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Convergence and monotonicity of the hormone levels in a hormone-based content delivery system

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Abstract The practical significance of bio-inspired, self-organising methods is rapidly increasing due to their robustness, adaptability and capability of handling complex tasks in a dynamically changing environment. Our aim is to examine an artificial hormone system that was introduced in order to deliver multimedia content in dynamic networks. The artificial hormone algorithm proved to be an efficient approach to solve the problem during the experimental evaluations. In this paper we focus on the theoretical foundation of its goodness. We show that the hormone levels converge to a limit at each node in the typical cases. We form a series of theorems on convergence with different conditions which are built on each other by starting with a specific base case and then we consider more general, practically relevant cases. The theorems are proved by exploiting the analogy between the Markov chains and the artificial hormone system. We examine spatial and temporal monotonicity of the hormone levels as well and give sufficient conditions on monotonic increase.

Keywords self-organizing algorithm, convergence, Markov chains

1 Introduction

Artificial hormone systems [1] are bio-inspired self-organizing algorithms that promise a robust and adaptive behavior [2] to cope with the problem of content

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delivery in dynamic networks [3]. This paper investigates the hormone-based algorithm and its extensions introduced by Sobe et al. [4], [5], [6] inspired by the endocrine system of higher mammals. This hormone-based system was developed for sharing small content units (e.g., a short video, video scene, picture, information) in a self-organising manner.

A content unit is atomic, i.e., cannot be further split during content delivery and each content unit is routed through a single path. The units represent the building blocks of more complex compositions (e.g., sequential streaming, parallel presentation etc., for details on unit compositions, see [7]).

In case of the artificial hormone algorithm, nodes are glands that create, consume and forward hormones through the network (the blood stream). Hormones indicate interest in a specific content unit. Content units react on hormones, by moving from lower towards higher hormone concentration. Therefore, the algorithm can successfully deliver the units on the requesting node if the hormone level increases strictly monotonically towards the requesting node.

The algorithm creates an artificial hormone system where requests for units are mapped to hormones. The hormone level can be represented by a real number and it may vary on the different nodes of the network. The hormones can be created by the network nodes and diffused over the network. There are several paths on which hormones can spread, and an evaporation mechanism is introduced for reducing the hormone levels. The hormone-based algorithm includes search for the requested unit and then the delivery of the units to the requesting clients. In the search phase, the hormone is spreading in the network. If the hormone reaches a node storing the requested unit then the increasing hormone levels attract the required unit and guide it on an appropriate path to the requester.

The artificial hormone algorithm proved to be an efficient approach to solve the content delivery problem during our experimental evaluations. In this paper we focus on the theoretical foundation of its goodness.

The hormone levels at the time of decisions on the directions of forwarding the units are formed after many iterations of the hormone update algorithm. We define a recursive function describing the hormone updates. The paper examines the convergence of the hormone levels in order to approximate the hormone levels with their limits. The artificial hormone system is not linear in the general case but the problem can be reduced to the convergence of a linear system by exploiting temporal monotonicity of the hormones. Our main result is that the hormone levels converge to a limit in the general case and we give a formula for their limits.

We study monotonicity of the limits of the hormone levels along a path of subsequent nodes in the network. We give sufficient conditions for the cases when the requested unit is copied in the system and when the hormone levels are increasing from the content sources towards the requesting node.

Section 2 gives a brief overview on the work related to the convergence analysis of the self-organising systems. Section 3 presents the former results about the applicability of the hormone based algorithm and introduces formu-

las, basic terms and properties which we can apply to the convergence analysis. Section 4 shows some results on temporal monotonicity of the hormone levels. Section 5 contains our main results on convergence. Section 6 considers the problem of spatial monotonicity in the network. Section 7 concludes the paper.

2 Related work

We provide a brief summary on the results of the convergence analysis of some bio-inspires methods. In ant colony optimization artificial ants build candidate solutions for a combinatorial optimisation problem by performing randomized walks on completely connected weighted graphs. Their convergence is proved in several papers [8], [9], [10] etc. Due to the randomness of the algorithm, the convergence can be proved in a probabilistic sense.

Gossip algorithms are distributed message passing methods widely used for information distribution and processing over ad-hoc and sensor networks. Furthermore, they can be used to solve the distributed averaging problem. Its convergence is proved and the steady state behaviour of the convergence is clearly characterised [11]. The convergence can be proved by using ergodic theory and its application to products of random matrices, which describes the averaging processes realised by the gossip methods.

Coupled oscillators can operate in a self-organising and adaptive manner by following the behaviour of swarms of fireflies. Kinglmayr and Bettstetter [12] proved by analysing the synchronisation precision over time that inhibitory coupling can lead to perfect synchrony independently of the initial conditions in case of delay-free environment and homogeneous oscillators. Furthermore, they give an upper precision bound on the synchronisation for systems with variable delays and heterogeneous oscillators. In [13], Leidenfrost, Elmenreich and Bettstetter show convergence and precision even in the presence of two-faced malicious faulty nodes for a modified fault-tolerant firefly algorithm.

The diffusion is a common method in dynamic load balancing [14], averaging in a network, reaching consensus [15], etc. Cybenko [14] found the conditions under which the diffusion converges to the uniform distribution. He applied the numerical analysis of matrix iterative schemes and he already mentioned the analogies with Markov chains as well. The structure of the diffusion matrix applied in load balancing is very similar to the one applied in hormone diffusion (the sum of the elements in each row is 1). However, the convergence results are different (hormones do not converge to their average) because the matrix is multiplied by vectors from different sides in the two models. Furthermore, nodes not forwarding the hormones make our model special and as we will see, they play a crucial role in the asymptotic behaviour.

Chemotaxis is a widely studied biological phenomena [16], [17], [18] where signal molecules (chemo) guide the movement (taxis) of living cells. It inspired computational algorithms as well where the signal controls the spreading of data in the network [19], [20]. Both hormone-based algorithm and chemotaxis move two kinds of objects, one of the objects (signal/hormone) moves signifi-

cantly faster than the other (data/content unit), the fast object spreads with diffusion, the slow objects follow the gradient of the fast object. The signal is often produced by the moving objects while the hormones are generated by the non-moving requests. Furthermore, the amount of data can be represented by a real value in chemotaxis, while the content unit can be represented by a simple indicator showing whether the content unit is located or not at a specific node.

Markov analysis is a well-known method in stochastic systems (see e.g., [21]). It has a wide range of application areas in life sciences [22], social sciences [23] and engineering including the self-organising systems as well [24]. The convergence of Markov chains is thoroughly studied in the last century and motivated several new results on matrix iterative schemes. Although the hormone based method is not a random process, we found that the underlying algebraic structure is the same at both problems which makes it possible to apply the convergence results on Markov chains to the hormone system.

3 The artificial hormone system

The section gives an overview on former results and experiences related to the artificial hormone system, provides a recursive formula for the hormone update function and introduces some basic terms and properties which we apply to the convergence analysis.

3.1 Applicability of the artificial hormone system

A series of previous works ([4], [25], [27], [26], etc.) shows that, if the initial parameters are set properly, the artificial hormone algorithm performs well in comparison with state-of-the art techniques. This subsection summarises the results related to scalability and practicality of the artificial hormone system.

Simulations are necessary in evaluations, because a distributed measurement system is hard to achieve, especially, if a system containing of multiple thousands of devices is evaluated. An open source simulator [5] is implemented to show the performance of the algorithm and to test its behavior under real circumstances.

