Patricia Thebault - Curriculum Vitae

DOB : 6 December, 1969
Laboratoire de recherche en Informatique (LaBRI)
University of Bordeaux, FRANCE
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DEGREE

2004   PhD in Bioinformatics, Toulouse University, France
Title : "CSP Formalisms and localization of structured motifs in genomic text".

1996   Master in Computer Science applied to Life Science, Toulouse University, France

1995   Master in Biochemistry, Poitiers University, France

SCIENTIFIC CARREER

Since 2016   co-Director of the International Track BAO (Bioinformatics and Omics) within the master of Bioinformatics of Bordeaux, coolaboration with EUSKAL HERRIKO UNIBERTSITATEA, Spain : **http://master-bioinfo- bordeaux.github.io**

Since 2012   Supervisor of the second year of the Master of Bioinformatics of Bordeaux, France.

2009-2013   Deputy Director of the Centre de Bioinformatique de Bordeaux, France.

2011-2014   Deputy Director of the MaBIOVIS team (Models and algorithms for Bio-informatics and information visualisation), LaBRI, Bordeaux, France.

2008-2014   Lecturer in the ERASMUS teaching exchange with the University of Applied Sciences in Bremen, Germany. (program ISTAB directed by Pr Tilman Achstetter)

Since 2007   Associate Professor in Bioinformatics, University of Bordeaux, France.

2005-2007   Postdoctoral Fellow, Grant INRIA Rhones-Alpes- University LyonI France.

2000-2002   Research engineer at INRA, Toulouse, France.

1998-2000   Research engineer at University Cork College, Cork, Ireland.

RESEARCH AREA

My current research deals with Bioinformatics and biological questions arising from biological networks and sequences. This involves investigations of RNA sequences and metabolic networks. I am

particularly interested in using modelisation to incoporate information resources into computational environments.

Publications and other scientific productions

- 14 papers in peer-reviewed international journals and 3 papers in special reviews Genome Annoucement.
- 3 publications in international conferences in computer science with reviewing committee and proceedings and 3 publications in workshop international conferences in computer science with reviewing committee.
- 5 software platforms: rNAV (RNA Navigator - Visual Exploration of sRNA mediated Regulatory Network), MetaboFlux (Multi-objective and multi-criteria method for flux analysis), Milpat (A structured motif definition based on CSPs and search algorithm), iANT (semi-automatic annotation environment), MIAH (automatic alignment of SSU rRNAs)

PUBLICATIONS

Selected Publications

- Bourqui R, Dutour I, Dubois J, Benchimol W, Thébault P. *rNAV 2.0: a visualization tool for bacterial sRNA-mediated regulatory networks mining,* **2017**. accepted in BMC Bioinformatics
- Sansen J, Thébault P, Dutour I, Bourqui R, "**Visualization of sRNA-mRNA Interaction Predictions**", in Proc. of the 20th International Conference on Information Visualisation (IV'16), pp. 342-347, **2016**.
- Thébault P, Bourqui R, Benchimol W, Gaspin C, Sirand-Pugnet P, Uricaru R, Dutour I. **Advantages of mixing bioinformatics and visualization approaches for analyzing sRNA-mediated regulatory bacterial networks**. Briefings in Bioinformatics. Sep; 16(5): 795–805. **2015**
- Ghozlane A, Bringaud F, Souedan H, Dutour I, Jourdan F and Thébault P. **Flux analysis of the Trypanosoma brucei glycolysis based on a multi-objective criteria bioinformatic approach.** Advances in Bioinformatics, 2012:159423. doi: 10.1155/2012/159423, **2012**
- Lemaitre C, Barré A, Citti C, Tardy F, Thiaucourt F, Sirand-Pugnet P, Thébault P. **A novel substitution matrix fitted to the compositional bias in Mollicutes improves the prediction of homologous relationships**. BMC Bioinformatics. 24;12:457. **2011**

