

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

Edward Andrew Susko

Citizenship: Canadian

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
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
(full tuition + stipend)
 1986 Entrance Award, Windsor

REFEREED CONTRIBUTIONS

1. **Susko, E.** (2017). Bayes Factor Biases for Non-nested Models and Corrections. *Accepted for Publication in The Canadian Journal of Statistics.*
2. Robicheau, 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.
3. Sokol, M. Žihala, D., Romain, D., Klimeš, V., Hradilová, M., Zadobrková, **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
4. Jones, C.T, **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.
5. Mingrone, J., **Susko, E.** and Bielawski, J. (2016). Smoothed bootstrap aggregation for assessing selection pressure at amino acid sites. *Molecular Biology and Evolution.* **33**:2976–2989.
6. 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.

7. **Susko, E.** (2015). Bayesian long branch attraction bias and corrections. *Systematic Biology*. **64**:243–255.
8. 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.
9. 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 Pygusua. *Current Biology*. **24**:1–11.
10. 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.
11. **Susko, E.** (2014). Tests for two trees using likelihood methods. *Molecular Biology and Evolution*. **31**:1029–1039.
12. **Susko, E.** (2013). Likelihood ratio tests with boundary constraints using data-dependent degrees of freedom. *Biometrika*. **100**:1019–1023.
13. 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.
14. 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.
15. **Susko, E.** and Roger, A.J. (2013). Problems with estimation of ancestral frequencies under stationary models. *Systematic Biology*. **62**:330–338.
16. 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.

17. **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.
18. 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.
19. 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.
20. 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.
21. **Susko, E.** (2011). Improved Least Squares Topology Testing and Estimation. *Systematic Biology*. **60**:668–675.
22. 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.
23. Wu, J. and **Susko, E.** (2011). A Test for Heterotachy Using Multiple Pairs of Sequences. *Molecular Biology and Evolution*. **28**:1661–1673.
24. **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.
25. 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.
26. **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.

27. Wu, J. and **Susko, E.** (2010). Rate-variation need not defeat phylogenetic inference through pairwise sequence comparisons. *Journal of Theoretical Biology.* **263**:587–589.
28. 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.
29. Wang, H., **Susko, E.** and Roger, A.J. (2009). PROCOV: maximum likelihood estimation of protein phylogeny under covarion models. *BMC Evolutionary Biology.* **9**:225.
30. Wu, J. and **Susko, E.** (2009). General Heterotachy and Distance Method Adjustments. *Molecular Biology and Evolution.* **26**:2689–2697.
31. **Susko, E.** (2009). Bootstrap Support is Not First Order Correct. *Systematic Biology.* **58**:211–223.
32. 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.
33. **Susko, E.** (2008). On the distributions of bootstrap support and posterior distributions for a star tree. *Systematic Biology.* **57**:602–612.
34. 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.
35. Leigh, J.W., **Susko, E.**, Baumgartner, M. and Roger, A.J. (2008). Testing phylogenetic congruence in phylogenomic analysis. *Systematic Biology.* **57**:104–115.
36. Wang, H., **Susko, E.**, Spencer, M. and Roger, A.J. (2008). Topological estimation biases with covarion evolution. *Journal of Molecular Evolution.* **66**:50–60.
37. 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.

38. **Susko, E.** and Roger, A.J. (2007). On reduced amino acid alphabets for phylogenetic inference. *Molecular Biology and Evolution*. **24**:2139–2150.
39. Spencer, M., Bryant, D. and **Susko, E.** (2007). Conditioned genome reconstruction: how to avoid choosing the conditioning genome. *Systematic Biology*. **56**:25–43.
40. 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.
41. 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.
42. Spencer, M., **Susko, E.** and Roger, A.J. (2006). Modeling prokaryote gene content. *Evolutionary Bioinformatics Online*. **6**:165–186.
43. **Susko, E.** (2006). Using minimum bootstrap support for splits to construct confidence regions for trees. *Evolutionary Bioinformatics Online*. **2**:137–151.
44. 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.
45. **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.
46. 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.

47. Shi, X., Gu, H., **Susko, E.** and Field, C. (2005). The comparison of confidence regions in phylogeny. *Molecular Biology and Evolution*, **22**:2285–2296.
48. Spencer, M. and **Susko, E.** (2005). Inferring the topology of species interactions from Markov chains. *Ecology*, **86**:3272–3278.
49. **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.
50. Spencer, M., **Susko, E.** and Roger, A.J. (2005). Likelihood, parsimony and heterogeneous evolution. *Molecular Biology and Evolution*, **22**:1161–1164.
51. Baptiste, 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.
52. **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.
53. **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.
54. 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.
55. 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.
56. **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.

