

## Miklós Csűrös

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AUGUST 14, 2013

### Education

**Ph. D. Computer Science**, Yale University, December 2000.

Advisors: Dana Angluin and Ming-Yang Kao.

Dissertation title: *Reconstructing Phylogenies in Markov Models of Evolution*.

**M. Phil. Computer Science**, Yale University, May 1997.

**M. Sc. & B. Sc. Electrical Engineering**, Technical University of Budapest (now called Budapest University of Technology and Economics), Hungary, July 1994.

Advisor: Gábor Lugosi

Thesis title: *Fast Algorithms in Computational Learning Theory*

Semester at Vienna University of Technology, Austria, Spring 1993.

Semester at Compiègne University of Technology, France, Fall 1990.

## Academic and professional experience

**Université de Montréal**, Department of Computer Science and Operations Research, Associate Professor with tenure (*professeur agrégé*) since June 2007; Assistant Professor (*professeur adjoint*), August 2001–May 2007.

**Rényi Institute of Mathematics**, Budapest, Hungary. Marie-Curie Transfer-of-Knowledge Visiting Experienced Researcher, May–July 2009 and September–December 2007.

**Collegium Budapest Institute for Advanced Study**, Budapest, Hungary. In-house Fellow, October 2007–July 2008.

**National Center for Biotechnology Information**, National Library of Medicine, National Institutes of Health, Bethesda, Md., USA. Visiting Researcher, May–June 2007.

**Institut National de Recherche en Informatique et en Automatique**, INRIA-Lorraine, Nancy, France. Visiting Researcher, June 2005.

**Baylor College of Medicine**, Human Genome Sequencing Center. Senior Technical Consultant, June–August 2001.

**Omixon/Chemistry Logic LLC**, Hungary. Scientific Consultant, 2009–2011.

**Genometrix, Inc.**, The Woodlands, Texas. Bioinformatics Department, Scientist, May 2000–May 2001.

**Curagen Corp.**, New Haven, Conn. Bioinformatics Department, Senior Software Developer, March–July 1999; Programmer, Summer 1997 and Summer 1996.

## Publications

### Manuscript under review

- [M1] M. Csűrös. Ambiguous inference of identity coefficients from independent biallelic loci, 2013. <http://www.iro.umontreal.ca/~csuros/papers/coancestry-identifiability.pdf>

### Journal articles

- [J2] H. Luo, M. Csűrös, A. L. Hughes and M. A. Moran. Evolution of divergent life history strategies in marine Alphaproteobacteria. *mBio*, **4**(4):e00373-13, 2013. DOI:10.1128/mBio.00373-13.
- [J3] E. Bareke, V. Saillour, J.-F. Spinella, R. Vidal, J. Healy, D. Sinnett and M. Csűrös. Joint genotype inference with germline and somatic mutations. *BMC Bioinformatics*, **14**(Suppl 5):S3, 2013. (Proceedings of the *Third RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-SEQ)*; 29 articles accepted from 41 submissions.) DOI:10.1186/1471-2105-14-S5-S3.
- [J4] E. V. Koonin, M. Csűrös and I. B. Rogozin. Whence genes in pieces: reconstruction of the exon-intron gene structures of the last eukaryotic common ancestor and other ancestral eukaryotes. [Review article] *WIREs RNA*, **4**:93–105, 2013. [1 citation] DOI:10.1002/wrna.1143.
- [J5] I. B. Rogozin, L. Carmel, M. Csűrös and E. V. Koonin. Origin and evolution of spliceosomal introns. [Review article] *Biology Direct*, **7**:11, 2012. [8 citations] DOI:10.1186/1745-6150-7-11.
- [J6] D. Chernikova, S. Motamedi, M. Csűrös, E. V. Koonin and I. B. Rogozin. A late origin of the extant eukaryotic diversity: divergence time estimates using rare genomic changes. *Biology Direct*, **6**:26, 2011. [Highly accessed] [10 citations] DOI:10.1186/1745-6150-6-26.
- [J7] M. Csűrös, I. B. Rogozin and E. V. Koonin. A detailed history of intron-rich eukaryotic ancestors inferred from a global survey of 100 complete genomes. *PLoS Computational Biology*, **7**(9):e1002150, 2011. [16 citations] DOI:10.1371/journal.pcbi.1002150.
- [J8] M. Csűrös. Count: evolutionary analysis of phylogenetic profiles with parsimony and likelihood. [Application note] *Bioinformatics*, **26**(15):1910–1912, 2010. [13 citations] DOI:10.1093/bioinformatics/btq315.

