

C U R R I C U L U M V I T A E

Edward Susko

ACADEMIC POSITIONS

2008-	FULL PROFESSOR	Dalhousie University
2003-2008	ASSOCIATE PROFESSOR	Dalhousie University
1998-2003	ASSISTANT PROFESSOR	Dalhousie University
1996-1998	NSERC POSTDOCTORAL FELLOW	University of Toronto

DEGREES

1996	PH.D.	Statistics, Waterloo
1992	M.SC.	Statistics, British Columbia
1990	B.A.	Mathematics, Windsor

AWARDS and HONOURS

2015-2020	Killam Professor of Mathematics and Statistics, Dalhousie University
2011	CRM-SSC Prize <i>Awarded by the Centre De Recherches Mathématiques and Statistical Society of Canada for outstanding research achievements by a statistical scientist within the first fifteen years following their PhD</i>
2005-2007	Fellow of the CIAR program in Evolutionary Biology
2002-2004	Associate Member of the CIAR program in Evolutionary Biology
2001	CJS Award <i>Awarded for the best paper in the Canadian Journal of Statistics</i>
1996	Pierre Robillard Award <i>Awarded by the Statistical Society of Canada for the best PhD thesis in the statistical sciences</i>
1996-1997	NSERC Postdoctoral Fellowship, University of Toronto
1992-1995	Mathematics Faculty Graduate Scholarship, Waterloo
1992-1994	NSERC Postgraduate Scholarship, Waterloo
1993	University Graduate Scholarship, Waterloo
1990-1992	NSERC Postgraduate Scholarship, British Columbia
1990	University Graduate Fellowship, British Columbia
1986-1990	Undergraduate Teaching Assistantship Award, Windsor <i>(full tuition + stipend)</i>
1986	Entrance Award, Windsor

REFEREED JOURNAL PUBLICATIONS

1. Mingrone, J., **Susko, E.** and Bielawski, J.P. (2019). ModL: exploring and restoring regularity when testing for positive selection *Bioinformatics. Advance Access*. <https://doi.org/10.1093/bioinformatics/bty1019>
2. Roger, A.J. and **Susko, E.** (2018). Evidence for an ancient origin of extant methanogenic archaeal lineages is weak. *Nature Ecology and Evolution*. **2**:1676–1677.
3. Jones, C.T, Youssef, N., Bielawski, J.P. and **Susko, E.** (2018). Phenomenological load on model parameters can lead to false biological conclusions. *Molecular Biology and Evolution*. **35**:1473-1488.
4. **Susko, E.**, Lincker, L. and Roger, A.J. (2018). Accelerated estimation of frequency classes in site-heterogeneous profile mixture models. *Molecular Biology and Evolution*. **35**:1266-1283.
5. Wang, H., Minh, B., **Susko, E.** and Roger, A.J. (2018). Modeling site heterogeneity with posterior mean site frequency profiles accelerates accurate phylogenomic estimation. *Systematic Biology*. **67**:216–235.
6. **Susko, E.** (2017). Bayes factor biases for non-nested models and corrections. *Canadian Journal of Statistics*. **9**:290-309.
7. Robicbeau, B.M., **Susko, E.**, Harrigan, A.M. and Snyder, M. (2017). The surprising link between the concerted evolution of rRNA genes, non-coding ‘junk’ DNA and eukaryotic genome size. *Genome Biology and Evolution*. **9**:380-397.
8. Sokol, M., Žihala, D., Romain, D., Klimeš, V., Hradilová, M., Zadroblková, **Susko, E.**, Roger, A.J., Čepička, I. and Elias, M. (2017). Nuclear genetic codes with a different meaning of the UAG and the UAA codon. *BMC Biology*. **15**:8
9. Jones, C.T, Youssef, N., **Susko, E.** and Bielawski, J.P. (2017). Shifting balance on a static mutation-selection landscape: a novel scenario of positive selection. *Molecular Biology and Evolution*. **34**:391-407.
10. Mingrone, J., **Susko, E.** and Bielawski, J.P. (2016). Smoothed bootstrap aggregation for assessing selection pressure at amino acid sites. *Molecular Biology and Evolution*. **33**:2976–2989.
11. Wang, H., **Susko, E.** and Roger, A.J. (2016). Split-specific bootstrap measures for quantifying phylogenetic stability and the influence of taxon selection. *Molecular Phylogenetics and Evolution*. **105**:114–125.
12. **Susko, E.** (2015). Bayesian long branch attraction bias and corrections. *Systematic Biology*. **64**:243–255.
13. Karin, E.L., **Susko, E.** and Pupko, T. (2014). Alignment errors strongly impact likelihood-based tests for comparing topologies. *Molecular Biology and Evolution*. **31**:3057–3067.

