

Artificial Immune Systems

Edited by

Emma Hart¹, Thomas Jansen², and Jon Timmis³

1 Napier University – Edinburgh, GB, e.hart@napier.ac.uk

2 University College Cork, IE, t.jansen@cs.ucc.ie

3 University of York, GB, jtimmis@cs.york.ac.uk

Abstract

This report documents the program and the outcomes of the Dagstuhl Seminar 11172 “Artificial Immune Systems”. The purpose of the seminar was to bring together researchers from the areas of immune-inspired computing, theoretical computer science, randomised search heuristics, engineering, swarm intelligence and computational immunology in a highly interdisciplinary seminar to discuss two main issues: first, how to best develop a more rigorous theoretical framework for algorithms inspired by the immune system and second, to discuss suitable application areas for immune-inspired systems and how best to exploit the properties of those algorithms.

Seminar 26.–29. April, 2011 – www.dagstuhl.de/11172

1998 ACM Subject Classification I.2.8 Problem Solving, Control Methods, and Search; Heuristic methods.

Keywords and phrases Artificial Immune Systems, Randomised Search Heuristics


Digital Object Identifier 10.4230/DagRep.1.4.100

1 Executive Summary

Emma Hart

Thomas Jansen

Jon Timmis

License  Creative Commons BY-NC-ND 3.0 Unported license
© Emma Hart, Thomas Jansen, Jon Timmis

Artificial immune systems (AISs) are inspired by biological immune systems and mimic these by means of computer simulations. They are seen with interest from immunologists as well as engineers. Immunologists hope to gain a deeper understanding of the mechanisms at work in biological immune systems. Engineers hope that these nature-inspired systems prove useful in very difficult computational tasks, ranging from applications in intrusion-detection systems to general optimization. Moreover, computer scientists identified artificial immune systems as another example of a nature-inspired randomized search heuristic (like evolutionary algorithms, ant colony optimization, particle swarm optimization, simulated annealing, and others) and aim at understanding their potential and limitations. While the relatively new field has its successful applications and much potential its theoretical foundation is still in its infancy. Currently there are several not well connected strands within AIS theory, not even a general agreement on what the central open problems are, and only a weak connection between AIS theory and AIS applications. The main goals of the proposed seminar include bringing together computer scientists and engineers to strengthen the connections within AIS theory, connections to other researchers working on the theory of randomized search heuristics, and to improve connectivity between AIS theory and applications.



Except where otherwise noted, content of this report is licensed under a Creative Commons BY-NC-ND 3.0 Unported license
Artificial Immune Systems, *Dagstuhl Reports*, Vol. 1, Issue 4, pp. 100–111
Editors: Emma Hart, Thomas Jansen, and Jon Timmis



DAGSTUHL REPORTS
Dagstuhl Reports
Schloss Dagstuhl – Leibniz-Zentrum für Informatik, Dagstuhl Publishing, Germany

Biological immune systems show great resilience in harsh environments and demonstrate the ability to cope with large amounts of sensory data as well as the unpredictability of the natural world. Indeed, a great deal of attention is now being paid to these aspects of the immune system by the wider computing research community.

Given the practical success of AIS, there is a serious lack of theoretical work in the area. Many AIS algorithms are based purely on clonal selection mechanisms, without any interaction between the different members of the cell populations. The dynamics of cell populations in the immune system have been modeled extensively using nonlinear dynamical systems. At present, however, there is no centrally agreed approach on how to tackle important theoretical issues in AIS. All too often theory is undertaken without the due attention to the practical implications. For theory to have a serious impact, collaboration between theoreticians and engineers is needed to identify key engineering issues, relevant theoretical issues and crucially how the theory can help support the engineering process. While starting point of the seminar and its driving force are deficits in the theoretical foundation of AIS its main goals are clearly beyond theory. At the heart of the seminar's motivation is the conviction that there is nothing more practical than a good theory.

