Replicator Formalism

A general account of replication

Ph.D. thesis

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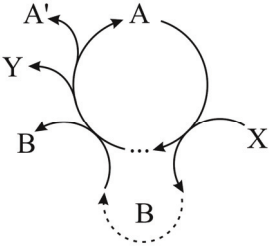

Everything we hear is an opinion, not a fact.
Everything we see is a perspective, not the truth.
Marcus Aurelius

Contents

Publications

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Abstract

Replicators are the most important objects of evolutionary biology. Their cumulative evolution lead to the emergence of complex, adaptive systems, like life. All major transitions of evolution are outcomes of the evolution of replicators. However, replication (and evolution) are universal concepts, independent of the level of biological organization, and even of biology.

A multitude of replicator candidates, and perhaps the same amount of definitions are available in the literature. Studies of (self-)replication in chemical, (proto-)biological, linguistic, cultural, neuronal, digital and kinetic systems have accumulated an impressive amount of theoretical and experimental knowledge in the last three decades.

To explore the consequences of the universality of replication and to cut through the bulk of misleading terms, I introduce the Replicator Formalism, a generalized theory of autocatalytic entities. To better understand models and be able to relate results of various fields dealing with replication, the formalism applies a pure, mostly field-independent language. It helps recognize key features of autocatalytic systems, like informational and material topology, and it both provides a classification of replication systems, and suggests evolutionary trajectories for certain transitions from lesser systems to evolved ones.

Several conclusions have been drawn using the formalism as conceptual and as modelling tool. These are: (1) replicator equivalency is relative, to be defined from a particular point of view; (2) the inheritance of information does not necessarily follow the inheritance of matter in replication; (3) phenotypic replication is direct replication lacking a distinct interactor; (4) there is a continuum between direct and Weismannian replication, Lamarckian being in-between them; (5) this continuum can be traversed by evolution: an evolutionary scenario for the emergence of division of labour is suggested, and tested in a stochastic model; (6) information can be stably maintained in Lamarckian systems, (7) informational replicators can coexist in a vehicle even if there is only stoichiometric coupling, but no phenotypic selection.

The Replicator Formalism gives a powerful theoretical and modelling framework to bridge various models and results of different fields.

1. Introduction

1.1. Preamble

Evolution via natural selection is based on the successive, erroneous replication of informational molecules. A population of replicators is a distinguished set of (biologically) interesting entities capable of multiplication, and in some cases, evolution as well. The definition of the replicator, however, could not grow up to this importance. Ever since the introduction of the term 'replicator' and emphasis made by Richard Dawkins (1976), it spurred a great amount of discussion in various scientific domains from biology through chemistry to linguistics, culture, computer sciences, especially artificial intelligence and artificial life. A multitude of definitions exist accordingly, each being usually specific to its field, cf. Muller 1966, Dawkins 1976 and 1982b, Hull 1980 and 1988b, Dawkins Maynard Smith 1986, Szathmáry & Maynard Smith 1993, Maynard Smith & Szathmáry 1995, Szathmáry 1995 and 2000, Sterelny et al. 1996, Aunger 2000 and 2002, Griesemer 2000b, Sperber 2000, Godfrey-Smith 2000, Nánay 2002, Hodgson & Knudsen 2008, and many more, see Appendix. Clearly, the replicator concept is common enough to infiltrate into many fields of science, though it remains a question how different examples of various fields can be related and compared.

Replicators are the single most important entities in evolutionary biology. Informational replicators are responsible for complex adaptive systems, which renders their role paramount in biology and related fields. Such highly successful adaptive systems include living organisms, the immune system, and perhaps cognitive capacities and language as well. The vague idea of memetics stems from the universal Darwinian concept (multiplication, variability, heredity) being extended to another complex adaptive system: culture (Dawkins 1976, Ball 1984, Szathmáry 1999, Sperber 2000, Aunger 2000). Replicators were also postulated to work in the brain by Calvin (1996), and Aunger (2002), and most recently the Neuronal Replicator Hypothesis assumes the existence of explicit neuronal replicators in the brain as spike patterns and/or topographic or topologic connections in the neuronal medium (Fernando et al. 2008, Fernando & Szathmáry 2009 and 2010, Fernando et al. 2010). These existing or putative replicators, theoretically, all share identical or similar dynamics as they all are manifestations of the basic Darwinian principle, but sometimes are disguised so heavily, that the relation is not apparent.

There are two main reasons for devising the replicator formalism. Firstly, current definitions and classifications cannot discriminate effectively between gene-like entities (being sufficiently abstract) and real organisms, or gene-like entities and simple autocatalytic cycle intermediates (e.g. glycolaldehyde in the formose reaction described by Butlerow (1861). There is obviously difference between these entities concerning their copying dynamics and exhibited similarity between parent and offspring. Secondly, some current definitions have not been formulated to include memes (e.g. Hull 1980 and 1988b), or other putative replicators of culture, but only genes. Memes (the gene-analogue cultural replicators introduced by Dawkins (1976, also in Dawkins 1982b), as we refer to them, are cultural traits, that are replicated by copying/imitation (e.g. words, concepts, songs, etc., see Plotkin 1994, Blackmore 1999, Kronfeldner 2007).

1.2. History of replicators

Replicators are everywhere. The most prominent example is clearly the gene, which was used by Dawkins to emphasize the gene's eye view approach to (evolutionary) biology. According to this, the answer to *cui bono*? (who benefits?), concerning an observable feature of living organisms, is always a mindless replicator in the background. This is in agreement with Theodosius Dobzhansky's famous statement (Dobzhansky 1973):

> "Nothing in biology makes sense except in the light of evolution."

Dawkins' seminal work and the debate it initiated proved that the replicator concept is elegant and parsimonious to be an effective theory of evolutionary biology. The replicator made its stand. Since then (and retroactively) many multiplying entities were termed replicators.

Consequently, it became evident that the mechanistic concept of replication (i.e. to explain the multiplication of entities) and the well-known chemical phenomenon of autocatalysis (the apparent self-catalyzation of certain chemicals) are related, and with it, the domain of replicators began to expand. For a review, see Zachar et al. (2010).

The recognition that replication is a universal phenomenon easy to reproduce in chemical systems, and the evolving methods to deal with combinatorial chemical systems lead to the impetus of a new field: systems chemistry. Artificial replicators are designed and synthetized since 1986 in the labs of Günter von Kiedrowski (von Kiedrowski 1986, Bag & von Kiedrowski 1996, von Kiedrowski 1999) and Julius Rebek (Tjivikua et al. 1990, Nowick et al. 1991, Rebek 1994, Conn & Rebek 1994). The ever-increasing literature of artificial chemical replicators include mostly peptides and nucleic acids (being polymers) and other small organic compounds

(Zielinski & Orgel 1987, Maddox 1991, Orgel 1992, Robertson et al. 2000, Paul & Joyce 2004). For a recent review of the field of combinatorial chemistry, see Peyralans & Otto (2009).

There are many inorganic chemical examples as well, though they are not listed here for sake of simplicity. I only mention the Belousov-Zhabotinsky reaction, which is perhaps the best known inorganic autocatalytic system. It is a family of oscillating chemical reactions with beautiful oscillatory visual patterns, being important as 1) it has very similar dynamics to that of the Lotka-Volterra model, and 2) it underlines the concept that simple chemical mechanisms are responsible for complex higher level structures. For more inorganic chemical examples, see Kumar & Nath (1997).

There is a wide range of abstract replicators and theoretical applications of the replicator concept. Certain chemical reaction-models were designed based on real-word oscillating reactions, like the Brusselator of Glansdorff & Prigogine (1971), the FKN mechanism (reduction of the complex chemical mechanism of the Belousov-Zhabotinsky reaction by Field et al. 1972), and the Oregonator by Field & Noyes (1974). One particularly important and complex chemical model is the chemoton, designed by Tibor Gánti to account for the minimal model of a cell (Gánti 1971, 2003). It consists of three autocatalytic subsystems (metabolism, template and boundary), and effectively models the growth and splitting dynamics of a protocell. It was studied in detail and is an extremely important model of theoretical biology, being relevant both to the origin of life, to cell-replication and to the organization and regulation of autocatalytic cycles. It was Gánti, who stated it the most clearly that not just whole autocatalytic cycles (like the chemoton itself) but their intermediates double as well with every turn of the cycle (Gánti 1971, Szathmáry 1995). This renders simple autocatalytic cycle intermediates as replicators as well (Maynard Smith & Szathmáry 1995, Gánti 2003). In addition, the chemoton suggests the possible existence of infrabiological systems missing one of the chemoton's three subsystem (cf. Szostak et al. 2001, Szathmáry 2005). These "impaired" systems still count as replicators and are important models of the cell-origin. Other hypothetic replicator systems were put forward by others to solve the origin of life: Eigen proposed the hypercycle (Eigen 1971, Eigen & Schuster 1977, Eigen & Schuster 1978) and reflexively autocatalytic protein sets (Eigen 1971), also by Dyson (1985), Kauffman (1986, 1993), and Ruiz-Mirazo et al. (2008). Szathmáry proposed the stochastic corrector model (Szathmáry & Demeter 1987, Zintzaras et al. 2002), which is a two level replicator: templates replicate inside compartments, and successful compartments replicate at a higher level. A different approach prefers replicating lipid microspheres (with limited heritable information, e.g. Segré et al. (2000).

The dynamics of oscillating systems (a possible phenomenological feature of coexisting replicators) was modeled as early as 1925 by Alfred J. Lotka and later by Vito Volterra in 1926. The Lotka-Volterra equations (now standard textbook elements) are important, as they were among the first to describe replicator dynamics phenomenologically. Schuster & Sigmund (1983) demonstrated how these equations translate to the replicator dynamics of Eigen and to Fisher's selection equation, establishing an explicit link between different replicator equations of evolutionary biology, which was later extended by Page & Nowak (2002). Approaches that are even more abstract were presented by Rosen as M-R systems (Rosen 1973, Ruiz-Mirazo et al. 2008). Maturana and Varela discussed autopoietic systems, dealing with the most general description of self-production, of which self-replication is an extremum (Varela et al. 1974, Ruiz-Mirazo et al. 2008). George Kampis designed component-production-systems along similar lines (Csányi & Kampis 1985, Kampis 1991).

Replicators quickly made their way to computers. Computer programs or viruses can be very successful *in silico* replicators (Spafford 1997, Bedau et al. 2000, Hodgson & Knudsen 2008). The vast field of Artificial Life is about recreating life via self-assembling and self-replicating components purely *in silico*. For example, short programs in the TIERRA software were designed to be able to evolve (Ray 1992). Examples that are more pragmatic are genetic algorithms, which are population-based optimization algorithms. They utilize Darwinian dynamics to evolve solutions via replication and selection of function parameters (genetic algorithms) or program representations (genetic programming) to solve/optimize a given problem (Koza 1992). A population of such code strings in a genetic algorithm setup contains explicit replicators with all genotype, phenotype and fitness defined artificially. A population of replicators undergoing selection and evolution provides a distributed and thus more effective search algorithm over a vast search space with multiple local optima compared to a single search-entity, e.g. a stochastic hill-climber.

The number of chemical (bio-, and physico-chemical) examples for autocatalytic reactions is enormous, only a few is listed here. Perhaps the most important autocatalytic cycles are those biochemical reactions, which are closely linked with the origin of life. The formose cycle proved that autocatalysis could lead to the replication of organic molecules (sugars) without enzymatic aid (Breslow 1959, Butlerow 1861, Szathmáry 1999). Regulated autocatalytic cycles in cells are e.g. the malate cycle and the Calvin cycle (Gánti 1987), the reductive carboxylic acid cycle (almost identical to an inversely operating citrate cycle, cf. Gánti 2003 p. 54., Kun et al. 2008).

There is a wide range of supramolecular systems, which exhibit replication-like behaviour: perhaps the best studied is the genetic material: DNA, genes or cistrons (Dawkins 1976, 1982b,

Hull 1980, 1988b). According to Dawkins, chromosomes and genomes can be replicators for some extent, especially if the organism reproduces asexually (Dawkins 1976, 1978, Hull 1981). In prebiotics, ribozymes are thought to have been the primordial replicators, preceding gene-protein systems (Crick 1968, Orgel 1968, Woese 1967). In cells, many biosynthetic molecule follows a hidden autocatalytic pathway, that manifests only in the long run: no single autocatalytic cycle for ATP, ADP, NAD+, THF, sugars, CoA, etc. can be isolated, but they do reproduce autocatalytically overall with the cell metabolism according to Kun et al. (2008). A particularly interesting field is the replication of prions (Prusiner 1982 and 1998, Pagel & Krakauer 1996, Shorter & Lindquist 2005). They can also be inherited epigenetically (Jablonka et al. 1998, Szathmáry 1999). Membrane inheritance can even be informational, if the composition of the membrane can be stably transmitted to successive generations (Cavalier-Smith 1995, 2004, Maynard Smith & Szathmáry 1999, Segré et al. 1998 and 2000, Segré, Ben-Eli, Deamer & Lancet 2001, Segré, Shenhav, Kafri & Lancet 2001). The self-replication of amphiphilic monolayers (Maoz et al. 1996), micelles and vesicles opened up the gate for the alternative of the metabolism-first scenario of the origin of life: proponents of the boundary-first approach study the replication and self-assembly of micelles and vesicles (Bachmann et al. 1992).

Various epigenetic inheritance systems are known as well which might pass on information with reproduction of the host cell, and evolve parallel to the genetic material present in the genome. Some cell organelles are able to replicate independently of the host cell replication, like mitochondria and plastids (Maynard Smith & Szathmáry 1995). Others replicate with the cell, like centrosomes (in animals, cf. Salisbury 2001) and spindle pole bodies (centrosome-equivalent in yeast), though they could only be non-informational replicators and usually they cannot form *de novo*. The chromatin marking system (Jablonka & Lamb 1995, Jablonka et al. 1998), structural inheritance systems like the cortical inheritance in ciliates (Sonneborn 1964), steady-state regulatory systems of the cytoplasm (Jablonka & Szathmáry 1995), like the inheritance of metabolic configurations (Gánti 2003, Kun et al. 2008), inheritance of determined and differentiated states of multicellular cell lineages (Jablonka 1994, Jablonka & Szathmáry 1995, Maynard Smith & Szathmáry 1995) are all epigenetic informational inheritance systems. There are further examples, like RNA mediated inheritance (paramutation) (e.g. Stam & Scheid 2005, also discussed at Koonin & Wolf (2009a). Several maternal effects (external to the genome) can be propagated to the offspring, for example antibodies of the immune system (Lemke et al. 2004), which renders such epigenetic inheritance systems Lamarckian (from the viewpoint of the

organism), as they inherit *acquired somatic changes* parallel to the genome of the organism. It must be noted however, that these changes are not written back to the genome directly.

According to Zachar & Szathmáry (2010), cellular or supracellular biological organisms can be replicators as well (see section 1.5). Similarly, the growth of individual living beings can be formulated as an autocatalytic cycle, just as the conventional eukaryotic cell cycle does. Developmental systems (e.g. Sterelny et al. 1996, p. 382) and organs, birds' nests, burrows, etc. can be thought of as replicators as well, though it must be noted here (to avoid Bateson's argument: "a bird is but a nest's way of making another nest"[1]) that they are non-informational, dependent replicators, depending on real informational, evolutionary replicators (as the nest depends on the bird or its genes). A detailed argument on the matter was presented in Zachar & Szathmáry (2010).

Higher-level units of selection can act as replicators as well, like the kin. Dawkins describes the individual (obviously the genome) as a genetic octopus extending to relatives (Dawkins 1978 p. 67.). Some consider even colonies, societies, populations, groups, or species (advocates of group selection) and ecosystems (the hypercycle of Eigen is basically a balanced ecosystem) as replicating entities. At lower levels of complexity, one should include viruses (Szathmáry 2006), viroids (Tsagris et al. 2008) and plasmids, noting that they are only operational if the appropriate working environment (the host cell) is provided. However, this is a general requirement for every replicator.

Culture is also hypothesized to be shaped by and to host replicators. Unquestionable the most (in)famous examples are memes (Dawkins 1976, 1982b, Ball 1984). Memetics, as an independent field, could not make its stand. Despite the initial uprising of memetic literature since the eighties, it still could not provide testable hypotheses, and lacks further progression (cf. Edmonds 2002, 2005), mostly because it lacks testable predictions stemming from non-existent population memetics. Nevertheless, there are candidates for cultural replicators. Words are excellent examples, as they are replicated from time to time and they seem to evolve with language. They are part of our epigenetic adaptive suite passed on with the replication of our

[1] See at Bateson (1978, p. 317.), also at Bateson (2006) and at Sterelny et al. (1996). Interestingly, Bateson did not make this claim to criticize Dawkins, but to point out that the passive side product (the nest) of an autocatalytic cycle (the bird) can as well feed back positively to the cycle. This does not mean that the nest transmits information back to the bird of course (Bateson stated this clearly, and Dawkins 2004 even more clear), but nevertheless renders the nest as a heterocatalytic aid, which ultimately loops back and aids its own production.

body, cf. Jablonka & Lamb (1995), and Maynard Smith & Szathmáry (1995). Accordingly, language, grammar, linguistic rules and constructions are more and more frequently seen as units of selection and evolution, cf. evolutionary and Darwinian linguistics (Croft 2002). More directly, there are ongoing projects trying to model linguistic and cognitive processes based on implicit replication of linguistic replicators between brains and inside brains (cf. Steels & Szathmáry 2008). Selection dynamics in the brain are already in science since Dawkins (1971): Changeux (1985) and Edelman (1987) have formulated hypotheses lacking replication. Real replication was then introduced by Calvin (1996) for structural units and by Aunger (2002) for connectivity patterns, to account for memetics as well. A true replication-selectional theory was put forward recently: the exceptionally bold but well-supported idea of the Neuronal Replication Hypothesis is on its way to become a valid theory of mind and cognitive functions (Fernando et al. 2008 and 2010, Fernando & Szathmáry 2009 and 2010). More simple examples can also be found, like contagious laughter (Sperber 2000), or examples from the financial domain, like fund (Mérő 2004). Debatable whether it is part of culture or not, but the classic non-genetic examples for cultural replication are Xerox copies (Dawkins 1976, 1982b, Godfrey-Smith 2000). In addition, if words, sentences, theories, and other items are replicators of culture, then it is equally valid to account books and artifacts as well, being vehicles for such cultural replicators (see upcoming paper on the classification of cultural inheritance by Számadó & Zachar (2011b).

Actual physically manifested macroscopic artificial replicators (called *clanking replicators*) are promising technological entities in the field of engineering, robotics and astromechanics (cf. Freitas et al. 1981), also for an extensive review of the field of kinematic self replicators from an engineer's point of view, see the excellent book by Freitas & Merkle (2004). Perhaps the most beautiful, elegant and simple representation of replication in macroscale was done by Lionel and Roger Penrose with the so-called Penrose block models (Penrose & Penrose 1957, Penrose 1958 and 1959). These are simple plywood blocks with handles allowing for some specific interactions between blocks. Astonishingly, many aspects of chemical (polymer-)replication could be reproduced with the blocks, like the semiconservative inheritance of DNA strands.

As is obvious, replicators are all over the place. Now the problem with this is that there is no clear definition that could sort out those examples that really shouldn't belong to the group, like the Queen's head printed on British postal stamps (Aunger 2002 p. 75), fire (discussed by Maynard Smith 1986), accumulating breadcrumbs (Griesemer 2000a), identical atoms of gold (Hull 1981), and other extreme cases.

1.3. Toward a better formalism

There are obvious differences among certain replicative systems (like genetic and cultural) that cause changes in the dynamics of information replication. It follows, that a universal formalism should focus on such general aspects that efficiently grasp the essence of replication, and do not change our basic concept of it too much for the new approach to be useless or repulsive. One can formulate an operative definition concerning only nucleotide replication, but it would not be general. To quote Orgel: "few of the features of RNA replication are essential for a general replication model" (Orgel 1992, p. 204.). Therefore, it is important to formulate the new definition the most generally, to account for the widest coverage. The formalism should define common and distinguishing aspects of presupposed replicators and should include or exclude candidates accordingly.

One particular problem of earlier approaches is that definitions are either too narrow (e.g. Hull 1980, 1988b) or too broad (e.g. definitions based on Muller's 1966 multiplication-heredity-variability criteria, which were later applied to the *units of evolution* instead of replicators by Maynard Smith 1986 and 1987). The former, by sticking to structure, do not allow the inclusion of memes, prions, and other replicators that transmit information in non-material ways. Too broad definitions allow the inclusion of for example organisms, or even supraindividual entities, but do not draw a clear line between sub-, and supracellular replicators. Accordingly, there are five general, intuitive requirements that were suggested by Zachar & Szathmáry (2010) that must be met by the replicator concept:

1. **Autocatalysis**: potentially autocatalytic mode of generation.
2. **Similarity**: potentially above-chance similarity between parent and offspring.
3. **Informational**: ability to pass on information to offspring. This is a requirement for informational replicators.
4. **Inclusivity**: The widest definition has to include genes, memes, and possibly other entities as well.[2]
5. **Specificity**: The definition must be able to distinguish between various multiplying entities: genes, memes, simple chemical cycle intermediates, lipid vesicles, kinetic multipliers, organisms, and higher-level entities in a clear and exact way.

[2] As it was Dawkins (1976) who has introduced the term replicator, it seems reasonable to focus on these two entities he has suggested.

These requirements are backed up by almost all definitions, and are supported by existing knowledge on inheritance systems. Accordingly, four questions are raised (after Zachar & Szathmáry 2010):

1. What is the qualitative and quantitative difference between genes, organisms, general autocatalytic intermediates and other multiplying entities?
2. What are the basic concepts behind the Mullerian criteria multiplication, heredity, and variability, and what part do they play in replication?
3. What is replicator identity and similarity? When do we say that two replicators are identical?
4. What is common and distinctive of genes and memes? What is the definition that puts memes and genes into the same box but not organisms?

Certain other questions infect our present concept of replication, and stem from the indefiniteness of earlier definitions. Is material input required for replication? Is material transmission required? What exactly do phenotypic replicators pass on to offspring (Szathmáry 1999)? The phenotype? Are prions real replicators? Are they phenotypic or genotypic? What kind of heredity they have? How do memes replicate? What is the exact nature of Lamarckian inheritance? How does it relate to Weismannian inheritance? These questions all boil down to the establishment (or lack of) basic principles. This thesis is an undertaking to define these fundamental principles to clear up the issues listed.

1.4. The necessity of autocatalysis

Replication is an autocatalytic process, and as such, it belongs primarily to the domain of formal chemistry. Orgel very clearly saw this when he stated (Orgel 1992, p. 203.):

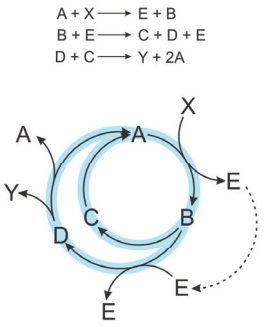
> "All replicating systems are, by definition, autocatalytic and all autocatalytic systems result, in some sense, in replication."

He also realized, the most important feature of a replicator is its potential to undergo evolution. Hence, he distinguished between *informational* and *non-informational* replicators which can and cannot be subject to evolution, respectively (*ibid.*).

Autocatalysis is discussed in depth in Zachar & Szathmáry (2010), here only the major points are recapitulated. The difference between dividing a glass of water and a true autocatalytic cycle lies in the stoichiometry. Without input, a litre of water divided would not give two litres. The 'reaction' cannot be rendered to be cyclic, not to mention autocatalytic. What is characteristic of

an autocatalytic entity is that it "can arise only if there is a pre-existing structure of the same kind in the vicinity" (Maynard Smith & Szathmáry 1995, p. 41.). However, parent and offspring can be totally different in e.g. structure, as long as they are functioning sufficiently similar to allow the cycle to close. Indeed, a new cell is not exactly the same as the old cell, but both have the potential to produce more cells. It is tempting to say here, that the parent and offspring must be similar in some "relevant aspects" (Aunger 2002, Godfrey-Smith 2000), but such indefiniteness does not help at all. The formalism presented here states that the old and new replicators must be *equivalent* from the viewpoint of selection (see 2.3.2 Selection), and not identical. Defining identity is problematic due to the arbitrariness of the level where two entities must be the same: it could be the level of cells, molecules, atoms, or even lower. Equivalency on the other hand is relative, depending on the selective environment defined for replicators.

An important consequence of autocatalytic closure is that not just intermediates of the cycle are replicators. Since products that provide positive effects to the growth of the cycle are ultimately catalyzing their own creation, they are considered replicators as well. For example nucleic acids and proteins *together* self-replicate (each is catalytically linked to the other). This also means that some replicators are *autonomous* (or *obligate autocatalyst*) like prions, putative ribozymes and organisms (birds for example), while some are *dependent* (or *facultative autocatalysts*) like DNA, proteins and nests. Thus there is a major difference between phenomenologically (kinetically) similarly behaving entities, as Blackmond (2009) captured it. For details, see Figure 1.



A, B, C, D: autocatalytic **intermediates**
A, B, C + D: autocatalytic seeds
A, B: obligate autocatalysts
C, D: facultative autocatalysts
E: indirect autocatalyst (autoinduction *sensu* Blackmond); also a heterocatalytic **product**
X: **input** material ("*food*")
Y: waste **product**
{A, B, C + D}: autocatalytic cycle

Figure 1. Terminology of autocatalytic cycles. Components can be input material, side products (e.g. waste), or intermediates, which drive the cycle. Cycle alternatives are also possible, if certain intermediates participate in OR-type branching (not depicted) instead of AND (like B → C + D). Facultative autocatalysts can only kick-start the cycle if their appropriate partner is present as well.

1.5. What is known about replicators

The replicator concept is infected with indefinite terms and definitions. It is clear however, and is generally accepted, that complex adaptive systems are products of inheritance systems, while inheritance systems are based on replicators. Aside the well-known genetic system, there are several epigenetic and even behavioral and linguistic inheritance systems as well, see Jablonka et al. (1998).

Perhaps the (biologically) most important attribute of replicators is their evolutionary potential. As Szathmáry & Maynard Smith (1993) have defined, limited hereditary replicators only have a few stable states as they are unable to pass on most of the variability in their structure. Unlimited hereditary replicators have a larger range of variation, with possibly more stable states than the population size. This allows members of the latter group to explore a vast search space, and renders them subjects to open ended evolution. In contrast, the evolution of limited hereditary replicators is highly restricted, as the search space is small.

The previous work on the replicator by Zachar & Szathmáry (2010) laid out the foundations of the formalism presented here. Major points are briefly recapitulated. Firstly, material overlap is not a necessity for replication. Actually, any necessity of material overlap would exile memes, prions, computer viruses, and other candidates as well from the land of replicators. Nevertheless, input is required for any autocatalytic entity, but it can be informational instead of material.

Secondly, the difference between autocatalytic intermediates and organisms is in the amount of heritable information. DNA can inherit many of the changes applied to its structure, while a cell can inherit a very small amount. However, this difference is clearly quantitative at the first place, as even polynucleotides cannot pass on all their structural changes (e.g. isotope substitutions), and there exist epigenetic methods for a cell to pass on more information than its nuclear DNA. As a conclusion, organisms are considered replicators, with a very large and variable part, and a very small heritable part (the genome).

Thirdly, any multiplying entity, which fits the multiplication criterion but lacks evolvability is still a replicator. Thus, exact (non-evolutionary) autocatalytic cycle intermediates with no heritable part are replicators. It follows from the fact, that exact replicators are natural extrema of hereditary replicators. For example, a gene is an exact replicator if proofreading is faultless, prohibiting short-term microevolution. Therefore, the *replicator* is not the same as *unit of evolution* (*sensu* Maynard Smith 1986), since exact replicators are not subjects to evolution, only selection. As a conclusion, even glycolaldehyde in the formose reaction is a replicator. Furthermore, even heterocatalytic products of autocatalytic cycles are claimed to be replicators,

though not necessarily autonomous and usually non-informational (but can be, see section 3.2 Evolution of division of labor). Such heterocatalytic side products are, for example, the expressed proteins of genes and nests of birds (cf. Figure 1 and Figure 7).

Concerning informational replicators, it was recognized that the (ideal) *genotype* and *phenotype* (in the narrow sense), and *development* and *templating* are abstractions, that can be represented as functions applied to the replicator. The phenotype is the function that partitions replicator space to equivalence classes according to actual selective forces. The genotype function specifies parts of the replicator that inherits **all** acquired changes. Accordingly, the genotype of a gene is encoded in the base order and the genotype of an organism is encoded in its genome plus all epigenetically heritable information. The **genes are the true replicators**, **as they approximate the ideal genotype the best** (in agreement with the *gene's eye view* of Dawkins (1976).

A simple model was presented to distinguish between multiplying entities, based on three parts of a replicator: the *heritable*, *variable* and the *non-variable* parts. These parts implicitly define those features that can 1) vary with the lifetime of the replicator and variations can be inherited; 2) can vary but no variation can be inherited; 3) cannot vary at all without rendering the replicator useless. This tripartite representation of the replicator is pictured in Figure 2.

A formula was presented to quantify the phenomenological similarity, S, of parent and offspring entities based on this model:

$$S = I\,(1 - V) + I\,V\,(1 - H)\,(1 - \upsilon) + I\,V\,H\,(1 - \upsilon)\,(1 - \mu) + I\,V\,H\,\upsilon\,\mu\,\varepsilon, \qquad (1)$$

where I stands for the total information content of the replicator (taken to be unity), V and H for the sizes of the variable and the heritable parts, V being a fraction of I and H being a fraction of V. Parameter υ is the probability that a feature of the variable part changes during a unit of time, while μ is the mutation rate suffered during the replicative process (the probability that a heritable feature is miscopied); ε gives the probability of the backmutation per module per replication. For large inventory sizes, the chance of backmutation is negligible. The overall similarity for various replicators predicted by the model is plotted in Figure 3.

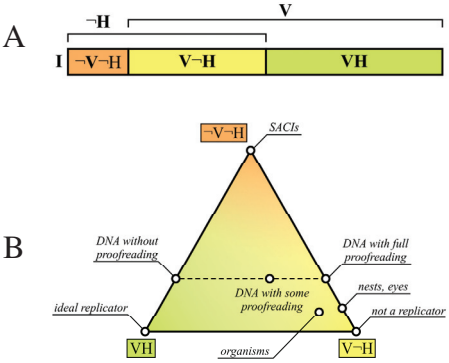


Figure 2. Tripartite representation of the general replicator. A) Subsets of the features of a replicator. V denotes parts of the replicator that can vary, H denotes parts that can vary and inherit changes, ¬ is the negation operator. VH is the subset of the features that can inherit changes, V¬H is the subset that cannot inherit changes, and ¬V¬H is the subset that cannot even vary. B) Shares of the three subsets in the whole of the replicator can be represented on a simplex. SACI = simple autocatalytic cycle intermediate (like glycolaldehyde in the formose reaction).

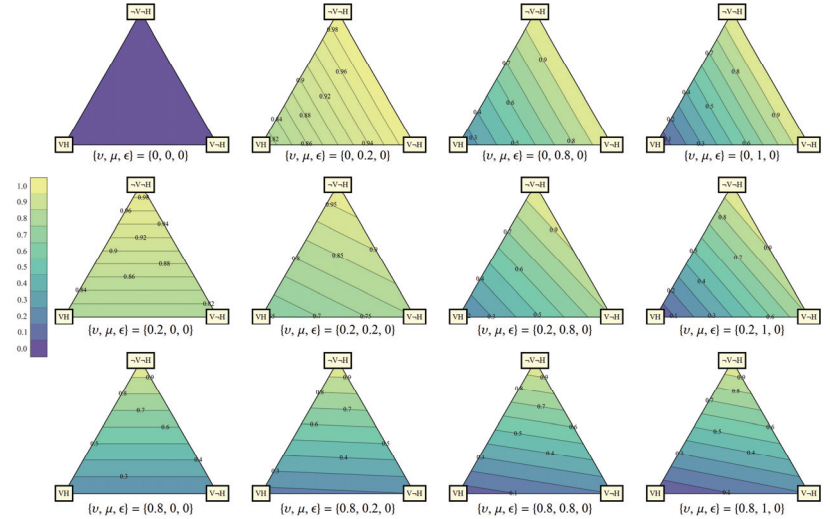


Figure 3. Similarity. Estimated between parent and offspring (both being modular) as a function of *V* and *H*. The chance of backmutation is taken to be negligible ($\varepsilon = 0$).

1.6. Problems of the replicator concept

1.6.1. PHENOTYPIC REPLICATION

One particularly persistent problem of the replicator concept is its lack of pinpointing **what** exactly is replicating. Is it matter, properties, information, or some kind of mixture of all? Most definitions are phenomenological (focusing on multiplication only) or indefinite in terms, see for example the definitions of Dawkins (1982b), Hull (1988b), Maynard Smith & Szathmáry (1995), Sperber (2000), and Aunger (2002) in the Appendix. Whichever is the case, it is true that the dynamics of a replicator primarily depends on what is expected of it to be replicated: DNA is expected to replicate base order, but not for example isotope substitutions in the sugar-phosphate chain. Concerning the inheritance of the latter DNA obviously fails. The distinction between Weismannian and Lamarckian replication also originates from this issue, as it is a distinction based on structural and informational division of labor. This will be discussed in turn.

Phenotypic replication is a term introduced by Szathmáry (1999) to denote those replicators that seemingly can inherit phenotypic properties directly, like prions, genetic membranes, and memes. It is indeed true, that these replicators exhibit different inheritance methods: they do have an underlying, digital structure, though it is not this pattern that is inherited, but rather its phenotypic representation. For example, the 3D conformation of prions, instead of their amino acid sequences (Figure 4). This justifies their emendation as a new subgroup in the set of replicators. However, the name ‘phenotypic’ is a bit confusing. The genotype by definition (Zachar & Szathmáry 2010) incorporates all those features that are inherited by the offspring, therefore any information that is inherited is part of the genotype. If there is any other phenotypic feature outside the genotype that is inherited, a paradox emerges: since the feature is inherited, it must be part of the genotype, thus cannot be outside of the genotype. Of course, prions (and also immune system components, viruses, memes, and even father’s watch) are inherited epigenetically compared to genes (Jablonka et al. 1992, Jablonka & Lamb 1989), though epigenetic means simply that 'not part of the genome'. Prion proteins are indeed epigenomic when inherited from body to body, but this just means that the actual genotype of an organism is the joint set of the genome and the traits inherited epigenetically – prions may very well rely on Weismannian dynamics when they propagate their conformation inside a cell.

At the level of prions, it is the protein conformation that is replicated from time to time (Prusiner 1998, Pagel & Krakauer 1996, Edmunds & Yool 1997). What makes it seemingly different compared to DNA replication is that it requires no material input. Given a set of wild

type proteins, a single infectious one can convert the whole population without any further material input. Of course, if there is no supply of native prion proteins via gene expression, no invasive conformation can propagate (although early theories hypothesized a template-based synthesis of new proteins on existing proteins, cf. Root-Bernstein (1983). Thus, input is still required for multiplication, be it material or informational. Furthermore, changing conformation of existing proteins does not differ much from the fact that a DNA polymerase is effectively changing the conformation of free monomers in the nucleus according to the template it reads.

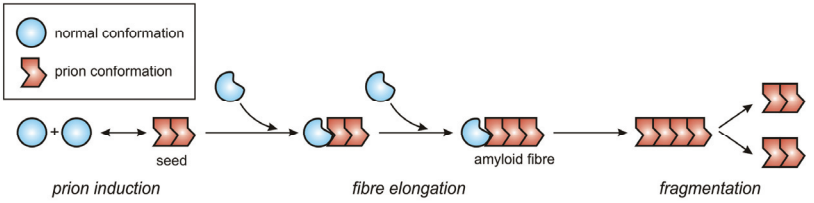


Figure 4. Replication of prion proteins. The prion conformation appears after a spontaneous conversion of native proteins. The prion seed converts further proteins by joining them to its two ends, thus the amyloid fiber starts to grow. As fibres fragment, new seeds are introduced, which further increase the speed of conversion (based on Shorter & Lindquist 2005).