14. Stairs, C.W., Eme, L., Brown, M.W., Mutsaers, C., **Susko, E.**, Dellaire, G., Soanes, D.M., van der Giezen, M. and Roger, A.J. (2014). A SUF Fe-S Cluster Biogenesis System in the Mitochondrion-Related Organelles of the Anaerobic Protist *Pygsuia*. *Current Biology*. **24**:1–11.
15. Wang, H., **Susko, E.** and Roger, A.J. (2014). An amino acid substitution-selection model adjusts residue fitness to improve phylogenetic estimation. *Molecular Biology and Evolution*. **31**:779–792.
16. **Susko, E.** (2014). Tests for two trees using likelihood methods. *Molecular Biology and Evolution*. **31**:1029–1039.
17. **Susko, E.** (2013). Likelihood ratio tests with boundary constraints using data-dependent degrees of freedom. *Biometrika*. **100**:1019–1023.
18. Hleap, J.S., **Susko, E.** and Blouin, C. (2013). Defining structural and evolutionary modules in proteins: A community detection approach to explore sub-domain architecture. *BMC Structural Biology*. **13**:20.
19. Wang, H., **Susko, E.** and Roger, A.J. (2013). The site-likelihood score is a good predictor of sites under positive selection. *Journal of Molecular Evolution*. **76**:280–294.
20. **Susko, E.** and Roger, A.J. (2013). Problems with estimation of ancestral frequencies under stationary models. *Systematic Biology*. **62**:330–338.
21. Zou, L., **Susko, E.**, Field, C. and Roger, A.J. (2012). Fitting nonstationary general-time-reversible models to obtain edge-lengths and frequencies for the Barry-Hartigan model. *Systematic Biology*. **61**:927–940.
22. **Susko, E.** and Roger, A.J. (2012). The Probability of correctly resolving a split as an experimental design criterion in phylogenetics. *Systematic Biology*. **61**:811–821.
23. Zou, L., Field, C., **Susko, E.** and Roger, A.J. (2011). The Barry and Hartigan general Markov model suffers from statistical non-identifiability. *Systematic Biology*. **60**:872–875.
24. Gaston, D., Roger, A.J. and **Susko, E.** (2011). A phylogenetic mixture model for the identification of functionally divergent protein residues. *Bioinformatics*. **27**:2655–2663.
25. Stokesbury, M.J.W, Neilson, J.D., **Susko, E.** and Cooke, S.J. (2011). Estimating mortality of Atlantic bluefin tuna (*Thunnus thynnus*) in an experimental recreational catch-and-release fishery. *Biological Conservation*. **144**:2684–2691.
26. **Susko, E.** (2011). Improved Least Squares Topology Testing and Estimation. *Systematic Biology*. **60**:668–675.
27. Wang, H., **Susko, E.** and Roger, A.J. (2011). Fast statistical tests for detecting heterotachy in protein evolution. *Molecular Biology and Evolution*. **28**:2289–2303.
28. Wu, J. and **Susko, E.** (2011). A Test for Heterotachy Using Multiple Pairs of Sequences. *Molecular Biology and Evolution*. **28**:1661–1673.

29. **Susko, E.** (2011). Large sample approximations of probabilities of correct evolutionary tree estimation and biases of maximum likelihood estimation. *Statistical Applications in Genetics and Molecular Biology*. **10**(1), Article 10.
30. Sangaralingam, A. **Susko, E.**, Bryant, D. and Spencer, M. (2010). Conditioned genome reconstruction: a case study with three ortholog databases *BMC Evolutionary Biology*. **10**:343.
31. **Susko, E.** (2010). First-Order correct bootstrap support adjustments for splits that allow hypothesis testing when using maximum likelihood estimation. *Molecular Biology and Evolution*. **27**:1621–1629.
32. Wu, J. and **Susko, E.** (2010). Rate-variation need not defeat phylogenetic inference through pairwise sequence comparisons. *Journal of Theoretical Biology*. **263**:587–589.
33. Blouin, C., Perry, S., **Susko, E.** and Roger, A.J. (2009). Reproducing the manual annotation of multiple sequence alignments using a SVM classifier. *Bioinformatics*. **25**:3093–3098.
34. Wang, H., **Susko, E.** and Roger, A.J. (2009). PROCOV: maximum likelihood estimation of protein phylogeny under covarion models. *BMC Evolutionary Biology*. **9**:225.
35. Wu, J. and **Susko, E.** (2009). General heterotachy and distance method adjustments. *Molecular Biology and Evolution*. **26**:2689–2697.
36. **Susko, E.** (2009). Bootstrap support is not first order correct. *Systematic Biology*. **58**:211–223.
37. Wang, H., Li, K., **Susko, E.** and Roger, A.J. (2008). A class frequency mixture model that adjusts for site-specific amino acid frequencies and improves inference of protein phylogeny. *BMC Evolutionary Biology*. **8**:331.
38. **Susko, E.** (2008). On the distributions of bootstrap support and posterior distributions for a star tree. *Systematic Biology*. **57**:602–612.
39. Wu, J. **Susko, E.** and Roger, A.J. (2008). An independent heterotachy model and its implications for phylogeny and divergence time estimation. *Molecular Phylogenetics and Evolution*. **46**:801–806.
40. Leigh, J.W., **Susko, E.**, Baumgartner, M. and Roger, A.J. (2008). Testing phylogenetic congruence in phylogenomic analysis. *Systematic Biology*. **57**:104–115.
41. Wang, H., **Susko, E.**, Spencer, M. and Roger, A.J. (2008). Topological estimation biases with covarion evolution. *Journal of Molecular Evolution*. **66**:50–60.
42. Baptiste, E., **Susko, E.**, Leigh, J., Trillo, I.R., Bucknam, J. and Doolittle, W.F. (2008). Alternative methods of concatenation of core life genes indicate a lack of resolution in deep nodes of the prokaryotic phylogeny. *Molecular Biology and Evolution*. **25**:83–91.
43. **Susko, E.** and Roger, A.J. (2007). On reduced amino acid alphabets for phylogenetic inference. *Molecular Biology and Evolution*. **24**:2139–2150.