The seminar took place from April 26th to April 29th 2011. It started with a series of talks aimed at providing a suitable level of introduction to the main areas of discussion to provide a levelling ground for all participants. The format of the seminar was then a series of short presentations by researchers on topics that ranged from swarm robotics to immunology and theoretical frameworks for algorithm analysis. These were then followed by a series of *breakout* group sessions which focussed discussion on the issues raised by the speakers with results from those discussions being reported back to the main group at regular intervals. Towards the end of the week, a convergence into four key topics emerges: (1) The principled development of bio-inspired algorithms and how the translation from computational models into usable algorithms is managed, (2) the relationship between evolution and immunity and how it might be possible to evolve an artificial immune system in complex engineering problems, specifically swarm robotic systems, (3) the development of a definitive clonal selection algorithm with appropriate theoretical analysis and (4) the development of novel immune algorithms and the use of models from computational immunology for both the understanding of immunological processes and the development of new algorithms. These four topics are to be taken forward as journal papers by participants from the seminar.

As a result of the seminar there will be a special issue published in *Natural Computing* a leading journal in the area that will not only publish papers outlined above, but provide a roadmap for the future direction of AIS and serve as, it is hoped, an authoritative guide to the area of artificial immune systems.

2 Table of Contents

Executive Summary

Emma Hart, Thomas Jansen, Jon Timmis 100

Overview of Talks

Training a network of mobile neurons

Bruno Apoloni 103

Immune inspired approaches to ab initio modelling

George M. Coghill 103

Theory of Randomized Search Heuristics

Benjamin Doerr 104

Making Affective Effective: Emotion Classification and AIS

Julie Greensmith 104

Applications of Immune Inspired Computing

Emma Hart 105

A Crash Course in Immunology and AIS

Emma Hart 105

Swarm-based Modeling and Visualization of the Immune System ... and more

Christian Jacob 106

AIS Theory

Thomas Jansen 106

Runtime Analysis of Clonal Selection Algorithms

Per Kristian Lehre 107

Real and artificial immune systems: oil and water or milk and cookies?

Chris McEwan 107

Less Bio, More Inspired

Robert Oates 108

The use of AIS techniques to protect an Artificial Hormone System

Mathias Pacher 108

Negative Selection Algorithms: Past, Present, Perspectives

Johannes Textor 108

On Fault Tolerance and Scalability of Swarm Robotic Systems

Alan FT Winfield 109

Run Time Analysis of Artificial Immune Systems

Christine Zarges 109

Working Groups

A principled approach to deriving immune inspired engineering principles

Marc Read, Chris McEwan, Emma Hart, Ed Clark, Julie Greensmith,

Uwe Aickelin 110

Participants 111

3 Overview of Talks

3.1 Training a network of mobile neurons

Bruno Apoloni (Università di Milano, IT)

License © ⓘ ⊖ Creative Commons BY-NC-ND 3.0 Unported license
© Bruno Apoloni

Joint work of Apoloni, Bruno; Simone, Bassis; Lorenzo, Valerio

Main reference Apoloni, Bruno; Simone, Bassis; Lorenzo, Valerio, “Training a network of mobile neurons,” Proc. IJCNN 2011

We introduce a new paradigm of neural networks where neurons autonomously search for the best reciprocal position in a topological space so as to exchange information more profitably. The idea that elementary processors move within a network to get a proper position is borne out by biological neurons in brain morphogenesis. The basic rule we state for this dynamics is that a neuron is attracted by the mates which are most informative and repelled by ones which are most similar to it. By embedding this rule into an Newtonian dynamics, we obtain a network which autonomously organizes its layout.

Thanks to this further adaptation, the network proves to be robustly trainable through an extended version of the backpropagation algorithm even in the case of deep architectures.

We test this network on two classic benchmarks and thereby get many insights on how the network behaves, and when and why it succeeds.

