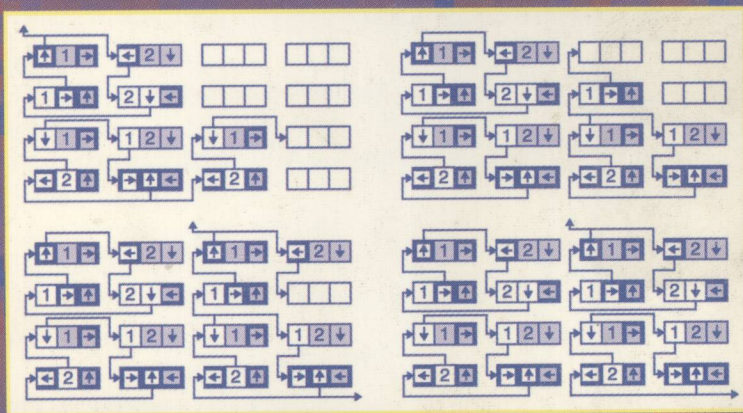


Auke Jan Ijspeert
Masayuki Murata
Naoki Wakamiya (Eds.)

Biologically Inspired Approaches to Advanced Information Technology

First International Workshop, BioADIT 2004
Lausanne, Switzerland, January 2004
Revised Selected Papers



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Foreword

The evolution of the Internet has led us to the new era of the information infrastructure. As the information systems operating on the Internet are getting larger and more complicated, it is clear that the traditional approaches based on centralized mechanisms are no longer meaningful. One typical example can be found in the recent growing interest in a P2P (peer-to-peer) computing paradigm. It is quite different from the Web-based client-server systems, which adopt essentially centralized management mechanisms. The P2P computing environment has the potential to overcome bottlenecks in Web computing paradigm, but it introduces another difficulty, a scalability problem in terms of information found, if we use a brute-force flooding mechanism.

As such, conventional information systems have been designed in a centralized fashion. As the Internet is deployed on a world scale, however, the information systems have been growing, and it becomes more and more difficult to ensure fault-free operation. This has long been a fundamental research topic in the field. A complex information system is becoming more than we can manage. For these reasons, there has recently been a significant increase in interest in biologically inspired approaches to designing future information systems that can be managed efficiently and correctly.

Essential for tackling the scalability problem is the introduction of modularity into the system. This requires defining the global goal, designing the activity of the local small entities, defining the interactions among the entities, and achieving the emergence of robust global behavior. The global goal is not the sum of the local goals, but more than that. Inspiration from biology, such as the concept of stigmergy (i.e., indirect communication via modifications of the environment), is particularly useful in the design of information systems that can adapt to unexpected environmental changes without preprogrammed system behavior. The development of biologically inspired information systems is steadily advancing, but it does not yet solve the above problems.

This book addresses how biological inspiration can help solving problems like this one, as well as many others in various domains in information technology. It presents the current state of the art of the field, and covers various important aspects of biologically inspired information systems.

Chapter 1 contains several papers related to the advancement of our understanding of biological systems for evolving information systems. Signorini et al. propose a case study where a familiar but very complex and intrinsically woven biocomputing system—the blood clotting cascade—is specified using a method from software design known as object-oriented design (OOD). Then, Shimizu et al. present an analysis of responses of complex bionetworks to changes in environmental conditions. Kashiwagi et al. discuss experimental molecular evolution showing flexibility of fitness, leading to coexistence and diversification in the biological system. Next, Mayer et al. introduce a method for adapting the recurrent layer dynamics of an echo-state network (ESN) without attempting to train the weights directly. They show that self-prediction may improve the performance of an ESN when performing signal mappings in the presence of additive noise. Also, Wang et al. describe a nonlinear

model for the rate of gene transcription, by employing a genetic algorithm to evolve the structure of a Bayesian network. Their methodology features a reconstruction resolution that is limited by data noise. Lastly, Johansson et al. first review the structure of the cerebral cortex to find out its number of neurons and synapses and its modular structure. The organization of these neurons is then studied and mapped onto the framework of an artificial neural network (ANN), showing that it is possible to simulate the mouse cortex today on a cluster computer, but not in real time.