- [J9] M. Csűrös and I. Miklós. Streamlining and large ancestral genomes in Archaea inferred with a phylogenetic birth-and-death model. *Molecular Biology and Evolution*, **26**(9): 2087–2095, 2009. [32 citations] DOI:10.1093/molbev/msp123.
- [J10] I. B. Rogozin, M. K. Basu, M. Csűrös and E. V. Koonin. Analysis of rare genomic changes does not support the unikont-bikont phylogeny and suggests cyanobacterial symbiosis as the point of primary radiation of eukaryotes. *Genome Biology and Evolution*, **1**:99–113, 2009. [23 citations] DOI:10.1093/gbe/evp011.
- [J11] M. Csűrös. Malin: maximum likelihood analysis of intron evolution in eukaryotes. [Application note] *Bioinformatics*, **24**(13):1538–1539, 2008. [9 citations] DOI:10.1093/bioinformatics/btn226.
- [J12] M. Csűrös, I. B. Rogozin and E. V. Koonin. Extremely intron-rich genes in the alveolate ancestors inferred with a flexible maximum likelihood approach. *Molecular Biology and Evolution*, **25**(5):903–911, 2008. [18 citations] DOI:10.1093/molbev/msn039.
- [J13] I. B. Rogozin, K. Thomson, M. Csűrös, L. Carmel and E. V. Koonin. Homoplasy in genome-wide analysis of rare amino acid replacements: the molecular-evolutionary basis for Vavilov’s law of homologous series. *Biology Direct*, **3**:7, 2008. [11 citations] DOI:10.1186/1745-6150-3-7.
- [J14] M. Csűrös, L. Noé and G. Kucherov. Reconsidering the significance of genomic word frequencies. [Genome analysis] *Trends in Genetics*, **23**(11):543–546, 2007. [10 citations] DOI:10.1016/j.tig.2007.07.008.
- [J15] M. Csűrös, J. A. Holey and I. B. Rogozin. In search of lost introns. *Bioinformatics*, **23**(13):i87–i96, 2007. [11 citations] DOI:10.1093/bioinformatics/btm190. (Proceedings of the *Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology & Sixth European Conference on Computational Biology (ISMB/ECCB)*; 66 articles accepted from 418 submissions.)
- [J16] M. Csűrös and B. Ma. Rapid homology search with neighbor seeds. *Algorithmica*, **48**(2):187–202, 2007. [5 citations] DOI:10.1007/s00453-007-0062-y.
- [J17] Rhesus Macaque Genome Sequencing and Analysis Consortium. Evolutionary and biomedical insights from the Rhesus macaque genome. *Science*, **316**(5822):222–234, 2007. [505 citations] DOI:10.1126/science.1139247.
- [J18] A. V. Sverdlov, M. Csűrös, I. B. Rogozin and E. V. Koonin. A glimpse of a putative pre-intron phase of eukaryotic evolution. [Genome analysis] *Trends in Genetics*, **23**(3):105–108, 2007. [7 citations] DOI:10.1016/j.tig.2007.01.001

