



EvoEvo Deliverable 6.6

Program of interdisciplinary dissemination workshop

Due date: M32 (July 2016)
Person in charge: Guillaume Beslon
Partner in charge: INRIA
Workpackage: WP6 (Management)
Deliverable description: Program of the interdisciplinary dissemination workshop that will be organized at the end of the project to disseminate ideas and concepts of EvoEvo in the biology and ICT communities.

Revisions:

Revision no.	Revision description	Date	Person in charge
1.0	Publication of the preliminary program	08/07/16	G. Beslon (INRIA)
1.1	Reorganization of the program to include participation of Eors Szathmary	30/07/16	G. Beslon (INRIA)
1.2	Publication of the final program validated by the partners	12/08/16	G. Beslon (INRIA)
1.3	Final version of the deliverable including links to the contributed abstracts	07/09/16	G. Beslon (INRIA)
1.4	Typo correction	12/09/16	P. Hogeweg (UU)



Table of Contents

1. Introduction	3
2. Aims and scope	3
3. Program	4
4. Abstracts of invited talks	6
4.1. Abstract for François Blanquart's talk.....	6
4.2. Abstract for Nobuto Takeuchi's talk.....	7
4.3. Abstract for Eors Szathmary's talk	7
5. URL of contributed abstracts	8
5.1. Evolvability drives innovation in viral genomes	8
5.2. Mutational load is ameliorated by increased transcriptional load-associated mutations, if these are biased towards duplications and deletions.....	8
5.3. Evolution of mutator populations in constant environments	8
5.4. Open-Endedness: Definitions and Shortcuts	8
5.5. In-silico experimental evolution highlights the influence of environmental seasonality on bacterial diversification	8
5.6. Evolution of r- and K-selected species of Virtual Microbes: a case study in a simple fluctuating 2-resource environment.....	8
5.7. Modeling the co-evolutionary dynamics of the <i>Lobaria pulmonaria</i> lichen symbiosis	8
5.8. EvoMachina: a novel evolutionary algorithm inspired by bacterial genome reorganization.	8
5.9. Evolution towards extinction in replicase models: inevitable unless.....	8
5.10. Physical interaction with automated music composition platforms	8



1. Introduction

This deliverable presents the program of the second EvoEvo workshop, to be held as a satellite of the 2016 Conference on Complex Systems in Amsterdam. This conference has been chosen because it attracts a large and interdisciplinary audience that perfectly fits with the objective of the workshop.

The program of the workshop is mainly composed of presentations of the different interdisciplinary results of the EvoEvo project (note that most of the presented abstracts are co-authored by two partners of the project; the corresponding extended abstracts are available on the project website: www.evoevo.eu/evoevo-2016/ - see detailed URL below) as well as three invited speakers conducting research directly related to the project.

2. Aims and scope

Variation and Selection are the two core processes of Darwinian Evolution. Yet, both are directly regulated by many processes that are themselves products of evolution (e.g. DNA repair, mutator genes, transposable elements, horizontal transfer, stochasticity of gene expression, sex, network modularity, niche construction...). This results in the ability of evolution to self-modify its operators, hence its dynamics. We call this process "Evolution of Evolution" or EvoEvo. Different EvoEvo strategies have been proposed in the literature, including regulation of variability, robustness/evolvability strategies and bet-hedging, but finding traces of these strategies in extant organisms is difficult. Moreover all these strategies are likely to interact one with the others, blurring their respective outcomes. However, new tools are now available that help understanding EvoEvo. On the one hand, large scale bioinformatic data analysis can be used to recognize signatures of evolution of evolution. On the other hand, large scale computational modelling of multi-level evolution is now becoming feasible, and promises to shed light on the conditions under which evolutionary mechanisms evolve as well as their consequences.

The aim of the EvoEvo workshop is to seek for a unified theory of Evolution of Evolution and bring together researchers from various fields in computational biology to tackle this challenge. The workshop will take place as a satellite workshop of CCS 2016, Amsterdam, NL. The EvoEvo workshop is an initiative of the EvoEvo consortium funded by the FP7 EU-FET grant EvoEvo (ICT-610427).

WORKSHOP CHAIRS

- **Guillaume Beslon**, INSA-Lyon, Université de Lyon (FR), LIRIS/Beagle team
- **Santiago Elena**, CSIC and Polytechnic University of Valencia (SP), IBMCP
- **Paulien Hogeweg**, Utrecht University (NL), Bioinformatics group
- **Dominique Schneider**, Université Grenoble Alpes (FR), TIMC-IMAG
- **Susan Stepney**, University of York (UK), Centre for Complex Systems Analysis



