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EDUCATION

2006 – 2009	<i>École Polytechnique Fédérale de Lausanne</i>	<i>Ph.D. in Computer Science (Nov. 2009)</i>
2003 – 2005	<i>University of New Mexico</i>	<i>Research Assistant</i>
1996 – 2000	<i>University of New Hampshire</i>	<i>Bachelors of Science</i>

EXPERIENCE

2013 – 2014	Institut de Biologie Computationnelle Postdoctoral fellow with Olivier Gascuel.	<i>Research</i>
2011 – 2013	Université de Montréal and McGill University Postdoctoral fellow with Nadia El-Mabrouk and Mathieu Blanchette.	<i>Research and teaching</i>
2009 – 2011	University of Ottawa and Université du Québec à Montréal Postdoctoral fellow with David Sankoff and Anne Bergeron.	<i>Research</i>
2006 – 2009	École Polytechnique Fédérale de Lausanne, Switzerland Graduate student under Bernard Moret. Gene-order comparison. <i>Teaching Assistant:</i> Algorithms in Computational Biology (for CS students). <i>Teaching Assistant:</i> Computational Biology (for Biology students).	<i>Research and teaching</i>
2003 – 2006	University of New Mexico Gene-order comparison. Orthology inference.	<i>Research</i>
2000 – 2002	Aprisma Management Technologies Network Management Suite. Promoted in half the expected time.	<i>Software Developer</i>
2000 – 2002	University of New Hampshire Calculus and Physics	<i>Teaching Assistant</i>

HONORS:

2012	Best Paper Award at RECOMB (one of two top conferences in computational biology)
2010	Dissertation Award finalist at EPFL
2005	Outstanding Graduate Student award at UNM Computer Science (awarded annually)

SERVICE:

Editorial Board JOURNAL OF COMPUTATIONAL BIOLOGY
BIOINFORMATICS (OXFORD)
ACM JEA – JOURNAL OF EXPERIMENTAL ALGORITHMS
IEEE/ACM TCBB – TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFO.
PLOS COMPUTATIONAL BIOLOGY
JOURNAL OF THEORETICAL BIOLOGY

JOURNAL REFEREE: BULLETIN OF MATHEMATICAL BIOLOGY
BMC BIOINFORMATICS
SIAM JOURNAL ON DISCRETE MATHEMATICS
ALGORITHM FOR MOLECULAR BIOLOGY
DISCRETE APPLIED MATHEMATICS
INFORMATION PROCESSING LETTERS
ALGORITHMS (MDPI)

	Program/Site chair	RECOMB-CG	2019
		RECOMB-CG	2010–2023
		RECOMB	2019–2023
		WABI	2011–2017,2019–2023
CONFERENCE COMMITTEE:		ISMB	2009,2015,2016,2018–2022
		ECCB	2020,2022
		ACM-BCB	2013,2016
		FUN	2010
		ABPC	2015,2016

PUBLICATIONS:

Number of publications in refereed international journals: 31

Refereed conference proceedings (important in Computer Science): 24, 14 extended into a full journal version

Citations (according to Google Scholar): 861

H-index (according to Google Scholar): 18

i10-index (according to Google Scholar): 29

Publications by topic:

- genome rearrangement – [32, 2, 36, 6, 38, 39, 40, 8, 41, 13, 19, 21, 22, 23, 24, 25, 26, 27, 28, 30, 55, 31]
- reconciliation, homology detection, and gene tree correction – [34, 12, 10, 33, 42, 14, 15, 16, 46, 20]
- tree consensus/comparison – [37, 3, 17, 18]
- phylogeny reconstruction – [29, 53]
- virus evolution – [35, 9, 11]
- transcriptomics – [7, 44]
- phylogenetic placement – [4]

Publications by algorithmic technique:

- approximation algorithm – [40, 15, 20, 31]
- linear programming – [38, 13]
- dynamic programming – [32, 36, 3, 42, 13, 17]
- reduction – [34, 38, 6, 8, 10, 15, 46, 25, 28]
- fixed parameter – [10]
- graphs and trees – [32, 34, 3, 36, 6, 38, 8, 9, 10, 12, 33, 15, 42, 14, 16, 17, 18, 46, 20, 21, 22, 25, 26, 28, 29, 55]
- combinatorial modeling – [32, 35, 6, 38, 8, 11, 18, 19, 21, 22, 23, 24, 26, 27, 28, 55]
- heuristic – [16, 18, 46, 25, 28, 29, 30, 53]
- probabilistic – [26, 4]