- [J19] The Honey Bee Genome Sequencing Consortium. Insights into social insects from the genome of the honeybee *Apis mellifera*. *Nature*, **443**:931–949, 2006. [654 citations] DOI:10.1038/nature05260.
- [J20] M. Csűrös. On the estimation of intron evolution. [Correspondence.] *PLoS Computational Biology*, **2**(7):e84, 2006. [5 citations] DOI:10.1371/journal.pcbi.0020084.
- [J21] M. Csűrös and I. Miklós. Statistical alignment of retropseudogenes and their functional paralogs. *Molecular Biology and Evolution*, **22**(12):2457–2471, 2005. [2 citations] DOI:10.1093/molbev/msi238.
- [J22] M. Csűrös and M. Ruzinkó. Single-user tracing and disjointly superimposed codes. *IEEE Transactions on Information Theory*, **51**(4):1606–1611, 2005. [5 citations] DOI:10.1109/TIT.2005.844097.
- [J23] A. Milosavljevic, R. A. Harris, E. J. Sodergren, A. R. Jackson, K. J. Kalafus, A. Hodgson, A. Cree, M. Csűrös, B. Zhu, P. J. de Jong, G. M. Weinstock and R. A. Gibbs. Pooled Genomic Indexing of Rhesus macaque. *Genome Research*, **15**(2):292–301, 2005. [7 citations] DOI:10.1101/gr.3162505.
- [J24] M. Csűrös. Maximum-scoring segment sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **1**(4):139–150, 2004. [3 citations] DOI:10.1109/TCBB.2004.43.
- [J25] M. Csűrös and A. Milosavljevic. Pooled genomic indexing (PGI): analysis and design of experiments. *Journal of Computational Biology*, **11**(5):1001–1021, 2004. [4 citations] DOI:10.1089/cmb.2004.11.1001.
- [J26] A. Milosavljevic, M. Csűrös, G. Weinstock and R. A. Gibbs. Shotgun sequencing, clone pooling, and comparative strategies for mapping and sequencing. *TARGETS: Applications of Genomics and Proteomics*, **2**(6):245–252, 2003. [Review article] DOI:10.1016/S1477-3627(03)02379-1. TARGETS is a peer-reviewed journal; its main readership is the drug industry. It has been published under the name *Drug Discovery Today: TARGETS* since 2004.
- [J27] M. Csűrös. Fast recovery of evolutionary trees with thousands of nodes. *Journal of Computational Biology*, **9**:277–297, 2002. [28 citations] DOI:10.1089/10665270252935467.
- [J28] M. Csűrös and M.-Y. Kao. Provably fast and accurate recovery of evolutionary trees through Harmonic Greedy Triplets. *SIAM Journal on Computing*, **31**:306–322, 2001. [10 citations] DOI:10.1137/S009753970037905X.

**Book chapter**

- [BC29] M. Csűrös. How to infer ancestral genome features by parsimony: dynamic programming over an evolutionary tree. In C. Chauve, N. El-Mabrouk and E. Tannier (Eds.), Springer-Verlag, 2013. Forthcoming.
- [BC30] M. Csűrös. Distance-based phylogeny reconstruction (fast-converging). 2 pages. Entry in M.-Y. Kao et al. (Eds.) *Encyclopedia of Algorithms*, Springer-Verlag, 2008.  
<http://www.springer.com/computer/foundations/book/978-0-387-30770-1>

**Peer-reviewed conference publications**

- [C31] M. Csűrös, Sz. Juhos and A. Bérces. Fast mapping and precise alignment of AB SOLiD color reads to reference DNA. Tenth Workshop on Algorithms in Bioinformatics (WABI), Springer LNBI 6293, 176–188, 2010. DOI:10.1007/978-3-642-15294-8\_15. [9 citations] (30 articles accepted from 83 submissions.)
- [C32] M. Csűrös. Approximate counting with a floating-point counter. *Sixteenth International Computing and Combinatorics Conference (COCOON)*, Springer LNCS 6196, 358–367, 2010. Preprint at Computing Research Repository, arXiv.org: 0904.3062 [cs.DS]. <http://arxiv.org/abs/0904.3062>. (54 articles accepted from 133 submissions.)
- [C33] M. Csűrös. Ancestral reconstruction by asymmetric Wagner parsimony over continuous characters and squared parsimony over distributions. *Sixth Annual RECOMB Satellite Workshop on Comparative Genomics*, Springer LNCS 5267, 72–86, 2008. DOI:10.1007/978-3-540-87989-3\_6. [1 citation] (19 articles accepted from 48 submissions.)
- [C34] M. Csűrös, M.-T. Cheng, A. Grimm, A. Halawani and P. Landreau. Segmentation with an isochore distribution. *Sixth Workshop on Algorithms in Bioinformatics (WABI)*, Springer LNCS 4175, 388–399, 2006. DOI:10.1007/11851561\_36. (36 articles accepted from 100 submissions.)
- [C35] M. Csűrös and I. Miklós. A probabilistic model for gene content evolution with duplication, loss, and horizontal transfer. *Tenth Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Springer LNCS 3909, 206–220, 2006. [18 citations] DOI:10.1007/11732990\_18. (40 articles accepted from 212 submissions.)

