

Jérôme WALDISPÜHL
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Research Interests

Modeling and predicting the folding of protein and RNAs, formal language theory, dynamic programming, transmembrane proteins, mutant RNAs, thermodynamics, statistical mechanics, evolution.

Current position

Since Jul. 2006 Instructor in Applied Mathematics, Massachusetts Institute of Technology.
Visiting appointment in the Department of Computer Science (CSAIL).

Education

November 2004 **PhD in Computer Science** with honors.
École Polytechnique (France)
Title: "Modeling and Predicting the Structure of Transmembrane Proteins"
Supervisor: Jean-Marc Steyaert.
Referees: Peter Clote, Marie-France Sagot.
Committee: Christian Choffrut (Chair), Alessandra Carbone, Philippe Dessen, Thomas Simonson.

July 2000 **M.S. in Computer Science** with honors.
École Polytechnique, E.N.S Ulm & Cachan, Universities of Paris 6, 7 & 11
Majors: computer algebra, algorithm analysis, combinatorics
M.S. thesis: "Analysis of Combinatorial Properties of Protein Folding".
Supervisor: Jean-Marc Steyaert.

June 1999 **B.S. in Mathematics** with honors.
University of Nice and Sophia-Antipolis (France)
Algebra, complex analysis, differential calculus, geometry, numerical analysis, probability, statistics, topology
B.S. thesis: "Ehrhart Polynomial, Cooccurrence Matrices and imagery".
Supervisor: Loïc Pottier.

Experience

Since Jul.2006 Instructor in Applied Mathematics, M.I.T.
Since Oct.2005 Postdoctoral Associate in Computer Science, M.I.T.
Jan.2005-Jun.2006 Postdoctoral Associate, Department of Biology, Boston College.
2003-2004 Instructor in Computer Science, University of Paris 7 (France).
2000-2003 Teaching assistant in Computer Science, École Polytechnique (France).

Awards and Honors

2000-2003 PhD Fellowship from the French Ministry for Research,
2000-2003 Teaching Fellowship (monitorat) from the Academy of Versailles (France),
1999-2000 Master Fellowship from the University of Paris 7 (France).

Research

Publications

Journal Articles:

- **J. Waldispühl***, S. Devadas, B. Berger and P. Clote*,
RNAmutants: a web server to explore the mutational landscape of RNA secondary structures,
Nucleic Acids Research, Web Server issue, *in press*.
(* authors equally contributed)
- **J. Waldispühl**, S. Devadas, B. Berger and P. Clote,
Efficient Algorithms for Probing the RNA Mutation Landscape,
PLoS Computational Biology, 4(8):e1000124, 2008 Aug. ISSN 1553-7358 (Electronic).
- **J. Waldispühl***, C.W. O'Donnell*, S. Devadas, P. Clote and B. Berger,
Modeling Ensembles of Transmembrane β -barrel Proteins,
PROTEINS: Structure, Function and Bioinformatics, vol. 71, Issue 3, p. 1097-1112, 2008.
(* authors equally contributed)
- **J. Waldispühl** and P. Clote,
Computing the partition function and sampling for saturated secondary structures of RNA, with
respect to the Turner energy model,
Journal of Computational Biology, Vol. 14, No. 2, p. 190-215, 2007.
- **J. Waldispühl**, B. Berger, P. Clote and J.-M. Steyaert,
Predicting Transmembrane β -barrel and Inter-strand residue interactions from Sequence
PROTEINS: Structure, Function and Bioinformatics, vol. 65, issue 1, p. 61-74, 2006.
- **J. Waldispühl**, B. Berger, P. Clote and J.-M. Steyaert,
transFold: A web Server for Predicting the Structure and Residue Contacts of Transmembrane
 β -barrels,
Nucleic Acids Research, vol. 34, Web Server issue, p. W189-W193, 2006.
- P. Clote, **J. Waldispühl**, B. Behzadi and J.-M. Steyaert,
Energy landscape of k-point mutants of an RNA molecule,
Bioinformatics Vol. 21, p. 4140-4147, 2005.
- **J. Waldispühl** and J.-M. Steyaert,
Modeling and Predicting All- α Transmembrane Proteins Including Helix-helix Pairing.
Theoretical Computer Science, special issue on Pattern Discovery in the Post Genome, p. 67-92,
2005.