Random shuffling of the prion domain (the part of the sequence of the protein where point mutations prevent the prion to propagate) indicates the infective phenotype (conformation) is quite robust against changes in its 'genotype', the amino-acid sequence, reported by Ross et al. (2004). This means that it is only the infective conformation that is transmitted, and not the altered amino-acid sequence: information is therefore coded in the conformation, rather than in the sequence (contrary to the case of nucleic acids). Thus, no change in the sequence can be inherited - just as anyone would have expected it according to the central dogma. It can be therefore argued, that there is no real information inherited, because the protein is either in its native or infectious conformation, but there are really no more alternatives. As it has turned out, this is not exactly true.

It was discovered that there can be multiple stable prion conformations for a given amino acid sequence (and not just wild type and infectious one), called strains (Safar et al. 1998, Prusiner 2004). These strains are known to have different phenotypes, i.e. possess differences on incubation time, caused symptoms, etc., see Bruce et al. (1991). If prions have various phenotypes, and these phenotypes cause differential survival, then prions are units of selection. Li et al. (2009) have demonstrated in a series of experiments that different selective regimes (e.g.

presence or absence of a prion inhibitor) cause the propagation of different prion strains, effectively demonstrating that prions are units of selection.

The next step is to ascertain that at least some mutations can be inherited selectively and stably during replication, i.e. during successive transfers of the conformation. The specifically arranged β-sheets inside the amyloid structure exposes the main polypeptide chain which may very well act as a template being modular, inheriting any change in the template. This template is assumed to be responsible for the transmission of conformation, i.e. the specific structure of the amyloid (Wickner et al. 2007). Li has also found that new variants appeared *de novo* during replication in the prion population (instead of being there in an initially heterogeneous population), indicating that mutations do affect prions (Li et al. 2009). Even more stunning is that they found different phenotypic properties and therefore different conformations to be heritable. Thus, we are dealing with at least limited heredity of prion proteins. According to Li, it seems that different strains can stably inherit phenotypic differences, which means that the conformation is inherited stably. Prions are therefore existing supramolecular hereditary replicators. The *a priori* difference compared to genetic replicators is debunked. The only real difference is in the medium and evolutionary potential: while genes are encoded in nucleic acid, with an enormous combinatorial search space, prions are encoded in 3D protein conformation with a presumable much smaller search space (due to the fact that only a small part of the vast conformational space is infectious), hence limited hereditary potential.

Therefore, I argue, that there is no such thing as a phenotypic replicator. If information is transmitted during replication, it is always part of the genotype. This may seem to be a simple change in terms from phenotypic to genotypic, but actually is an indication of the fact, that the same Darwinian dynamics apply to prions and genes. Prion replication is merely the replication of a pattern of information (Pagel & Krakauer 1997), namely the specific conformation of the protein, therefore the genotype of the prion is nothing more than bits of information representing the conformation (or a single bit if only native and infectious conformations are allowed). The fact that this information is coded in the 3D structure of the protein rather than in some digital code should not make replication different.

1.6.2. LAMARCKIAN INHERITANCE

The other interesting aspect of the same example, prion replication, is the obvious Lamarckian tone if their inheritance is considered at the cell-level. If the cell is viewed as a replicator, it is apparent that the genetic material and possible prion conformers follow different inheritance

routes when the cell, as a whole, is replicated. The genetic material is inherited the Weismannian way, as lifetime changes to the soma are not written to the germline. Contrarily, changes to the protein population of a cell via prions do get replicated when the cell replicates, hence the epigenetic and Lamarckian terms. A detailed investigation of Lamarckian inheritance is in preparation by Számadó & Zachar (2011a), here the issue is only briefly discussed.

According to Jean Baptiste Lamarck (1809) evolution happens due to the change of the environment forcing the living organisms to adapt to these changes. The mechanism of adaptation is the incorporation of changes resulting from use and disuse by means of inheritance of acquired characters, provided that these changes can be found in both parents. Note that this does not necessarily cover all external effects, like artificially cutting the tail of mice, as Weismann (1892) has proved it: taillessness is not an outcome of individual adaptation (*use and disuse*). Thus, interpreting Lamarck, adaptation happens on the level of organisms and not on the level of population, or on the level of genes. In summary, Lamarck outlined a theory in which organism-level (directed) variation caused by environmental adaptation, acquired in the lifetime of an organism, is transmitted to further generations. Worded by Koonin and Wolf: „[Lamarckian inheritance] is based on variation directly caused by an environmental cue and resulting in a specific response to that cue" (Koonin & Wolf 2009a, p. 8.).

The term 'Lamarckian' is used in many situations (see Pagel & Krakauer 1997, Jablonka et al. 1998, Lemke et al. 2004, Hodgson & Knudsen 2006b, Koonin & Wolf 2009a), and is used in connection with various concepts. Accordingly, it refers to different methods depending on context, see Kronfeldner (2005, 2007) (biological, cultural, socio-economics, etc.). There are three major concepts, which are more or less generally attributed to Lamarckian inheritance and which (each or together) render it to be the opposite of Weismannian inheritance in some sense (after Számadó & Zachar 2011a):

1. *Inheritance of acquired characters*: propagation of lifetime changes to the offspring (Jablonka & Lamb 1995, Blackmore 1999).
2. *Use and disuse*: the use of an organ induces the functional improvement of the organ (directed phenotypic changes).
3. *Parental filter*: any phenotypic change will only be inherited if both parents have it, according to Lamarck 1809 (biased inheritance).

These points immediately raise several problematic issues. First, where are acquired changes stored in the parent? In the genome? Or epigenetically? While for organisms the answer is clear (only epigenetic inheritance systems could inherit organism-level acquired changes), this might not be obvious for other replicators.

Secondly, what kind of acquired changes Lamarckian inheritance should pass on? Only directed or undirected changes as well? For the description of directed and undirected changes, see Kronfeldner (2007) and Paenke et al. (2007).

Thirdly, if "acquired" is used in a looser sense referring to all kind of changes, then for example DNA itself would be Lamarckian, as DNA inherits *all* changes it acquires – this is why it is termed a *hereditary* informational replicator. Clearly, this is not what Lamarck has in mind. Obviously, the distinction between Lamarckian and Weismannian inheritance is only valid at the organism-level. If there are no germ line and soma, there is no sense talking about inheritance of acquired changes. The thesis sets out to answer some of these questions as the formalism unveils.

1.7. Limited and unlimited heredity

A major question of inheritance systems is the origin of modular information. Modular information, however, is only useful, if it can be inherited, with changes. The crucial concept of hereditary replicators was introduced by Szathmáry & Maynard Smith (1993, p. 201.):

> "[...] we introduce the terms 'unlimited' and 'limited hereditary replicators'. [...] Limited hereditary replicators, owing to their structural peculiarities, can exist and be replicated in only a few stable states, whereas unlimited hereditary replicators can encode for a practically infinite set of varieties."

Modular information, encoded by unlimited hereditary replicators, offers a combinatorial search space to discover. If this search space is vast enough, open-ended evolution can drive the inheritance system (of unlimited hereditary replicators) toward novel adaptations. But how did a digital information storage system emerge from a non-digital, chemical reaction-network?

The emergence of unlimited hereditary replicators in case of the template-first scenario is somewhat ready-made. The presence of digital information storage is already granted in the RNA world, so it is not required to evolve some means to stably store and transmit information, to begin with. Of course, the problems of elongation (to increase combinatorial potential) and error threshold are still unresolved, but these are not discussed here for sake of simplicity.

On the other hand, if metabolism or boundary is granted first, but no template polymers, even modular information storage becomes a severe problem to deal with. The achievements of those advocating the metabolism-first scenario are briefly mentioned here, as the basic model of reflexively autocatalytic networks is one of great importance, and is used as an example throughout the thesis.

Composomes of the Graded Autocatalysis Replication Domain model (GARD, devised by Segré et al. 1998, Segré et al. 2000, Segré, Ben-Eli, Deamer & Lancet 2001, Segré, Shenhav, Kafri & Lancet 2001) are presumed molecular assemblies able to grow, split and inherit compositional information. Given a set of amphiphilic molecules, vesicle formation can be induced in fluid phase (Figure 5). If the component molecules are not identical, the vesicle has compositional information, hence the name *composome*. The further growth of the composome is driven by catalytic inclusion of available molecules of the environment. What is important is that this facilitating effect is provided by the already included molecules of the composome. Therefore one can assume, that the outcome of a seemingly stochastic growth process is somewhat determined by 1) the actual members of a composome; and 2) the possible list of catalytic effects between components. Reaching a certain size, the composome splits, producing two daughter vesicles, with components randomly distributed among them.

The growth and multiplication of the system effectively renders the GARD model reflexively autocatalytic on the level of vesicles: already present members of the composome catalyze the inclusion of new components, yielding two offspring vesicles ultimately. It is clear that there is inheritance, as offspring composition is correlated with parent composition, thus the system contains heritable information. However, the compositional information cannot be maintained reliably for a long time (as was proven by Vasas et al. 2010) due to the stochastic processes of growth and fission. According to this, composomes are only limited hereditary replicators, and even this limited amount of information cannot be maintained for a long time due to stochasticity. Nevertheless, the GARD model teaches us an insightful lesson about how limited heredity could have emerged from the replication of non-polymeric entities.

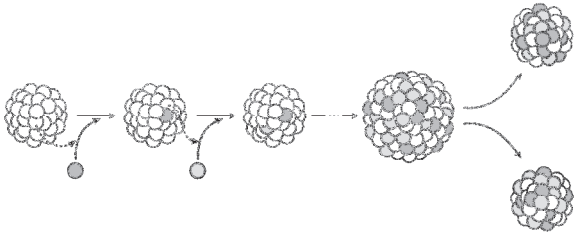


Figure 5. The hypothetic GARD model. Lipid molecules assemble to form a vesicle. The vesicle grows stochastically by incorporating new components. Inclusion is catalyzed by present members of the ensemble (dashed arrows). After reaching a critical size, physical forces cause the stochastic splitting of the vesicle, yielding two daughter vesicles compositionally related to the parent. Due to this limited inheritance of composition, such microspheres are called *composomes*.

1.8. Structure of the thesis

To deal with different informational topologies of inheritance systems, a bottom-up approach is applied in chapter 2 to build up a consistent formalism from smaller, well-defined concepts. By this way, the benefit is twofold: first, a classification of various replicational systems emerge; and second, a possible evolutionary trajectory these systems might took from simple to complex could be drafted.

To underline the clarity and adaptability of the formalism, several experiments are performed. These are discussed in chapter 3. First, in section 3.1, a mathematical formalism is presented to estimate impact of mutation at levels of representation, depending on the informational topology of replication. Next, in section 3.2 the general replicator representation is introduced and a potential scenario for the emergence of division of labour is tested. Thirdly, in section 3.3, a kinetic investigation is presented: the coexistence of replicators with different growth rates in the chemoton is analyzed.

A discussion follows in chapter 4, which deals with three major issues. Section 4.1 gives a consistent definition for Lamarckian inheritance. Section 4.2 explains phenotypic replication in detail, providing an appropriate context for it, in light of the findings of the thesis. 4.3 then discusses some details of the levels of selection in complex inheritance systems.

Chapter 5 gives a classification based on the terms discussed and introduced during the thesis, giving a full hierarchy of the replicator family tree. The last, sixth chapter concludes the thesis and gives some thoughts about future research.

2. The formal model of replication

To give a full account of replication, four aspects are discussed: *causal*, *selectional*, *stoichiometric,* and *informational*. Each layer deals with a major concept of replication, and is responsible for *correlation*, *variation*, *multiplication,* and *heredity*, respectively. The latter three are known as the criteria of **units of evolution** (see Muller 1966, Maynard Smith 1986, 1987). Correlation is only implicitly included in this definition.

2.1. Notations and Abbreviations

The narrow and broad senses of various concepts (genotype, phenotype, template, and replicator) are distinguished in the formalism. The narrow sense always refers to an abstraction of the entity, while the broad sense denotes the smallest individual physical entity responsible directly for the narrow sense. For example, a gene's *genotype in the narrow sense* (GN) is the abstract base order of the coding DNA strand (i.e. a sequence of letters). The *genotype in the broad sense* (GB) is the actual physical representation of the GN: the double helix of the DNA. For clarification, refer to Figure 24. *Units* of various concepts indicate that the concept refers to a population of such units, instead of a single entity.

X, Y, Z, …	distinct entities	S or St	equivalence relation at time t
E, F, G, …	set of entities	p(X)	phenotype function of entity X at time t
M	medium of an entity	t(X)	template function of entity X
C	codon set of a modular entity	g(X)	genotype function of entity X
$X \Rightarrow Y$	transformation of entity X to Y	d(X)	development function of entity X
$\Theta: E \rightarrow F$	transformation map	PN/PB	phenotype in the narrow/broad sense
$T: E \rightarrow F$	transmission map (modular Θ)	TN/TB	template in the narrow/broad sense
$\Theta: CE \rightarrow CF$	transformation map of codons underlying a transmission	GN/GB	genotype in the narrow/broad sense

2.2. Causal aspect (Correlation)

The causal aspect deals with the simplest condition of replication: correlation. For causation as an explicit condition of replication, see e.g. Aunger (2002), Godfrey-Smith (2000) and Sterelny et al. (1996). Causality means that due to some causal effect, there will be correlation between parent and offspring entities, otherwise they bear no information on one another, and thus no replication is done. Consequently, there must be a rule responsible for the consistency of

the reaction, yielding the same output given the same input. The causal aspect in itself, however, cannot specify the exact nature and quantity of similarity, since no one has established a viewpoint from which parent and offspring should look similar or different (other than equality up to the last quark). This will be defined under section 2.3 Selectional aspect (Variation). The causal backbone of any reaction is provided by a transformation rule.

2.2.1. TRANSFORMATION

Transformation is a **mapping**, $\boldsymbol{\Theta}$, defined on a set of entities E:

$$\boldsymbol{\Theta}: E \rightarrow E,$$

such that it derives entity $Y \in E$ from entity $X \in E$, meaning that X is *causally responsible* for the nature of Y. A certain transformation is indicated with a wide arrow: $X \Rightarrow Y$.

A transformation is not to be mistaken with a *reaction*, which uses standard arrow notation. A transformation omits input and waste materials, stoichiometric and kinetic factors or catalytic effects, it only focuses on the *causal topology* of the reaction. As we will see, this causal topology is the foundation of any *informational topology*, which cannot be represented directly in standard reaction equations.

The transformation need not be deterministic (i.e. a proper function). It can yield Y with probability less than 1 and other entities with probability larger than 0. This can be denoted as:

$$X \Rightarrow Y_1 \mid Y_2 \mid Y_3 \mid \ldots$$

A probabilistic transformation written in standard chemical reaction format:

$$X \rightarrow p_1\, Y_1 + p_2\, Y_2 + p_3\, Y_3 + \ldots,$$

where p_i is the net amount of the i^{th} entity after the reaction (p_i can be zero).

The actual outcome of a probabilistic transformation must depend on exogenous factors, i.e. it *must be independent* of the nature of X. From the viewpoint of replication, two things are important. First, obviously the more deterministic a multiplicative system is the more stably it can produce the same replicators ($X \Rightarrow X$). Second, probabilistic transformation can yield attractor-based inheritance (Hogeweg 1998, Szathmáry 2000), where information, maintained as a population of replicators, heavily depends on the dynamical control space of replicators. This will be discussed under 2.6.1 Informational replication.

2.3. Selectional aspect (Variation)

At what point and for what extent must the offspring of the replicator be similar to its parent? Consider a simple chemical autocatalytic cycle of molecule X, which is doubled in amount during one turn of the cycle. Once, due to a mistake, the new product Y rises, which differs in some aspect from X. Still the cycle can go on unharmed with Y, producing new X-s. Would then Y differ from X? One could say that if Y is heritable, and new cycles would produce Y instead of X, then Y differs from X. However, if Y is not heritable, i.e. both X and Y can substitute the other without causing any change in the reactions, they then only differ in their structures, but not in functions. Therefore, why should anyone differentiate among them? Now, there could be a huge difference concerning e.g. their macroscopic functions, like color, which may help marketing one but not the other. The important point here is that from one aspect X and Y are similar (the chemical aspect), while they differ from another (marketing).

This means that replicator equivalency is a matter of **relativity** that cannot be decided without specifying an explicit viewpoint. By saying that a replicator and its offspring are similar, one has to specify the viewpoint where from they do function or look similar. If one defines such a viewpoint by introducing a **selective force**, only then can similarity or difference between parent and offspring be specified. Note, that still two entities can differ in their structures, or information content if they are equivalent under a selective force. Therefore, similarity has multiple aspects as well: *structural*, *functional*, *material, informational*, and possibly more. Different aspects may not assume the same equivalency. Only if all similarity aspects converge will two entities be totally identical.

Note that the following definition of sorting is based on the definitions of selection at Hull (1988b, p. 408) and of sorting at Vrba (1989, p. 117), and is the more clear-cut version introduced by Zachar & Szathmáry (2010). The present approach explicitly differentiates between selection and sorting. It must be emphasized that it is the equivalence relation (induced by sorting) that defines the phenotype, therefore **the phenotype can be defined without genotype, or even without replication**. Fitness is the one-dimensional representation of the phenotype. If there is a population of multiple entities differing in some sense, then they can be units of sorting and selection according to this variation. The selective force can be any natural or artificial function (e.g. resource limitation, disease, etc.). The phenotype of an entity can be represented by another, distinct entity, called the interactor. Shifting the task of interfacing the selective force to a distinct entity (the interactor) opens up the possibility for division of labor, which is an indispensable prerequisite of Weismannian inheritance (see later).

2.3.1. SORTING

A sorting event is a **process**, acting on a particular population of entities E, in a particular environment, during which some entities cease functioning while others persist, according to a unique function of the entities. Sorting therefore defines an **equivalence relation** S on the list of entities E, $S \subset E \times E$ that sorts entities into equivalence classes according to their phenotype function p.

2.3.2. SELECTION

Selection is a **process**, and is the successive chain of an indefinite number of sorting events. As sorting at time t defines a specific equivalence relation S_t, selection defines a set of sorting events and a set of **equivalence relations** $\{S_t, S_{t+1}, S_{t+2}, \ldots\}$.

2.3.3. PHENOTYPE

The phenotype is a **function** p of a set of entities E, about which a particular sorting equivalence relation S sorts entities into equivalence classes. The phenotype is therefore that function p: $E \rightarrow p(E)$ for which it is true, that $\forall\ e_1, e_2 \in E$: $e_1\ S\ e_2 \Leftrightarrow p(e_1) = p(e_2)$. Informally, **for every pair of entities, they are in relation S iff their phenotypes are identical.** The phenotype function thus maps entities to such a set, $p(E)$, that, if partitioned by the equality relation (=), has the exact same structure as the partition of E implied by the sorting relation S (see Figure 6).

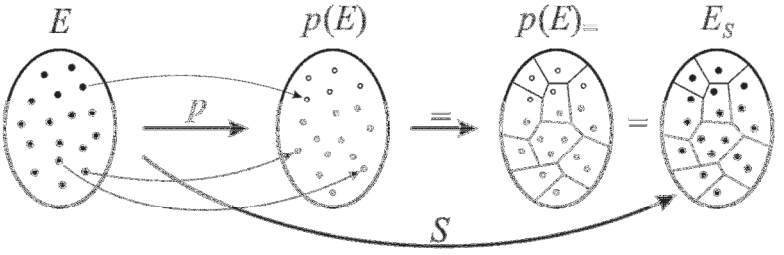


Figure 6. Sorting. A list of entities E (leftmost) is sorted into equivalent phenotype classes (domains of the rightmost set) according to a sorting function S. The function about which S sorts is the phenotype p. The first projection (the phenotype function p) is one-to-one. Next, $p(E)$ is partitioned by the equality relation = to yield $p(E)_=$. S is such, that the partitioned set E_s gained by applying the sorting relation S directly to E, is identical to $p(E)_=$.

As it was mentioned earlier, replicator equivalency is a matter of relativity. Without specifying the observer (i.e. an aspect), no valid statements can be made concerning equivalency (i.e. whether two replicators are equivalent or not). Phenotype, and more basically, replicator identity is defined in a way that is similar to the definition of consciousness in the Turing test (Turing 1950). Without context, two similarly sentient beings (or replicators) cannot be tell apart, or distinguished in any sensible way. Replicator identity is basically an indistinguishability problem, which upon an objective agent decides. Selection or sorting poses an objective and indirect viewpoint, just like an experimenter or judge does in the Turing test. Until a sorting function cannot distinguish among replicators, they are considered equivalent.

It must be emphasized here, that while the sorting relation defines the actual phenotype and fitness of the entities, both phenotype and fitness depend on inherent properties of the entities, like structure and information content. The definition merely reflects the well known fact that an organism may have a different fitness in a different environment. Accordingly, a replicator's fitness (though is its own property), is defined by the selective environment as well.

2.3.4. SIMILARITY

Similarity is a distance **metric** d defined over the set of entities, or more precisely, over the set of phenotypes of entities, partitioned by a sorting equivalence relation S. Equivalence is a special case of similarity, when $d(e_1, e_2) = 0$. This definition of similarity defines *selective similarity*. Other metrics can be defined based on structural, functional, material, informational, or other types of equivalencies. Only if all similarity aspects converge can two entities be considered identical.

2.3.5. UNITS OF SORTING

An **entity** is a unit of sorting, if there potentially exists a population E of such entities, and, according to the equivalence relation S of a particular sorting event of the environment, they are not all equivalent, possessing different phenotypes.

Notice that this definition only refers to variation, but not multiplication. To have indefinite number of sorting events (iterative selection), multiplication is needed, otherwise the population of entities will disappear within finite time. If replication is informational, units become subjects of evolution. Table 1 summarizes the relation of units of sorting, selection, and evolution.

Table 1. Units. Extending the classification of Maynard Smith (1987), unit of sorting was introduced in Zachar et al. (2010). Note that units of evolution form a subgroup of units of selection, which in turn are special units of sorting.

	Variation	*Multiplication*	*Heredity*
units of sorting	X		
units of selection	X	X	
units of evolution	X	X	X

2.3.6. INTERACTOR

The interactor is a distinct **entity** Z transformed from a unit of sorting, X, representing directly the phenotype of X:

$$Z = \boldsymbol{\Theta}(X) \quad \text{where} \quad Z \neq X \quad \text{and} \quad p(X) = p(Z),$$

that is the phenotype of X is equivalent to the phenotype of Z under *S*. Note that there is an underlying transformation $X \Rightarrow Z$.

In chemical and biological systems, the interactor is a product of the replicator-cycle. Therefore, the interactor (Z) is correlated with the replicator (X): it is a transformation (or even translation) of the replicator. At the same time, replication is affected by the interactor in the long run (as selection affects the interactor) and is usually inevitable for the cycle to turn. Therefore, the interactor is a heterocatalytic result of the autocatalytic cycle of the replicator (cf. Figure 7). In a more formal way: since the selectional relation *S* sorts according to phenotypes, and the phenotype is a direct function of Z, therefore *S* affects the population of Z directly. *S* also affects X indirectly, if there is any backward link from Z to X, that is the change selection induces is channeled toward X (e.g. if the interactor dies, so does the replicator it represents).

Examples abound. Proteins are interactors of genes, expressed memes are interactors of (neuro)memes (e.g. Aunger 2002, Blackmore 1999, Dawkins 1976 and 1982b, Sperber 2000). There can be higher-level interactors (cf. *vehicle* of Dawkins 1982a) and interactors outside the body as well (cf. *extended phenotype* of Dawkins 1982b).

The notion of the interactor is context-dependent, for example proteins are not always interactors. Imagine a situation of gene replication with direct gene-selection (as in a prebiotic setup). Although proteins are still translated, they would not be used in any way to affect the

distribution of genes. In this case, there would be **no** interactor, since proteins do not change the next-generational distribution of the genes.

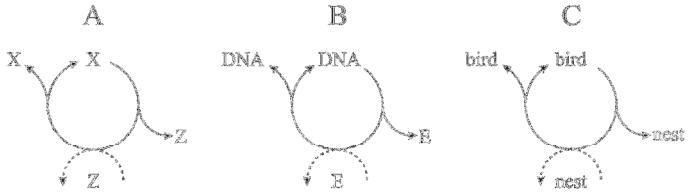


Figure 7. The interactor. A) general representation of the interactor. Z, the interactor is usually a result of a transformation from X. Dashed arrows indicate indirect effects on the cycle (e.g. catalysis). B) An enzyme E, as an interactor, is a direct heterocatalytic result of the autocatalytic cycle of the replicator, the DNA. C) a nest can be thought of as a heterocatalytic product of the life cycle of a bird. Input and waste materials are omitted.

In case of genes, both replicators and interactors are modular. This however need not be so. Non-modular replicators may have non-modular interactors. What is important here is that the $X \Rightarrow Z$ transformation (defined by $\boldsymbol{\Theta}$) should be deterministic instead of probabilistic. The more deterministic $\boldsymbol{\Theta}$ is, the more stable would be the effect of the interactor over the cycle, providing thus stable functioning of the cycle over time. $\boldsymbol{\Theta}$ thus need not be unambiguous (i.e. can be probabilistic), but then the efficiency of interaction decreases, as the phenotype would not represent uniquely and stably the replicator. Different replicators should therefore map to interactors in either a one-to-one or many-to-one way for greater efficiency.

This definition of the interactor is coherent with the one given by Hull: "an entity that interacts as a cohesive whole with its environment in such a way that this interaction *causes* replication to be differential" (1988b, p. 408). However, interactor does not refer to replication here. The idea of interactor is broader: if there are units of sorting, these units can be represented by interactors. Thus, the interactor is a unit of sorting itself, but is not necessarily a unit of selection, therefore it does not have to multiply. Therefore, it is not necessarily related to replication, but it definitely needs sorting.

There is always one phenotype function associated to a particular sorting (i.e. at one level of selection), but it is possible that multiple interactors contribute to that phenotype. That is why the interactor is not always the *phenotype in the broad sense* (PB). The PB can be the replicator itself (memes), an interactor (protein), or a set of interactors (soma). Since the phenotype is the direct function of the interactor (which is defined by X), the interactor is therefore responsible for the *extended phenotype* function *p'* of X.

Without the interactor, no division of labor is possible. For example, prebiotic ribozyme replicators presumably did not have a separate interactor, therefore they lacked division of labor. One can say, that the ribozyme replicator is itself the interactor, as it is responsible for its own selection. Even Hull's original definition (Hull 1980, 1988b) does not specify explicitly, that the interactor cannot be the replicator itself. If the interactor is a different entity, there is at least partial division of labor between the replicator and itself: the interactor is the entity that is responsible for interfacing and channeling selection toward the replicator, while the replicator is responsible for multiplication. If the replicator is informational (i.e. hereditary), the division of labor could be complete. The replicator conserves the genotypic information while the interactor deals with selection, or more broadly, with environment.

The interactor usually uses a different element set than the replicator (that is $\mathbf{M}_X \neq \mathbf{M}_Z$), therefore it is generated by translation. However, this is not necessary. The interactor can be created by transcription, or in a non-informational way. Copying is unlikely (hence the condition $Z \neq X$), as the interactor would then compete with its parent replicator for monomers, therefore it would not be a representation of the phenotype of the replicator, so division of labor would not be present. Nevertheless, certain artificial cases can be fabricated to prove the possibility of valid interactors of the case $\mathbf{M}_X = \mathbf{M}_Z$.

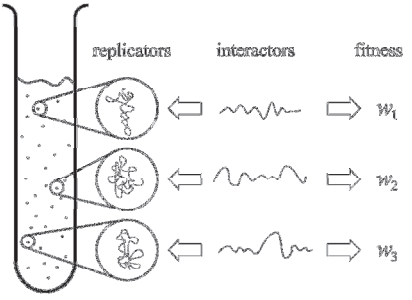


Figure 8. Hypothetic interactor experiment. For each ribozyme in the test tube, an arbitrarily chosen external RNA sequence is chosen to be the interactor by the experimenter. Interactor phenotypes are evaluated and fitness values w_i are assessed according to artificial selection criteria and replicators in the test tube are artificially replicated by selective replicases according to the fitness order. In this case, both replicators and interactors share the same monomers, and the link between them is purely symbolic.

For example, consider a test tube, where ribozymes replicate in a controlled way, by the experimenter (Figure 8). Each ribozyme is represented by another, unique ribozyme interactor, artificially assigned to the test ribozymes, outside of the test tube. In each turn, the interactors are evaluated: artificial selection assigns a fitness value to each one, and then the original ribozymes are replicated artificially according to their fitness values. In this case, test ribozymes are replicators, while assigned ribozymes are their interactors, working on their behalf. Note, that the function assigning interactors to replicators is **completely holistic, and symbolic**. The DNA-

protein system has a similar symbolic function (assigning codons to amino acids in a mostly arbitrary way), although it is compositional: each different DNA strand starting with AGU will have a protein starting with serine. Contrarily, in the above toy example, phenotype similarity of replicators cannot be predicted based on the similarity of their sequences.

2.4. Stoichiometric aspect (Multiplication)

The most obvious feature of a replicator is inevitably its replicative potential. Multiplication is a quantitative matter, which, if granted, ensures that the replicator can be present for practically infinite time. If the entity cannot multiply, it will be degraded in finite time. *Autocatalysis is the observable phenomenon of replication*. An entity that replicates is a unit of selection.

2.4.1. REPLICATION

Replication is a **mapping**, described by a set of successive transformations

$$e_1 \Rightarrow e_2 \Rightarrow e_3 \Rightarrow \ldots$$

and net reactions

$$\{e_1 \rightarrow r_1\, e_2,\ e_2 \rightarrow r_2\, e_3,\ \ldots\}$$

for which it is true that $\forall i$: $r_i > 1$ and $\forall i,j$: $p(e_i) = p(e_j)$, where p is the phenotype function, that is defined by a selectional relation S. Thus replication, when applied consecutively, yields an increasing number of phenotypically identical entities. Replication R is therefore a recursive mapping:

$$\mathrm{R}: E \rightarrow E, \quad \mathrm{R} = \Theta^n,$$

where $n \in \mathbf{N}$ stands for the possibly infinite iterations of replication. Since $e_2 = \Theta(e_1)$, $e_3 = \Theta(e_2)$, ..., it follows that $e_i = (\Theta \circ \Theta \circ \ldots \circ \Theta)e_1$ and $\forall i$: $p(e_1) = p(e_i)$, thus Θ has to be a transmission of such that it can maintain phenotypic identity **and** further transformation. Only if the replicator is modular, can one allow correlated rather than identical phenotypes. This will be discussed in section 2.6.1 Informational replication.

Note, that entity X is autocatalytic if and only if the stoichiometric factor $r > 1$ **and** the dynamics of the reaction ensure growth:

$$\mathrm{X} \underset{d}{\overset{k}{\rightleftharpoons}} r\mathrm{X},$$

that is the net growth of X, defined by kinetic parameters $k > d$, can be characterized by the following equation ($x = [X]$):

$$\frac{dx}{dt} = a\,x^e, \quad \{a, e\} > 0.$$

Thus the definition of replication has a **causal** ($\Rightarrow$), a **stoichiometric** (r), a **selectional** (p) and a **kinetic** (k/d) aspect. This also means that the term *replication* can be used in a limited form, e.g. *stoichiometric replication* if only the equation $X \rightarrow 2X$ is known, which does not necessarily imply real replication, since the kinetic setup is unknown.

As absolute replicator identity cannot be defined[3], the relative equivalency is used to establish the equality of phenotypes $p(Y)$ and $p(X)$. Since equivalence depends on selection, **replication is only defined if selection is defined** to begin with (i.e. sorting, or at least a relation). Consequently, replicators are units of sorting, and, since they can multiply, they are units of selection as well, according to Maynard Smith (1987). Whether an entity is actually a replicator thus depends on the sorting function of the actual environment. Again, it must be emphasized, that on one hand, internal properties are responsible for the replication-ability of an entity. On the other hand however, the working environment is equally important in defining replication, as it is possible to have an environment, where all DNA sequences have the same phenotypes (thus there is no differential survival and no evolution), or where there are no monomers (and thus no multiplication).

Furthermore, since identity is not specified as a strict criterion, X and Y can actually use different media as building blocks, until the equivalency condition holds. Therefore it is not part of the definition that media are identical, that is $\mathbf{M}_X = \mathbf{M}_Y$ (although, for chemical and biological examples this is usually fulfilled). This is true for any subtype of replication. For example, the replication of a printed book may not result in another book but in a set of scanned images. These may seem to be different entities, and not parent and offspring. From a legal viewpoint however (i.e. law being the selective factor), the act is still considered reproduction, as the information in the book did get replicated. This happened multiple times when Google Books

[3] The indentity of two objects can be defined in many levels (subatomic, atomic, molecular, etc.), though emphasizing any of these as the decisive level of replicator identity is arbitrary. DNA sequences can have identical base orders, though different metilation patterns. Therefore, no absolute identity is sought here, but the more satisfactory relative approach is used, which requires the explicit specification of the level of selection (i.e. base-order, metilation pattern, or both).

scanned items of publishers denying rights to do so (e.g. Google versus French publisher La Martiniere).

Replication can be informational or non-informational according to Orgel (1992), depending on the amount of heritable information (see section 2.5). Non-informational replicators are also called analogue (Szathmáry 1995, 1999), holistic (Maynard Smith & Szathmáry 1999, Szathmáry 1999), or processive (Szathmáry 1995) replicators. A replicator is a unit of selection and an informational replicator is a unit of evolution, according to (Maynard Smith 1987).

The *replicator in the narrow sense* (RN) is only defined in case of informational replicators: it is the **genotype**. The *replicator in the broad sense* (RB) is a distinct entity that is multiplied. For informational replicators, the replicator itself is solely responsible for the genotype, and approximates it the best by minimizing its variable but non-heritable part (see section 1.5). The *replicator in the extra-broad sense* (RXB) denotes the whole autocatalytic cycle (i.e. all intermediates, cf. Gánti 1971), and every product of the cycle, which has a positive feedback on the replication of the cycle (heterocatalytic products). Intermediates of the cycle are transformed to yield the next stage. Selection may act on multiple of the intermediates directly: these together form the *interactor in the broad sense* (IB) of the cycle.

Note, that the reaction $X \rightarrow 2X$ can have an indefinite number of intermediates (input and waste material are omitted):

$$X \rightarrow Y \rightarrow ... \rightarrow 2X,$$

which can also be rearranged into a cycle, to fully reflect autocatalytic cycles. The important fact is that if both X and Y are modular (i.e. all transformations are compositional), it is not necessary for all steps to be unambiguous. If X is transformed probabilistically to Y, an **appropriate** reverse transmission of unambiguous nature would still yield X from Y, thus information is maintained. This will be discussed under section 2.5 Informational aspect (Heredity).

2.4.2. UNITS OF SELECTION

An **entity** e is a unit of selection, if there potentially exists a population P of entities (for an indefinite time), and, according to the equivalence relation set $\{S_t, S_{t+1}, S_{t+2}, \ldots\}$ of a particular selective force of the environment, they are not all equivalent, possessing different phenotypes. Formally, entity e_i is a *unit of selection* iff:

$$\forall i\colon e_i \in P, \forall t \in \mathbf{N}\colon \exists j\colon e_j \in P, i \neq j, p(e_i, t) \neq p(e_j, t),$$

where $p(e, t)$ indicates the fitness of e_i at time t. Informally, e is a unit of selection if there exists at least one other entity in the population with a different fitness.