- [C36] M. Csűrös. Likely scenarios of intron evolution. *Third RECOMB Satellite Workshop on Comparative Genomics*, Springer LNCS 3678, 47–60, 2005. [27 citations] DOI:10.1007/11554714\_5. (14 articles accepted from 21 submissions.)
- [C37] M. Csűrös and B. Ma. Rapid homology search with two-stage extension and daughter seeds. *Eleventh International Computing and Combinatorics Conference (COCOON)*, Springer LNCS 3595, 104–114, 2005. [5 citations] DOI:10.1007/11533719\_13. (96 articles accepted from 353 submissions.)
- [C38] M. Csűrös. Algorithms for finding maximal-scoring segment sets. *Fourth Workshop on Algorithms in Bioinformatics (WABI)*, Springer LNCS 3240, 62–73, 2004. (Full version: [J24].) <http://www.iro.umontreal.ca/~csuros/papers/mle-segmentation-wabi.pdf>. [4 citations] (39 articles accepted from 117 submissions.)
- [C39] M. Csűrös. Performing local similarity searches with variable length seeds. *Fifteenth Annual Symposium on Combinatorial Pattern Matching (CPM)*, Springer LNCS 3109, 373–387, 2004. [6 citations] <http://www.iro.umontreal.ca/~csuros/papers/seed-tree-cpm.pdf>. (36 articles accepted from 79 submissions.)
- [C40] M. Csűrös and M. Ruzinkó. Single-user-tracing superimposed codes. *IEEE Symposium on Information Theory (ISIT)*, p. 255, 2004. (Full version: [J22].) DOI:10.1109/ISIT.2004.1365290.
- [C41] M. Csűrös, B. Li and A. Milosavljevic. Clone-array pooled shotgun mapping and sequencing: design and analysis of experiments. *Fourteenth International Conference on Genome Informatics (GIW)*, 186–195, 2003. [3 citations] <http://www.jsbi.org/pdfs/journal1/GIW03/GIW03F019>. (25 articles accepted from 44 submissions.)
- [C42] M. Csűrös and A. Milosavljevic. Pooled genomic indexing (PGI): mathematical analysis and experiment design. *Second International Workshop on Algorithms in Bioinformatics (WABI)*, Springer LNCS 2452, 10–28, 2002. (Full version: [J25].) <http://www.iro.umontreal.ca/~csuros/papers/pgi-wabi.pdf> [1 citation] (41 articles accepted from 83 submissions.)
- [C43] M. Csűrös. Fast recovery of evolutionary trees with thousands of nodes. *Fifth Annual International Conference on Computational Molecular Biology (RECOMB)*, 104–113, 2001. (Full version: [J27].) DOI:10.1145/369133.369178. [28 citations] (35 articles accepted from 128 submissions.)

- [C44] M. Csűrös and M.-Y. Kao. Recovering evolutionary trees through Harmonic Greedy Triplets. *Tenth Annual ACM-SIAM Symposium on Discrete Algorithms (SODA)*, 261–270, 1999. (Full version: [J28].) [11 citations]
- [C45] D. Angluin and M. Csűrös. Learning Markov chains with variable memory length from noisy output. *Tenth Annual Conference on Computational Learning Theory (COLT)*, 298–308, 1997. [2 citations] DOI:10.1145/267460.267517.

### Software

- [SW46] QuadGT: SNP calling for germline and somatic mutations from mapped sequencing reads, 2013. (Publication: [J3]) <http://www.iro.umontreal.ca/~csuros/quadgt/>
- [SW47] Short read alignment and mapping modules in the Omixon Variant Toolkit, and the Omixon Gapped Solid Alignment Plug-In from CLC bio, 2011. (The modules implement the algorithms of [C31].) <http://www.omixon.com/omixon/abouttoolkit.htm> and <http://www.clcbio.com/clc-plugin/omixon-precisealign/>
- [SW48] M. Csűrös. Count software package (evolutionary analysis of phylogenetic profiles), 2009–2013. (Application note: [J8]) [http://www.iro.umontreal.ca/~csuros/gene\\_content/count.html](http://www.iro.umontreal.ca/~csuros/gene_content/count.html).
- [SW49] M. Csűrös. Malin software package (analysis of intron evolution), 2005–2011. (Application note: [J11]) <http://www.iro.umontreal.ca/~csuros/introns/malin/>.



## Research funding

	<b>Duration</b>	<b>Grant</b>	<b>Amount</b>	<b>My role</b>
(i)	2011–2016	NSERC discovery grant	CA\$120,000	principal investigator
(ii)	2008–2011	FQRNT team grant	CA\$142,560	team member
(iii)	2006–2011	NSERC discovery grant	CA\$125,000	principal investigator
(iv)	2003	CFI & FQRNT infrastructure grant	CA\$212,972	principal investigator
(v)	2002–2006	NSERC discovery grant	CA\$100,000	principal investigator
(vi)	2003–2004	Subcontract in NIH grant	US\$12,000	subcontractor
(vii)	2002–2005	FCAR strategic program	CA\$62,000	principal investigator
	2001–2004	University faculty startup funds	CA\$65,000	principal investigator

**(i) “Bioinformatics for comparative and evolutionary genomics.”** 2011–2016. Individual discovery grant from the Natural Sciences and Engineering Research Council of Canada (NSERC). Total funding: \$120,000.