44. Spencer, M., Bryant, D. and **Susko, E.** (2007). Conditioned genome reconstruction: how to avoid choosing the conditioning genome. *Systematic Biology*. **56**:25–43.
45. Wang H., Spencer, M., **Susko, E.** and A. J. Roger (2007). Testing for Covarion-like Evolution in Protein Sequences. *Molecular Biology and Evolution*. **24**:294–305.
46. Filée, J., Bapteste, E., **Susko, E.**, Krisch, H.M. (2006). A selective barrier to horizontal gene transfer in the T4-type bacteriophages has preserved a core genome with the viral replication and structural genes. *Molecular Biology and Evolution*. **23**: 1688–1696.
47. Spencer, M., **Susko, E.** and Roger, A.J. (2006). Modeling prokaryote gene content. *Evolutionary Bioinformatics Online*. **6**:165–186.
48. **Susko, E.** (2006). Using minimum bootstrap support for splits to construct confidence regions for trees. *Evolutionary Bioinformatics Online*. **2**:137–151.
49. Inagaki, Y. **Susko, E.** and Roger, A.J. (2006). Recombination between elongation factor 1 α genes from distantly-related archaeal lineages. *Proceedings of the National Academy of Sciences*. **103**:4528–4533.
50. **Susko, E.**, Leigh, J., Doolittle, W.F. and Bapteste, E. (2006). Visualizing and assessing phylogenetic congruence of core gene sets: a case study of the γ -proteobacteria. *Molecular Biology and Evolution*. **23**:1019–1030.
51. Wang, H., **Susko, E.** and Roger, A.J. (2006). On the correlation between genomic G+C content and optimal growth temperature in prokaryotes: data quality and confounding factors. *Biochemical and Biophysical Research Communications*. **342**:681–684.
52. Shi, X., Gu, H., **Susko, E.** and Field, C. (2005). The comparison of confidence regions in phylogeny. *Molecular Biology and Evolution*, **22**:2285–2296.
53. Spencer, M. and **Susko, E.** (2005). Continuous-time Markov models for species interactions. *Ecology*, **86**:3272–3278.
54. **Susko, E.**, Spencer, M. and Roger, A.J. (2005). Biases in Phylogenetic Estimation can be caused by Random Sequence Segments. *Journal of Molecular Evolution*, **61**:351–359.
55. Spencer, M., **Susko, E.** and Roger, A.J. (2005). Likelihood, parsimony and heterogeneous evolution. *Molecular Biology and Evolution*, **22**:1161–1164.
56. Bapteste, E. , **Susko, E.**, Leigh, J., MacLeod D., Charlebois, R.L., and W.F. Doolittle (2005). Do orthologous gene phylogenies really support tree thinking? *BMC Evol. Biol.*, **5**:33.
57. **Susko, E.** and Roger, A.J. (2004). Estimating and comparing the rates of gene discovery and expressed sequence tag (EST) frequencies in EST surveys. *Bioinformatics*, **20**:2279–2287.
58. **Susko, E.**, Inagaki, Y. and Roger A.J. (2004). On inconsistency of the neighbour joining method and least squares estimation when distances are incorrectly specified. *Molecular Biology and Evolution*, **29**:1629–1642.

59. Inagaki, Y., **Susko, E.**, Fast, N.M. and Roger, A.J. (2004). Covarion shifts cause a long branch attraction artifact that unites microsporidia and archaeobacteria in EF-1 α phylogenies. *Molecular Biology and Evolution*, **21**:1340–1349.
60. Shan, Y., Milios, E., Roger, A., Blouin, C. and **Susko, E.** (2003) Automatic recognition of regions of intrinsically poor multiple alignment. *Proceedings of the 2003 IEEE Bioinformatics Conference (CSB2003)*. 482–483.
61. **Susko, E.**, Field, C., Blouin, C. and Roger, A.J. (2003). Estimation of rates-across-sites distributions in phylogenetic substitution models. *Systematic Biology*, **52**, 594–603.
62. Inagaki, Y., Blouin, C., **Susko, E.** and Roger A.J. (2003). Assessing functional divergence of EF-1 α and its paralogues in eukaryotes and archaeobacteria. *Nucleic Acids Research*, **31**, 4227–4237.
63. **Susko, E.** (2003). Confidence regions and hypothesis tests for topologies using generalized least squares. *Molecular Biology and Evolution*, **20**, 862–868.
64. **Susko, E.** (2003). Weighted Tests of Homogeneity for Testing the Number of Components in a Mixture. *Journal of Computational Statistics and Data Analysis: Special Issue on Mixtures*, **41**, 367–378.
65. **Susko, E.** and Nadon, R. (2002). Estimation of a residual distribution with small numbers of repeated measurements, *Canadian Journal of Statistics*, **30**, 383–400.
66. **Susko, E.**, Inagaki, Y., Field, C., Holder, M.E. and Roger, A.J. (2002). Testing for Differences in Rates Across Sites Distributions in Phylogenetic Subtrees. *Molecular Biology and Evolution*, **19**, 1514–1523.
67. **Susko, E.**, Chen, J. and Kalbfleisch, J.D. (2001). A Diagnostic Tool for Mixture Models. *Journal of Statistical Computation and Simulation*, **69**, 293–314.
68. **Susko, E.**, Bronskill, M.J., Graham, S.J. and Tibshirani R. (2001). Estimation of Relaxation Time Distributions in Magnetic Resonance Imaging. *Canadian Journal of Statistics*, **29**, 379–394. *Winner of the 2001 CJS Award for the best paper in the Canadian Journal of Statistics*
69. **Susko, E.**, Kalbfleisch, J.D. and Chen, J. (1998). Constrained Nonparametric Mixture Maximum Likelihood Estimation. *Canadian Journal of Statistics*, **26**, 601-617.
70. Joe, H., Steyn, D. and **Susko, E.** (1996). Analysis of Trends in Tropospheric Ozone in the Lower Fraser Valley, British Columbia. *Atmospheric Environment*, **30**, 3413-3421.
71. Liu, J. and **Susko, E.** (1992). On Strict Stationarity and Ergodicity of a Non-linear ARMA Model. *Journal of Applied Probability* **29**, 363-373.

ADDITIONAL PUBLICATIONS

1. Jones, C.T. **Susko, E.** and Bielawski, J.P. (2018). Looking for Darwin in genomic sequences: validity and success depends on the relationship between model and data. In *Evolutionary Genomics: Statistical and Computational Methods*. Maria Anisimova (ed.) 2nd edition (In Press), Humana press.