57. 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.
58. **Susko, E.** (2003). Confidence regions and hypothesis tests for topologies using generalized least squares. *Molecular Biology and Evolution*, **20**, 862–868.
59. **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.
60. **Susko, E.** and Nadon, R. (2002). Estimation of a residual distribution with small numbers of repeated measurements, *Canadian Journal of Statistics*, **30**, 383–400.
61. **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.
62. **Susko, E.**, Chen, J. and Kalbfleisch, J.D. (2001). A Diagnostic Tool for Mixture Models. *Journal of Statistical Computation and Simulation*, **69**, 293–314.
63. **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*
64. **Susko, E.**, Kalbfleisch, J.D. and Chen, J. (1998). Constrained Nonparametric Mixture Maximum Likelihood Estimation. *Canadian Journal of Statistics*, **26**, 601-617.
65. 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.

66. Liu, J. and **Susko, E.** (1992). On Strict Stationarity and Ergodicity of a Non-linear ARMA Model. *Journal of Applied Probability* 29, 363-373.

UNREFEREED CONTRIBUTIONS

1. **Susko, E.** (2016). Tree Support Measures. In: Kliman, R.M. (ed.), *Encyclopedia of Evolutionary Biology*. vol. 4, pp. 256–260. Oxford: Academic Press.
2. **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.
3. 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).
4. 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.
5. **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.
6. **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.**, Minh, B. and Roger, A.J. (2017). Modeling Site Heterogeneity with Posterior Mean Site Frequency Profiles Accelerates Accurate Phylogenomic Estimation. *Under Revision for Systematic Biology.*

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

- 2014-2019 **23,000/yr**
NSERC Discovery Grant
- 2013 **\$10,854**
NSERC Equipment Grant
Brown, J., Dilcher, K., Faridi, S., Field, C.A., Iron, D., Janssen, J.,
Kolokolnikov, T. (*PI*), Nowakowski, R. and **Susko, E.A.**
- 2008-2013 **\$21,000/yr**
NSERC Discovery Grant
- 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. (*PI*)
Susko, E.A.
- 2007 **\$55,591**
NSERC Equipment Grant
An Xserve computer cluster for phylogenetic
and comparative genomic analyses
Archibald, J.M., Roger, A.J. (*PI*)
Simpson, A.G. and **Susko, E.A.**
- 2006-2009 **\$141,917/yr**
CIHR Operating Grant
Integron metagenomics
Doolittle, W.F. (*PI*), Stokes, Hatch and **Susko, E.A.**
- 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 **\$63,200**
NSERC Equipment Grant
Bielawski, J., Dowd, M., Field, C.A., Hamilton, D.,
Smith, B. and **Susko, E.A.**
- 2003-2008 **\$19,000/yr**
NSERC Discovery Grant

2002-2006 **\$4,442,900**
 Genome Canada Grant
 A comparative understanding of prokaryotic evolution
 and diversity: from genomics to metagenomics
 Doolittle, W.F. (*PI*), Mulligan, M.E.,
 Rannala, B., Roger, A.J., Smith, B.R. and **Susko, E.A.**

2000 **\$70,476**
 NSERC Equipment Grant
 Field, C.A., Hamilton, D., Smith, B. and **Susko, E.A.**

1999-2003 **\$12,000/yr**
 NSERC Operating Grant

1999 **\$17,100**
 NSERC Equipment Grant
 Field, C.A., Hamilton, D., Smith, B. and **Susko, E.A.**

REFeree AND REVIEW RESPONSIBILITIES

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

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

American Naturalist (1)
 Annals of Statistics (1)
 Annals of Applied Statistics (1)
 Bioinformatics (12)

Biometrics (1)
Biometrika (1)
BMC Bioinformatics (3)
BMC Biology (1)
BMC Evolutionary Biology (8)
BMC Genomics (1)
Canadian Journal of Statistics (6)
Clinical Cancer Research (1)
Computational Statistics and Data Analysis (2)
Discrete Applied Mathematics (1)
Evolutionary Bioinformatics (2)
Evolutionary Biology Online (1)
FEBS Letters (1)
Genome (1)
Genome Biology and Evolution (6)
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 (30)
Molecular Phylogenetics and Evolution (1)
Philosophical Transactions of the Royal Society, Series B: Biological Sciences (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 (21)
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 (3)
Promotion Reviewer (1)