**(ii) “Molecular evolutionary analysis for improved annotation of genes and transposons in eukaryotic genomes.”** 2008–2011. Team grant from Québec’s *Fonds de recherche sur la nature et les technologies* (FQRNT). Team composition: principal investigator Paul Harrison (McGill University), members Thomas Bureau (McGill) and myself. Total funding: \$142,560.

**(iii) “Comparative analysis of molecular sequences.”** 2006–2011. Individual discovery grant from the Natural Sciences and Engineering Research Council of Canada (NSERC). Total funding: \$125,000.

**(iv) “Computer laboratory for large-scale sequence analysis.”** 2003. Individual infrastructure grant from the Canada Foundation for Innovation (CFI) and Québec’s *Fonds de recherche sur la nature et les technologies* (FQRNT). Total funding: \$212,972. Financial sources: 40% from CFI, 40% from FQRNT, 17% in-kind contribution from industry partners and 3% from the University.

**(v) “Large-scale comparative analysis of biomolecular sequences.”** 2002–2006. Individual discovery grant 250391–02 from the Natural Sciences and Engineering Research Council of Canada (NSERC). Total funding: \$100,000.

**(vi) “Clone pooling methods for physical mapping.”** 2003–2004. Subcontract in the cooperative research project 1 U01 RR018464 from the US National Institutes of Health awarded to Aleksandar Milosavljevic (Baylor College of Medicine). Subcontract funding: US\$12,000.

- (vii) **“Large-scale comparative physical mapping.”** 2002–2005. Individual strategic program grant NATEQ 2003–SC–87439 from Québec’s *Formation de chercheurs et l’aide à la Recherche* (FCAR). Total funding: \$62,000 (\$45,000 in operating grant and \$17,000 in equipment grant) and 25% teaching load reduction. The grant was accompanied by a \$250,000 salary contribution given to the university for the years 2002–2007.

## Teaching

**Université de Montréal**, Department of Computer Science and Operations Research, Associate Professor, since June 2007; Assistant Professor, August 2001 — May 2007.

Data Structures (second-year undergraduate): Fall 2012, 60 students; Winter 2012, 42 students; Fall 2011, 36 students; Winter 2011, 32 students; Fall 2010, 43 students; Winter 2010, 38 students; Winter 2009, 13 students; Winter 2007, 12 students; Winter 2006, 30 students.

Biosciences/computer science II (third-year undergraduate): Fall 2012, 4 students.

Programming II (first-year undergraduate): Winter 2011, 48 students; Summer 2010, 9 students; Fall 2009, 20 students.

Research topics in bioinformatics [themes in different years: evolutionary genomics, DNA algorithmics, genome sequencing] (graduate): Fall 2009, 3 students; Fall 2006, 2 students; Fall 2005, 7 students; Fall 2004, 7 students; Fall 2003, 4 students.

Programming I (first-year undergraduate): Fall 2008, 45 students.

Bioinformatics (third-year undergraduate): Winter 2006, 7 students; Winter 2005, 6 students; Winter 2004, 12 students; Winter 2003, 16 students.

Concepts of Programming Languages (second-year undergraduate): Winter 2002, 72 students.

Introduction to Theoretical Computer Science (second-year undergraduate): Fall 2001, 73 students.

**Baylor College of Medicine**, Department of Molecular and Human Genetics, Guest Lecturer in the course “Computational Methods in Molecular Biology,” May 2001.

**Yale University**, Department of Computer Science, Teaching Assistant, 1995–1998.

Algorithmic Techniques for Bioinformatics (senior/graduate): 1 semester.

Cryptography and Computer Security (senior/graduate): 3 semesters.

Mathematical Tools for Computer Science (sophomore): 3 semesters.

Theoretical Methods in Computer Science (senior/graduate): 1 semester.

Algorithms (sophomore/junior): 2 semesters.

Theory of Distributed Systems (senior/graduate): 1 semester.

Introduction to Computer Science (freshman): 3 semesters.

Elements of Computing (freshman): 1 semester.