3.2 Immune inspired approaches to ab initio modelling

George M. Coghill (University of Aberdeen, GB)

License © ⓘ ⊖ Creative Commons BY-NC-ND 3.0 Unported license
© George M. Coghill

Joint work of Coghill, George M.; Pang, Wei

Main reference Pang, W. & Coghill, GM. (2011), “An immune-inspired approach to qualitative system identification of biological pathways,” Natural Computing, vol 10, no. 1, pp. 189–207.

URL <http://dx.doi.org/10.1007/s11047-010-9212-2>

Model-based systems and qualitative reasoning (MBS&QR) provides a means of reasoning about the structure and behaviour of dynamic systems in situations where information about the system of interest is sparse or incomplete. In domains such as systems biology the data available are mixed: some are sparse, some are detailed and some are qualitative. In such circumstances MBS&QR may enable one to simulate, construct or modify imprecise models of metabolic systems.


We have developed a number of MBS&QR tools to facilitate this: a fuzzy qualitative reasoning system to provide abstract simulations, diagnostic machinery and Artificial Immune System based model learners. For this latter the results of the learning are very promising for ab initio system identification.

A version utilizing CLONALG generates results comparable to deterministic model learning for small models, but which comes into its own for larger systems.

Comparative studies with an improved version of optAINet reveal improved identification speeds for larger systems

3.3 Theory of Randomized Search Heuristics

Benjamin Doerr (MPI für Informatik – Saarbrücken, DE)

License  Creative Commons BY-NC-ND 3.0 Unported license
© Benjamin Doerr

In this survey talk, I will give a high-level summary of what happened in the area of theoretical analyses of randomized search heuristics. After the talk, I'm hoping for interesting discussions on whether this can serve as a roadmap for the developing theory of artificial immune systems or what should be done differently.

By theory, I shall adopt the strict view of proving precise statements by mathematical means. I shall then highlight three research directions that were followed in the theory of randomized search heuristics.

Artificial example problems: These did a good job in refuting common misbeliefs, for example, that unimodal functions are always easy to optimize via hill-climbers.


Run-time analysis. Inspired by classical randomized algorithms theory, we may also try to bound the run-time of a randomized search heuristic. Usually, we do not regard the actual run-time, but count the number of fitness evaluations.

This reflects the common assumption that this is the most costly part in many randomized search heuristic applications.

Black-box complexity: Since classic algorithms theory greatly profited from a powerful complexity theory, a similar methodology might be helpful for randomized search heuristics as well. If again we take the number of search point evaluations as complexity measure, this leads to the notion of (unrestricted) black-box complexity. It is currently discussed to what extent this notion yields useful insight on the problem difficulty for randomized search heuristics. Most likely, the class of all black-box optimization algorithms should be restricted in a way that excludes overly powerful, but unrealistic heuristics.

3.4 Making Affective Effective: Emotion Classification and AIS

Julie Greensmith (University of Nottingham, GB)

License  Creative Commons BY-NC-ND 3.0 Unported license
© Julie Greensmith

URL <http://www.ima.ac.uk/greensmith>

Affective computing is an emerging multidisciplinary field within computer science with the aim of incorporating of emotions into computational systems.

The nature of this incorporation can occur via the use of emotion data from users of such systems. Equally it can represent the display of emotions by computational systems to enhance the experience of the user through the generation of an emotive dialogue.


There are a number of challenges in working with affective systems centered on using emotions. Emotions are dynamic, they change over time depending on the internal and external milieu of the individual. Emotions are personal, with individuals portraying different emotions in a number of different physiological and social ways. Emotions are subjective, as it is difficult to find a universal taxonomy or strict definition for any individual emotion. Specific identifiable patterns or physiological signatures of emotion simply do not exist between individuals.

This makes it an interesting problem in terms of the application of computational intelligence techniques. However, little research exists in the area of the application of

intelligent classification techniques to the ascertainment of emotions from physiological data. In this talk I presented the wearable biosensor technology used to collect physiological data and propose an approach for the modelling and classification of this data using ensemble based artificial immune system classification methods. In addition I proposed and gained feedback on a framework combining AIS algorithms to process multiple levels and types of emotional response.