The number of nodes varied from 50 to 10,000 at the different simulation scenarios. The network topology was represented by a connected Erdős-Rényi random graphs and scale-free graphs. Multiple requests for different units lead to a different set of hormones being handled in parallel by the network. During the simulations, each node generated sequential requests continuously: if one request is fulfilled the next one is sent by the client. Each node contained several content units. The number of different content units was between several hundreds and several thousands.

Requests for the same unit result in a superimposed hormone landscape for that unit. In this case, a unit might be attracted by two hormone trails.

Without replication, the unit must move to different requesters in order. The requester that receives the unit first is determined by the strength of hormone reaching the unit (from the requester). In order to avoid such detours, we investigated a number of replication mechanisms. A series of experiments showed that by relying on local information only in combination with replication mechanisms, the algorithm can scale up to at least 1,000 nodes and can cover up to 50 % node churn [5], [4], [6].

A middleware named as SEAHORSE (SElforganizing Artificial HORmone SystEm) [6] was introduced that generalizes the artificial hormone system algorithm to a middleware for search and delivery of information units. Simulations were executed in order to examine its application in different technical fields including distributing multimedia content at a social event (for example spectators at a sports event such as a triathlon) and information dissemination in smart electrical grid. In the first use case, SEAHORSE enabled tens of thousands of participants to produce and share multimedia content continuously and instantaneously. The selection of the parameters of the algorithm were analyzed in detail and it was found that different network sizes can be executed on the same parameter set. The algorithm scaled well, e.g., time to full coverage comparison was doubled when the number of nodes increased from 100 to 10,000 in the second case study. The performance of the artificial hormone system was compared with pull-based Gossip and the artificial algorithm used by SEAHORSE performed better.

We introduced and implemented an ILP-based optimization method in order to determine the optimal values of Quality of Service (QoS) parameters (average delay, number of failed unit deliveries) of the content delivery system in a centralized manner. The optimums served as bounds during the evaluation of the hormone-based algorithm [28]. The evaluation showed that that the delay of the self-organizing content distribution tends towards the optimum.

3.2 The hormone update function

Sobe [26] presents the steps of the hormone update algorithm and their detailed explanations. The subsection considers the steps of the algorithm in order to give a recursive formula for the hormone level.

Given a graph describing the topology of the network with n nodes and each node may exchange data with its neighbours. Given a requesting node n_r as well that would like to get a content unit stored in one of the nodes (n_i, $i = 1..n$) of the network. In order to find and deliver the requested unit, each node of the network runs the same algorithm in a self-organising manner i.e., none of the nodes has global knowledge on the network but the nodes make their decisions on local information only.

The main steps of the hormone-based algorithm as follows are continuously repeated in each node of the network:

1. handle incoming requests
2. diffuse hormones

3. move units
4. evaporate known hormones

We give a recursive formula for the hormone levels in the next subsections. We will use the notation as follows for the hormone levels:

– $\overline{\mathbf{h}}^{(s)}(t) = (h_1^{(s)}(t), h_2^{(s)}(t), ..., h_n^{(s)}(t))$: the vector containing the hormone levels at different nodes in iteration t after the sth step of the algorithm

The initial values of the hormone levels are considered constant zero in each algorithmic step: $\overline{\mathbf{h}}^{(s)}(0) = \overline{\mathbf{0}}$

3.2.1 Handle incoming requests (Step 1)

In the algorithmic step of handling incoming requests, the requesting node starts the presentation of the unit if the requested unit is present on it. Otherwise, it generates hormones in order to indicate the demand for the unit. The hormone level $\overline{\mathbf{h}}^{(1)}(t+1)$ can be calculated from the hormone level $\overline{\mathbf{h}}^{(4)}(t)$ after the end of the previous step as follows:

$$\overline{\mathbf{h}}^{(1)}(t+1) = \overline{\mathbf{h}}^{(4)}(t) + \overline{\mathbf{b}}^{(1)}(t+1)$$

Where

– $\overline{\mathbf{b^{(1)}}}(t) = (b_1^{(1)}(t), b_2^{(1)}(t), ..., b_n^{(1)}(t))$: the vector containing the generated hormones at different nodes in iteration t

If the content is not present on requesting node n_r the requesting node generates η_0 and η hormones in the first and the subsequent iterations, respectively. The value of the additive term can be given as follows:

$$b_i^{(1)}(t) = \begin{cases} \eta_0 & i = r, t = 1 \\ \eta & i = r, t > 1 \\ 0 & i \neq r \end{cases}$$

3.2.2 Diffuse hormones (Step 2)

In the step of diffusing hormones, a part of the hormone on each node is distributed among the neighbors. The hormone level $\overline{\mathbf{h}}^{(2)}(t)$ after diffusing hormones can be calculated as follows:

$$\overline{\mathbf{h}}^{(2)}(t) = (\overline{\mathbf{h}}^{(1)}(t) + \overline{\mathbf{b}}^{(2)}(t))\mathbf{D}$$

Where

– $\mathbf{D}$: The diffusion matrix describing the spreading of the hormone between nodes.
– $\overline{\mathbf{b}}^{(2)}(t) = (b_1^{(2)}(t), b_2^{(2)}(t), ..., b_n^{(2)}(t))$: the vector containing the additive terms coming from the hormone diffusion at different nodes in iteration t.

A specified ratio denoted by α of the hormone level at each node is distributed among the neighboring nodes proportionally to the weights w_{ij} expressing the quality of the link from node n_i to n_j. The values of the diffusion matrix can be defined as follows:

$$\mathbf{D} = \begin{pmatrix} 1-\alpha & \alpha \cdot w_{12} & \dots & \alpha \cdot w_{1n} \\ \alpha \cdot w_{21} & 1-\alpha & \dots & \alpha \cdot w_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ \alpha \cdot w_{n1} & \alpha \cdot w_{n2} & \dots & 1-\alpha \end{pmatrix}$$

The special features of the matrix $\mathbf{D}$ are that its elements are all non-negative, less than or equal to one and their sum for each row is equal to one. If the requested unit is stored on the node, the hormone is deleted from the node first. The value of the additive term can be given as follows:

$$b_i^{(2)}(t) = \begin{cases} -h_i^{(1)}(t) & x_i(t) = \text{true} \\ 0 & x_i(t) = \text{false} \end{cases}$$

where $x_i(t)$ is a boolean indicating whether the requested content is present on node n_i in iteration t.

3.2.3 Move units (Step 3)

When the hormone reaches a node storing the requested content unit, a decision is made to which neighbour to copy the unit from the node. Although Step 2 deletes the hormone from the node that stores the unit, the hormone level is not zero because it can be diffused there from the neighbouring nodes after the deletion.

The unit is copied to the neighbour with the highest hormone level, if this value is higher than the hormone level on the current node plus the migration threshold m. Copying takes several iterations because the content units are much larger than the packets containing the hormones.

This step does not change the hormone level: $\overline{\mathbf{h}}^{(3)}(t) = \overline{\mathbf{h}}^{(2)}(t)$. It has an indirect effect on the hormone update function because $x_i(t)$ indicating the presence of the requested content on a node changes after completing the copy of the unit to the new location.