2. **Susko, E.** (2016). Tree Support Measures. In: Kliman, R.M. (ed.), *Encyclopedia of Evolutionary Biology*. vol. 4, pp. 256–260. Oxford: Academic Press.
3. **Susko, E.** and Roger, A.J. (2009). Chapter 13. Statistical analysis of expressed sequence tags. In: *Methods in Molecular Biology - ESTs: Generation and Analysis*, John Parkinson (Ed.), Humana Press. **533**::277–287.
4. Nadon, R., Woody, E., Shi, P., Rghei, N., Hubschle, H., **Susko, E.**, & Ramm, P. (2002). Statistical inference in array genomics. In *Microarrays for the Neurosciences: An Essential Guide*, Daniel Geschwind & Jeffrey Gregg Eds. Cambridge, MA: MIT Press (pp. 109-140).
5. Nadon, R., Shi, P., Skandlis, A., Woody, E., Hubschle, H., **Susko, E.**, Rghei, N. and Ramm, P. (2001). Statistical Inference Methods for Gene Expression Arrays. In "Microarrays: Optical Technologies and Informatics", M. L. Bittner, Y. Chen, A. N. Dorsel, E. R. Dougherty, Eds. *Proceedings of SPIE*, **4266**, 46–55.
6. **Susko, E.**, Kalbfleisch, J.D. and Chen, J. (1999). Computational approaches for Mixture Estimation. In *Proceedings of the Interface: Models, Predictions and Computing*, Ken Berk and Mohsen Pourhadi, Editors, **31**, 432-438.
7. **Susko, E.** and Lindsay, B.G. (1996) Likelihood Ratio Statistic Tests of Mixture Hypotheses for Multinomial Models. *Technical Report 96-5, Center for Likelihood Studies, Department of Statistics, Penn State University*

SUBMITTED or UNDER REVISION

1. Wang, H., **Susko, E.** and Roger, A.J. (2018). The relative importance of modeling site pattern heterogeneity versus partition-wise heterotachy in phylogenomic inference. *Under revision for Systematic Biology*.
2. Roger, A., Munoz-Gomez, S., Hess, S., Burger, G., Lang, B., **Susko, E.**, and Slamovitz, C. (2018). An updated phylogeny of the Alphaproteobacteria reveals that the parasitic Rickettsiales and Holosporales have independent origins. *Submitted to The ISME Journal*.

THESES

DOCTORAL DISSERTATION TITLE: Nonparametric Maximum Likelihood Estimation for Mixture Models. *Winner of the 1996 Pierre Robillard Award, awarded by the Statistical Society of Canada for the best PhD thesis in the statistical sciences.*

SUPERVISORS: John D. Kalbfleisch and Jiahua Chen

M.Sc. THESIS TITLE: Segmented Regression Modelling with an Application to German Exchange Rate Data.

SUPERVISOR: Jian Liu

GRANTS

2015-2020	2,000/yr	Killam Professor Support Susko, E.
2014-2019	23,000/yr	NSERC Discovery Grant Statistical Methods for Molecular Evolution Susko, E.
2013	\$10,854	NSERC Equipment Grant High-performance computing cluster for research and training in mathematics and statistics Brown, J., Dilcher, K., Faridi, S., Field, C.A., Iron, D., Janssen, J., Kolokolnikov, T. (<i>PI</i>), Nowakowski, R. and Susko, E.
2008-2013	\$21,000/yr	NSERC Discovery Grant Statistical Evolutionary Bioinformatics Susko, E.
2008	\$3,000,000	TULA Foundation Grant Founding of Centre for Comparative Genomics and Evolutionary Bioinformatics Archibald, J.M, Beiko, R.G., Bielawski, J., Blouin, C., Doolittle, W.F., Gray, M.W., Simpson, A.G.B., Roger, A.J. (<i>PI</i>), Susko, E.
2007	\$55,591	NSERC Equipment Grant An Xserve computer cluster for phylogenetic and comparative ge- nomic analyses Archibald, J.M., Roger, A.J. (<i>PI</i>) Simpson, A.G. and Susko, E.
2006-2009	\$141,917/yr	CIHR Operating Grant Integron metagenomics Doolittle, W.F. (<i>PI</i>), Stokes, Hatch and Susko, E.
2004-2006	\$60,000/yr	NPCDS Grant Canadian Consortium on Statistical Genomics Bingham, D., Bryan, J., Chipman, H., Kustra, R., Murdoch, D., Nadon, R., Susko, E. and Tibshirani, R.J.
2004	\$28,000	NSERC Equipment Grant Upgrade of sun computer system with new cluster Bielawski, J., Dowd, M., Field, C.A., Hamilton, D., Smith, B. and Susko, E.
2003-2008	\$19,000/yr	NSERC Discovery Grant Mixture models and molecular evolution Susko, E.
2002-2006	\$4,442,900	Genome Canada Grant A comparative understanding of prokaryotic evolution and diversity: from genomics to metagenomics Doolittle, W.F. (<i>PI</i>), Mulligan, M.E., Rannala, B., Roger, A.J., Smith, B.R. and Susko, E.
2000	\$70,476	NSERC Equipment Grant Sun server for system upgrade Field, C.A., Hamilton, D., Smith, B. and Susko, E.
1999-2003	\$12,000/yr	NSERC Operating Grant Nonparametric Mixture Models Susko, E.

1999 **\$17,163** NSERC Equipment Grant
Computer upgrade for computationally intensive statistics research
Field, C.A., Hamilton, D., Smith, B. and Susko, E.