### Students advised

Naïm Poonja-Tremblay, M. Sc. in Bioinformatics, Université de Montréal. Expected graduation in 2014.

Eric Bareke, Post-doctoral researcher, Hôpital Ste-Justine, co-supervision with Daniel Sinnott, 2012–2013.

Billel Benzaid, Ph. D. in Bioinformatics, Université de Montréal, co-supervision with Nadia El-Mabrouk, Université de Montréal. Expected graduation in 2014.

Louis Philip Benoît-Bouvrette, M. Sc. in Bioinformatics, Université de Montréal. Graduated in March 2011 (“*Analyse de la corrélation conditionnelle dérivée de la coévolution d’un système de trois gènes par un modèle du maximum de vraisemblance.*” [Analysis of conditionally correlated evolution in a system of three genes using a maximum likelihood model]). Co-supervision with Sylvie Hamel, Université de Montréal.

Amandine Bemmo, M. Sc. in Bioinformatics, Université de Montréal, co-supervision with Jacek Majewski, McGill University. Graduated in August 2009 (“*Performances de la puce exon et son application dans l’analyse de l’épissage alternatif associé à la métastase du cancer de sein*” [Performance of the exon array and its application in the analysis of alternative splicing associated with metastatic breast cancer]).

Benjamin Provencher, M. Sc. in Computer Science, Université de Montréal. Graduated in August 2009 (“*Recherche d’éléments répétés par analyse des distributions de fréquences d’oligonucléotides*” [Search for repetitive elements using oligonucleotide frequency distributions]).

Mahshid Shakiba, M. Sc. in Computer Science, Université de Montréal, graduated in August 2006 (“Phylogenetic shadowing using a model selection process”), thesis among the best 15% at university.

Ming-Te Cheng, M. Sc. in Computer Science, Université de Montréal, graduated in June 2006 (“Methods for multi-class segmentation of molecular sequences”), thesis among the best 15% at university.

Hervé Saint-Amand, undergraduate Summer project in 2003 (visualization of profile Hidden Markov Models).

## Service

**Editorial appointments:** Member of the editorial board for the journal *Biology Direct*, 2013; Bioinformatics area editor for *Encyclopedia of Algorithms*, Springer-Verlag, 2008. (Second edition is currently in preparation.) <http://www.springer.com/computer/foundations/book/978-0-387-30770-1>

**Workshop organizer:** Invited minisymposium on Bioinformatics, Third Biennial Canadian Discrete and Algorithmic Mathematics Conference (CanaDAM), May 31–June 3, 2011, Victoria, B.C., Canada. <http://canadam.math.ca/2011/>

### Program committee member

◇ **FAW 2012**

Sixth International Frontiers of Algorithmics Workshop, May 14–16, Beijing, China. <http://faw-aaim2012.pku.edu.cn/>

◇ **ISMB 2012, 2011, 2010, 2009, 2008**

Twentieth Annual International Conference on Intelligent Systems for Molecular Biology, July 15–17, 2011, Long Beach, Cal. <http://www.iscb.org/ismb2012>

Nineteenth Annual International Conference on Intelligent Systems for Molecular Biology, July 15–19, 2011, Vienna, Austria. <http://www.iscb.org/ismb2011>

Eighteenth Annual International Conference on Intelligent Systems for Molecular Biology, July 11–13, 2010, Boston, Mass. <http://www.iscb.org/ismb2010>

Seventeenth Annual International Conference on Intelligent Systems for Molecular Biology, June 27–July 2, 2009, Stockholm, Sweden. <http://www.iscb.org/ismb2009/>

Sixteenth Annual International Conference on Intelligent Systems for Molecular Biology, July 19–23, 2008, Toronto, Ontario. <http://www.iscb.org/ismb2008/>

◇ **ACM BCB 2011**

ACM Conference on Bioinformatics, Computational Biology and Biomedicine, August 1–3, 2011, Chicago, Ill. <http://acmbcb.org/>

◇ **RECOMB-CG 2011, 2009, 2008, 2007, 2006**

Ninth RECOMB Satellite Workshop on Comparative Genomics, October 8–10, 2011, Galway, Ireland. <http://recombcg.org/>

Seventh RECOMB Satellite Workshop on Comparative Genomics, September 27–29, 2009, Budapest, Hungary. <http://www.renyi.hu/conferences/recomb-cg2009/>