Research articles

- Bourqui R, Dutour I, Dubois J, Benchimol W, Thébault P. *rNAV 2.0: a visualization tool for bacterial sRNA-mediated regulatory networks mining,*. accepted in BMC Bioinformatics, **2017**
- Thébault P, Bourqui R, Benchimol W, Gaspin C, Sirand-Pugnet P, Uricaru R, Dutour I. **Advantages of mixing bioinformatics and visualization approaches for analyzing sRNA-mediated regulatory bacterial networks**. Briefings in Bioinformatics. Sep; 16(5): 795–805. **2015**
- Ghozlane A, Bringaud F, Souedan H, Dutour I, Jourdan F and Thébault P. **Flux analysis of the Trypanosoma brucei glycolysis based on a multi-objective criteria bioinformatic approach.** Advances in Bioinformatics, 2012:159423. doi: 10.1155/2012/159423, **2012**
- Tardy F, Baranowski E, Nouvel LX, Mick V, Manso-Silvàn L, Thiaucourt F, Thébault P, Breton M, Sirand-Pugnet P, Blanchard A, Garnier A, Gibert P, Game Y, Poumarat F, Citti C. **Emergence of atypical Mycoplasma agalactiae strains harboring a new prophage and associated with an alpine wild ungulate mortality episode.** Appl Environ Microbiol. Jul;78(13):4659-68, **2012**
- Dupuy V, Manso-Silván L, Barbe V, Thebault P, Dordet-Frisoni E, Citti C, Poumarat F, Blanchard A, Breton M, Sirand-Pugnet P, Thiaucourt F. **Evolutionary History of Contagious Bovine Pleuropneumonia Using Next Generation Sequencing of Mycoplasma mycoides Subsp. mycoides "Small Colony".** PLoS One.;7(10):e46821. **2012**
- Lemaitre C, Barré A, Citti C, Tardy F, Thiaucourt F, Sirand-Pugnet P, Thébault P. **A novel substitution matrix fitted to the compositional bias in Mollicutes improves the prediction of homologous relationships**. BMC Bioinformatics. 24;12:457. **2011**
- Lacroix V, Cottret L, Thébault P, Sagot MF: **An Introduction to Metabolic Networks and Their**

Structural Analysis. IEEE/ACM Trans. Comput. Biology Bioinform. 5(4): 594-617. **2008**
- Thébault P, DeGivry S, Schiex T and Gaspin C. **Searching RNA motifs and their intermolecular contacts with constraint networks** *Bioinformatics*, 22(17):2074-2080, **2006**.
- Renalier M.H., Joseph S., Gaspin C., Thébault P., and Mougin Héléne. **The tRNA modification Cm56 is catalized either by a specific 2'-O-methylase, or a C/D sRNP upon Archaea.** *RNA journal*. 11(7):1051-63, **2005**
- Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thébault P., Vandenbol M., Weidner S., Galibert F. **Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.** *Proc. Natl. Acad. Sci. U.S.A.*.98:9877-9882, **2001**.
- Galibert *et al*. Science. **The composite genome of the legume symbiont Sinorhizobium meliloti**. *Science*. 293:668-672, **2001**.
- Salanoubat M, *et al. Nature*, 415(6871):497-502, **2002**.
- Thébault P, Monestié P, McGrath A and Higgins D. **MIAH : automatic alignment of eukaryotic SSU rRNAs**. *Bioinformatics* 15(4):341-342, **1999**
- Chetouani F, Monestié P, Thébault P, Gaspin C and Michot B. **ESSA: An integrated and interactive computer tool for analysing RNA secondary structure**. *Nucleic Acids Res.* 25(17) : 3514-3522, **1997**

Peer-reviewed International conferences in computer science with proceedings
- Sansen J, Thébault P, Dutour I, Bourqui R, "**Visualization of sRNA-mRNA Interaction Predictions**", in Proc. of the 20th International Conference on Information Visualisation (IV'16), pp. 342-347, **2016**.
- Dubois J, Ghozlane A, Thébault P, Dutour I, Bourqui R.**"Genome-wide detection of sRNA targets with rNAV", IEEE Symposium on Biological Data Visualization,** BioVis 2013, Proc. BioVis 2013, Atlanta, USA., pp. 81-88, **2013**
- Dubois J, Cottret L, Thebault P, Bringaud F, Ghozlane A, Jourdan F, Auber D and Bourqui R. **Systrip: a visual environment for the investigation of time-series data in the context of metabolic networks. IV 2012,** 16th IEEE international conference on Information Visualisation 8-13th July , Montpellier, France, **2012.**

Invitation to Workshops
- William Benchimol, Patricia Thébault , Thomas Bandres, Jonathan Dubois, Isabelle Dutour, Romain Bourqui. **rNAV, a new software mixing bioinformatics and visualization approaches for analysing bacterial sRNA-mediated regulatory networks**. 6th Bordeaux RNA Club Workshop, June 26-27, **2014**.
- Patricia Thebault, A multi-objective heuristic integrating biological data for flux analysis in metabolic networks, **Open Source Software for Systems, Pathways, Interactions and Networks** (SPIN-OSS) retreat being held at the Wellcome Trust Genome Campus, EBI, England, 14-16´November **2012**.
- Patricia Thebault, Outils Bioinformatiques dédiés à la prédiction de cibles de petits ARNs : Application à des données de RNA-SEQ de *Mycoplasma pneumoniae*. **RNA CLUB**, Institut Européen de Chimie et Biologie (IECB), Bordeaux, France, 30 sept **2010**.