3.2.4 Evaporate (Step 4)

The evaporation reduces the hormones by a constant value if possible and then deletes the hormone if its value is below a specified threshold. This step ensures that the hormones on alternative paths will disappear from the system after delivering the unit at the destination. The hormone level after evaporating hormones $\overline{\mathbf{h}}^{(4)}(t)$ can be calculated as follows:

$$\overline{\mathbf{h}}^{(4)}(t) = \overline{\mathbf{h}}^{(2)}(t) + \overline{\mathbf{b}}^{(4)}(t)$$

Where

η_0	Generated hormone level at a new request
η	Increase of the hormone level after each iteration at the requesting node
α	Percentage of hormones to be forwarded to the neighbors
ϵ	Hormone evaporation value
T	Minimum hormone strength
m	Minimum hormone difference to move unit (migration threshold)

Table 1 Summary of the parameters of the algorithm. We apply the same notation as Sobe [26]. The only difference is that T is used for minimum hormone strength instead of t because t denotes the index of the iteration in this paper.

– $\overline{\mathbf{b}}^{(4)}(t) = (b_1^{(4)}(t), b_2^{(4)}(t), ..., b_n^{(4)}(t))$: the vector containing the evaporations at different nodes in iteration t

ϵ and T give the constant evaporation value and the threshold of deletion, respectively. The value of the additive term can be given as follows:

$$b_i^{(4)}(t) = \begin{cases} -\epsilon, & h_i^{(2)}(t) \geq T + \epsilon \\ -h_i^{(2)}(t), & h_i^{(2)}(t) < T + \epsilon \end{cases}$$

3.2.5 One entire iteration

The above steps can be accumulated into one formula for a whole iteration. The monotonicity is evaluated for unit guidance after Step 2 (Diffuse hormones), therefore we focus on the hormone level after this step.

The hormone update function can be presented as follows:

$$\overline{\mathbf{h}}(t+1) = (\overline{\mathbf{h}}(t) + \overline{\mathbf{b}}(t+1))\mathbf{D}$$

Where

– $\overline{\mathbf{h}}(t) = (h_1(t), h_2(t), ..., h_n(t))$: the vector containing the hormone levels at different nodes before the evaluation for unit forwarding ($\overline{\mathbf{h}}(t) = \overline{\mathbf{h}}^{(2)}(t)$)
– $\mathbf{D}$: The diffusion matrix (See Subsection Diffuse hormones (Step 2)).
– $\overline{\mathbf{b}}(t) = (b_1(t), b_2(t), ..., b_n(t))$: the vector containing the accumulated additive terms at different nodes in iteration t

The value of the accumulated additive term can be given as follows (see Table 1 for the summary of the parameters):

$$b_i(t) = \begin{cases} \eta_0 & i = r, t = 1 \\ \eta - \epsilon & i = r, t > 1, h_i(t-1) > T + \epsilon \\ \eta & i = r, t > 1, h_i(t-1) \leq T + \epsilon \\ -\epsilon & i \neq r, h_i(t-1) > T + \epsilon \\ -h_i(t) & i \neq r, h_i(t-1) \leq T + \epsilon \end{cases}$$

3.3 The diffusion matrix

In this section, we introduce some terms and properties related to the diffusion matrix which are useful in the convergence analysis of the hormone-based algorithm.

3.3.1 Basic terms and properties

The hormones diffuse in a deterministic manner in the algorithm. Due to the next lemma, the results on the well-studied transition probability matrix of Markov chains can be applied to the diffusion matrix of the hormone-based system although the diffusion of the hormones does not follow a Markov-process. In this subsection, we introduce some terms into the artificial hormone system which correspond to some basic terms of Markov chains (e.g., regularity, fixed row vector of the transition matrix, absorbing Markov chain).

Lemma 1 *For an artificial hormone system, there exists a Markov chain whose transition probability matrix is equal to the diffusion matrix of the system.*

Proof: The lemma follows from the fact that the elements of the diffusion matrix $\mathbf{D}$ are all non-negative, less than or equal to one and their sum for each row is equal to one. The elements of matrix $\mathbf{D}$ correspond to the transition probabilities of the Markov chain. □

Definition 1 A hormone system is called *regular* if some power of the diffusion matrix has only positive elements.

In other words, for some l, the hormones can diffuse from any state to any state in exactly l steps in a regular system. The following lemma gives a condition for regularity which holds for the typical hormone systems.

Lemma 2 *If the network is strongly connected and* $0 < \alpha < 1$ *then the hormone system is regular.*

Proof: We give a graph theoretical proof. Since diffusion matrix $\mathbf{A}$ is a nonnegative matrix, $(\mathbf{A}^k)_{ij}$ is positive if and only if there exists at least one edge sequence of length k between nodes i and j. If the network is strongly connected, there exist k for every pair of nodes i and j such that $(\mathbf{A}^k)_{ij}$ is positive. If $0 < \alpha < 1$ then loop edges are added at each node. By circulating in loop edges, the edge-sequences can be extended to any length. For this reason, if l is equal to the maximal shortest paths length between two nodes in the network, then all elements of the lth power of the diffusion matrix are positive. □

For this reason, the hormone systems are regular in the most cases. A counterexample for the regularity is when the directed network graph has no loop edges and it is acyclic or bipartite graph.

Definition 2 A hormone system is called *time-homogeneous* if both the diffusion matrix and the location of the units are the same after each iteration.

The hormone levels are used in the decisions on the direction where to forward the content units. The decision is made when copying a content unit is completed. For this reason, our convergence analysis refers to the period of the iterations of the hormone update function while a unit is copied. In this period, the locations of the content units are unchanged.

The following term of the fixed row plays a key role in convergence.

Definition 3 A row vector $\overline{\mathbf{w}}$ with the property $\overline{\mathbf{w}}\mathbf{D} = \overline{\mathbf{w}}$ is called a *fixed row vector* for diffusion matrix $\mathbf{D}$. A fixed row vector with the property $\sum_{i=1}^{n} w_i = 1$ (w_i is the ith component of $\overline{\mathbf{w}}$) is called a *normalised fixed row vector* for $\mathbf{D}$.

Lemma 3 *The fixed row vector does not depend on the algorithm parameters but only on the weights between the network nodes.*

Proof: Let us introduce $\mathbf{D}'$ denoting the matrix representing the weights between the nodes. The diffusion matrix can be expressed by using $\mathbf{D}'$ as follows:

$$\mathbf{D} = (1 - \alpha)\mathbf{E} + \alpha\mathbf{D}'$$

where $\mathbf{E}$ represents the unit matrix. Let us replace $\mathbf{D}$ with the above expression in the definition of the fixed vector.

$$\overline{\mathbf{w}}[(1 - \alpha)\mathbf{E} + \alpha\mathbf{D}'] = \overline{\mathbf{w}}$$

This implies that

$$\overline{\mathbf{w}}(-\alpha\mathbf{E} + \alpha\mathbf{D}') = \overline{\mathbf{0}}$$

We may assume $\alpha \neq 0$ otherwise, no hormone is distributed among the nodes. Therefore, we may divide both sides by α.

$$\overline{\mathbf{w}}(-\mathbf{E} + \mathbf{D}') = \overline{\mathbf{0}}$$
$$\overline{\mathbf{w}}\mathbf{D}' = \overline{\mathbf{w}}$$

According to the above equations, the fixed vectors of matrix $\mathbf{D}$ are also fixed vectors for $\mathbf{D}'$. $\mathbf{D}'$ and therefore its fixed vectors do not depend on any parameter of the algorithm but on the weights between the network nodes. □

The hormone system may contain nodes that receive hormones but do not forward them to any neighbors: the nodes containing the requested unit and the nodes with hormone level below the threshold T. The hormone level drops to zero at these nodes according to the formal description of the update algorithm in Section 3. We introduce some terms related to these nodes.