3.5 Applications of Immune Inspired Computing

Emma Hart (Edinburgh Napier University, GB)

License  Creative Commons BY-NC-ND 3.0 Unported license
© Emma Hart

Joint work of Hart, Emma; Timmis, Jon

Main reference Hart,E and Timmis,J., “Applications of AIS: The Past, the Present and the Future,” *Applied Soft Computing* 8(1), 2008, pp. 191–201

URL <http://dx.doi.org/10.1016/j.asoc.2006.12.004>

The field of Artificial Immune Systems (AIS) has seen a number of successful algorithms developed over the past 20 years. AIS algorithms can be considered as either evolutionary or swarm like and they are inspired by a variety of immunological processes. Recently there has been a drive to provide theoretical underpinnings of some of these algorithms. Despite these successes, in this talk we highlight issues that might potentially hinder further development of the field. We explicitly separate immune properties and immune functionality and use this classification to highlight potential of engineered systems that can exploit either immune properties or immune function. We discuss ad-hoc sensor networks and swarm robotic systems that naturally map to suitable immune functions and properties. We highlight issues of translating immune models into engineered immune-inspired solutions. We argue that functionality driven design will lead to systems that don't necessarily replicate biological mechanisms but replicate biological functionality.

3.6 A Crash Course in Immunology and AIS

Emma Hart (Edinburgh Napier University, GB)


License  Creative Commons BY-NC-ND 3.0 Unported license
© Emma Hart

Joint work of Hart, Emma; Jon Timmis

This talk provides a high level introduction to immunology and to the algorithms and application areas that have been developed from looking to the immune system for inspiration. It introduces immune mechanisms such as negative selection, clonal selection and danger theory. These are related to computational algorithms that have been developed to address applications in optimisation, anomaly detection and classification.

3.7 Swarm-based Modeling and Visualization of the Immune System ... and more

Christian Jacob (University of Calgary, CA)

License  Creative Commons BY-NC-ND 3.0 Unported license
© Christian Jacob

Joint work of Jacob, Christian; von Mammen, Sebastian; Davison, Timothy; Sarraf, Abbas; Sarpe, Vladimir; Esmaili, Afshin; Phillips, David; Yazdanbod, Iman

The Lindsay Virtual Human (LINDSAY) project creates a 3-dimensional, interactive computer model of male and female anatomy and physiology for medical education. The software developed in the LINDSAY project provides an exploration tool for medical students that complements their experiences and learning in the classroom, with simulators, and with patients.


Lindsay Presenter (LPresenter) is our first prototype of a presentation tool for interactive, 3-dimensional anatomical contents, to be used by instructors in medical schools. LPresenter can also be used by students to review contents from the lectures, prepare for exams, use quiz-type inquiry, or help with general as well as specific inquiry of anatomical structures. LPresenter has a built-in anatomy database and searchable atlas, which provides easy access to anatomical contents.

Lindsay Composer (LComposer) provides access to simulations of physiological processes. LComposer is the software tool that integrates physiology contents into medical teaching and learning resources as a computer-based modeling and exploration tool for human physiology. Similar to LPresenter, LComposer allows to program and compose physiological scenarios, which would illustrate key concepts of human physiology related to medical education. LComposer also incorporates a graphical programming environment, so that simulations and computer models can be assembled without any prior programming experience.

I presented first results from our LINDSAY Virtual Human project and demonstrated our first steps towards integrating simulations of immune system processes into multi-scale physiology simulations.

3.8 AIS Theory

Thomas Jansen (University College Cork, IE)

License  Creative Commons BY-NC-ND 3.0 Unported license
© Thomas Jansen

With help by and thanks to





- Uwe Aickelin, University of Nottingham,
- Ed Clark, University of York,
- Robert Oates, University of Nottingham,
- Thomas Stibor, TU München,
- Johannes Textor, Universität Lübeck,
- Christine Zarges, TU Dortmund.