EDITORIAL ACTIVITIES

2010– Associate Editor, Systematic Biology
2007–2018 Associate Editor, Canadian Journal of Statistics

REVIEW RESPONSIBILITIES

American Naturalist (1)
Annals of Statistics (1)
Annals of Applied Statistics (1)
Bioinformatics (12)
Biometrics (2)
Biometrika (1)
BMC Bioinformatics (3)
BMC Biology (1)
BMC Evolutionary Biology (9)
BMC Genomics (1)
Canadian Journal of Statistics (6)
Clinical Cancer Research (1)
Computational Statistics and Data Analysis (2)
Current Biology (2)
Discrete Applied Mathematics (1)
Evolutionary Bioinformatics (2)
Evolutionary Biology Online (1)
FEBS Letters (1)
Genes (1)
Genome (1)
Genome Biology and Evolution (7)
IEEE/ACM Transactions on Computational Biology and Bioinformatics (1)
Journal of Applied Probability (1)
Journal of Molecular Evolution (1)
Journal of Multivariate Analysis (1)
Journal of Theoretical Biology (5)
Methods in Ecology and Evolution (1)
Molecular Biology and Evolution (31)
Molecular Phylogenetics and Evolution (1)
Nature (2)
Nature Communications (1)
Nature Methods (1)
Philosophical Transactions of the Royal Society, Series B: Biological Sciences (1)
PloS One (1)
Probability Theory and Related Fields (1)
Proceedings of *Mathematics of Evolution and Phylogenetics* (1)

Recomb-2005 (2)
Science (2)
Statistical Science (1)
Statistica Sinica (1)
Systematic Biology (22)
Trends in Ecology and Evolution (2)
Theoretical Population Biology (1)
Zoology (1)

Operating Grant Reviewer, NSERC (18)
Marsden Fund Grant Reviewer, New Zealand (2)
NSF Reviewer, Systematic Biology Panel (2)
US-Israel BSF Reviewer (1)
Tenure Reviewer (5)
Promotion Reviewer (1)

EVENT ADMINISTRATION

2015–2016 SSC 2016 Program Chair
2011–2015 SSC 2015 Local Arrangements Chair
2013 Program Committee Member for ISMB 2013
2012 NSERC Mathematics and Statistics Evaluation Group Committee Member
2011 Program Committee Member for ACM Conference on Bioinformatics,
Computational Biology and Biomedicine (BCB) 2011
2010 Program Committee Member for ISMB 2010
2006–2007 Organizing Committee, SMBE 2007
2006 Program Committee Member for Asia Pacific Bioinformatics Conference 2007
2005–2010 Editorial Board, Systematic Biology
2005–2007 Pierre Robillard Committee, Statistical Society of Canada
2005 Program Committee Member for ISMB 2005

COMMITTEE MEMBERSHIP

2016–2019 SSC/CRM Award Committee
2016– NSERC Mathematics and Statistics Liaison Committee
2012 NSERC Mathematics and Statistics Evaluation Group Committee Member
2005–2010 Editorial Board, Systematic Biology
2005–2007 Pierre Robillard Committee, Statistical Society of Canada

SELECTED PRESENTATIONS

1. Montreal, Canada, June, 2018. Estimation of Frequency Classes in Site-heterogeneous Phylogenetic Mixture Models 2018 Annual Meeting of the Statistical Society of Canada (SSC). Invited Speaker.
2. Halifax, Nova Scotia, October 2017. Bayes Factor Biases for Non-nested Models and Corrections. Mathematics and Statistics Colloquium, Dalhousie University.

3. Waterloo, Ontario, July 2017. Bayes Factor Biases for Non-nested Models and Corrections. Celebrating 50 years of Statistics and Actuarial Science. Invited Speaker.
4. Wolfville, Nova Scotia, October 2015. Phylogenetic Estimation and Inference. The Atlantic Universities Mathematics, Statistics and Computer Science Conference. Plenary Speaker.
5. Boston, Massachusetts, August 2014. Tests for Two Trees using Likelihood Methods. Joint Statistical Meetings (JSM). Invited Speaker.
6. Centre de recherches mathématiques (CRM), Montreal, Canada, September 2013. Tests for Two Trees using Likelihood Methods. Workshop on Mathematics of Sequence Evolution: Biological Models and Applications. Invited Speaker.
7. Ann Arbor, Michigan, September 2012. Likelihood Ratio Tests with Boundary Constraints. Symposium in Honor of Jack Kalbfleisch. Invited Speaker.
8. Montpellier, France, June 2012. Testing Phylogenies. Mathematical and Computational Evolutionary Biology 2012. Keynote Speaker.
9. Waterloo, Ontario, December 2011. Properties of Measures of Uncertainty in Phylogenetic Inference. Department of Statistics, University of Waterloo. Invited Talk.
10. Antigonish, Nova Scotia, October 2011. Properties of Measures of Uncertainty in Phylogenetic Inference Keynote address at the AARMS Special Session on high-dimensional data.
11. Centre de Recherches de Mathématiques, Université de Montréal, September 2011. Properties of Bayesian Posteriors and Bootstrap Support in Phylogenetic Inference. Invited Talk.
12. Wolfville, Nova Scotia, June 2011. Statistical Issues in Molecular Evolution: Measures of Uncertainty. Invited talk. CRM-SSC Medal Address, Annual Meeting of the Statistical Society of Canada.
13. Halifax, Nova Scotia, May 2009. The Star Tree Paradox, Posterior Probabilities and Bootstrap Support. Invited talk. Canadian Society for Ecology and Evolution Annual Meeting.
14. Halifax, Nova Scotia, June 2007. On Reduced Amino Acid Alphabets for Phylogenetic Inference. Invited talk. CIFAR Evolutionary Biology Program. 19th Annual Meeting.
15. Seattle, Washington, August, 2006. Using bootstrap support for splits to construct confidence regions for trees. Invited talk. Joint Statistical Meetings.
16. White Point, Nova Scotia, September 2003. A little bit of energy in our trees. Invited talk jointly with Andrew J. Roger and Christian Blouin, CIAR Evolutionary Biology Program. 17th Annual Meeting.
17. Toronto, Ontario, September 2003. Organizer and discussant of phylogenetics session of National Program in Complex Data Sets (NPCDS) inaugural workshop in Statistical Genomics.