Peer-refereed Proceedings (proceedings published in journal):

- **J. Waldispühl**, C.W. O'Donnell, S. Will, S. Devadas, R. Backofen and B. Berger,
Simultaneous Alignment and Folding of Proteins,
13th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009),
Lecture Notes in Computer Science, Research in Computational Molecular Biology, p. 339-355, 2009.
- **J. Waldispühl**, B. Behzadi and J.-M. Steyaert,
An Approximate Matching Algorithm for Finding (Sub-)Optimal Sequences in S-attributed Grammars,
First European Conference on Computational Biology (ECCB 2002),
Bioinformatics Vol. 18, p. 250-259, 2002.

Patent:

- **J. Waldispühl** and J.-M. Steyaert,
Method for modelling three-dimensional topological structures of a protein,
Publication Number: WO/2006/032949, Publication Date: 30.03.2006, International Filing Date: 24.09.2004.

Softwares and Web Servers:

- RNAmutants* Algorithms for studying the RNA mutation landscape,
Download: <http://RNAmutants.csail.mit.edu>,
Web Server: <http://bioinformatics.bc.edu/clotelab/RNAmutants/>,
- partiFold* Structure prediction of transmembrane proteins (previously *transFold*),
Web Server: <http://partifold.csail.mit.edu/>,
- RNAstat* Boltzmann partition function computing and rational sampling of RNA locally optimal structures
- amsag2c* Automatic generation of the approximate parsing algorithm AMSAG.

Poster Papers:

- **J. Waldispühl**, S. Devadas, B. Berger and P. Clote,
Efficient algorithms for probing the RNA mutation landscape & prediction of deleterious mutations,
Poster at the RNA in Biology, Bioengineering and Nanotechnology workshop at the Institute of Mathematics and Application, Minneapolis, USA.
- **J. Waldispühl**, C.W. O'Donnell, N. Palmer, S. Devadas, P. Clote and B. Berger,
Modeling Ensemble of Transmembrane β -barrels,
Poster at the 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2007), Vienna, Austria.
- **J. Waldispühl**, B. Berger, P. Clote and J.-M. Steyaert
Predicting Transmembrane β -barrels and Inter-strand residue interactions from Sequence: Application to OmpA of *E. Coli*,
Poster at 2006 Merck/MIT annual meeting, Cambridge, USA.
- **J. Waldispühl** and P. Clote,
A study of the Energy Landscape of RNA,
Poster at the Ninth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2005), Cambridge, USA.
- **J. Waldispühl** and J.-M. Steyaert,
Modeling and Predicting All- α transmembrane Proteins,
Poster at the second European Conference on Computational Biology (ECCB 2003), Paris, France.
- B. Behzadi, **J. Waldispühl** and J.-M. Steyaert,
Can RNA Super-Optimal Structure improve predictions?
Poster at the first Belgium Bioinformatics Conference (BBC 2003), Louvain, Belgium.
- **J. Waldispühl** and J.-M. Steyaert,
Modeling Membrane Protein Structures with S-attribute Grammars,
Poster at the "troisièmes Journées Ouvertes en Biologie Informatique et Mathématiques" (JOBIM 2002), Saint-Malo, France.

Others:

- Modeling and Predicting the Structure of Transmembrane Proteins, PhD thesis, École Polytechnique, November 2004.
- A Study of Combinatorial Properties of Protein Folding, M.S. thesis, École Polytechnique, July 2000.
- Erhart Polynomial, Cooccurrence Matrices and Applications to Medical Imaging, B.S. thesis, University of Nice and Sophia-antipolis, July 1999.

Talks

International Conferences:

1. **May 2009:**
13th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009), Tucson AZ.
"Simultaneous Alignment and Folding of Protein Sequences"
2. **July 2008:**
13th Annual Meeting of the RNA society, Berlin, Germany.
"Algorithms for Exploring the Mutation Landscape of RNA Molecules".
3. **December 2005:**
LIX Symposium: Bioinformatics: algorithms, structures and statistics, Palaiseau, France.
"Predicting Transmembrane β -barrel and Inter-strand residue interactions from Sequence"
4. **November 2002:**
First European Conference on Computational Biology (ECCB 2002), Saarbrücken, Germany.
"An Approximate Matching Algorithm for Finding (Sub-)Optimal Sequences in S-attributed Grammars"

International Workshops:

1. **July 2008:**
4th RNA Ontology Consortium meeting, Berlin, Germany.
"Representation and meaning of multiple sequence alignments using RNAmutants".
2. **January 2008:**
IMA Annual Program Year Workshop on Protein Folding, Minneapolis, USA.
"Modeling Ensembles of Transmembrane β -barrel Proteins".
3. **July 2006:**
Computational approaches to functional and regulatory RNAs, Benasque, Spain.
" k -point mutants and k -superoptimal secondary structures"