Aim of the brief overview talk is to provide a very basic orientation in the field of artificial immune system and relevant theoretical approaches. As four main topics clonal selection, negative selection, dendritic cells and immune networks are identified. For each of these we identify a biological basis, prominent systems or algorithms, and theoretical approaches and

provide pointers to literature. As key issues in AIS theory we briefly discuss the aspects of equivalence to other known approaches, affinity and complexity.

3.9 Runtime Analysis of Clonal Selection Algorithms

Per Kristian Lehre (Technical University of Denmark, DK)

License     Creative Commons BY-NC-ND 3.0 Unported license
© Per Kristian Lehre

The recent progress in runtime analysis of evolutionary algorithms (EAs) has been facilitated by the introduction of appropriate analytical techniques. However, many of these techniques are primarily suited for the analysis of EAs with a parent population size of one, and not the population-based EAs that are often used by practitioners.

The first part of the talk gives a brief introduction to some analytical techniques that have recently become available for EAs with larger population sizes (Lehre PPSN2010 & GECCO2011). In particular, we introduce a variant of the well-known artificial fitness level technique which can be used to derive upper bounds the expected runtime of non-elitist EAs with populations.

In the second part of the talk, we discuss whether these techniques can be helpful for researchers in the artificial immune systems community, in particular for the study of clonal selection algorithms.

3.10 Real and artificial immune systems: oil and water or milk and cookies?

Chris McEwan (Edinburgh Napier University, GB)

License     Creative Commons BY-NC-ND 3.0 Unported license
© Chris McEwan


The seminal work in artificial immune systems set out to establish a productive interface between computer science and immunology. As the field gained popularity, the focus of research shifted towards "novel approaches" to applied problems in optimisation and artificial intelligence. With this shift, the once shared goal of hypothesising how the immune system might realise such functionality was compromised, and with it, any opportunity for AIS to establish itself as an independent body of work that contributes novel ideas to the immunological and engineering domains.

In this talk, I will address better aligning the real and artificial immune systems. This approach centers on the role of theory in providing mechanistic explanations behind such systems. I will argue that AIS should always be able to provide a biological interpretation, regardless of validity or plausibility; otherwise, they are only trivially "immune inspired". At the same time, AIS should be communicable with minimal references to biological nomenclature; otherwise, it is difficult to assert novelty and worth as computing artifacts.

Only once both desiderata are met can one claim to have achieved "immune-inspired computing". To meet both at the same time requires theoretical support for moving between the two mindsets. I contend that here lies the current and future contribution of AIS as a body of work.

3.11 Less Bio, More Inspired


Robert Oates (University of Nottingham, GB)

License  Creative Commons BY-NC-ND 3.0 Unported license
© Robert Oates

This talk represents a deliberately hyperbolic argument against the utility of the field of AIS and bio-inspired computing in general, in order to stimulate debate about the field's short-comings and, hopefully, inspire a well-structured counter-argument. It highlights issues surrounding the fidelity of the underlying biological models to the systems they purport to represent and questions the "cell-by-cell" approach to developing immune-inspired algorithms. Far from concluding, the talk ends with a series of open questions to act as jumping off points for a deeper audience discussion.

3.12 The use of AIS techniques to protect an Artificial Hormone System

Mathias Pacher (Universität Frankfurt am Main, DE)

License  Creative Commons BY-NC-ND 3.0 Unported license
© Mathias Pacher


Joint work of Pacher, Mathias; Brinkschulte, Uwe

We present an Artificial Hormone System (AHS) which is able to allocate tasks on resources of a distributed system. The AHS holds "organic" properties like self-configuration, self-optimization, and self-healing. We proved that the AHS works perfectly well under normal circumstances. However, in case of hardware failures or malicious attacks the effects on the AHS may be fatal: Its real-time bounds may be violated or there may be task loss or system overload which leads to damages of the resources of the distributed system.

We try to use or adapt AIS algorithms to counteract the effects arising from failures and attacks. We show a first approach demonstrating that AIS algorithms may help protect the AHS.