18. Harrison Hot Springs, British Columbia, October 2002. Inconsistency of distance methods under model mis-specification. Invited talk, CIAR Evolutionary Biology Program. 16th Annual Meeting.
19. Hamilton, Ontario, May 2002. The Estimation of T_2 Distributions in Magnetic Resonance Imaging. CJS Award Lecture, Annual Meeting of the Statistical Society of Canada.
20. Hamilton, Ontario, May 2002. Testing for rate variation in phylogenetic subtrees. Invited talk, Annual Meeting of the Statistical Society of Canada.
21. Val-David, Quebec, October 2001. Models for Rate Variation. Invited Talk. CIAR Evolutionary Biology Program. 15th Annual Meeting.
22. Hamburg, Germany, July 2001. Diagnostics for Mixture Models and Weighted Homogeneity Tests. Invited talk, Mixtures 2001, Hamburg, Germany.
23. Dalhousie University, September 2000. Issues in the Analysis of Microarray Data.
24. Schaumburg, Illinois, June 1999. Computational Methods for Mixture Estimation. Invited talk, Proceedings of the 31st Symposium of the Interface between Computing Science and Statistics.
25. Dalhousie University, July 1998. Residual Diagnostics for Normal Mixture Models.
26. Dalhousie University, January 1998. The Estimation of T_2 Distributions in Magnetic Resonance Imaging.
27. New Brunswick, June 1996. Nonparametric Maximum Likelihood Estimation for Mixture Models. Pierre Robillard Lecture, Annual Meeting of the Statistical Society of Canada.
28. University of Toronto, February 1997. Nonparametric Maximum Likelihood for Mixture Models.
29. University of Toronto, Department of Computer Science, October 1996. Computational approaches for Mixture Estimation.
30. McMaster University, December 1995. Constrained Maximum Likelihood Estimation for Mixture Models.
31. Montreal, July 1995. Likelihood Ratio Statistic Tests of Mixture Hypotheses for Multinomial Models. Joint Annual Meetings of Statistical Society of Canada and Institute of Mathematical Statistics.
32. Waterloo, May 1994. Mixture Models. Hidden Markov Model Seminar Series.
33. Banff, Alberta, May 1994. The Asymptotic Distribution of the Likelihood Ratio Statistic in Mixture Models. Annual Meeting of Statistical Society of Canada.
34. Corvallis, Oregon, 1992. On the Estimation of Segments in Regression Modeling. Western Regional Meeting of Institute of Mathematical Statistics and Biometric Society.

TEACHING EXPERIENCE

2008-	FULL PROFESSOR	Dalhousie University
2003-2008	ASSOCIATE PROFESSOR	Dalhousie University
1998-2003	ASSISTANT PROFESSOR	Dalhousie University
1996-1998	INSTRUCTOR	University of Toronto
	POST DOCTORAL FELLOW	
1995-1996	SESSIONAL INSTRUCTOR	University of Waterloo
1992-1995	TEACHING ASSISTANT	University of Waterloo
	RESEARCH ASSISTANT	
1990-1992	TEACHING ASSISTANT	University of British Columbia
	RESEARCH ASSISTANT	
1986-1990	TEACHING ASSISTANT	University of Windsor

COURSES TAUGHT

1st year

Introuctory Statistics, Dalhousie University.

2nd year

Exploratory Data Analysis, Dalhousie University. An introduction to statistical computing and methodology using S-Plus.

Introduction to Probability and Statistics, Dalhousie University.

Introductory Statistics, Dalhousie University.

Statistical Theory, University of Toronto. Introductory statistics course.

3rd year

Applied Probability, University of Waterloo. An introduction to stochastic processes.

Regression Analysis, Dalhousie University.

Intermediate Statistical Theory, Dalhousie University.

4th year/graduate

Data Mining and Statistical Pattern Recognition, graduate course, Dalhousie University.

Advanced Statistical Theory I & II, 4th year/graduate course, Dalhousie University.

Methods of Applied Statistics, 4th year/graduate course, University of Toronto. Linear models, generalized linear models and some multivariate techniques.

Mixture Models, graduate course, Dalhousie University. Topics course covering random effects, finite and nonparametric mixtures.

Probability Theory and Measure, graduate course, Dalhousie University.

Statistical Issues in Molecular Evolution, graduate course, Dalhousie University.

Stochastic Processes, 4th year/graduate course, Dalhousie University.

Survival Analysis, 4th year/graduate course, Dalhousie University.