Journal Publications

- [1] G.W. Coombs, S.L. Baines, B.P. Howden, [K.M. Swenson](#), and F.G. O'Brien. Diversity of bacteriophages encoding Pantone-Valentine leukocidin in temporally and geographically related *Staphylococcus aureus*. *PLoS one*, 15(2):e0228676, 2020. PDF.
- [2] [K.M. Swenson](#) and M. Blanchette. Large-scale mammalian genome rearrangements coincide with chromatin interactions. *Bioinformatics*, 35(14), 07 2019. PDF.
- [3] B.-F. Wang and [K.M. Swenson](#). A faster algorithm for computing the kernel of maximum agreement subtrees. *ACM/IEEE Trans. on Comput. Biology and Bioinformatics*, 6 2019. PDF.
- [4] B. Linard, [K.M. Swenson](#), and F. Pardi. Rapid alignment-free phylogenetic identification of metagenomic sequences. *Bioinformatics*, 35(18):3303–3312, 01 2019. PDF.
- [5] P. Simonaitis, A. Chateau, and [K.M. Swenson](#). A general framework for genome rearrangement with biological constraints. *Algorithms for Mol. Biol.*, 14(15), 2019. PDF.
- [6] P. Simonaitis and [K.M. Swenson](#). Finding local genome rearrangements. *Algorithms for Mol. Biol.*, 13(1):9, 2018. PDF.
- [7] S. Blanquart, J.-S. Varré, Paul Guertin, A. Perrin, A. Bergeron, and [K.M. Swenson](#). Assisted transcriptome reconstruction and splicing orthology. *BMC Genomics*, 17(10):157–164, 2016. PDF.

