

Sébastien MORETTI

Curriculum Vitae

Personal address: 14 rue de l'eau vive, FR-25300 Doubs
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CURRENT POSITION

Bioinformatician Engineer – Computer Scientist
Swiss Institute of Bioinformatics, Vital-IT group
Department of Ecology & Evolution, Lausanne University
Switzerland

EDUCATION & EXPERIENCES

- 2006-now Contract engineer, Swiss Institute of Bioinformatics, Vital-IT group
Department of Ecology & Evolution (DEE), University of Lausanne, Switzerland
Projects: Genome-wide metabolic network reconstruction ([MetaNetX](#))
Java applet development and enhancement of the [MyHits](#) web site.
[Web services](#) implementation via Soaplab and Taverna.
Advisor: Dr. M. Pagni (Vital-IT)
Projects: [Bgee](#) (gene expression evolution db) database, tool and web site development.
[Selectome](#) (positive selection db) database, tools and web site development.
Advisor: Pr. M. Robinson-Rechavi (SIB/Evol Bioinfo Group & DEE, University of Lausanne)
- 2003-2006 Contract engineer, Sanofi-Aventis in the Genomic and Structural Information lab. (CNRS),
University of Luminy, Marseilles, France
Projects: Structural and genomic research about kinase proteins.
Multiple Sequence Alignments [tools](#) development.
Advisors: Dr. C. Notredame (CNRS), Dr. V. Saudek (Aventis), Pr. J.-M. Claverie (CNRS)
- 2001-2003 Contract engineer, Génoplante-Biogemma, Biotechnology and Plant Innovation lab. (ENSAT),
Toulouse, France
Projects: Set up an automated annotation system for Sunflower EST program.
Advisor: Pr. L. Gentzbittel (ENSAT)
- 2000-2001 Master Science in Functional Genomics Engineering, Universities Paris VII & Evry, France
Projects: SNP physical maps construction for target genes, phylogeny, two-hybrid analyses.
Advisor: Pr. B. Giros (INSERM, Psychiatry and Neurobiology unit, Créteil, France)
- 1999-2000 Master Y2 in Population Biology, Genetics and Eco-ethology, University of Tours, France
Thesis: Pheromonal polymorphism for the European Corn Borer (*Ostrinia nubilalis* Hbn.).
Advisor: Dr. B. Frérot (INRA, Phytopharmacy and Semiochemicals unit, Versailles, France)
- 1998-1999 Master Y1 in Population Biology and Ecosystems, University of Lyons I, France
Thesis: Round of duplication in Vertebrate gene families.
Parasitoid pheromonal interference in egg laying site.
Advisors: Dr. M Gouy & Pr. M Boulétreau (CNRS, Biometry & Evolution Biology, Lyons, France)

SKILLS

Bioinformatics & Computer Science

Annotation, gene prediction, SNP identification, structure analysis and visualization, EST clustering, multiple sequence alignment, phylogeny.
Databanks management and up-date, BASE & SRS installation and administration, installation of bioinformatic tool for application server.

OS, Servers & Programming

OS: Linux (administration), Unix, Mac OS X, Windows.
Servers: Apache, Tomcat and SVN management.
IT: Server administration, RPM building.
Programming: Perl, Java, Shell (bash), R, HTML, CSS, XML, CGI scripts and Javascript.
Notions: C, C++, JSP, Python and PHP.

Databases

SQL, MySQL (administration), Perl DBI.

Statistics

Parametric and non-parametric statistics.

Biology

Evolution biology, molecular biology, population genetics, eco-ethology.

Languages

English	read, written and spoken
French	mother language
German	elementary knowledge

WEB SITES & SOFTWARE

Web sites

<http://bgee.unil.ch/>
<http://selectome.unil.ch/>
<http://tcoffee.vital-it.ch/>
<http://wsembnet.vital-it.ch/>
<http://www.metanetx.org/>
<http://myhits.vital-it.ch/>
<http://www.vital-it.ch/>
<http://www.expasy.org/>

Software & Plugins

ProtoGene: Turning amino acid alignments into bona-fide CDS nucleotide alignments.
SoS: Mapping of SNPs onto Structures (<http://bioanalyse.free.fr/Software/>).
Plugins for the molecular viewer PyMOL (<http://bioanalyse.free.fr/Software/>).

