



Project no. : **200767**
Project acronym: **APO-SYS**
Project title: **Apoptosis systems biology applied to cancer and AIDS.**

Instrument: Collaborative project

Thematic Priority: Large-scale integrating project

Deliverable reference number and title

DL4: Training for mastering the interface for pathway map description integration (Month 3, Partners 3, 14, 15A, 19, 21, 9, 5, 7, 2, 18, 8, 1, 10, 10A) (WP6.1).

Due date of deliverable: **30/04/2008**

Actual submission date: **05/06/2008**

Start date of project:
1 of February 2008

Duration:
4 years

Organisation name of lead contractor for this deliverable:
Institut Curie (Beneficiary no 3)

Project co-funded by the European Commission within the Sixth Framework Programme (2002-2006)		
Dissemination Level		
PU	Public	X
PP	Restricted to other programme participants (including the Commission Services)	
RE	Restricted to a group specified by the consortium (including the Commission Services)	
CO	Confidential, only for members of the consortium (including the Commission Services)	

Description of DL4 with completion date “Month 3”

Editor : Emmanuel Barillot

DL4 (WP6-1): Training for mastering the interface for pathway map description integration (Month 3, Partners 3, 14, 15A, 19, 21, 9, 5, 7, 2, 18, 8, 1, 10, 10A).

One of the main goal of APO-SYS is to build mathematical models of apoptosis and use them to understand cancer and AIDS. These models are based on the accumulation of knowledge available both in the literature and in the mind of the experts from the partnership, and must be confronted to the experimental data produced in APO-SYS or coming from other sources. The first step in building models for the pathways of apoptosis, as for any other biological process, is to summarize the current knowledge of experts into a common and meaningful picture (as stated by (Kitano, 2003) : *A solid definition and comprehensive graphical representation of biological networks is essential for efficient and accurate dissemination of information on biological models*). This means in particular using the adequate tools for capturing and representing this information, and navigating into the pathway maps. At Institut Curie (partner 3) we have some experience of this question and adopted a well-known software to address it, and also developed a complementary tool. After careful selection, we based our developments in pathway charting on CellDesigner (Kitano et al, 2005), a systems biology software already widely used in the scientific community and with whom we designed in a previous work a comprehensive map of the Rb/E2F pathway (Calzone et al, 2008). We also build an interface, BiNoM (Zinovyev et al, 2007), which is a plug-in to the well known graph software Cytoscape and allows analysis of networks created with CellDesigner.

In order to have all partners in APO-SYS using the same language and tools for pathways charting and analysis, we have organized a workshop for pathway charting at Institut Curie, where the participants have been trained on real cases to the practice of both CellDesigner and BiNoM. This workshop was hold by Andrei Zinovyev and Laurence Calzone, both from Institut Curie. The detailed program can be found on the APO-SYS web site (under Announcements and Workshops/Training), at <http://bioinfo-out.curie.fr/training/CGH-PATHWAYworkshop/>, as well as the documents used and distributed at the workshop. Nineteen participants from the APO-SYS partnership attended the workshop, including the two organizers (**Appendix 1**). Note that this training session was jointly organized with another session on “omics” data analysis (WP7.5) (**Appendix 2**).

Appendix 1

List of participants :

Nelli	Kunkel	Division of Molecular Genetic Epidemiology German Cancer Research Center
Bowang	Chen	Division of Molecular Genetic Epidemiology German Cancer Research Center
Lorenzo	Galluzzi	INSERM, U848 - Unit "Apoptosis, cancer and immunity" Institut Gustave Roussy, France
Nadya	Morozova	CNRS, Villejuif, France
Kumar	Rajiv	DKFZ, Heidelberg, Germany
Per	Lund	Université de Strasbourg, France
Kohonen	Pekka	VTT Medical Biotechnology-Technical Research Centre of Finland
Fabio	Manzo	Student of Lucia Altucci, Università di Napoli
Marco	Corazzari	National Institute for infectious Diseases
Tuula	Kallunki	Institute of Cancer Biology-Denmark
Einat	Zalckvar	Department of Molecular Genetics-Weizmann Institute of Science-Israel
Christian	Hellwig	RCSI, Department of Physiology & Medical Physics
Heinrich	Huber	RCSI, Department of Physiology & Medical Physics
Nicolas	Servant	Institut Curie, Paris, France
Philippe	Hupé	Institut Curie, Paris, France
Andrei	Zinovyev	Institut Curie, Paris, France
Laurence	Calzone	Institut Curie, Paris, France
Juliette	Aury-Landas	Institut Curie, Paris, France
Emmanuel	Barillot	Institut Curie, Paris, France
Igor	Ulitsky	Tel Aviv University, Israel

