Julien Maupetit

PhD in Structural Bioinformatics - Software / Web Developer

Personal Data

Place and Date of Birth:	Saint Denis (93), France | 14 October 1980
Address:	4, Rue Nationale, 63110, Beaumont, France
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Education

Nov 2007 — PhD's Degree in Bioinformatics, **Paris Diderot University**, Paris, France
Supervisor: Dr P. Tufféry

July 2004 — Master's Degree in Bioinformatics, **Paris Diderot University**, Paris, France
Grade: *magna cum laude*

July 2002 — Bachelor's Degree in Biochemistry, **Paris Diderot University**, Paris, France
Grade: *magna cum laude*

Principal Positions Held

Current / Dec 2011 — Web Developer & Co-Manager at ComSource
Front & Back End Web development
Entrepreneurship has always been in my mind. My passion for the web and its design decided me to join the ComSource web agency to develop tailored solutions for the web.

Nov 2011 / Sep 2008 — **Frozen Position**
Research Engineer at Paris Diderot University
(RPBS & INSERM UMR-S973), Paris, France
Structural bioinformatics - Web development - System administration
Supervisors: Dr P. Tufféry and Dr B. Villoutreix
Since I obtained my position, my principal activities have been: (i) structural bioinformatics and chemoinformatics web servers / programs development, (ii) structural bioinformatics assistance with biological wet laboratories, and (iii) platform / laboratory hosting / computing / storage resources administration.

Aug 2008 / Oct 2007 — Assistant Professor at IBPC (CNRS UPR9080), Paris, France
Bioinformatics teaching - Peptide structure prediction
Supervisor: Pr P. Derreumaux
The technics developped during my PhD applied to peptide structures appears strongly relevant. Hence, we designed PEP-FOLD, a fast method for large scale *de novo* peptide and miniprotein structure prediction.

Sep 2007 Oct 2004	PhD at Paris Diderot University (INSERM U726), Paris, France *Protein structure prediction* Supervisor: Dr P. Tufféry In a post-genomic context, plenty of proteins, identified by their sequence, have no experimentaly resolved structure, and fall out the range of application of comparative modelling methods. The goal of my PhD was to explore a new *de novo* protein structure prediction approach.
Summer 2003	Summer Intern at Paris Diderot University (INSERM U726) and Pasteur Institute, Paris, France *Molecular visualization* Supervisor: Dr P. Tufféry Development and integration of a PDB files parser in a molecular visualization widget.
May 2003 Jan 2003	Intern at Paris Diderot University (EA3508), Paris, France *Molecular biology* Supervisor: Pr J. London Transgenic mice genotyping.
Summer 2002	Summer Intern at Hospital Bichat (INSERM U409), Paris, France *Molecular biology* Supervisor: Dr M.E. Martin Hepcidin involvement in particular hemochromatosis – IRE/IRP system in transgenic mice over-expressing the superoxyde dismutase.

Teaching Experience

2005-2011, Paris Diderot University (300h)

Master	Introduction to XHTML/CSS Introduction to LaTeX Introduction to BioPython Python programing C programing Interfacing C and Python with Swig	Protein structure prediction Microarray data analysis Molecular phylogeny Bioinformatics tools
Bachelor	Bioinformatics tools	

2006, 1st Medils Summer School, Split, Croatia (4h)

PhD	Comparative protein modelling	Normal modes analysis

Publications

Peer reviewed articles

[1] J. Maupetit, R. Gautier, and P. Tufféry. "SABBAC: online Structural Alphabet-based protein BackBone reconstruction from Alpha-Carbon trace". In: *Nucleic Acids Res* 34.Web Server issue (July 2006), W147–51. DOI: 10.1093/nar/gkl289.

[2] J. Maupetit, P. Tufféry, and P. Derreumaux. "A coarse-grained protein force field for folding and structure prediction". In: *Proteins* 69.2 (Nov. 2007), pp. 394–408. DOI: 10.1002/prot.21505.

[3] L. Regad, F. Guyon, J. Maupetit, P. Tufféry, and A. C. Camproux. "A Hidden Markov Model applied to the protein 3D structure analysis". In: *Computational Statistics and Data Analysis* 52.6 (Feb. 2008), pp. 3198–3207. DOI: 10.1016/j.csda.2007.09.010.

[4] J. Maupetit, P. Derreumaux, and P. Tufféry. "PEP-FOLD: an online resource for de novo peptide structure prediction". In: *Nucleic Acids Res* 37.Web Server issue (July 2009), W498–503. DOI: 10.1093/nar/gkp323.

