Molecular Processes as a Basis for Autonomous Networking

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***Abstract* – Autonomous networking has become the buzzword for attempts of building high-scalable network architectures, which are self-organizing, self-maintaining and self-healing. Few of these approaches were successful and none has shown to provide all the promised functions. We try to study the processes in computer networks using molecular processes as the paradigm. This novel approach shows many similarities between computer networking and cellular mechanisms. In this paper, we focus on the area of network security as one research area with high demand for high-scalable mechanisms providing the needed functionality. After identifying similarities between nature and technology, we discuss potential research domains, which are high potentials for learning directly from biology at the example of security attacks in networks. We see the proposed mechanism as a generic approach for autonomous networking. The countermeasures against attacks in computer networks are only a special example to introduce the mechanisms.**

***Keywords* – Autonomous Networking, Bio-Inspired Computing, Network Modeling, Next Generation Networks**

I. INTRODUCTION

We investigated the possibilities to utilize the infinite experience of the nature to solve current question in computer science, focused on problems in networking. Among other things, this approach was motivated by a book from Nobel prize laureate Prof. Manfred Eigen [7]. Unlike most activities in bioinformatics where computerized methods are employed to study natural processes in more detail, we discovered that at least some of our nowadays problems might be easier to understand and even to be solved if we directly learn from natural mechanisms. In this paper, we focus on mechanisms known from molecular biology, which we can adopt to improve internet technology.

During the last couple of years, great progress was made to make computer networks more stable, more efficient, and more secure. Nevertheless, we also experience that there are still many open issues, especially in terms of network security. Distributed denial of service (DDoS) attacks, worms, and viruses are getting more aggressive and much harder to prevent [9]. Autonomous networking should help to solve these problems. We try to fill this buzzword with some content learned from natural processes and show potential solutions using mechanisms for network security as an example.

In simple configurations of low-speed networks, well-known mechanisms can be employed to examine all the network traffic, to filter unknown or suspicious data packets, and to program firewall rules denying most kinds of attack traffic [3, 11]. Unfortunately, these mechanisms fail in today's high-speed backbone networks. Restrictions are given in CPU capacity and availability of free memory for processes and queues. Therefore, it is not possible to run all kinds of monitor processes and filters at once directly on the network components.

Our idea is to limit the active processes to those which are required by the current situation in the network, e.g. if a particular worm is being distributed, only a prevention scheme for this event is required. How can this be done? The solution is provided by achievements of molecular biology. In every single cell of an organism, the program for all reactions and mechanism is coded in the DNA and is activated exactly in the situation when it is needed. Every signal from the extracellular environment is recognized specifically and results in a specific signal transduction cascade. Signal transduction normally initiate the translation of the necessary genes which finally leads to a cellular answer, e.g. to maintain the cellular function, but also to react to pathological situations, e.g. any kind of inflammation, virus invasion, etc.

The same procedure seems to be adequate for reactions in computer networks. If we are able to describe solutions for typical problems in form of processes and their course of actions, we can build flexible network components with low resource requirements and a high efficiency in terms of network operations. Fortunately, we can employ methods from software engineering for such descriptions. Monitor components act as the receptors and try to identify the behavior of the network. Due to the availability of sampling methodologies and statistical methods, such monitoring can be done even in high-speed network environments [6, 13]. We already addressed similar scalability issues in other areas such as network measurements [5].

Based on the recognized behavior of the network, new processes can be created and activated using the permanent description of the available mechanisms. Afterwards, countermeasures are possible against the current attacks. This is possible because only these processes exist in memory and are activated which are required in the current situation.

We see the proposed mechanism as a generic approach for autonomous networking. The detection of security attacks and the following activation of countermeasures is only a special example to introduce the mechanisms.

In this paper, we show the similarities between the signaling mechanisms in cellular systems and networking entities responsible for packet forwarding, intrusion detection, and firewalling. Based on these similarities we identify the most important research issues.

The rest of the paper is organized as follows: in section II, the cellular mechanisms are described followed by a description of a general networking architecture including network security mechanisms in section II. Possible research issues resulting from an analysis of the similarities between both the cellular systems and computer networks are discussed in section III. A section describing related work and some conclusions complete this paper.