2.4.3. REPLICATOR

A replicator is a **unit of selection**, where selection implies differential survival of a population of entities. Since selection is defined for indefinite time, the population has to be present for an indefinite time, thus multiplication (replication) is necessary (but not heredity), otherwise members of the population will go extinct in finite time. A "replicator that is potentially the ancestor of indefinitely long line of descendant replicators," is a *germ-line replicator* (Dawkins 1982b, p. 83.). Only a germ-line replicator can replicate for a potentially infinite time.

This definition of *units of selection* is fully coherent with the one given by Maynard Smith (1987), and with the definition of the replicator at Szathmáry & Maynard Smith (1993) and Zachar & Szathmáry (2010). In Orgel's term (1992), this definition refers to both informational and non-informational replicators (to be discussed in turn).

In summary, **a replicator is an entity that is capable of autocatalytic growth and which produces new entities that are equivalent to it in terms of phenotype** (Fernando et al. 2011).

2.5. Informational aspect (Heredity)

The informational aspect is inevitable for replicators to have evolutionary potential. However, to maintain the generality of the formalism, it must be discussed in a replication-free way. Basic concepts apply to various chemical or biological cases, where there is no replication at all.

In a given transformation, parts of the source entity may map to parts of the target entity. Source and target are *modular* in this case, and the transformation is compositional, called *transmission*. Since the modules (*codons*) of the source define the modules of the target, the source entity is called a *template*. Modular replicators are called informational ones, while non-modulars are non-informational (Orgel 1992), holistic (Szathmáry 2000), or processive (Szathmáry 1995) replicators.

2.5.1. MODULARITY

Modularity is an **attribute** of an entity in a specific transformation $X \Rightarrow Y$, if there is a mapping $\boldsymbol{T}$ for which it is true that

$$Y = \boldsymbol{T}(X), \quad \text{where} \quad \boldsymbol{T} = \boldsymbol{\Theta}^n : \mathbf{C}_X{}^n \rightarrow \mathbf{C}_Y{}^n,$$

where $n \in \mathbf{N}$ and $n > 1$, and $\mathbf{C}_X$ and $\mathbf{C}_Y$ are the codon spaces of X and Y, respectively[4]. The equation tells that Y can be created by applying $\boldsymbol{T}$ on X, where $\boldsymbol{T}$ is a mapping of the modules of X to the modules of Y, and X consists of $n > 1$ modules.

If $n = 1$, the transformation is *holistic*, if $n > 1$ the transformation is *compositional*, and X is modular. In general, modularity is a property of an entity that is constructed from a set of monomers of nearly equal ranks (like DNA). However, consider the following thought experiment. In a hypothetic transformation, each unique DNA sequence is "transformed" to a random unique integer. Now the smallest change in the structure of DNA may yield a completely different number, therefore one cannot say that nucleotides in the DNA have equal ranks. Thus modularity, in the strict sense, is a property of an entity and is **specific for a given transformation**. In addition, if X is modular, then Y has to be modular as well.

2.5.2. COMPOSITIONALITY

Compositionality or holisticity is an **attribute** of a mapping. The projection $\boldsymbol{T}$ of a transformation $X \Rightarrow Y$ is compositional, if X is modular (i.e. $\boldsymbol{T} = \boldsymbol{\Theta}^n$: $\mathbf{C}_X{}^n \rightarrow \mathbf{C}_Y{}^n$ where $n > 1$), and holistic, if X is non-modular (i.e. $n = 1$). Informally, a transformation is compositional if the mapping from the entity space $\boldsymbol{T}$: $E \rightarrow E$ requires fewer assignments than the size of E (number of entities), and holistic, if for each $X \in E$ there is a specific assignment yielding the appropriate $Y \in E$ (see Table 2). Note that if a transmission is compositional, both X and Y are modular: the n modules of X are transformed to the n modules of Y, one by one. Compositional transformation is called *transmission*.

Table 2. The relationship between modularity and compositionality of transformations.

	modularity (source and target are...)	*complexity* (transformation is...)
simple transformation	non-modular	holistic
transmission	modular	compositional

[4] For example, the codon space of DNA during gene-expression consists of the 64 codons, while the corresponding codon-space of proteins contains the 20 aminoacids (plus the stop function).

For example, the RNA → DNA transcription or the DNA → protein translation is compositional (requiring 4 and 64 rules, respectively). Conversely, if each possible DNA sequence is mapped to a unique random number, then the mapping is holistic, and cannot be represented by elementary rules. Note that in the latter case, the DNA still can be considered modular in the chemical sense, but since one cannot predict the assigned number based on the sequence of the nucleotides, one cannot say that modules are of nearly equal rank: the addition of one nucleotide completely changes the outcome (the assigned number), and there is no correlation. Therefore, in this though experiment, DNA is not considered modular.

Compositionality and holisticity are universal terms used in information transmission, be it of any kind, chemical or linguistics. Compositionality in general is defined as: the properties of a complex expression are determined by its structure and the properties of its constituents (after Szabó 2008). In linguistics, the compositional mapping of meaning to form (or back) means that subparts of meaning map to subparts of form. In contrast, in a holistic representation system (like postulated protolanguages) there is no systematic mapping between subparts of the signal and subparts of the meaning (see Tallerman 2007, Wray 1998, Zachar 2011).

Compositionality may (somewhat confusingly) refer to the fact, that the heritable information of a replicator is coded by a composite set of modules (i.e. by an assembly), like "compositional genomes" in Doron Lancet's GARD model (Segré et al. 2000, Lancet & Shenhav 2009), see in section 2.6.3 Order of inclusion. Compositionality *sensu* Lancet simply refers to informational (i.e. modular, digital) replication.

2.5.3. TRANSMISSION

Transmission is a compositional transformation **mapping** $\boldsymbol{T}$: $F \rightarrow G$ such that:

$$\forall\, n > 1\colon \forall\, f \in F\colon f \in \mathbf{C}_F{}^n \quad \text{and} \quad \forall\, g \in G\colon g \in \mathbf{C}_G{}^n \quad \text{thus}$$

$$\boldsymbol{T} = \boldsymbol{\Theta}^n, \text{ where } \boldsymbol{\Theta}\colon \mathbf{C}_F \rightarrow \mathbf{C}_G, \text{ thus } \boldsymbol{T}\colon \mathbf{C}_F{}^n \rightarrow \mathbf{C}_G{}^n,$$

where F and G are entity (or sequence) spaces of X and Y, respectively. Informally, a transmission is a transformation X ⇒ Y, where X is modular. Y is created based on the template X as Y = $\boldsymbol{T}$(X). Transmission $\boldsymbol{T}$ is the extension of the transmission $\boldsymbol{\Theta}$ defined on modules of F to the full sequence space F. Note, that X and Y need not be sequences at all, they can have any dimensions.

As a matter of fact, $\boldsymbol{T}$ does not map from F to G, but from $t(F)$ to $t(G)$, and another function, d, provides the final Y:

$$X \xrightarrow{t} t(X) \xrightarrow{T} t'(Y) \xrightarrow{d} Y,$$

$$Y = d(\boldsymbol{T}(t(X))).$$

Function t defines the parts/features of X conveying the template information and d is the inverse of t. This inverse function of t can be called *development*, and is more pronounced in organisms of higher complexity. Development basically interprets the template information $t(X)$, or its translation $t'(Y)$, to yield the final entity Y. The more simple the molecule is, the more t and d approximate the identity function for which it is true that $id(X) = X$. The important formalism is the t-$\boldsymbol{T}$-d triplet (*extract-transmit-develop*). For example in case of (asexual) organisms, X is the parent organism, $t(X)$ is its genome, $t(Y)$ is the genome of its offspring, d is the quite complex function of development, and $\boldsymbol{T}$ is the identity function (plus mutation).

If the transmission is deterministic, there is always a fixed dispatch table $\boldsymbol{\Theta}$ consisting of the elementary rules of projection, just as the genetic code table provides 64 rules for DNA → protein translations. This table works deterministically both forward and backward. In case of language inheritance however, there is no such universal code table. This, on one hand, allows for a practically infinite search-space for languages (that are not constrained by any kind of code-restriction), on the other hand it allows the potential loss of information (since recipient may use a different "code-table"). One solution to avoid information loss in language is either to increase compositionality of X and therefore reduce the overall number of rules that must be learned in a code-table. Note that for holistic languages, much more rules must be learned than in compositional ones (Kirby 2000). The other solution is to use iterated learning (Smith et al. 2003), especially with external pools of fixed translational codes (i.e. books, DVDs, etc.), that help the recipient to decode the same information that was encoded using these devices.

In summary, given a transformation $X \Rightarrow Y$, if X is **modular**, than Y is modular as well, and the transformation is a **compositional transmission**, mapping the **template** information of X to Y according to the projection $\boldsymbol{T}$.

2.5.4. TEMPLATE

The *template in the narrow sense*, $t(X)$, is an abstraction (a **function)** of a modular entity X in a specific transmission, which, if changed, may cause a change in the product entity (the *transcript*). The *template in the broad sense*, X, is a modular entity that contributes information (the template in the narrow sense) to the transcript.

In case of DNA replication, the template of the new DNA is one strand of the original one. Since the template is not a replication-specific concept, it must be noted that the polynucleotide chain is also the template for proteins.

Obviously, a template is not necessarily a replicator, and the transmission is not necessarily replication. The transcript of the template is not necessarily a template for a following step, closing the loop. While the genotype is specific for replication, the template is a more extended concept of information transmission. The genotype (of a replicator) is a specific template, where the media and dictionaries of template and transcript are the same. Furthermore, in case of replicators, the template **must not** be destroyed, otherwise there is no multiplication. Thus, the template of a replicator always acts as an (auto)catalyst, implying that catalysts and templates are separate sets with a possible intersection. There could be transmissions where the template is destructed, which means that it is neither replicated nor regenerated, thus it is not a catalyst.

2.5.5. CODON

A codon is an **element** of the domain of a transformation $\boldsymbol{\Theta}$: $\mathbf{C}_F \rightarrow \mathbf{C}_G$ being the part of a transmission $\boldsymbol{T}$: $\mathbf{C}_F{}^n \rightarrow \mathbf{C}_G{}^n$ ($n \in \mathbf{N}$, $n > 1$). The **target codon** is an element of the codomain $\mathbf{C}_G$. The target codon is not to be mistaken with the anticodon, which is a target codon specific for the mRNA → tRNA translation. It follows, that a codon is thus **specific for an entity and for a transmission**. A DNA triplet is a codon, specific for translation, but not for transcription; conversely, a base of the DNA is a codon for transcription, but not for translation. Moreover, in translation, single amino acids are the corresponding target-codons.

2.5.6. AMBIGUITY

Ambiguity is an **attribute** of a transmission $\boldsymbol{T}$, if it is not a proper mathematical function. The transmission is ambiguous, if the mapping $\boldsymbol{T}$ is a probabilistic one-to-many mapping. Conversely, the transmission is unambiguous, if $\boldsymbol{T}$ is either a many-to-one or a one-to-one mapping. In terms of codon spaces, $\boldsymbol{T}$ is ambiguous if $|\mathbf{C}_F| < |\mathbf{C}_G|$, and unambiguous if $|\mathbf{C}_F| \geq |\mathbf{C}_G|$.

2.5.7. ELEMENTARY TRANSMISSIONS

Elementary transmissions listed here describe the simplest projections from source entity to product, according to the transmission mapping $\boldsymbol{T} = \boldsymbol{\Theta}^n$. Figure 9 illustrates the four elementary

transmission types. More complex inheritance pathways (like Weismannian and Lamarckian inheritance) are built of elementary transmissions.

2.5.7.1. Translation

Translation is a case of transmission, where $\boldsymbol{\Theta}$ is a surjective, but not injective mapping (i.e. a many-to-one function, unambiguous). Translation (if not bijective) compresses the information content of the template to a lower resolution (thus for example the offspring sequence is shorter than the parent). Translation is a projection from a larger to a smaller sized codon space. For example, proteins are translated from the 64-element codon alphabet to a 20-element alphabet of amino acids (plus stop codon, cf. Figure 9). During translation, the resolution of the information content decreases, but this does not necessarily mean loss of information: while the exact DNA sequence is lost, and cannot be reconstructed from the protein exactly as it was, still any reconstruction would code for the same protein. Thus DNA and protein here are isomorphic.

2.5.7.2. Reverse translation

Reverse translation is a case of transmission, where $\boldsymbol{\Theta}$ is the inverse of a surjective, but not injective mapping (i.e. inverse of translation). Since such an inverse mapping is a one-to-many mapping, it is therefore ambiguous and is not a mathematical function. The actual realization of a reverse translation involves probabilistic (possibly random) choice among the possible outcomes, thus reverse translation is a probabilistic transmission. Note that reverse translation inflates the information content of the template to a higher resolution. A hypothetical example is the reverse translation of proteins to DNA, where amino acids are mapped to codons in a probabilistic way. This mapping would therefore be ambiguous (cf. Figure 9), and the outcome (the DNA) would be bloated as there are 3 times more bits in it than in the protein, though both DNA and protein sequences are isomorphic, representing the same thing.

2.5.7.3. Transcription

Transcription is a case of transmission, where $\boldsymbol{\Theta}$ is a surjective and injective, therefore bijective mapping (a one-to-one function, unambiguous). Transcription is a projection between codon spaces of equal size. An example is the DNA → RNA transcription, where the resolution does not change, only the alphabet (cf. Figure 9).

2.5.7.4. Copying

Copying is a special case of transcription, where $\mathbf{C}_F = \mathbf{C}_G$, i.e. the media of both source and target are identical (the domain and codomain of the mapping equal). Example is DNA replication, where neither resolution nor alphabet changes during the process (cf. Figure 9).

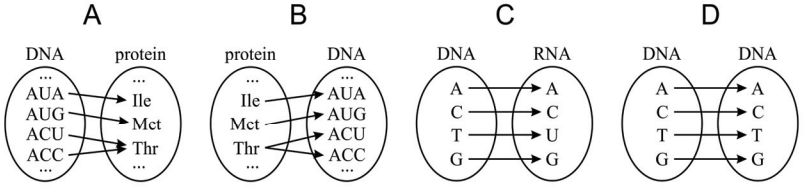


Figure 9. The four basic types of transmissions (i.e. compositional/informational transformations). The transmission mapping can be used to transform arbitrarily large sequences (or sets) of entities. Here, only the codons spaces (C_F and C_G) are presented. A) translation; B) reverse translation (hypothetic); C) transcription; D) copying.

The ambiguity of a transmission depends solely on the codon lengths and inventory sizes of the domain and codomain sets for deterministic transmissions (Figure 10). Presumably, any inheritance system favors unambiguous transmission over ambiguous one, though, as it will be shown, ambiguous transmission does not necessarily imply loss of information.

Codon robustness r specifies the number of target codons associated with the codon: if transmission is unambiguous, $r = 1/n$ ($n \in$ N) where n different codons map to the same target codon. If $r > 1$ (r $\in$ N), transmission is ambiguous, and a codon can be mapped to r different target codons (see Figure 11). The actual mapping process assigning target codons to a codon during translation is irrelevant, but it must be probabilistic, as an ambiguous translation is not a proper mathematical projection.

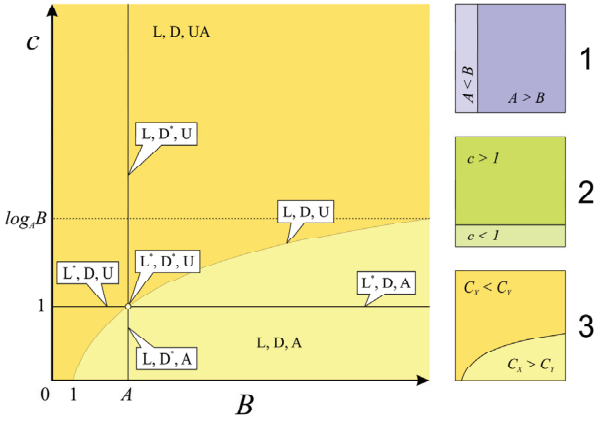


Figure 10. Transmissional properties. Properties depend on the sizes of the domain and the codomain codon spaces. The codon size of the domain (c on y-axis) and the inventory size of the codomain (B on x-axis) are taken to be continuous for sake of simplicity. The codomain codon size is taken to be 1, and the domain inventory set (A) is 4. The three properties defined by c, A and B are: length change/fixed length(L/L*), dictionary change/fixed dictionary (D/D*), ambiguous/unambiguous (A/U). Figures on the right indicate how the parameter space is partitioned according to 1) the relation of the inventory sizes; 2) the size of c; and 3) the relation of the two codon-space sizes, C_X and C_Y. Note that the point where $B = A$ and $c = 1$ indicates transcription, or (if the two inventory sets are identical) copying. In reality, the parameter space is not fully continuous, i.e. A and B have integer values, while ($0 < c \leq 0.5$ and $c \in$ Q) or ($c > 1$ and $c \in$ N).

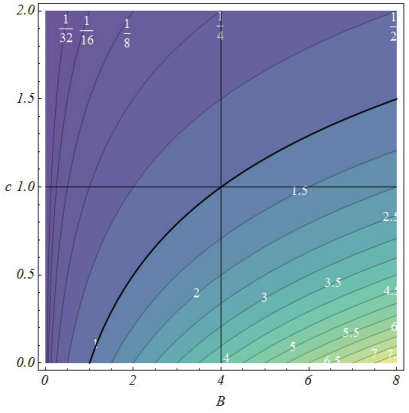


Figure 11. Codon space robustness (applied to Figure 10). Contours and color indicate the actual number of codons associated with one target codon of the codomain ($b_{B\to A}$). Horizontal line indicates the target codon length of the codomain ($d = 1$), vertical line indicates the domain inventory size ($A = 4$). A rational number $1/n$ means that n codons of the domain map to the same target codon of the codomain. Note that the plot assumes that each target codon has an equal number of codons mapping into them (this is not true for the genetic code though, where the average robustness is 21/64 (at $B = 21$ and $c = 3$).

2.5.8. COMPLEX TRANSMISSIONS

Complex transmissions are composed of successive elementary transmissions. The correlation of entities along transmissions defines an **informational topology**, representing the travel of information from one entity to others. Both Weismannian and Lamarckian inheritance (as specified here), and other putative inheritance methods realize an informational topology between components, and are thus complex information transmissions. Since inheritance is about maintaining information, complex transmissions are analyzed from the viewpoint of information loss. It must be noted here, that mutation is not part of any transmission (i.e. is not endogenous), but is understood as an *a posteriori* external noise applied to the result of transmission.

The loss of information in a reaction can only be determined, if one knows what the result should be (based on known input). For example, replication is lossy, if it cannot reproduce the original parent. Consequently, an elementary transmission cannot be deemed lossy or not. Even if the first transmission is ambiguous, a fitting second transmission may yield the original entity (thus the process effectively becomes replication), maintaining thus the expected amount of information (cf. Figure 12 D). In case of complex transmissions, information can only be maintained, if the original entity can potentially be reconstructed. If there is no way, that the original entity can be reconstructed, the overall transmission is lossy. Of course, there is information loss during a single translation (for example a serine molecule does not remember from which RNA codon it was translated), but this does not mean, that no information can be maintained in a replicative system.

Therefore, **only complex transmission pathways can be really lossy**. To analyze such complex transmissions, the simplest general representation is introduced here:

$$X \Rightarrow Y \Rightarrow Z \Rightarrow W.$$

In case of replication, we expect Z = X and W = Y, however, this is not necessary, as it will be proven in turn. Also, according to the *replicator equivalency criterion* defined earlier, the minimal conditions are Z ~ X and W ~ Y, where ~ stands for equivalency

A replication method is lossy, if during the process information is irreversibly lost, and cannot be maintained due to the (possibly more than one) mappings used. That is Y !~ Z and X !~ W, or more precisely: $t(Y) \neq t(Z)$ and $t(X) \neq t(W)$. If replication is lossy, it means that it cannot potentially maintain information for an indefinite time, and has therefore limited evolutionary potential.

Figure 12 describes the basic ways of complex information transformation. Assuming that the original entity X is always retained, the final product (X or W) is therefore generated in surplus (this is not depicted), according to specific transformational rules. Excluding mutations, the only source of change is the possible probabilistic nature of the mappings used in the various basic transformations (i.e. transcription, translation, reverse translation).

1. **Direct replication** (Figure 12 A). Entity X is a simple replicator with no division of labor, and no intermediate stage. Example is a (putative) prebiotic ribozyme, which is itself responsible for both conserving information and interfacing selection. Unfortunately, the most advanced artificially selected polymerase ribozyme at the moment is of ~200 nucleotides long and can only replicate sequences up to a length of 95, thus it cannot replicate itself (Wochner et al. 2011). Present examples include von Kiedrowski's self-replicating oligomers, though with limited heredity (von Kiedrowski 1986).

2. **Replication with exact intermediate** (Figure 12B). Both X and its intermediate Y can be maintained stably without loss of information. Therefore, both X and Y are replicators, and Y (facing selection *S*) is an interactor as well. Still, division of labor is not present, as changes applied to both X and Y are inherited, thus there is no dedicated entity for either keeping information intact and interfacing selection. Any informational autocatalytic chemical cycle with at least one intermediate belongs here, for example replication of RNA +/- strands (where the + strand generates a - strand, that generates a + strand, and so on). If either X or Y is omitted (as they do not convey extra information), the system falls back to direct replication (Figure 12 A).

3. **Weismannian replication** (Figure 12 C). X is the replicator, Y is the interactor. Information introduced to Y cannot be propagated to X, and Y alone is responsible directly for selection, thus a full division of labor is present. Example is the idealized gene-protein inheritance system.

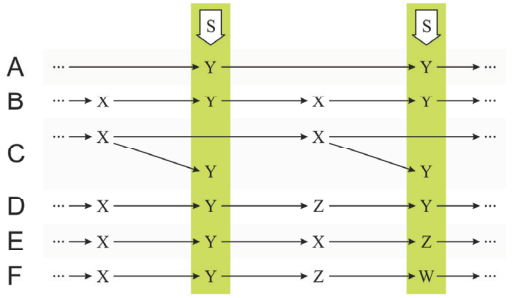


Figure 12. Complex ways of information transformation. Only the informational (or correlational) topology of inheritance is given, but not stoichiometry. Mutation is ignored, changes are only due to the nature of elementary transmissions (i.e. mappings). Selection always acts on the component under S. A) Direct replication, no intermediate component. B) Direct replication with intermediate. C) Weismannian replication. D) Probabilistic direct replication: Y can be transformed to different intermediates. Since there is no division of labour (Y is the information storage and the interactor) replication is Lamarckian. E) Replication depends on whether Z is transformed to X again or not. F) Non-replication: lossy complex transformation, where neither X, nor Y can be reconstructed. More details in text.

4. **Replication with variable intermediate (Lamarckian replication)** (Figure 12 D). Intermediate Y is not necessarily recreated by translation (but by ambiguous processes), therefore it seems, that it is not a replicator. However, since both Y and Z still code for the very same X, they are phenotypically equivalent, disregarding their real structure, therefore they *are* replicators. Thus the **only information that can be stably maintained is the information content of X, the intermediate under direct selection, but not Y, the variable intermediate** (contrary to Figure 12 B). Again, here is no clear division of labor, as there are two stages, but both of them can inherit changes. Nevertheless, only one stage is responsible for direct selection: Y. A hypothetic example would be the DNA → protein → DNA → … system, where a certain amino acid can be retranslated to various codons. It must be noted, that even if information is maintained, the evolution of such systems may differ from the dynamics of direct replication or Weismannian systems. Due to intermediate steps, the mutation rate can be higher than in case of direct copying systems, and the non-trivial neutrality kernel (Toussaint & von Seelen 2007) may change significantly, as Z differs from Y. This is investigated in section 3.1. One example is language learning: grammatical *rules* (set of constructions, Y (cf. Goldberg 2003) are used to create utterances (X), and therefore to externalize language *L*. In any case, the learner receives only the utterances, and has to acquire *L* either by inferring the original rules, or by creating a new set of rules: Z. Z would be a holistic representation of X, and therefore it differs from Y. In

this case, there seems to be no explicit replication of Y, however it must be emphasized, that both Y and Z (and respectively, the compositional and holistic rule sets) code for the same *L*. Therefore *L* does get replicated time to time. This mirrors the fact that mental concepts in human minds (like language, memories, color, etc.) can be encoded in completely different ways even if they are phenomenologically equivalent. Both the compositional and holistic rule sets are equivalent, if selection cannot discriminate about the external language representations. Of course, if evolution is involved, or there is a bottleneck on learning, the selection situation and the evolutionary potential of the various representations of *L* will differ heavily. Since language evolution and acquisition is a well-researched field, there are plenty of work about the effect of information loss during transformation (cf. Smith et al. 2003). In general, memes are assumed to exhibit this kind of informational transmission when replicating from parent to offspring, as it was recognized by Maynard Smith & Szathmáry 1999, p. 140.).

5. **Replication with ambiguous translation** (Figure 12 E). This type is not a distinct subtype of replication, as will be explained in turn. Since the transmission of Y is ambiguous, this type of replication can only be stable, if two conditions are matched. First, the phenotype of Y always has to be the same, that is $p(X) = p(Z)$. Secondly, it must be ensured, that W is translated back to Y. If conditions are met, this type falls back to Figure 12 B. If not, it is the lossy process of Figure 12 F. Presumably, evolution of such inheritance systems tends toward the more exact replication of Figure 12 B, i.e. toward unambiguous translation.

6. **Lossy process** (Figure 12 F). Since no X or Y can be maintained stably, this is not a stable replication method. Still if W and X are equivalent (i.e. share the same phenotype, but are not necessarily identical), the system can be replicative. There is, however, no guarantee, that in a next step, the new transcript (which probably will not be identical to the original one due to loss of information) will have the same phenotype. Note that if X and W are equivalent, that means that Y and Z are equivalent as well, as their phenotypes are realized in X and W.

Note, that in case of Figure 12 D the offspring is created by using the information of an intermediate stage. This is the primary inheritance method allocated to memes (Maynard Smith & Szathmáry 1999). In cultural evolution it is the intermediate external product (utterance, artifact), not the mental concept (idea, though) that gets copied (i.e. *copy product vs. copy recipe*, see Blackmore (1999), and Számadó & Zachar (2011a). Usually copying the product involves the necessary *inference* of the recipe underlying the product. In a formal way, it is always *copying the product* if there is at least one intermediary stage (the product) between parent and offspring entities, however, it does not necessary mean that inference, or guessing is involved. If

however the intermediate stage is not enough to reconstruct the primary stage, either inference must be used, or the process becomes lossy.

As a conclusion, I claim that there are **three distinct types of complex transmissions, which are replicative in nature: direct replication, Weismannian replication and Lamarckian replication**. It must be noted however, that as direct and Weismannian replicators signify the far ends of the continuum, Lamarckian replicator is anything in-between the two. Lamarckian replication is nevertheless different enough to be distinguished. It requires two linked entities, thus is different from direct replication (which does not require an intermediate), but similar to Weismannian inheritance. Though functions of information conservation and interfacing selection are not separated, thus it is similar to direct replication but different to Weismannian.

As a conclusion, it can be stated that both Weismannian and Lamarckian replications are defined only for informational replication, i.e. without any kind of modular template information (and transmission), there is no sense to refer to these specific inheritance methods.

2.5.9. INFERENCE (RECONSTRUCTION)

Inference is process, being part of a complex transmission where the parent entity X by default cannot be replicated without loss of information, only if an external source is used to infer parent information Figure 13. Via inference, X can be reconstructed better than random from Y, thus offspring X' approximates X better than random.

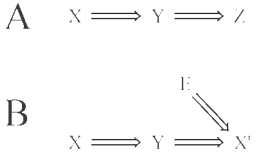


Figure 13. Inference. A) By default a generative process cannot reproduce X reliably as Y does not hold enough information (Z !~ X). B) Using an external source E to infer information about the parent, X can be reconstructed successfully.

Note that in this case, part of the recurring X is encoded in the external environment. If inference can fully reconstruct the original information, then the second transmissional process (Y ⇒ Z or now Y ⇒ X) must be unambiguous, i.e. is a *translation*.

Language acquisition and similar tasks are prime examples of replication with inference: external sources like textbooks are used heavily during learning processes. It is also generally accepted that during cultural replication, memes are reconstructed by learners instead of simply copied (cf. Kronfeldner 2007, Sperber 2000, p. 505.). It is true, that cultural replication differs from simple template copying, although it is not true to account reconstruction as a process that is completely different of other ways of transmissions. As a matter of fact, social learning is also

a way of transmitting information. Reconstruction simply means that the acceptor receives (i.e. copies) limited amount of information (like an external artifact) about the original mental concept, and using this limited amount he has to infer or guess the original concept. The information transformation is lossy translation, which implies that guessing (or external references) has to be used, i.e. the process by default is ambiguous. One particular solution to decrease the error rate of transmission in case of complex cultural items is to transmit a blueprint of the item instead of the item itself. This is *recipe copying* (Blackmore 1999), or instruction copying (Dawkins 1999), which in most cases is better than direct *product copying*. However, in certain situations, only the latter channel is available, which is still better than nothing (the issue is further discussed in Számadó & Zachar 2011b).

2.6. All aspects combined

Simple or cycle stoichiometry (by Gánti 1987) is not able to capture the informational aspect of replication. **There is a topology of information transmission underlying any reaction**, which cannot be represented directly by a stoichiometric equation. Extending this concept, one can realize, that there can be multiple different topologies underlying a particular reaction network. The information may originate from completely different parents than those providing the building material or those facilitating assembly. Though it seems obvious to track information in case of replicators, nevertheless any genealogical link between parent and offspring replicators must specify which aspect(s) it focuses on.

For example, during RNA transcription at least three components are involved: the DNA template, the synthetized RNA chain and the RNA polymerase, however information only travels from DNA to RNA, and not from the polymerase to RNA. The selectional aspect works similarly: proteins provide the phenotype function for genes, therefore selection acts directly on proteins, but not on genes. The polymerase hardly conveys any novel information to the RNA: it just makes the favored reactions (the elongation of the polynucleotide chain) happen with a much higher probability.

As a conclusion, material and informational topology (i.e. the traversal of matter and information between entities and reaction steps) could be different, see Figure 14. It is possible that the replicator only provides material, but there is no informational template: rules of chemistry ensure that the reactions of the formose cycle yield the same result if the same initial conditions are provided. On the other hand it is also possible that no material is provided by the replicator at all (Figure 14 C): Sperber's linked audio recorders (Sperber 2000, also at Aunger

2002, p. 78.), Penrose's block models (Penrose & Penrose 1957), memes, computer viruses, and also prions work like this. The only thing that is replicated is the configuration of matter, but no matter is provided by the parent entity at all. About the material aspect see the discussion of Zachar & Szathmáry (2010) on Griesemer's material-based classification (Griesemer 2000a).

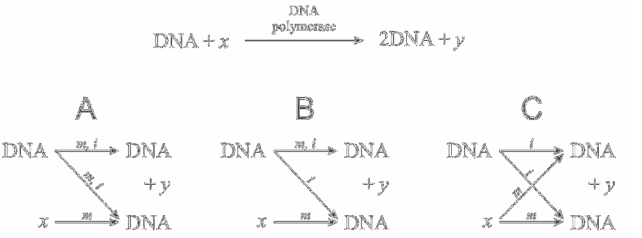


Figure 14. The informational and material aspect of replication. The simplified stoichiometric equation at the top (with *x* and *y* as input and waste materials) can be resolved in various ways, according to the flow of matter (*m*) and information (*i*). A) DNA in reality replicates in a semiconservative way; B) theoretically DNA can be conservative by only providing matter for one of the offspring, or C) DNA may provide only template information, but no matter.

Concerning the material and informational aspects, one can come to the conclusion, that non-informational replication is about the replication of material entities, while copying of template molecules is about replication of properties: patterns of information (cf. Nánay 2009). This is true in the sense, that property copying can happen without the explicit generation of new entities, that is if a set of these entities is already given. A fitting example is prion propagation, where conformation can only be replicated if there is a population of prion proteins, generated by standard gene expression.

Prions are interesting in the sense that they may be able to replicate in various ways. Besides the simple non-informational conformation switch, recent findings indicate a possible informational way as well. The specifically arranged β-sheets inside the amyloid structure of the prion protein expose the main polypeptide chain, which can act as a template, inheriting possibly acquired changes. This template is assumed to be responsible for the transmission of conformation, i.e. the specific structure of the amyloid (Wickner et al. 2007). It was also found that new variants appeared *de novo* during replication in the prion population (instead of being there in an initially heterogeneous population), indicating that there can be mutations in prion conformation as well (Li et al. 2009). These conformations are heritable for some extent according to Li, which renders prions to be limited heredity replicators.

2.6.1. INFORMATIONAL REPLICATION

Informational replication *sensu* Orgel (1992) is a special case of **replication**, where $Y = d(\boldsymbol{T}(t(X)))$. Function t specifies the template of X, $\boldsymbol{T}$ is a translation process, therefore Y is the translation of X, and X is the template of Y. Basically informational replication is replication with transmission.

Note that informational replication need not be based on copying, as it is not necessary that X and Y are identical. They only have to be equivalent under the given selective force. A perfect example is the hypothetic reverse-translational inheritance (see Figure 16 B for topology, and section 3.1 for performance of Lamarckian inheritance): no single transmission is copying, though the outcome of the successive steps is as if there is copying going on. Another example is the limited inheritance of the GARD model (Segré et al. 1998): there is correlation between parent and offspring, though exact similarity cannot be maintained (hence the limited inheritance attribute).

An informational replicator is a unit of evolution, according to (earliest) Maynard Smith 1987). Since informational replicators are subjects to evolution compared to non-informational ones (with at most limited evolutionary potential), prior works on replication were mostly targeted on them. The notion of informational replication can be paralleled with the notion of *self-reproduction* of von Neumann (1966). Solé gives a basic correspondence between the logic components of self-replication and the machinery and template of the living cell (Solé 2009 p. 275), which can be further generalized in the way it was done so far in this work.

If the transformation process is informational, and information transmission from parent to offspring is deterministic, the maintenance of information in the population is *storage-based* according to Hogeweg (1998) and Szathmáry (2000). It means that the trajectory of the population only depends on the parents. If transformation is probabilistic, then the outcome of replication can be probabilistic (but not necessarily, see section 3.1). In this case, the actual nature of the offspring depends not just on the properties of the parents but on environmental factors as well, controlling the probabilistic inclusion of modules. Any system relying on ambiguous (probabilistic) replication is therefore at least partially *attractor-based* (Hogeweg 1998, Szathmáry 2000). See Table 3 for a classification. Attractor-based systems might utilize exact replication methods, but the outcome of successive replication-selection depends on the dynamic setup of the system (for example on a probabilistic code-table) and not on the information encoded in entities. Thus, identity of parent and offspring is preserved by the dynamical stability (basin of attraction) rather than the informational stability of replicators.

Attractor-based systems not necessarily require informational molecules. Storage-based replication on the other hand requires the existence of a template with a fixed spatial or temporal ordering: this will be discussed in the next section (2.6.3 Order of inclusion). In a storage-based system, practically all possible states are equally stable, and starting from whatever initial setup, the system can stably maintain it (granted that mutation rates are low enough).

