

## Miklós Csűrös

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### 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) since June 2007; Assistant Professor, 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.

**Chemistry Logic LLC**, Hungary. Scientific Consultant September–December 2009.

**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

### Journal articles

- [1] 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. DOI:10.1093/molbev/msp123.
- [2] 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. DOI:10.1093/gbe/evp011.
- [3] M. Csűrös. Malin: maximum likelihood analysis of intron evolution in eukaryotes. [Application note] *Bioinformatics*, **24**(13):1538–1539, 2008. DOI:10.1093/bioinformatics/btn226
- [4] 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. DOI:10.1093/molbev/msn039
- [5] 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. DOI:10.1186/1745-6150-3-7.
- [6] M. Csűrös, L. Noé and G. Kucherov. Reconsidering the significance of genomic word frequencies. [Genome analysis] *Trends in Genetics*, **23**(11):543–

546, 2007.

DOI:10.1016/j.tig.2007.07.008.

- [7] M. Csűrös, J. A. Holey and I. B. Rogozin. In search of lost introns. *Bioinformatics*, **23**(13):i87–i96, 2007. 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.)
- [8] M. Csűrös and B. Ma. Rapid homology search with neighbor seeds. *Algorithmica*, **48**(2):187–202, 2007. DOI:10.1007/s00453-007-0062-y.
- [9] Rhesus Macaque Genome Sequencing and Analysis Consortium. Evolutionary and biomedical insights from the Rhesus macaque genome. *Science*, **316**(5822):222–234, 2007. DOI:10.1126/science.1139247.
- [10] 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. DOI:10.1016/j.tig.2007.01.001
- [11] The Honey Bee Genome Sequencing Consortium. Insights into social insects from the genome of the honeybee *Apis mellifera*. *Nature*, **443**:931–949, 2006. DOI:10.1038/nature05260.
- [12] M. Csűrös. On the estimation of intron evolution. [Correspondence.] *PLoS Computational Biology*, **2**(7):e84, 2006. DOI:10.1371/journal.pcbi.0020084.
- [13] M. Csűrös and I. Miklós. Statistical alignment of retropseudogenes and their functional paralogs. *Molecular Biology and Evolution*, **22**(12):2457–2471, 2005. DOI:10.1093/molbev/msi238.
- [14] M. Csűrös and M. Ruzinkó. Single-user tracing and disjointly superimposed codes. *IEEE Transactions on Information Theory*, **51**(4):1606–1611, 2005. DOI:10.1109/TIT.2005.844097.
- [15] 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. DOI:10.1101/gr.3162505.
- [16] M. Csűrös. Maximum-scoring segment sets. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **1**(4):139–150, 2004. DOI:10.1109/TCBB.2004.43.

- [17] M. Csűrös and A. Milosavljevic. Pooled genomic indexing (PGI): analysis and design of experiments. *Journal of Computational Biology*, **11**(5):1001–1021, 2004. DOI:10.1089/cmb.2004.11.1001.
- [18] 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.
- [19] M. Csűrös. Fast recovery of evolutionary trees with thousands of nodes. *Journal of Computational Biology*, **9**:277–297, 2002. DOI:10.1089/10665270252935467.
- [20] 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. DOI:10.1137/S009753970037905X.

### Book chapter

- [21] M. Csűrös. Distance-based phylogeny reconstruction (fast-converging). 2 pages. Entry in M.-Y. Kao et al. (Eds.) *Encyclopedia of Algorithms*, Springer-Verlag. To appear. <http://refworks.springer.com/algorithms/>.

### Peer-reviewed conference publications

- [22] 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. (19 articles accepted from 48 submissions.)
- [23] 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.)
- [24] 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. DOI:10.1007/11732990\_18. (40 articles accepted from 212 submissions.)

- [25] M. Csűrös. Likely scenarios of intron evolution. *Third RECOMB Satellite Workshop on Comparative Genomics*, Springer LNCS 3678, 47–60, 2005. DOI:10.1007/11554714\_5. (14 articles accepted from 21 submissions.)
- [26] 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. DOI:10.1007/11533719\_13. (96 articles accepted from 353 submissions.)
- [27] M. Csűrös. Algorithms for finding maximal-scoring segment sets. *Fourth Workshop on Algorithms in Bioinformatics (WABI)*, Springer LNCS 3240, 62–73, 2004. (Full version: [16].) <http://www.iro.umontreal.ca/~csuros/papers/mle-segmentation-wabi.pdf>. (39 articles accepted from 117 submissions.)
- [28] M. Csűrös. Performing local similarity searches with variable length seeds. *Fifteenth Annual Symposium on Combinatorial Pattern Matching (CPM)*, Springer LNCS 3109, 373–387, 2004. <http://www.iro.umontreal.ca/~csuros/papers/seed-tree-cpm.pdf>. (36 articles accepted from 79 submissions.)
- [29] M. Csűrös and M. Ruzinkó. Single-user-tracing superimposed codes. *IEEE Symposium on Information Theory (ISIT)*, p. 255, 2004. (Full version: [14].) DOI:10.1109/ISIT.2004.1365290.
- [30] 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. <http://hc.ims.u-tokyo.ac.jp/JSBi/journal/GIW03/GIW03F019/>. (25 articles accepted from 44 submissions.)
- [31] 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: [17].) <http://www.iro.umontreal.ca/~csuros/papers/pgi-wabi.pdf> (41 articles accepted from 83 submissions.)
- [32] 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: [19].) DOI:10.1145/369133.369178. (35 articles accepted from 128 submissions.)
- [33] 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: [20].)