3. Program

9h30 – 9h50	Introduction talk: Paulien Hogeweg (Utrecht University, Utrecht, NL) <i>What's EvoEvo?</i>								
9h50 – 10h30	Invited talk: François Blanquart (Imperial College, London, UK) <i>Epistasis and the structure of fitness landscapes: are experimental fitness landscapes compatible with Fisher's geometric model?</i>								
10h30 – 11h	Coffee break								
11h – 11h40	Invited talk: Nobuto Takeuchi (University of Tokyo, Tokyo, JP) <i>The origin of genes through spontaneous symmetry breaking</i>								
11h40 – 13h	Session 1 "EvoEvo at the molecular level" <hr/> <table><tr><td>11h40 – 12h</td><td>Guillaume Beslon (INRIA, Lyon, FR), Vincent Liard (INRIA, Lyon, FR), Santiago Elena (CSIC, Valencia, SP) <i>Evolvability drives innovation in viral genomes</i></td></tr><tr><td>12h – 12h20</td><td>Enrico Sandro Colizzi (Utrecht University, Utrecht, NL), Paulien Hogeweg (Utrecht University, Utrecht, NL) <i>Mutational load is ameliorated by increased transcriptional load-associated mutations, if these are biased towards duplications and deletions</i></td></tr><tr><td>12h20 – 12h40</td><td>Jacob Pieter Rutten (INRIA, Lyon, FR), Paulien Hogeweg (Utrecht University, Utrecht, NL), Guillaume Beslon (INRIA, Lyon, FR) <i>Evolution of mutator populations in constant environments</i></td></tr><tr><td>12h40 – 13h</td><td>Susan Stepney (University of York, York, UK), Guillaume Beslon (INRIA, Lyon, FR)</td></tr></table>	11h40 – 12h	Guillaume Beslon (INRIA, Lyon, FR), Vincent Liard (INRIA, Lyon, FR), Santiago Elena (CSIC, Valencia, SP) <i>Evolvability drives innovation in viral genomes</i>	12h – 12h20	Enrico Sandro Colizzi (Utrecht University, Utrecht, NL), Paulien Hogeweg (Utrecht University, Utrecht, NL) <i>Mutational load is ameliorated by increased transcriptional load-associated mutations, if these are biased towards duplications and deletions</i>	12h20 – 12h40	Jacob Pieter Rutten (INRIA, Lyon, FR), Paulien Hogeweg (Utrecht University, Utrecht, NL), Guillaume Beslon (INRIA, Lyon, FR) <i>Evolution of mutator populations in constant environments</i>	12h40 – 13h	Susan Stepney (University of York, York, UK), Guillaume Beslon (INRIA, Lyon, FR)
11h40 – 12h	Guillaume Beslon (INRIA, Lyon, FR), Vincent Liard (INRIA, Lyon, FR), Santiago Elena (CSIC, Valencia, SP) <i>Evolvability drives innovation in viral genomes</i>								
12h – 12h20	Enrico Sandro Colizzi (Utrecht University, Utrecht, NL), Paulien Hogeweg (Utrecht University, Utrecht, NL) <i>Mutational load is ameliorated by increased transcriptional load-associated mutations, if these are biased towards duplications and deletions</i>								
12h20 – 12h40	Jacob Pieter Rutten (INRIA, Lyon, FR), Paulien Hogeweg (Utrecht University, Utrecht, NL), Guillaume Beslon (INRIA, Lyon, FR) <i>Evolution of mutator populations in constant environments</i>								
12h40 – 13h	Susan Stepney (University of York, York, UK), Guillaume Beslon (INRIA, Lyon, FR)								



	<i>Open-Endedness: Definitions and Shortcuts</i>
13h – 14h45	Lunch & CCS Keynote Lecture
<i>14h45 – 15h30</i>	Invited talk: Eors Szathmary (Parmenides Center for the Conceptual Foundations of Science, Pullach/Munich, Germany) <i>Evolution of Evolvable Systems</i>
<i>15h30 – 16h30</i>	Session 2 “EvoEvo at the population level”
<i>15h30 – 15h50</i>	<u>Charles Rocabert (INRIA, Lyon, FR),</u> <u>Carole Knibbe (INRIA, Lyon, FR),</u> <u>Jessika Consuegra (Univ Grenoble Alpes, Grenoble, FR),</u> <u>Dominique Schneider (Univ Grenoble Alpes, Grenoble, FR),</u> <u>Guillaume Beslon (INRIA, Lyon, FR)</u> <i>In-silico experimental evolution highlights the influence of environmental seasonality on bacterial diversification</i>
<i>15h50 – 16h10</i>	<u>Bram van Dijk (Utrecht University, Utrecht, NL),</u> <u>Thomas Cuypers (Utrecht University, Utrecht, NL),</u> <u>Paulien Hogeweg (Utrecht University, Utrecht, NL)</u> <i>Evolution of r- and K-selected species of Virtual Microbes: a case study in a simple fluctuating 2-resource environment</i>
<i>16h10 – 16h30</i>	<u>Julia Adams (Wellesley College, Wellesley, UK)</u> <u>Simon Carrignon (Supercomputing Center, Barcelona, SP),</u> <u>Aina Olle (Pompeu Fabra University, Barcelona, SP),</u> <u>Salva Duran (Pompeu Fabra University, Barcelona, SP)</u> <i>Modeling the co-evolutionary dynamics of the Lobaria pulmonaria lichen symbiosis</i>