Definition 4 In the hormone system, a node is called a *deleting node* in iteration t if its hormone level drops to zero in any algorithmic step of iteration t. The other nodes not deleting their whole hormone level are called *preserving nodes*. The hormone system is called *deleting* if it has at least one deleting node and if the hormones from every node can diffuse to a deleting node.

If only the rows and columns of preserving nodes is held from a diffusion matrix of a hormone update functions then the resultant matrix corresponds to matrix $\mathbf{Q}$ of an absorbing Markov chain.

Definition 5 In a deleting hormone system, matrix $\mathbf{Q}$ gives the diffusion rates between the preserving nodes.

The deleting hormone systems can be characterised by absorbing Markov chains. A state s_i of a Markov chain is called *absorbing* if it is impossible to leave it (i.e., $p_{ii} = 1$). A Markov chain is *absorbing* if it has at least one absorbing state and if from every state it is possible to go to an absorbing state (not necessarily in one step). In an absorbing Markov chain, a state which is not absorbing is called *transient*.

Lemma 4 *For an artificial hormone system, there exists an absorbing Markov chain whose matrix containing the transition probabilities between the transient states is equal to* $\mathbf{Q}$ *of the hormone system if the network is strongly connected.*

Proof: The deleting and preserving nodes correspond to the absorbing and the transient states, respectively, of the Markov chains. The transition probabilities are equal to the elements of the diffusion matrix of the hormone system except the transition probabilities from the absorbing nodes. For the absorbing node n_i, $p_{ii} = 1$. Due to the connectivity, absorbing nodes can be reached from each transient node. Matrix $\mathbf{Q}$ contains the transition probabilities between the transient states. □

3.3.2 Convergence of the powers of the diffusion matrix

Since the diffusion matrix may represent the transition matrix of a Markov chain, we decided to apply the results on the well-studied Markov chains to the convergence analysis of the artificial hormone system. In this subsection, some theorems on the powers of the diffusion matrix are presented that can be applied to prove the convergence of the hormone levels. They can be proved by applying the properties of the transition probability matrix of Markov chains to the diffusion matrix. The related theorems on Markov chains can be found in the book of Grinstead and Snell [21].

The following theorem claims that the powers of a diffusion matrix of a regular hormone system form a convergent sequence.

Lemma 5 *If* $\mathbf{D}$ *is a diffusion matrix for a regular hormone system, then* $\lim_{n\to\infty} \mathbf{D}^n = \mathbf{W}$, *where* $\mathbf{W}$ *is matrix with all rows the same vector* $\overline{\mathbf{w}}$.

It follows from the Fundamental Limit Theorem for Regular Chains and Lemma 1. □

The common row of $\mathbf{W}$ is equal to the fixed row vector of $\mathbf{D}$ ($\overline{\mathbf{w}}\mathbf{P} = \overline{\mathbf{w}}$) and it is the only fixed row vector.

Lemma 6 *Let* $\mathbf{D}$ *be the diffusion matrix for a regular hormone system and* $\overline{\mathbf{v}}$ *a vector whose length is equal to the number of nodes and for which the sum of its components is 1. Then* $\lim_{n\to\infty} \overline{\mathbf{v}}\mathbf{P}^n = \overline{\mathbf{w}}$, *where* $\overline{\mathbf{w}}$ *is the unique fixed row vector for* $\mathbf{P}$.

It follows from a similar theorem on Markov chains and Lemma 1. □

Lemma 7 *Let* $\mathbf{D}$ *be the diffusion matrix for a regular hormone system, let* $\mathbf{W}$ *be the limit of the sequence of its powers. Then the matrix* $\mathbf{E}-\mathbf{D}+\mathbf{W}$ *has an inverse. The series of* $\mathbf{E}+(\mathbf{D}-\mathbf{W})+(\mathbf{D}^2-\mathbf{W})+...$ *converges to the inverse of* $\mathbf{E}-\mathbf{D}+\mathbf{W}$.

It follows from a similar theorem on Markov chains and Lemma 1. □

As we mentioned in the previous subsection, the absorbing Markov chains are relevant for the artificial hormone systems if the hormone systems contain nodes deleting the hormones.

Lemma 8 *In a deleting hormone system, the powers of* $\mathbf{Q}$ *containing the diffusion rates between the preserving nodes converge to the zero vector. (i.e.,* $\mathbf{Q}^n \to \mathbf{0}$ *as* $n \to \infty$*).*

It follows from a similar theorem on absorbing Markov chains and Lemma 4.

If the considered hormone system is deleting then the hormone would disappear from the system without continuous production due to the above theorem. According to the next theorem, the sum of the matrix powers converges.

Lemma 9 *For a deleting hormone system the matrix* $\mathbf{E}-\mathbf{Q}$ *has an inverse. The series of* $\mathbf{E}+\mathbf{Q}+\mathbf{Q}^2+...$ *converges to the inverse of* $\mathbf{E}-\mathbf{Q}$.

It follows from a similar theorem on absorbing Markov chains and Lemma 4.

4 Monotonicity in time

This section concentrates on the monotonicity of the hormone level on a specific node as a function of the iteration t. The hormone levels may decrease (e.g. at evaporation) and increase (e.g. at generation) within one iteration in the different steps of the algorithm. However, if the hormone levels always in the same algorithmic step of the subsequent iterations are considered then the sequence of the hormone levels at a node proves to be monotonic in many cases. The hormone system is monotone increasing in time at node n_i in iteration t if $\overline{\mathbf{h}}_i^{(s)}(t) \geq \overline{\mathbf{h}}_i^{(s)}(t-1), s \in \{1,2,3,4\}$.

Lemma 10 *If the hormone system is time-homogeneous and the hormone level increases monotonically in time at each node in iteration* $t_0, t_0 > 1$ *then it does in each iteration* $t \geq t_0$ *as well.*

Proof: The lemma can be proved by mathematical induction on the steps of the algorithm. In the iteration t_0, the monotonicity follows from the condition of the theorem. Now, let us assume that the hormone level were monotonically increasing in algorithmic step s of iteration t. The aim of the inductive step is to prove that it is monotonically increasing at each node in the next step as well: $h_i^{(s)}(t+1) \geq h_i^{(s)}(t)$ if $h_i^{(s-1)}(t+1) \geq h_i^{(s-1)}(t)$ for $1 < s \leq 4$, and if $h_i^{(4)}(t) \geq h_i^{(4)}(t-1)$ for $s = 1$.

Let us consider the algorithmic steps one after the other. Step 1 Handle incoming requests provides higher hormone level by η than in the previous algorithmic step in iteration t if $t > 1$, therefore, it provides greater or equal hormone levels than in the previous iteration if the hormone levels were monotone increasing in the previous iteration step as well. It is true for Step 2 Diffuse hormones as well for any iteration if the hormone system is time-homogeneous. Step 3 Move units does not change the hormone level. Step 4 Evaporate hormones is also appropriate because more hormone remains after the evaporation if the hormone level was higher before it. Therefore, the hormone level is monotonically increasing in iteration $t+1$ if it was in iteration t. The inductive step is ready. □

The condition of monotonicity at each node seems to be strict but the following lemma gives a simple condition for monotonicity in all iterations.

Lemma 11 *If the hormone system is time-homogeneous and the hormone level at the requesting node increases in the second iteration then the hormone level at each node monotonically increases in time in each iteration. The condition of the monotonicity of the hormone level at the requesting node in the second iteration is* $\eta \geq \min(\eta_0, \epsilon + \alpha\eta_0)$.