SUPERVISION

2017-	Etai Markowski MSc	Constructing confidence sets phylogenetic trees using likelihood methods
2017-	Ziwei Jin MSc	Nonparametric bootstrapping of likelihood ratio statistics

2014–	Chris Jones PhD	Codon models that incorporate spatial-temporal variability and phenotypic change Co-supervisor with J.P. Bielawski
2010–	Joey Mingrone PhD	Statistical methods for detecting positive selection Co-supervisor with J.P. Bielawski
2004-2017	Huaichun Wang PDF	Statistical Issues in Phylogenetics Co-supervisor with A.J. Roger
2016	Léa Lincker	Frequency mixture models Research Internship (France) Co-supervisor with A.J. Roger
2015	Benjamin Potter BSc	Computing transition probabilities for the general birth-death process (Honours Project)
2014	Moyan Mei BSc	Least squares methods in phylogenetics (Honours Project)
2005-2011	Liwen Zou PhD	Construction of amino acid rate matrices and extensions of the Barry and Hartigan model for phylogenetic inference Co-supervisor with C. Field and A.J. Roger
2011	Malcolm Cameron BSc	Outliers and influence in phylogenetics through least squares methods (Honours Project)
2006-2010	Jihua Wu PhD	Distance method adjustments and a test for general heterotachy in phylogenetic estimation
2008-2009	He Gao MSc	Corrected Log Det evolutionary distance estimation
2007-2008	Yifei Hu MSc	Testing for a genomic clock
2005-2006	Paul Sheridan MSc	Generalized least squares methods in phylogenetics
2004-2006	Matthew Spencer PDF	Gene content models Co-supervisor with A.J. Roger
-2004-2006	Leah Gerber MSc	Overdispersion and Fisheries Models Co-supervisor with R. Myers
2005	Jihua Wu MSc	A random branch length model for rate heterogeneity in phylogenetics
2004-2005	Liwen Zou MSc	Estimation of rate matrices from sequence data Co-supervisor with C. Field
2005	Isabelle Nadeau	Site-specific models of evolution Summer Student - Co-supervisor with A.J. Roger
2002	Wei Xu MSc	Covariation models in molecular evolution Co-supervisor with C. Field
2001	Bo Lin MSc	Maximum likelihood estimation of phylogenetic trees
2001	Sofia Mosesova BSc	Handwritten Digit Recognition (Honours Project)

THESIS COMMITTEE MEMBERSHIP

2016–	Noor Youssef PhD
2016–	Lihui Liu PhD
2017	Tianshu Huang MSc
2016	Chongci Chang MSc
2016	He Hao MSc
2010-2015	Sergio Hleap PhD (Mol Biol and Biochem)
2013	Wei Dai MSc

2012	Wei Chen MSc
2009-2012	Javier Alfaro MSc (Mol Biol and Biochem)
2006-2012	Dan Gaston PhD (Mol Biol and Biochem)
2006-2010	F. Ferretti PhD (Biol)
2009	Sonja Pritchett MSc
2005-2009	Jessica Leigh PhD (Mol Biol and Biochem)
2007	Mei Chen MSc
2004-2007	Derek Tittensor PhD (Biol)
2006	Wenyi Jiang MSc
2006	Xiaofei Shi PhD
2005	Aditya Aggarwal MSc (CS)
2005	Le Bao MSc
2005	Connie Stewart PhD
2005	Krista Collins MSc
2002-2005	Saeed Hashemi PhD (CS)
2003	Yunfeng Shan (CS) MSc
2002	Julia Baum (Biol) MSc
2001	Xiofei Shi MSc
2000	Paul Scott MSc
2000	Joanna Mills PhD
1999	J. Concepción Loredó-Osti PhD

EXTERNAL EXAMINATIONS

2016	Y. Zhai (British Columbia)	PhD
2011	A. Rea (Auckland)	PhD
2006	Erica Nahm (Acadia)	MSc

ADMINISTRATIVE RESPONSIBILITIES

2016–	Consulting Director, Department of Mathematics and Statistics, Dalhousie University
2016–	SSC/CRM Award Committee
2016–	NSERC Mathematics and Statistics Liaison Committee
2016	Chair, Tenure and Promotion Subcommittee, Department of Mathematics and Statistics, Dalhousie University
2015-2016	Chair, Search Committee for CRC Chair (Tier II) Dalhousie University
2015-2016	SSC 2016 Program Chair
2012-2016	SSC Program Committee Member
2011-2015	SSC 2015 Local Arrangements Chair
2014	Tenure and Promotion Subcommittee, Department of Mathematics and Statistics, Dalhousie University
2014	Chair, Math Director Search Committee, Dalhousie University
2012–2014	SSC Research Committee Member

2012–2014 Atlantic Regional Representative to SSC
 2013 Hiring Committee, Department of Mathematics and Statistics,
 Dalhousie University
 2012 Hiring Committee, Department of Mathematics and Statistics,
 Dalhousie University
 2011–2012 Senator, Dalhousie University
 2010 Chair Advisory Committee (Physics), Faculty of Science,
 Dalhousie University
 2006–2010 Executive Committee, Computational Biology and Bioinformatics Program,
 Dalhousie University
 2005–2010 Graduate Coordinator, Division of Statistics, Dalhousie University
 2002–2009 Scientific Committee, National Program on Complex Data Structures
 2007 Reappointment Committee member, Division of Statistics,
 Dalhousie University
 2007 Tenure Committee member, Division of Statistics, Dalhousie University
 2007 Tenure Committee member, Division of Statistics, Dalhousie University
 2007 Chair, Pierre Robillard Committee, Statistical Society of Canada
 2006–2007 Organizing Committee, SMBE 2007
 2006–2007 Chair Advisory Committee (Chemistry), Faculty of Science,
 Dalhousie University
 2006 Tenure Committee member, Division of Statistics, Dalhousie University
 2006 Chair, Appointments Committee, Division of Statistics,
 Dalhousie University
 2006 Appointments Committee, Division of Statistics, Dalhousie University
 2005–2007 Pierre Robillard Committee, Statistical Society of Canada
 2005 Tenure Committee member, Division of Statistics, Dalhousie University
 2005 Chair, Promotion Committee, Division of Statistics, Dalhousie University
 2005 Program Committee member for ISMB 2005
 2003–2005 Chair, Computing Resources Committee,
 Department of Mathematics and Statistics, Dalhousie University
 2002 Computing Resources Committee,
 Department of Mathematics and Statistics, Dalhousie University
 2002 Hiring Committee, Division of Statistics, Dalhousie University
 2002 Seminar coordinator, Division of Statistics, Dalhousie University
 2000–2002 Atlantic Regional Representative to SSC
 2001 Math Director search Committee, Department of Mathematics and Statistics,
 Dalhousie University
 2000–2001 Hiring Committee, Division of Statistics, Dalhousie University
 2000 Atlantic Genomics Centre - Education Committee
 1999 Hiring Committee, Division of Statistics, Dalhousie University

CONSULTING

2016–2009 Director of Consulting Service, Dalhousie University
 Consultant for Department of Fisheries and Oceans
 Post-release mortality in Atlantic bluefin tuna sport fishery.