In Chap. 2, Zhou et al. present an emotion-based hierarchical reinforcement learning (HRL) algorithm for environments with multiple sources of reward. The architecture of the algorithm is inspired by the neurobiology of the brain and particularly by those areas responsible for emotions, decision making and behavior execution, namely the amygdala, the orbito-frontal cortex and the basal ganglia, respectively. Then, Bouchard et al. present two ways in which dynamic self-assembly can be used to perform computation, via stochastic protein networks and self-assembling software. They describe their protein-emulating agent-based simulation infrastructure, which is used for both types of computations, and the few agent properties sufficient for dynamic self-assembly. Next, Yoshimoto et al. design a system to support the dynamic formation of human relationships between strangers in networked virtual space. The system attempts to locate the most suitable virtual space for the content of their conversation. Graves et al. apply long short-term memory (LSTM) recurrent neural networks (RNNs) to more realistic problems, such as the recognition of spoken digits. Without any modification of the underlying algorithm, they achieve results comparable to state-of-the-art hidden Markov model (HMM)-based recognizers on both the TIDIGITS and TI46 speech corpora. Then, Sharlin et al. discuss tangible user interfaces (TUIs) and their potential impact on cognitive assessment and cognitive training, and present Cognitive Cubes as an applied test bed. Lee et al. discuss the principle of the artificial immune system and propose a virus detection system that can detect unknown viruses. Yu et al. discover that a model based on lateral disinhibition in biological retinas allows us to explain subtle brightness-contrast illusions. Finally, Choe et al. investigate how artificial or natural agents can autonomously gain understanding of their own internal (sensory) state, and, in the context of a simple biologically motivated sensorimotor agent, they propose a new learning criterion based on the maintenance of sensory invariance.

In Chap. 3, Rubin et al. describe the response properties of a compact low-power analog circuit that implements a model of a leaky integrate-and-fire neuron, with spike-frequency adaptation, refractory period and voltage-threshold-modulation properties. Next, based on the nine construction rules of the so-called Tom Thumb algorithm, Mange et al. show that cellular division leads to a novel self-replicating loop endowed with universal construction and computation. Another self-property is presented by Petraglio et al., who describe an approach to the implementation on an electronic substrate of a process analogous to the cellular division of biological organisms. Finally, Upegui et al. present a functional model of a spiking neuron, where some features of biological spiking neurons are abstracted, while preserving the functionality of the network, in order to define an architecture with low implementation cost in field programmable gate arrays (FPGAs).

In Chap. 4, first, Kondo et al. introduce an adaptive state recruitment strategy that enables a learning robot to rearrange its state space conveniently according to the task

complexity and the progress of the learning. Next, Joshi et al. use simple linear readouts from generic neural microcircuit models for learning to generate and control the basic movements of robots. Then, Labella et al. show that a simple adaptation mechanism, inspired by ants' behavior and based only on information locally available to each robot, is effective in increasing the group efficiency. The same adaptation mechanism is also responsible for self-organized task allocation in the group. Finally, Vardy et al. present a detailed account of the processing that occurs within a biologically inspired model for visual homing. They also describe a cellular vision matrix that implements CGSM and illustrate how this matrix obeys cellular vision.

Chapter 5 contains the papers related to distributed/parallel processing systems. Tsuchiya et al. develop an adaptive mechanism with the aim of enhancing the resiliency of epidemic algorithms to perturbations, such as node failures. It dynamically adjusts the fan-out, the number of receiver partners each node selects, to changes in the environment. Gruau et al. present an implementation of the blob object using the "programmable matter" platform of cellular automaton simulation. Then they describe an implementation of blob division, the machine implementation of computer node duplication. Buchli et al. propose a distributed central pattern generator model for robotics applications based on phase-sensitivity analysis. Finally, Izumi et al. consider an ant-based approach to the agent traversal problem, and propose a novel lightweight implementation of the ant system where the unnecessary traffic of the network is reduced.