- [8] [K.M. Swenson](#), P. Simonaitis, and M. Blanchette. Models and algorithms for genome rearrangement with positional constraints. *Algorithms for Molecular Biology*, 11(1):1–10, 2016. PDF.
- [9] S. Bérard, A. Chateau, N. Pompidor, P. Guertin, A. Bergeron, and [K.M. Swenson](#). Aligning the unalignable: bacteriophage whole genome alignments. *BMC Bioinformatics*, 17(1):1–13, 2016. PDF.
- [10] R. Dondi, N. El-Mabrouk, and [K.M. Swenson](#). Gene tree correction for reconciliation and species tree inference: complexity and algorithms. *J. Discrete Algorithms*, 2014. PDF.
- [11] [K.M. Swenson](#), P. Guertin, H. Deschenes, and A. Bergeron. Reconstructing the modular recombination history of staphylococcus aureus phages. *BMC Bioinformatics*, 14(Suppl 15):S17, 2013. PDF.
- [12] M. Lafond, M. Semeria, [K.M. Swenson](#), E. Tannier, and N. El-Mabrouk. Gene tree correction guided by orthology. *BMC Bioinformatics*, 14(Suppl 15):S5, 2013. PDF.
- [13] P. Holloway, [K.M. Swenson](#), D. Ardell, and N. El-Mabrouk. Ancestral genome organization: an alignment approach. *J. Comput. Biology*, 20(4):280–295, 2013. PDF.
- [14] [K.M. Swenson](#) and N. El-Mabrouk. Gene trees and species trees: irreconcilable differences. *BMC Bioinformatics*, 13(Suppl 19):S15, 2012. PDF.
- [15] O. Tremblay-Savard and [K.M. Swenson](#). A graph-theoretic approach for inparalog detection. *BMC Bioinformatics*, 13(Suppl 19):S16, 2012. PDF.
- [16] [K.M. Swenson](#), A. Doroftei, and N. El-Mabrouk. Gene tree correction for reconciliation and species tree inference. *Algorithms for Mol. Biol.*, 7(31), 2012. PDF.
- [17] [K.M. Swenson](#), E. Chen, N.D. Pattengale, and D. Sankoff. The kernel of maximum agreement subtrees. *ACM/IEEE Trans. on Comput. Biology and Bioinformatics*, 9(4):1023–1031, 2012. PDF.
- [18] N.D. Pattengale, A.J. Aberer, [K.M. Swenson](#), A. Stamatakis, and B.M.E. Moret. Uncovering hidden phylogenetic consensus in large datasets. *ACM/IEEE Trans. on Comput. Biology and Bioinformatics*, 8(4):902–911, 2011. PDF.
- [19] [K.M. Swenson](#), G. Badr, and D. Sankoff. Listing all sorting reversals in quadratic time. *Algorithms for Mol. Biol.*, 6(11), 2011. PDF.
- [20] A. Ouangraoua, [K.M. Swenson](#), and C. Chauve. A 2-approximation for the minimum duplication speciation problem. *J. Comput. Biology*, 18(9), 2011. PDF.
- [21] A. Ouangraoua, [K.M. Swenson](#), and A. Bergeron. Theory and practice of ultra-perfection. *J. Comput. Biology*, 18(9), 2011. PDF.
- [22] G. Badr, [K.M. Swenson](#), and D. Sankoff. Listing all parsimonious reversal sequences: new algorithms and perspectives. *J. Comput. Biology*, 18(9), 2011. PDF.
- [23] [K.M. Swenson](#), V. Rajan, Y. Lin, and B.M.E. Moret. Sorting signed permutations by inversions in $O(n \log n)$ time. *J. Comput. Biology*, 17(3):489–501, 2010. PDF.
- [24] Y. Lin, V. Rajan, [K.M. Swenson](#), and B.M.E. Moret. Estimating true evolutionary distances under rearrangements, duplications, and losses. *BMC Bioinformatics*, 11(Suppl 1):54, 2010. PDF.
- [25] V. Rajan, A.W. Xu, Y. Lin, K M. Swenson, and B.M.E. Moret. Heuristics for the inversion median problem. *BMC Bioinformatics*, 11(Suppl 1):54, 2010. PDF.
- [26] I. Miklós, B. Mélykúti, and [K.M. Swenson](#). The metropolized partial importance sampling mcmc mixes slowly on minimum reversal rearrangement paths. *ACM/IEEE Trans. on Comput. Biology and Bioinformatics*, 7(4), 2010. PDF.
- [27] [K.M. Swenson](#), Y. Lin, V. Rajan, and B.M.E. Moret. Hurdles and sorting by inversions: combinatorial, statistical, and experimental results. *J. Comput. Biology*, 16(10):1339–1351, 2009. PDF.
- [28] [K.M. Swenson](#), Y. To, J. Tang, and B.M.E. Moret. Maximum independent sets of commuting and noninterfering inversions. *BMC Bioinformatics*, 10(Suppl 1), 2009. PDF.
- [29] [K.M. Swenson](#) and B.M.E. Moret. Inversion-based genomic signatures. *BMC Bioinformatics*, 10(Suppl 1), 2009. PDF.
- [30] [K.M. Swenson](#), M. Marron, J.V Earnest-Deyoung, and B.M.E. Moret. Approximating the true evolutionary distance between two genomes. *ACM J. Experimental Algorithmics*, 12:1–17, 2008. PDF.
- [31] M. Marron, [K.M. Swenson](#), and B.M.E. Moret. Genomic distances under deletions and insertions. *Theor. Computer Science*, 325(3):347–360, 2004. PDF.

Book Chapters

- [32] A. Bergeron and [K.M. Swenson](#). Un siècle de réarrangements génomiques. In Gilles Didier and Stéphane Guindon, editors, *Modèles et méthodes pour l'évolution biologique*, pages 127–150. ISTE Editions Ltd, 27-37 St George's Road, London, UK, 2022. PDF.
- [33] M. Lafond, [K.M. Swenson](#), and N. El-Mabrouk. Error detection and correction of gene trees. In C. Chauve, N. El-Mabrouk, and E. Tannier, editors, *Models and Algorithms for Genome Evolution*, pages 261–285. Springer London, 2013. PDF.