II. CELLULAR MECHANISMS

All organisms share one common information system which is the DNA (or RNA in some viruses) and which code for the organization of the whole organism. This organization is a highly regulated process from the single cell up to complex organs of the body. The hierarchy in the organism is very high. Every process, e.g. movement, metabolism, communication etc. is organized by interactions of several organs. Organs represent an assembly of one or more tissues, which fulfill a common function. One tissue is build by different cell types. One cell type consists of identical cells, which are associated and communicate with each other to fulfill a common function within the tissue. Single cells communicate with each other as well as with cells of other tissues by sending signals to which the target cells respond by specific gene expression. In this way, a signal can be carried out and influence the function of higher units such as the organs, e.g. cellular processes which induce the immune response during inflammation.

In this paper we want to focus on the mechanisms how cells interact with their environment in general and, secondly, on intracellular processes which select specifically the cellular response to an extracellular stimulus out of the pool of information given by the DNA.

A. Cellular Signaling

The functionality of an eukaryotic cell relies on the complex network of biochemical processes. Within these processes, single reactions take place in a coordinated fashion. They can take place simultaneously and successively. Therefore, these processes must be highly regulated and controlled. This also means that these mechanisms are very specific for the given result.

The main goals of cellular processes are to regulate the intracellular metabolism (biosynthesis of metabolites and enzyme activity) and to communicate with their environment. Physical or chemical attractions from the environment are signals for the cell to change intracellular processes. Chemical attractions can be low-molecular metabolites, hormones, or ions. They can be sent by other cells of the same tissue or by cells from other tissues and organs. Furthermore, physical parameters such as heat, pressure, or electrical signals can induce cellular reactions.

B. Intercellular Communication

Communication between cells can occur by different processes.

First, cells can release soluble molecules such as hormones etc. that are transported via the blood (long distance in the organism, e.g. hormones) to the target cell. Other soluble factors are released into the extracellular space to reach the neighboring cells in a short distance (Fig 1 A). These molecules are recognized by the target cells and induce a specific biochemical answer. By the release of soluble factors many cells can be activated simultaneously which results in a coordinated reaction of the organ or organism.

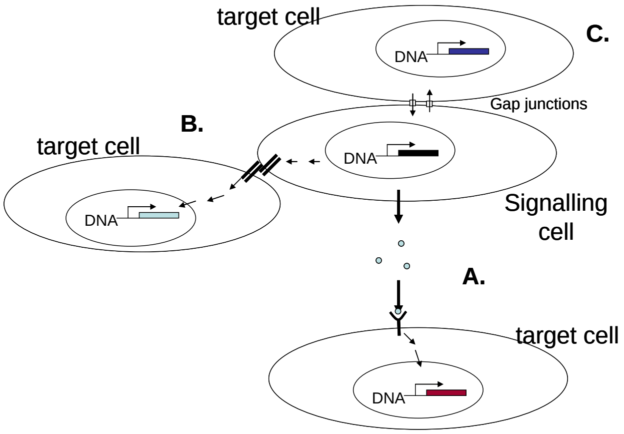

Fig 1. Intercellular communication. One cell can communicate with the neighboring cells via A. soluble factors, B. receptor interactions, C. direct contact, e.g. “gap junctions”. The target cells react on the current stimulus by gene transcription.

Secondly, cells can also communicate via cell surface molecules. In this process, a surface molecule of one cell or even a soluble molecule, which is released by one cell, directly binds to a specific receptor molecule on another cell (Fig 1 B). Thirdly, communication between cells occurs via direct connections between two neighboring cells, for example “gap junctions”. These junctions are channels, which allow a direct exchange of metabolites (Fig 1 C).

C. *Intracellular Communication*

In either case, the signal from the extracellular source is transferred through the cell membrane. Inside of the target cell, complex signaling cascades are involved in the transfer of the signal (signal transduction) which finally result in gene expression or an alteration in enzyme activity and therefore, define the cellular response.

Because of the great variety of signal transduction pathways, only one example for receptor-mediated signal transduction is presented here which might have a great relevance for computer networks: The MAPK signaling pathway is a major pathway in eukaryotic cells, which is activated by different types of receptors, e.g. receptor-tyrosine-kinases or G-protein-coupled receptors [15]. The principle of these pathways is described here in general on this example.