SELECTED PRESENTATIONS

1. Wolfville, Nova Scotia, October 2015. Phylogenetic Estimation and Inference. The Atlantic Universities Mathematics, Statistics and Computer Science Conference. Plenary Speaker.
2. Boston, Massachusetts, August 2014. Tests for Two Trees using Likelihood Methods. Joint Statistical Meetings (JSM). Invited Speaker.
3. 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.
4. Ann Arbor, Michigan, September 2012. Likelihood Ratio Tests with Boundary Constraints. Symposium in Honor of Jack Kalbfleisch. Invited Speaker.
5. Montpellier, France, June 2012. Testing Phylogenies. Mathematical and Computational Evolutionary Biology 2012. Keynote Speaker.
6. Waterloo, Ontario, December 2011. Properties of Measures of Uncertainty in Phylogenetic Inference. Department of Statistics, University of Waterloo. Invited Talk.
7. Antigonish, Nova Scotia, October 2011. Properties of Measures of Uncertainty in Phylogenetic Inference Keynote address at the AARMS Special Session on high-dimensional data.
8. Centre de Recherches de Mathématiques, Université de Montréal, September 2011. Properties of Bayesian Posteriors and Bootstrap Support in Phylogenetic Inference. Invited Talk.

9. 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.
10. Halifax, Nova Scotia, May 2009. The Star Tree Paradox, Posterior Probabilities and Bootstrap Support. Invited talk. Canadian Society for Ecology and Evolution Annual Meeting.
11. Halifax, Nova Scotia, June 2007. On Reduced Amino Acid Alphabets for Phylogenetic Inference. Invited talk. CIFAR Evolutionary Biology Program. 19th Annual Meeting.
12. Seattle, Washington, August, 2006. Using bootstrap support for splits to construct confidence regions for trees. Invited talk. Joint Statistical Meetings.
13. 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.
14. Toronto, Ontario, September 2003. Organizer and discussant of phylogenetics session of National Program in Complex Data Sets (NPCDS) inaugural workshop in Statistical Genomics.
15. Harrison Hot Springs, British Columbia, October 2002. Inconsistency of distance methods under model mis-specification. Invited talk, CIAR Evolutionary Biology Program. 16th Annual Meeting.
16. 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.
17. Hamilton, Ontario, May 2002. Testing for rate variation in phylogenetic subtrees. Invited talk, Annual Meeting of the Statistical Society of Canada.
18. Val-David, Quebec, October 2001. Models for Rate Variation. Invited Talk. CIAR Evolutionary Biology Program. 15th Annual Meeting.
19. Hamburg, Germany, July 2001. Diagnostics for Mixture Models and Weighted Homogeneity Tests. Invited talk, Mixtures 2001, Hamburg, Germany.

20. Dalhousie University, September 2000. Issues in the Analysis of Microarray Data.
21. Schaumburg, Illinois, June 1999. Computational Methods for Mixture Estimation. Invited talk, Proceedings of the 31st Symposium of the Interface between Computing Science and Statistics.
22. Dalhousie University, July 1998. Residual Diagnostics for Normal Mixture Models.
23. Dalhousie University, January 1998. The Estimation of T_2 Distributions in Magnetic Resonance Imaging.
24. New Brunswick, June 1996. Nonparametric Maximum Likelihood Estimation for Mixture Models. Pierre Robillard Lecture, Annual Meeting of the Statistical Society of Canada.
25. University of Toronto, February 1997. Nonparametric Maximum Likelihood for Mixture Models.
26. University of Toronto, Department of Computer Science, October 1996. Computational approaches for Mixture Estimation.
27. McMaster University, December 1995. Constrained Maximum Likelihood Estimation for Mixture Models.
28. 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.
29. Waterloo, May 1994. Mixture Models. Hidden Markov Model Seminar Series.
30. Banff, Alberta, May 1994. The Asymptotic Distribution of the Likelihood Ratio Statistic in Mixture Models. Annual Meeting of Statistical Society of Canada.
31. 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

Introductory 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, 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