National Workshops:

1. **March 2003:**
Annual meeting of the inter-disciplinary group on RNA (AReNA) Orsay, France.
"AMSAG: A approximate parsing algorithm for S-attribute Grammars and Application to the prediction of RNA secondary structures"

2. **January 2003:**
Annual IMPG meeting "Functional Bioinformatics and genetic regulation systems", Marseille-Luminy, France.
"Modeling and Predicting All- α Transmembrane Proteins with Multi-tape S-attribute Grammars"

Seminars:

1. **March 23, 2009:** Biozentrum, University of Basel, Basel, Switzerland.
"Ensemble Predictions of RNA and Protein Structures"
2. **March 11, 2009:** Symposium of the Cluster of Excellence "Multimodal Computing and Interaction", Saarland University, Saarbrücken, Germany.
"Ensemble Predictions of RNA and Protein Structures"
3. **February 23, 2009:** School of Computer Science, McGill University, Montreal, Canada.
"Ensemble Predictions of RNA and Protein Structures"
4. **November 2008:** IRIC, University of Montreal, Montreal, Canada.
"Modeling Structural Ensemble of Transmembrane Proteins".
5. **November 2008:** Computer Science Department, Brown University, Providence, USA.
"Ensemble-based computational structure modeling".
6. **May 2008:** Computer Science Department (LRI), Université Paris-Sud, Orsay, France.
"Algorithms for Exploring the Mutation Landscape of RNA Molecules".
7. **April 2008:** Computer science department, Tufts, Medford, USA.
"Algorithms for Exploring the Mutation Landscape of RNA Molecules".
8. **March 2008:** Computer science laboratory, MIT, Cambridge, USA.
"Algorithms for Exploring the Mutation Landscape of RNA Molecules".
9. **March 2006:** Applied mathematics department, MIT, Cambridge, USA.
"Modeling and Predicting the structure of Transmembrane Proteins"
10. **March 2006:** Department of Biology, Carleton University, Ottawa, Canada.
"Structural Bioinformatics : Tools and Methods to understand the folding of Biological Sequences"
11. **December 2005:** Department of Biology, Boston College, Chestnut Hill, USA.
"Predicting Transmembrane β -barrel and Inter-strand residue interactions from Sequence"
12. **October 2005:** Computer science laboratory, MIT, Cambridge, USA.
"Energy landscape of k-point mutants of an RNA molecule"
13. **May 2005:** Computer Science Department (LRI), Université Paris-Sud, Orsay, France.
"Structural Bioinformatics : Tools and Methods to understand the folding of Biological Sequences"
14. **March 2005:** Computer science laboratory, MIT, Cambridge, USA.
"Modeling and Predicting the structure of Transmembrane Proteins"
15. **April 2004:** Computer Science Department, Université Paris 7 Diderot, Paris, France.
"Modeling the secondary structure of RNA with pseudo-knots"
16. **September 2003:** Computer Science Department, Université Paris 7 Diderot, Paris, France.
"Reconstructing NMR data"

17. **July 2003:** Bioinformatics Research Center, University of Glasgow, Glasgow, UK.
“Modeling and Predicting All- α Transmembrane Proteins”
18. **February 2003:** Computer Science Department, Université Paris 7 Diderot, Paris, France.
“Modeling and Predicting All- α Transmembrane Proteins with Multi-tape S-attribute Grammars”
19. **July 2002:** French Atomic Energy Commission, Orsay, France.
“Modeling All- α Transmembrane Proteins with S-attribute Grammars”
20. **November 2001:** Computer Science Department (LRI), Université Paris-Sud, Orsay, France.
“Modeling Membrane Protein Structures with S-attribute Grammars”

Others activities

- Referee for the journals "Bioinformatics", "Journal of Computational Biology", "Theoretical Computer Science", "Journal of Mathematical Biology", "in-silico biology", "IEEE/ACM Transactions on Computational Biology and Bioinformatics" and "Journal of Molecular Biology", and the conferences "ISMB 2007", "RECOMB 2006", "ICALP 2002".
- Organizing committee of the LIX symposium: "Bioinformatics: algorithms, structures and statistics", Palaiseau, December 2005.
- PhD student representative, computer science department council, École Polytechnique, Palaiseau, France, 2003-2005.
- Chief of the technical staff, South West European Regional programming Contest of ACM, École Polytechnique, Palaiseau, France, November 2004.
- Member of the technical staff, South West European Regional programming Contest of ACM, École Polytechnique, Palaiseau, France, November 2003.
- École Polytechnique PhD student representative, Academy of Versailles, France, 2001-2002.
- Organizing committee of the LIX Bioinformatics workshop, Palaiseau, December 2002.