TEACHING

Master training bioinformatics course (Oct 2007).

Phylogeny and Evolution using bioinformatics - EMBnet course for doctorals and post-doctorals (Sept 2007).

Installation of T-coffee web server - Course for CNRS and CRS4 T-coffee users (Sept 2006).

Multiple Sequence Alignments and T-Coffee tools - Course for SwissProt team (June 2006).

Query biological databases and BLAST - Course for a small group of Biogemma engineers (October 2002).

PUBLICATIONS

Journal publications

Daub JT, Moretti S, Davydov II, Excoffier L, Robinson-Rechavi M.

Detection of Pathways Affected by Positive Selection in Primate Lineages Ancestral to Humans

Molecular Biology and Evolution, 2017; 34(6), 1391-1402.

Morgat A, Lombardot T, Axelsen KB, Aimo L, Niknejad A, Hyka-Nouspikel N, Coudert E, Pozzato M, Pagni M, Moretti S, Rosanoff S, Onwubiko J, Bougueleret L, Xenarios I, Redaschi N, Bridge A.

Updates in Rhea - an expert curated resource of biochemical reactions

Nucleic Acids Res., 2017; 45(Database issue), D415-D418.

Moretti S, Martin O, Van Du Tran T, Bridge A, Morgat A, Pagni M.

MetaNetX/MNXref - reconciliation of metabolites and biochemical reactions to bring together genome-scale metabolic networks

Nucleic Acids Res., 2016; 44(Database issue), D523-526.

Ison J, Rapacki K, Ménager H, Kalaš M, Rydza E, Chmura P, Anthon C, Beard N, Berka K, Bolser D, Booth T, Bretaudeau A, Brezovsky J, Casadio R, Cesareni G, Coppens F, Cornell M, Cuccuru G, Davidsen K, Vedova GD, Dogan T, Doppelt-Azeroual O, Emery L, Gasteiger E, Gatter T, Goldberg T, Grosjean M, Grüning B, Helmer-Citterich M, Ienasescu H, Ioannidis V, Jespersen MC, Jimenez R, Juty N, Juvan P, Koch M, Laibe C, Li JW, Licata L, Mareuil F, Mičetić I, Friborg RM, Moretti S, Morris C, Möller S, Nenadic A, Peterson H, Profiti G, Rice P, Romano P, Roncaglia P, Saidi R, Schafferhans A, Schwämmle V, Smith C, Sperotto MM, Stockinger H, Vařeková RS, Tosatto SC, de la Torre V, Uva P, Via A, Yachdav G, Zambelli F, Vriend G, Rost B, Parkinson H, Løngreen P, Brunak S.

Tools and data services registry: a community effort to document bioinformatics resources

Nucleic Acids Res., 2016; 44(Database issue), D38-D47.

SIB Swiss Institute of Bioinformatics Members

The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases

Nucleic Acids Res., 2016; 44(Database issue), D27-D37.

Moretti S, Laurencyzy B, Gharib WH, Castella B, Kuzniar A, Schabauer H, Studer RA, Valle M, Salamin N, Stockinger H, Robinson-Rechavi M.

Selectome update: quality control and computational improvements to a database of positive selection.

Nucleic Acid Res., 2014; 42(Database issue), D917-D921.

Bernard T, Bridge A, Morgat A, Moretti S, Xenarios I, Pagni M.

Reconciliation of metabolites and biochemical reactions for metabolic networks.

Brief. Bioinformatics, 2014; 15(1), 123-135.

Roux J, Privman E, Moretti S, Daub JT, Robinson-Rechavi M, Keller L.

Patterns of positive selection in seven ant genomes

Molecular Biology and Evolution, 2014; 31(7), 1661-1685.

Piasecka B, Lichocki P, [Moretti S](#), Bergmann S, Robinson-Rechavi M.

The hourglass and the early conservation models - co-existing evolutionary patterns in vertebrate development.

Plos Genetics, 2013; 9(4), e1003476.

Ganter M, Bernard T, [Moretti S](#), Stelling J, Pagni M.

MetaNetX.org: a website and repository for accessing, analyzing, and manipulating metabolic networks.

Bioinformatics, 2013; 29(6), 815-816.

Cohen D, Bogeat-Triboulot MB, Vialet-Chabrand S, Merret R, Courty PE, [Moretti S](#), Bizet F, Guilliot A, Hummel I.