Conference Publications

- [34] [K.M. Swenson](#), A. Elghraoui, F. Valafar, S. Mirarab, and M. Weller. Quantifying hierarchical conflicts in homology statements. In *Proc. 19th Workshop Comp. Genomics (RECOMB-CG'22)*, volume 13234 of *Lecture Notes in Computer Science*, pages 146–167, 2022. PDF.
- [35] A. Bergeron, M-J. Meurs, R. Valiquette-Labonté, and [K.M. Swenson](#). On the comparison of bacteriophage populations. In *Proc. 19th Workshop Comp. Genomics (RECOMB-CG'22)*, volume 13234 of *Lecture Notes in Computer Science*, pages 3–20, 2022. PDF.
- [36] P. Simonaitis, A. Chateau, and [K.M. Swenson](#). Weighted minimum-length rearrangement scenarios. In *Proc. 19th Int'l Workshop Algs. in Bioinformatics (WABI'19)*, volume 143 of *Leibniz International Proceedings in Informatics (LIPIcs)*, pages 13:1–13:17, Dagstuhl, Germany, 2019. PDF.
- [37] J. Truszkowski, O. Gascuel, and [K.M. Swenson](#). Rapidly computing the phylogenetic transfer index. In *Proc. 19th Int'l Workshop Algs. in Bioinformatics (WABI'19)*, volume 143 of *Leibniz International Proceedings in Informatics (LIPIcs)*, pages 20:1–20:12, Dagstuhl, Germany, 2019. PDF.
- [38] P. Simonaitis, A. Chateau, and [K.M. Swenson](#). A general framework for genome rearrangement with biological constraints. In *Proc. 16th Workshop Comp. Genomics (RECOMB-CG'18)*, volume 11183 of *Lecture Notes in Bioinformatics*, pages 49–71. Springer Verlag, Berlin, 2018. PDF *.
- [39] S. Pulicani, P. Simonaitis, E. Rivals, and [K.M. Swenson](#). Rearrangement scenarios guided by chromatin structure. In *Proc. 15th Workshop Comp. Genomics (RECOMB-CG'17)*, volume 10562 of *Lecture Notes in Bioinformatics*, pages 141–155. Springer Verlag, Berlin, 2017. PDF.
- [40] P. Simonaitis and [K.M. Swenson](#). Finding Local Genome Rearrangements. In *Proc. 17th Int'l Workshop Algs. in Bioinformatics (WABI'17)*, volume 88 of *Leibniz International Proceedings in Informatics (LIPIcs)*, pages 24:1–24:13, Dagstuhl, Germany, 2017. PDF *.
- [41] [K.M. Swenson](#) and M. Blanchette. Models and algorithms for genome rearrangement with positional constraints. In *Proc. 15th Int'l Workshop Algs. in Bioinformatics (WABI'15)*, pages 243–256. Springer Verlag, Berlin, 2015. PDF *.
- [42] M. Lafond, [K.M. Swenson](#), and N. El-Mabrouk. An optimal reconciliation algorithm for gene trees with polytomies. In *Proc. 12th Int'l Workshop Algs. in Bioinformatics (WABI'12)*, volume 7534 of *Lecture Notes in Computer Science*, pages 106–122. Springer Verlag, Berlin, 2012. PDF.
- [43] P. Holloway, [K.M. Swenson](#), D. Ardell, and N. El-Mabrouk. Evolution of genome organization by duplication and loss: an alignment approach. In *Proc. 16th Ann. Int'l Conf. Comput. Mol. Biol. (RECOMB'12)*, volume 7262 of *Lecture Notes in Computer Science*, pages 94–112. Springer Verlag, Berlin, 2012. PDF *.
- [44] A. Ouangraoua, [K.M. Swenson](#), and A. Bergeron. On the comparison of sets of alternative transcripts. In *Proc. 8th Inter. Symp. on Bioinform. and Applic. (ISBRA'12)*, volume 7292 of *Lecture Notes in Computer Science*, pages 201–212. Springer Verlag, Berlin, 2012. PDF.
- [45] [K.M. Swenson](#), E. Chen, N.D. Pattengale, and D. Sankoff. The kernel of maximum agreement subtrees. In *Proc. 7th Inter. Symp. on Bioinform. and Applic. (ISBRA'11)*, volume 6674 of *Lecture Notes in Computer Science*, pages 123–135. Springer Verlag, Berlin, 2011. PDF *.
- [46] C. Zheng, [K.M. Swenson](#), E. Lyons, and D. Sankoff. OMG! orthologs in multiple genomes - competing graph-theoretical formulations. In *Proc. 11th Int'l Workshop Algs. in Bioinformatics (WABI'11)*, volume 6833 of *Lecture Notes in Computer Science*, pages 364–375. Springer Verlag, Berlin, 2011. PDF.
- [47] [K.M. Swenson](#), G. Badr, and D. Sankoff. Listing all sorting reversals in quadratic time. In *Proc. 10th Int'l Workshop Algs. in Bioinformatics (WABI'10)*, volume 6293 of *Lecture Notes in Computer Science*, pages 102–110. Springer Verlag, Berlin, 2010. PDF *.