2016	Léa Lincker, Research Internship - France (Co-supervisor with Andrew Roger) Frequency mixture models
2015	Benjamin Potter (Honours Project) Computing transition probabilities for the general birth-death process
2014–	Chris Jones PhD (Co-supervisor with Joe Bielawski) Codon models that incorporate spatial-temporal variability and phenotypic change
2014	Moyan Mei (Honours Project) Least squares methods in phylogenetics
2011	Malcolm Cameron (Honours Project) Outliers and influence in phylogenetics through least squares methods
2010–	Joey Mingrone PhD (Co-supervisor with Joe Bielawski) Statistical methods for detecting positive selection
2008-2009	He Gao MSc Corrected Log Det evolutionary distance estimation
2007-2008	Yifei Hu MSc Testing for a genomic clock
2006-2010	Jihua Wu PhD Distance method adjustments and a test for general heterotachy in phylogenetic estimation
2005-2011	Liwen Zou PhD Construction of amino acid rate matrices and extensions of the Barry and Hartigan model for phylogenetic inference
2005	Isabelle Nadeau (Summer Student) Site-specific models of evolution (Co-supervisor with A.J. Roger)
2005-2006	Paul Sheridan MSc Generalized least squares methods in phylogenetics
2005	Jihua Wu MSc

2004– A random branch length model for rate heterogeneity in phylogenetics
 Huaichun Wu Postdoctoral Fellow
 Covarion models (Co-supervisor with A.J. Roger)
 2004-2006 Matthew Spencer Postdoctoral Fellow
 Gene content models (Co-supervisor with A.J. Roger)
 2004-2006 Leah Gerber MSc
 Overdispersion and Fisheries Models (Co-supervisor with R. Myers)
 2004-2005 Liwen Zou MSc
 Estimation of rate matrices from sequence data (Co-supervisor with C. Field)
 2002 Wei Xu MSc
 Covarion 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 WORK

2016–	L. Liu	PhD
2016	C. Chang	MSc
2016	Y. Zhai (British Columbia - External Examiner)	PhD
2016	H. Hao	MSc
2014–	S. Carson	PhD
2013	W. Dai	MSc
2012	W. Chen	MSc
2011	A. Rea (Auckland - External Examiner)	PhD
2010-2015	S. Hleap (Mol Biol and Biochem)	PhD
2009-2012	J. Alfaro (Mol Biol and Biochem)	MSc
2009	S. Pritchett	MSc
2007	M. Chen	MSc
2006-2012	D. Gaston (Mol Biol and Biochem)	PhD
2006	W. Jiang	MSc
2006	X. Shi	PhD
2006-2010	F. Ferretti (Biol)	PhD
2006	E. Nahm (Acadia)	MSc
2005	A. Aggarwal (CS)	MSc

2005	L. Bao	MSc
2005-2009	J. Leigh (Mol Biol and Biochem)	PhD
2005	C. Stewart	PhD
2005	K. Collins	MSc
2002-2005	S. Hashemi (CS)	PhD
2004-2007	D. Tittensor (Biol)	PhD
2003	Y. Shan (CS)	MSc
2002	J. Baum (Biol)	MSc
2001	X. Shi	MSc
2000	P. Scott	MSc
2000	J. Mills	PhD
1999	J. Loredó	PhD

ADMINISTRATIVE RESPONSIBILITIES

- 2016 Chair, Tenure and Promotion Subcommittee,
Department of Mathematics and Statistics, Dalhousie University
- 2016– Consulting Director,
Department of Mathematics and Statistics, Dalhousie University
- 2016–2019 SSC/CRM Award Committee
- 2016– NSERC Mathematics and Statistics Liaison Committee
- 2015– Chair, Search Committee for CRC Chair (Tier II)
Dalhousie University
- 2015– SSC 2016 Program Chair
- 2011–2015 SSC 2015 Local Arrangements Chair
- 2014 Tenure and Promotion Subcommittee,
Department of Mathematics and Statistics, Dalhousie University
- 2012– SSC Program Committee Member
- 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
- 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– Executive Committee, Computational Biology and Bioinformatics Program,

Dalhousie University

2006 Chair, Appointments Committee, Division of Statistics,
Dalhousie University

2006 Appointments Committee, Division of Statistics, Dalhousie University

2005–2010 Graduate Coordinator, 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

2002–2009 Scientific Committee, National Program on Complex Data Structures

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

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

2000–2002 Atlantic Regional Representative to SSC

1999 Hiring Committee, Division of Statistics, Dalhousie University

CONSULTING

2009 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 Consulnant 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. `bptaxon_split`, `rbic_taxon_split`, `taxa_split_support`, `tree2treein`: C language source 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.
2. `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.
3. `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.
4. `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.
5. `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.
6. `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.
7. `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.
8. `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.
 9. `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.
 10. `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.
 11. `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.
 12. `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.
 13. `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.

14. `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