Chapter 6 treats networking-related issues. Dicke et al. look at the ability of an ant colony optimization algorithm to evolve new architectures for storage area networks, in contrast to the traditional algorithmic techniques for automatically determining fabric requirements, network topologies, and flow routes. Then, Sasabe et al. propose a new algorithm that considers the balance between supply and demand for media streams, inspired by biological systems, in P2P (peer-to-peer) networks. Le Boudec et al. investigate the use of an artificial immune system (AIS) to detect node misbehavior in a mobile ad hoc network using DSR (dynamic source routing), which is inspired by the natural immune system of vertebrates. Another network control method inspired by biology is presented by Wakamiya et al. where they adopt a pulse-coupled oscillator model based on biological mutual synchronization such as that used by flashing fireflies for realizing scalable and robust data fusion in sensor networks.

Chapter 7 is devoted to the application of bio-inspired approaches to image processing. Seiffert et al. develop a new image compression method based on artificial neural networks (ANN), and apply it to biomedical high-throughput screening (HTS). Next, Avello et al. develop naive algorithms for key-pharse extraction and text summarization from a single document, which is inspired by the protein biosynthesis process. The last paper of this section is by Lee et al., who propose a biologically motivated trainable selective attention model based on an adaptive resonance theory network that can inhibit an unwanted salient area and only focus on an interesting area in a static natural scene.

Chapter 8 contains several important topics. Oltean proposes an evolutionary approach for solving a problem for which random search is better than another standard evolutionary algorithm. Next, Kurihara analyzes a simple adaptive model of competition called the Minority Game, which is used in analyzing competitive

phenomena in markets, and suggests that the core elements responsible for forming self-organization are: (i) the rules place a good constraint on each agent's behavior, and (ii) there is a rule that leads to indirect coordination. Finally, Sorensen explores the genealogy of the contemporary biological influence on science, design and culture in general to determine the merits of the tendency and lessons to learn, and argues that biomimetics rests on bona fide scientific and technical grounds in the pursuit of dynamic IT, but also on other, more external factors.

June 2004

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Masayuki Murata
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Preface

This state-of-the-art survey reports advancements of information technologies inspired by biological systems. It was comprehensively discussed for the first time during the 1st International Workshop on Biologically Inspired Approaches to Advanced Information Technology (Bio-ADIT 2004) held at EPFL, Switzerland, on January 29–30, 2004. This book continues the discussion of bio-inspired approaches for future information technologies, as perceived by the authors, including the achievements that were originated by the authors. To ensure the content quality, each paper was revised after the workshop took place, according to the helpful comments made by the reviewers, and fruitful discussions during the workshop.

Probably, mimicking biological systems should not be an aim per se for engineers, and one can see that many useful engineering developments have little to do with biology (the use of metals, wheels, or rockets come to mind). However, nature offers us a large array of fascinating phenomena such as replication, self-organization, self-repair, and adaptive behavior that are clearly of tremendous importance to current and future IT technologies. Actually, the contributions published in this book underline the international importance of this field of research; 37 contributions are contained from Australia, Austria, Belgium, Canada, France, Germany, Japan, Korea, Romania, Spain, Sweden, Switzerland, Taiwan, UK, and USA. It strongly indicates the importance of the field and the world-wide movement into this field.

The book consists of papers ranging from basic biological research to the application of biologically inspired algorithms and concepts to various aspects of information systems. The first chapter aims at providing a roadmap for the whole book and serves as a summary of the book's content. The book then moves to the analysis of biological systems for IT evolution. The following sections cover the application of biological inspiration to software, hardware, robotics, distributed/parallel processing, network, and image processing systems.