- [34] 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. DOI:10.1145/267460.267517.

## Software

- [35] M. Csűrös. Count software package (evolutionary analysis of phylogenetic profiles), 2009. [http://www.iro.umontreal.ca/~csuros/gene\\_content/count.html](http://www.iro.umontreal.ca/~csuros/gene_content/count.html).
- [36] M. Csűrös. Malin software package (analysis of intron evolution), 2009. (Application note: [3]) <http://www.iro.umontreal.ca/~csuros/introns/malin/>.

## Non-refereed reports

- [37] M. Csűrös. Approximate counting with a floating-point counter. Technical report, Computing Research Repository, arXiv.org: 0904.3062 [cs.DS], 2009. <http://arxiv.org/abs/0904.3062>.
- [38] M. Csűrös. A linear-time algorithm for finding the longest segment which scores above a given threshold. Technical report, Computing Research Repository, arXiv.org: cs/0512016 [cs.DS], 2006. <http://arxiv.org/abs/cs/0512016>.

## Research funding

**FQRNT** (Québec’s *Fonds de recherche sur la nature et les technologies*), team grant (PI: Paul Harrison, McGill University; three team members), Team member, 2008–2011, \$142,560.

**NSERC** (Natural Sciences and Engineering Research Council of Canada) discovery grant, Principal Investigator, 2006–2011, \$125,000. (“...the committee’s recommendation of level funding should be viewed positively” — NSERC’s *Message to Applicant*)

**NSERC** (Natural Sciences and Engineering Research Council of Canada) discovery grant, Principal Investigator, 2002–2006, \$100,000.

**FCAR** (Québec’s *Fonds de formation de chercheurs et l’aide à la recherche*) programme stratégique de professeurs-chercheurs, établissement de nouveaux chercheurs

(Strategic grant program — new researcher), Principal Investigator, 2003–2006, \$62,000 and 25% teaching load reduction. This grant is accompanied by a \$250,000 salary contribution given to the university for the years 2002–2007.

**CFI** (Canada Foundation for Innovation) infrastructure grant, Principal Investigator, 2004, \$214,070.

**NIH** (National Institutes of Health) NCCR U01 research grant subcontract, (Principal Investigator for the grant: Aleksandar Milosavljevic, Baylor College of Medicine). 2003–2004, US\$12,000.

**Université de Montréal** faculty startup funds, 2001, \$65,000.

## 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): Winter 2010, 38 students; Winter 2009, 13 students; Winter 2007, 12 students; Winter 2006, 30 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 II (first-year undergraduate): Fall 2009, 20 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

Louis Philip Benoit-Bouvette, M. Sc. in Bioinformatics, Université de Montréal, expected completion in 2010 [co-evolution of genes, functional modules in archaeal genomes]. 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]). Now a Ph. D. student at McGill.

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]). Now at the National Research Centre Canada.

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. Now Lecturer at Yazd University, Iran.

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. Now at Genome Québec Innovation Centre, McGill University.

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

## Service

### University

Université de Montréal, Bioinformatics Undergraduate Studies Committee member, 2004–

Université de Montréal, Bioinformatics Program Steering Committee member, 2003–

Université de Montréal, Co-Director of Graduate Programs in Bioinformatics, 2002–2004

Université de Montréal, Bioinformatics Graduate Studies Committee member, 2001–2002

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 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 (seven times) of Masters thesis defense committees at Université de Montréal, since Fall 2001.

- ◇ Chair (twice) and member (twice) of qualifying examination committees for Ph. D. candidacy in Computer Science at Université de Montréal, since Fall 2001.
- ◇ Chair (once) and member (twice) of qualifying examination committees for Ph. D. candidacy in Bioinformatics at Université de Montréal, since Fall 2001.