Developmental and Environmental Regulation of Aquaporin Gene Expression across Populus Species: Divergence or Redundancy?

PLoS One, 2013; 8(2), e55506.

Artimo P, Jonnalagedda M, Arnold K, Baratin D, Csardi G, de Castro E, Duvaud S, Flegel V, Fortier A, Gasteiger E, Grosdidier A, Hernandez C, Ioannidis V, Kuznetsov D, Liechti R, [Moretti S](#), Mostaguir K, Redaschi N, Rossier G, Xenarios I, Stockinger H.

ExpASY: SIB bioinformatics resource portal.

Nucleic Acids Res., 2012; 40(Web Server issue), W597-W603.

[Moretti S](#), Murri R, Maffioletti S, Kuzniar A, Castella B, Salamin N, Robinson-Rechavi M, Stockinger H.

gcodeml: A Grid-enabled Tool for Detecting Positive Selection in Biological Evolution.

Studies in Health Technology and Informatics, 2012; 175, 59-68.

Di Tommaso P, [Moretti S](#), Xenarios I, Orobityg M, Montanyola A, Chang JM, Taly JF, Notredame C.

T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension.

Nucleic Acids Res., 2011; 39(Web Server issue), W13-W17.

Kraut A, [Moretti S](#), Robinson-Rechavi M, Stockinger H, Flanders D.

Phylogenetic Code in the Cloud - Can it Meet the Expectations?

Studies in Health Technology and Informatics, 2010; 159, 55-63.

Proux E, Studer RA, [Moretti S](#) and Robinson-Rechavi M.

Selectome: a database of positive selection.

Nucleic Acids Res., 2009; 37(Database issue), D404-D407.

[Moretti S](#), Wilm A, Higgins DG, Xenarios I, Notredame C.

R-Coffee: a web server for accurately aligning noncoding RNA sequences.

Nucleic Acids Res., 2008; 36(Web Server issue), W10-W13.

Bastian F, Parmentier G, Roux J, [Moretti S](#), Laudet V, Robinson-Rechavi M.

Bgee: Integrating and Comparing Heterogeneous Transcriptome Data Among Species.

in DILS: Data Integration in Life Sciences. *Lecture Notes in Computer Science*, 2008; 5109:124-131.

[Moretti S](#), Armougom F, Wallace IM, Higgins DG, Jongeneel CV, Notredame C.

The M-Coffee web server: a meta-method for computing multiple sequence alignments by combining alternative alignment methods.

Nucleic Acids Res., 2007; 35(Web Server issue):W645-8.

Armougom F, Poirot O, Moretti S, Higgins DB, Bucher P, Keduas V, Notredame C.

APDB: a web server to evaluate the accuracy of Multiple Sequence Alignment using Structural Information.

Bioinformatics, 2006; 22(19):2439-40.

Armougom F, Moretti S, Keduas V, Notredame C.

iRMSD, a local measure of sequence alignment accuracy using structural information.

ISMB 2006 - Bioinformatics, 2006; 22(14):e35-9.

Moretti S, Reinier F, Poirot O, Armougom F, Audic S, Keduas V, Notredame C.

Protogene: Turning amino acid alignments into bona-fide CDS nucleotide alignments.

Nucleic Acids Res., 2006; 34(Web Server issue):W600-3.

Armougom F, Moretti S, Poirot O, Audic S, Dumas P, Schaeli B, Keduas V, Notredame C.

Espresso: Automatic incorporation of Structural Information in Multiple Sequence Alignments using 3D-Coffee.

Nucleic Acids Res., 2006; 34(Web Server issue):W604-8.

Ben C, Hewezi T, Jardinaud M-F, Bena F, Ladouce N, Moretti S, Tamborindéguy C, Liboz T, Petitprez M and Gentsbittel L.

Comparative analysis of early embryonic sunflower cDNA libraries.

Plant Mol. Biol., 2005 ;57(2):255-70.

Posters

Moretti S, Armougom F, Saudek V, Notredame C.

Protogene: Turning amino acid alignments into bona-fide CDS nucleotide alignments.

10th Evolutionary Biology Meeting, Marseilles, 2006.

REFEREES

Dr. Cédric NOTREDAME (**CRG/CNRS**)

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Dr. Vladimir Saudek (**Sanofi-Aventis**)

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