Proof: In the first iteration ($t = 1$), the monotonicity is a trivial consequence of the zero initial values. Let us turn to iteration $t = 2$. Similarly to the previous lemma, it can be proved that the hormone update steps except Step 1 Handle incoming requests provide greater or equal hormone level for iteration $t = 2$ if the hormone levels were increasing in iteration $t = 1$. The problem with Step 1 in the second iteration is that the increase η in this iteration may be smaller than the increase η_0 in the first iteration.

Let us examine the condition of the monotonicity at the requesting node in the second iteration. The hormone level is initially η_0 at the requesting node. In the second iteration, it is $(1 - \alpha)\eta_0 - \epsilon + \eta$ if the hormone was not deleted in the evaporation step and η otherwise. We can get after a short calculation that the hormone level in the second iteration after Step 1 Handle incoming requests is greater than η_0 if $\eta > \min(\eta_0, \epsilon + \alpha\eta_0)$. If this condition is fulfilled, then the hormone levels are monotonic at each node in step $t = 2$. In this case, Lemma 10 implies monotonicity in each iteration $t \geq 2$ as well. □

We are interested whether the set of preserving nodes is extending or shrinking. According to the following corollary, the set of preserving nodes never shrinks.

Corollary 1 *If the hormone system is time-homogeneous and the hormone level is monotonically increases with time at each node in iteration* $t_0, t_0 > 1$ *then the size of the set of preserving nodes is monotone increasing in each iteration* $t \geq t_0$.

Proof: If the hormone level is larger than 0 at node n_i in iteration $t_0, t_0 > 1$ and the hormone level monotonically increases with time at each node in the same iteration then the hormone level remains positive at node n_i in each iteration $t \geq t_0$. This implies the corollary because preserving nodes refer to nodes with nonzero hormone levels. □

5 Convergence results for the hormone levels

In this section, we examine the convergence of the hormone levels at the nodes of the network. The hormone based algorithm diffuses hormone in the network and looks for the requested content unit. If the unit is found it is always forwarded from the storing node to its neighbor with the highest hormone level. Therefore, the direction of forwarding depends on the relative values of the hormone levels in the network. After the unit arrives to the new location, a decision is made again where to copy or move it further.

We assume that the hormone update is running repeatedly while a unit is forwarded and it is iterated for several times before the decision is made on the direction of forwarding the units based on the current hormone levels. The hormone spreads much faster than the content unit because the size of the content unit is much larger than the one of the messages containing the hormones. This is especially true for multimedia content. The hormone is represented as a real value which can be encoded as a few bytes while the size of the multimedia units was between 100KB and 16 MB in the simulation scenarios. Since the number of iterations between the decisions is usually large, convergence analysis can characterise the behaviour of the hormone system.

Since the decision on direction is based on the hormone levels at the time when copying a content unit is completed, we examine the convergence of the hormone values during the period before this time while a unit is being copied. The location of the content unit is unchanged in this period.

5.1 Zero additive term

In this subsection, the additive term in the hormone update function is assumed to be constant zero except at the first iteration.

Theorem 1 *If the hormone system is regular and time-homogeneous and the additive term is zero for iterations* $t > 1$ $(\overline{\mathbf{b}}(t) = \overline{\mathbf{0}}, \forall t > 1)$ *then the hormone level converges at each node. The limit of the hormone level vector is* $\eta_0 \overline{\mathbf{w}}$ *where* $\overline{\mathbf{w}}$ *is the normalised fixed vector of the diffusion matrix.*

Proof: The hormone level at the first iteration can be formulated as follows:

$$\overline{\mathbf{h}}(1) = (\overline{\mathbf{h}}(0) + \overline{\mathbf{b}}(1))\mathbf{D} = \overline{\mathbf{b}}(1)\mathbf{D}$$

The additive term in the first iteration is simply $\overline{\mathbf{b}}(1) = \overline{\mathbf{b}}^{(1)}(1)$. Its components for the ith node can be defined as follows:

$$b_i(1) = \begin{cases} \eta_0 & i = r \\ 0 & i \neq r \end{cases}$$

Let us introduce vector $\overline{\mathbf{v}}$ for which $\eta_0 \overline{\mathbf{v}} = \overline{\mathbf{b}}(1)$. Its components can be defined as follows:

$$v_i = \begin{cases} 1 & i = r \\ 0 & i \neq r \end{cases}$$

If the additive term is zero

$$\overline{\mathbf{h}}(t) = \overline{\mathbf{h}}(1)\mathbf{D}^{t-1} = \overline{\mathbf{b}}(1)\mathbf{D}^{t} = \eta_0\overline{\mathbf{v}}\mathbf{D}^{t}$$

Theorem 6 can be applied to the limit of the hormone levels:

$$\lim_{t\to\infty}\overline{\mathbf{h}}(t) = \overline{\mathbf{h}}(1)\mathbf{D}^{t-1} = \eta_0\lim_{t\to\infty}\overline{\mathbf{v}}\mathbf{D}^{t} = \eta_0\overline{\mathbf{w}} \tag{1}$$

□

The content unit is guided towards the increasing hormone levels. As a consequence of the above theorem, the relative values of the hormones on the nodes are determined only by the fixed vector of the diffusion matrix ($\overline{\mathbf{w}}$). According to Lemma 3, it means that they depend neither on the algorithm parameters nor the location of the requesting node but only on the weights between the nodes. The above result is not surprising if we think on the analogy with Markov chains. The regular Markov chains converge to the stationary distribution (also called as equilibrium distribution) independently from the starting distribution. The zero additive term has practically low relevance because η and ϵ are usually not zero. However, the above results will be applied in the next subsection.

5.2 Constant additive term

In this section, the additive term of the hormone update function may differ from zero but it is assumed to be constant after the first iteration.

Theorem 2 *If the hormone system is regular and time-homogeneous, additive term* $\overline{\mathbf{b}}$ *is constant at each node in iterations* $t > 1$ *and* $c = \sum_{i=1}^{n} b_i > 0$ *then the hormone levels are asymptotically equivalent with the linear function* $t \cdot c \cdot \overline{\mathbf{w}}$ *where* $\overline{\mathbf{w}}$ *is the normalised fixed vector of the diffusion matrix. Furthermore,*

$$\lim_{t\to\infty}(h(t) - t\cdot c\cdot\overline{\mathbf{w}}) = \eta_0\overline{\mathbf{w}} + \overline{\mathbf{b}}(\mathbf{E}-\mathbf{D}+\mathbf{W})^{-1} - \overline{\mathbf{b}} \tag{2}$$

Proof: If the additive term is constant, the hormone level can be formulated as follows:

$$\overline{\mathbf{h}}(t) = (\overline{\mathbf{h}}(t-1) + \overline{\mathbf{b}})\mathbf{D} = \overline{\mathbf{h}}(1)\mathbf{D}^{t-1} + \overline{\mathbf{b}}\sum_{i=1}^{t-1}\mathbf{D}^{i}$$

$$\lim_{t\to\infty}\overline{\mathbf{h}}(t) = \lim_{t\to\infty}\overline{\mathbf{h}}(1)\mathbf{D}^{t-1} + \lim_{t\to\infty}\overline{\mathbf{b}}\sum_{i=1}^{t-1}\mathbf{D}^{i} \tag{3}$$

The first term of the above sum converges $\eta_0\overline{\mathbf{w}}$ according to the previous theorem. Now, let us turn to the second term. It follows from Lemma 7 that

$$\lim_{t\to\infty}(\sum_{i=0}^{t}\mathbf{D}^{i} - t\cdot\mathbf{W}) = (\mathbf{E}-\mathbf{D}+\mathbf{W})^{-1}$$