We wish to record our appreciation of the efforts of all the authors who helped to make this book happen, while we regret that it was not possible to include all the individual contributions. We are indebted to Daniel Mange and Shojiro Nishio, General Co-chairs, for managing the workshop. We would also like to again acknowledge the financial support from three sponsors for the original workshop: the Osaka University Forum, the Swiss Federal Institute of Technology, Lausanne, and the 21st Century Center of Excellence Program of the Ministry of Education, Culture, Sports, Science and Technology (MEXT) of Japan under the program title “Opening up New Information Technologies for Building a Networked Symbiosis Environment.”

June 2004

Auke Jan Ijspeert
Masayuki Murata
Naoki Wakamiya

Table of Contents

1. Biosystems for IT Evolution

Object-Oriented Specification of Complex Bio-computing Processes: A Case Study of a Network of Proteolytic Enzymes	1
<i>Jacqueline Signorini, Patrick Greussay</i>	
Analysis of Responses of Complex Bionetworks to Changes in Environmental Conditions	13
<i>Hiroshi Shimizu, Takashi Hirasawa, Keisuke Nagahisa, Suteaki Shioya</i>	
Experimental Molecular Evolution Showing Flexibility of Fitness Leading to Coexistence and Diversification in Biological System	28
<i>Akiko Kashiwagi, Wataru Noumachi, Masato Katsuno, Mohammad T. Alam, Itaru Urabe, Tetsuya Yomo</i>	
Echo State Networks and Self-Prediction	40
<i>Norbert M. Mayer, Matthew Browne</i>	
Learning Bayesian Networks by Lamarckian Genetic Algorithm and Its Application to Yeast Cell-Cycle Gene Network Reconstruction from Time-Series Microarray Data	49
<i>Sun-Chong Wang, Sai-Ping Li</i>	
Towards Cortex Sized Attractor ANN	63
<i>Christopher Johansson, Anders Lansner</i>	

2. Bio-inspired Software Systems

Biologically Inspired Reinforcement Learning: Reward-Based Decomposition for Multi-goal Environments	80
<i>Weidong Zhou, Richard Coggins</i>	
Dynamic Self-Assembly and Computation: From Biological to Information Systems	95
<i>Ann M. Bouchard, Gordon C. Osbourn</i>	
Implementation and Evaluation of a System to Support Human Relationship Formation in Networked Virtual Space	111
<i>Yoshiharu Yoshimoto, Yuichi Itoh, Yoshifumi Kitamura, Fumio Kishino</i>	
Biologically Plausible Speech Recognition with LSTM Neural Nets	127
<i>Alex Graves, Douglas Eck, Nicole Beringer, Juergen Schmidhuber</i>	

Spatial Tangible User Interfaces for Cognitive Assessment and Training	137
<i>Ehud Sharlin, Yuichi Itoh, Benjamin Watson, Yoshifumi Kitamura, Steve Sutphen, Lili Liu, Fumio Kishino</i>	
Biologically Inspired Computer Virus Detection System	153
<i>Hyungjoon Lee, Wonil Kim, Manpyo Hong</i>	
Explaining Low-Level Brightness-Contrast Illusions Using Disinhibition	166
<i>Yingwei Yu, Takashi Yamauchi, Yoonsuck Choe</i>	
Autonomous Acquisition of the Meaning of Sensory States Through Sensory-Invariance Driven Action	176
<i>Yoonsuck Choe, S. Kumar Bhamidipati</i>	
3. Hardware Systems	
Characterizing the Firing Properties of an Adaptive Analog VLSI Neuron	189
<i>Daniel Ben Dayan Rubin, Elisabetta Chicca, Giacomo Indiveri</i>	
Embryonic Machines That Divide and Differentiate	201
<i>Daniel Mange, André Stauffer, Enrico Petraglio, Gianluca Tempesti</i>	
Artificial Cellular Division by Self-Inspection	217
<i>Enrico Petraglio, Daniel Mange, André Stauffer, Gianluca Tempesti</i>	
A Hardware Implementation of a Network of Functional Spiking Neurons with Hebbian Learning	233
<i>Andrés Upegui, Carlos Andrés Peña-Reyes, Eduardo Sánchez</i>	
4. Robotics	
A Study on Designing Robot Controllers by Using Reinforcement Learning with Evolutionary State Recruitment Strategy	244
<i>Toshiyuki Kondo, Koji Ito</i>	
Movement Generation and Control with Generic Neural Microcircuits ...	258
<i>Prashant Joshi, Wolfgang Maass</i>	
Efficiency and Task Allocation in Prey Retrieval	274
<i>Thomas H. Labella, Marco Dorigo, Jean-Louis Deneubourg</i>	
Anatomy and Physiology of an Artificial Vision Matrix	290
<i>Andrew Vardy, Franz Oppacher</i>	