[5] B. Néron, H. Ménager, C. Maufrais, N. Joly, J. Maupetit, S. Letort, S. Carrere, P. Tufféry, and C. Letondal. "Mobyle: a new full web bioinformatics framework". In: *Bioinformatics* 25.22 (Nov. 2009), pp. 3005–11. DOI: 10.1093/bioinformatics/btp493.

[6] J. Maupetit, P. Derreumaux, and P. Tufféry. "A fast method for large-scale de novo peptide and miniprotein structure prediction". In: *J Comput Chem* 31.4 (Mar. 2010), pp. 726–38. DOI: 10.1002/jcc.21365.

[7] J. Maupetit, A. Saladin, and P. Tufféry. "Prédiction en ligne de la structure des protéines : un état des lieux". In: *Spectra Analyse* 39.276 (Nov. 2010), pp. 27–33.

[8] P. Schmidtke, V. Le Guilloux, J. Maupetit, and P. Tufféry. "fpocket: online tools for protein ensemble pocket detection and tracking". In: *Nucleic Acids Res* 38 Suppl (July 2010), W582–9. DOI: 10.1093/nar/gkq383.

[9] D. Lagorce, J. Maupetit, J. Baell, O. Sperandio, P. Tufféry, M. A. Miteva, H. Galons, and B. O. Villoutreix. "The FAF-Drugs2 server: a multistep engine to prepare electronic chemical compound collections". In: *Bioinformatics* 27.14 (2011), pp. 2018–20. DOI: 10.1093/bioinformatics/btr333.

[10] L. Regad, A. Saladin, J. Maupetit, C. Geneix, and A.-C. Camproux. "SA-Mot: a web server for the identification of motifs of interest extracted from protein loops". In: *Nucleic Acids Res* 39.Web Server issue (2011), W203–9. DOI: 10.1093/nar/gkr410.

[11] P. Thevenet, Y. Shen, J. Maupetit, F. Guyon, P. Derreumaux, and P. Tuffery. "PEPFOLD: an updated de novo structure prediction server for both linear and disulfide bonded cyclic peptides." In: *Nucleic Acids Res* [Accepted] (2012).

Proceedings

[12] H. Ménager, V. Gopalan, B. Néron, S. Larroudé, J. Maupetit, A. Saladin, P. Tufféry, Y. Huyen, and B. Caudron. "Bioinformatics applications discovery and composition with the Mobyle suite and MobyleNet". In: *RED 2010*. Vol. [Accepted]. Lecture Notes in Computer Science. 2011.

[13] Y. Shen, J. Maupetit, P. Derreumaux, and P. Tufféry. "PEP-FOLD: biased approach for the de novo prediction of peptide and miniprotein structure". In: *JOBIM 2011*. 2011. URL: http://www.pasteur.fr/ip/easysite/pasteur/fr/recherche/communication-scientifique/conferences-et-congres-scientifiques/conferences-service-colloques-institut-pasteur/jobim-2011.

[14] E. Strauser, M. Naveau, H. Ménager, J. Maupetit, Z. Lacroix, and P. Tufféry. "Semantic Map for Structural Bioinformatics: enhanced service discovery based on high level concept ontology". In: *RED 2010*. Vol. [Accepted]. Lecture Notes in Computer Science. Springer, 2011.

Oral communications

[15] J. Maupetit, F. Guyon, A. C. Camproux, P. Derreumaux, and P. Tufféry. *Candidate Fragments Prediction and their Assembly with a Greedy Algorithm and a Coarse-Grained Force Field to solve Protein Folding*. JOBIM. 2007. URL: http://crfb.univ-mrs.fr/jobim2007.

[16] J. Maupetit, B. Néron, H. Ménager, C. Maufrais, N. Joly, C. Letondal, and P. Tufféry. *Mobyle @ RPBS - A web portal for structural bioinformatics and chemoinformatics*. BIOGRALE. 2008. URL: http://pbil.univ-lyon1.fr/pf_bioinfo/breve86.html.

[17] J. Maupetit and P. Tufféry. *Mobyle vers Playmoby - Déploiement de web services*. BioWorkflow. 2008. URL: http://migale.jouy.inra.fr/bioworkflow/.

[18] J. Maupetit and P. Tufféry. *Mobyle @ RPBS // MobyleNet*. MobyleNet. 2009. URL: http://mobylenet.rpbs.univ-paris-diderot.fr.

