

GUILLAUME BOURQUE

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WORK EXPERIENCE

2007 – ...	Senior Group Leader & Assoc Director Computational & Mathematical Biology, Genome Institute of Singapore, <i>Singapore</i>
2004 – 2007	Group Leader Computational & Mathematical Biology, Genome Institute of Singapore, <i>Singapore</i>
2005 – ...	Adjunct Assistant Professor Mathematics Department, National University of Singapore, <i>Singapore</i>
2002	Bioinformatics Consultant MazLab, Inc., <i>Montréal, Qc</i>
1998 – 2001	Teaching Assistant University of Southern California, <i>Los Angeles, CA</i>
1996 – 1997	Research Assistant Centre de Recherches Mathématiques, Université de Montréal, <i>Montréal, Qc</i>

EDUCATION

2002 – 2004	Postdoctoral Researcher Centre de Recherches Mathématiques, Université de Montréal, <i>Montréal, Qc</i> Development of novel algorithms for the analysis of time-series gene expression data. Advisor: David Sankoff.
1998 – 2002	Ph.D. in Applied Mathematics University of Southern California, <i>Los Angeles, CA</i> Algorithms for phylogenetic tree reconstruction based on genome rearrangements. Advisor: Pavel Pevzner.
1998 – 2000	M.A. in Applied Mathematics University of Southern California, <i>Los Angeles, CA</i>
1995 – 1998	B.Sc. in Computer Science and Mathematics Université de Montréal, <i>Montréal, Qc</i>
1993 – 1995	International Baccalaureate and D.E.C. Collège Jean-de-Brébeuf, <i>Montréal, Qc</i>

RESEARCH FUNDING

2007 – 2009	NIH RFA Grant (RFA-CA-07-001), USA, US\$ 1,000,000 PI: Edison Liu, Role: Co-Inv Pair-end-ditag technologies for the complete annotation of fusion genes.
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2006 – 2011	A*STAR-SSCC Grant (SSCC-06-007), Singapore, S\$ 850,000 PI: Paul Robson, Role: Co-Inv Improved Derivations of Human Embryonic Stem Cells Via Modelling of the Preimplantation Genetic Regulatory Network.
2006 – 2010	BMRC-NMRC Grant (05/1/31/19/423), Singapore, S\$ 1,500,000 PI: Patrick Tan, Role: Co-Inv Systematic Identification of Oncogenic Cellular Pathways and Processes in Gastric Cancer for Patient Stratification and Personalized Therapy.
2005 – ...	GIS Internal Grant (GIS05-114101), Singapore PI: Guillaume Bourque Comparative Genomics: Theory and Application Platform.

SCHOLARSHIPS AND AWARDS

2002 – 2004	Postdoctoral Research Fellowship Nature and Technology Quebec Research Fund (FCAR)
2000 – 2002	Postgraduate Scholarship (PGS B) Natural Sciences and Engineering Research Council of Canada (NSERC)
1998 – 2000	Postgraduate Scholarship (PGS A) Natural Sciences and Engineering Research Council of Canada (NSERC)
1999 – 2001	Outstanding Academic Achievement Office of International Services, USC
2000	Trigg Summer Fellowship Department of Mathematics, USC
1997	CREPUQ scholarship to study abroad San Francisco State University

PUBLICATIONS AND SOFTWARE

1. H. Zhao, **G. Bourque**. 2009. Recovering Genome Rearrangements in the Mammalian Phylogeny. *Genome Res.* In press.
2. **G. Bourque**, B. Leong, V.B. Vega, X. Chen, K.G. Srinivasan, J.-L. Chew, Y. Ruan, C.-L. Wei, H.H. Ng, E.T. Liu. 2008. Evolution of the mammalian transcription factor binding repertoire via transposable elements. *Genome Res.* 18(11):1752-62.
3. Y.F. Pan, K.D.S.A. Wansa, M.H. Liu, B. Zhao, S.Z. Hong, P.Y. Tan, K.S. Lim, **G. Bourque**, E.T. Liu, E. Cheung. 2008. Regulation of estrogen receptor-mediated long-range transcription via evolutionarily conserved distal response elements. *J. Biol. Chem.* 283(47):32977-88
4. X. Chen, X. Han, P. Yuan, F. Fang, E.M. Huss, V.B. Vega, E. Wong, Y.L. Orlov, W. Zhang, J. Jiang, Y.H. Loh, H.C. Yeo, Z.H. Yeo, V. Narang, K.R. Govindarajan, B. Leong, A. Shahab, Y. Ruan, **G. Bourque**, W.K. Sung, N. Clarke, C.L. Wei, H.H. Ng. 2008. Integration of external signaling pathways with the core transcriptional network through transcription factor colocalization hotspots in embryonic stem cells. *Cell* 133(6):1106-17.