5. Bio-inspired Distributed/Parallel Processing

An Adaptive Mechanism for Epidemic Communication	306
<i>Tatsuhiko Tsuchiya, Tohru Kikuno</i>	
The Blob Division (A “Hardware-Free”, Time Efficient, Self-Reproduction on 2D Cellular Automaton)	317
<i>Frédéric Gruau, Gabriel Moszkowski</i>	
Distributed Central Pattern Generator Model for Robotics Application Based on Phase Sensitivity Analysis	333
<i>Jonas Buchli, Auke Jan Ijspeert</i>	
Ant-Based Approach to Mobile Agent Traversal.....	350
<i>Taisuke Izumi, Toshimitsu Masuzawa</i>	

6. Bio-inspired Networking

An Ant Inspired Technique for Storage Area Network Design	364
<i>Elizabeth Dicke, Andrew Byde, Dave Cliff, Paul Layzell</i>	
Media Streaming on P2P Networks with Bio-inspired Cache Replacement Algorithm	380
<i>Masahiro Sasabe, Naoki Wakamiya, Masayuki Murata, Hideo Miyahara</i>	
An Artificial Immune System Approach to Misbehavior Detection in Mobile Ad Hoc Networks	396
<i>Jean-Yves Le Boudec, Slaviša Sarafijanović</i>	
Scalable and Robust Scheme for Data Gathering in Sensor Networks	412
<i>Naoki Wakamiya, Masayuki Murata</i>	

7. Image Processing

Biologically Inspired Image Compression in Biomedical High-Throughput Screening	428
<i>Udo Seiffert</i>	
Naïve Algorithms for Keyphrase Extraction and Text Summarization from a Single Document Inspired by the Protein Biosynthesis Process	440
<i>Daniel Gayo-Avello, Darío Álvarez-Gutiérrez, José Gayo-Avello</i>	
Biologically Motivated Trainable Selective Attention Model Using Adaptive Resonance Theory Network	456
<i>Sang-Bok Choi, Sang-Woo Ban, Minho Lee, Jang-Kyoo Shin, Dae-Wha Seo, Hyun-Seung Yang</i>	

8. Other Topics

Searching for a Practical Evidence of the No Free Lunch Theorems 472
 Mihai Oltean

How Collective Intelligence Emerge in Complex Environment? 484
 Satoshi Kurihara, Kensuke Fukuda, Toshio Hirotsu, Osamu Akashi,
 Shinya Sato, Toshiharu Sugawara

The Genealogy of Biomimetics:
Half a Century's Quest for Dynamic IT 496
 Mikkel Holm Sørensen

Author Index 513

Object-Oriented Specification of Complex Bio-computing Processes: A Case Study of a Network of Proteolytic Enzymes