Since $\sum_{i=1}^{t} \mathbf{D}^i = \sum_{i=0}^{t} \mathbf{D}^i - \mathbf{E}$ and $\lim_{t\to\infty} \sum_{i=1}^{t} \mathbf{D}^i = \lim_{t\to\infty} \sum_{i=1}^{t-1} \mathbf{D}^i$

$$\lim_{t\to\infty} (\sum_{i=1}^{t-1} \mathbf{D}^i - t \cdot \mathbf{W}) = (\mathbf{E} - \mathbf{D} + \mathbf{W})^{-1} - \mathbf{E}$$

Let us multiply the above equation by $\overline{\mathbf{b}}$.

$$\lim_{t\to\infty} (\overline{\mathbf{b}} \sum_{i=1}^{t-1} \mathbf{D}^i - t \cdot \overline{\mathbf{b}}\mathbf{W}) = \overline{\mathbf{b}}(\mathbf{E} - \mathbf{D} + \mathbf{W})^{-1} - \overline{\mathbf{b}} \tag{4}$$

According to Lemma 5, each row of $\mathbf{W}$ is equal to vector $\overline{\mathbf{w}}$, therefore,

$$\lim_{t\to\infty} (\overline{\mathbf{b}} \sum_{i=1}^{t-1} \mathbf{D}^i - t \cdot (\sum_{i=1}^{n} b_i)\overline{\mathbf{w}}) = \overline{\mathbf{b}}(\mathbf{E} - \mathbf{D} + \mathbf{W})^{-1} - \overline{\mathbf{b}} \tag{5}$$

If $\sum_{i=1}^{n} b_i \neq 0$, we may divide both sides by $t \cdot (\sum_{i=1}^{n} b_i)\overline{\mathbf{w}}$ and we get that

$$\lim_{t\to\infty} \frac{\overline{\mathbf{b}} \sum_{i=1}^{t-1} \mathbf{D}^i}{t \cdot (\sum_{i=1}^{n} b_i)\overline{\mathbf{w}}} = 1$$

By using the notation of asymptotic equivalence, we may write:

$$\overline{\mathbf{b}} \sum_{i=1}^{t-1} \mathbf{D}^i \sim t \cdot (\sum_{i=1}^{n} b_i)\overline{\mathbf{w}} \tag{6}$$

From Eqs. (1), (3) and (6),

$$\overline{\mathbf{h}}(t) \sim \eta_0 \overline{\mathbf{w}} + t \cdot (\sum_{i=1}^{n} b_i)\overline{\mathbf{w}} \sim t \cdot (\sum_{i=1}^{n} b_i)\overline{\mathbf{w}}$$

Eq. (2) comes from Eqs. (1), (3) and (5). □

According to the theorem, the hormones levels diverge and are unbounded. However, this may happen only if the network does not contain any deleting nodes. Otherwise, the deleting node would delete hormone amount that is proportional to the increasing hormone levels, therefore, the additive term cannot be constant. For this reason, the conditions of the theorem for the constant additive term is rather strict because the additive term may be positive at each node only if the requested content unit cannot be found in the network and the hormone can spread over the whole network.

5.3 Fixed set of deleting nodes

Let us replace the condition of the constant additive term with the more general condition that the set of preserving (or deleting) nodes is fixed. In this case, the deleting nodes can be dropped from the system because they will never forward hormone towards the other nodes. This subsection reformulates the theorems in the previous subsections for a hormone system with a fixed set of preserving nodes.

Theorem 3 *If the hormone system is deleting and time-homogeneous, the set of deleting nodes is fixed and the additive term is zero at the preserving nodes in iterations $t > 1$ then the hormone levels converge to zero at each node.*

Proof: Let $\overline{\mathbf{h}'}(t)$ denote the hormone levels on the preserving nodes. If the additive term is zero

$$\overline{\mathbf{h}'}(t) = \overline{\mathbf{h}'}(t-1)\mathbf{Q} = \overline{\mathbf{h}'}(1)\mathbf{Q}^{t-1}$$
$$\lim_{t\to\infty} \overline{\mathbf{h}'}(t) = \lim \overline{\mathbf{h}'}(1)\mathbf{Q}^{t-1}$$

We know from Lemma 8 that $\mathbf{Q}^n \to \mathbf{0}$ as $n \to \infty$, therefore,

$$\lim_{t\to\infty} \overline{\mathbf{h}'}(t) = \overline{\mathbf{0}} \qquad \square$$

Theorem 4 *If the hormone system is deleting and time-homogeneous, the set of deleting nodes is fixed and the additive term $\overline{\mathbf{b}}$ is constant nonzero at the preserving nodes in iterations $t > 1$ then the hormone levels converge at each node. The limit of the vector containing the hormone levels is*

$$\lim_{t\to\infty} \overline{\mathbf{h}'}(t) = \overline{\mathbf{b}'}[(\mathbf{E}-\mathbf{Q})^{-1} - \mathbf{E}]$$

where $\overline{\mathbf{b}'}$ denotes the additive term on the preserving nodes.

Proof: If $\overline{\mathbf{b}'}$ is constant, the hormone level can be calculated as follows:

$$\overline{\mathbf{h}'}(t) = (\overline{\mathbf{h}'}(t-1) + \overline{\mathbf{b}'})\mathbf{Q} = \overline{\mathbf{h}'}(1)\mathbf{Q}^{t-1} + \overline{\mathbf{b}'}\sum_{i=1}^{t-1}\mathbf{Q}^i$$

$$\lim_{t\to\infty} \overline{\mathbf{h}'}(t) = \lim_{t\to\infty} \overline{\mathbf{h}'}(1)\mathbf{Q}^t + \lim_{t\to\infty} \overline{\mathbf{b}'}\sum_{i=1}^{t-1}\mathbf{Q}^i$$

The first term of the above sum converges to zero according to the proof of the previous theorem (Theorem 3). For this reason, the hormone levels converge to the second term of the sum.

$$\lim_{t\to\infty} \overline{\mathbf{h}'}(t) = \lim_{t\to\infty} \overline{\mathbf{b}'}\sum_{i=1}^{t-1}\mathbf{Q}^i = \lim_{t\to\infty} \overline{\mathbf{b}'}\sum_{i=0}^{t}\mathbf{Q}^i - \overline{\mathbf{b}'} \tag{7}$$

The sum of powers of $\mathbf{Q}$ converges to $(\mathbf{E}-\mathbf{Q})^{-1}$ according to Lemma 9:

$$\lim_{t\to\infty} \overline{\mathbf{h}'}(t) = \overline{\mathbf{b}'}(\mathbf{E}-\mathbf{Q})^{-1} - \overline{\mathbf{b}'} = \overline{\mathbf{b}'}[(\mathbf{E}-\mathbf{Q})^{-1} - \mathbf{E}] \qquad \square$$

5.4 General case

Theorem 5 *If the hormone system is deleting and time-homogeneous and there is an iteration t_0 for which the hormone level monotonically increases with time at each node then the hormone levels converge at each node.*

Proof: From Corollary 1, the set of preserving nodes is monotonically increasing, therefore, there exists a maximal set of preserving nodes whose size does not change any more. The components of the additive term $\overline{\mathbf{b'}}$ is constant for the preserving nodes in iterations $t > 1$. They can be simply calculated as follows:

$$b'_i = \begin{cases} \eta - \epsilon & i = r \\ -\epsilon & i \neq r \end{cases}$$

For this reason, we can apply Theorem 4 for the maximal set of preserving nodes (i.e., minimal set of deleting nodes) and for the fixed additive term specified above.

$$\lim_{t\to\infty} \overline{\mathbf{h'}}(t) = \overline{\mathbf{b'}}[(\mathbf{E} - \mathbf{Q})^{-1} - \mathbf{E}] \tag{8}$$

where $\mathbf{Q}$ denotes the matrix of the diffusion rates between the nodes of the maximal set of preserving nodes. □

We remark that although the condition on monotonicity in time for each node seems to be restrictive, Lemma 11 gives a simple sufficient condition for it. Furthermore, a systems is deleting if it contains the requested unit and there is a path from every node to a node containing the unit. For this reason, the conditions of the lemma are fulfilled in the most of the practically relevant cases.