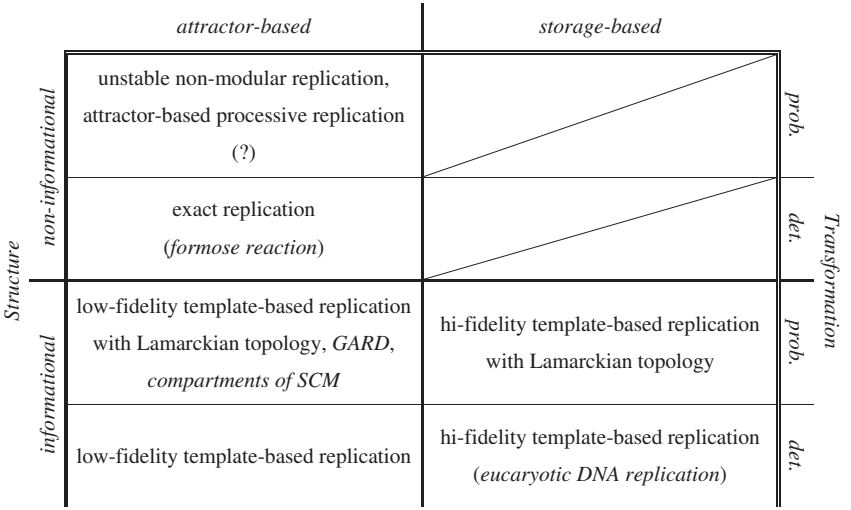
For example, the GARD model is attractor based, as both growth and splitting of composomes are stochastic, which cannot guarantee the reproduction of the original composome. Furthermore, as it was discovered by Vasas et al. 2010), the catalytic matrix is by default compartmentalized (i.e. it inherently defines groups of mutual components) which is responsible for the seemingly stable short-time inheritance of compositions. Genomes of the vesicles in the stochastic corrector model are also compositional and attractor-based (cf. Szathmáry 2006, p. 1764). Another example is DNA replication with high mutation rate. If copying fidelity is below the error threshold, no information at all can be maintained selectively in the population, just the distribution of Hamming-neighbours, the *quasispecies*, which is an attractor. Thus the outcome of replication is not defined by sequence composition but by the magnitude of mutation rate.

Practically, a replication method can be probabilistic in two ways. Either there is an externally induced error over the information-transmission channel of replication (as in case of polynucleotide replication), or the replication channel is inherently loosing information, for example because of a probabilistic code table. Both can be anticipated, and countered. External mutation rate is reduced by the eukaryotic cell using DNA error correction methods. Internal probabilistic transformation can be countered by an appropriate inverse transformation, as it will be discussed in 3.1 Replication fidelity of informational .

To conclude, it is claimed, that **probabilistic transmission can yield attractor-based dynamics**, and, furthermore, **there is a continuous space of possible replicator systems between storage-based and attractor-based systems**. This seems to be supported by the nanotechnologist Chris Phoenix, who claims that offspring might have different attractor-configurations than parents, and if the attractor space is sufficiently large with several attractor-configurations, unlimited heredity is possible (in Freitas & Merkle 2004, p. 149.).

Table 3. Classification of replicational systems based on structural, maintenance and transformation attributes. SCM stands for the stochastic corrector model of Szathmáry & Demeter 1987). The Lamarckian topology is discussed in section 3.1. Here I refer to the above statement (on page 48) that successive probabilistic transformations can yield deterministic replication. Note, that storage based inheritance is not possible in case of non-informational replicators.

Maintenance of information



In summary, **an informational replicator is a replicator that is capable of producing new entities that are either equivalent or correlated (either positively or negatively) with the parent in the given environment**. Conversely, a non-informational replicator is one which can produce equivalent entities, but for which correlation (similarity distance) cannot be defined, thus it cannot produce offspring that has fitness correlated with the parental fitness (Fernando et al. 2011).

2.6.2. UNITS OF EVOLUTION

An **informational replicator** is a unit of evolution, if there potentially exists a population *P* of entities, and if the replicator can stably maintain its information complexity for an indefinite time.

2.6.3. ORDER OF INCLUSION

Informational replicators rely on some sort of template to convey information (and accidental changes) to the offspring. Information can be encoded by the *quantity*, *proportion* or *arrangement* of signal modules as Gánti has specified it (Gánti 1987, p. 116., Griesemer & Szathmáry 2009, p. 482.).

If the spatial arrangement of components encodes the information, replication is template replication, and is deterministic in the sense that the template (ideally) fully determines the information content of the offspring. Attractor-based systems, however, not necessarily use a fixed spatial structure, therefore spatial order may not matter (cf. genetic membranes and lipid vesicles, especially the GARD model). At the same time, temporal order of modules may matter. Consider reflexively autocatalytic cycles and networks, where previous inclusions may facilitate the inclusion of specific modules in the future. This is obviously not present in DNA replication: just compare the polymerization of the leading and lagging strands. One can draw the general conclusion: during replication if spatial order of modules matters, temporal order is not necessary. Conversely, if temporal order is forced, spatial order does not matter (cf. Table 4). Accordingly, fuzzy inheritance systems with neither spatial nor temporal order, or rigid systems with both orders are unknown. It is even questionable whether they are theoretically possible at all. Since information is the order of bits, it seems plausible that no completely fuzzy informational replicator can exist. Whether spatially and temporally restricted informational replicators exist is unknown. Surely, they must be very strict and exactly replicating systems.

Temporal order \ *Spatial order*	no	yes
no	*fuzzy systems*? (possibly no)	*ribozymes*, *DNA*
yes	*GARD*	*rigid systems*? (redundant)

Table 4. Order of module inclusion. Classification of informational replicator systems based on spatial and temporal order of incorporation of different modules. Completely fuzzy (no spatial or temporal order) or completely rigid systems are not known.

As it was stated, temporal and spatial order are defined only for modular, informational replicators. The particular ordering defines in what order components are incorporated into the new replica during a replicational process. Thus it provides a physical or abstract template, defining the composition of the offspring to be similar (correlated) to the parent.

Spatial ordering refers to the situation where inclusion of components does not depend on the presence/absence of previously included components, but only on a spatially fixed structure, the *physical template*, just like DNA or ribozyme replication. This means that the replica theoretically can be built up in any order, and temporarily skipping a position should not disturb

the process in any form. This is true for DNA replication, as the lagging strand is composed in a different order than the leading strand, indicating that results can be identical independent of the temporal order of the inclusion of nucleotides. Spatial ordering means that successive replication of the same sequence might happen in different temporal order, still yielding the very same result.

Contrarily, temporally ordered replicators do not require a physical template. Components are incorporated in a given order *because* previously incorporated components define the domain of components that can be included later. **Temporal ordering can act as an abstract template** that is not coded in a physical structure but in the pairwise affinity of components.

The ordering in the GARD model is defined by a catalytic matrix M, where $M_{i,j}$ specifies the catalytic effect of component i on the inclusion of component j (after Segré et al. 2000). Temporal ordering means that for example component j can only be included *after* component i has been already included. The $M_{i,j}$ can mean inhibition if negative. Diagonal elements define autocatalytic, while offdiagonals define heterocatalytic effects.

If the M matrix has only the first off-diagonal filled with positive values, and every other cell is zero, it defines a sequential incorporation of components, which deterministically gives the same result every time the initial seed is provided. Therefore, a highly "contrasted" catalytic matrix can force a deterministic inclusion, and consequently, **a temporally ordered replicator without an explicit template can mimic a storage-based template replicator**. A replicator that could self-replicate according to multiple temporal orders could be faster and less prone to break down due to lack of certain resources in the environment, though there may be a specificity issue. Temporal ordering also provides a "recipe" to which the system can stick to. This abstract recipe increases copying fidelity from time to time, without explicitly requiring a template. By this way, a reproducing system can be an informational replicator even without explicit copying used during replication!

As a consequence, informational replication can be classified by two aspects: whether information is coded in a physical storage (the template), or other types of dynamic attractors are provided, and whether inclusion of new modules are done according to spatial or temporal order.

Table 5. Classification of inheritance systems according to structure and type of transmission.

Maintenance	*Structure*		
	holistic (*non-informational replicators*)	compositional (*informational replicators*)	
		spatially ordered	temporally ordered
attractor-based	unstable non-modular replication (*cycles depending on environmental factors*)	physycal template coupled with stochastic dynamics (*Paulien Hogeweg's replicator networks*)	affinity-based stochastic informational replication (*GARD*)
storage-based		physical template-based replication (*DNA*, *RNA*)	autocatalytic cycles storing information in the order of intermediates? (*?*)

Note however, that even if the matrix defines a linear inclusion order, it does not guarantee that the outcome of replication will be identical to the source, as splitting might cause the offspring to lack any component that catalyses the inclusion of other necessary components. Therefore, to have deterministic replication, both inclusion and separation has to be deterministic OR the composition of the successive steps has to be deterministic (just like in case of Lamarckian replication, in section 3.1).

2.6.4. GENOTYPE

The genotype is a **function** *g* of an entity X, defining the parts that can potentially pass on changes (acquired during lifetime of entity, incorporated into the said part) to offspring Y during replication.

In any informational replication, the *genotype in the narrow sense* (GN) is the template *t*(X), the *genotype in the broad sense* (GB) is X. Note that the genotype is specific for (informational) replication, while the template is a more general term referring to any kind of (informational) transmission.

2.6.5. DIRECT REPLICATION

A special case of informational **replication** without interactor, where X' = T_1(X) with T_1 being copying and the phenotype of replicator X is represented directly as p(X). The direct informational topology is depicted in Figure 15 A. Examples systems are basically any autocatalytic entity that replicates without the intervention/help of an interactor. The theory of RNA world hypothesizes the early existence of self-replicating ribozymes, which could replicate each other (or even themselves) without the help of enzymes, or encapsulating vehicles. Prions replicate directly, with no intermediate stages and no distinct interactors.

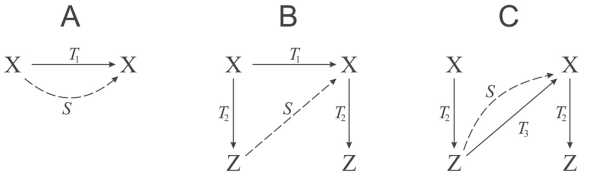


Figure 15. Topologies of inheritance systems. A: Direct replication; B: Weismannian inheritance; C: Lamarckian inheritance. The replicator is X, its interactor is Z. Normal arrows indicate causality along transformations, dashed arrows indicate the indirect effect of sorting S on the distribution of the next-generation of replicators. T_1 is copying, T_2 is translation, T_3 is reverse translation. With more entities introduced, topologies that are more complex can be devised.

2.6.6. LAMARCKIAN REPLICATION

A special case of informational **replication** with interactor, where X' = $T_3(T_2(X))$ with T_3 being ambiguous. The phenotype of replicator X is represented directly by another entity, Z = T_2(X), thus $p(X) = p'(Z)$. Informally, Lamarckian replication is an inheritance system involving an interactor, that is a translation of the replicator, morover, the new replicator inherits information from the interactor. The Lamarckian informational topology is depicted in Figure 15 C. Examples abound in culture: songs, words, grammatical rules, elements of language and other cultural items.

Note that the composition $T_3 \circ T_2$ need not be ambiguous or lossy. If it can stably maintain information, Lamarckian replication approximates direct replication. What makes Lamarckian replication different of direct informational replication is the presence of an intermediate entity, which is under direct selection (thus is an interactor). Variations introduced to the interactor are inherited. The overall amount of information maintained in the system is solely defined by Z,

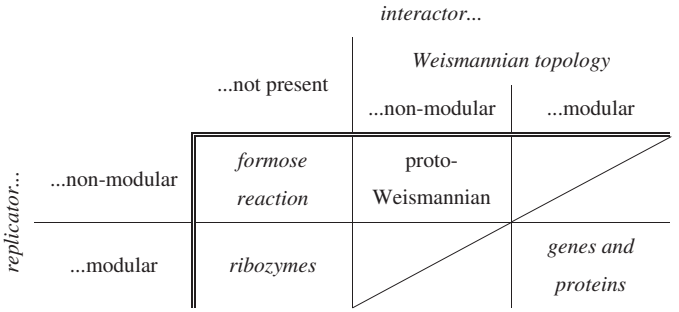
thus it is a replicator as well. Thus, Lamarckian replication is a direct replication process with variable intermediates. Lamarckian inheritance is discussed further Discussion.

2.6.7. WEISMANNIAN REPLICATION

A special case of informational **replication** with interactor, where the phenotype of replicator X is represented directly by another entity, $Z = T_2(X)$, thus $p(X) = p'(Z)$, and T_2 is an unambiguous transmission process. Informally, Weismannian replication is an inheritance system involving an interactor, that is a translation of the replicator. The Weismannian informational topology is depicted in Figure 15 B. The well-known example is the gene-protein system, where both genes and proteins are modular, and thus replication is informational. Though it must be noted, that DNA replication itself is direct. The Weismannian topology is revealed only if genes are enclosed in vehicles, like cells.

For informational replicators, it can be allowed that phenotypes may not be identical, but are correlated, to open up the gate for adaptive evolution via mutations. In addition, this may involve the change of *T* through successive iterations. As it was established under 2.4.1 Replication, *T* must be able to maintain phenotypic correlation and further transmission.

Table 6. Inheritance systems depending on replicator and interactor modularity. Due to the definition of transmission and modularity, the interactor cannot be modular if the replicator is non-modular and vice versa. Proto-Weismannian systems, where both the replicator and the interactor are holistic are not known, although are theoretically possible (see Table 7).



Weismannian replication is only defined if replication is informational and the interactor is present. Does it mean that *non-informational Weismannian replication* is not possible, even theoretically? No, but since Weismannian inheritance is about *heredity*, it seems logical, that a non-hereditary entity cannot be Weismannian. Still, there can be non-hereditary replication

systems with interactors, but these should not be called Weismannian (cf. Table 6). Theoretically, if DNA were not possible to inherit changes (not even potentially), it would be a non-hereditary replicator/interactor system, where both DNA and proteins are modular, though without inheritance, genes would be non-informational replicators.

Note that usually the media of the replicator X and its copy Y is the same ($\mathbf{M}_X = \mathbf{M}_Y$), and T_1 is a bijective mapping (transcription, or more likely copying, that is why Y is represented as X in Figure 15), but this is not necessary. Theoretically, the new replicator can be a product of translation as well, until the two conditions are met: first, phenotypes are the same ($p(X) = p(Y)$), and second, Y must be able to produce X ($X \Rightarrow Y \Rightarrow X$).

One important consequence of the Weismannian topology is *division of labor*. A Weismannian inheritance systems separates the two functions (conserving information and interacting with the environment) and distributes roles to two entities, X and Y. Prebiotic evolution, as we think, happened along the following steps: an initial holistic autocatalytic system gained modularity, became informational, and later recruited proteins to be the vehicles/interactors for them ($1 \rightarrow 3 \rightarrow 4$ in Table 7).

Table 7. Evolution of the Weismannian inheritance system. SACI = simple autocatalytic cycle intermediate.

	without interactor	*with interactor*
non-informational replication	1. simple non-informational replication (*formose cycle, SACIs*)	2. proto-Weismannian replication (*?*)
informational replication	3. Direct informational replication (*ribozymes, Eigen's biosequences, prions*)	4. Weismannian replication (*genes and proteins*)

toward a dedicated information-carrier ↓

toward a dedicated interface →

However, there could have been an alternate way: the holistic system first co-opted proteins, retaining a holistic replicator → interactor transformation, and later became modular ($1 \rightarrow 2 \rightarrow 4$). Although transitions $1 \rightarrow 3$ (origin of RNA world) and $2 \rightarrow 4$ (hypothetic) are analogous, going from $1 \rightarrow 2$ (hypothetic) and $3 \rightarrow 4$ (origin of translation) are not, and this difference could be the cause of the course real evolution took. Even if there is no theoretical

objection against the proto-Weismannian stage 2, if transition $1 \rightarrow 2$ is not possible, such systems could not exist in reality. Why would it worth to have a dedicated interactor, if there is no real information to inherit? There may be an answer, although at present we cannot imagine a selective scenario that results a proto-Weismannian system. Moreover, from a proto-Weismannian system to traverse to a real Weismannian system both the replicator and the interactor should become informational simultaneously, which is less parsimonious than expecting the successive steps of first becoming informational ($1 \rightarrow 3$) and then evolving/recruiting the interactor ($3 \rightarrow 4$). The last part of the latter scenario is tested with stochastic experiments in section 3.2 Evolution of division of labor.

2.6.8. VEHICLE

The vehicle is an **entity**, a unit of sorting/selection acting as the interactor of a set of replicators physically encapsulated in the vehicle. The vehicle as a compartment *defines a new level of selection* different from the one acting directly on the replicators (or their more direct interactors) inside it. The link between the vehicle and the replicator is tight: if the vehicle disassembles/dies, so does the replicator inside it.

The creation of the vehicle V using the information of replicators is development (*d*):

$$\{X_1, X_2, ...\} \Rightarrow V,$$
$$\{X_1, X_2, ...\} \xrightarrow{t} t(X_1, X_2, ...) \xrightarrow{T} t'(V) \xrightarrow{d} V,$$

where $\{X_1, X_2, ...\}$ are enclosed replicators, the template information for vehicle V is $t(X_1, X_2, ...)$ and the inverse function of t is the development function of the vehicle.

This definition of the vehicle originates from Dawkins (1982a), and from the concept of reproducer at Griesemer (2000b). Accordingly, new vehicles come to being by reproduction (i.e. a specific way of replication), and they can develop by growth. The general example for the vehicle is the soma (contrasting the germline). Compartments are also vehicles, like in case of the stochastic corrector model (Szathmáry & Demeter 1987), or the compartmentalized hypercycle (Zintzaras et al. 2002), although neither of these compartments are built using the information encoded in the replicators inside. They nevertheless act as interactors, since their functions (e.g. reproduction rate, segregation bias) are defined by the replicators inside them. Note that this is not true for most of the models of the chemoton, including the one presented here (section 1.1), as the survival/reproduction of the chemoton usually does not depend on the template(s) inside.

3. Experiments

3.1. Replication fidelity of informational replicators

This section presents a model of Lamarckian replication, which can be analyzed to estimate the overall copying fidelity of Lamarckian replicators, to test against Weismannian replicators' copying fidelity. A simple replication-selectional model is used to check mathematical results against stochastic simulations.

3.1.1. MODEL

For sake of clarity, the two stages of a replicator are denoted A and B. To get a grip on the stages, it can be thought of as A stands for the DNA sequence and B for the protein (as it happens to be the case for standard genetic inheritance). Figure 16 shows the simplest informational topologies of such systems, based on Figure 15.

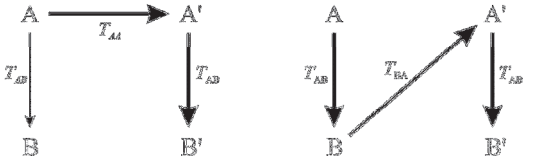


Figure 16. Informational topology. Left: Weismannian inheritance; right: Lamarckian inheritance. Heavy arrows indicate the route information travels during replication and generation. Elementary transmissions are denoted as arrows with *T*. Transmissions are subjects to noise (mutation), which is not shown in the figure.

Clearly, the two inheritance methods differ in topology, but the consequences of this difference is not trivial. Depending on the nature of the individual transmission steps, Lamarckian inheritance can approximate Weismannian inheritance. In the followings, I will compare the two inheritance systems in detail.

Instead of focusing on the actual per-digit copying fidelity in replication of Weismannian and Lamarckian replicators, one must realize that (according to the statement made on page 48) it is the B stage, the stage under selection, that is important, and should be tracked during replication. Now the B stage might consists of less digits than the A stage, due to the compressing nature of translations. This renders calculations needlessly cumbersome. However, both A and B consist

of the same number of codons. Accordingly, we must deal with the copying fidelity of *codons* instead of single *digits*.

For analysis, a simple inheritance system is chosen with the following characteristics:

Table 8. Simple parameter set for investigating replication fidelity.

		A	**B**
sequence length	n	30	10
inventory size	a	2	2
transmission method		uniformly ordered	uniformly ordered
sequence space size	σ	2^{30}	2^{10}
codon length	c	3	1
codon space size	s	8	2
codon space	S	{000, 001, 010, 011, 100, 101, 110, 111}	{0, 1}
codon branch	b	4	¼
transmission map		000 → 0 001 → 0 010 → 0 011 → 0 100 → 1 101 → 1 110 → 1 111 → 1	0 → { 000, 001, 010, 011 1 → { 100, 101, 110, 111

Note that if sequence length, inventory size and transmission method is defined, any other property can be calculated easily. A uniformly ordered transmission map means that the ordered set of source codons maps to the ordered set of target codons with uniform probability, evenly distributing target codons with source codons in successive order. It can be replaced by perhaps more realistic transmission maps, see Table 9. Uniform random transmission still distributes target codons among source codons evenly, though not in successive order. Random transmission does not force an even distribution.

Table 9. Different methods to generate the transmission map.

uniform ordered	*uniform random*	*random*
000 → 0	000 → 0	000 → 1
001 → 0	001 → 1	001 → 0
010 → 0	010 → 1	010 → 1
011 → 0	011 → 0	011 → 1
100 → 1	100 → 0	100 → 0
101 → 1	101 → 1	101 → 1
110 → 1	110 → 0	110 → 1
111 → 1	111 → 1	111 → 1

The probabilistic nature of a possible reverse translation is clearly visible as the transmission map of the B stage maps the same B codon (0 or 1) into multiple A codons, in any of the cases in Table 9. Simple probabilistic choice is used to resolve reverse translation: one of the possible target codons is chosen randomly, each with equal probability.

As Lamarckian inheritance has the B sequence as the stable stage during successive replication events, it is necessary to compare the overall replication probability of the B-sequences to the same B-sequence replication probability of Weismannian replication. Furthermore, sequence replication fidelity depends on the codon replication probability and the number of codons in a sequence. Therefore it is sensible to simplify the case to measure codon replication fidelity on the first hand. Using the model, I intend to answer the question: *What is the probability P_r that replicating an A codon yields the same B codon, as is the original B codon of the original A sequence?*

To understand difference between the two topologies, each informational route is broken down to elementary transmissions, where mutation always acts on the *result* of a transmission, as is depicted in Figure 17.

To calculate the probability value, certain matrices have to be introduced. Let the translation matrix T_{ij} be a matrix of size $s_i \times s_j$ of which the element $T_{ij(pq)}$ gives the probability of translating the p^{th} codon of the codon space of i to the q^{th} codon of the codon space of j. For translation, this matrix has 1 and 0 as its elements, while for retranslation 0 and $1/b$, where b is the codon branch value, and is always chosen as the larger from the two codon branch values b_i and b_j, thus $b \geq 1$ and $b \in \mathbf{N}$. For irregularly distributed translations, b is defined as the sum of appropriate columns of T_{ij}. By the definition of copying (on page 44), T_{ii} is the identity matrix of size s_i.

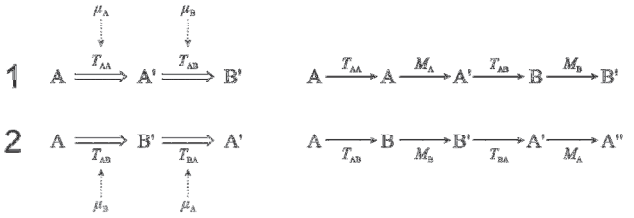


Figure 17. Detailed informational topologies, generating the B stage. 1) Weismannian inheritance. 2) Lamarckian inheritance. T_{ij} denotes translation from stage i to stage j (note that copying can be defined as T_{AA}), μ_i denotes per-digit mutation rate applied to stage i. On the left is the linearized version of Figure 16, on the right is the explicit application of translational and mutational mappings, where M_i denotes the mutational probability matrix of the codon space of i.

The codon mutation matrix M_i is a square matrix of size $s_i \times s_i$ of which the element $M_{i(pq)}$ defines the probability that the p^{th} codon of the codon space of i is mutated to the q^{th} codon of the same space, assuming a per-digit mutation rate of μ_i. More precisely, the probability of mutating sequence (or codon) p to sequence (or codon) q is:

$$M_{i(pq)} = \begin{cases} 1 & \mu = 0 \wedge k = 0 \\ \left(\frac{\mu}{a-1}\right)^k & \mu = 1 \wedge k = n, \\ (1-\mu)^n \left(\frac{\mu}{a-1}\right)^k - k & \text{True} \end{cases} \qquad (2)$$

where alphabet size a, length n and mutation rate μ are specific for the given stage, and k is the Hamming distance of sequences p and q. For the codon mutation matrix M_i, n is given as c_i, the codon length of stage i. Examples of T and M matrices (for the parameter configuration of Table 8) are shown in Table 10.

Table 10. Transmission and mutation matrices.

T_{AB}

	0	1
000	1	0
001	1	0
010	1	0
011	1	0
100	0	1
101	0	1
110	0	1
111	0	1

T_{BA}

	000	001	010	011	100	101	110	111
0	$\frac{1}{4}$	$\frac{1}{4}$	$\frac{1}{4}$	$\frac{1}{4}$	0	0	0	0
1	0	0	0	0	$\frac{1}{4}$	$\frac{1}{4}$	$\frac{1}{4}$	$\frac{1}{4}$

M_A

	000	001	010	011	100	101	110	111
000	$(1-\mu_A)^3$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)\mu_A^2$	μ_A^3
001	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^3$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^2\mu_A$	μ_A^3	$(1-\mu_A)\mu_A^2$
010	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^3$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^2\mu_A$	μ_A^3	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)\mu_A^2$
011	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^3$	μ_A^3	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)\mu_A^2$
100	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^2\mu_A$	μ_A^3	$(1-\mu_A)^3$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^2\mu_A$
101	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^2\mu_A$	μ_A^3	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^3$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^2\mu_A$
110	$(1-\mu_A)\mu_A^2$	μ_A^3	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^3$	$(1-\mu_A)^2\mu_A$
111	μ_A^3	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)\mu_A^2$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^2\mu_A$	$(1-\mu_A)^3$

M_B

	0	1
0	$1-\mu_B$	μ_B
1	μ_B	$1-\mu_B$

First, formalize P_r for the Weismannian topology. Let P_W be the probability that an A codon is replicated such, that it returns the same B codon the original was coding for. First, let us define

the probability that the i^{th} codon of stage A (A_i) is copied, mutated, translated, and again mutated to yield the j^{th} codon of stage B (B_j):

$$\omega_{ij} = P(m_B(t_{AB}(m_A(t_{AA}(A_i)))) = B_j). \tag{3}$$

Since t_{AA} is the identity function, it can be ignored (but not its mutation, m_A). Since ω_{ij} has to be defined for all codons $i \in s_A$ and $j \in s_B$, it is convenient to return the matrix form of ω (being of $s_A \times s_B$ size):

$$\omega = (M_A.T_{AB}).M_{B.} \tag{4}$$

From this, the overall probability of fidelity, P_W, can be calculated by multiplying ω with T_{AB} (this factors out the impossible translations), and averaging the result. P_W gives the average probability that an A codon is replicated to yield an isomorphic A' codon, both encoding the same B codon:

$$P_W = \frac{\sum_j^{s_B}\left(\sum_i^{s_A} T_{AB\,i\,j}\,\omega_{i\,j}\right)}{s_A}. \tag{5}$$

Similarly to ω_{ij}, we define λ_{ij} as the probability that A_i is translated, mutated, retranslated, and again mutated to yield B_j in case of the Lamarckian topology:

$$\lambda_{ij} = P(m_A(t_{BA}(m_B(t_{AB}(A_i)))) = B_j). \tag{6}$$

Note that here no translation can be ignored, and also the application order of mutation functions m_A and m_B is reversed, according to Figure 16 and Figure 17. The result is:

$$\lambda_{ij} = M_{Aij}\sum_k^{s_B} T_{BAki}\sum_l^{s_B} M_{Blk}\,T_{ABjl}, \tag{7}$$

from which the overall probability is:

$$P_L^* = \frac{\sum_i^{s_A}\sum_j^{s_A} M_{Aij}\sum_k^{s_B} T_{BAki}\sum_l^{s_B} M_{Blk}\,T_{ABjl}}{s_A}. \tag{8}$$

Now P^*_L gives the probability of exactly replicating A_i. However, since we are interested in the B stage, consequently the question should be: *what is the probability that the outcome of replication is* ***isomorphic*** *to the source, that is it stays in the same neutral subspace where the parent codon was*? Simply put: what is the probability that A_j translates to the same thing A_i translates to (ignoring mutation)? The answer is simple:

$$P_L = P_L^* \cdot b_A, \tag{9}$$

where b_A is the average number of A codons assigned to a B codon (codon branch).

Codon robustness (defined by the codon branch b_A) naturally translates to sequence robustness: β_b is the number of sequences allocated to the same target sequence in regard of the given transmission. It can be calculated easily as:

$$b_A = s_A/s_B \tag{10}$$

$$\beta_A = b_A{}^m, \quad m = n_A/c_A = n_B/c_B, \tag{11}$$

where m is the codon number (that is identical for both A and B sequences, in any deterministic model).

3.1.2. RESULTS

Probabilities were tested against iterations of sequences undergoing translation and mutation, according to the following setup:

- for Weismannian codons: iterating over the range (0, 1) for μ_A and μ_B, for each $\{\mu_A, \mu_B\}$ value pair 1000 random A-codons were chosen, and for each codon it was tested, whether the test is true:

$$t_{AB}(A) == m_B(t_{AB}(m_A(A))). \tag{12}$$

- for Lamarckian codons: iterating over the range (0, 1) for μ_A and μ_B, for each $\{\mu_A, \mu_B\}$ value pair 1000 random A-codons were chosen, and for each codon it was tested, whether the test is true:

$$t_{AB}(A) == m_A(t_{BA}(m_B(t_{AB}(A)))). \tag{13}$$

An example of the agreement between calculated and measured probability data is illustrated in Figure 18.

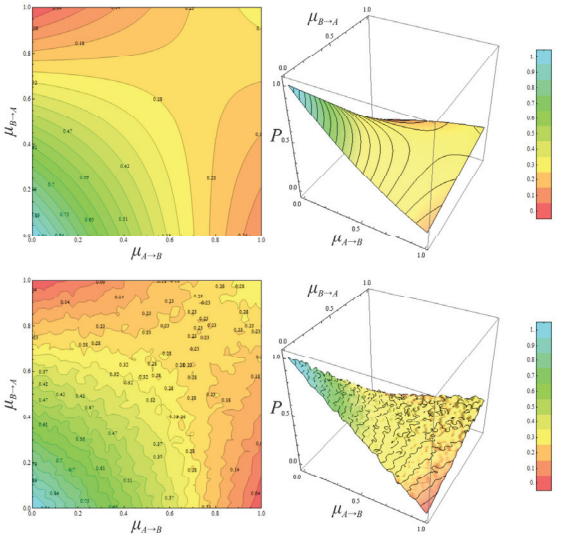


Figure 18. Replication probability comparison. Top row: calculated P_L using eq. 9; bottom row: measured P_L, average codon replication probability for Lamarckian inheritance, depending on the per-digit mutation rates of translation and retranslation ($\mu_{A\to B}$ and $\mu_{B\to A}$ respectively). Left and right plots show the same surface. For each value of $\mu_{A\to B}$ and $\mu_{B\to A}$, 1000 random iterations were done to measure the probability (for bottom row).

For no mutation, one can observe what is naively expected: inheritance is exact, and perfect. With mutation, results show that for almost all cases Weismannian and Lamarckian probability surfaces have a near perfect agreement (Figure 19). For random transmissions the difference becomes slightly pronounced, but still is negligible. The identity of probability surfaces breaks down the moment the second translation (B → A) is not the inverse of the forward translation (A → B), in case of Lamarckian inheritance (Figure 20). This means that the two successive transmissions do not complement each other to form an information-maintaining process: replication is inherently lossy, independent of the mutation rates. In such cases, the probability value of the Lamarckian replicator (for every parameter combination) is far below 1. This shows that inherently information-loosing transmissions cannot perform exact copying (stably for all sequences) **even if there is no exogenous mutation rate** on the transmission channel. Therefore, the two sources for information loss, external error rate (*mutation*) and internal *transmissional degradation* must be distinguished!

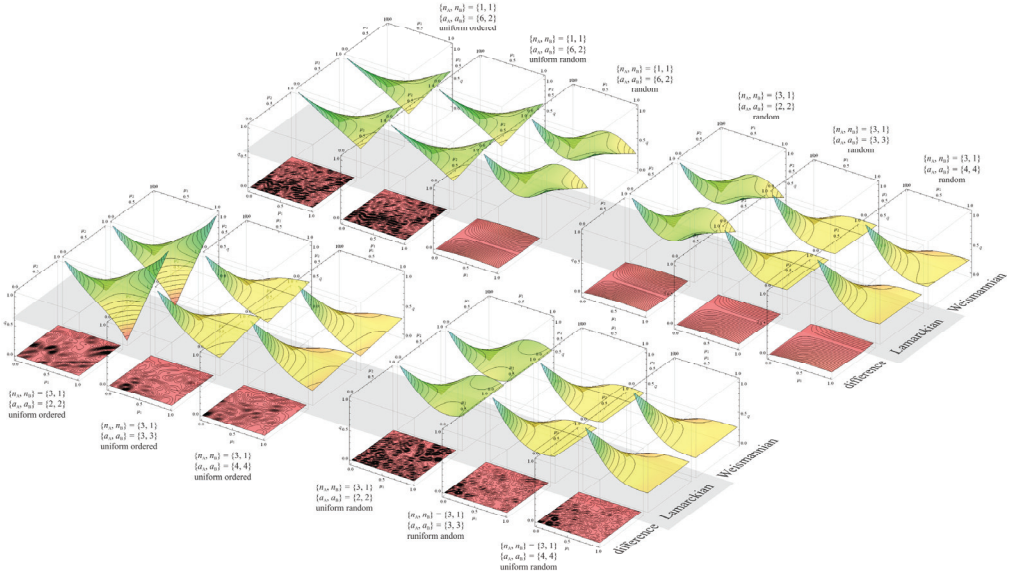


Figure 19. Average codon replication probability. Each column is a specific parameter set, containing three plots (for the three rows): Weismannian P_W, Lamarckian P_L, and their difference: $|P_W - P_L|$. Differences are due to numerical error, indicating the two methods to be identical.

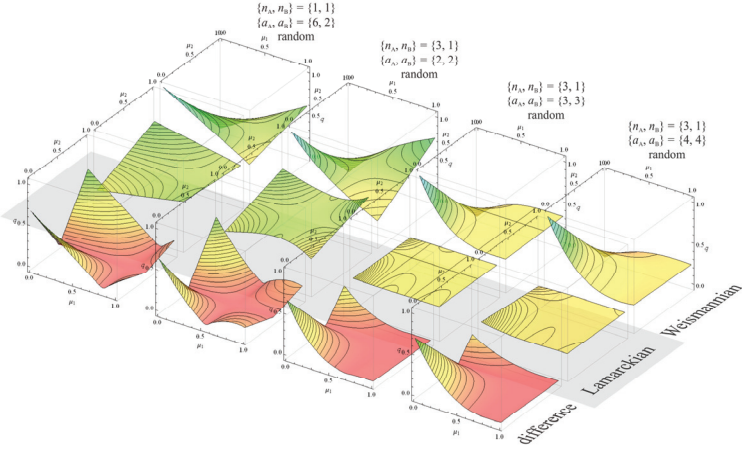


Figure 20. Average codon replication probability for lossy transmission. For each parameter set, the three plots are: Weismannian P_W, Lamarckian P_L, and their difference: $|P_W - P_L|$.

For small inventory sizes, there is more chance to achieve tolerable overall error rates, as there is a higher chance that two consecutive mutations bring the given bit back to its original state. As an extremum, at $a = 2$ (i.e. two-letter alphabet), there are two cases for which exact copying can be reached. Furthermore, only for $a = 2$ is it possible to have 0 possibility of exact replication: when only one of the two transmissions is erroneous but not the other, mutation inevitable destroys information (see Figure 19, front row, leftmost plots).