3.13 Negative Selection Algorithms: Past, Present, Perspectives

Johannes Textor (Universität Lübeck, DE)

License  Creative Commons BY-NC-ND 3.0 Unported license
© Johannes Textor

Joint work of Textor, Johannes; Elberfeld, Michael; Liśkiewicz, Maciej

Main reference M. Liśkiewicz, J. Textor, "Negative selection algorithms without generating detectors," Proc. Genetic and Evolutionary Computation Conference (GECCO'10), pp. 1047–1054, ACM, 2010.

URL <http://dx.doi.org/10.1145/1830483.1830673>

Negative selection algorithms are immune-inspired binary classifiers that are trained on only negative examples. Though initially a considered promising approach, there was so far no success in applying negative selection algorithms to real-world machine learning problems. One of the major obstacles was the computational demand, which was generally exponential in the size of the input data.

By casting negative selection algorithms in the formal framework of algorithmic learning theory, we showed that the while efficient implementations of the scheme are indeed unlikely to exist, one can efficiently *simulate* the scheme, e.g. by constructing a finite automaton whose accepted language is equal to the set of all strings that the algorithm would assign a positive label to.

We give a brief overview of how this approach provided new insight into the computational complexity of negative selection algorithm - based classification for some important classes of patterns that were used in the artificial immune systems literature. For some pattern classes, including the prominent *r*-chunk and *r*-contiguous patterns, we provide polynomial time solutions while previously, there were only exponential time implementations available.

Moreover, we discuss how negative selection algorithms are becoming increasingly important tools in theoretical immunology, where they function as a formal model of the negative selection process itself.

References

- 1 M. Liśkiewicz and J. Textor. Negative selection algorithms without generating detectors. In *Proceedings of Genetic and Evolutionary Computation Conference (GECCO'10)*, pages 1047–1054. ACM, 2010.
- 2 M. Elberfeld and J. Textor. Negative selection algorithms on strings with efficient training and linear-time classification. *Theoretical Computer Science*, 412:534–542, 2011.

3.14 On Fault Tolerance and Scalability of Swarm Robotic Systems

Alan FT Winfield (University of the West of England - Bristol, GB)

License © © ⊖ Creative Commons BY-NC-ND 3.0 Unported license
© Alan FT Winfield

Joint work of Bjercknes, Jan Dyrre; Winfield, Alan FT

Main reference Bjercknes JD and Winfield AFT, “On Fault-tolerance and Scalability of Swarm Robotic Systems,” Proc. Distributed Autonomous Robotic Systems (DARS 2010), Lausanne, November 2010.

There is a common assumption that swarm robotic systems are robust and scalable by default. This talk will present an analysis based on both reliability modelling and experimental trials of a case study swarm performing team work, in which failures are deliberately induced. The case study has been carefully chosen to represent a swarm task in which the overall desired system behaviour is an emergent property of the interactions between robots, in order that we can assess the fault tolerance of a self-organising system. Our findings show that in the presence of worst-case partially failed robots the overall system reliability quickly falls with increasing swarm size. We conclude that future large scale swarm systems will need a new approach to achieving high levels of fault tolerance.

3.15 Run Time Analysis of Artificial Immune Systems

Christine Zarges (TU Dortmund, DE)

License © © ⊖ Creative Commons BY-NC-ND 3.0 Unported license
© Christine Zarges

In this talk, artificial immune systems, in particular clonal selection algorithms used for optimization, are considered from the perspective of general randomized search heuristics.


An overview on recent theoretical results on the run time of simple algorithms is presented.

In the first part, we discuss several mutation operators that are used in practical algorithms and point out benefits and drawbacks of such mechanisms. In the second part, the use of the concept of static pure aging is investigated and compared to a similar mechanism from the field of evolutionary computation. We close by pointing out interesting and important aspects for future work.