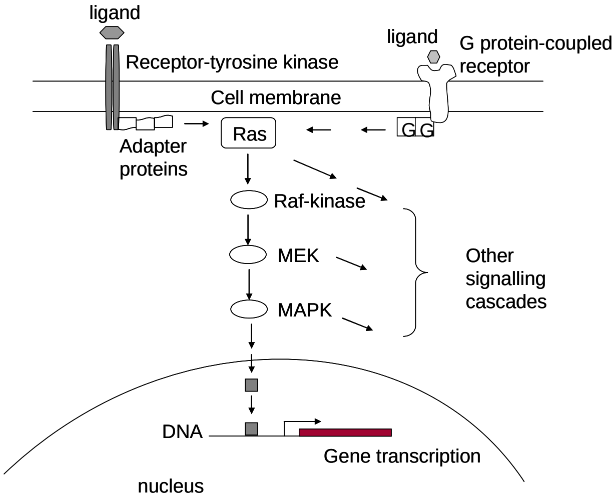

Fig 2. Intracellular signal transduction, shown on the example of MAPKinase pathway. Different ligands can activate different receptor types which result in MAP kinase activation.

Upon binding of the signaling factor (ligand), the receptor is activated. This activation is mostly attended by a phosphorylation or conformational change of the receptor, which make it possible for adapter proteins inside of the cell to bind to the receptor. Similarly, these adapter proteins are activated. The signal is carried on to a signaling molecule called Ras. As shown in Fig 2, the activation of different types of receptors comes together in the activation of Ras. The signal is carried on by protein kinases. Protein kinases phosphorylate other proteins. Phosphorylated protein kinases are able to conver the phosphorylation to the next kinase. Finally, a transcription factor is activated by this signaling cascade which move into the cell nucleus and bind to the DNA. The binding of a specific transcription factor to a specific binding site on the DNA result in gene transcription, which finally induce a specific cellular response.

This example shows only one straight-forward signaling pathway. For example, the same protein kinases Ras, MEK and MAPK are also involved in other signaling cascades. Thus, signaling cascades are often highly networked, but at least result in a very specific gene transcription and, therefore, result in a very specific cellular response [12].

III. NETWORK ARCHITECTURE

The main goal of this section is to describe the relevant elements of general network architectures. We start at a high abstraction level, the internetworking structure of the global Internet and dig deeper until we reach the internal operation of a single networking node. The focus lies on the characterization of the information and data paths in the network concerning packet forwarding, network monitoring, and firewalling as well as management functions including intrusion detection mechanisms.

A. *Internetworking Structure*

From a high-level point of view, an Internet consists of a multitude of individual networks. Each of theses networks, which are called domains, hides its internal structure from the outside world. Such a scenario is shown in Fig 3.

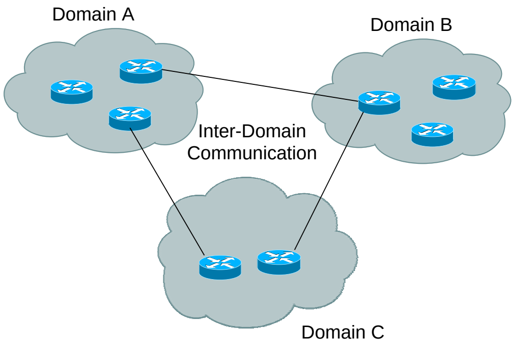

Fig 3. Internetworking Structure. Large internets consist of multiple network domains

Because, in reality, all these domains are managed from different service providers, the interaction between the domains is limited, mainly due to unequal configurations and mistrust.

Looking at security issues, this is a serious problem. Denial of service attacks can be only detected if the knowledge about the network traffic in multiple domains can be shared. Mechanisms are required for an inter-domain signaling and interaction. So far, there are no or at least few of such mechanisms developed or even deployed. The interaction between the domains is currently restricted to the exchange of routing information using inter-domain routing protocols.

B. *Intra-Domain Mechanisms*

If we look a little closer and examine the components of single domains (still with the focus on network security), there are, among other entities, routers, monitoring probes, firewall, and intrusion detection systems. These entities and their data and signaling paths are shown in Fig 4. It is important to understand that this is only a logical point of view. In reality, some or even all of these functions can be implemented in a single box.