Bibliography

Calzone L, Gelay A, Zinovyev A, Radvanyi F, Barillot E.

A comprehensive modular map of molecular interactions in RB/E2F pathway.

Mol Syst Biol. 2008;4:173. Epub 2008 Mar 4.

Zinovyev A, Viara E, Calzone L, Barillot E.

BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks.

Bioinformatics. 2008 Mar 15;24(6):876-7. Epub 2007 Nov 16.

Kitano H, Funahashi A, Matsuoka Y, Oda K.

Using process diagrams for the graphical representation of biological networks.

Nat Biotechnol. 2005 Aug;23(8):961-6.

Kitano H.

A graphical notation for biological networks. BioSilico, 2003, 1, 169–176.

Appendix 2 :

Announcement for the joined workshop WP6.1 and WP7.5
(<http://www.apo-sys.eu/aposys/Announcements/Announcements.htm>)

APO-SYS form for the joint workshop on data analysis and pathway charting Paris, April 29th and 30th

As planned in WP 6 and 7, we will organize a workshop for pathway charting and modeling, and a workshop for data analysis. Due to a number of constraints, it turns out that the only available dates are 29 and 30 of April and these workshops will be organized jointly at this date at Institut Curie, Paris. The workshop is divided in three parts: transcriptome analysis, DNA copy number analysis, and pathway charting. Please fill in this form if you would like to attend.

The sessions :

DNA copy number analysis: this session will be presented by Stéphane Liva and Philippe Hupé (Emmanuel Barillot group, Institut Curie, partner 3) and will cover:

CAPweb, a pipeline for DNA copy number array management (<http://bioinfo-out.curie.fr/CAPweb/>)

VAMP, a user interface for DNA copy number array analysis (<http://bioinfo-out.curie.fr/actudb/>)

Transcriptome analysis: this session will be presented by Igor Ulitsky (Ron Shamir group, Tel Aviv Univ., partner 14) and will cover :

Expander (Gene expression analysis: clustering, bi clustering, classification etc.)

MATISSE (Identification of pathways with correlated expression patterns)

AMADEUS (Motif finding in promoters and 3' UTRs).

Pathway charting and integration: this session will be presented by Igor Ulitsky (Ron Shamir group, Tel Aviv Univ., partner 14) and Laurence Calzone and Andrei Zinovyev (Emmanuel Barillot group, Institut Curie, partner 3) and will cover:

SPIKE (Signaling pathway knowledgebase)

CellDesigner (a tool for charting pathways, <http://www.celldesigner.org/>) and BiNoM (for analysing pathways and querying pathway databases, <http://bioinfo-out.curie.fr/projects/binom/>)

APO-SYS form for the joint workshop on data analysis and pathway charting
Paris, April 29th and 30th

Who are you ?

Name of participant:

Affiliation :

Apo-sys partner number :

Which session would you like to attend to ?

Transcriptome analysis : Yes / No

DNA copy number analysis : Yes / No

Pathway charting : Yes / No

Motivations (Optional)

In order to tune the workshop to the needs and the agenda of the participants, we are asking you to briefly describe the relevant projects you are working on that may benefit from the workshop (half a page maximum).

For transcriptome and DNA copy number please explain the biological system used, the scientific question(s) under investigation and the experiment design (including technology used, replicates and number of arrays).

For the pathway charting session please explain the biological system you are studying, describe the pathway (molecular interaction) data you may have collected and the concrete biological questions you would like to solve using mathematical modeling of pathways.