16h30 – 17h	Coffee break
17h – 18h	Session 3 “Using EvoEvo to built artificial systems”
17h – 17h20	Tim Hoverd (University of York, York, UK), Susan Stepney (University of York, York, UK) <i>EvoMachina: a novel evolutionary algorithm inspired by bacterial genome reorganisation</i>
17h20 – 17h40	Simon Hickinbotham (University of York, York, UK), Paulien Hogeweg (Utrecht University, Utrecht, NL) <i>Evolution towards extinction in replicase models: inevitable unless...</i>
17h40 – 18h	Jonas Abernot (INRIA, Lyon, FR), Simon Hickinbotham (University of York, York, UK) <i>Physical interaction with automated music composition platforms</i>

4. Abstracts of invited talks

4.1. Abstract for François Blanquart’s talk

Epistasis and the structure of fitness landscapes: are experimental fitness landscapes compatible with Fisher’s geometric model?

The fitness landscape defines the relationship between genotypes and fitness in a given environment and underlies fundamental quantities such as the distribution of selection coefficient and the magnitude and type of epistasis. A better understanding of variation in landscape structure across species and environments is thus necessary to understand and predict how populations will adapt. An increasing number of experiments investigate the properties of fitness landscapes by identifying mutations, constructing genotypes with combinations of these mutations, and measuring the fitness of these genotypes. Yet these empirical landscapes represent a very small sample of the vast space of all possible genotypes, and this sample is often biased by the protocol used to identify mutations. Here we develop a rigorous statistical framework based on Approximate Bayesian Computation to address these concerns and use this flexible framework to fit a broad class of phenotypic fitness models (including Fisher’s model) to 26 empirical landscapes

representing nine diverse biological systems. Despite uncertainty owing to the small size of most published empirical landscapes, the inferred landscapes have similar structure in similar biological systems. Surprisingly, goodness-of-fit tests reveal that this class of phenotypic models, which has been successful so far in interpreting experimental data, is plausible in only three of nine biological systems. More precisely, although Fisher's model was able to explain several statistical properties of the landscapes—including the mean and SD of selection and epistasis coefficients—it was often unable to explain the full structure of fitness landscapes.

4.2. Abstract for Nobuto Takeuchi's talk

The origin of genes through spontaneous symmetry breaking

The heredity of the modern cell is provided by a small number of non-catalytic template molecules—the gene. This basic feature of modern-type heredity, however, is believed to have been absent at the earliest stages of evolution. The RNA world hypothesis posits that the heredity of the first, primitive cell (protocell, for short) was provided by a population of dual-functional molecules serving as both templates and catalysts. How could genes originate in protocells? Here, I will discuss the possibility that gene-like molecules emerge in protocells through spontaneous symmetry breaking between the complementary strands of replicating molecules. Our model assumes a population of primitive cells, each containing a population of replicating molecules. Protocells are selected towards maximizing the catalytic activity of internal molecules, whereas molecules tend to evolve towards minimizing it. This conflicting evolutionary tendencies at different levels induce symmetry breaking, whereby one strand of replicating molecules maintains catalytic activity and increases its copy number, whereas the other completely loses catalytic activity and decreases its copy number—like genes. The evolution of these gene-like molecules increases the equilibrium fitness of protocells. Our results implicate conflicting multilevel evolution as a key cause of the evolution of genetic complexity.

4.3. Abstract for Eors Szathmary's talk

Evolution of Evolvable Systems

I shall survey experimental and theoretical results from an ERC Advanced project with that name (<https://www.parmenides-foundation.org/research/projects/evoevo/>). I shall focus on three issues:

- Experimental approach to infrabiological systems,
- Major transitions theory 2.0 (especially the filial transitions),
- Learning in evolution versus Evolution in learning.



5. URL of contributed abstracts

5.1. Evolvability drives innovation in viral genomes

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_Beslon.pdf

5.2. Mutational load is ameliorated by increased transcriptional load-associated mutations, if these are biased towards duplications and deletions

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_Colizzi.pdf

5.3. Evolution of mutator populations in constant environments

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_Rutten.pdf

5.4. Open-Endedness: Definitions and Shortcuts

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_stepney.pdf

5.5. In-silico experimental evolution highlights the influence of environmental seasonality on bacterial diversification

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_Rocabert.pdf

5.6. Evolution of r- and K-selected species of Virtual Microbes: a case study in a simple fluctuating 2-resource environment

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_vanDijk.pdf

5.7. Modeling the co-evolutionary dynamics of the *Lobaria pulmonaria* lichen symbiosis

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_Adams.pdf

5.8. EvoMachina: a novel evolutionary algorithm inspired by bacterial genome reorganization

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_Hoverd.pdf

5.9. Evolution towards extinction in replicase models: inevitable unless...

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_Hickinbotham.pdf

5.10. Physical interaction with automated music composition platforms

http://www.evoevo.eu/download/evoevo_workshop_2016/EvoEvo2016_Abernot.pdf