2001 Consultant for Bedford Institute of Oceanography
 Mixture model analysis of cod otolith data

2000– Consultant for Health Canada
 Bayesian methods for predictive microbiology

1998–2000 Consultant for Imaging Research, St. Catherines, Ontario
 Analysis of Micro-array data, mixture modeling, programming, general advice

PUBLICLY AVAILABLE SOFTWARE DEVELOPMENT

<http://www.mathstat.dal.ca/~tsusko/>

1. MAMMaL: (M)ultinomial (A)pproximate (M)ixture (Ma)ximum (L)ikelihood. Software to estimate frequency vectors for classes in an amino acid mixture-of-frequencies model.
Susko, E., Lincker, L. and Roger, A.J. (2018). Accelerated Estimation of Frequency Classes in Site-heterogeneous Profile Mixture Models. *Molecular Biology and Evolution*. **35**:1266–1283.
2. `bptaxon_split`, `rbic_taxon_split`, `taxa_split_support`, `tree2treein`: C language source code for some of the methods described in
 Wang, H., **Susko, E.** and Roger, A.J. (2016). Split-specific Bootstrap Measures for Quantifying Phylogenetic Stability and the Influence of Taxon Selection. *Molecular Phylogenetics and Evolution*. **105**:114–125.
3. `pbf`, `infoprior`, `pbfs`: C language source for some of the methods described in
Susko, E. (2015). Bayesian Long Branch Attraction Bias and Corrections. *Systematic Biology*. **64**:243–255.
4. `khns` and `trees2df`: C language source for some of the methods described in
Susko, E. (2014). Tests for Two Trees using Likelihood Methods. *Molecular Biology and Evolution*. **31**:1029–1039.
5. `pr4design`, `pr4addbranch`, `pr4deltaxa` and `pr4list`: C language source for some of the methods described in
 Susko, E. and Roger, A.J. (2012). The Probability of Correctly Resolving a Split as an Experimental Design Criterion in Phylogenetics. *Systematic Biology* **61**:811–821.
6. `glsphyl`, `glsphylest`, `wlsnphyl`, `wlsphylest`: C language source for some of the methods described in
Susko, E. (2011). Improved Least Squares Topology Testing and Estimation *Systematic Biology* **60**:668–675.
7. `aBP`: C language source for some of the methods described in
Susko, E. (2010). First-Order correct bootstrap support adjustments for splits that allow hypothesis testing when using maximum likelihood estimation. *Molecular Biology and Evolution*. **27**:1621–1629.
8. `pahadist`: C language source for some of the methods described in

9. Wu, J. and **Susko, E** (2009). General Heterotachy and Distance Method Adjustments. *Molecular Biology and Evolution*. **26**:2689–2697.
10. `minmax-chisq`: C language source for some of the methods described in **Susko, E.** and Roger, A.J. (2007). On reduced amino acid alphabets for phylogenetic inference. *Molecular Biology and Evolution*. **24**:2139–2150.
11. `min_BP`, `ranked_spl`: C language source code for the methods described in **Susko, E.** (2006). Using minimum bootstrap support for splits to construct confidence regions for trees. *Evolutionary Bioinformatics Online*. **2**:137–151.
12. `chk1.idx.k`, `gapc`, `heatmap.d` and `heatmap.nod`: R functions for the methods described in **Susko, E.**, Leigh, J., Doolittle, W.F. and Baptiste, E. (2006). Visualizing and assessing phylogenetic congruence of core gene sets: a case study of the γ -proteobacteria. *Molecular Biology and Evolution*. **23**:1019–1030.
13. `cov_est`, `egene_est_single`, `egene_est_multiple`, `expr_est` and `equal_est`: C language source code for the methods described in **Susko, E.** and Roger, A. (2004). Estimating and comparing rates of gene discovery and expressed sequence tag (EST) frequencies in EST surveys. *Bioinformatics*, **20**:2279–2287.
14. `glsprot`, `glsdna`, `glsprot_eig`, `glsdna_eig`: C language source code for the methods described in **Susko, E.** (2003). Confidence regions and hypothesis tests for topologies using generalized least squares. *Molecular Biology and Evolution*, **20**, 862–868.
15. `dist_est`: C language source code for the methods described in **Susko, E.**, Field, C., Blouin, C. and Roger, A.J. (2003). Estimation of rates-across-sites distributions in phylogenetic substitution models. *Systematic Biology*, **52**, 594–603.
16. `bivar`: C language source code for the methods described in **Susko, E.**, Inagaki, Y., Field, C., Holder, M.E. and Roger, A.J. (2002). Testing for Differences in Rates Across Sites Distributions in Phylogenetic Subtrees. *Molecular Biology and Evolution*, **19**, 1514–1523.
17. `wthom.test`: R functions for the methods described in **Susko, E.** (2003). Weighted Tests of Homogeneity for Testing the Number of Components in a Mixture. *Journal of Computational Statistics and Data Analysis: Special Issue on Mixtures*, **41**, 367–378.

PATENTS

International Application No. PCT/IB01/01625

Publication No. WO 02/20824 A2

Applicant: Imaging Research Inc.

Title: Process for estimating random error in chemical and biological assays