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 *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*
2005-2007	Fellow of the CIAR program in Evolutionary Biology
2002-2004	Associate Member of the CIAR program in Evolutionary Biology
2001	CJS Award *Awarded for the best paper in the Canadian Journal of Statistics*
1996	Pierre Robillard Award *Awarded by the Statistical Society of Canada for the best PhD thesis in the statistical sciences*
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 JOURNAL PUBLICATIONS

1. Baker, B.A, Gutiérrez-Preciado, A. Rodiriguez del Rio, A., McCarthy, C.G.P., López-Garcia, P., Huerta-Cepas, J., **Susko, E.**, Roger, A.J., Eme, L. and Moreira, D. (2024). Expanded phylogeny of extremely halophilic archaea shows multiple independent adaptations to hypersaline environments. *Accepted for Publication in Nature Microbiology* `https://doi.org/10.1038/s41564-024-01647-4`

2. Markowski, E. and **Susko, E.** (2024). Performance of Topology Tests under Extreme Selection Bias. *Molecular Biology and Evolution*. **41**:msad280.

3. Hehenberger, E., Gao, J., Wilken, S., Hoadley, K. Sudek, L., Poirier, C., Dannebaum, R., **Susko, E.** and Worden, A.Z. (2023). Reprogramming of the tRNA epitranscriptome and codon usage bias underpin nutrient limitation responses in marine algae. *Molecular Biology and Evolution*. **40**:msad251.

4. Baños, H., **Susko, E.** and Roger, A.J. (2023). Are profile mixture models over-parameterized? *Systematic Biology Advance Access*. `https://doi.org/10.1093/sysbio/syad063`

5. Jones, C.T., Meynell, L., Neto, C. **Susko, E.** and Bielawski, J.P. (2023). The role of the ecological scaffold in the origin and maintenance of whole-group trait altruism in microbial populations. *BMC Ecology and Evolution*. **23**:11.

6. **Susko, E.** (2022). Complex Statistical Modelling for Phylogenetic Inference. *Canadian Journal of Statistics*. **50**:1339–1354.

7. Jones, C., **Susko, E.**, and Bielawski, J.P. (2022). Evolution of the connectivity and indispensability of a transferable gene: the simplicity hypothesis. *BMC Ecology and Evolution*. **22**:140.

8. Youssef, N. **Susko, E.**, Roger, A.J. and Bielawski, J.P. (2022). Evolution of amino acid propensities under stability-mediated epistasis. *Molecular Biology and Evolution*. **39**:msac030

9. Ho, L.S.T. and **Susko, E.** (2022). Ancestral state reconstruction with large numbers of sequences and edge-length estimation. *Journal of Mathematical Biology*. **84**:21

10. Muñoz Gómez, S., **Susko, E.**, Williamson, K., Eme, L., Slamovitz, C.H., Moreira, D. Purificación, L. and Roger, A.J. (2022). A site-and-branch-heterogeneous model on an expanded dataset favor mitochondria as sister to known Alphaproteobacteria *Nature Ecology & Evolution*. **6**:253–262.

11. Youssef, N. **Susko, E.**, Roger, A.J. and Bielawski, J.P. (2021). Shifts in amino acid preferences as proteins evolve: a synthesis of experimental and theoretical work. *Protein Science*. **30**:2009–2028

12. McCain, J.S.P., Tagliabue, A., **Susko, E.**, Achterberg, E.P., Allen, E., Bertrand, E.M. (2021). Cellular costs underpin micronutrient limitation in phytoplankton. *Science Advances*. **7**:eabg6501.

13. **Susko, E.**, Steel, M. and Roger, A.J. (2021). Conditions under which distributions of edge length ratios on phylogenetic trees can be used to order evolutionary events. *Journal of Theoretical Biology*. **526**:110788.

14. **Susko, E.** and Roger, A.J. (2021). Long Branch Attraction Biases in Phylogenetics. *Systematic Biology*. **70**:838–843.

15. Youssef, N., **Susko, E.** and Bielawski, J.P. (2020). Consequences of stability-induced epistasis for substitution rates. *Molecular Biology and Evolution*. **37**:3131–3148.

16. Jones, C., Youssef, N., **Susko, E.** and Bielawski, J. (2020). A phenotype-genotype codon model for detecting adaptive evolution. *Systematic Biology*. **69**:722–738.

17. **Susko, E.** and Roger, A.J. (2020). On the Use of Information Criteria for Model Selection in Phylogenetics. *Molecular Biology and Evolution*. **37**:549–562.

18. Wang, H., **Susko, E.** and Roger, A.J. (2019). The relative importance of modeling site pattern heterogeneity versus partition-wise heterotachy in phylogenomic inference. *Systematic Biology*. **68**:1003–1019.

19. Mingrone, J., **Susko, E.** and Bielawski, J.P. (2019). ModL: exploring and restoring regularity when testing for positive selection *Bioinformatics*. **35**:2545–2554.

20. Muñoz-Gómez, S., Hess, S., Burger, G., Lang, B., **Susko, E.**, Slamovitz, C. and Roger, A. (2019). An updated phylogeny of the Alphaproteobacteria reveals that the parasitic *Rickettsiales* and *Holosporales* have independent origins. *eLife*. **8**:e42535.

21. 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.

22. 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.

23. **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.

24. 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.

25. **Susko, E.** (2017). Bayes factor biases for non-nested models and corrections. *Canadian Journal of Statistics*. **9**:290-309.

26. 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.

27. 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

28. 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.

29. 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.

30. 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.