[19] J. Maupetit, A. Saladin, and P. Tufféry. *La plate-forme RPBS : analyse fonctionnelle des structures protéiques in silico*. APLIBIO day. 2011. URL: http://renabi.genouest.org/platforms/aplibio/.

[20] J. Maupetit, A. Saladin, and P. Tufféry. *The RPBS Platform - in silico functional analysis & prediction of protein structures ... and molecular 3D printing!* GGMM. 2011. URL: http://ggmm2011.wordpress.com.

Posters

[21] J. Maupetit, P. Derreumaux, and P. Tufféry. *A Greedy Algorithm for Protein Structure Reconstruction: Improvements and Applications*. GCB. 2006. URL: http://www.gcb2006.de/.

[22] J. Maupetit, F. Guyon, J. Martin, A. C. Camproux, P. Derreumaux, and P. Tufféry. *Assessing a New Approach for Protein Structure Modeling Combining Structural Alphabet Local Conformation Prediction and Greedy Algorithm for Reconstruction*. CASP7. 2006. URL: http://predictioncenter.org/casp7/.

[23] S. Larroudé, J. Maupetit, H. Ménager, B. Néron, A. Saladin, B. Caudron, and P. Tufféry. *MobyleNet: user-centered large spectrum service integration over distributed sites*. ISMB. 2010. URL: http://www.iscb.org/ismb2010.

[24] J. Maupetit, B. O. Villoutreix, and P. Tufféry. *3D Printing service @ RPBS*. JOBIM 2010. 2010. URL: http://www.jobim2010.fr.

[25] J. Maupetit, B. O. Villoutreix, and P. Tufféry. *3D Printing service @ RPBS*. Obernai 2010. 2010. URL: http://infochim.u-strasbg.fr/new/spip.php?rubrique15.

[26] D. Lagorce, J. Maupetit, J. Baell, O. Sperandio, P. Tufféry, M. A. Miteva, H. Galons, and B. O. Villoutreix. *The FAF-Drugs2 server: a multi-step engine to prepare electronic chemical compound collections*. BABE. 2011. URL: http://www.omicsonline.org/BABE2011/.

[27] A. Saladin, J. Maupetit, H. Ménager, B. Néron, B. Caudron, and P. Tufféry. *MobyleNet: a network of trusted platforms for seamlessly sharing a large spectrum of services*. GGMM. 2011. URL: http://ggmm2011.wordpress.com.

[28] Y. Shen, J. Maupetit, P. Derreumaux, and P. Tufféry. *Mini protein fast fold de novo generation using biased conformation search*. PepCon. 2011. URL: http://www.bitlifesciences.com/PepCon2011/.

[29] Y. Shen, J. Maupetit, P. Derreumaux, and P. Tufféry. *PEP-FOLD: biased approach for the de novo prediction of peptide and miniprotein structure*. GGMM. 2011. URL: http://ggmm2011.wordpress.com.

Intern supervision

2011 — 3 months
SBMap3, Structural Bioinformatics Semantic Map Redesign
B. Delepine, Bachelor in Bioinformatics
Redesign SBMap interface with modern javascript tools instead of a Java Applet.

2010 — 5 months
SBMap2, Structural Bioinformatics Semantic Map
E. Strauser, Master of Bioinformatics
SBMap Java applet user interface and graphical navigation improvements.

PyPDB, a toolbox to work with PDB files
F. Briand, Master of Bioinformatics
Design of a command line tool to manipulate PDB files, its packaging and integration in the RPBS Mobyle portal.

2009 — 3 months
PyPDB, a python class to work with PDB files
C. Habib, Bachelor in Bioinformatics
Python code cleanup and documentation, integration of PDB-XML files support.

2008 — 5 months
SBMap, Structural Bioinformatics Semantic Map
M. Naveau, Master of Bioinformatics
Structural bioinformatics concepts ontology automatic update integration in an web administration interface.

Computer Skills

Operating systems:	GNU/Linux (expert), MacOS X, Windows
Programming languages:	Python, Bash, C, R (statistics)
Web development:	{ *front end* } HTML5, CSS3, SASS (Compass), Javascript/AJAX (jQuery)
	{ *back end* } PHP, Python (Django, CGI)
Databases:	SQL (MySQL, SQLite)
Graphic Art:	ADOBE Photoshop, Illustrator

Interests and Activities

Web technologies, Python, Open-Source, Programming
Guitar playing, Actor in a theater company