

Marie-Dominique Devignes

- Background
 - Ecole Normale Supérieure, section Biology, Paris, 1977-1982
 - Agregation in Physiology-Biochemistry, 1980
 - PhD in Molecular Biology, 1982, University Paris VII.
 - Doctorat d'Etat ès Sciences (equivalent to the Habilitation à diriger les Recherches), 1988.
 - Master in Computer Sciences Secondary Proficiency, University Nancy-1, 2001
- Research Associate at CNRS since 1983, she worked at the Institut Jacques Monod in Paris from 1980 to 1989, in
 Charles Auffray's laboratory in Nogent sur Marne then in Villejuif from 1990 to 2001, and since that time at the
 LORIA: Laboratorie Lorrain de Recherche en Informatique et ses Applications in Nancy where she develops
 research in Bioinformatics
- Member of the ORPAILLEUR team (directed by Amedeo Napoli), her research mainly concerns data integration
 and mining for knowledge discovery in the life sciences. Application domains are candidate gene identification for
 complex genetic diseases, pharmacogenomics, protein-protein interactions and drug discovery.
- Coordinator since 2005 of two transversal projects funded by the French government and the Région Lorraine:
 BIOINFO (2005-2006) and MBI ("Modelling of Biomolecules and their Interactions", 2007-2013), including an
 experimental computer platform for sharing resources. More details on http://bioinfo.loria.fr.
- Member since September 2007 of the LORIA Direction Team, in charge of the transversal theme: "Computer Science and Life Sciences".
- Invited in several program committees of international workshops and as an expert for reviewing interdisciplinary PhD theses and applications at the ANR funding agency.
- Co-founder and scientific advisor of a start-up created in 2009: Harmonic Pharma (www.harmonicpharma.com).
- Presently supervising 3 PhD theses with colleagues at the LORIA, Nancy Hospital and IGBMC (Strasbourg).



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Recent publications

- GHEMTIO L, <u>DEVIGNES MD</u>, SMAIL-TABBONE M, SOUCHET M, LEROUX V, and MAIGRET B (2010)
 Comparison of three pre-processing filters efficiency in virtual screening: identification of new putative LXR B regulators as a test case. In press in *Journal of Chemical Information and Modeling*.
- <u>DEVIGNES MD</u>, FRANIATTE P, MESSAI N, NAPOLI A et SMAIL-TABBONE M (2010) BioRegistry: automatic
 extraction of metadata for biological database retrieval and discovery. *International Journal on Metadata, Semantics and Ontologies*, 5: 184-193.
- YILMAZ S, JONVEAUX P, BICEP C, PIERRON L, SMAIL-TABBONE M, <u>DEVIGNES MD</u> (2009) Gene-Disease Relationship Discovery based on Model-driven Data Integration and Database View Definition. *Bioinformatics*, 25:230-236.
- COULET A, SMAIL-TABBONE M, BENLIAN P, NAPOLI A, <u>DEVIGNES MD</u> (2008) Ontology-guided data preparation for discovering genotype-phenotype relationships. *BMC Bioinformatics*, 9 (suppl4), 9 pages.
- COULET A, SMAÏL-TABBONE M, BENLIAN P, NAPOLI A, <u>DEVIGNES MD</u> (2006a) SNP-Converter: an Ontology-Based solution to Reconcile Heterogeneous SNP Descriptions for Pharmacogenomic Studies, *Lecture Notes in Bioinformatics*, 4075: 82-93, Springer.

Book chapters

- COULET A, SMAÏL-TABBONE M, NAPOLI A, and <u>DEVIGNES MD</u> (2010) Ontology-Based Knowledge Discovery in Pharmacogenomics. In press in *Advances in Computational Biology*, book series Advances in Experimental Medicine and Biology, AEMB, Springer.
- DEVIGNES MD et SMAÏL-TABBONE M (2009). Maîtriser les ressources numériques: biologie « in silico ». In Biologie, l'ère numérique. M Roux Ed. Editions du CNRS, Paris, pp199-231.