Thus in case of the Lamarckian topology, smaller inventory size allows for larger replication fidelity, as with increasing alphabet size overall fidelity drops to a general level, mostly independent of the mutational rates at all (Figure 20, rightmost plots). However, probabilities of Lamarckian topology could never get close to the probability surface of the Weismannian topology in such lossy complex transmissions. The only chance for it is if the reverse transmission table is – by chance – randomly generated to be the inverse of the forward transmission table. This case would then be equal to the *uniform random* method of Table 9.

Stochastic simulations support these results. A simple stochastic replication-selectional system was built to test the equality/difference of Weismannian and Lamarckian inheritance for certain cases. A standard selective scenario was used, where the population settles at the best fitness due to selective birth (replication) and random death. Population size is initially 1, and is allowed to grow to 100. Sequence length of A is $n_A = 15$, of B is $n_B = 5$, inventory size is $a_A = a_B = 2$, which gives sequence space sizes as 2^{15} and 2^5 for A and B, respectively. Sequence lengths were chosen to fit both transmissional requirements (i.e. a large-enough codon branching value was chosen: $b_A = 3$), and the population size: if possible number of A-sequences is too large, both the Lamarckian *and* the Weismannian population would end up with an A-diversity larger than the actual population size. Mutation rates were chosen to yield identical sequence-replication chances for B, according to previous results, thus:

$$\mu_{A\to A} = \mu_{A\to B} = \mu_{B\to A} = 0.1. \tag{14}$$

Results indicate, that both populations reach optimal fitness with the same pace, and equilibrial diversity of B sequences are identical (around 9). It cannot settle at 1 (as there is only one best-fitnessed sequence allowed by the landscape, see the *Nk* fitness landscape under section 3.2.1), as the mutation rate guarantees the continuous appearance of new variants. The only distinct difference between the two simulations is in the magnitude of A-diversity. According to eq. 11, the A-sequence robustness for Lamarckian replication is β_A is $3^5 = 243$, which is larger than the allowed population size.

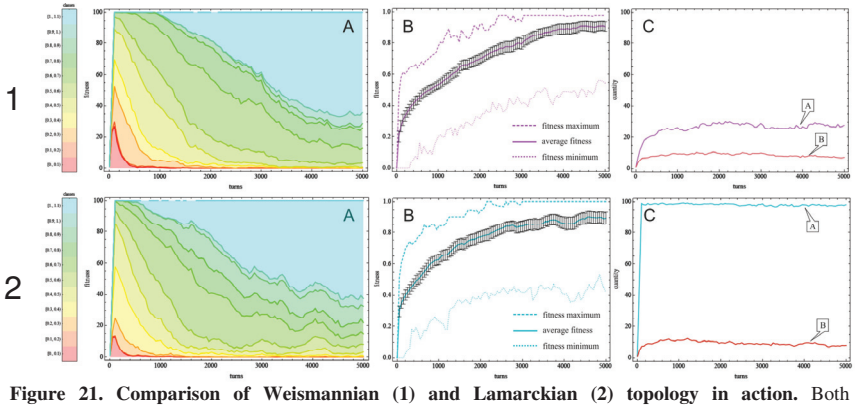


Figure 21. Comparison of Weismannian (1) and Lamarckian (2) topology in action. Both populations were allowed to grow up to a size of 100, with standard replication-selectional dynamics. Only the first 5000 turns are shown, as populations reach equilibrium before that. A) Distribution of replicators according to fitness classes; B) fitness statistics; C) absolute number of different types of *A* and *B* sequences in the population. It is clear that Lamarckian replicators maintain a larger *A*-diversity, as was expected. Each plot is an average of 10 independent simulations. Details are in text.

3.1.3. DISCUSSION

According to the calculations and the toy model, Weismannian topology equals Lamarckian topology, from the viewpoint of B sequences iff T_{AB} equals T_{BA}. Still there is a difference between Weismannian and Lamarckian topologies (thus the distinction of is justifiable). In the latter case, the interactor can pass on acquired variations, while this is still not true for Weismannian replication. Furthermore, the major divergence is that A-sequence diversity is kept high in case of Lamarckian inheritance.

If however the reverse translation step is not the inverse of the preceding translation, there is true information loss in the A → B → A' process, and as is, the two topologies are not equal any longer. As a matter of fact, Lamarckian replication is not even replication any longer, as it cannot maintain information reliably. In this case, probability for Lamarckian inheritance drops severely, compared to the probability of Weismannian replication.

Results clearly show, that replication can be exact in case of probabilistic transmissions. The Lamarckian replication consists of a deterministic (forward translation) and a probabilistic transmission (reverse translation). Therefore, a probabilistic transmission in a complex transmission chain (in a replication process) is not necessarily enough for the replication to be

lossy. If it is preceded with an appropriate inverse transmission, the probabilistic effect is cancelled.

Results also indicate, that maximal mutation rates still can yield exact replication, if inventory size is $a_A = a_B = 2$. In such cases, two consecutive steps of mutation (for *backward* and *forward* translations in Lamarckian inheritance and *copying* and *translation* in Weismannian inheritance) yield the original sequence. Of course, this is not a realistic situation, but indicates that information still can be maintained in such cases. As a consequence, the quasispecies distribution depending on $\mu_{AB} = \mu_{BA}$ obviously has two identical ends, with two error thresholds (Figure 22).

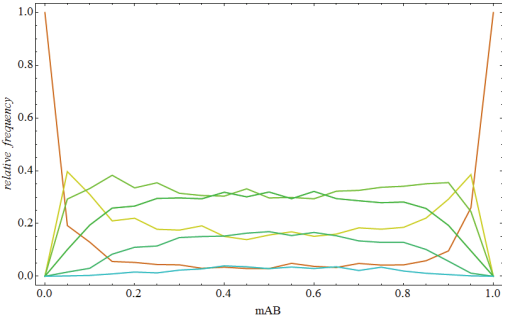


Figure 22. Error threshold of a replicator population of $a = 2$ and two transmission steps (after Swetina & Schuster 1982). The x-axis indicates the value of $\mu_{AB} = \mu_{BA}$. Increasing mutation rates decreases replication fidelity, and without fidelity, the master copy (red line) cannot be maintained in the population, and neighboring mutant groups dominate the population (other lines). However, if inventory size is 2, high mutation rates can help, as backmutations cause the re-appearance of the original sequence during replication. This is invariable true for Weismannian and Lamarckian replicators. The reverse transmission is the inverse of the forward transmission table. Sequence lengths are: $n_A = 15$, $n_B = 5$, inventory sizes are: $a_A = a_B = 2$, population size is 200. Only the distribution of B sequences was plotted in equilibrium.

Stochastic simulations confirm, that a population of Lamarckian replicators, even with fully variable intermediates, could evolve just like a population of Weismannian replicators evolve. The difference between the Weismannian and Lamarckian inheritance in this setup is purely in the amount of robustness of the system: the A-sequence diversity is always larger for the Lamarckian replicator. This is because of the underlying codon robustness, which, in turn, causes the robustness of the sequence space.

It is clear that the same dynamics can emerge from different topologies: Weismannian and Lamarckian replicators can maintain identical amounts of information concerning B sequences, though Lamarckian inheritance operates with a larger A-diversity. This might be a hindrance, when high A-sequence specificity is required, though can be a benefit, when it is necessary to have larger diversity, for example in case of rapidly changing environments (see e.g. Paenke et al. 2007).

3.2. Evolution of division of labor

The difference between various types of informational replicators is primarily in the selectional aspect and the informational topology: which entities are under direct selection (provide directly the *phenotype*) and which ones convey information for replication (provide *genotype*; see 4.1 Lamarckian inheritance). As it was already explained under 2.5.8 Complex transmissions, at one end of the continuum is direct replication, where only one entity is responsible for both selectional and informational functionalities. At the other end of the continuum is Weismannian replication, where the two entities and two functions are clearly separated, and division of labour is complete. Consequently, it is claimed here that this continuum can be traversed gradually, from direct to Weismannian replication, via Lamarckian intermediate stages (cf. Figure 39). Division of labor, accompanied several major transitions during evolution of life (Maynard Smith & Szathmáry 1995). This particular division between replicator and interactor (analogous to the division between germline and soma) is extremely important as it allows evolution to improve replication fidelity by magnitudes.

3.2.1. MODEL

A stochastic toy model is devised to investigate the possibility of the above drafted scenario. A replication-selectional system is modelled, where the population of sequence replicators undergoes selection and evolution through time. To understand how different entities may contribute to the genotype and phenotype functions, let us first introduce the graph of general replication (Figure 23). A general replicator consists of a finite number of entities (these can be thought of as intermediates and products of an autocatalytic cycle), and generator rules defining the generation of these entities.

A specific subset of all informational replicators is replicators with life cycles consisting exactly two entities. Both Weismannian and Lamarckian replicators belong to this subset. An even simpler instance is a direct replicator, which does not even have an intermediate, thus is consisting of a single entity. The informational and selectional topology of a general two-entity, informational replicator is shown in Figure 24.

The graph of Figure 24 makes the Replicator Formalism explicit by showing how the genotype and phenotype relate to entities. Both the genotype and phenotype are functions of the entities: $G = g(A, B)$, $P = p(A, B)$. Note that both G and g are able to specify the genotype exactly, however g is a function, while G is the result of applying the function to A and B. This

indicates the fact that the genotype is an *abstract concept* (a function, *g*), though it can be denoted with the *theoretical genotype* (an entity, G, like the pure informational base order in a gene), or even with the *realized genotype*: the relevant parts of A and B (like the gene itself, as a material piece of DNA).

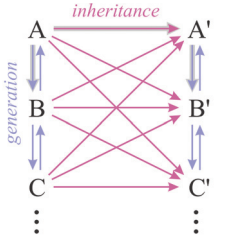


Figure 23. Graph of general replication. A replicator is a set of entities of different nature (A, B, C, ...), which are created from each other according to generation rules (blue arrows). During replication of the replicator, its entities contribute information to the next generation of entities A', B', ... in various ways (purple arrows). Heavy arrows highlight a particular topology on the general graph: Weismannian inheritance. Note that the graph is general to be extended with further components

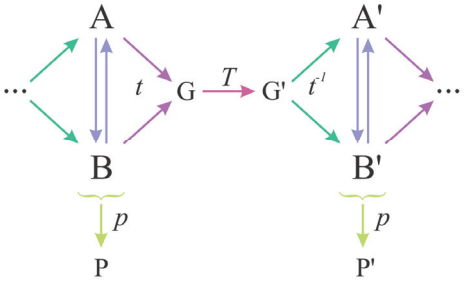


Figure 24. Details of a general 2-entity informational replicator. Two entities, A and B replicate, and define genotype (G) and phenotype (P) Violet arrows indicate function *t* that derives the genotype template from entities A and B: G = *t*(A, B). Blue arrows denote possible development routes that produce B from A, or vice versa. The purple arrow *T* denotes the actual transmission of genotype information (not necessarily copying!) Turquoise arrows indicate the inverse function of *t*, producing A and/or B from inherited genotypic information. Green arrows mark the phenotype function *p*, which defines the phenotype as a function of entities A and B: P = *p*(A, B). Note that not all arrows are necessary to be present for a particular instance of informational replication.

The scenario to evolve Weismannian replication out of direct replicators is depicted on Figure 25. It assumes that the first step is the appearance of a neutral side product, B. B is produced by the initial autocatalytic cycle of an informational entity, A. Furthermore, B is assumed informational as well (since it is created by modular transmission from A). In addition, B is neutral in the sense that it affects neither replication nor selection. This product might later evolve to provide some functionality for the replicator, that positively affects its replication rate

(fitness). The replicator becomes the composite of A-B. At this point, it is assumed that A and B together are responsible for the reproductive success of the replicator. Furthermore, B is allowed to stand in for A, substituting it in replication, in the actual copying process. By this, we ensure that if better, B can take over the whole replication business from A. If selective forces are chosen appropriately, we expect division of labour to arise from the undifferentiated situation, where every entity can play every role.

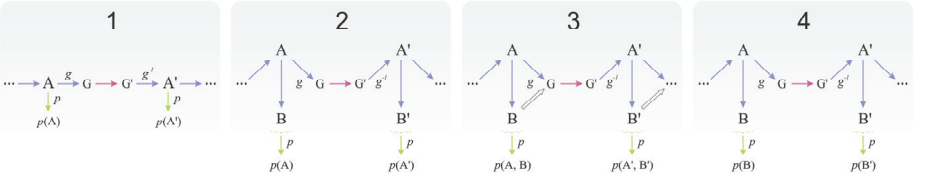


Figure 25. Scenario for the evolution of division of labour. Time goes from left to right: 1) Simple autocatalytic entity: A. 2) A harmless, neutral product is introduced: B. 3) The product begins to compete with the original entity, and contributes to both the phenotype and the genotype. 4) Ultimately, the roles are divided: entity A deals exclusively with the genotype, while B with the phenotype only: note how the phenotype depends only on B. Empty arrows indicate mandatory contribution of the side product to inheritance.

It may seem more straightforward that, when B is introduced, it only begins to contribute to the phenotype, but not the genotype. While this seems perfectly plausible, it is also plausible to suppose that side products of early replicators with considerably similar structure and complexity did compete with the original entity for transmitting information to the offspring, cf. heritable processive cycles. Furthermore, until real compartmentalization happened during prebiotic evolution, no one could expect early replicators not to contribute directly to their own phenotypes. As they were not enclosed and separated from the outside environment according to the RNA world scenario, it is perfectly logical to assume that they were responsible for their own pehnotypes, and not via free-floating interactors. Supporting the whole of this scenario, Crick wrote (in Sagan 1975):

> "We see on Earth that there are two molecules, one of which is good for replication and one of which is good for action. Is it possible to devise a system in which one molecule does both jobs, or are there perhaps strong arguments, from systems analysis, which might suggest (if they exist) that to divide the job into two gives a great advantage, This is a question to which I do not know the answer."

Now division of labour is clearly advantageous in circumstances and environments where genes and proteins work. Whether there are situations, where a lack of division is more profitable cannot be told in general. There are cases (like prion propagation), where there is no apparent division of labour, though whether this is an evolved fact providing some benefit or is a consequence of the impossibility to develop full separation is an open question. The division of labour problem is a complex issue, and both its causes and means have to be considered to understand how evolution preferred the division (cf. Maynard Smith & Szathmáry 1995).

Consequently, replicators of the model were left to evolve with the less restricted assumption set: both A and B entities are allowed to contribute to both the genotype and the phenotype. Entities are represented as one dimensional sequences drawn from a finite inventory set of length n_A and n_B, while the genotype and phenotype are sequences indicating positions in A and B belonging to the genotype or the phenotype (or none or both). Figure 26 shows an example of such a replicator, with sequence length $n_A = 20$ and $n_B = 10$, inventory size $a_A = a_B = 2$, and codon length $c_A = 2$, $c_B = 1$. Codons are randomly distributed between genotype and phenotype. To prevent interference of digits of different sequences in a given function (genotype or phenotype), it is not allowed to allocate digits of same positions of A and B to the same function. Because of this, it is always a codon instead of a digit that is allocated to a certain functionality, and allocation is exclusive. Thus, if the i^{th} codon of A is allocated to the genotype, it is not possible to allocate the i^{th} codon of B to the genotype as well. In other words, a bit of the genotype (or phenotype) is either an A or a B codon, but cannot be neither or both. Consequently, in any situation, even if the genotype is distributed randomly among A and B, there **is** a definite genotype, which can be derived from A and B sequences unambiguously.

The details of the example of Figure 26 are listed below for clarification:

sequences	A	01010001100010011000
	B	1000000101
genotype specification	*g*	BAABABBBBA
actual genotype sequence	G	{1}{01}{00}{0}{10}{0}{0}{1}{0}{00}
phenotype specification	*p*	AABBBABBAB
actual phenotype sequence	P	{01}{01}{0}{0}{0}{00}{0}{1}{10}{1}

According to the evolutionary scenario, the initial replicator population should consist of direct replicators, where there is no B sequence at all. For sake of simplicity, the lack of B is modeled as a completely inert B sequence that does not contribute to anything, but is already

present. Of course, this does not deal with the question of how interactors appeared on the first place, but this is not in the scope of this work. Thus assuming that a harmless side product already produced for the autocatalytic core of A, it is sensible to start the investigation from this point. At the end, we can expect four different outcomes (aside from totally random distribution), listed in Figure 27.

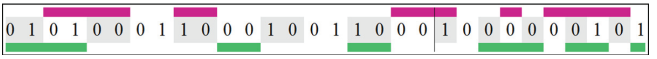


Figure 26. Example Lamarckian replicator. Left is sequence A of length 20, right is sequence B of length 10. Shading indicates individual codons. Top purple and bottom green bars mark codons that contribute to the genotype and the phenotype, respectively.

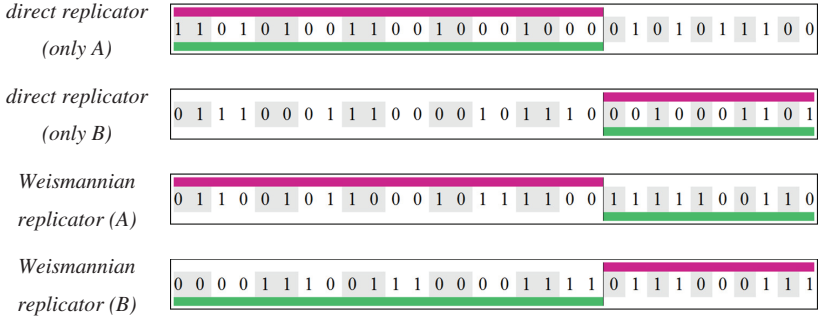


Figure 27. Possible outcomes of evolution. Note the two mirror pairs, only A and only B, and standard and reverse Weismannian replicators: if one of the pair can be evolved in the model, the other can be evolved similarly, swapping appropriate parameters.

There are two major selective forces that could drive the evolution of such a replication-selectional system (in general): selection for better fitness; and selection for higher replication fidelity. The tradeoff of these two factors defines the outcome of the evolutionary trajectory of the population. To force a particular entity (A or B) to be responsible for the genotype, high fidelity replication is required for the given entity, to be able to maintain information over time. To force an entity to be responsible for the phenotype, it is required to yield good enough phenotypes, with high fitness. However, it is also important that well fitted phenotypes are heritable, otherwise they cannot be maintained in the population. Of course, in case of an unrestricted fitness landscape, where every sequence has a high fitness, no division of labour is expected. Thus, an appropriate fitness landscape has to be chosen to facilitate division of labour. Accordingly, mutation rates of transmission channels are to be chosen in a way to facilitate one

entity to undertake, and ultimately monopolize inheritance, while the other becomes solely responsible for the phenotype and selection.

Replication efficiency is controlled by adjusting the fitness landscape. A correlated landscape is simulated using Kaufmann and Levin's *Nk* model of rugged fitness landscape (Kauffman & Levin 1987, Kauffman et al. 1988, Kauffman & Weinberger 1989). The *Nk* model is a stochastic method to generate fitness for digital sequences. The name indicates the two basic parameters: N, the length of sequences, and k the number of epistatic neighbours (both parameters are uniform for all sequence). The size of epistatic neighborhood k, as a single parameter, controls the 'ruggedness' (correlatedness) of the adaptive landscape. The *Nk* model is well-studied and understood (Weinberger 1991, Fontana et al. 1993, Altenberg 1997) and is applied to various fields of evolutionary biology, like DNA sequence evolution (Kauffman & Levin 1987), immune system maturation (Kauffman & Weinberger 1989) and ecosystem coevolution (Kauffman 1993).

The *Nk* model assumes a set of epistatic connections for components of the sequences of a replicator. These epistatic neighbours together define partial subvalues for the phenotype (and thus for fitness). The actual fitness of a replicator is the average of N fitness components: F_i, contributed by each sequence position i. Each positions' fitness component F_i is determined by its own value, x_i, and the values at k other epistatic loci (so k must fall between 0 and N - 1). Thus, the fitness function is:

$$F(x) = \frac{\sum_{i=1}^{N} F_i(x_i, \{x_{i,1}, x_{i,2}, \ldots, x_{i,k}\})}{N}, \tag{15}$$

where x_i gives the i^{th} position in sequence x, and $\{x_{i,1}, x_{i,2}, ..., x_{i,k}\}$ defines the k epistatic neighbours for the i^{th} position (where $\{i_1, ..., i_k\} \subset \{1, ..., i-1, i+1, ..., k\}$).

Thus, for each sequence component contributing to the fitness, the epistatic map defines a neighbourhood of size k. The actual sequence element at position i and its epistatic neighbours define the subsequence s_i of length $k + 1$ that is used to calculate the fitness contribution F_i (the sub-fitness value). F_i is a function that for any given position i and subsequence $s_i = \{x_{i,1}, x_{i,2}, ..., x_{i,k}, x_{i,k+1}\}$ returns a random value of the uniform distribution (0, 1). What is important is that F_i should return the **same value for the same neighbourhood at the same position**. Note that same neighborhoods at different positions yield independent values.

If $k = N - 1$, that is the number of epistatic neighbours is the maximum, each position is connected to each other. This yields a random landscape, as any bit change in the sequence yields a completely new subsequence, and consequently, a completely new subfitness for each

position. If $k = 0$, thus there are no epistatic neighbours, each position is responsible for only itself and is independent of other positions, yielding therefore a fully correlated landscape.

The neighbourhood can be arranged in any particular way suiting the experiment, it does not need to be a continuous subsequence (see Figure 28). Furthermore, it is not required that the i^{th} sequence component should contribute to the i^{th} phenotype element (see Figure 28 D and E). Here the 'block' epistatic map was used introduced by Perelson & Macken 1995). The block map algorithm allows for a variable k for different phenotype components, as its primary parameter is the number of blocks b (Figure 28). The block map assumes that the phenotype consists of a set of independent domains, and mutations in one domain (block) affects the contribution of that block alone. The overall correlation of fitness and sequence distance (Hamming distance) is guaranteed by the fact that each sequence uses the very same epistatic map and subfitness values assigned for the particular subsequences. Note that $b = 1$ for the block map equals $k = N - 1$ for adjacent neighbourhood, as the epistatic map is completely filled (yielding thus a random landscape). Similarly, $b = N$ equals $k = 0$, where there is only one cell filled for every position, though not necessarily in the order of positions. This setup yields a fully correlated landscape.

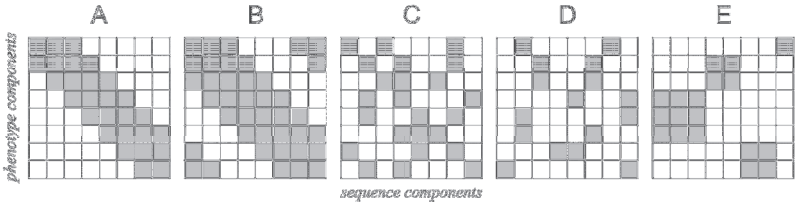


Figure 28. Epistatic maps for the *Nk* fitness landscape. Gray cells in a row indicate an epistatic connection between the marked sequence components for the given phenotype component. A) Kauffmann's adjacent neighborhood ($k = 3$). B) Adjacent neighborhood assuming a cyclical sequence ($k = 4$). C) Random neighborhood, with filled diagonal ($k = 2$). D) Random neighborhood without diagonal ($k = 2$). E) Block map ($b = 4$). After Altenberg (1997).

Thus, a landscape L is depending on N, k, and inventory size a (alphabet size). For a fixed k and given a, the lookup table to store all possible subfitness values would be:

$$\lambda = N\, a^{k+1}, \tag{16}$$

i.e. an a^{k+1}-sized matrix (one subfitness value for each possible subsequence) for each position. For variable k, for example for block map, this modifies as:

$$\lambda = \sum_{i=1}^{N} a^{k_i+1}, \tag{17}$$

where k_i indicates the neighbourhood size at the i^{th} position. This could get immensely large for large sequences and/or for large inventory sizes. However, the *Nk* landscape does not have to be pre-computed: subfitness values can be generated on the fly, as the pseudorandom number generator can be exploited to return a specific subfitness value w_i consistently, when a specific subsequence at position i (in a specific environment) is encountered (after Altenberg 1997):

$$w_{i,e} = \psi(F_i(x_i, \{x_{i,1}, x_{i,2}, ..., x_{i,k}\}), e) = \Psi(i, s_i, e), \tag{18}$$

where $i \in \{1, 2, ..., N\}$, subsequence s_i is the actual epistatic neighbourhood of the i^{th} sequence component, itself included, and e is an index for the given environment (or session).

The only problem with the *Nk* model is that, by default, it generates a correlated distribution of fitnesses around the mean value of the preallocated fitness range, usually the (0, 1) interval, but the actual sequence having the best fitness cannot be predicted. A method however, is introduced here that allows for adjusting and fine-tuning the landscape by seeding the *a priori* random landscape with sequences that have pre-allocated fitness values. The neighborhood subsequences of the seeded sequences are extracted according to the epistatic map, and then all of these subsequences (at the appropriate position) are associated with the predefined fitness values (and stored in the lookup table). These allocations then can be used to overwrite the randomly generated subfitnesses for the specific encounters during simulation. As each seed produces *N* subsequences with pre-allocated subfitnesses, the number of entries in the lookup table scales linearly with the number of seeds: the memory-consumption of this method is comparably less than storing the whole landscape in memory as a lookup table of all subfitness values, see eq. 16. Adding seeds still retains the correlatedness, though appropriately skews the distribution, see Figure 29.

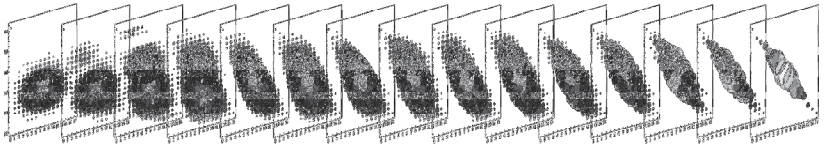


Figure 29. Fitness distribution in a correlated and seeded *Nk* landscape. Fitness (*y*-axis) depends on Hamming distance (*x*-axis), compared to best sequence. Block number, *b*, increases from 1 (left) to 15 (right), shifting toward a fully correlated landscape on the right. $N = 15$, $a = 2$, the two seeds specified for the landscape are: 111111111111111 with fitness 1, and 000000000000000 with fitness 0. Bubble sizes are proportional to the amount of sequences at coordinates. Fitness was partitioned to bins of width 0.05.

Now to cope with the fact that both A and B sequences may contribute to fitness, certain problems has to be handled. Since subfitness values are assigned to individual digits, it means that there might be different number of subsequences and subfitnesses for A and B (if they have different sequence lengths), which makes fitness-calculation problematic for replicators with mixed phenotypes. Therefore there are two parallel (shadow) fitness landscapes, L_A and L_B, defined for A and B sequences, respectively. During fitness assessment, the phenotype specification defines which codons to use from which sequence. For each codon at the given position, the appropriate subfitness value is calculated from the appropriate shadow landscape. If a codon has length $c > 1$, than the returned c subfitness values are averaged for the codon length. Therefore, each codon contributes exactly one subfitness value. These subfitnesses from the A and B shadow landscapes are then averaged according to eq. 13, to yield a fitness value that defines the actual landscape (which is rather hard to visualize, having at least 4 dimensions).

Fitness seeds were chosen to simulate the superiority of B over A codons in terms of fitness. A-codon fitnesses were rescaled to lie in the (0, 0.5) interval, while B-codon fitnesses are in the (0, 1) interval (Figure 30).

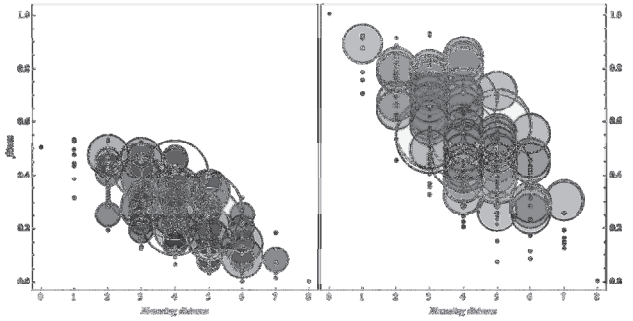


Figure 30. Fitness landscapes for A and B sequences. The landscape for A sequences has fitness maximized at 0.5 (left), while B sequences can climb up to 1.0 (right). Actual fitness of a replicator is calculated by averaging the subfitness values of the positions of A and B sequences contributing to the phenotype. Bubble sizes are proportional to the amount of sequences at given coordinates. Fitness was partitioned to bins of width 0.05.

Replication fidelity is controlled by mutation rates. There are 3 mutation rates for the three transmissions: A → A, A → B, B → A, see Figure 31. Any new entity inherits three features from its parent: 1) the sequence information that is specified by the genotype; 2) the genotype specification; and 3) the phenotype specification. The latter two is represented and transmitted in the form of sequences of length s_i/c_i consisting of the letters A and B. The sequence information

is used to produce a new A' sequence initially. The B' sequence (as is the side product of the autocatalytic cycle of A) is generated from the new A' (and not directly from the inherited genotype), as is pictured in Figure 25 and Figure 31. The sequence information and both the genotype and phenotype specifications are subjects to mutation during transmission. By this way, the genotype and phenotype functions can evolve as well, in parallel to sequences.

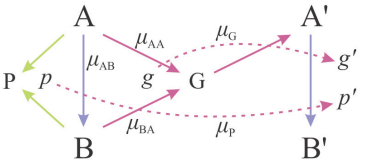


Figure 31. Mutation rates of transmission steps. Both genotype (g) and phenotype (p) specifications are inherited along with sequence information of A and B (dashed arrows) - all via erroneous channels (hence μ symbols). The theoretical genotype of the left hand side replicator has three parts: the inherited sequence information G, and the function specifications g and p.

Setting the B → A process less reliable than the A → A transmission by choosing appropriate mutation rates for the two processes, the system is forced to utilize A codons to transmit replicator information rather than using B codons. The mutation rate of the A → B process is left at zero, as it is irrelevant for the case: whatever is the outcome of evolution (cf. Figure 27), each replicator relies on the same B-generation process, and thus any change in μ_{AB} would affect every replicator the same way.

3.2.2. Results

To test the behaviour of the model, several benchmark simulations were run. In case no sequence-mutation is allowed and only the genotype specification g could change, the genotype settles at 50%A – 50%B – the expected and trivial outcome. That is, if sequence mutation does not drive selection and evolution, the genotype specification randomly distributes between A and B codons evenly. A good example for such a replicator is Figure 26, where both g and p are at 40%A and 60%B (being a mere coincidence, that both g and p ratios are identical).

For sake of simplicity, A and B sequences are of identical dimensionality, thus translation does not play any role here. Accordingly, by setting the mutation rate of the A → A process lower than the B → A process, it can be ensured that A codons are preferred to encode genetic information over B codons. This is because the new replica always generated by starting with an A-sequence, in any case. In detail: if the genotype function g contains reference to an A codon,

then the new entity will inherit that A codon. During replication, it is always the A sequence of the new entity that is built first, based on the genotype. Accordingly, if the parent genotype g contains a reference to a B codon, this B codon will be passed on to the offspring, but it will be translated to A-codon.

Initial populations were set to be only-B populations, where B codons contribute to both the genotype and the phenotype, exclusively. Initial sequences were allocated lowest possible fitness (0.0). Figure 33 shows that while average fitness climbs toward the global optimum, the genotype steadily increases until more than 70% of it is monopolized by A codons. To achieve a dominant A-genotype, retranslation from B sequences must be set quite high: $\mu_{AA} = 0.001$, $\mu_{BA} = 0.1$. This guarantees that A sequences are copied with higher fidelity. Though the difference of two orders of magnitude between μ_{AA} and μ_{BA} is quite unrealistic. Figure 34 shows a similar run, but with a more realistic mutation rate setup. The difference between sequence mutation rates was set to be one order of magnitude: $\mu_{AA} = 0.005$, $\mu_{BA} = 0.05$. By setting the fitness landscape more rugged ($b = 4$) and allowing more time to evolve, the population reaches the same outcome, where A codons clearly dominate over B codons in the genotype specification g.

If mutation rates μ_{AA} and μ_{BA} are equal, then the genotype settles around 50%, as A codons are no better choice to maintain information than B codons (Figure 35). This explicitly demonstrates that it is possible to force division of labour by deliberately setting the fitness landscape and the translational mutations to drive evolution of sequences and genotype/phenotype specifications.

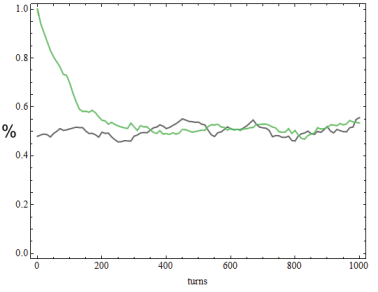


Figure 32. Share of A-codons in the genotype, with and without selection. Sequences are not allowed to mutate, only the genotype specification g. As a result, g settles at 50%, i.e. A and B codons contribute to g 50-50%, none being better than the other in inheriting information. Black line indicates g-share of A-codons, when population starts from random initial genotype distributions (that is, the genotype is initialized with roughly 50-50% of A and B codons). The green line indicates the g-share of A-codons starting from a population with all-A genotypes (that is, initial genotype is provided entirely by A-codons). Population size is 20, $\mu_G = 0.1$, $n_A = n_B = 10$, $a_A = a_B = 2$. Each curve is a result of 10 iterations.

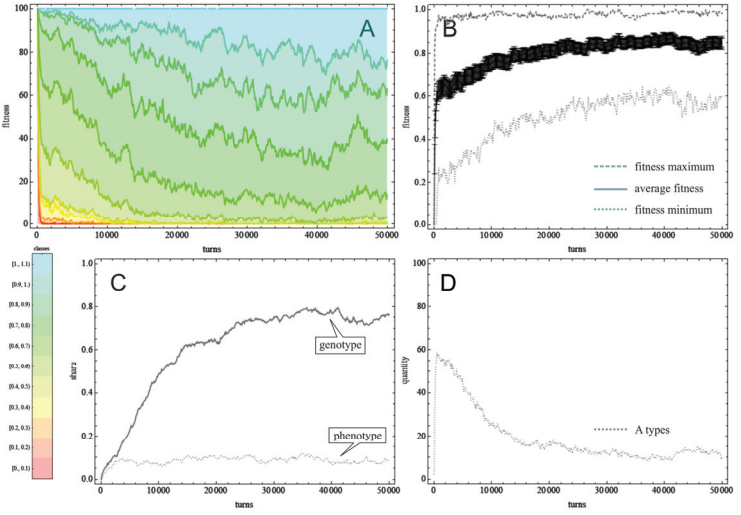


Figure 33. Emergence of division of labour. A) fitness distribution of replicators, the higher the fitness the cooler the color is. B) Maximum, average and minimum fitness values of replicators. C) Share of sequence-A digits in the genotype and phenotype functions. D) Number of different A-sequences in the population. Population size is 100, $n_A = n_B = 8$, $a_A = a_B = 2$, $\mu_{AA} = 0.001$, $\mu_{BA} = 0.1$, $\mu_G = \mu_P = 0.005$, transmission table is uniformly ordered, block epistatic map, $b = 8$, random weighted birth, and random death. Each plot is the average of 10 independent runs.

