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Abstract:

Jablonka and Lamb have presented a number of different possible mechanisms for finessing design. The extra-genetic nature of these mechanisms has led them to challenge orthodox neo-Darwinian views. However, these mechanisms are for calibration and have been designed by natural selection. As such they add detail to our knowledge, but neo-Darwinism is sufficiently resourced to account for them.

Main text:

Evolutionary theory is about design. Organic life demonstrates design at different levels, from the functional fit between the parts of an organism, to the adaptive fit between the whole organism and its environment. There is no getting away from the requirement to explain this. The most successful evolutionary theory to date is neo-Darwinism, which has, at its core, gene-level selection. Jablonka and Lamb (J&L) seek to challenge the explanatory hegemony of gene-level selection with a case for three other sources of intrinsic design. Using diverse evidence and adopting an accessible style, J&L's book is a useful addition to debate. However, we take issue with their interpretation both of the evidence and of evolutionary theory.

At the centre of J&L's thesis is a concern with information. They define information in terms of source and receiver; the input from the source becomes informative if the receiver interprets it. Thus, information denotes a functional relationship between an input and a system; a system will only respond systematically to those inputs for which it is prepared, or designed.

DNA molecules are organised systems that respond to particular inputs, leading to the assembly of polypeptide chains. The nucleotides on a strand of DNA have a one-to-one relationship with RNA nucleotides such that the latter's sequence may be

predicted from the former. This specificity is maintained in messenger RNA (mRNA) with a one-to-one correspondence between mRNA sequence and the sequence of amino acids in a protein. From there the rest unfolds (or folds) with greater complexity. Protein folding and mechanisms underlying gene expression are not fully understood. Views of how DNA works might well be altered in light of new science, but, whatever new mechanisms are uncovered, they will doubtless conform to information theory. It might be said that this notion of information is axiomatic.

J&L take issue with neo-Darwinian inheritance. While we might conservatively say that parental nucleic acids are inherited and initiate development, J&L would add that various other factors (epigenetic and behavioural) can alter design later in development in ways not directly captured by the regularities of genetics, and these factors are inherited differently. They proceed by analogy:

DNA replication is compared with photocopying: a process indifferent to content. Photocopying differs from teaching and learning, because different content can be more or less difficult to learn; and, by content J&L can only mean inputs. This content-sensitivity has an affect on what can be transmitted, whereas DNA just replicates and any accidental variation can only be tested through selection, which is wasteful (it is not clear from what perspective this is wasteful). This analogy nudges us to think that some downstream re-designing in light of ecological facts is likely in order to reduce waste; some systems might be content sensitive and calibrate themselves accordingly. And this, of course, is the role for the other three sources of design that J&L lay claim to.

Downstream recalibration cannot be caused solely by extra-genetic, inherited content. Any content sensitivity that one encounters can only be the consequence of a system that is specifically designed to take and react to inputs. So, one can imagine a complex decision-rule architecture that will capture a large number of possible environmental variations, and thus a large number of differing inputs. Organisms in the same species have this architecture set differently according to local environmental idiosyncrasies, and this will have different content-sensitive effects; but, we must note that the degrees of freedom for such calibration are finite. This, incidentally, is how learning works (Gallistel, 1999).

Calibrating processes are fascinating, and J&L have given us rich detail on a number of candidate mechanisms. One interesting fact about these mechanisms is their co-dependence of parts and of the whole system to its inputs, which equates to the evidence for design. As such J&L require a theory of design to account for them. Again the most successful theory is neo-Darwinism, to which J&L offer no alternative. Minimally we must say that the finite possible calibrations that can be made by developmental processes reflect facts about the ecology and evolutionary history of a species.

We come now to J&L's description of genetic, mutational change. Irrespective of the nature of the genetic system, a key neo-Darwinian supposition is that genetic change is random with respect to the function selected. In chapter 3, J&L offer a helpful typology of the kinds of non-random change which have been observed. They describe three tribes whose social structure is by analogy to germline mutation strategies: 1. a conservative tribe, members of which stick with what works and

devote resources to the maintenance of tradition, 2. a tribe of explorers who foster individual discovery by all members and have no respect for tradition, 3. a tribe of interpreters who engage in creative enterprise constrained by tradition. Given a certain level and scope of variation, we are led into the intuition that the most successful strategy is the interpreters', which corresponds with a strategy of induced mutations in which random nucleotide change is triggered by specific events and/or in specific genomic regions.

This is an interesting example and the plausibility is further enhanced when J&L remind us that the adaptive value of sex and recombination is studied within orthodox evolutionary circles. But there are several missing elements. First, such evolutionary research is often concerned with questions about levels of selection. A key aim of many theorists has been to explain the evolution of sex in terms of individual-level selection, which has been achieved in the context of the Red Queen hypothesis. So J&L must consider their criterion of plausibility in this light. Might it not be best for individual genomes to tend towards conservative stances? Pleiotropic gene effects, which raise the costs of mutations, would not seem to tilt the scales one way or the other (contra J&L) and might easily be overcome by mutations in specific regulatory domains or in genes with tissue-specific expression. Indeed the optimal stance adopted might vary between lineages and between parts of the genome. The answer to this question does not seem obvious to us and it may be best to stay close to the evidence (which presently supports neither fully *directed* mutations nor an adaptive strategy underlying adaptive induced mutations; see Brisson, 2003).

In summary, we welcome J&L's efforts to bring together research in genetics and development in the context of evolution. But, while they discuss many interesting calibrating processes, J&L do not offer any alternative theory of design to explain these. This does not amount to a fundamental challenge to the explanatory resources of classical neo-Darwinism.

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