5. C.H. Lin, **G. Bourque***, P. Tan*. 2008. A Comparative Synteny Map of Burkholderia Species Links Large-scale Genome Rearrangements to Fine-scale Nucleotide Variation in Prokaryotes. *Mol. Biol. Evol.* 25(3):549-58 (*corresponding authors).
6. H. Zhao, **G. Bourque**. 2007. Recovering True Evolutionary Events on Phylogenetic Trees. In *Proceedings of the 5th RECOMB Workshop on Comparative Genomics*, San Diego, USA, LNCS 4751:149-161.
7. X.D. Zhao, J.L. Chew, X. Han, J. Liu, K.P. Chiu, A. Choo, A. Shahab, V.A. Kuznetsov, **G. Bourque**, S. Ho, Y. Ruan, H.H. Ng, C.-L. Wei. 2007. Whole Genome Mapping of Histone H3 Lys 4 and 27 Trimethylation Reveals Distinct Genomic Compartments in Human Embryonic Stem Cells. *Cell Stem Cell* 1(3):286.
8. J.U. Pontius, J.C. Mullikin, D. Smith, K. Lindblad-Toh, S. Gnerre, M. Clamp, J. Chang, R. Stephens, B. Neelam, N. Volfovsky, A.A. Schffer, R. Agarwala, K. Narfstrm, W.J. Murphy, U. Giger, A.L. Roca, A. Antunes, M. Menotti-Raymond, N. Yuhki, J. Pecon-Slattey, W.E. Johnson, **G. Bourque**, G. Tesler, S.J. OBrien. 2007. The Domestic Cat Genome Sequence: Annotation and Comparative Inferences. *Genome Res.* 17:1675-1689.
9. Y. Ruan, H.-S. Ooi, S.W. Choo, K.P. Chiu, X.D. Zhao, K.G. Srinivasan, F. Yao, C.Y. Choo, P. Nuwantha, R. Kalpana, W.G.W. Bin, A. Shahab, W.-K. Sung, **G. Bourque**, N. Palanisamy, C.-L. Wei. 2007. Fusion Transcripts and Transcribed Retrotransposed Loci Discovered through Comprehensive Transcriptome Analysis using Paired-End diTagging (PET). *Genome Res.* 17(6):828-838.
10. C.-Y. Lin, V.B.B. Vega, J.S. Thomsen, T. Zhang, S.L.L. Kong, M. Xie, K.-P. Chiu, L. Lipovich, D.H. Barnett, F. Stossi, A. Yeo, J. George, V.A. Kuznetsov, Y.K. Lee, T.H. Charn, N. Palanisamy, L.D. Miller, E. Cheung, B. Katzenellenbogen, Y. Ruan, **G. Bourque**, C.-L. Wei, E.T. Liu. 2007. Whole-Genome Cartography of Estrogen Receptor α Binding Sites. *PLoS Genetics* 3(6):e87.
11. V.B. Vega, C.-Y. Lin, K.S. Lai, X. Su, H.F. Teh, J.S. Thomsen, S.L. Kong, M. Xie, A.L. Yeo., W.K. Sung, **G. Bourque**, E.T. Liu. 2006. Multi-platform genome-wide identification and modeling of functional human estrogen receptor binding sites. *Genome Biol.* 7(9):R8.
12. J. Xu, B.P. Srinivas, S.Y Tay, A. Mak, X. Yu, S.G.P. Lee, H. Yang, K.R. Govindarajan, B. Leong, **G. Bourque**, S. Mathavan, and S. Roy. 2006. Genome-wide expression profiling in the Zebrafish embryo identifies target genes regulated by hedgehog signaling during vertebrate development. *Genetics* 174: 735-752.
13. Y.-H. Loh, W. Wu, J.-L. Chew, V.B. Vega, W. Zhang, X. ChenLoh, **G. Bourque**, et al. 2006. The Oct4 and Nanog transcription network that regulates pluripotency in mouse embryonic stem cells. *Nature Genetics* 38(4):431-440.
14. **G. Bourque**, G. Tesler, P.A. Pevzner. 2006. The convergence of cytogenetics and rearrangement-based models for ancestral genome reconstruction. *Genome Res.* 16(3):311-313.
15. H.X. Yu, J.-M. Chia, **G. Bourque**, M.V. Wong, S.H. Chan, E.C. Ren. 2005. A population-based LD map of the human chromosome 6p. *Immunogenetics.* 57(8): 559-565.
16. **G. Bourque**, Y. Yacef, and N. El-Mabrouk. 2005. Maximizing synteny blocks to identify ancestral homologs. In *Proceedings of RECOMB Comparative Genomics Satellite Workshop*. LNBI 3678: 21-34.
17. W.J. Murphy, D.M. Larkin, A. Everts-van der Wind, **G. Bourque**, G. Tesler, L. Auvil, J.E. Beever, B.P. Chowdhary, F. Galibert, L. Gatzke, C. Hitte, S.N. Meyers, E.A. Ostrander, G. Pape, H.G. Parker, T. Raudsepp, M.B. Rogatcheva, L.B. Schook, L.C. Skow, M. Welge, J.E. Womack, S.J. OBrien, P.A. Pevzner, H.A. Lewin. 2005. Dynamics of mammalian chromosome evolution inferred from multispecies comparative maps. *Science* 309(5734): 613-617.