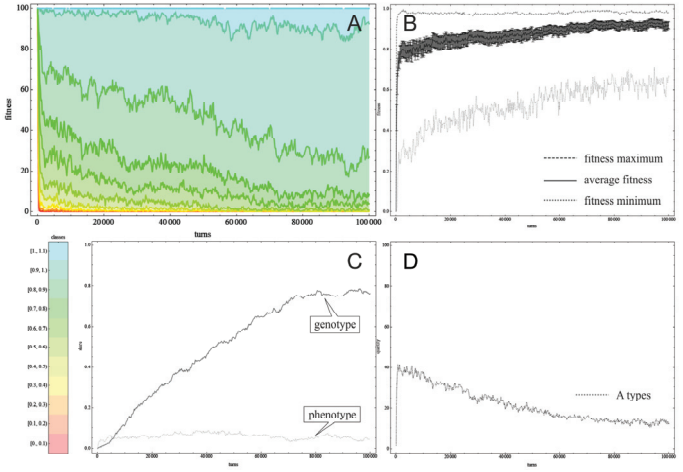


Figure 34. Simulations with smaller mutation rates. Population size is 100, $n_A = n_B = 8$, $a_A = a_B = 2$, $\mu_{AA} = 0.005$, $\mu_{BA} = 0.05$, $\mu_G = \mu_P = 0.001$, transmission table is uniformly ordered, block epistatic map, $b = 4$, random weighted birth, and random death. Each plot is the average of 10 independent runs.

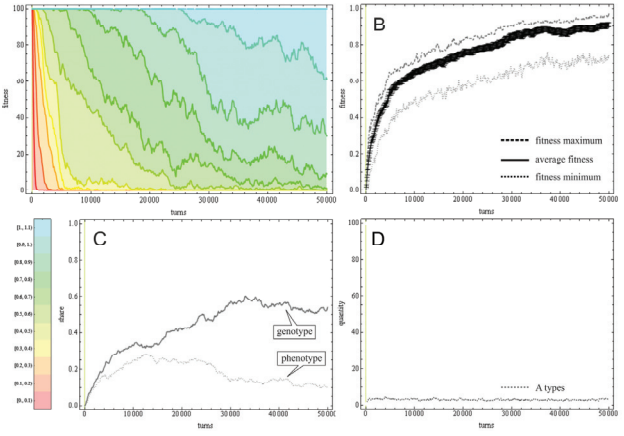


Figure 35. Simulations with equal mutation rates. $\mu_{AA} = \mu_{BA} = 0.005$, which results in the genotype being shared equally between A and B codons, as no one is better than the other in transmitting information. Population size is 100, $n_A = n_B = 8$, $a_A = a_B = 2$, $\mu_G = \mu_P = 0.001$, transmission table is uniformly ordered, block epistatic map, $b = 8$, random weighted birth, and random death. Each plot is the average of 10 independent runs.

3.2.3. DISCUSSION

This experiment demonstrates how a particular domain of a genome can transit from direct replication to Weismannian through a Lamarckian stage. Sequences form only a part of the implicit genome (hence the word domain), since other parts are transmitted independently. Genotype and the phenotype specifications *g* and *p* are **not coded** in the A or B sequences, but are part of the assumed genome of the replicator. They are still explicitly inherited, as specific sequences. These are not modeled at the same representation level as A and B sequences are, and are evolving somewhat independently of A and B sequences. Nevertheless, the model shows that a part of the genome is able to evolve gradually toward transmitted via Weismannian inheritance.

The model does not specify what kind of information is inherited from the two sequences A and B. One can think of them as simple sequence mutations in coupled autocatalytic template cycles, or as lifetime-acquired adaptations of the soma (and germline), or even learnt knowledge the organism acquired through social information transmissions in a cultural evolutionary setup. The Formalism states that independent of the level of organization, the Lamarckian topology should produce the same dynamics.

Results indicate that while average fitness increases to a certain point quite quickly, due to direct sequence evolution, to reach global optimum would require much more time than is allowed for the simulations. This is because the evolution of the genotype and phenotype specifications is at least a magnitude slower than sequence evolution. This is true even if *g* and *p* mutation rates are identical to sequence mutation rates. This is because of their indirect effects, which do not allow direct evolution of genotype and phenotype.

Further research should is aimed to examine the exact internal dynamics of such complex informational systems. Here, only the genotype-specification was examined, and the phenotype was assumed to be already at optimal distribution. It would be interesting to try to find such environmental setup, which can force a “regime shift” of a direct. That is, starting from a population of direct replicators with all-A genotypes and all-A phenotypes and evolving all-B genotypes and an all-B phenotypes. Even more interesting would be to examine a regime shift in a Weismannian system: starting from all-A genotype and all-B phenotype and evolving an all-B genotype and all-A phenotype.

These experiments surely must include some kind of environment-change during simulation, changing possible both the fitness landscapes and mutation rates in mid-simulation. This is not implemented at present.

It is also alarming, that the difference between the two translational mutations ($\mu_{A\to A}$ and $\mu_{B\to A}$) must be at least one or two orders of magnitude to take effect. Surely, other processes might have been in work during the trajectory from direct to Weismannian inheritance. The origin of the DNA and the genetic code is a well-studied field with many theories and models that could be compared and included in the scenario explained here. For example, the works of Richard Michod (cf. Michod 1983) deal with the emergence of nonenzymatic, template-directed replication, and the origin of first organisms, bootstrapping from an initially non-replicating chemical reaction network.

3.3. Compartmentalized replicators

3.3.1. REPLICATORS IN THE CHEMOTON

A next step in replicator evolution was compartmentalization. It could have happened before a dedicated interactor emerged (i.e. the proteins for DNA genes), though is generally accepted that ribozymes themselves are not capable of organizing into protocells without explicit protein enzymes. Therefore, the boundary subsystem either was recruited by an already evolved DNA + protein system, or was evolved independently of polynucleotides (as metabolism-first theories suggest). In this section, I will investigate the possible coexistence of template replicators in a compartment, the chemoton, in a setup where replicator templates and interactors are strongly coupled stoichiometrically. As a matter of fact, the chemoton is not just an interactor, but itself is the vehicle of the template replicators housed inside of it.

A particularly promising approach to simulate early compartmentalization is provided by the chemoton model devised by Gánti (1971, 1978, 2003). Gánti proposed that life should be analyzed by investigating chemical supersystems that at the same time are also biological minimal systems. The chemoton is a model for a minimal protocell able to reproduce and stably maintain its integrity, and being the simplest system that satisfies all the absolute life criteria (Gánti 1971), it is also a unit of life (Szathmáry 2002). What is even more important, chemotons can be units of evolution (Maynard Smith 1987), if hereditary variants appear (see extension of the basic chemoton model in next section).

The chemoton consists of three autocatalytic subsystems: a metabolic (self-reproducing chemical cycle, M), an informational (template polymerization cycle, T) and a boundary subsystem (B) enclosing the former two. The chemical reactions of the three subsystems are linked stoichiometrically, which coordinates the growth and division of the cell so that the system is also autocatalytic as a whole. Although the subsystems are stoichiometrically coupled, the dynamics of the system still depends on kinetic factors.

The metabolic subsystem produces the components necessary for its own self-reproduction and those of the other two subsystems. The boundary subsystem provides compartmentalization and keeps the volume of the sphere between certain boundaries whereby it ensures the necessary concentrations, which in turn are necessary for the appropriate rate of reactions. The template system controls quantitatively the chemical processes of the whole supersystem (Gánti 2003). If the growing chemoton reaches a certain size, physical forces are assumed to initiate fission,

producing two daughter cells (cf. Carletti & Fanelli 2007, similarly to the fission in GARD, and other boundary-first models of lipid vesicles). The cyclic nature of all subsystems causes the supersystem to behave cyclically as well, therefore not just intermediates of the chemical cycles, or subsystems, but the chemoton as a whole is an autocatalytic entity, and a replicator as such.

By the introduction of an information carrier template molecule in the system (being thus an informational replicator *sensu* Orgel), at least limited heredity (Szathmáry & Maynard Smith 1993) can be achieved: splitting microspheres are able to pass on changes in their template molecules to offspring. In the basic model described in Gánti (1971) the template consists of only one type of monomer (it is a homopolymer), and the only real information the system carries is the distribution of polymers of different lengths. Although information is limited, it is still information. If there is no practical limit on polymer length and composition, unlimited heredity and open-ended evolution can be achieved.

The chemoton is an abstract, idealized model that can serve as a blueprint for the synthesis of coupled autocatalytic systems; a prime aim of the newborn science of systems chemistry. Although, there is no successful physical manifestation *in vitro* so far, there are promising initiatives (Szostak et al. 2001). It has nevertheless been tested *in silico* in great detail, and has been proved to work under broad conditions, both in deterministic (Békés 1975, Csendes 1984, Fernando & di Paolo 2004, Fernando 2005) and stochastic setups (Van Segbroeck et al. 2009).

3.3.2. COEXISTENCE IN THE EXTENDED CHEMOTON

Recently, Zachar, Fedor and Szathmáry devised an extended model of the chemoton, to investigate internal competition of informational replicators in the chemoton (Zachar et al. 2011). They introduced a second template cycle T_2, being in competition with the first one, T_1 (see Figure 36), making it thus similar to the stochastic corrector model (SCM). Consequently, chemotons may be units of open-ended evolution, according to the type and ratio of different templates hosted. Contrasting the SCM however, the stable coexistence of various templates integrated in the chemoton does not depend on the phenotypic effects these templates have on the chemoton itself (i.e. what they code for, being altruistic or parasitic at all). The templates do not have any direct effect on the survival of the chemoton, and, as a matter of fact, there is no selection at all at the level of the chemoton, as we were only interested in the internal dynamics of coexistence. Without restrictions on the effect of template replicators on their integrator (the chemoton), we allow *a priori* for a far wider range of replicators to be able to coexist compared to the SCM.

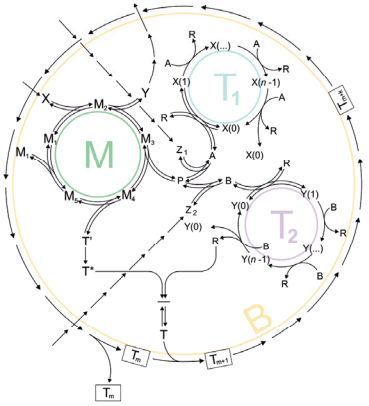


Figure 36. Topology of the extended chemoton. **M =** Metabolism, **T_1, T_2 =** Template cycles, **B =** Boundary. In this particular depiction two alternative template cycles feed on monomers A and B (producing polymers X and Y, respectively), converted from precursor P, which is produced by the metabolism. Both informational subsystems produce the membrane precursor R that is necessary for the membrane to grow and the chemoton to divide. Food molecules Z_1 and Z_2 are required for the template monomers A and B, respectively.

Subexponentially growing replicators are known to be able to coexist stably according to Scheuring & Szathmáry 2001), although the molecular mechanism behind parabolic growth outside the chemoton is due to single and double strands of replicators: by forming a double strand, replicators become inert, inhibiting further multiplication thus limiting the rate of replication (von Kiedrowski 1986). The chemoton implies subexponential growth in a different way: it couples its metabolic cycle with the template cycle stoichiometrically, therefore the cycle feeding on metabolism cannot be faster than the metabolism itself. By limiting the rate of metabolism to a subexponential rate, the chemoton ensure that template replication is limited as well.

The metabolic speed is set by the reversible reactions in the metabolic cycle: Any autocatalytic cycle grows exponentially if and only if no side-product can accumulate to block the forward reactions. If any reaction producing side-products (including the reaction doubling the original molecule) is either irreversible or products are immediately consumed in irreversible reactions, the cycle would grow exponentially. For the chemoton, this means that the metabolism can only grow exponentially if reactions producing Y, P and T' are irreversible, and no Y, P or T' can build up. This is ensured by the immediate take-up of P and T' by the other cycles and the quick removal of Y (waste) from the system. In any other case (i.e. in realistic setups), the metabolic subsystem grows subexponentially, or even linearly.

Therefore, homopolymers grow subexponentially, and coexist stably (see Figure 37 A). Furthermore, since there is no monomer-competition between homopolymers feeding on different monomers, these homopolymers are only indirectly competing with each other via the

available space in the chemoton (cf. carrying capacity). Since replication is subexponential, and division happens regularly, no faster homopolymer can wipe out the slower ones.

The chemoton can take the limits of coexistence even farther. The representation of the chemical supersystem can be greatly simplified, and both the metabolism and membrane can be omitted. The metabolism can be substituted by incorporating food or precursor input to the system directly. The boundary can be ignored as well, as its only relevant function at this point is to set the pace for the oscillatory behaviour by initiating division when the surface/volume ratio reaches a certain value. Consequently, the function of the boundary molecule T can be replaced by simply dividing the chemoton when all of its remaining components reach a certain amount. The simplest model of the two template cycles of the chemoton therefore is as follows:

$$\begin{aligned} a + x &\xrightarrow{k_x} 2\,x\,, \\ b + y &\xrightarrow{k_y} 2\,y\,, \end{aligned} \tag{19}$$

where x and y are template concentrations for X and Y (not distinguishing between different stages of polymerization), k_x and k_y are the reaction rate constants for template X and template Y, and a and b are concentrations of monomers A and B, respectively. Thus both x and y are potentially exponential replicators.

As the precursors are omitted, equations of eq. 19 assume that monomers A and B are provided by the metabolism at either a linear flux rate or constantly, yielding linear or exponential growth, respectively. If decay rate d is applied to A, B, X and Y, growth becomes regulated, that is, subexponential. According to these factors, the two templates with different k values may coexist in the dividing chemoton without one diluting the other to extinction (as it happens with exponential replicators competing for space or resources). Figure 37 shows coexisting and diverging pairs of replicators in the chemoton. A stochastic simulation was also performed using the Gillespie algorithm-based *BlenX* language with similar results (see Zachar et al. 2011).

Now the chemoton has its internal mechanisms under regulated control in the sense that it has its template cycles coupled stoichiometrically to metabolism. This means that there is an inherent internal method of regulation that is provided by the reverse nature of metabolism. Due to reverse reactions, the metabolic cycle cannot run amok, but is slowed down when producing too much products. This ultimately decreases the rate of monomer-creation (coupled with spontaneous dissociation) yielding subexponential growth for monomers and templates.

Furthermore, by introducing a common precursor, P, for monomers A and B, even explicitly exponential replicators can be forced to coexist. Accordingly, the chemoton can be extended to the following set of reactions, which is more realistic than the model of eq. 19:

$$\left\{ m \xrightarrow{k_m} 2\,m + p,\ p \xrightarrow{k_a} a,\ p \xrightarrow{k_b} b,\ x + a \xrightarrow{k_x} 2\,x,\ y + b \xrightarrow{k_y} 2\,y \right\} \tag{20}$$

and appropriate differential equations:

$$dm = k_m\, m, \tag{21}$$

$$dp = k_m\, m - k_a\, p - k_b\, p, \tag{22}$$

$$da = k_a\, p - a\, k_x\, x, \tag{23}$$

$$db = k_b\, p - b\, k_y\, y, \tag{24}$$

$$dx = a\, k_x\, x, \tag{25}$$

$$dy = b\, k_y\, y. \tag{26}$$

The equations follow previous works (e.g. Fernando & di Paolo 2004) using deterministic and continuous analysis assuming a set of standard nonlinear kinetic differential equations.

It is possible for two replicators with different growth rates to coexist within the chemoton, due to the regulating effect of the common precursor (see Figure 38 A, B). However, if the rate of metabolism is increased, it does not limit the growth of the superior template, X, any more causing thus the dilution of Y (see Figure 38 C). Therefore, by keeping the rate of metabolism low (i.e. around the value of replication rates: $k_m \approx k_x \approx k_y$), even competing exponential replicators with different replication rates can stably coexist, if they compete for a shared monomer precursor. Thus the chemoton does not even requires subexponential growth for coexistence (growth curves in Figure 38 are all exponential).

The above results of the extended chemoton readily suggest a further extension. It is possible to include heteropolymers as well (built up of different monomers), not just homopolymers. Heteropolymers imply a combinatorial explosion on the information maintainable inside compartments. Preliminary results indicate that simple heteropolymer sequences consisting of two types of monomers can still coexist, when sequences are sufficiently different, that is their Hamming distance is large enough. Otherwise, monomer-competition ensures that the faster growing template wipes the slower one out of the compartment. Because of the size limitations and the preliminary nature of these results, the mentioned experiments are omitted here, and left for a future publication.

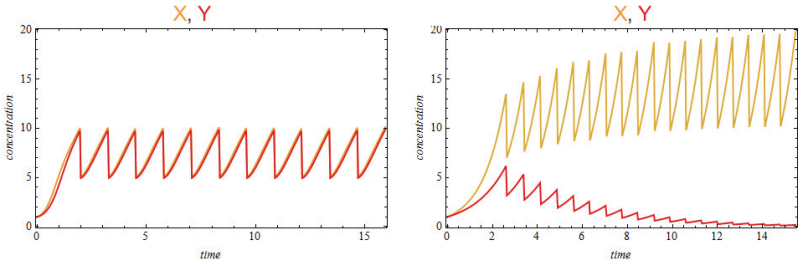


Figure 37. Two replicators in the chemoton. Metabolism is represented implicitly as the availability of monomers A and B. Growth rates for the dimers X and Y are $k_x = 1.0$, $k_y = 0.7$, and division happens when $X + Y > 20$. Initial concentrations are $A_0 = B_0 = X_0 = Y_0 = 1$. A) Coexistence of two subexponentially growing replicators: growth is regulated by the decay factor $d = 0.1$ of monomers and dimers. A and B have linear influx rates $f = 5$. B) Extinction of exponentially growing replicator: A and B have constant concentrations and there is no decay ratio for either the monomers or the dimers.

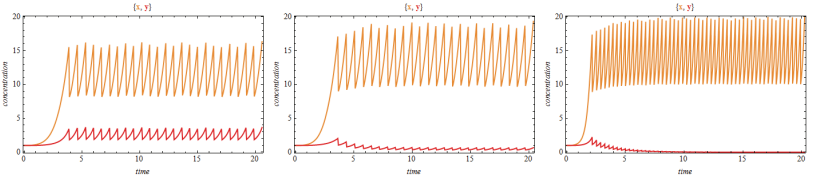


Figure 38. Coexistence of exponential replicators due to sharing a common monomer-precursor. Division happens when $X + Y > 20$. Initial concentrations are $A_0 = B_0 = P = 0$, $M = X_0 = Y_0 = 1$. A) Coexistence of replicators with different implicit growth rates: $k_x = 1.0$, $k_y = 0.1$, when $k_m = k_a = k_b = 1.0$. B) Coexistence of replicators with different monomer conversion rates: $k_a = 1.0$, $k_b = 0.1$, when $k_m = k_x = k_y = 1.0$. C) If the rate limiting k_m is increased ($k_m = 2.0$, $k_x = k_a = k_b = 1.0$, $k_y = 0.1$), the inferior replicator will practically go extinct (though the theoretical curve never reaches zero).

Analytic solution for the chemoton equations are rather complicated to derive, due to the strong nonlinearity of the system (because of decay factors) and the periodically occurring discrete division. Since the chemoton divides when its internal state reaches a certain critical value (for example, volume/surface ratio reaches a limit), the regulation of concentration is discrete in time. Volume and surface values can be modelled simply by assuming that the chemoton divides when the amount of all molecules (M, T, B) reaches a certain value. Since discrete division cannot be modelled analytically with differential equations, discrete regulation must be translated to continuous decay by assuming an Eigen-type flow reactor with continuous nonlinear outflow.

Thus, by default division happens when the membrane, and with it the overall volume reaches a certain size. With increase of volume, all enclosed molecular species increase in amount, until reaching the size limit at c. This means that at successive divisions, it is true that all molecular amounts add up to c ($\Sigma s_i = c$ where s_i indicates the i^{th} chemical species present in the chemoton). One can also assume that in equilibrium template molecules are regulated to always yield the same amount (c_{temp}) after successive divisions, that is: $\Sigma t_i = c_{temp}$, for all polymerization stages i.

The total growth of the system is $2\ k_m\ m$, which – in equilibrium – must equal the outflow of the system. Assuming that each chemical species is regulated by a continuous nonlinear outflow according to its actual concentration, we get a modified equation for the growth of the i^{th} species:

$$ds_i^* = ds_i - s_i\ (2\ k_m\ m). \qquad (27)$$

Comparison reveals that the flow-reactor approximation has a very good match with the discrete-time division model, apart from cases with small chemoton size (small c) or large difference in template replication rate (large k_y). In summary, nonlinear continuous outflow could be used to provide qualitatively similar results as those of the non-continuous (discrete) division model. This both means that replicators with exponential growth tendencies can coexist in the chemoton just like they would do in a continuous flow reactor, and that analytic solution could be derived more easily in case of the continuous than for discrete cases. This analysis is in progress.

4. Discussion

4.1. Lamarckian inheritance

As was discussed in section 1.6.2, Lamarckian inheritance is about the inheritance of acquired changes, about use and disuse and about being the antithesis of Weismannian inheritance. Using the replicator formalism, an exact definition can be given for Lamarckian inheritance.

First, it must be made clear that the inheritance of acquired characters and directed variation arising of use and disuse are two independent concepts. An acquired change can be directed or undirected, but both can be inherited. This implies that changes originating from use and disuse and changes from any other external source (like injury) cannot be distinguished on the level of information transmission, without losing the general meaning of "acquired." Since the variation introduced to the genotype (in-generation or next-generation) has no smell, inheritance cannot distinguish between directed or undirected changes. Therefore, any part that is changed (and is inherited) is part of the genotype. Koonin and Wolf states: "The crucial difference between 'Darwinian' and 'Lamarckian' mechanisms of evolution is that the former emphasizes random, undirected variation whereas the latter is based on variation directly caused by an environmental cue and resulting in a specific response to that cue" (Koonin & Wolf 2009a, p. 8.) which implicitly includes that both Darwinian (or Weismannian) and Lamarckian mechanisms are able to transmit any kind of change. If therefore the difference between Weismannian and Lamarckian inheritance is *only* in the directedness of changes, it would mean that the two topologies of information-transformation are identical, i.e. the two inheritance systems are otherwise the same. Now as this is obviously not true, the difference between Weismannian and Lamarckian inheritance lies elsewhere, and is not only about the directed or undirected nature of changes. At this point, we have to stick with the definitive difference of Lamarckian inheritance being able to pass on acquired variations.

If we accept, that changes can be directed or undirected, and that both mechanisms (Weismannian and Lamarckian) are able to transmit both types, four different cases can be distinguished. If directed variation is combined with inheritance, the specific form of directed Lamarckian inheritance arises (see Table 11). Directed in this sense means that those traits will be preferred (both phenotypic or genotypic changes) which are more adaptive in the given selectional setup. Who or what mechanism decides about this preference is out of the scope of this thesis.

Table 11. Changes in the phenotype and in the genotype (after Számadó & Zachar 2011a).

		Genotype inherits changes in the phenotype?	
		yes	*no*
Phenotype changes	*undirected*	undirected (blind) Lamarckian inheritance	Weismannian inheritance
	directed	directed (biased) Lamarckian inheritance	Weismannian inheritance with phenotypic plasticity

It follows from Table 11, that **Lamarckian and Weismannian inheritance systems are only possible if phenotypic changes are stored elsewhere than genotypic changes**, otherwise there is no difference between such changes. For example, if *in vitro* polynucleotide replication is considered, one can state that any phenotypic change to a replicator possibly changes the genotype (the base order). Consequently, both Weismannian and Lamarckian inheritance are only defined if there is an *a priori* distinction of soma and germline, that is there is division of labour between conserving data and interacting with the environment. The abstract correspondents of the germline and soma are the *genotype* and *vehicle* (which is an *interactor,* Hull 1988a, 1988b), respectively, or if they are not separated: the abstract *genotype* and the physical *body* of the replicator. It follows, that **if there is no interactor involved in a replication process, it could not be termed either Weismannian or Lamarckian**. Koonin & Wolf (2009a, p. 9) state: "the Lamarckian modality is associated primarily, if not exclusively, with the organismal level of complexity, and does not apply to the most fundamental level of evolution", i.e. to genes and alike. What they failed to see is that while their statement is valid, it is not restricted to the organismal level. Of course, most well-known examples refer to somatic inheritance (e.g. maternal antibodies, etc.), but as the soma and germline are instances of the more generalized concepts of vehicle and genotype it follows that the type of inheritance (being Weismannian or Lamarckian) can be applied to any replicator with a vehicle.

Thus, if all conditions are met for Lamarckian inheritance, the possibility to inherit changes originating from the function of e.g. a given organ (i.e. from the phenotype) means that information is inherited from the physical realization of the phenotype, which is the interactor. It is the interactor *interacting with*, or *adapting to* the selective environment, rather than the genotype itself. Therefore, the inheritance of acquired traits *sensu* Lamarck explicitly requires the **existence of two more-or-less distinct physical entities, one for adapting to the**

environment (the interactor) and one to store heritable information (the genotype). Figure 39 summarizes the relation of inheritance systems.

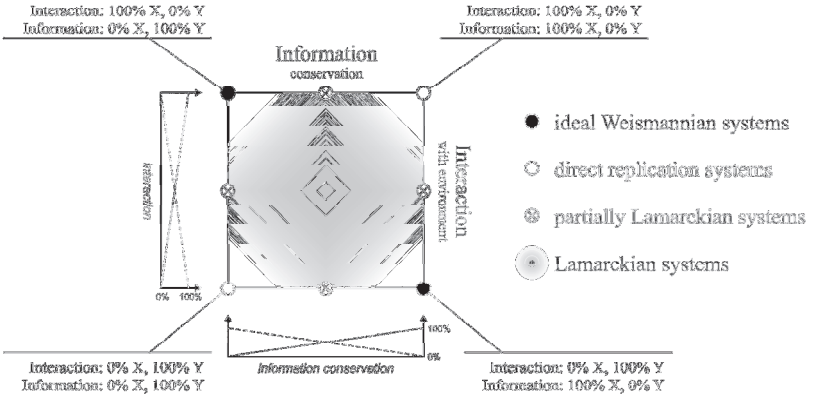


Figure 39. The functional continuum of inheritance systems. Inheritance systems are described by the interplay of two entities, X and Y, and two functionalities: *information* conservation and *interaction* with environment. Filled circles represent ideal Weismannian replicator/interactor systems, empty circles represent systems where only one entity plays both roles (i.e. no Weismannism or Lamarckism is defined), while any system around the center of the plot would be Lamarckian. For example, the upper left corner indicates that Y is responsible solely for information storage while X is responsible for interaction, meaning thus that Y is a perfect germline and X is a perfect soma, and the process is ideal Weismannian inheritance.

Now if the interactor is represented as a distinct entity (even if it is a vehicle, containing all the replicators), the topology of information-transmission can be drawn. Simplifying Figure 15, one can come to the conclusion that there are three basic inheritance methods, depending on 1) the level of selection; and 2) the route of information transmission, as is shown in Figure 40.

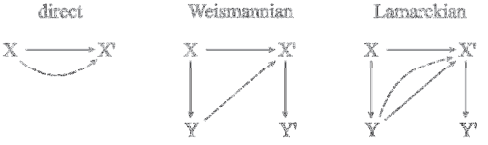


Figure 40. Inheritance methods depending on the presence/absence of an interactor, and the topology of information transmission. Dashed arrows indicate indirect effects caused by selection.

As it was implied in Figure 39, the share of functionalities between entities is not discrete or exclusive, there can be partial solutions as well, where both entities share the same functionality (interfacing or storing). Consequently, and as it was proven in section 2.5.8, Lamarckian inheritance has two extrema. If both roles (storing phenotypic and genotypic changes) are played by one entity (either X or Y), the method simplifies to the case of direct replication. This happens when the Lamarckian method of Figure 40 lacks the X → X' transmission. On the other hand, if entities fully separate roles, and there is a perfect division of labour, inheritence method is that of Weismannian. In that case, the Lamarckian method lacks the Y → X' arrow. Thus, theoretically, there is a continuum of informational inheritance systems where Weismannian, Lamarckian and direct inheritance systems can gradually evolve toward each other. This was explored under 3.2 Evolution of division of labor.

Considering all the facts so far, the formal definition of Lamarckian replication is as follows:

Lamarckian replication is a special case of informational replication with a distinct interactor, but without fully separated roles of storing heritable information.

Consequently, both entities (the replicator and the interactor) may inherit information. Furthermore, the special nature of Lamarckian inheritance may induce other important factors.

First, it is true, that the replicator is the template of the interactor, but the interactor is also the template of the next generation of the replicator. In case of the direct replicator → replicator transmission is missing (X → X' in Figure 40), the interactor becomes an equally valid replicator as the other entity (though replication becomes direct).

Secondly, as the interactor is usually translated from the replicator using a many-to-one mapping (e.g. proteins from DNA), or one-to-many mapping (the same genotype might induce different phenotypes of organisms), it is clear that the X → Y → X' route **must** include a probabilistic transmission, to stably yield such X' as result, that is equivalent to X (otherwise the whole process is not replication any more). Though it does not directly result from the topology of transmissions, but it is usually true, that the **indirect X → Y → X' route is lossy**, and cannot stably maintain all the information present in X by itself alone. Contrarily, the **direct X → X' route does not loose information**. This is the most important fact that ultimately distinguishes Lamarckian from direct or Weismannian inheritance. The information loosing nature of the Lamarckian topology can be countered by the presence of the direct genetic replication of X. An information-loosing replication method on its own is not really replication, as it cannot stably maintain information for an indefinite time.

An important remark is in order. According to this definition of Lamarckian replication, the **inheritance of memes is not Lamarckian**. As memes (or any kind of cultural replicators) replicate between human brains, there is no way mental information of one brain can be transmitted *directly* to the other brain, parallel to the indirect method of words, spoken or written. This would involve telepathy, or direct neuronal topology-transmission – both impossible at the moment. Thus, as memetic inheritance fails to deliver such direct inheritance methods, it lacks one crucial property to be Lamarckian in nature (Weismannian inheritance was excluded in the first place because of same reasons). Then what kind of replication is involved in memetic inheritance? As the brain → words → brain transmission is highly lossy in nature (there is no debate over this), it means that memetic inheritance at all lacks any direct, stable inheritance method, which ultimately means that memes are not replicators. While many already made this conclusion based on other considerations, there is still a very strong bias for believing that cultural inheritance does involve replication.

There is a way to resolve this situation other than discarding memes at all as replicators. First, the iterative nature of imitation, social learning, etc. can greatly enhance the fidelity of a replication step. Second, parallel replication methods **do** exist in cultural inheritance, thus there can be more than one route to establish information transmission from one brain to the other. Information about how to make a tool for example can be passed on by direct verbal communication, via written instructions, visual guides over the internet, and so on. It is true, that none of these is completely without loss of information, but overall, they do quite a good job maintaining information (culture) reliably for quite a long time. This was made possible by 1) the early emergence of compositional languages, 2) the invention of writing, 3) invention of printing, and 4) further, more and more stable ways of storing and spreading information. These issues are discussed in depth in two upcoming papers by Számadó & Zachar (2011a and 2011b). Accordingly, memetic replication is depicted in Figure 41.

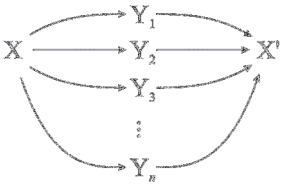


Figure 41. Cultural inheritance may exploit multiple parallel pathways between individuals. X denote mental structures in the brain (items of the internal culture), Y-s indicate various transmission intermediates, like words, books, other artifacts (items of the external culture), that are used by the acceptor to inference original X.

The metaphorical interpretation of cultural inheritance states that it is not the individual who acquires changes but the cultural items themselves. If understood literally, culture would involve

the biological inheritance of acquired cultural traits. According to some, since culture does not use the genetic inheritance system but social transformation, it cannot be said to be Lamarckian (cf. Kronfeldner 2007, p. 501, Hull 1982, p. 309-311 and Hull 2001, p. 121). Nevertheless, the informational topology clearly follows the Lamarckian way, as it was demonstrated.

4.2. Phenotypic replication

According to the formalism presented here, there is no such thing as phenotypic replication. This is because the phenotype is not an entity, but an abstraction of the replicator, specific for a certain environment, therefore it cannot be copied. It could be the replicator, or its translation, the interactor, that is responsible directly for the phenotype. Phenotypic traits, that seem to be passed on in case of organisms, are part of the phenome. What actually distinguishes phenotypic replicators from e.g. genetic replicators, on one hand, is that for example prions do not have distinct interactors. On the other hand, other phenotypic replicators like memes do have interactors (external utterances), but then the difference lies in the topology of information: memes inherit information directly from the interactors.

Therefore, phenotypic replication refers to informational replication where either there is no interactor (as in case of prions), or the template of the interactor is the replicator, and the template of the replicator is the interactor itself (memes). Due to this particular circularity, the extrema of Lamarckism was proven to be the same as either Weismannian replication or direct informational replication (cf. section 2.5.8). The three different topologies are depicted in Figure 15. This also means that the genotype of a "Lamarckian" organism is not necessarily coded in one medium (the DNA) but may be dispersed in various media (DNA, chromosome methilation, immune system, brain, etc.).

Phenotypic replicators indeed form a different subgroup of replicators, though the term “phenotypic” is misleading. Originally, it was meant to distinguish the possible digital information in prions and memes from the phenotypic representations (3D conformation, and e.g. communicative performance) indicating that it is not the sequence that gets transmitted, but rather the representation of the phenotype. The true difference however between genetic and phenotypic replicators, is not in the medium heritable information is encoded to (DNA sequence, prion conformation, phonemes, letters) but in the topology of information transmission: which intermediates are correlated with others, and which are under direct selection?

In case of genetic replicators, the actual genotype is well-concealed from selection, and the interactor interfaces the environment instead of the underlying replicator. Prions and memes

however are directly exposed to the environment, and inherit whatever changes they acquire (prions with limited, memes with unlimited heredity).

4.3. The levels of selection

In a complex adaptive system, there are multiple levels where mutation can drive evolution. For example in a Weismannian system, mutation can change the lowest level of representations (the genome, as point mutations in the base-order of DNA) or higher levels of representation (e.g. doubling or reshuffling whole genes, or even changes in the phenome). Depending on the level of mutation, the experienced mutational kernel may vary greatly, either enhancing or blocking adaptive evolution. Accordingly, many levels can be specified, though not all of these are isomorphic, see Figure 42.

The first, innermost set represents the innermost replicators in a complex adaptive system (like DNA in cells). In general, it is an autocatalytic cycle, with multiple stages, that drives replication. Accordingly, each stage of the cycle (A, B, ...) is isomorphic, representing the same amount of information (*levels of the germline*). Nevertheless, even these isomorphic levels could react differently to mutation, thus selection can discriminate between the stages (still being at the same level). Enclosing the autocatalytic cycle into a higher-level vehicle might define a new level of selection, if the vehicle is a unit of selection (like the cell). It can be further enclosed in an even higher-level vehicle (the organism), and so on (toward the extended phenotype). There are two important points here. First, mutation applied to these hierarchic levels (*levels of the soma*) do not necessarily propagate to inner levels and/or next generation entities. This depends on the actual inheritance system(s) at work. Second, selection on any of these levels usually affects both lower and higher level entities. These effects can be **direct** (like gene expression at the cell level has direct upward effects; cell death has a direct downward effect), or **indirect** (gene expression propagates upward rather indirectly to the topmost organism level; gene evolution caused by organism-level selection is indirect downward).

For example, at the lowest level, non-informational chemical replicators might drive the metabolism of an enclosing vehicle. It is possible, that the composition of the population of these replicators inside the vehicle is forced to an attractor because of the kinetic setup. Now, if the vehicle is replicated as well, it is possible that the composition of the population of exact non-informational replicators is transmitted stably to daughter cells. If there are multiple attractors that are inherited stably, **there could be informational replication and limited heredity at a**

higher level than the level of the exact replicators. One can realize how enormously complex such a system can be from an informational point of view.

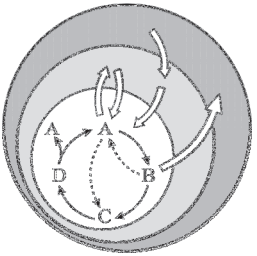


Figure 42. The two dimensions of levels of selection. Entities at the same level are informational isomorphs (like A, B, C and D), while entities enclosed in other entities are not necessarily isomorphic as they might depend unidirectionally on each other, without directly closing the informational loop. Normal and dashed arrows indicate in-level transmissions, empty arrows between-level transmissions (the two orthogonal dimensions).

