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David Bourgais

Objectives

Bioinformatics, Chemoinformatics, Consulting, Project manager

Professional experience

Since September 2010, **Scientist Computational Chemistry**: Galapagos SASU, Romainville, France and Mechelen, Belgium.
November 2005 – July 2010, **bioinformatics/computer science consulting**: BioXpr S.A, Namur, Belgium.
June 2004 – December 2004, **Bioinformatics scientist**: Unité Santé et Environnement du Centre Hospitalier Universitaire Laval, Quebec, Canada.
May 2003 – January 2004, **Bioinformatics/computer science engineer**: Centre d’Analyses Protéomiques, Institut de Biologie Structurale et Microbiologie, Marseille, France.
November 2002 – January 2003, **Computer science technician**: Trophos SA, Marseille, France.

Education

2001 - 2002: **Master in computer science**.
2000 - 2001: Neurobiology diploma.
1999 - 2000: Master in cell biology, Genetics and developmental biology.

Computer science

Operating systems: Linux (Debian, RHEL), Windows Server 2008, Sun Solaris 8, Irix.
Languages: Java (J2EE), C, C++, C#, Perl, R (bioconductor), PHP, PL/SQL, JavaScript, HTML.
RDBMS: Oracle, PostgreSQL, MySQL.
Web servers: Apache, IIS.
Office productivity: Microsoft Office, OpenOffice.
Virtualization: VMWare server, Oracle VirtualBox.
Business reporting: Dotmatics Browser, Vortex, TIBCO Spotfire.

Languages

Technical and scientific English (read, written and spoken, TOEIC, 2002).
Spanish (notions).
Vietnamese (notions).

Extra-professional activities

Web site moderator: www.developpez.com.
Sports: karate, swimming.
International exchange: Vietnam, Canada, Germany, Iceland.

Appendix

Data manager/software developer

- Requirements analysis on Galapagos 3 sites (Mechelen in Belgium, Romainville in France, Leiden in Netherland), expectations and technical specifications writing, solutions propositions.
- Compound logistics: supervision and registering external compounds orders. Data management and technical support to the department.
- DMPK: providing IT resource and software development for automatic reports generation.
- Medicinal chemistry: molecule properties calculation (Fsp3, TPSA, BEI, LE, LLE). Generation of SD file, structure correction.
- Development of a R script to process microarrays from Agilent or Affymetrix. Reporting from this R script to Translational Sciences department for QC, PCA and genes clustering and profiling. Annotation of genes set with GeneOntology and KEGG.
- Solutions development using existent system, writing new queries regarding expectations for an Oracle 10g database, developing new PHP scripts.
- Users training and communication about the development of new functionalities regarding their expectations.
- Servers administrator of Dotmatics software Browser and Vortex :
    - On site software deployment in Mechelen, Belgium, and Romainville, France
    - Screenings projects development for each chemistry teams
    - Users trainings
    - Pivots (SQL) and aggregation functions (Java) writing for Browser software
    - Plug-ins writing for the migration Spotfire -> Vortex (Jython, Java)
    - Dotmatics Users Meetings attendee and speaker (September 2011 and 2012, Bishops Stortford, England), named by Dotmatics as an example for aggregation functions on heterogeneous data by Dotmatics.

Bioinformatics and computer science consulting

- **Bioinformatics Consulting** for BioXpr SA/NV customers (from big pharmaceutical to biotechnology start-up companies, hospitals, universities):
    - Feasibility studies, marketing, specifications report writing
    - Database Administrator: PostgreSQL/MySQL/ORACLE databases management for high data range (BLAST, transcriptomics and proteomics experimental results databases, volumetric access greater than 500 per day), backup strategy development, users management, on-site deployment
    - Project manager: Stand-alone and Web software project driving, analysis studies, developers hiring, developers time management (GANTT chart), AQ, on-site deployment
    - Overall bioinformatics achievements : web portal to bioinformatics services (public or vendors software, own BioXpr software) with authentication (J2EE, PHP)

- **Author** of a stand-alone software to predict nucleotidic probes and primers (PCR, siRNA) using C++ for core software and Java 5 SE for HMI

- **Author** of a stand-alone software to visualize biological molecular networks (interactoms, pathways) using OpenGL for graphical rendering (display lists and Vertex Buffer Objects) and Java 6 SE for general programming. Networks are under XML, MITAB (HUPO PSI-MI) and text format

- **Bioinformatics achievements**:
    - Genomes annotation: database analysis and modeling (UML), database manager and developer using PostgreSQL
    - Proteomics: mass spectrometry analysis using software pipe-line (Perl 5 CGI)

    - Clinical studies: database analysis and modeling (UML) with a constant interaction with project partners (hospital Mont-Godinne, Liège University, Namur University), database manager and developer using PostgreSQL. Web site development to import partners data, visualise data into per patient page and export statistical analysis or data into Excel format (PHP 4 and Java 5 SE). Consulting for statistical analysis using R

- **Business development**:
    - Organisation group member of BeLiveIT days (http://www.beliveit.be), BioXpr evangelist to potential customer during event
    - Assistant member of the Infopole administration committee (http://www.infopole.be)

- **System administration**: Subversion server installation and configuration, Perl 5 script development to manage Subversion client or to backup Subversion repositories

Proteomics research associate

- **Author** of software pipe-line for mass spectrometry processing. The developed LIMS is based on PeptideProphet and ProteinProphet software (Keller et al, personal contact with Andrew Keller) and on ThermoElectron SEQUEST. Processed data are stored into a designed Oracle 9 database under a Sun Solaris 8 OS.

- **Author** of the Namek 0.5 software (GNU General Public License) using Java 1.4.2 SE.

Publications

- **Co-Author**: "PARPs database: a LIMS systems for protein-protein interaction data mining or laboratory information management system", BMC Bioinformatics. 2007 Dec 19;8 : 483.

- **Co-Author:** "*Proteome Profiling of the Epithelial Ovarian Cancer Cell Line TOV-112D"*, Molecular and Cellular Biochemistry, 2005, 275 : 25 – 55.

- **Co-Author:** oral communication *"Proteome Profiling of the Epithelial Ovarian Cancer Cell Line TOV-112D"* Proteome Society, Vancouver, Canada (01/24/2005) and American Association for Cancer Research, Wawaii, USA (01/26/2005).

- **Co-Author:** "Redundant functions but temporal and regional regulation of two alternatively spliced isoforms of semaphorin 3F in the nervous system ", Molecular and Cellular Neurosciences, 2003 Oct;24(2): 409-18.