18. **G. Bourque**, E. M. Zdobnov, P. Bork, P. A. Pevzner, and G. Tesler. 2005. Comparative architectures of mammalian and chicken genomes reveal highly variable rates of genomic rearrangements across different lineages. *Genome Res.* 15: 98–110.
19. International Chicken Genome Sequencing Consortium, (including **G. Bourque**). 2004. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 432: 695–716.
20. **G. Bourque** and D. Sankoff. 2004. Improving gene network inference by comparing expression time-series across species, developmental stages or tissues. *J Bioinform Comput Biol.* 2(4):765–83.
21. Rat Genome Sequencing Project Consortium (including **G. Bourque**). 2004. Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature* 428(6982):493–521.
22. **G. Bourque**, P. A. Pevzner, and G. Tesler. 2004. Reconstructing the genomic architecture of ancestral mammals: Lessons from human, mouse, and rat genomes. *Genome Res.* 14(4):507–516.
23. G. Andelfinger, C. Hitte, R. Guyon, F. Galibert, G. Tesler, **G. Bourque**, P. Pevzner, E. Kirkness, L. Etter, D.W. Benson. 2004. Detailed comparative mapping and gene order analysis of the canine *ctvm* locus and syntenic regions in human, mouse, and rat genomes. *Genomics* 83(6): 1053–1062.
24. W.J. Murphy, **G. Bourque**, G. Tesler, P.A. Pevzner, and S.J. OBrien. 2003. Reconstructing the genomic architecture of mammalian ancestors using multispecies comparative maps. *Human Genomics* 1(1): 30–40.
25. **G. Bourque**. 2002. Algorithms for phylogenetic tree reconstruction based on genome rearrangements. PhD Thesis, Advisor P. Pevzner.
26. **G. Bourque** and P. Pevzner. 2002. Genome-Scale Evolution: Reconstructing Gene Orders in the Ancestral Species. *Genome Res.* 12(1): 26–36.
27. **G. Bourque**. 2002. MGR. Web tool at www-cse.ucsd.edu/groups/bioinformatics.
28. D. Sankoff, M. Blanchette and **G. Bourque**. 1997. Breakpoint Phylogenies. In *Genome Informatics*, Miyano, S., and Takagi, T., eds., Universal Academy Press, Tokyo, 25–34.

BOOK CHAPTERS

1. H. Zhao, **G. Bourque**. 2009. Chromosomal Rearrangements in Evolution. In *Evolutionary Genomics and Systems Biology*, Caetano-Anolles G. ed, John Wiley & Sons.
2. G. Tesler, **G. Bourque**. 2008. Computational tools for the analysis of rearrangements in mammalian genomes. In *Phylogenomics. Series: Methods in Molecular Biology*, Murphy W.J. ed, Humana Press, 422 : 145-70.
3. **G. Bourque**, G. Tesler. 2008. Computational tools for the analysis of rearrangements in mammalian genomes. In *Bioinformatics: Data, Sequence Analysis and Evolution. Series: Methods in Molecular Biology*, Keith J.M. ed, Humana Press, 452 : 431-55.
4. **G. Bourque** and L. Zhang. 2006. Models and Methods in Comparative Genomics. In *Advances in Computers, Special Volume: Computational Biology*, C.-W. Tseng ed., Volume 68, Elsevier, ISBN-10: 0-12-012168-9.