Accordingly, the following factors are identified that may contribute to a complex inheritance system:

- **in-level topology**: lowest-level autocatalytic cycles may exhibit different selection at different intermediates of the cycle, with different mutation rates and with different exploration distributions, due to complex transmissions between intermediates of the cycle;
- **between-level topology**: there can be various transmission processes going from various levels downward (incorporation of acquired traits) or upward (gene-expression, regulation, etc.);
- **between-generation topology**: the information passed on to the offspring could be collected from various levels (cf. genetic and epigenetic inheritance);
- **transmission property**: in-level, between-level and between-generation transmission processes can be unambiguous (DNA replication, RNA translation), ambiguous (protein retranslation), or lossy (cultural transmission);
- **selectional topology**: selection can cause direct and indirect effects both downward or upward between levels, or directly at the same level on different intermediates of the cycle;
- **recursive embedding**: there can even be individual autocatalytic cycles in higher levels, further increasing the complexity (e.g. maternal antibodies are replicating at a different level inside the organism than germline DNA, however both are passed on to offspring);
- **other topologies**: lastly, it is possible for each single transmission to have different informational, material, etc. topologies (according to Figure 15).

It is futile and pointless to address all possible situations, as the number of combinations is infinite. As a conclusion, the level-of-evolution debate is left intact here. One must notice

however, that the alarming complexity of adaptive, linked inheritance systems can be described using a limited set of general, low-level patterns. These patterns were examined and detailed in the formalism presented here (like the trio of informational topologies: direct, Weismannian and Lamarckian replication).

According to the multilevel selection discussed above, some remarks are in order. From the viewpoint of adaptation, it is often more convenient to change the interactor or the vehicle (i.e. the phenome), than its original hard plan, the genes. Mutations in the former may more often induce useful '*functional*' changes, than mutations in the latter, which would rather change the low-level representation, i.e. the '*positional*' information of the entity (see Figure 43). The actual effect of a mutation however greatly depends on how a certain entity is represented. Since interactors are translations of underlying replicators, they represent a different degree of compositionality. In this sense, mutations may have a more functional effect, if affecting higher level entities, like the interactor, than lower level entities, like the replicator. After all, more compositional representations, yield higher-impact changes (like chromosome recombination) than low-level representations, e.g. point mutations in the DNA.

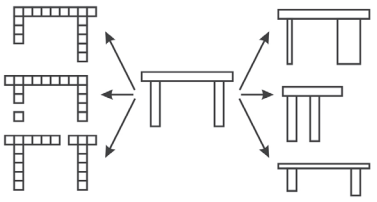


Figure 43. Low-level and high-level mutations. The outcome of evolution depends on what level mutations act on. Lower level (positional) representations usually tolerate more changes (as there are more modules), but produce less useful mutations (tables on the left), while higher level (functional) representations may yield useful functional variants (right). This is of course depends on the exact nature of representations (figure was kindly provided by Chrisantha Fernando).

Following this logic, one can argue that the best way of adaptation is to change the phenome directly. Obviously, this does not have long-lasting effects in case of Weismannian inheritance systems, but this phenomenon can be exploited in case of Lamarckian topology.

The general idea is that depending on the level of representation, a mutation may induce changes of different magnitude (cf. Figure 44). This depends on three factors:

1. the topology of information-network (the full graph);
2. the nature of transmissions (double arrows) (unambiguous, ambiguous, lossy);
3. the nature of mutations (μ_i, applied to nodes).

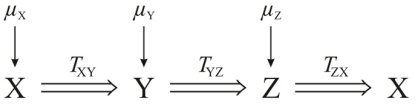


Figure 44. Propagation of mutation-induced changes along the topology of replication of an informational replicator. T_{XY}, T_{YZ} and T_{ZX} are various transmissions between autocatalytic cycle intermediates X, Y, and Z; μ_X, μ_Y and μ_Z are mutational distributions applied to the intermediates. Mutation, in general, is part of a transmissional channel, though for simplicity, transmission and mutation can be separated. Therefore, mutations are always applied to nodes *after* transmissions, that is, the outcome of the T_{XY} transmission is mutated to yield the erroneous translation of X.

To end up with the original entity X at the end of the whole process, all mutations must be neutral (or there should be no mutation at all), and all elementary transmissions should comply so that the whole process becomes unambiguous (from X to X). Otherwise, if the overall process is ambiguous, it would suffer from a seemingly larger mutation rate than the one actually implied by environment (the cumulative effect of all μ_i). The very same effect was proved for the GARD model, where the overall mutation rate may be larger than the actual reproduction rates, due to the stochastic nature of growth and replication (see Vasas et al. 2010).

The most important consequence of the informational topology is the fact that the overall *a posteriori* mutation rate can be estimated if both the *a priori* mutation rates and transmissions are known. If there are N different (successive) stages of replication, and every transmission is transcription, then the overall mutation rate (assuming that no back mutation happens) is:

$$\overline{\mu} = \prod_{i=1}^{N} \mu_i. \tag{28}$$

Thus if all μ_i are equal, the overall mutation rate scales rapidly with the number of intermediate stages. If, however, transmissions are translations, replication gets complicated (a calculation was provided for Weismannian and Lamarckian topologies in section 3.1). Since replication has to yield X starting from X, a translation from X to Y necessarily involves an inverse mapping (reverse translation) to yield X' from Y. If no mutation is allowed then all the stages of replication are isomorphic. If mutation is present, then neutral changes are allowed to appear in intermediate stages that do not affect the result (stages are still isomorphic). The important point however is that in Lamarckian topology, intermediate stages maintain a higher diversity, thus they have a better chance that certain neutral mutants may drive out the population from a local optimum.

5. Classification

The formalism reveals that many aspects of previous replicator definitions are redundant or refers to the same thing. A brief discussion is given to relate, sort and filter these concepts, establishing thus a fixed terminology. A hierarchical classification was provided by Zachar & Szathmáry (2010), which is now reworked and extended, according to new results. Many of the cited concepts and definitions can be found in the Appendix.

5.1. Types of replication

The replicator continuum can be partitioned according various properties, defined by the four basic aspects outlined in chapter 2.

Undoubtedly, the most important and evolutionarily most interesting type of replicators are informational ones. The concept of **informational** and **non-informational** replicators (*sensu* Orgel 1992), is present in various disguises in many definitions. Maynard Smith, focusing on selectional and evolutionary potential, used the terms *units of selection* and *units of evolution* (Maynard Smith 1987, Szathmáry & Maynard Smith 1993). As it was already discussed, all replicators are units of selection, and informational replicators are the only true units of evolution. Later, Szathmáry introduced the terms *processive* (or *holistic*) and *modular* mode of replication (Szathmáry 1995, 2000), to signify the structural requirement of informational replication. Accordingly, informational replicators must be modular, and their replication is compositional. Wächtershäuser distinguished between autocatalytic processes by the scale of evolution they can undergo, as processes being capable of only *macroevolution* and of macro-, and *microevolution*. Consequently, he termed the former as *piecemeal* uptake of components, contrasting modular buildup during replication (Wächtershäuser 1988). While non-informational replicators are replicated piecemeal, a complementary pair readily suggests itself: informational replication proceeds *bitwise*. Later, Wächtershäuser used the terms *analogue* and *digital*, which correspond to replication *without* and *with template* (Wächtershäuser 1994), respectively to non-informational and informational replicators. In summary, all these definitions refer to the same things and the partition the replicator space identically. However, there are other classifications that yield different partitions.

For example, Griesemer referred to such replication processes as *exact* and *inexact* replication, focusing on development (Griesemer 2000b, p. 74). In his words, exact replicators are AC intermediates without any form of development, while inexact replication is the

replication of reproducers with full development. According to the Formalism, exact replication refers to replication where the development function is reduced to nothing (i.e. *d = identity* considering section 2.6.1). Though Griesemer did not require informational replicators for development, the Formalism explicitly states, that development requires an informational template, thus inexact replicators of Griesemer are informational replicators with a complex development function, while exact replicators correspond to either non-informational replicators, or the *genotype in the narrow sense* of informational replication: it has *d = identity*.

The informational domain of replicators can be further partitioned to subtypes. The r**epresentation of information** defines a varied subhierarchy. Concerning **encoding**, Gánti specified that information could be stored in the quantity, proportion, or arrangement of signals (modules) (Gánti 1987, p. 116.). The **dimensionality** of encoded information is also an important feature: polynucleotides like DNA and RNA encode information in one dimension. Lipid vesicles, genetic membranes, and similar structures maintain information in a 2D surface. As Gánti recognized for the chemoton, compared to von Neumann's self-reproducing spatial automaton: "[...] the organization of fluid automata is independent of the direction of geometrical space, thus the new parts coming into existence do not destroy the organization of the fluid machine (though they influence its operation)." (Gánti 2003, p. 43). Prion proteins assumingly have their infective potential encoded in their 3D structure. The neuronal substrate might encode neuronal replicators in three-dimensional topology according to the Neuronal Replicator Hypothesis. Important specification for the representation is the actual **medium** into which information is encoded: the range of possibilities is extremely wide. From simple chemicals like nucleotides, amino acids, through lipid composomes and fluid mosaic membranes to neuronal and *in silico* bits almost anything can code the information that is to be replicated.

A further division in the informational domain of replicators is defined by the **dependency of components**. Dependency can be *spatial* or *temporal*. Spatial dependency means that the construction of an informational replicator depends on a spatially arranged physical pattern. Accordingly, the temporal order of included components (modules, building blocks) during construction does not matter, only the final spatial pattern. Contrarily, if dependency is temporal, inclusion sequence of components is fixed in time, but not spatially. This can be the result of a very strict and chain-like affinity landscape of components. *Spatial* informational replicators can be storage based (like DNA, ribozymes), compared to *affinity based* informational replicators, which usually have multiple attractors (lipid vesicles, GARD). The replication of the former is governed by structural dependency, which manifests in *spatial order*, while the replication of the

latter is regulated by the pairwise affinity of components, resulting in an explicit *temporal order*, but not necessarily in spatial order.

There are replicator types, which are context-dependent: properties of the replicator do not define these types on their own, but it is the actual environment that specifies it.

The **hereditary potential** of a replicator is one such aspect. Szathmáry & Maynard Smith introduced the concepts of limited and unlimited hereditary potential (Szathmáry & Maynard Smith 1993), to pinpoint the evolutionary capacities of certain replicators, which are context-dependent. It means that the potential of a replicator depends on the actual environment it is replicating in, including such variables as population and search space size. Later, this dichotomy was refined to include and explicitly differentiate non-informational replicators as replicators with no hereditary potential (Zachar & Szathmáry 2010).

Another contextual distinction is between storage-, and attractor-based **maintenance** of information Hogeweg (1998), also at Szathmáry (2000). The actual method of how information is maintained in case of a population of replicators is rather independent of the nature of the individual replicators and depends on the dynamics of the embedding environment. Inheritance of the replicator networks of Hogeweg (1994), composomes of the GARD model at Segré et al. (1998) and the maintenance of the quasispecies (Eigen 1971) are all attractor-based, while maintenance of the genetic information is storage based. Now, a hypothetic gene with probabilistic codon-translation would have to obey both template-information and the dynamics of the probabilistic affinity of codons and anticodons, being thus partially storage-, and attractor-based. Consequently, there is a continuous bridge between storage and attractor based systems, and one can assume that more error-prone, attractor-based, probabilistic systems gradually evolve toward more precise deterministic ones, just as it happened with DNA error-correction, climbing over the error threshold. Escaping the attractors of the environment/affinity-defined dynamics of a system must have been one of the most important steps in early template evolution. Many attractor-based systems are still at work in organisms. Steady-state inheritance systems are responsible for the inheritance of certain properties of the cytoplasm, like the presence/absence of gene products, which further regulate their own expression, cf. Jablonka & Szathmáry (1995).

The autocatalytic nature of replicators allows for such autocatalytic cycles, where no component is replicated individually, but the collective effort of all the components replicate the group as a whole. According to Gánti, still all the intermediates of such (reflexively) autocatalytic cycles are replicators, though they do not replicate individually, but as part of a set. Collective replication is thus a complex case of an autocatalytic cycle where almost all members

are facultative autocatalysts (cf. Figure 1). Thus, some replicators are **solitary**, while collectively replicating ones are called **ensemble** replicators (Szathmáry 2000). Examples are the components of composome in the GARD model, as they only replicate with the replication of the composome. The solitary/ensemble dimension is orthogonal to all other dimensions, but is strongly biased toward informational replicators. This is because both solitary and ensemble replicators assume a set of components (building blocks, cycle intermediates) that together perform replication and together form a replicator. Such composite replicators are often modular (if they are able to inherit changes), which is the definition of informational replication

If multiple entities are involved in replication, their material, selectional, and informational relationships define dynamics. One such particularly important interaction is provided by the **interactor** (Hull 1980), which is a distinct entity dealing with selection. The interactor does not require that the replicator should be informational (see Figure 8), though, usually, only informational replicators have interactors. The presence of the interactor (or even a vehicle) redefines the level of selection, which could change the dynamics of the system. If no interactor is defined, replication is *direct*, if there is a distinct interactor, various interesting topologies of the intermediates can emerge in the replication system.

Such topologies – according to the formalism - are defined by 1) the **level of selection** (the interactor) 2) and the **generation of intermediates**. Intermediates are causally related and their transformations from on to another stage can be defined by either deterministic or probabilistic transformations (or transmissions, in case of informational replicators). According to these specifications, the most significant topologies are *direct*, *Weismannian* and *Lamarckian* inheritance. It must be emphasized, that this distinction is only defined for informational replicators: there is no sense talking about non-informational Weismannian replication at all. Also, the exact definition of genotype and phenotype in the formalism above makes it clear, that the distinction of **genotypic/phenotypic replication** (Szathmáry 1999) *per se* is fallacious, as even in case of such replicators, information is inherited either the direct, Weismannian or Lamarckian way, but the phenotype can never be copied (only the phenome). Furthermore, with the appearance of the interactor, **division of labour** becomes possible, as there are two entities to share tasks, see Table 6. In case of Weismannian inheritance, *full division of labour* is present between replicator and interactor (and germline and soma, if the concepts are extended). Lamarckian inheritance systems exhibit only *partial division of labor*, as the interactor itself is a replicator. As direct replicators do not have an interactor, *no division of labour* is possible.

The informational topology of replicators is not the only one: there can be different topologies for material, functional, or other aspects. For sake of simplicity, these are not discussed further

here, noting though that e.g. material topologies follow the same general lines that were designed for informational topologies.

Replication has two more orthogonal aspects: **probability** and **entropy**. Probability specifies, that according to the nature of successive elementary transmissions forming the chain of a complex transmission, replication can be *probabilistic* or *deterministic*. It is probabilistic, if ambiguous transmissions are involved, which means a variable intermediate in the cycle. Such variable intermediates can maintain higher levels of robustness. According to entropy, replication can be *stable* or *lossy*. Lossy replication (due to the specific topology and transmissions in the transmission chain, cf. point 6 of section 2.5.8) eventually degrade the original information content of the replicator, or results in attractor-based inheritance, where the information that is maintainable, is defined by the mutational rate (i.e. the dynamic control space) instead of the cycle intermediates. Note however, that such lossy replication, by the strictest sense, is not replication at all, as it cannot reliably and stably maintain information for an indefinite time. It follows that in case of probabilistic or lossy transmissions, not all sequences are equally stable. The maintenance of information and entropy represent orthogonal dimensions, as it was indicated in Table 3.

5.2. Classification

The set of aspects defined in the Formalism specifies the dimensions along which the replicator continuum can be classified. Unfortunately, these dimensions are mostly orthogonal, thus a clear-cut full hierarchy cannot be drawn. Instead, a basic hierarchy of some of the dimensions is given in Figure 45.

A description of known replicators based on these dimensions is provided in Table 12. For example, a **gene** is an informational, Weismannian biological replicator. The transmission of replication is an almost deterministic copying mechanism (unambiguous), and information is maintained storage-based. The inclusion of new modules has no temporal, only spatial order (i.e. the actual inclusion time of a base does not matter, only the position where it is bound). Information is encoded in the 1D arrangement and ratio of modules.

Contrarily, the GARD model assumes an ensemble replicator-set which can only replicate *together* if reaches a certain size, that is informational, with direct replicative topology, and is a micelle-like assembly of molecules. Replication is probabilistic (ambiguous) due to probabilistic growth and split processes and is mostly attractor-based. Still the assembly works as a vague template, causing some very limited storage-based behaviour as well, though this eludes in the

long run. The inclusion of modules depend on the previous inclusions, but not on the position of components, thus temporal order does matter, while spatial order doesn't. Information is encoded in a 2D surface, in the proportion of different molecules.

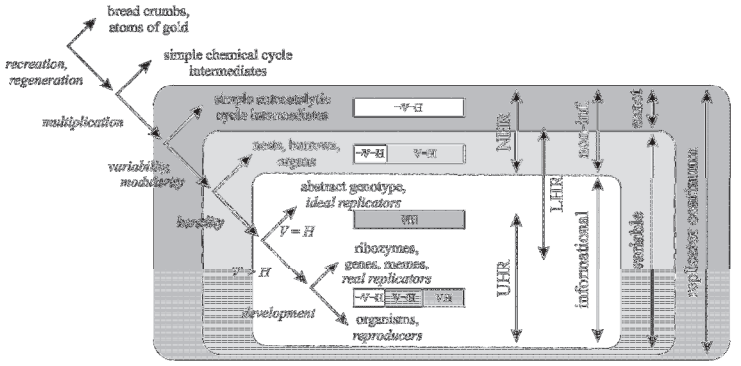


Figure 45. Hierarchy and classification of multiplying entities based on multiplication, variation and heredity. Each downward arrow introduces a new feature. Inset diagrams show the parts of the given replicator regarding the model of Figure 3. The replicator continuum can be categorized along various dimensions: classes based on the informational aspect are shown on the right. UHR, LHR, and NHR stand for unlimited, limited, and non-hereditary, respectively.

Accordingly, the set of replicators is divided to exact (holistic/processive) and variable (modular) replicators. All exact and some variable replicators are non-informational, while many replicators with variable structure can inherit variability, thus are informational replicators. Informational replicators might use a physical template encoded in some spatial structure or a temporal template defined by catalytic effects of components on new recruits. Both physical and affinity "templates" can replicate deterministically (as physico-chemical laws allow it), thus the maintenance of information is storage-based. Alternatively, replication can be probabilistic, maintaining information defined dynamical attractors rather than stored sequence-like information. The amount of information that can be maintained, in general, is much larger for storage-based systems.

From another viewpoint, informational replicators are distinguished based on informational and selectional topology of components. Prions, ribozymes, and nucleic acids in general are assumed to replicate according to a direct informational topology, as there is no interactor. Organisms, cells, and genes with proteins are subject to Weismannian inheritance. However, organisms also can replicate some of their information in a Lamarckian way. Similarly, memes

are subject to Lamarckian inheritance, with reverse translation and inference. It must be noted however, that reverse translation can be reverted to simple replication, and Lamarckian inheritance to direct inheritance in situations where there is full division of labour between the interactor and the replicator. In case of an A → B → A' → B' → ... transmission, if B is under selection directly but not A, then the system can be simplified to direct replication: B → B' → ... Nevertheless, such direct inheritance systems with reverse translation present in the chain of replication are replicators with variable intermediates, meaning that the intermediate offspring still exhibit a higher amount of robustness than is expected in cases where there is no ambiguous translational step.

Table 12. Classification of inheritance systems. en = ensemble, sol = solitary, W = Weismannian, L = Lamarckian, S = storage-based, A = attractor-based, D = deterministic, P = probabilistic, LH = limited hereditary, UH = unlimited hereditary, *q* = quantity, *p* = proportion, *a* = arrangement, n/s = not specified. Extended from Szathmáry (2000). Note that the formose reaction is not an inheritance system, as it has no hereditary potential. Underlined letters indicate the higher level of replication if multiple levels are present in the given system.

	informational	*genotype is encoded in...*	*interactor*	*level of replication*	*set*	*transmission topology*	*maintenance*	*transmission probability*	*material overlap*	*development*	*evolutionary potential*	*inclusion order*	*dimensionality of encoded information*	*encoding*
crystal growth	hardly	cell errors	none	unit cells	sol	direct	S	D	no	no	very LH	spatial	3	*a*
Penrose plywoods	could be	block properties (marks)	none	blocks	sol	direct	S	D	yes	no	LH	spatial	1, 2	*q, p, a*
RA protein networks	yes	composition of network	none	protein population	en	direct ?	A	n/s	can be	?	LH	temporal?	n/s	*q, p, a*
genes (DNA)	yes	base order	proteins	nucleotides, sequences	sol	W	S	D	yes	no	UH	spatial	1	*p, a*
GARD	yes	composome composition	non	composomes	en	direct	A	P	yes	growth	LH	temporal	2	*q, p*
hypercycle	can be	templates	can be	cycles and hypercycles	sol, en	n/s	S	D, P	can be	no	LH/UH	n/s	n/s	n/s
SCM	yes	set of templates	compartment as vehicle	templates and compartments	sol, en	W	A	D, P	yes	growth	LH/UH	spatial	1	*q, p, a*
ribozymes (RNA)	yes	base order	none	nucleotides	sol	direct	S	D	no?	folding	LH/UH	spatial	1	*p, a*
formose reaction	no	–	none	intermediates and cycle	sol	direct	S	D	yes	no	none	–	–	–

	informational	*genotype is encoded in...*	*interactor*	*level of replication*	*set*	*transmission topology*	*maintenance*	*transmission probability*	*material overlap*	*development*	*evolutionary potential*	*inclusion order*	*dimensionality of encoded information*	*encoding*
prions	could be?	3D conformation	none	prion proteins	sol	direct	S	D	no	no	LH	–	3	*q, p, a*
genetic membranes	yes	protein composition	none	vesicles	en	direct	A	P	yes	growth	LH	temporal	2	*q, p,* (*a*)
chemoton	yes	template composition	compartment as vehicle, metabolic intermediates	templates and chemotons	sol, en	W	S, A	D, P	yes	yes	UH	spatial	1	*q, p, a*
cells	yes	genome, epigenetic traits	the cell as a vehicle	genome and cell	sol, en	L/W	A/S	D, P	yes	yes	LH/UH	temporal, spatial	1, 3	*q, p, a*
Eukaryotic cell differentiation	yes	cytoplasm config., chromatin marking, etc.	cell	"epigenome" and cells	en	L	A/S	D, P	yes	yes	LH/UH	temporal, spatial	1, 3	*q, p, a*
Neuronal Replicator Hypothesis	yes	topology, spike pattern	cognitive performance	neurons, groups of neurons	sol	L/W	S?	?	no?	?	UH	spatial?	2, 3	*q, p, a*
words	yes	?	linguistic performance	words, minds	sol	L (W)	S?	P, D	no	?	UH	temporal	1	*q, p, a*
grammatical rules	yes	?	production & parsing efficiency	constructions, rules	sol	L (W)	S/A	P, D	no	?	UH	probably temporal	?	*q, p, a*
memes	yes	?	cultural items	items, concepts, minds	sol	L (W)	S/A	P, D	no	?	UH	spatial, temporal	multi?	*q, p, a*
computer viruses	yes	bits of memory	various functions of the virus	viruses	sol	direct	S	D	no	no	LH	spatial	1	*q, p, a*

6. Conclusions

Replicators are crucial objects of evolutionary biology. Their cumulative evolution lead to the emergence of complex, adaptive systems, like life, the immune system, and perhaps language, culture and cognitive capacities as well. Major evolutionary transitions are results of the evolution of replicators. However, replication (and all related concepts) is a universal phenomenon, independent of biology. Consequently, a multitude of replicator candidates were suggested in various fields. Studies of self-assembly, reproduction and (self-)replication in chemical, (proto-)biological, linguistic, cultural, neuronal, digital and kinetic systems have accumulated an impressive amount of theoretical and experimental knowledge in the last three decades.

The replicator concept was thoroughly revised in the thesis with the help of the Replicator Formalism, a generalized, field-independent theoretical framework of replication. It is a bottom-up approach based on earlier works presented in Zachar & Szathmáry (2010) and Zachar et al. (2010). The two major reasons for establishing the formalism were to provide a conceptual hierarchy of various replicator classes (to classify candidate replicators from simple autocatalytic intermediates to organisms), and to suggest a possible evolutionary hierarchy, outlining certain steps in the origin of inheritance systems. As the concepts of replicator, interactor, genotype, phenotype, template, vehicle, and many more are independent of any level of organization and field of science, they were extended to their full potential, to cover the widest possible replicator-space.

Accordingly, the formalism provides a non-biological, clear and informational way to identify and analyze different replication systems. Using the formalism as a conceptual tool, useful insight was gained about the nature of inheritance systems. The formalism also has provided a platform for modelling. A complex modelling and simulation environment was developed in the symbolic programming platform *Mathematica* (by Wolfram Research), for experimenting with a wide range of informational replicators and inheritance systems in replication-selectional scenarios[5]. Important findings of the formalism and major results of the experiments are briefly discussed here.

The theory of replication and the Replicator Formalism especially build on the four orthogonal aspects of replication: *causal*, *selectional*, *stoichiometric,* and *informational*. Aspects

[5] The modelling software is available upon request.

define the criteria of units of evolution: *correlation*, *variation*, *multiplication,* and *heredity*, respectively (Muller 1966, Maynard Smith 1986 and 1987). Non-informational replicators lack the informational aspect, therefore lack heredity. Causality and the selectional aspect are independent of each other, which means that selection does not require causal transformation and vice versa: entities in a population can undergo selection without any transformation or information-transmission potential.

The group of units of evolution (with attributes variability, multiplication, and heredity) and units of selection (variability and multiplication) were extended accordingly to include units of sorting. Such entities are able to undergo a single selection event, but there is no guarantee that they multiply. Consequently, they might not be subjects to successive selection events. While units of selection refer to any replicator and units of evolution to any informational replicator, units of sorting define a group of entities *preceding* real replication.

It was proven that replicator equivalency is relative. This means that parent and offspring entities do not have to be similar in "some relevant aspects," or maintain structural identity or even similarity at all. The only thing important is that parent and offspring are phenotypically identical, and – as part of this equivalence – the offspring is able to produce more phenotypically identical entities. Whether it is structure, conformation, information, or any kind of pattern that is inherited and makes the offspring phenotypically similar to the parent is irrelevant, while the equivalence relation holds! In addition, relativity means that whether an entity is actually a replicator or not, depends on the sorting function of the actual environment.

The useful concept of the interactor introduced by Hull was generalized. Accordingly, the interactor is a unit of selection. The interactor need not be informational. If informational, than the replicator is the template of the interactor. The interactor is indispensable for more complex inheritance systems: both Weismannian and Lamarckian inheritance methods require the presence of an interactor. This interactor can even enclose the (genetic) replicators: such interactors are called vehicles. The vehicle is the generalization of the soma; the genotype is the generalization of the germline.

Based on these details, it was realized that there is a topology of information transmission underlying any replication, defining the route of information through the various entities involved in replication. This topology cannot be represented directly by a stoichiometric equation, as it does not necessarily agree with the material topology (how parts of entities combine/separate during reactions). The informational topology is defined by templates. The template is the extended concept of the genotype: even non-replicative transmissions rely on information templates. The genotype in the narrow sense defines the set of parts of the replicator,

which, if changed, inherits changes. For example, the genotype in the narrow sense is the abstract base order of a gene, while the genotype in the broad sense is the actual coding, physical DNA strand.

The three basic inheritance methods (direct, Weismannian, and Lamarckian) of informational replication were discussed. If there is no distinct interactor involved in a replication process it cannot be termed either Weismannian or Lamarckian. Therefore, the Weismannian and Lamarckian topologies are only valid, if there is a (partially) separate germline and soma (or replicator and interactor). In other words, Lamarckism and Wiesmannism are only possible if the phenotypic changes are stored elsewhere than genotypic changes. Consequently, DNA always replicates directly, without intermediates, as there is no interactor is involved. Only at the *level of organism*, but not at the level of the gene, it is true that genetic inheritance is Weismannian. Thus, replication and inheritance are clearly distinguished.

Furthermore, *copying* is not the same as r*eplication*: copying is an elementary transformation, while informational replication (though phenomenologically is a copying process) can be composed of various transmission methods not necessarily copying. The following example should help to see the difference. In GARD, there is (limited) informational replication, though no copying takes place at all: there is no template, and no bit-by-bit copying of components. Similarly, calculations about the replication fidelity of the Lamarckian replicator show that copying can be simulated with two inverse translation processes, where there is no direct bit-by-bit copying, but information transmission happens via an intermediate stage.

The problem with such composite replication methods is that they are prone to be information loosing, as usually there is no way to guarantee that the translation step is followed by its inverse retranslation, which could yield the original replicator. If replication is lossy in total, other methods are required to maintain the information in the system, otherwise information will degrade, and inheritance becomes attractor-based, instead of being storage-based (relying on e.g. sequence information explicitly). The cultural inheritance system seems to be able to deal with this inherent decay, by maintaining parallel ways of information replication (speech, gestures, tonality), relying on stable and high-fidelity information storing devices (e.g. books), and by using iterative processes extensively (like imitation).

A concise definition was given for Lamarckian inheritance. It is defined as a special case of informational replication with a distinct interactor, but without fully separated roles of storing heritable information. As such, Lamarckian inheritance systems are assumed to predate more evolved Weismannian ssytems, where there is full division of labour. It was proven that Lamarckian inheritance is in-between the continuum spanning from direct to Weismannian

inheritance. By allocating two entities (replicator and interactor) to two functions (storage of heritable information and interfacing selection), an informational system can shift from direct to Weismannian replication traversing intermediate Lamarckian stages. This was tested in a stochastic replication-selectional model, indicating that such evolutionary trajectories are indeed possible.

In Lamarckian inheritance, all intermediate stages are replicators, and are isomorphic. This means that they can maintain the same amount of information – however, this information is defined by the intermediate with the most conservative nature. It is possible that variable intermediates maintain high diversity, but this diversity is not inherited stably. This extra information of the system can only be maintained partially, if there are attractors for the variable intermediates. This was supported by both analytic results and stochastic experiments. If reverse translation is the inverse of the forward translation, Lamarckian inheritance can maintain the same amount of information, than Weismannian. The moment the two transmissions cease to be the inverse of each other, performance drops severely, as the replication process becomes information loosing. This renders the Lamarckian method practically useless. It is no more the information in sequences that defines the outcome of long-term replication, but the dynamic attractors of the replicator-space.

These models of inheritance illustrate the fact, that loss of information in replication can only be understood in case of successive transformations. Information loss can originate from at least three sources:

1. **Exogenous mutation**: noise of external origin. Present in any system, as there is no perfect storage based inheritance. Error correction (inference) can help overcome it.
2. **Probabilistic translation**: noise of internal origin. The translation in itself is *a priori* probabilistic in nature, and this ambiguity cannot be escaped. It can be countered, if inverse process follows to restore original entity.
3. **Lossy transmission**: a complex transmission can be lossy, of the probabilistic nature of one transmission is not resolved via an inverse processes, thus the outcome is *a posteriori* ambiguous. Inference still can help by using other, external sources to complement missing data.

Real lossy inheritance (technically, it is not really inheritance, as it cannot maintain information reliably, cf. GARD) is thus a process where there is no error correction, no appropriate inverse transmission process, and no inference is available.

A quantitative model is presented in section 3.1 that can effectively estimate the overall robustness of a Weismannian or Lamarckian inheritance system. It naturally follows that the

model can be extended to deal with other, arbitrarily complex inheritance systems, not just the above two. It can also be easily extended to estimate the amount of information that can be maintained in case of complex transmission chains).

It was proven that phenotypic replication is a *contradictio in adjecto*, and is misleading as such. Always the genotype is inherited. The group of phenotypic replicators (prions, memes) are however, indeed special replicators which only inherit information, but not material, and which largely ignore the underlying digital representations provided (like prions). Prions also lack interactors. Technically, they are informational replicators replicating either directly (prions) or via variable intermediates (memes) and with no material transmission. As such, almost all direct replicators should belong to here (like Penrose plywoods, Sperber's linked audio recorders, etc.), though not DNA, which on one hand replicates semiconservatively (thus there is material overlap), and on the other hand, requires the protein interactors to intervene selection.

Summarizing, one can conclude that there might have been multiple evolutionary trends traversing the vast replicator continuum. It is obvious that units of sorting preceded units of selection, and lastly came the units of evolution. In general, the evolution of inheritance systems advances from non-informational to informational replication, toward minimizing the variable but not heritable part, from holistic to compositional representation, from attractor-based inheritance (i.e. autocatalytic sets) to storage-based inheritance (templates), from probabilistic to deterministic transmission, and from direct replication through Lamarckian toward Weismannian inheritance (cf. Szathmáry 2000). For Weismannian inheritance to evolve, at least two important selective factors are required: an interactor that can yield better phenotypes, than the replicator itself can; and a replicator that can inherit information better, than the interactor can. One way to guarantee that only the interactor deals with the selective environment directly is to enclose replicators *inside* the interactor, forming a vehicle. Several models of the origin of life deals with this scenario, the most significant one is the chemoton.

The chemoton, as a minimal vehicle model, provides insight about the dynamic coexistence of informational replicators. Competing exponential replicators with different replication rates were proved to be able to stably coexist in a growing and splitting (oscillating) compartment, if they are forced to compete for a shared monomer precursor generated by a shared metabolism. The chemoton does not even require subexponential growth for coexistence: the faster exponential replicator does not wipe out the slower one, due to the regulating effect of the metabolism. This finding suggests that the constraint on coexistence of different templates, as assumed in the formulation of Eigen's paradox, may be generally more relaxed than previously thought. These results are important, because the chemoton efficiently decouples the internal replication rate of

its replicators from the vehicle-level replication rate (contrarily the stochastic corrector model), as the chemoton as a whole is nut under selection, thus internal replicators do not have external phenotypic effects.

Preliminary results indicate that dynamics that are even more interesting can be achieved with the chemoton if heteropolymers are allowed to appear during polymerization. According to these results, the composition of different templates has a very complex, strange, and unexpected effect on coexistence. Namely, the order of modules in the sequence has an effect on the outcome of coexistence. This effect was not studied so far, and as such, is a completely new way to approach the paradox of prebiotics. Parallel to analyzing sequence-effects, a better analytic solution is searched as well to model the chemoton, which can be solved for explicit template compositions.

As the chemoton is a theoretical realization of a complex inheritance system (with informational replicators and vehicle interactors), it is of utmost important to further extend the capabilities of the model. It would be interesting to study how the chemoton could deal with the various inheritance methods the Replicator Formalism suggests. Could it be coded to exhibit real Weismannian inheritance? For this, it is required that replicators have same kind of phenotypic effect at the vehicle level. This would involve a stochastic corrector-like model, with chemotons as compartments. In addition, the scenario for division of labor presented here could be fully reconstructed inside the chemoton. Accordingly, an experiment could be designed, where replicators inside the chemoton evolve from a simple replicative stage (with directly replicating templates) toward either Lamarckian or Weismannian replications, as the vehicle becomes responsible for fitness, and – possibly – takes part in the inheritance of information as well (for example as a steady-state epigenetic information source).

Such modells would allow the further investigation of the adventage\disadvantage of different informational topologies, and the effect of mutation at different levels in an advanced chemoton. It must be emphasized here, that even the chemoton is a highly abstract representation of a living cell. But as such, it is one of the most significant models of life, and provides a perfect playground for such investigations, as it is more realistic, than any of the models presented in this thesis.