Sixth RECOMB Satellite Workshop on Comparative Genomics, October 13–15,

2008, Paris, France. <http://igm.univ-mlv.fr/RCG08/>  
Fifth RECOMB Satellite Workshop on Comparative Genomics, September 16–18,  
2007, San Diego, Cal. <http://casb.ucsd.edu/recombcg07/>  
Fourth RECOMB Satellite Workshop on Comparative Genomics, September 24–  
26, 2006, Montréal, Qué. <http://www.crm.umontreal.ca/Genomics06/>

◇ **CPM 2010**

Twenty-first Annual Symposium on Combinatorial Pattern Matching, June 21–23,  
2010, New York, NY. <http://cs.nyu.edu/parida/CPM2010/>

◇ **WABI 2009, 2008**

Ninth Workshop on Algorithms in Bioinformatics, September 11–13, 2009, Philadel-  
phia, Penn. <http://www.wabi09.org/>

Eighth Workshop on Algorithms in Bioinformatics, September 15–17, 2008, Karl-  
sruhe, Germany. <http://algo2008.org/doku.php/wabi>

◇ **ECCB 2008**

Seventh European Conference on Computational Biology, September 22–26, 2008,  
Cagliari, Italy. <http://eccb.iscb.org/2008/>

◇ **BIOT 2007**

Fourth Biotechnology and Bioinformatics Symposium, October 19–20, 2007, Col-  
orado Springs, Col. <http://www.biotconf.org/biot07.shtml>

◇ **PSI 2006**

Sixth International Andrei Ershov Memorial Conference: Perspectives of System  
Informatics, June 27–30 2006, Novosibirsk, Akademgorodok, Russia.

◇ **JOBIM 2004**

Journées Ouvertes Biologie, Informatique, Mathématiques, June 2004, Montréal,  
Qué.

**Organizing committee member**

◇ Seventh RECOMB Satellite Workshop on Comparative Genomics, Septem-  
ber 27–29, 2009, Budapest, Hungary.

◇ Fourth RECOMB Satellite Workshop on Comparative Genomics, Septem-  
ber 24–26, 2006, Montréal, Qué.

◇ Journées Ouvertes Biologie, Informatique, Mathématiques (JOBIM), June  
2004, Montréal, Qué.

**Grant reviewer for:** Natural Sciences and Engineering Research Council of Canada, Health Research Board of Ireland, Israel Science Foundation.

**Ad hoc reviewer for:** *Algorithmica*, *Algorithms for Molecular Biology*, *Bioinformatics*, *BioEssays*, *BMC Evolutionary Biology*, *BMC Genomics*, *Discrete Applied Mathematics*, *Genome Research*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, *IEEE Computer*, *IEEE Transactions on Information Theory*, *INFORMS Journal on Computing*, *Journal of Computational Biology*, *Journal of Theoretical Biology*, *Molecular Biology and Evolution*, *Nucleic Acids Research*, *PLoS Genetics*, *PLoS ONE*, *Random Structures and Algorithms*, *SIAM Journal on Computing*, *Trends in Genetics*; *IWOCA* (2013), *WABI* (2003, 2004, 2005, 2010, 2012), *RECOMB* (2003, 2004, 2006, 2008), *ISIT* (2003), *COLT* (2005), *APBC* (2006, 2009, 2010).

### Administrative services

- ◇ Université de Montréal, Bioinformatics Undergraduate Program director, September 2011–
- ◇ Université de Montréal, Bioinformatics Undergraduate Studies Committee member, 2004–2007
- ◇ Université de Montréal, Co-Director of Graduate Programs in Bioinformatics, 2002–2004
- ◇ Université de Montréal, Bioinformatics Graduate Studies Committee member, 2001–2002; 2008–2011
- ◇ Yale University Graduate Student Assembly, elected departmental representative, 1997
- ◇ Yale University Graduate School, English Testing and Training Review Committee member, Spring 1997

### Thesis committees

- ◇ External reader for Ph.D. dissertation in Computer Science at University of Waterloo, Spring 2010.
- ◇ External reader for Ph.D. dissertation in Computer Science at Université de Sherbrooke, Fall 2009.



