

PROJECT SUMMARY

Evolution is the major source of complexity on Earth at the origin of all the species we can observe, interact with or breed. On a smaller scale, evolution is at the heart of the adaptation process for many species, in particular micro-organisms (e.g. bacteria, viruses...). Microbial evolution results in the emergence of the species itself, and it also contributes to the organisms' adaptation to perturbations or environmental changes. These organisms are not only organised by evolution, they are also organised to evolve.

The EvoEvo project will develop new evolutionary approaches in information science and will produce algorithms based on the latest understanding of molecular and evolutionary biology. Our ultimate goal is to address open-ended problems, where the specifications are either unknown or too complicated to express, and to produce software able to operate in unpredictable, varying conditions.

We will start from experimental observations of micro-organism evolution, and abstract this to reproduce EvoEvo, in biological models, in computational models, and in application software. Our aim is to observe EvoEvo in action, to model EvoEvo, to understand EvoEvo and, ultimately, to implement and exploit EvoEvo in software and computational systems.

The EvoEvo project will have impact in ICT, through the development of new technologies. It will also have impact in biology and public health, by providing a better understanding of micro-organism adaptation (such as the emergence of new pathogens or the development of antibiotic resistances).

CONTACT

<http://www.evoevo.eu>
contact@evoevo.eu

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Project name: Evolution of Evolution

Project acronym: EvoEvo

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Subprogramme area: ICT-2013.9.6

Contract type: Collaborative project (generic)

Call: EVLIT (Evolving Living Technologies)



THE UNIVERSITY of York

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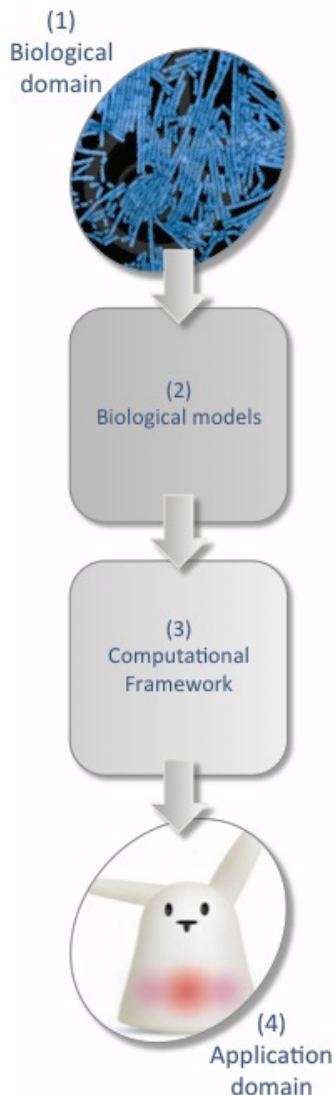
– EVOLUTION OF EVOLUTION –

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WORK PROGRAM

EvoEvo will achieve its main objective through the achievement of four scientific and technological objectives organized to bridge biological knowledge to ICT applications.



- 1) **BIOLOGICAL DOMAIN**
Observe, quantify and characterize EvoEvo in *Escherichia coli* and *Tobacco etch Virus* through experimental evolution.
- 2) **COMPUTATIONAL BIOLOGY**
Simulate “evolution of evolution” by mean of individual-based models and *in silico* experimental evolution.
- 3) **COMPUTATIONAL FRAMEWORK**
Design a computational evolutionary platform to exploit EvoEvo in applicative software.
- 4) **APPLICATION DOMAIN**
Apply EvoEvo to real ICT problems and propose proofs of concept for the approaches developed in the project.

KEY CONCEPTS

Evolution of Evolution is a process that acts through modification of organisms genotype-to-phenotype mapping. In the project, four characteristics of mapping will be studied in real organisms, modelled through computational evolution and used in a real application.

- **VARIABILITY**
The ability to generate new phenotypes by mutations or by stochastic fluctuations. Variability is one of the central processes of evolution.
- **ROBUSTNESS**
The ability to support mutational events or environmental variations without losing fitness.
- **EVOLVABILITY**
The ability to increase the proportion of favourable adaptive events through reorganization of the genotype-to-phenotype mapping.
- **OPEN-ENDEDNESS**
The ability to generate new challenges while evolving.

SYSTEMS OF INTEREST

- **MICRO-ORGANISMS**
Two model micro-organisms will be studied: the bacterium *E. coli* and *Tobacco etch virus*. Both models will be studied from the genomic to the phenotype and population levels.
- **COMPUTATIONAL MODELS**
Two different simulation frameworks (“aevoI” and “pearls-on-a-string”) will be used and merged to create an integrated model.
- **APPLICATIONS**
Two different applications will be used as proof of concept: on-line data stream clustering and evolution of a personal companion.

PARTNERS



Guillaume Beslon, INRIA Grenoble Rhône-Alpes, Beagle Team, Lyon, France

INRIA is associated with INSA-Lyon, Université Claude Bernard-Lyon 1 and the LIRIS Laboratory



Dominique Schneider, Université Joseph Fourier Grenoble 1, Laboratoire Adaptation et Pathogénie des Microorganismes, Grenoble, France.



Paulien Hogeweg, Utrecht University, Theoretical Biology and Bioinformatics Group, Utrecht, Nederland.



Susan Stepney, University of York, York Centre for Complex Systems Analysis, York, UK



Santiago Elena, Consejo Superior de Investigaciones Científicas, Instituto de Biología Molecular y Celular de Plantas, Valencia, Spain