In summary, the Replicator Formalism gives a powerful theoretical and modelling framework, and provides a generalization tool to bridge various models and results of different fields. This universality begs for further research by including more exotic replication systems in the research pipeline, like the one postulated by the Neuronal Replicator Hypothesis (Fernando et al.

2010) or grammatical rules and constructions in language acquisition and evolution (Steels & Szathmáry 2008).

Abbreviations

SACI	simple autocatalytic cycle intermediate
GARD	Graded Autocatalysis Replication Domain model
SCM	stochastic corrector model

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Appendix

Definitions of relevant concepts

AUTOCATALYSIS

Autocatalysis

Szathmáry 1995, p. 282.

"The intermediates of [an autocatalytic] cycle are stages of a 'life' cycle of a replicator. [...] ...the intermediates of the [autocatalytic] cycle *will also* reproduce."

p. 283.

"[...] what members of autocatalytic cycles as limited hereditary replicators lack is the ability to undergo microevolution: heredity is almost always exact. [...] It seems reasonable to assume that autocatalytic cycles come in only a relatively small number of types: their intermediates are limited hereditary replicators (Szathmáry & Maynard Smith 1993, Maynard Smith & Szathmáry 1995)

Szathmáry 2000, p. 1670.

"[...] a molecular autocatalyst must be a replicator."

Blackmond 2009, p. 386.

"[...] an autocatalytic reaction is defined as a system in which a reaction product serves as a catalyst for its own production. This definition associates an autocatalytic reaction with the process of self-replication, which is essential to the origin of life."

Gánti 2003], p. 45.

"[…] the products catalyze the formation of the same compounds."

Plasson et al. 2011, p. 1.

$$\frac{dx_i}{dt} = k(\boldsymbol{X}) \cdot x_i^n + f(\boldsymbol{X}), \quad k > 0;\ n > 0;\ |k| \gg |f| \quad (1)$$

"$\boldsymbol{X}$ is the vector of all the concentrations x_j. An autocatalysis for the compound x_i exists when the conditions of Eq. (1) are fulfilled. The term $k(\boldsymbol{X}) \cdot x_i^n$ describes the autocatalytic process itself, while $f(\boldsymbol{X})$ describes the sum of all other contributions coming from the rest of the chemical system."

Wikipedia 2011a

"A single chemical reaction is said to have undergone autocatalysis, or be autocatalytic, if the reaction product itself is the catalyst for that reaction."

Obligate autocatalysis

Kun et al. 2008, p. 2.

"Thus, the autocatalytic metabolite set of an organism includes all compounds that can be synthesized by small molecule metabolism, have an autocatalytic nature, and that must be present within the cell because otherwise the network, or part of it, would halt. We refer to such cases as obligate autocatalysis."

Autoinduction

Blackmond 2009, p. 386.

"[...] a reaction product or side product accelerates the rate of a kinetically meaningful step of a reaction sequence without directly producing more of itself. Autoinductive processes may exhibit kinetic signatures similar to autocatalytic processes."

Autocatalytic set

Wikipedia 2011a

"A set of chemical reactions can be said to be "collectively autocatalytic" if a number of those reactions produce, as reaction products, catalysts for enough of the other reactions that the entire set of chemical reactions is self sustaining given an input of energy and food molecules.

An autocatalytic set is a collection of entities, each of which can be created catalytically by other entities within the set, such that as a whole, the set is able to catalyze its own production. In this way the set as a whole is said to be autocatalytic. Autocatalytic sets were originally and most concretely defined in terms of molecular entities, but have more recently been metaphorically extended to the study of systems in sociology and economics."

Hordijk & Steel 2004, p. 453.

"Informally, a set of reactions R' is [reflexively autocatalytic and F-generated] if every reaction is catalysed by at least one molecule involved in a reaction in R', and every reactant in R' can be constructed from the food set F by successive applications of reactions from R'."

Hordijk et al. 2010, p. 1735.

"Given a network of catalyzed chemical reactions, a (sub)set *R* of such reactions is called:

Reflexively autocatalytic (RA) if every reaction in *R* is catalyzed by at least one molecule involved in any of the reactions in *R*;

F-generated (F) if every reactant in *R* can be constructed from a small "food set" *F* by successive applications of reactions from *R*;

Reflexively autocatalytic and *F*-generated (RAF) if it is both RA and F."

SELECTION

Sorting event

Pocklington & Best 1997, p. 6.

"[...] instances where one alternative versus another is differentially replicated."

Selection

Hull 1988b, p. 408-409.

"*selection* - a process in which the differential extinction and proliferation of interactors cause the differential perpetuation of the relevant replicators."

Vrba 1989, p.113.

"Selection is the interaction,between heritable, varying, emergent characters of individuals, and the common environmental elements experienced by the variant individuals, that causes differences in birth and/or death raets among them."

Pocklington & Best 1997, p. 3.

"[...] three necessary conditions for change due to selection:

- a source of variation
- a method of replication
- covariance between variants and their replication success"

Griesemer 2000b, p. 68.

"Further, I suggest that what distinguishes the Darwinian process of natural selection from mere sorting (Vrba and Gould, 1986), is that the former always involves entities that are, or are composed of, or are parts of, entities with the capacity to multiply."

p. 70.

"Maynard Smith's approach makes units of evolution (satisfying *M*, *V*, and *H*) more basic than units which may evolve *by means of* natural selection (also satysfying *F*)."

Hull et al. 2001, p. 513.

"[...] we define selection as repeated cycles of replication, variation and environmental interaction so structured that environmental interaction causes replication to be differential."

Units of selection

Pocklington & Best 1997, p. 3.

"Units of selection, defined as those patterns which differentially replicate, are essential to any evolutionary model."

Interactor

Hull 1980, p. 318.

"interactor: an entity that directly interacts as a cohesive whole with its environment in such a way that replication is differential"

Hull 1988b, p. 408-409. also at Hull 1988a p. 27.

"*interactor* - an entity that interacts as a cohesive whole with its environment in such a way that this interaction *causes* replication to be differential"

Hodgson & Knudsen 2006b, p. 14.

"If an entity is an interactor, then it must satisfy all of the following minimal conditions (Hodgson & Knudsen, 2004b). For each interactor there is a corresponding non-empty 'component' set of replicators, such that the following conditions apply: (1) *shared dependence of component replicators*: if the interactor perishes, then all its component replicators are also likely to perish, (2) *shared organisation of components*: every component replicator is hosted by its interactor and principally interacts with the outside world through the interactor, (3) *relative independence of non-component replicators*: the interactor and any non-component replicator are independent in the sense that the survival of one does not largely depend on the survival of the other, and (4) *property-dependent replication*: the properties of an interactor determines the expected number of successor replicators within a given environment."

p. 15.

"[...] interactors at multiple levels may correspond to entities at lower levels that both fulfil the role of being interactors and replicators."

Level of Selection

Lewontin 1970, p. 8.

"The rate of evolution is limited by the variation in fitness of the units being selected. This has two consequences from the point of view of comparison between levels of selection. First, the rapidity of response to selection depends upon the heritability of differences in fitness between units. The heritability is highest in units where no internal adjustment or reassortment is possible since such units will pass on to their descendent units an unchanged set of information. Thus, cell organelles, haploid organisms, and gametes are levels of selection with a higher heritability than diploid sexual genotypes, since the latter do not perfectly reproduce themselves, but undergo segregation and recombination in the course of their reproduction. In the same way, individuals have a greater heritability than populations and assemblages of species."

INHERITANCE

Attractor/storage-based

Szathmáry 2000, p. 1671.

"The system is also attractor based (Hogeweg 1998) since it is the dynamical nature of the network of reactions that makes replication possible, and the identity of the network is preserved by its dynamical stability (the system's basin of attraction). Information carried by gene-like replicators is, in contrast, storage based (Hogeweg 1998): to a good approximation all possible gene sequences are equally stable and transmissible, using the same copying mechanism."

Vasas et al. 2010, p. 1475.

"Hogeweg distinguished between attractor-based and storage-based inheritance, where the latter category clearly refers to gene-based systems. We concur that this distinction is crucial in analyzing quasibiological systems. The essence of nucleic acids from the point of view of inheritance is exactly that they can store a lot of information at roughly equal energy/stability levels, exactly the property one requires from "storage". Information in attractor-based systems crucially depends on the limited number of alternative stable states, as exemplified by our analysis of the GARD model."

Lineage

Hull 1988b, p. 408-409.

"*lineage* - an entity that persists indefinitely through time either in the same or an altered state as a result of replication."

Darwinian/Lamarckian inheritance

Calvin 1997 (paraphrased from The Cerebral Code)

"There must be a pattern involved.

The pattern must be copied somehow (indeed, that which is copied may serve to define the pattern). [Together, 1 and 2 are the minimum replicable unit - so, in a sense, we could reduce six essentials to five. But I'm splitting rather than lumping here because so many "sparse Darwinian" processes exhibit a *pattern* without *replication*.]

Variant patterns must sometimes be produced by chance - though it need not be purely random, as another process could well bias the directionality of the small sidesteps that result. Superpositions and recombinations will also suffice.

The pattern and its variant must compete with one another for occupation of a limited work space. For example, bluegrass and crab grass compete for back yards. *Limited* means the workspace forces choices, unlike a wide-open niche with enough resources for all to survive. Observe that we're now talking about *populations* of a pattern, not one at a time.

The competition is biased by a multifaceted environment: for example, how often the grass is watered, cut, fertilized, and frozen, giving one pattern more of the lawn than another. That's Darwin's **natural selection**.

New variants always preferentially occur around the more successful of the current patterns. In biology, there is a skewed survival to reproductive maturity (environmental selection is mostly juvenile mortality) or a skewed distribution of those adults who successfully mate (sexual selection). This is what Darwin later called an **inheritance principle**. Variations are not just random jumps from some standard starting position; rather, they are usually little sidesteps from a pretty-good solution (most variants are worse than a parent, but a few may be even better, and become the preferred source of further variants)."

Jablonka et al. 1998, p. 206.

"Mechanisms allowing the inheritance of acquired characters have evolved several times during the history of life, and understanding their evolution is crucial to understanding the transition to new levels of individuality."

p. 207.

"[...] in modern biology lamarckism is usually equate4d with the inheritance of acquired characters. Other parts of the Darwin's and Lamarck's theories are usually ignored."

Pál & Miklós 1999, p. 22.

"The machanism of Lamarckian evolution can be summarized in three statements: (i) a change in a character can be induced by the environment. (ii) the induced change can be transmitted to the following generations, even if the original inducing stimuli are no longer present, and (iii) the induced phenotypes are adaptive in the given environment. The "soft" version of Lamarckism includes only the first two points, while the "hard" version covers all three points."

Hull et al. 2001, p. 514.

"The distinction between Darwinian and Lamarckian iheritance depends on the distinction between genotype and phenotype. According to the inheritance of acquired characteristics, the environment modifies the phentoype of an organism so that it is better adapted to the environmental factors that produced this phenotypic change in the first place – better adapted than those organisms that were not modified in this way. The phenotypic change is then transmitted somehow to the genetic material so that it is passed on in reproduction. Thus, according to this view, species can rapidly adapt to environmental change."

Hodgson & Knudsen 2006a, .p. 346.

"– **Darwinism** is a causal theory of evolution in complex or organic systems, involving the inheritance of genotypic instructions by individual units, a variation of genotypes, and a process of selection of the consequent phenotypes.

– **Lamarckism** is a doctrine admitting the possibility of the (genotypic) inheritance of acquired (phenotypic) characters by individual organisms in evolutionary processes.

– **Weismannism** (or neo-Darwinism) is a doctrine denying the possibility of the (genotypic) inheritance of acquired (phenotypic) characters by individual organisms in evolutionary processes."

Reproduction, reproducer

Miller 1978, p. 363.

"Reproduce – the subsystem which is capable of giving rise to other systems similar to the one it is in. This process fundamentally involves transmission of information, the template of the new system. The matter-energy which is organized to compose the new system, However, must also be processed. The care of the next generation of systems until they become independent and self-supporting is also a function of this subsystem. In all systems the reproducer operates by many complex, reversible functions, but the ultimate effect is to bring about an irreversible, historical change, the creation of the new systems of a new generation."

Dawkins 1982a, p. 9.

"Each new vehicle comes into being through an act of reproduction. New parts of vehicles come into being through growth."

p. 11.

"It makes sense if we are regarding reproduction as the process by which a new vehicle comes into existence, and growth as the process by which an existing vehicle develops."

Griesemer 2000b, p. 77.

"Reproducers are entities that multiply by material overlap of propagules conferring the capacity to develop. Inheritors are entities that multiply by material overlap of propagules conferring the capacity to develop by *evolved* mechanisms. Replicators are entities that multiply by material overlap of propagules conferring the capacity to develop by evolved, *coding* mechanisms."

Inheritor

Griesemer 2000b, p. 77.

"Reproducers are entities that multiply by material overlap of propagules conferring the capacity to develop. Inheritors are entities that multiply by material overlap of propagules conferring the capacity to develop by *evolved* mechanisms. Replicators are entities that multiply by material overlap of propagules conferring the capacity to develop by evolved, *coding* mechanisms."

Szathmáry 2002, p. 188.

"[...] inheritors must have a hereditary subsystem that carries information for the system as a whole."

Development

Griesemer 2000b, p. 74.

"Development is minimally the acquisition of the capacity to reproduce."

Vehicle

Dawkins 1982a, p. 9.

"Each new vehicle comes into being through an act of reproduction. New parts of vehicles come into being through growth."

p. 11.

"It makes sense if we are regarding reproduction as the process by which a new vehicle comes into existence, and growth as the process by which an existing vehicle develops."

p. 167.

"But just as we had a nested hierarchy of would-be replicators - small and large fragments of genome - so there is a hierarchy of nested vehicles. Chromosomes and cells are gene vehicles within organisms. In many species organisms are not dispersed randomly but go around in groups. Multispecies groups form communities or ecosystems. At any of these levels the concept of vehicle is potentially applicable. Vehicle selection is the differential success of vehicles in propagating the replicators that ride inside them. In theory selection may occur at any level of the hierarchy."

Hull 1988a

"The physical body that houses the replicator and gets it from place to place is referred to as the vehicle, or interactor (Hull 1988b)."

Epigenetic inheritance system

Jablonka & Lamb 1995, p. 80.

"An epigenetic ineritance system (EIS) is a sysetm that enables a particular functional state or structural element to be transmitted from one cell generation to the next, even when the stimulus that originally induced it is no longer present. In other words, EISs are the systems that enable the transmission of various phenotypic expressions of the genetic information in an individual."

REPLICATION

Replication, replicator, raplicate

Dawkins 1976, p. 17-18.

"[...] Some varieties would have been inherently more stable than others. Certain molecules, once formed, would be less likely than others to break up again. These types would become relatively numerous in the soup, not only as a direct logical consequence of their 'longevity', but also because they would have a long time available for making copies of themselves. Replicators of high longevity would therefore tend to become more numerous and, other things being equal, there would have been an 'evolutionary trend' towards greater longevity in the population of molecules.

But other things were probably not equal, and another property of a replicator variety that must have had even more importance in spreading it through the population was speed of replication or 'fecundity'."

"[...] the individual molecules lasted a long time, or they replicated rapidly, or they replicated accurately. Evolutionary trends toward these three kinds of stability took place in the following sense: if you had sampled the soup at two different times, the later sample would have contained a higher proportion of varieties with high longevity/fecundity/copying-fidelity. This is essentially what a biologist means by evolution when he is speaking of living creatures, and the mechanism is the same—natural selection."

Hull 1980, p. 318.

"*replicator:* an entity that passes on its structure directly in replication"

Dawkins 1982b, p. 83-84.

"I define a *replicator* as anything in the universe of which copies are made" ... "An *active replicator* is any replicator whose nature has some influence over its probability of being copied." ... "A *germ-line replicator* (which may be active or passive) is a replicator that is potentially the ancestor of indefinitely long line of descendant replicators." ... "The reason active germ-line replicators are important units is that, wherever in the universe they may be found, they are likely to become the basis for natural selection and hence evolution."

Csányi & Kampis 1985, p. 303.

"It is suggested that replication—a copying process achieved by a special network of interrelatedness of components and component-producing processes that produces the same network as that which produced them—characterizes the living organization. The information "used" in this copying process, whether it is stored by special means or distributed in the whole system, is called replicative information."

Hull 1988b, p. 408-409.

"*replicator* - an entity that passes on its structure largely intact in successive replications."

Maynard Smith & Szathmáry 1995, p.20-21.

"...it is important to emphasize that autocatalysis is not the same as replication. For replication, it is not sufficient that an *A* gives rise to two *A*s: it is also necessary that, if the *A* is replaced by *B* (or a *C* or a *D*), then the cycle should give rise to two *B*s (or *C*s, or *D*s). in autocatalysis, there is no variation, and hence no heredity. Autocatalysis is an important first step towards replication, but it is not the whole road."

p. 41-42.

"[The replicator] may mean a structure that can arise only if there is a preexisting structure of the same kind in the vicinity. Such structures we will call 'simple replicators': as an example, peroxisomes ... [...] Some replicators, however, are able to exist in several forms - A, B, C, etc. - and, when they replicate, the new structure resembles the old. We will call such structures 'hereditary replicators'. A DNA molecule is such a

hereditary replicator, and the number of possible distinct structures is indefinitely large: DNA molecules, therefore, are 'indefinite hereditary replicators'. It is possible, however, that here are also structures, which can exist in a limited number of heritable states: these we will call 'limited hereditary replicators'."

p. 43.

"These models [models of nucleation, Penrose plywoods] show that entities can be replicators without having variation or heredity, and that they can have variation and heredity limited to relatively few types. For sustained evolution, however, we require indefinite hereditary replicators."

p. 58.

"A replicator is an entity that only arises by the division or copying of a preexisting entity."

Sterelny et al. 1996, p. 396.

"...the following elements are part of the biologically interesting notion of replication. If B is a copy of A:

(i) A plays a causal role in the production of B

(ii) B carries information about A in virtue of being relevantly similar to A. This similarity is often functional: B has the same, or similar functional capacities to A. Indeed we should probably think of "copy" as a three-term relation: B is a copy of A with respect to C. where C is often some function of A.

(iii) B respects the xerox condition: B is a potential input to a process of the same type that produced it.

(iv) Copying is a teleological notion. For B to be a copy of A it must be the output of a process whose biofunction is to conserve function. On this view, the mere similarity of B to A does not suffice for B to be a copy of A. A fossil of a leaf is not a copy of a leaf. B must be meant to be similar to A; that similarity is why those mechanisms exist. Copying is a process with the function of producing from one token another which is relevantly similar."

Sperber 2000, p. 7.

"For B to be a replication of A,

(1) B must be caused by A (together with background conditions)

(2) B must be similar in relevant respects to A

(3) The process that generates B must obtain the information that makes B similar to A from A."

Godfrey-Smith 2000, p. 414.

"Y is a *replicate* of X if and only if: (i) X and Y are similar (in some relevant aspects), and (ii) X was causally involved in the production of Y in a way responsible for the similarity of Y to X. Replication is any process by which a replicate is produced."

Griesemer 2000b, p. 77.

"Reproducers are entities that multiply by material overlap of propagules conferring the capacity to develop. Inheritors are entities that multiply by material overlap of propagules conferring the capacity to develop by *evolved* mechanisms. Replicators are entities that multiply by material overlap of propagules conferring the capacity to develop by evolved, *coding* mechanisms."

Aunger 2002, p. 73.

"...replication is a relationship between a copy and some source exhibiting the following characteristics:

Causation: The source must be causally involved in the production of the copy

Similarity: The copy must be like its source in relevant aspects

Information transfer: The process that generates the copy must obtain the information that makes the copy similar to its source from that same source, and

Duplication: During the process, one entity gives rise to two (or more)"

p. 339.

"Four minimal conditions for replication: These criteria are closely related to those found in Sperber 2000, with supplementary input from Godfrey-Smith (in press) and Maynard Smith 1987."

Hodgson & Knudsen 2006a, p. 21.

"[the genotype] carries generative information through time and somehow passes it from structure to structure."

Zachar & Szathmáry 2010, p. 21-22.

"*Replicator*: any autocatalytic entity for which there is a selection process defined. Selection is a process acting on a particular population of entities in a particular environment, which sorts entities according to their phenotypes."

"*Abstract informational replicator*: a replicator in the narrow sense: the abstract genotype itself that is multiplied. The genotype is that part of an entity which can potentially pass on changes (acquired during lifetime of entity, incorporated into the said part) to offspring during a multiplication process, called copying.

Realistic informational replicator: a replicator in the broad sense: any multiplying entity that has a heritable genotype - that is, the smallest entity that houses the genotype."

Fernando et al. 2011, p. 2.

"The fundamental method of determining whether an entity is a replicator is to seed the system with a single copy (or a small quantity) of the putative replicator and observe whether the initial period of growth of the replicator (i.e. of equivalent entities) is exponential. By comparing this to the spontaneous formation of equivalent entities in the absence of seeding, one can determine the extent to which entities are replicated vs. spontaneously assembled. The above operational definition identifies entities capable of autocatalytic

growth. A sufficient condition for a replicator is that it is an entity capable of autocatalytic growth."

Fernando 2011, pers. comm.

"A replicator is an entity that is capable of autocatalytic growth (multiplication) and which produces new entities that are equivalent to it in terms of fitness. An informational replicator is a replicator that is capable of producing new entities that are either equivalent or correlated (positively or negatively) with the parent in fitness. A neuronal replicator is an informational replicator that exists in the brain as a pattern of neuronal connectivity or activity."

Informational/non-informational replicators

Orgel 1992, p. 203.

"All replicating systems are, by definition, autocatalytic and all autocatalytic systems result, in some sense, in replication. [...] Two very different types of replicating systems must be considered. The first does not involve direct replication of a polymeric molecule, but may help to create an environment favourable for such replication. Systems involving the autocatalytic synthesis of one of the building blocks of a replicating polymer, or the components of a membrane, might be of this kind. I refer to such systems as non-informational autocatalytic systems. The second type of systems involves the replication of informational polymers made up from two or more different polymers. Here, the conservation of sequence information is paramount, so I refer to such systems as informational replicating systems."

p. 204.

"Non-informationl replicating system are not genetic systems. They cannot evolve by natural selection, because they do not store information in a stable way." "Apart from the requirements described above, few of the features of RNA replication are essential for a general replication model."

Processive/modular replicators

Szathmáry 1995, p. 284.

"It seems worth while to make clear the distinction between replicating oligonucleotides and other autocatalytic molecules lacking a digital sequence. Both are limited hereditary replicators, but the former are able to undergo microevolution whereas the latter are not. The crucial difference is in the mechanism of replication: oligonucleotides are copied by the template effect of a sequence composed of digits (modules) belonging to a restricted alphabet, whereas the other type of autocatalysts lack modular growth, so replication proceeds piecemeal (Wächtershäuser 1988). This enables the system to take small heritable steps in sequence space (see Maynard Smith 1970). I suggest the term *processive* and *modular* replicators. A string of module is a one-dimensonal array [...]"

Limited/unlimited heredity

Szathmáry & Maynard Smith 1993, p. 201.

"[...] we introduce the terms 'unlimited' and 'limited hereditary replicators'. The term replicator has been suggested by R. Dawkins, for a genetically active unit whose structure is copied repeatedly. Limited hereditary replicators, owing to their structural peculiarities, can exist and be replicated in only a few stable states, whereas unlimited hereditary replicators can encode for a practically infinite set of varieties."

Szathmáry 1999, p. 2.

"Limited hereditary is context-dependent, since we require that the number of possible types should be smaller than the number of actual individuals present."

Trivial replication

Nánay 2002, p. 116.

"I'll call a process trivial replication if no new, spatially distinct entity is formed during the replication process. If new, spatially distinct entities are formed, then the replication is non-trivial. This is the first distinction within the category of replication processes. The second one is somewhat more interesting, involving one of the keywords in evolutionary biology: variation."

Phenotypic replication

Szathmáry 1999, p. 5.

"Phenotypic replication is a process whereby the phenotype, or function, of one object is transmitted to the other, without any modular copying effect."

Ensemble replication

Segré et al. 2000, p. 4112.

..."self-replication as the collective property of ensembles of relatively simple molecules, interconnected by networks of mutually catalytic interactions."

Szathmáry 2000, p. 1670.

"Imagine first a set of replicating DNA molecules such as occurs in the macro-nucleus of hypotrych ciliates. In this case the set is replicating only because all its elements are. Ensemble replication is quite a different process - only the set as a whole is able to replicate."

Evolution

Lewontin 1970, p. 1.

"1. Different individuals in a population have different morphologies, physiologies, and behaviours (phenotypic variation).

2. Different phenotypes have different rates of survival and reproduction in different environments (differential fitness).

3. There is a correlation between parents and offspring in the contribution of each to future generations (fitness is heritable).

These three principles embody the principle of evolution by natural selection. While they hold, a population will undergo evoltionary change."

"Natural selection occurs even when two bacterial strains are growing logarithmically in an excess of nutrient broth if they have different division times."

Csányi 1980, p. 427.

“Evolution is the process in the course of which an open system existinf in an energy-flow leaves the state of equilibrium an in its structures replicative information evolves that continually increases and converges toward a maximum until the whole system becomes one, coordinated replicative unit.”

Koza 1992

"- An entity has the ability to reproduce itself.

- There is a population of such self-reproducing entities.

- There is some variety among the self-reproducing entities.

- Some difference in ability to survive in the environment is associated with the variety."

Szathmáry & Maynard Smith 1997, p. 555.

"Existing organisms are not replicators (that is, new individuals do not arise by copying), but reproducers that contain replicators."

"We will argue that mere heredity is not enough. Evolution requires “unlimited heredity”: that is, the existence of replicators that can exist in an indefinitely large number of forms. Although heredity with a small number of possible types can exist without copying, it seems very probable that unlimited heredity requires template copying of replicators with a modular structure."

Open-ended evolution

Ruiz-Mirazo et al. 2008, p. 69.

"[…] we will here refer to open-ended evolution (rather than Darwinian evolution) as a process in which there is the possibility for an indefinite increase in complexity."

Units of evolution

Williams 1966, p. 25.

"In evolutionary theory, a gene could be defined as any hereditary information for which there is a favourable or unfavourable selection bias equal to several or many times its rate of endogenous change."

Williams 1966, p. 24.

"[A genes is] That which segregates and recombines with appreciable frequency."

Maynard Smith 1987, p. 120.

"[...] if there is a population of entities with multiplication, variation, and heredity, and if some of the variations alter the probability of multiplying, then the population will evolve. Further, it will evolve so that the entities come to have adaptations [...]"

Szathmáry & Maynard Smith 1993, p. 198.

"*Multiplication*: If there is entity A, then it must give rise to more of the same. A simple example is when a mother cell divides into two daughter cells.

Heredity: There are different kinds of entities A, B, C, etc. Through multiplication, each has to produce more A, B, and C objects, respectively.

Variability: Heredity is not perfect. Sometimes (infrequently) A produces A’ entities, similar, but not identical to itself. It may be the case that A’ = B. The most common type of change is called mutation.

If the different types of entity differ in their ability to *survive* and *reproduce*, then in a population of them *evolution by natural selection* can take place."

Szathmáry & Maynard Smith 1997, p. 558.

"(1) Multiplication: Entities should give rise to more entities of the same kind."

Szathmáry 2002, p. 182.

"Units of evolution must: (i) multiply, (ii) have heredity, and (iii) heredity must not be totally accurate (variability). Furthermore, some of the inherited traits must affect the chance of reproduction and/or survival of the units. If all these criteria are met, then in a population of such entities evolution by natural selection can take place."

Koonin & Wolf 2009b, p. 3.

“[...] the fundamental, Distinct Unit of Evolution (FUE) is any genetic element with a unique [independent] evolutionary history, rather than an organism or a species.”

Major transitions of evolution

Maynard Smith & Szathmáry 1995, p. 6.

"One feature is common to many of the transitions: entities that were capable of independent replication

before the transition can replicate only as part of a larger whole after it."

Jablonka & Lamb 2006, p. 237.

"Maynard Smith and Szathmáry suggested that all of these transitions were associated with changes in the way that information is stored, transmitted or interpreted. They argued that higher-level entities could evolve through selection acting on lower-level units because the latter can benefit more by cooperating than by competing."

CULTURAL EVOLUTION

Units of cultural transmission

Pocklington & Best 1997, p. 6.

"The appropriate units of selection will be the largest units of socially transmitted information that reliably and repeatedly withstand transmission."

Meme

Dawkins 1976, p. 192.

"A meme is a replicator, a unit of cultural transmission, and unit of imitation."

"Memes propagate themselves in the meme pool by leaping from brain to brain via imitation."

"Fidelity, fecundity, longevity are the ways in which a meme is defined as successful."

Kronfeldner 2007, p. 504.

"Normally, those mental contents, which I will call ideas here, that can be culturally shared are regarded as memes."

Plotkin 1994, p. 251.

"The unit of cultural heredity analogous to the gene."

Plotkin 1997, p. 159.

"What is transmitted between individuals in a social group, equivalent to genes."

p. 252-3.

"Essential units of a social group's common cultural currency." "Cultural entities, descent with modification."

Visser 1994, p. xix. (note that Visser does not herself use the word meme, but much of her book is about repeated cultural practices)

"In our "consumer" culture, we are constantly confronted with crowds of objects and with changing fashions in behaviour."

"It is important to know how we are all implicated in the existence of these culturally resonant objects, and in their form."

Sperber 1996, p. 26:

"Socio-cultural representations"

p. 33.

"A cultural representation is made up of many versions, mental (or private) ones and public ones."

"Each mental, private version results from the interpretation of a public representation that is itself an expression of a mental expression."

"Cultural representations so understood are sometimes a fuzzy combination of private and public representations inhabiting a given social group."

Mithen 1999, p. 210:

"The hectic and ongoing pace of cultural evolution unleashed by the appearance of cognitive fluidity continues to change the developmental contexts of young minds, resulting in new types of domain specific knowledge [memes]."

Blackmore 1999, p. 43

"A meme is whatever is passed on by imitation. Imitation includes any kind of copying of ideas and behavior from one person to another."

Wikipedia 2011b

“A meme is an idea, behavior or style that spreads from person to person within a culture. While genes transmit biological information, memes are said to transmit ideas and belief information. A meme acts as a unit for carrying cultural ideas, symbols or practices, which can be transmitted from one mind to another through writing, speech, gestures, rituals or other imitable phenomena. Supporters of the concept regard memes as cultural analogues to genes in that they self-replicate, mutate and respond to selective pressures.”

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Summary

Replicators are the most important objects of theoretical biology. Their cumulative evolution lead to the emergence of complex, adaptive systems, like life. Most of the major transitions of evolution are outcomes of the evolution of replicators. However, replication (and evolution) are universal concepts, independent of the level of biological organization, and even of biology.

A multitude of replicator candidates, and perhaps the same amount of definitions are available in the literature. Studies of (self-)replication in chemical, (proto-)biological, linguistic, cultura, neuronal, digital and kinetic systems have accumulated an impressive amount of theoretical and experimental knowledge in the last three decades.

To explore the consequences of the universality of replication and to cut through the bulk of misleading terms, I introduce the Replicator Formalism, a generalized theory of autocatalytic entities. To better understand models and be able to relate results of various fields dealing with replication, the formalism applies a pure, objective language, independent of any specific field. It helps to recognize key features of autocatalytic systems, like informational and material topology, and it both provides a classification of replication systems, and suggests evolutionary trajectories for certain transitions from lesser systems to evolved ones.

Several conclusion were devised using the formalism as a conceptual and as a modelling tool. These are: (1) replicator equivalency is a matter of relativity, and can only be defined from an arbitrary point of view; (2) there could be possibly different material, informational and selectional topologies behind inheritance systems; (3) phenotypic replication is direct replication lacking a distinct interactor; (4) there is a continuum between direct and Weismannian replication, Lamarckian being in-between them; (5) this continuum can be traversed by evolution: an evolutionary scenario for the emergence of division of labour is suggested, and tested in a stochastic model; (6) information can be stably maintained in Lamarckian systems, (7) informational replicators can coexist in a vehicle even if there is only stoichiometric coupling, but no phenotypic selection.

The Replicator Formalism gives a powerful theoretical and modelling framework, providing a tool to bridge various models and results of different fields.

Összefoglaló

Az evolúcióbiológia legfontosabb objektumai a replikátorok. A replikátorok folytatólagos evolúciója felelős a komplex, adaptív rendszerek kialakulásáért, mint amilyen az élő sejt, az immunrendszer, vagy (egyes elméletek szerint) az emberi agy bizonyos kognitív funkciói is. A nagy evolúciós lépések mind a replikátorok illetve öröklődési rendszereik evolúciójának fontos mérföldkövei.

A definíciók és replikátornak tekintett autokatalitikus (azaz önszaporító) rendszerek száma olyan hatalmas az irodalomban, hogy a téma teljes mélységében gyakorlatilag feldolgozhatatlan. A replikáció jelenségét számos tudományterület vizsgálta, többnyire a saját szemszögéből. Ennek megfelelően lehengerlő mennyiségű elméleti és kísérletes megközelítéssel találkozunk a kémiai, (proto-)biológiai, nyelvi, kulturális, neuronális, informatikai, robotikai, mérnöki és más tudományterületek elmúlt harminc évnyi irodalmában. Mindemellett a replikáció és evolúció fogalmai teljesen univerzálisak és függetlenek a biológiai rendszerektől. Mivel *minden* evolúciós, adaptív rendszer replikátorokra épül, legyen az biológiai, kémiai vagy kulturális, szükségszerűen ugyanazok az általános elvek és mechanizmusok érvényesülnek bármely rendszer esetében. Munkámban ezt az univerzalitást vizsgáltam meg.

A disszertációban bemutatom az általam levezetett Replikátor Formalizmust, amely a replikáció univerzalitását szem előtt tartva tisztázza az autokatalitikus rendszerek alapvető fogalmait és tulajdonságait. Mivel a formalizmus az egyes tudományterületektől független nyelvre épül, a segítségével lehetőség van a fogalmak kiterjesztésére és általánosítására, s ennek következtében a különféle replikátorok egységes tárgyalására. A kulcsfontosságú tulajdonságok (pl. az információáramlás útja) azonosítása lehetővé tesz egy egységes osztályozást, és kijelöli a replikációs rendszerek lehetséges evolúciós pályáját, amely mentén kialakulhattak.

A formalizmust egyrészt egységes fogalmi keretként, másrészt modellezési eszközként használva az alábbi konlúziókat vontam le: (1) A replikátor-azonosság relatív, s csak abban az esetben definiálható, ha egy (önkényes) nézőpontot is megállapítunk – ez többnyire a szelekció. (2) Az öröklődési rendszerek szelekciós, anyag-, és információ-áramlási útvonalai nem feltétlenül esnek egybe. (3) A fenotipikus replikáció a közvetlen replikáció egy alesete. (4) A közvetlen és weismanni öröklődés közötti kontinuum folytonos. A köztes rendszerek öröklődése lamarcki. (5) Ez a kontinuum evolúciósan áthidalható: egy sztochasztikus modell keretében vizsgáltam meg a weismanni öröklődésre jellemző munkamegosztás evolúciós kialakulását. (6) A lamarcki öröklődésre jellemző replikációs folyamatok vizsgálatával igazoltam, hogy elméletben ugyanannyi információ tartható fenn lamarcki, mint weismanni öröklődés esetén. (7) A chemoton determinisztikus reakciódinamikai modelljét felhasználva megvizsgáltam az információs replikátorok hordozóba zárt stabil együttélésének egy lehetséges módját, mely megoldást nyújt a prebiotika paradoxonjára.

Az eredmények szerint a replikátor formalizmus hatékony eszköz a különféle öröklődési rendszerek tanulmányozásához, mind fogalmi, mind modellezési szinten.