6 Monotonicity in the network

This section concentrates on the monotonicity of the hormone level along a path between the node containing the requested unit and the requesting node. For brevity, we refer to the node containing the requested unit as a content source. We give sufficient conditions when the content unit is copied from the content sources. We also examine monotonic increase at the neighbours of the content source and at the further nodes along the path to the requesting node. We restrict our examination to the stationary solution ($\overline{\mathbf{h}}(t+1) = \overline{\mathbf{h}}(t) = \overline{\mathbf{h}}$) represented by the limit of the hormone levels. First, we give some basic formulas for the stationary solutions.

$$\overline{\mathbf{h}} = (\overline{\mathbf{h}} + \overline{\mathbf{b}})\mathbf{D} \tag{9}$$

where $\overline{\mathbf{h}}$ denotes a stationary solution and the additive term $\overline{\mathbf{b}}$ is also fixed.

The above equation can be applied to express the hormone level on a single node as follows:

$$h_i = (1 - \alpha)(h_i + b_i) + \alpha \sum_{j \in N_i} w_{ji}(h_j + b_j) \tag{10}$$

where h_i and b_i denote the stationary hormone level and the additive term, respectively, at node n_i. N_i refers to the set of indexes of the neighbours of node n_i.

Let N_i' denote the set of indexes of the nondeleting neighbours of node n_i. Since $-h_i = b_i$ for the deleting nodes, they can be dropped from the right side of Eq. (10). Now, let us apply the above equation to nonedeleting node n_i:

$$h_i = (1-\alpha)(h_i + b_i) + \alpha \sum_{j \in N_i'} w_{ji}(h_j + b_j) \tag{11}$$

If n_i is deleting, the equation can be further simplified:

$$h_i = \alpha \sum_{j \in N_i'} w_{ji}(h_j + b_j) \tag{12}$$

In the preceding section, we gave sufficient condition for the convergence of the hormone levels. One can easily check that the limit provided by Theorem 4 serves as a stationary solution. The next theorem gives a lower bound on the hormone levels on a content source.

Lemma 12 *If the hormone system converges to a stationary solution and the requested unit can be found on $s_1 > 0$ different nodes then there is at least one node among the content sources where the hormone level is at least*

$$\frac{1}{s_1}[\eta - (n - s_1)(\epsilon + T)]$$

Proof: In a stationary solution, the total amount of hormone increase is equal to the total amount of hormone decrease. Diffusing hormones preserves the total sum of the hormones in the system since the sum of the weights of outgoing edges from a node is equal to one. The step of handling incoming requests increases the amount of hormones while evaporation and deleting the hormone on the node containing the requested unit decreases the hormone levels.

Let S_1 and S_2 denote the set of nodes containing the requested unit and the further deleting nodes, respectively. s_i gives the size of S_i, $i = (1, 2)$. Furthermore, let s_0 denote the number of the nondeleting nodes.

In the stationary state, the generated and the deleted hormone levels are equal with one another:

$$\eta = s_0\epsilon + \sum_{i \in S_1} h_i + \sum_{i \in S_2} h_i \tag{13}$$

Let n_m denote the content source with the largest hormone level.

$$\eta \leq s_0\epsilon + s_1 h_m + s_2(\epsilon + T) \tag{14}$$

This implies that

$$h_m \geq \frac{1}{s_1}[\eta - s_0\epsilon - s_2(\epsilon+T)] \geq \frac{1}{s_1}[\eta - (s_0+s_2)(\epsilon+T)] = \frac{1}{s_1}[\eta - (n-s_1)(\epsilon+T)]$$

□

The requested unit is not forwarded from its original location if the hormones do not reach any content sources.An easy consequence of the above lemma provides a sufficient condition guaranteeing to find the content unit.

Corollary 2 *If the hormone system converges to a stationary solution, the requested unit can be found in the network and* $\eta > (n - s_1)(\epsilon + T)$ *then the artificial hormone system finds the content unit in the network.*

Proof: According to the previous lemma, there exists content source n_m in the network for which $h_m > 0$. □

The algorithm guides the content unit from the source to its neighbour with the highest hormone level. The next theorem provides a lower bound on the highest hormone level among the neighbours of a content source and defines a condition when the content unit will be copied from its original locations.

Theorem 6 *If the hormone levels converge to a stationary solution, none of the content sources is adjacent with the requesting node and the following inequality holds*

$$m \leq \frac{\eta - (n - s_1)(\epsilon + T)(1 - \alpha \sum_{j \in N_i'} w_{ji})}{s_1 \alpha \sum_{j \in N_i'} w_{ji}} + \epsilon \tag{15}$$

then the content unit will be copied from its original location.

Proof: Let us apply Equation (12) describing the stationary solution to deleting node n_i not adjacent with the requesting node:

$$h_i = \alpha \sum_{j \in N_i'} w_{ji}(h_j - \epsilon) \tag{16}$$

Let h_m denote the maximum hormone level among the neighbours of n_i.

$$h_i \leq (h_m - \epsilon)\alpha \sum_{j \in N_i'} w_{ji} \tag{17}$$

It implies that

$$h_m \geq \frac{h_i}{\alpha \sum_{j \in N_i'} w_{ji}} + \epsilon \tag{18}$$

The difference of the hormone levels at the content source and at its neighbour with the largest hormone level can be expressed as follows:

$$h_m - h_i \geq \frac{h_i(1 - \alpha \sum_{j \in N_i'} w_{ji})}{\alpha \sum_{j \in N_i'} w_{ji}} + \epsilon \tag{19}$$

As a consequence of the above inequality and Lemma (12), a lower bound can be expressed for the difference:

$$h_m - h_i \geq \frac{[\eta - (n - s_1)(\epsilon + T)](1 - \alpha \sum_{j \in N_i'} w_{ji})}{s_1 \alpha \sum_{j \in N_i'} w_{ji}} + \epsilon \tag{20}$$

The content unit will be copied from its original location if the differerence is larger than threshold m. □

We can give another condition on copying from the content source:

Theorem 7 *If the hormone levels converge to a stationary solution, content source n_i is not adjacent with the requesting node, the hormone level reaches it (i.e., $h_i > 0$) and $\sum_{j \in N_i'} w_{ji} < \frac{1}{\alpha}$ and $m < \epsilon$ then the content unit will be copied from its original location.*

Proof: It can be proved similarly to the previous theorem that Inequation (19) holds in this case as well. Let us consider the right side of the inequality. The following inequalities hold under the conditions of the theorem:

$$h_i(1 - \alpha \sum_{j \in N_i'} w_{ji}) > 0, \epsilon > m$$

In this case, $h_m - h_i$ is larger than migration threshold m according to Inequation (19). □

We have given a lower bound on the highest hormone level among the neighbours of the content source. We go one step further: the next lemma can be used for providing lower bound on the largest hormone level for the neighbours of node n_i where n_i is the neighbour of the content source.