- ◇ External reader for Ph.D. dissertation in Mathematics at University of Ottawa, Fall 2008.
- ◇ External reader for M.Sc. thesis in Biology at McGill University, Summer 2007.
- ◇ External reader for Ph.D. dissertation in Computer Science at Université Paris VII, Fall 2004.
- ◇ Chair (six times) and member (eight times) of Masters thesis defense committees at Université de Montréal, since Fall 2001.
- ◇ Chair (twice) and member (three times) of qualifying examination committees for Ph. D. candidacy in Computer Science at Université de Montréal, since Fall 2001.
- ◇ Chair (once) of thesis committee (Ph. D. in Computer Science) at Université de Montréal, Spring 2010.
- ◇ Dean's Representative (once) of thesis committee (Ph. D. in Bioinformatics) at Université de Montréal, Fall 2009.
- ◇ Chair (once) and member (twice) of qualifying examination committees for Ph. D. candidacy in Bioinformatics at Université de Montréal, since Fall 2001.

## Awards and honors

Québec's FCAR Strategic Program — New Researcher, 2002.

Official Citation of the Connecticut General Assembly, Connecticut Immigrant Day, 1999

Yale Fellowship, 1994 Fall – Spring 1998

Soros Foundation Travel Grant, 1994.

Technical University of Budapest Fellowship, Spring 1993

Fellowship of the Faculty of Electrical Engineering of the Technical University of Budapest, Spring 1993 and 1994

European Community (TEMPUS) Scholarship, Summer–Fall 1990

## Talks

### Invited and contributed talks at conferences and workshops

*Mathematical and Computational Approaches in High-Throughput Genomics: Workshop on Evolutionary Genomics*, Institute for Pure & Applied Mathematics, University of California Los Angeles, November 2011; invited speaker. <http://www.ipam.ucla.edu/programs/genws3/>

*Asia-Pacific Bioinformatics Conference*, Bangalore, India, January 2010; keynote speaker. <http://cs.nyu.edu/parida/APBC2010/>

*Phylogeny Workshop*, Alfréd Rényi Institute of Mathematics, Budapest, Hungary, June 2009; invited speaker. <http://www.renyi.hu/conferences/phylo09/>

*Bayesian Phylogeny Workshop*, Alfréd Rényi Institute of Mathematics, Budapest, Hungary, June 2008; invited speaker. <http://www.renyi.hu/conferences/bp2008/>

*Annual Scientific Meeting of the Hungarian Society for Bioinformatics*, Budapest, Hungary, October 2007; invited speaker.

*Bertinoro Computational Biology Meeting*, Italy, June 2007; invited oral presentation. <http://www.mcb.mcgill.ca/research/bertinoro/2007/>

*First Meeting of the Hungarian Society for Bioinformatics*, Budapest, Hungary, June 2006; contributed talk.

*International Workshop on Applied Probability*, Storrs, Conn., May 2006; invited speaker.

*Congrès de l'Association francophone pour le savoir (ACFAS)*, Montréal, May 2004; invited oral presentation.

*Bertinoro Computational Biology Meeting*, Italy, June 2003; invited oral presentation. <http://www.dsi.uniroma1.it/~ale/BICI/BCB/>

*DIMACS-CTS Conference on the Interconnections among Codes, Designs, Graphs, and Molecular Biology*, National Chiao Tung University, Hsinchu, Taiwan, May 2002; contributed oral presentation. <http://dimacs.rutgers.edu/Workshops/Chiaotung/>

*DIMACS Symposium on Estimating Large Scale Phylogenies: Biological, Statistical, and Computational Problems*, Princeton University, June 1998; invited oral presentation. <http://dimacs.rutgers.edu/Workshops/Phylogenies/>

### Seminars

School of Computer Science, University of Waterloo, March 2010.

Penn Bioinformatics Forum, University of Pennsylvania, September 2009.

Department of Computer Science, Swiss Federal Institute of Technology, Zürich, May 2009.

Biological Research Center, Hungarian Academy of Sciences, Szeged, May 2008.

McGill Centre for Bioinformatics, McGill University, February 2006.

Computational Biology Branch, National Center of Biotechnology Information, NLM/NIH, January 2006.

Alfréd Rényi Institute of Mathematics, Hungarian Academy of Sciences, November 2005.

Department of Chemistry, McGill University, May 2005.

Department of Computer Science, University of Waterloo, October 2004.

Department of Computer Science, University of Western Ontario, October 2004.

Computer and Automation Research Institute, Hungarian Academy of Sciences, July 2004.

McGill Centre for Non-linear Dynamics, Montréal, September 2003.

CRM Summer School: The mathematics of bioinformatics, Montréal, August 2003.

Department of Biochemistry, Université de Montréal, November 2001.

School of Computer Science, McGill University, April 1999.