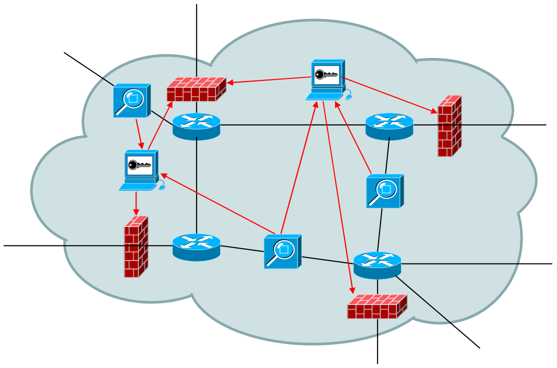

Fig 4. Communication in a single network. Typical entities are routers (packet forwarding), monitoring probes, firewall, and controlling IDS systems

The routers are responsible for the raw packet forwarding. Sometimes, statistical information is sent to management or IDS systems. Network monitors are employed to analyze the traffic in the network in order to detect suspicious data flows or unusual network behavior. Based on such information, examinations that are more precise can be initiated, e.g. based on attack signatures, and countermeasures against attacks are possible. The intrusion detection systems signal the signatures of violent hosts to the firewall systems. At this place, rules are installed which prevent any further attacks from the identified intruders.

Today, there are some intrusion detection systems available, a few of them as open source software. Unfortunately, they do not work in highly distributed configurations and their interaction is limited. Research needs to be done to improve these mechanisms, especially the interoperation between all kinds of networking components.

C. *Single Node*

In the last step, we zoom into a single network node and analyze the primary components in order to compare them later with corresponding parts in cellular environments. Fig 5 provides a schematic overview. Shown are only these parts, which we think are directly improvable by studying cellular mechanisms.

First, each network node has interfaces connecting it to other network nodes. Logically, each interface has two sub-interfaces. One for inter-node communication and one for the raw data transfer. Internally, each interface consists of input and output queues with fixed but configurable size and behavior, e.g. the selected queuing algorithm.

Secondly, limited resources such as CPU capacity and memory are available for sharing among numerous tasks. These tasks finally do the work in such a network node. There are tasks, which handle the routing tables and algorithms, others coordinate the packet forwarding and still others perform security checks and inter-node communication. Tasks "exist" per default, i.e. they are started when the system is booted. Other tasks can be created on demand allowing a high flexibility.

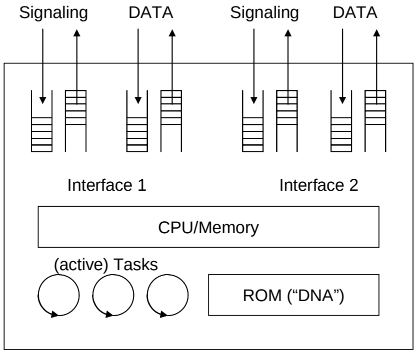

Fig 5. Schematic overview of the resources in a single network node those are required for processing and signaling.

In terms of network security, it would be desirable to have tasks searching for any known (and unknown?) kind of security threads while at the same time forwarding data packets at very high data rates. Unfortunately, this is not possible because the main resources such as CPU capacity and memory are very limited.

Therefore, the primary question is which task to run at which time. Also, not all tasks and algorithms can exist in memory waiting to get started if needed. Other solutions are required when and how to create such new tasks from saved high-level descriptions of their composition and behavior.

IV. SIMILARITY ANALYSIS AND RESEARCH ISSUES

Following to the description of cellular mechanisms and the networking architecture, we discuss potential research issues in this section by analyzing similarities between both worlds. We divide this section into three parts. First, we start with the comparison of the structure at different layers followed by the analysis of the external signaling pathways. Finally, we examine the internal behavior of individual components.

A. *Composition of the Components*

A first obvious result is the cognition that cellular structures are directly comparable with networking structures. The interaction of different cell types in tissues is also comparable to networking domains (as discussed in the next subsection). If we zoom into both systems, the same similarities appear as tissues are made of different cells, each focused on its very specific purpose. Network nodes, on the other hand, are also very specific for their particular tasks such as packet forwarding or network monitoring.

Currently, we only assume the possibility that some of the known processes of cellular interactions might be useful and can be copied to advance the specificity of answers in the network technology. Nevertheless, in computer science, great effort was made in simulating mechanisms based on such constructive building blocks. We intend to create object-oriented programming modules representing network nodes, their internal behavior, and their external communication mechanisms. An analyzing and studying computer network with such simulations is common in the network research area. The novel approach is to reuse the same programming for simulations on cellular structures and signaling pathways. We expect interesting results from this work.

B. External Signaling Pathways

The primary difference in the external signaling pathways between communication networks and cellular systems is the presence of data traffic in typical computer networks sharing the same infrastructure that is used for inter-node communication. Besides this fact, the concepts of inter-node communication and cellular signaling are similar. A typical problem in communication networks is the scalability of mechanisms, e.g. routing or configuration tasks.