Teachings

Description

- 2008-2009 **Foundation of Computational Structural Biology (18.417)**
Graduate course in mathematics department of M.I.T. (lecturer)
15 students, 40 hours
Single variable calculus (18.01)
Undergraduate course in the mathematics department of M.I.T.
40 students, 100 hours
- 2007-2008 **Foundation of Computational Structural Biology (18.417)**
Graduate course in mathematics department of M.I.T. (lecturer)
10 students, 40 hours
Multivariable calculus (18.02)
Undergraduate course in the mathematics department of M.I.T.
40 students, 100 hours
- 2006-2007 **Foundation of Computational Structural Biology (18.417)**
Graduate course in mathematics department of M.I.T. (lecturer)
15 students, 40 hours
Single variable calculus (18.01)
Undergraduate course in the mathematics department of M.I.T.
40 students, 100 hours
- 2004-2005 **Programming in Java**
B.S. in Mathematics and Computer Science (3rd year) of the University of Paris 7 Diderot
20 students, 45 hours
Introduction to programming
B.S. in Computer Science (1st year) of the University of Paris 7 Diderot
25 students, 30 hours
C Programming
B.S. in Computer Science (4th year) of the École Polytechnique
25 students, 20 hours
- 2003-2004 **Algorithmic and Programming in Java**
B.S. in Computer Science (3rd year) of the École Polytechnique
25 students, 40 hours
C Programming
B.S. in Computer Science (4th year) of the École Polytechnique
25 students, 20 hours
Unix System Programming
B.S. in Computer Science (3rd year) of the University of Paris 7 Diderot
30 students, 20 hours
Theory of Computation
B.S. in Computer Science (4th year) of the University of Paris 7 Diderot
15 students, 24 hours

Advanced C Programming

B.S. in Bioinformatics (4th year) of the University of Paris 7 Diderot
15 students, 24 hours

Automata's & Formal Languages

B.S. in Bioinformatics (3rd year) of the University of Paris 7 Diderot
30 students, 20 hours

2002-2003

Algorithmic and Programming in Java

B.S. in Computer Science (3rd year) of the École Polytechnique
25 students, 40 hours

C Programming

B.S. in Computer Science (4th year) of the École Polytechnique
25 students, 30 hours

2001-2002

Algorithmic and Programming in Java

B.S. in Computer Science (3rd year) of the École Polytechnique
25 students, 40 hours

Scientific Programming with Scilab

B.S. in Computer Science (4th year) of the École Polytechnique
20 students, 10 hours

C Programming

B.S. in Computer Science (4th year) of the École Polytechnique
25 students, 20 hours

2000-2001

Algorithmic and Programming in Java

B.S. in Computer Science (3rd year) of the École Polytechnique
25 students, 80 hours

Bioinformatics

B.S. in Biology (4rd year) of the École Polytechnique
25 students, 4 hours

Bioinformatics Project Coordinator

B.S. in Computer Science (3rd year) of the École Polytechnique
40 students, 20 hours

Summary

By teaching level:

Type	1st-2nd years	3rd year	4th year	Grad.	Total
Lectures	-	75 h.	124 h.	120 h.	319 h.
Recitations	330 h.	200 h.	38 h.	-	568 h.
Project	-	20 h.	-	-	20 h.
Total	330 h.	245 h.	162 h.	120 h.	907 h.

By topic:

course	1st-2nd years	3rd year	4th year	Grad.
Algorithmic	-	200 h.	-	-
C Programming	-	-	124 h.	-
Theory of Computation	-	-	24 h.	-
Calculus	300 h.	-	-	-
Bioinformatics	-	-	-	120 h.
Formal Languages	-	20 h.	-	-
Java Programming	30 h.	55 h.	-	-
Unix Programming	-	20 h.	-	-
Others	-	-	14 h.	-

References

Prof. Bonnie Berger,
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Massachusetts Institute of Technology
Cambridge, MA 02139, USA
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Fax: (617) 253-5429.
Email: bab@mit.edu.

Prof. Srinivas Devadas,
Computer Science and AI Lab,
Massachusetts Institute of Technology,
Cambridge, MA 02139, USA.
Phone: (617) 253-0454.
Fax: (617) 253-6652.
Email: devadas@mit.edu.

Prof. Peter Clote,
Department of Biology,
Boston College,
Chestnut Hill, MA 02467, USA.
Phone: (617) 552-1332.
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