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Abstract. We propose a case study where a familiar but very complex and intrinsically woven bio-computing system – the blood clotting cascade – is specified using methods from software design known as object-oriented design (OOD). The specifications involve definition and inheritance of classes and methods and use design techniques from the most widely used OOD-language: the Unified Modeling Language (UML), as well as its Real-Time-UML extension. First, we emphasize the needs for a unified methodology to specify complex enough biological and biochemical processes. Then, using the blood clotting cascade as a example, we define the class diagrams which exhibit the static structure of procoagulant factors of proenzyme-enzyme conversions, and finally we give a dynamic model involving events, collaboration, synchronization and sequencing. We thus show that OOD can be used in fields very much beyond software design, gives the benefit of unified and sharable descriptions and, as a side effect, automatic generation of code templates for simulation software.

1 Introduction

OOD for Non-software Complex Systems:

Object-oriented programming (OOP) is now the major paradigm for software design. To specify and design very complex programs, OOP requires new methods recently built upon description languages. Prior to programming, these languages yield a complete specification for the states and processes which constitute the planned task. One other reason of the success of these description languages (UML, Real-Time UML) [1], [7], [6] has to do with the power of sharing a prototype description between independent teams working in loose cooperation.

It is now a standard issue that OOP gave birth to a large set of object oriented design (OOD) methods. This structured set of methods has become a recognized craft as well as a technical methodology. The methods give specifications kept separate from the target programs which will be subsequently hand-coded or computer-generated from the description yielded by OOD.

The time has come to consider that OOD has all the power needed to specify complex domains beyond program design. They could not rely until now on: 1/ a unified and stable description methodology; 2/ a way of using concepts such as encapsulation, classes sharing and embedding, static properties and dynamic process inheritance; 3/ an opportunity to share and recombine descriptions built by separate research teams; 4/ the ability of automatically generating the code templates for simulation software associated with the specified situations.

We thus propose, using a typical example in bio-computing – the set of processes of the blood clotting cascade – a case study which hopefully demonstrate the need for a unified description methodology. For that purpose, our tool will be the most widely used and standardized language today for OOD: Unified Modeling Language (UML)¹.

At this stage of development of biochemical models, we believe that it is necessary to use standard and stable object-oriented specification tools in contrast with non-standard tools such as Statecharts or LCS [13]: first, it will thus be possible to combine several specifications coming from unrelated research teams; second, we strongly believe that we need a large number of case studies in biochemical modeling before even thinking of trying to use the language of mathematics or formal semantics; (even after more than thirty years of software design research, formal methods are still very far from accepted as standard), last it is probably too soon to try an integrated multilevel description of a complex organism, even with reactive systems. Biochemical processes are *not* formal objects, and we are at the very beginning of trying to build approximate computational models. What we need is a deeper understanding of what biological components need to be adequately described; proof methods, at this stage, would not be even mildly interesting. However, it is very possible that unexpected or unknown bio-processes could be exposed, as a side-effect of modeling. The last word, obviously, will come from biological validation.

What Is the Blood Clotting Cascade:

The process of blood clotting and the subsequent dissolution of the clot following repair of the injured tissue is termed hemostasis. It is based on an ordered series of proenzyme-enzyme conversions, also referred as the proteolytic cascade [5]. Proteolytic enzymes are proteins that can cut other proteins in pieces. As they can be extremely dangerous, they usually are formed and transported in the plasma as proenzymes (zymogens), an inactive form which on activation undergoes proteolytic cleavage to release the active factor from the precursor molecule. The coagulation pathway functions as a series of positive and negative feedback loops which controls the activation process. It ensures the formation of the cross-linked fibrin clot that plug injured vessels and prevent blood loss through the action of thrombin. All the plasma proteins involved in coagulation, mainly produced in the liver, are clotting factors designated by Roman numeral descriptors. They reflect the order of their discovery rather than their sequence in the clotting cascade. Factors XII, XI, X, IX, VII, prothrombin are proenzymes which are converted to active enzymes during coagulation.

¹ We use Rational Rose 2000 UML, Rational Software Corp.