4 Working Groups

4.1 A principled approach to deriving immune inspired engineering principles

Marc Read, Chris McEwan, Emma Hart, Ed Clark, Julie Greensmith, Uwe Aickelin

License  Creative Commons BY-NC-ND 3.0 Unported license
© Marc Read, Chris McEwan, Emma Hart, Ed Clark, Julie Greensmith,
Uwe Aickelin

Our group discussions concerned the derivation of a principled approach to deriving immune inspired engineering principles from immune system simulations. Drawing on the group's experience in developing complex immune simulations and attempting to create immune inspired algorithms, a principled approach to extracting from detailed simulations the minimal and essential set of principles required to capture a phenomenon of interest (PoI) was outlined.

These detailed simulations are typically developed to aid in exploring an immune domain, with no view to contribute to bio-inspired engineering solutions.

However, such simulations may be deemed to have captured some PoI with respect to engineering solutions, such as self-organisation or memory. Our approach advocates a principled approach to distilling such simulations to their *minimal representations*; the simulation may capture a great deal of immunological detail that is not essential to the PoI.

The *minimal representation* represents the smallest set of entities and their interactions required to capture the PoI. Distilling a detailed simulation to the minimal representation requires that one establish tests to demonstrate the presence of the PoI; the distillation process entails iteratively stripping complexity from the original simulation to the point that the PoI can no longer be maintained. Sensitivity analysis is identified as a means of indicating which elements of the simulation may be stripped; by attributing variation of a system's outputs to variation in its inputs, sensitivity analysis can reveal which cells and molecules of the system are non-critical with respect to the PoI.

Our approach is not intended as a replacement of the conceptual framework [1], or "immuno-engineering" [2]. Rather it elucidates some of the processes expressed within these concepts, and how the parties within and around the field of artificial immune systems relate to the provision of bio-inspired engineering solutions.

References

- 1 Susan Stepney, Robert E. Smith, Jonathan Timmis, Andy M. Tyrrell, Mark J. Neal and Andrew N. W. Hone. *Conceptual Frameworks for Artificial Immune Systems*. International Journal of Unconventional Computing, 1(3):315-338, 2005.
- 2 J. Timmis, E. Hart, A. Hone, M. Neal, A. Robins, S. Stepney and A. Tyrrell. *Immuno-Engineering*. 2nd IFIP International Conference on Biologically Inspired Collaborative Computing, 20th IFIP World Computer Congress, Milan, Italy, September 2008. IEEE Press Vol: 268/2008 pp. 3-17. 2008.

Participants

- Uwe Aickelin
University of Nottingham, GB
- Luca Albergante
Università di Milano, IT
- Bruno Apoloni
Università di Milano, IT
- Helio J.C. Barbosa
Lab. Nacional de Computação Científica-Petrópolis, BR
- Ed Clark
University of York, GB
- George M. Coghill
University of Aberdeen, GB
- Benjamin Doerr
MPI für Informatik – Saarbrücken, DE
- Julie Greensmith
University of Nottingham, GB
- Emma Hart
Edinburgh Napier University, GB
- Christian Jacob
University of Calgary, CA
- Thomas Jansen
University College Cork, IE
- Per Kristian Lehre
Technical Univ. of Denmark, DK
- Chris McEwan
Edinburgh Napier University, GB
- Yevgen Nebesov
Leibniz Univ. Hannover, DE
- Robert Oates
University of Nottingham, GB
- Pietro Oliveto
University of Birmingham, GB
- Mathias Pacher
Univ. Frankfurt am Main, DE
- Mark Read
University of York, GB
- Thomas Stibor
TU München, DE
- Dirk Sudholt
University of Birmingham, GB
- Johannes Textor
Universität Lübeck, DE
- Jon Timmis
University of York, GB
- Alan FT Winfield
University of the West of England – Bristol, GB
- Carsten Witt
Technical Univ. of Denmark, DK
- Lidia Yamamoto
Université de Strasbourg – Strasbourg, FR
- Christine Zarges
TU Dortmund, DE