Lemma 13 *If the hormone levels converge to a stationary solution, node n_i is nondeleting, it is not adjacent with the requesting node, it has at least one nondeleting neighbour and the following inequality holds*

$$\frac{\epsilon}{\alpha} > (\sum_{j \in N_i'} w_{ji} - 1)(h_i - \epsilon) \tag{21}$$

then n_i has at least one neighbour n_m for which $h_m > h_i$.

Proof: The stationary equation (9) can be formulated as follows for a single node n_i whose neighbours do not contain the requested content unit:

$$h_i = (1 - \alpha)(h_i - \epsilon) + \alpha \sum_{j \in N_i'} w_{ji}(h_j - \epsilon) \tag{22}$$

Let h_m denote the maximum among the neighbours of n_i. Its introduction into Eq. (22) results in the following inequality:

$$h_i \leq (1 - \alpha)(h_i - \epsilon) + \alpha \sum_{j \in N_i'} w_{ji}(h_m - \epsilon)$$

After equivalent transformations we can get that

$$h_m \geq \frac{h_i + \epsilon(\sum_{j \in N_i'} w_{ji} - 1 + \frac{1}{\alpha})}{\sum_{j \in N_i'} w_{ji}} \tag{23}$$

$$h_m - h_i \geq \frac{(h_i - \epsilon)(1 - \sum_{j \in N_i'} w_{ji}) + \frac{\epsilon}{\alpha}}{\sum_{j \in N_i'} w_{ji}} \tag{24}$$

According to this inequality, $h_m > h_i$ if the inequality (21) holds. □

The next lemma can be used for the further nodes after the neighbour of the content source along a path to the requesting node. It provides a less strict sufficient condition for the monotonic increase than the preceding lemma does.

Lemma 14 *If the hormone levels converge to a stationary solution, node n_i is nondeleting and not adjacent with the requesting node, it has at least two nondeleting neighbours, one of them (n_s) has smaller hormone level than n_i and the following inequality holds*

$$\frac{\epsilon}{\alpha} + w_{si}(h_i - h_s) > (\sum_{j \in N_i'} w_{ji} - 1)(h_i - \epsilon) \tag{25}$$

then n_i has at least one neighbour n_m with larger hormone level than n_i.

Proof: The proof is analogous to the one of the preceding lemma but h_s is introduced in addition to h_m into Eq. (22), therefore, the details of the proof are omitted. □

We can assume that the adjacency in the network represents a symmetric relation i.e. if there is an edge with positive weights w_{ij} from node n_i to n_j then w_{ji} is also positive.

Let us introduce χ_i to indicate whether node n_i has at least two nondeleting neighbours and one of them has smaller hormone level than n_i:

$$\chi_i = \begin{cases} 1 \ \exists n_s, n_m \in N_i' : h_i > h_s \wedge i \neq m \\ 0 \ otherwise \end{cases}$$

We use this notation in the next lemma on spatial monotonicity in the artificial hormone system.

Theorem 8 *If the hormone levels converge to a stationary solution and each nondeleting node n_i has at least two neighbours, at least one of them is nondeleting and the following inequality holds*

$$\frac{\epsilon}{\alpha} + \chi_i w_{si}(h_i - h_s) > (\sum_{j \in N_i'} w_{ji} - 1)(h_i - \epsilon) \tag{26}$$

then any paths with strictly monotonically increasing hormone levels starting from a deleting node lead to the requesting node or to one of the neighbours of the requesting node.

Proof: Let $n_{i_0}, n_{i_1}, n_{i_2}, ..., n_{i_l}$ denote the subsequent items of the path with monotonically increasing hormone levels where n_{i_0} denote a deleting node and the n_{i_l} is the last node of the path. The path can be continued until it reaches a local maximum. Node n_{i_0} has a nondeleting neighbour n_{i_1}. n_{i_1} cannot represent a local maximum under the conditions of the theorem due to Lemma 13.

If $j > 1$ then n_{i_j} has a neighbour with smaller hormone level ($n_{i_{j-1}}$). If n_{i_j} has two nondeleting neighbours then Lemma 14 guarantees a neighbour with larger hormone level. Now, let us examine the case when n_{i_j} has only one nondeleting neighbours, the others are deleting. In this case, $n_{i_{j-1}}$ is the nondeleting neighbour and $h_{i_{j-1}} < h_{i_j}$ due to the monotonicity of the path. Since $w_{i_j,i_{j-1}} < 1$, it follows from Lemma 13 that $n_{i_{j-1}}$ should have larger hormone level than h_{i_j}, which is a contradiction. For this reason, we can exclude the case that n_{i_j} has only one nondeleting neighbour. The above lemmas guarantee monotonicity for all nodes except the requesting node and its neighbours. □

The theorem defines conditions guaranteeing a path with monotone increasing hormone levels from the content source towards the requesting node. A sufficient but not necessary condition of the monotonicity if the sum of the incoming weights is less than 1 because in this case the inequality in the theorem holds. We remark, that if the hormone levels are considered before the hormone diffusion step then the monotone paths are guaranteed to lead to the requesting node under the conditions of the theorem.

7 Summary

The paper presents the first convergence and monotonicity results on an artificial hormone system developed for multimiedia delivery. In order to examine the convergence of the hormone levels in the system, we gave recursive formulas for the hormone levels. We determined the limits of the hormone values at the nodes of the network under different conditions. We started with a basic hormone distribution system, then we gradually removed the restrictions and at the end, we examined a general case. Although the artificial hormone method in our scope is a deterministic algorithm, it shows analogy with the Markov chains and the proofs on the convergence are based on the theorems of the Markov chains.

Table 2 gives an overview on the asymptotic behaviour of the examined artificial hormone system under different conditions. If the hormone levels are divergent then the requested content units trying to follow the increasing hormone levels may fail to get to the destination. The results in the paper show that convergence can be guranteed by properly forming and parameterising the hormone system if the system contains the requested content unit. If the requested content unit cannot be found in the network the hormone levels can linearly increase without any upper bound which causes overflow in the network levels after many iterations. We found that the hormone levels converge to a limit in the most general case.

Furthermore, we were also interested in whether the hormone levels guide the unit to the requesting node. In some special cases (no deleting nodes and either no additive term or constant additive term), the relative values of the hormone in the network depend neither on the algorithm parameters nor the location of the requesting node but only on the fixed vector ($\overline{\mathbf{w}}$) of the diffusion

Table 2 The convergence of the hormone based algorithm in different cases

Condition	*Additive term*	*Convergence*
regular	$\overline{\mathbf{0}}$	convergent
regular	constant, $\sum_{i=1}^{n} b_i > 0$	divergent, unbounded
deleting	$\overline{\mathbf{0}}$	convergent to $\overline{\mathbf{0}}$
deleting	constant, $\sum_{i=1}^{n} b'_i > 0$	convergent
deleting, monotonic increasing in time	no restriction	convergent

matrix. In these systems, the units would be forwarded always to the same direction independently where the requesting node is. However, these cases are practically not relevant because they assume no deleting nodes in the network.

We studied the conditions of the monotonic increase of the hormone levels from the content sources towards the requesting node. Sufficient conditions were given when the hormone level reaches the requested content unit and when the content unit is copied from its original location which are inevitable for the proper operation. A sufficient but not necessary condition of the monotonicity is that the sum of the incoming weights is less than one. These results help in better understanding the behaviour of the artificial hormone system and in defining the structure and parameters of the system.

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