



Bartosz Wilczyński  
Obrońców Tobruku 32/2  
01-494 Warszawa  
bartek@mimuw.edu.pl  
<http://www.mimuw.edu.pl/~bartek>

Warszawa, August 17th, 2010

# Curriculum Vitae

## *Personal information*

Date of birth	July, 30th, 1979
Place of birth	Częstochowa, Poland
Work address	Banacha 2 02-097 Warszawa
Marital status	married, 2 children
Nationality	Polish

## *Education*

2003–2008	Ph.D. in Mathematics (with honours), Institute of Mathematics, Polish Academy of Sciences
1998–2003	M.Sc. in Computer Science, University of Warsaw, College of Inter-Faculty Individual Studies in Mathematics and Natural Sciences (MISMaP).

## *Professional experience*

II 2010–	Assistant professor, <i>Institute of Informatics</i> , University of Warsaw.
IV 2008–II 2010	Post doctoral fellow, <i>European Molecular Biology Laboratory</i> , Heidelberg, Germany.
X 2003–II 2008	Graduate student, <i>Institute of Mathematics, Polish Academy of Sciences</i> , Warsaw, Poland.
X 2002–VIII 2003	Research scholar, <i>Lawrence Livermore National Laboratory</i> , Livermore, USA.

## *Awards*

2007–2008	Stipend for young researchers in the Start programme of the Foundation for Polish Science.
2008	Distinction of the PhD thesis

## *Participation in research projects*

Participant in the following projects funded by the Polish Ministry of Science and Higher Education:

3 T11F 021 28	Algorithmic and computational problems in bioinformatics, 2005-2007
3 T11F 022 29	Mathematical models of gene regulatory networks, 2005-2007
N N301 065236	Algorithmic problems in Systems Biology and Bioinformatics, 2008-

## *Peer reviewed publications*

2010	<ul style="list-style-type: none"><li>• <b>Dynamic CRM occupancy reflects a temporal map of developmental progression</b>, Bartek Wilczynski, Eileen EM Furlong, <i>Molecular Systems Biology</i> 6:383</li></ul>
------	---

## (continued)

- **Challenges for modeling global gene regulatory networks during development: Insights from Drosophila**, *Bartek Wilczynski, Eileen EM Furlong*, *Developmental Biology* 340(2):161-169 (review)
- 2009 • **Finding evolutionarily conserved cis-regulatory modules with a universal set of motifs**, *Bartek Wilczynski, Norbert Dojer, Mateusz Patalak and Jerzy Tiuryn*, *BMC Bioinformatics* 2009, 10:82
- **Biopython: freely available Python tools for computational molecular biology and bioinformatics**, *Peter J. A. Cock, Tiago Antao, Jeffrey T. Chang, Brad A. Chapman, Cymon J. Cox, Andrew Dalke, Iddo Friedberg, Thomas Hamelryck, Frank Knauff, Bartek Wilczynski, Michiel J.L. de Hoon*, *Bioinformatics* 2009 25(11):1422-1423 (application note)
- **BNFinder: Exact and efficient method for learning Bayesian networks**, *Bartek Wilczynski, Norbert Dojer*, *Bioinformatics* 2009 25(2):286-287 (application note)
- 2008 • **A Stochastic Extension of R.Thomas Regulatory Network Modelling**, *Bartek Wilczyński*, *Banach Center Publications* 80 (2008), 271-276
- 2007 • **Reconstruction of Mammalian Cell Cycle Regulatory Network from Microarray Data using Stochastic Logical Networks**, *Bartek Wilczyński, Jerzy Tiuryn*, *Lecture Notes in Bioinformatics* 4695:121-135, ed. Calder and Gilmore
- 2006 • **Applying Dynamic Bayesian Networks to Perturbed Gene Expression Data**, *Norbert Dojer, Anna Gambin, Bartek Wilczyński, Jerzy Tiuryn*, *BMC Bioinformatics*, 2006, 7:249.
- **Using local gene expression similarities to discover regulatory binding site modules** *B. Wilczyński, TR. Hvidsten, A.Kryshtafovych, J. Tiuryn, J. Komorowski, K. Fidelis*, *BMC Bioinformatics* 2006, 7:505
- **Regulatory Network Reconstruction using Stochastic Logical Networks**, *Bartek Wilczyński, Jerzy Tiuryn*, *Lecture Notes in Bioinformatics* 4210:145-157, ed. Priami C.
- **Automated modeling of genetic control in Arabidopsis thaliana**, *Anna Gambin, Katarzyna Bozek, Bartek Wilczyński, Jerzy Tiuryn*, *Journal of Fruit and ornamental plant research*, 2006, XIV(Supp. 1):163-171
- 2005 • **Discovering regulatory binding site modules using rule-based learning**, *T.R. Hvidsten, B. Wilczyński, A. Kryshtafovych, J. Komorowski and K. Fidelis*, *Genome Research*, 15:856-866, 2005.
- 2003 • **A rule-based framework for gene regulation pathways discovery**, *B.Wilczyński, T.R. Hvidsten, A. Kryshtafovych, L. Stubbs, J. Komorowski, K. Fidelis*, *Computational Systems Bioinformatics* 2003: 435-436, Stanford, 11-14. August, 2003. (short paper)

### *Theses*

- 2007 Stochastic Logical Networks: a mathematical framework for regulatory network reconstruction, *Doctoral dissertation*, Institute of Mathematics, PAS.
- 2003 Probabilistic model for DNA-chip probe design (in Polish), *M.Sc. thesis*, University of Warsaw.

### *Scientific software development*

- Biopython → member of the core development team of Biopython, a widely used (>100 citations) collection of software libraries useful in Bioinformatics (<http://biopython.org>)

## (continued)

- BNfinder → main developer of BNfinder, a fast implementation of an exact algorithm for finding the structure of dynamic and static Bayesian Networks. (<http://bioputer.mimuw.edu.pl/software/bnf>)
- MEMOfinder → architect and maintainer of MetaMotifFinder, a meta-server for *de novo* motif finding in DNA sequences. (<http://bioputer.mimuw.edu.pl/software/mmf>)
- BIAS → main developer of the BioInformatic Application Server (BIAS), a tool facilitating deployment of scientific applications as webservice. Used to generate www interfaces for BNfinder and MEMOfinder. (<https://launchpad.net/bias>)
- ReNe → sole developer of the ReNe library for reconstruction of regulatory networks using Stochastic Logical Networks, using Hidden Markov Models. Fully described in the PhD thesis.