- [48] A. Ouangraoua, A. Bergeron, and K.M. Swenson. Ultra-perfect sorting scenarios. In *Proc. 6th Workshop Comp. Genomics (RECOMB-CG'10)*, volume 6398 of *Lecture Notes in Computer Science*, pages 50–61. Springer Verlag, Berlin, 2010. PDF *.
- [49] A. Ouangraoua, K.M. Swenson, and C. Chauve. An approximation algorithm for computing a parsimonious first speciation in the gene duplication model. In *Proc. 6th Workshop Comp. Genomics (RECOMB-CG'10)*, volume 6398 of *Lecture Notes in Computer Science*, pages 290–302. Springer Verlag, Berlin, 2010. PDF *.
- [50] N.D. Pattengale, K.M. Swenson, and B.M.E. Moret. Uncovering hidden phylogenetic consensus. In *Proc. Bioinformatics Research and Applications, 6th International Symposium, ISBRA'10*, volume 6053 of *Lecture Notes in Computer Science*, pages 128–139. Springer Verlag, Berlin, 2010. PDF *.
- [51] G. Badr, K.M. Swenson, and D. Sankoff. Listing all parsimonious reversal sequences: new algorithms and perspectives. In *Proc. 6th Workshop Comp. Genomics (RECOMB-CG'10)*, volume 6398 of *Lecture Notes in Computer Science*, pages 39–48. Springer Verlag, Berlin, 2010. PDF *.
- [52] K.M. Swenson, V. Rajan, Y. Lin, and B. M. E. Moret. Sorting signed permutations by inversions in $O(n \log n)$ time. In *Proc. 13th Ann. Int'l Conf. Comput. Mol. Biol. (RECOMB'09)*, volume 5541 of *Lecture Notes in Computer Science*, pages 386–399. Springer Verlag, Berlin, 2009. PDF *.
- [53] K.M. Swenson, W. Arndt, J. Tang, and B.M.E. Moret. Phylogenetic reconstruction from complete gene orders of whole genomes. In *Proc. 6th Asia Pacific Bioinformatics Conf. (APBC'08)*, pages 241–250, 2008. PDF.
- [54] K.M. Swenson, Y. Lin, V. Rajan, and B.M.E. Moret. Hurdles hardly have to be heeded. In *Proc. 6th Workshop Comp. Genomics (RECOMB-CG'08)*, volume 5267 of *Lecture Notes in Computer Science*, pages 241–251. Springer Verlag, Berlin, 2008. PDF *.
- [55] K.M. Swenson, N.D. Pattengale, and B.M.E. Moret. A framework for orthology assignment from gene rearrangement data. In *Proc. 3rd Workshop Comp. Genomics (RECOMB-CG'05)*, pages 153–166. Springer Verlag, Berlin, 2005. PDF.
- [56] K.M. Swenson, M. Marron, J.V. Earnest-DeYoung, and B.M.E. Moret. Approximating the true evolutionary distance between two genomes. In *Proc. 7th SIAM Workshop on Algorithm Engineering & Experiments (ALENEX'05)*, pages 121–129. SIAM Press, Philadelphia, 2005. PDF *.
- [57] M. Marron, K.M. Swenson, and B.M.E. Moret. Genomic distances under deletions and insertions. In *Proc. 9th Int'l Conf. Computing and Combinatorics (COCOON'03)*, volume 2697 of *Lecture Notes in Computer Science*, pages 537–547. Springer Verlag, Berlin, 2003. PDF *.

* conference article corresponding to a full journal publication