### **Editorship**

- ◇ Area editor for Bioinformatics on the editorial board of the *Encyclopedia of Algorithms*, Springer-Verlag, 2008. <http://www.springer.com/computer/foundations/book/978-0-387-30770-1>

## Conferences and journals

### Program committee member:

#### ◇ **ISMB 2010, 2009, 2008**

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/>

#### ◇ **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, Philadelphia, Penn. <http://www.wabi09.org/>

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

#### ◇ **RECOMB-CG 2008, 2007, 2006**

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/>

#### ◇ **ECCB 2008**

Seventh European Conference on Computational Biology, September 22–26, 2008, Cagliari, Italy. <http://www.eccb08.org/>

#### ◇ **BIOT 2007**

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

#### ◇ **PSI 2006**

Sixth International Andrei Ershov Memorial Conference: Perspectives of System Informatics, June 27–30 2006, Novosibirsk, Akademgorodok, Russia. <http://www.iis.nsk.su/PSI06>

◇ **JOBIM 2004**

Journées Ouvertes Biologie, Informatique, Mathématiques, June 2004, Montréal, Qué. <http://www.congresbcu.com/jobim2004/>

**Organizing committee member:**

- ◇ Seventh RECOMB Satellite Workshop on Comparative Genomics, September 27–29, 2009, Budapest, Hungary.
- ◇ Fourth RECOMB Satellite Workshop on Comparative Genomics, September 24–26, 2006, Montréal, Qué.
- ◇ Journées Ouvertes Biologie, Informatique, Mathématiques (JOBIM), June 2004, Montréal, Qué.

**Ad hoc reviewer for:** *Algorithmica*, *Bioinformatics*, *BioEssays*, *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*, *SIAM Journal on Computing*, *Trends in Genetics*; *WABI* (2003, 2004, 2005), *RECOMB* (2003, 2004, 2006, 2008), *ISIT* (2003), *COLT* (2005), *APBC* (2006, 2009, 2010).

## 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 and posters

### Conferences and workshops

*Asia-Pacific Bioinformatics Conference*, Bangalore, India, January 2010; keynote speaker.

*Phylogeny Workshop*, Budapest, Hungary, June 2009; invited speaker.

*Bayesian Phylogeny Workshop*, Budapest, Hungary, June 2008; invited speaker.

*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.

M. Shakiba and M. Csűrös. Three monkeys: phylogenetic shadowing using a model selection process. *RECOMB Workshop on Comparative Genomics*, Montréal, Québec, September 2006; poster.

*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.

G. Lunter, I. Miklós and M. Csűrös. Reticular alignment: a new heuristic for multiple sequence alignment using transducers and suboptimal alignments. *RECOMB*, Venice, Italy, April 2006; poster.

M. Csűrös and I. Miklós. Statistical alignment of retropseudogenes and their functional paralogs via a common ancestor. *FEBS Congress and IUBMB Conference*, Budapest, Hungary, July 2005; poster (abstract in *FEBS Journal*, **272**(s1):A3-029P, 2005).

*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.

A. Milosavljevic, M. Csűrös, E. Sodergren, G. Weinstock, A. R. Jackson, R. A. Gibbs, B. Li. Clone-array pooled shotgun methods for *de novo* and comparative physical mapping. *The 68th Symposium: The Genome of Homo Sapiens*, Cold Spring Harbor Laboratory, May 2003; poster.

A. R. Jackson, M. Csűrös, E. Sodergren, G. Weinstock, R. A. Gibbs, and A. Milosavljevic. Mapping of BACs covering over 10% of the Rhesus macaque genome onto Human genome via Pooled Genomic Indexing. *The Biology of DNA, 50th anniversary celebratory meeting*, Cold Spring Harbor Laboratory, March 2003; poster.

A. R. Jackson, F. Yu, M. Csűrös, E. Sodergren, G. Weinstock, R. A. Gibbs, and A. Milosavljevic. Mapping of 2256 Rhesus macaque BACs onto Human genome via Pooled Genomic Indexing. *Advances in Genome Biology and Technology*, Marco Island, Florida, February 2003; poster.

A. Jackson, M. Csűrös, E. Sodergren, G. Weinstock, R. A. Gibbs, and A. Milosavljevic. Comparative clone mapping and sequence assembly: preliminary results on rhesus macaque vs. human. *2nd Cold Spring Harbor Laboratory/Wellcome Trust Conference on Genome Informatics*, Hinxton, UK, September 2002; poster selected for oral presentation.

*DIMACS-CTS Conference on the Interconnections among Codes, Designs, Graphs, and Molecular Biology*, National Chiao Tung University, Hsinchu, Taiwan, May 2002; contributed oral presentation.

M. Csűrös, A. R. Jackson, E. Sodergren, G. Weinstock, R. A. Gibbs, and A. Milosavljevic. Pooled Genomic Indexing. *15th Annual Cold Spring Harbor Meeting on Genome Sequencing and Biology*, May 2002; poster.

M. Csűrös and A. Milosavljevic. Pooled Genomic Indexing. *RECOMB: Currents in Computational Molecular Biology*, pp. 44–45, 2002; poster.

*DIMACS Symposium on Estimating Large Scale Phylogenies: Biological, Statistical, and Computational Problems*, Princeton University, June 1998; invited oral presentation.

## Seminars

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.