We believe that there are high potentials in examining the mechanisms for signal transduction in cellular systems and applying them to communication systems.

The most impressing issues are given by the autonomic behavior of individual cells. During inflammation cells of the affected tissue send signals to recruit cells of the immune system from the blood. One of these signals can be IL-1β, a small soluble factor that affects e.g. signal transduction of endothelial cells. Endothelial cells are found on the luminal site of all blood vessels and represent the connection between the blood and the surrounding tissue. In these cells, binding of IL-1β to its receptor result in the gene transcription and translation of E-selectin protein. This protein is one of the first proteins that are involved in the interaction between the endothelium and cells of the immune system in order to recruit them to the center of the current inflammation. This example show how a specific signal is transferred from the signaling cell (in the inflamed tissue) to a target cell (the endothelial cells) in the environment and result in a local cellular answer which in turn can recruit help from far away.

Similar mechanisms are helpful in communication networks. Again, we focus on network security. Considering an intrusion detection system, it is working all the time on analyzing network traffic. If suspicious traffic is detected, the system might, as usual today, contact its management system or an attached firewall to enforce countermeasures. This methodology has many drawbacks, e.g. the relevance of the possible and undisturbed communication between the IDS and the management/firewall node. If the mechanisms known from the blood system could be applied, the detection of problems in the network could be distributed the same way to neighboring nodes which themselves can introduce countermeasures or which can redistribute the message until any assistant systems get knowledge about the problem and initiate countermeasures.

C. Internal Behavior of Individual Components

The same autonomic behavior applied to network nodes would help us making communication networks more efficient. There are a number of topics to discuss. Much pressure is on high scalable and effective intrusion detection with automatically involved countermeasures. We are working on such mechanisms allowing us to monitor, analyze, and process as much traffic as possible depending on the current knowledge about ongoing attacks. Processing power of individual nodes is first allocated for the supervision of ongoing attacks and the effectiveness of taken countermeasures. Then, the remaining capacities are directed to the analysis of unknown traffic and the detection of new attack traffic.

Also on this platform a lot of similarities between the biological processes of signal transduction and communication networks can be expected. The knowledge on the specificity of receptor-ligand interactions as well as the specificity of intracellular signaling pathways and the cellular answer that result from the particular pathway might give impressions how these problems can be solved in computer networks.

For example, gene activation as a result of a signaling cascade is often influenced by the presence of intracellular inhibitor and effector molecules which are, in turn, regulated by other control mechanisms in the cell [2, 8]. These molecules appropriate the specific gene translation and, therefore, influence the cellular answer. This means that a signal transduction cascade is often not a straight-line cascade, but can be networked with other signaling cascades and all these processes succeed highly coordinated and regulated.

V. RELATED WORK

The first approaches to identify mechanisms in nature helping to solve technological problems, especially in computer science date back to the mid 1990s. The human immune systems was used for investigations on computer viruses and their detection [4]. This is still the best-known example of so-called bio-inspired computing [10].

The group of Prof. Suda is investigating an architecture, which they named the bio-networking architecture [16].

The basis of their project is a middleware named the bio-networking platform [14], which aims to incorporate working mechanisms known from swarms of bees and ant colonies in order to achieve a high level of autonomy and reliability.

We believe that there is still much work to be done in the research field of bio-inspired networking. That this is a hot topic is also demonstrated, for example, by the current research-funding program of the NSF [1].

VI. CONCLUSIONS AND FURTHER WORK

In conclusion it can be said that we were able to show many similarities in the signal transduction of biological systems and computer networks.

The attempt to adopt mechanisms from the basis of the organism, the single cell, might be useful for further studies because the cell has to maintain its own assembly and thus react specifically on changes of their direct environment without the necessity to know about all interactions in the organism. The effectiveness of cellular signaling to communicate can be copied when single processes of information transfer in cellular systems are interpreted and analyzed for their utility on computer networks.

In conclusion, actual problems of computer networks have to be discussed on the model that each part in the network corresponds to an adequate structure in the organism. Looking at the defined adequate structure in the organism, the mechanisms of interaction with other parts of the system can be analyzed in detail and assigned for computer networks.

We are going on in our research activities creating a model which represents the signaling pathways in communication networks and allows us to incorporate the studied mechanisms from biology. From such a model, simulative analyses can be done to show the advantages of our new algorithms.

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