5. **G. Bourque.** 2006. Analyzing genome rearrangements. In *Bioinformatics: From Genomes to Therapies*. Lengauer T. ed, Wiley-VCH. ISBN-10: 3-527-31278-1.
6. **G. Bourque.** 2005. Chromosome phylogeny. In *Encyclopedia of Genomics, Proteomics and Bioinformatics*. Dunn M., Jorde L., Little P. and Subramaniam S. eds., Wiley. Volume 7, Section 4.

SCIENTIFIC PRESENTATIONS

- Evolution of the mammalian transcription factor binding repertoire via transposable elements. Genomic Impact of Transposable Elements, Asilomar, USA. Feb 2009.
- Evolution of the mammalian transcription factor binding repertoire via transposable elements. Frontiers in Bioinformatics and Systems Biology Colloquium. UC San Diego, USA. Feb 2009.
- Informatics Solution to Medical Genomics. HUGO-Asia meeting. Cebu, Philippines. April 2008.
- The Hitchhikers guide to mammalian transcription factors binding sites. Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor Laboratory, USA. April 2008.
- Decoding the human genome and implications for human health. Bharathidasan University, India. March 2008.
- Genome-wide binding site map of mammalian transcription factors reveals rapid evolutionary turnover. Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor Laboratory, USA, March 2007.
- New paired-end sequencing technologies for the characterization of transcription factor binding sites and mRNA populations. IRCM, Montreal, Canada, September 2006.
- Chromosome rearrangements in evolution and cancer. Workshop on Genomics. IMS, NUS, Singapore, November, 2005.
- Maximizing synteny blocks to identify ancestral homologs. 3rd RECOMB Comparative Genomics Satellite Workshop, Dublin, Ireland, September 2005.
- Improving gene network inference by comparing expression time-series across species, developmental stages or tissues. Statistical Methods in Microarray Data Analysis. Institute for Mathematical Sciences, Singapore, January 2004.
- A Comparative Approach for Multiple Gene Network Inference Using Time-Series Gene Expression Data. IMA/RECOMB Satellite Workshop on Comparative Genomics. Minneapolis, USA, October 2003.
- Gene network inference using time-series gene expression data. Conference organized by RBMC. Montréal, Canada, May 2003.
- Heuristic for Genome Rearrangements in Multi-Chromosomal Species (poster presentation). Recomb 2001.

TUTORIALS

- Decoding the human genome. Singapore Science Center. Nov 2007.

- Pancake Flipping, Bill Gates and Genome Rearrangements. Math-CS Camp. National University of Singapore. July 2006.
- Chromosome rearrangements in evolution and cancer. Workshop on Genomics. Institute for Mathematical Sciences, National University of Singapore. Nov 2005.
- Combinatorial Methods in Genomics. Asian Mathematical Conference, National University of Singapore. July 2005.
- Gene Expression Analysis and Modeling. CRM summer school on bioinformatics. Montréal, Canada, August 2003.
- Microarray Data Analysis Techniques. Tutorial organized by BioneQ. Montréal, Canada, June 2003.

STUDENT SUPERVISION

- Sharon Tan. Undergraduate student. Fine-Scale Mapping of Recurrent Genomic Aberrations in Breast Cancer using Paired-End diTags (PETs). 2008.
- Chew Tian Wei. Undergraduate student. Transcription Factor Binding Sites in Mammalian Genomic Repeats. 2008. Project won a Gold medal at the Singapore Science and Engineering Fair (SSEF).
- Thidathip Wongsurawat. Master student. Genome-wide comparison of recombination and rearrangement hotspots. 2006.
- Melvin ZhiYong (co-sup with H-W Leong). Undergraduate student. Rearrangements in genomes with unequal content. 2005.
- Do Hoang (co-sup with H-W Leong). Undergraduate student. Simulating evolution and testing phylogenetic reconstruction methods. 2005.

OTHER ACTIVITIES

- Conference Organizing Committees
 - RECOMB'2008, Singapore, March 2008.
 - Genome Informatics Workshop (GIW'07), Singapore, December 2007.
 - (Co-chair) GEM⁴ Conference on Cancer, Singapore, July 2007.
 - (Co-chair) 4th RECOMB Satellite Workshop on Comparative Genomics, Montreal, September 2006.
 - Workshop on BioAlgorithms, Singapore, July 2006.
 - Workshop on Genomics. Institute for Mathematical Sciences, Singapore, November 2005.
- Editorial Board
 - PLoS ONE
 - Algorithms for Molecular Biology
- Reviewer for:
Genome Research, PLoS Computational Biology, Bioinformatics, Physiological Genomics, IEEE Transactions on Computational Biology and Bioinformatics, BMC Genomics.