

traffic, telecommunications, even business-communication networks.

A multi-disciplinary team of four research groups plans to create new computer simulations of cell-signalling networks (CSNs) in the ESIGNET project. Through mathematical modelling and software development, they aim to investigate biological **CSNs** and computational methods for evolving artificial **CSNs.** One practical outcome will be open-source code for 'filling in' the unknown parts of partially characterised CSNs. Researchers in the life sciences and in drug discovery could be among the beneficiaries.

# Evolutionary cell signalling

ell signalling is a key area in biology which deals with how cellular processes in biological organisms may be regulated by signals from other cells or cues from the environment. Investigating how cell signalling is carried out in the human body and what happens if components of the signalling pathway are defective is critical in understanding how diseases such as cancer develop and spread through the body. Abnormalities in cell-signalling pathways have been implicated in the progress of many other diseases and illnesses, such as cholera, rheumatoid arthritis and diabetes. This is one reason why pharmaceutical companies have concentrated a lot of resources on the development of drugs that target key components of signal pathways, and kits and assays for detection of diseases.

CSNs contain molecules with which they respond to and transduce signals. As inputoutput systems, CSNs may be likened to computers – their biochemical reactions to appropriate electronic circuits. The aim of the ambitious ESIGNET project is to develop software to simulate biological CSNs. The work involved demands a combination of expertise in biology, computer science and control engineering which is not found in any single Member State. Bringing together researchers from the United Kingdom, Germany, the Netherlands and Ireland, this is a project with clear European added value.

## **Artificial CSNs**

To achieve their aims, the team will first have to develop languages for data entry and for representing the computational properties of CSNs. They will implement fast evolutionary algorithms for subjecting artificial CSNs to a computational evolutionary process as a means of generating descendants that behave just like biological CSNs. The resulting software will take as an input a desired computational task and calculate for its output a CSN capable of carrying out that task. In a parallel effort, the partners will use existing simulation software to investigate real CSNs and mathematical modelling to describe their properties so that artificial CSNs can be developed with matching properties.

In real life, CSNs often share components – in this way one signal-transduction pathway may regulate another. The consortium will create software to mimic this 'cross-talking' in artificial counterparts. To validate the evolved CSNs, the team will develop software to transfer them to



Within biology, ESIGNET

will give a completely

new perspective on the

properties of real CSNs

and new ways to study

them.

## ESIGNET NEST ADVENTURE

Evolutionary computation techniques are already used in industry for optimising jobs.

### AT A GLANCE

*Official title Evolving cell signalling networks in silico* 

#### Coordinator

United Kingdom: University of Birmingham, School of Computer Science

#### Partners

- The Netherlands: Technical University Eindhoven
- Germany: Friedrich Schiller University
- Ireland: Dublin City University

#### Further information

Dr Jonathan Rowe School of Computer Science University of Birmingham Birmingham, B15 2TT, United Kingdom Fax: +44 121 414 4281 E-mail: jer@cs.bham.ac.uk

Duration 36 months

*Project costs* € 1 599 999

*EU funding* € 1 599 999

Project reference Contract No. 12789 (NEST)

Web: http://www.cordis.lu/nest

existing molecular-dynamic and artificialchemistry packages. They can then test them in realistic molecular simulations.

## CSN 'predictor' and other applications

In addition to providing useful insights for biologists into the workings of CSNs, software developed during the project's three-year duration has the potential to

improve productivity in several industry sectors. The team will develop a 'predictor', for example, to allow unknown components of partially known pathways to be identified. The input for this software module will be a description of an

incompletely identified CSN and a specific computation; the output will enumerate possible candidates. Experimental *in vitro* methods for analysis of real CSNs are timeconsuming and costly, so this could be useful in the pharmaceutical industry for drug development as well as for scientific research. Looking to the future, members of the ESIGNET team believe that findings from the project could well have applications in investigations into quite different networks – traffic networks, telecommunications networks, even business-communication networks, for example. Evolutionary computation techniques are already used in industry for optimising jobs. As this project will increase experience in this field of computing, there may be benefits too for

> human resource management in Europe.

The possibilities do not end there. 'Closure' occurs when cross-talking CSNs self-regulate and thereby maintain homeostasis in the system. A question the partners are looking for

answers to is: "How well can CSNs maintain closure in the face of abrupt changes in their environment?" If answers are found, they may hold lessons in the design of more resilient control systems in engineering.



© European Commission, 2005 The Commission accepts no responsibility or liability whatsoever with regard to the information presented in this document.