Hadrien Mary

62 rue de la Colombette
31000 Toulouse, France
28/04/1987 (25 years)

Driving license
Phone: +33 6 25 30 33 27
Email: hadrien.mary@gmail.com

Education

Since september 2012 : **Bioinformatic engineer** at LBCMCP (CNRS UMR5088) in **Tournier team**, *Toulouse – France*

* Cell biology, imaging, modelling, microscopy

2009 - 2011 : **Master degree in Biocomputing**, *University of Bordeaux*

* Phylogeny, Genomics, Biocomputing, Metabolomic

* Programming, Database design and management, Algorithmics

2009 : **Bachelor's degree in Biology of Organisms**, *University of Bordeaux*

* Biostatistics, Ecology, Genetics

* Biochemistry, Cellular Biology, Molecular Biology

2008 : **Erasmus year** – European Union student exchange program. High school of biology, *University of Complutense in Madrid*

* Iberic ecology, Evolutive genetics, Biostatistics

2005 : Higher National Diploma, *Basque country – France*

Professional experience

March – September 2011 : Six month internship at **IMB** (The Institute for Molecular Bioscience), *University of Queensland, Brisbane, Australia*, under the supervision of Nick Hamilton

High-throughput image segmentation and statistic analysis

* High-throughput image segmentation using **CellProfiler**

* Images come from optical fluorescence microscope and contained Salmonella infected cells

* The aim was to identify new proteins / genes reducing infection

* Development of a software to analyse and interpret data from the segmentation

* ProfileExtractor allow a fast and accurate data visualization to be able to identify interesting wells according to a set of parameters

* Source code: http://github.com/hadim/profileextractor

* Publication coming soon [1] (contact Nick Hamilton, see References, to get details)

Mammalian kidney **branching morphogenesis modelling**

* Mouse kidney 3D reconstruction analysis

* Development of a new branching morphogenesis model using L-system approach

* Development of Lsysdrawer: L-system 3D visualization software using VTK

* Source code: http://github.com/hadim/lsysdrawer

May 2010 : Two month internship at **LaBRI** (Informatic Research Laboratory of Bordeaux), *University of Bordeaux, France*, under the supervision of Marie Beurton Aimar

Development of MAS Meta (Multi Agent System for metabolism simulation)

* Conception of a high performance parallelisation algorithm
* MAS implementation using GPU computing trough OpenCL (Open Computing Language)
* Converting old CUDA program originally designed for 3D image segmentation
* http://bitbucket.org/marelo/mas-metabo
* C++, OpenCL, OpenGL, CUDA, XML

February 2010 : Two month internship at **CBiB** (Center for bioinformatics of Bordeaux), *University of Bordeaux, France*, under the supervision of Patricia Thebault

Development of GUI for MetaboFlux, a software to analyse metabolic networks

* In charge of the coordination between the developpers team (4 students) and the customer
* Specification establishment asked by the customer
* Documentation generation with Doxigen (documentation generator)
* Detailed report about code structure and software specifications
* Tutorials movies about MetaboFlux GUI use to help biologist (video editor : Kdenlive)
* Python, PyGTK, SBML, XML

2003 - 2007 : Various student jobs like waiter, commis chef, babysitting, domestic help and gardener (All located in Saint Jean de Luz and around)

Special Skills

Computing and data processing:

Programming language : Python, C/C++, Java, Perl, PHP, R (statistics), Ruby

GPU computing : CUDA, OpenCL

Database : MySQL, PostgreSQL

Revision control systems : Git, Mercurial, SVN

Imagery processing and analysis: CellProfiler, ImageJ, GIMP

3D visualization: OpenGL, VTK, VPython

User Interface libraries: Qt, GTK

Markup language : GraphML, SBML, Latex, XML, HTML

Operating system : GNU/Linux, Windows, Mac OS X

Bioinformatics:

Knowledge of **bioinformatics tools and databases** for the analysis and research of nucleic and proteic sequences

* NCBI, EBI, Ensembl, BLAST, FASTA, Clustal, etc
* Good knowledge of the tools' algorithms

High-throughput **image analysis**: segmentation with CellProfiler

Modelling: L-system, MAS (Multi-Agent based modelling approaches), Neural Network, Genetic Algorithm

Metabolic flux analysis: 13C-Flux, CellDesigner, PySCeS, Cytoscape, Omix, COPASI

Web development:

Drupal developpment (open source CMS)

* Administrator of the master student website. http://embib.toile-libre.org

* MySQL and Apache administration server

* Key technologies : PHP, HTML, CSS

Wordpress developpment (open source CMS)

* Website integration and deployment

*Custom design creation

* Plugin creation for specific customer requirement

Django developpment (Python web framework)

Use of modern web technology such as HTML5, CSS3, jQuery and so forth.

Languages:

french : native language

spanish : fluent (one year in Madrid – Spain in 2007)

english : fluent (six month in Brisbane – Australia in 2011)

References

Nick Hamilton (researcher and group leader of Hamilton group)

IMB (The Institute for Molecular Bioscience, Brisbane, Australia)

mail : n.hamilton@imb.uq.edu.au

website : http://www.imb.uq.edu.au/index.html?page=91481&pid=91492

phone : +61 7 3346 2033

Marie Beurton-Aimar (researcher and leader of the biocomputing master degree)

LaBRI (Informatic Research Laboratory of Bordeaux, France)

mail : marie.beurton@labri.fr

website : http://dept-info.labri.fr/ beurton/

phone : +33 5 40 00 35 25

Patricia Thébault (researcher)

CBiB (Center for bioinformatics of Bordeaux, France)

mail : patricia.thebault@u-bordeaux2.fr

website : http://cbi.labri.fr

phone : +33 5 57 57 48 61

Various

Level 3 **scuba diving** CIPP certified : considering to pass instructor degree

Surfing, biking, swimming, and running.

Very interested in **game of Go** : an ancient board game for two players that is noted for being rich in strategy despite its simple rules.

Chess, poker

Bibliography

[1] Kerr MC, Castro N, Mary H, et al. "Screening the contribution of the PX family to Salmonella pathogenesis".