

Dr Pierre-Yves Dupont

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📄 <http://pydupont.github.io/CV>

PERSONAL

Date of Birth 24/4/1984
Nationality French
Residency New Zealand
Languages French (mother tongue), English (advanced)

EDUCATION

2011: PhD in Computational Biology, INRA, Clermont Ferrand, France

2008: Masters in Computational Biology, Bordeaux University, France, *Class Major*

2007: Bachelor in Computer Sciences, Bordeaux University

2005: Bachelor in Biology, Geology and Earth Sciences, Bordeaux University, Diploma to become biology and geology teacher in high school

POSITIONS

Postdoctoral researcher in computational biology at Massey University, Palmerston North, New Zealand; 2012 – current

Lateral gene transfer in fungi: Identifying the cross-species toolbox for metabolic innovation. This work involves the development of different web applications, scripts and software to analyse and display complex data.

PhD studentship at INRA, Clermont Ferrand, France; 2008 – 2011

Thesis on developing bioinformatics tools to combine information from metabolomics, transcriptomics and promotor studies to characterize metabolic pathways involved in liver cancers. Collaboration with Polytechnic school (Palaiseau, France) to develop software for biological pathway modelling and biochemical dynamics analysis.

Masters Internship at European Institute of Biology and Chemistry, Bordeaux, France; 2008

Evaluation of a docking software (Autodock v.4) and development of an automatic procedure to compute docking of multiple ligands on kinase receptors using a computation cluster.

Bachelor Internship at Bordeaux University, Bordeaux, France; 2007

Development of software for visualisation and detection of internal movements in biomolecules.

SKILLS

Operating systems: Daily use of Windows 7 and 10 computers as well as Linux (Fedora, Ubuntu and Mint) from GUI or CLI. Good command of Mac OS X

Languages and Libraries: Good command of languages Ruby, Python (including Pandas, Matplotlib, Plotly, ScikitLearn and SQLAlchemy) and Java. Common practice of C++, R and Perl and L^AT_EX. Basic knowledge of PHP.

Web technologies: Advanced knowledge of Ruby on Rails. Good practice of HTML5, CSS3 and Javascript (including JQuery and Underscore.js), SQL (MySQL), ZURB Foundation (HTML responsive front-end), Reveal.js (HTML presentation framework)

Modeling and development practices: Good knowledge of UML diagrams, Test Driven Development, Continuous Integration and versioning systems (git, svn, cvs), Docker

SOFTWARE AND DATABASES

Genomic annotation of *Epichloe festucae* E2368 gene models

Publically available at: <http://epichloe.massey.ac.nz>. This Ruby on Rails web application contains functional annotations for all *E. festucae* E2368 gene models. It includes links to major international bioinformatics databases. It is used by international researchers and considered as one of the major tools for studies on fungal endophytes.

Genomic annotation of perennial ryegrass (*Lolium perenne*) gene models

Publically available at: <http://ryegrass.massey.ac.nz>. This Ruby on Rails database contains functional annotations for over 50,000 predicted perennial ryegrass genes.

Hybrid Lineage Transcriptome Explorer (HyLiTE)

Publically available at: <http://sourceforge.net/projects/hylite>. HyLiTE is a software allowing the analysis of high-throughput transcriptome data from allopolyploid species

Geneprom

Geneprom is a Ruby on Rails web application developped during my PhD. It allowed users to study regulatory elements present in gene promoters.

MPSA (Metabolic Pathway Software Analyzer)

This is a Java plugin for VANTED. It allows the integration of data from different biological analysis methods to have a better understanding of metabolic pathways and their regulation.

I also worked on the developement of a proprietary information system for academic research (written in C++) during my PhD. Some more of my work, including the slides of my teaching, can be found in my Sourceforge (<http://sourceforge.net/u/pydupont/profile/>) and Github (<https://github.com/pydupont>) personal pages.

TEACHING

I have been involved in teaching to both undergraduate students and academic staff. I have taught Microarray analysis to third year students at Massey University in 2015 and to medical students in Clermont-Ferrand University, France in 2010 and 2011. I also created an introductory course to Unix and Python programming for Massey University staff (2013-2014). I have given short talks about different topics like SVN and GIT, Ruby on Rails and Lisp.

PUBLICATIONS

Fungal endophyte infection of ryegrass reprogrammes host metabolism and alters development

Dupont PY, Eaton CJ, Wargent JJ, Fechtner S, Solomon P, Schmid J, Day RC, Scott B, Cox MP; New Phytologist; *In press*

*A core gene set describes the molecular basis of mutualism and antagonism in *Epichloë* spp.*

Eaton CJ, **Dupont PY**, Solomon P, Clayton W, Scott B, Cox MP; Molecular Plant-Microbe Interactions; 2015; 28(3):218-231

HyLiTE: accurate and flexible analysis of gene expression in allopolyploid species

Duchemin W, **Dupont PY**, Campbell MA, Ganley A and Cox MP; BMC Bioinformatics, 2015; 16:8

Computational identification of transcriptionally co-regulated genes, validation with the four ANT isoform genes

Dupont PY, Guttin A, Issartel JP, Stepien G; BMC Genomics, 13:482

Computational analysis of the transcriptional regulation of the adenine nucleotide translocator isoform 4 gene and its role in spermatozoid glycolytic metabolism

Dupont PY, Stepien G; Gene, 487(1):38-45

Description and assessment of a model for GSK-3beta database virtual screening

Ventimila N, **Dupont PY**, Laguerre M, Dessolin J; J Enzyme Inhib Med Chem, 25(2):152-7