31. **Susko, E.** (2015). Bayesian long branch attraction bias and corrections. *Systematic Biology*. **64**:243–255.

32. 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.

33. 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.

34. 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.

35. **Susko, E.** (2014). Tests for two trees using likelihood methods. *Molecular Biology and Evolution*. **31**:1029–1039.

36. **Susko, E.** (2013). Likelihood ratio tests with boundary constraints using data-dependent degrees of freedom. *Biometrika*. **100**:1019–1023.

37. 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.

38. 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.

39. **Susko, E.** and Roger, A.J. (2013). Problems with estimation of ancestral frequencies under stationary models. *Systematic Biology*. **62**:330–338.

40. 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.

41. **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.

42. 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.

43. 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.

44. 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.

45. **Susko, E.** (2011). Improved Least Squares Topology Testing and Estimation. *Systematic Biology.* **60**:668–675.

46. 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.

47. Wu, J. and **Susko, E.** (2011). A Test for Heterotachy Using Multiple Pairs of Sequences. *Molecular Biology and Evolution.* **28**:1661–1673.

48. **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.

49. 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.

50. **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.

51. Wu, J. and **Susko, E.** (2010). Rate-variation need not defeat phylogenetic inference through pairwise sequence comparisons. *Journal of Theoretical Biology.* **263**:587–589.

52. 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.

53. Wang, H., **Susko, E.** and Roger, A.J. (2009). PROCOV: maximum likelihood estimation of protein phylogeny under covarion models. *BMC Evolutionary Biology.* **9**:225.

54. Wu, J. and **Susko, E** (2009). General heterotachy and distance method adjustments. *Molecular Biology and Evolution.* **26**:2689–2697.

55. **Susko, E**. (2009). Bootstrap support is not first order correct. *Systematic Biology.* **58**:211–223.

56. 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.

57. **Susko, E.** (2008). On the distributions of bootstrap support and posterior distributions for a star tree. *Systematic Biology.* **57**:602–612.

58. 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.

59. Leigh, J.W., **Susko, E.**, Baumgartner, M. and Roger, A.J. (2008). Testing phylogenetic congruence in phylogenomic analysis. *Systematic Biology*. **57**:104–115.

60. Wang, H., **Susko, E.**, Spencer, M. and Roger, A.J. (2008). Topological estimation biases with covarion evolution. *Journal of Molecular Evolution*. **66**:50–60.

61. Bapteste, 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.

62. **Susko, E.** and Roger, A.J. (2007). On reduced amino acid alphabets for phylogenetic inference. *Molecular Biology and Evolution*. **24**:2139–2150.

63. Spencer, M., Bryant, D. and **Susko, E.** (2007). Conditioned genome reconstruction: how to avoid choosing the conditioning genome. *Systematic Biology*. **56**:25–43.

64. 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.

65. 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.

66. Spencer, M., **Susko, E.** and Roger, A.J. (2006). Modeling prokaryote gene content. *Evolutionary Bioinformatics Online*. **6**:165–186.

67. **Susko, E.** (2006). Using minimum bootstrap support for splits to construct confidence regions for trees. *Evolutionary Bioinformatics Online*. **2**:137–151.

68. Inagaki, Y. **Susko, E.** and Roger, A.J. (2006). Recombination between elongation factor 1α genes from distantly-related archaeal lineages. *Proceedings of the National Academy of Sciences*. **103**:4528–4533.

69. **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.

70. 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.

71. Shi, X., Gu, H., **Susko, E.** and Field, C. (2005). The comparison of confidence regions in phylogeny. *Molecular Biology and Evolution*, **22**:2285–2296.

72. Spencer, M. and **Susko, E.** (2005). Continuous-time Markov models for species interactions. *Ecology*, **86**:3272–3278.

73. **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.

74. Spencer, M., **Susko, E**. and Roger, A.J. (2005). Likelihood, parsimony and heterogeneous evolution. *Molecular Biology and Evolution*, **22**:1161–1164.

75. 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.

76. **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.

77. **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.

78. Inagaki, Y., **Susko, E**., Fast, N.M. and Roger, A.J. (2004). Covarion shifts cause a long branch attraction artifact that unites microsporidia and archaebacteria in EF-1α phylogenies. *Molecular Biology and Evolution*, **21**:1340–1349.

79. 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.

80. **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.

81. Inagaki, Y., Blouin, C., **Susko, E**. and Roger A.J. (2003). Assessing functional divergence of EF-1α and its paralogues in eukaryotes and archaebacteria. *Nucleic Acids Research*, **31**, 4227–4237.

82. **Susko, E**. (2003). Confidence regions and hypothesis tests for topologies using generalized least squares. *Molecular Biology and Evolution*, **20**, 862–868.

83. **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.

84. **Susko, E**. and Nadon, R. (2002). Estimation of a residual distribution with small numbers of repeated measurements, *Canadian Journal of Statistics*, **30**, 383–400.

85. **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.

86. **Susko, E**., Chen, J. and Kalbfleisch, J.D. (2001). A Diagnostic Tool for Mixture Models. *Journal of Statistical Computation and Simulation*, **69**, 293–314.

87. **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*

88. **Susko, E**., Kalbfleisch, J.D. and Chen, J. (1998). Constrained Nonparametric Mixture Maximum Likelihood Estimation. *Canadian Journal of Statistics*, **26**, 601-617.

89. 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.

90. 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. Roger, A.J., **Susko, E.** and Leger, M.M. (2021) Evolution: Reconstructing the Timeline of Eukaryogenesis. *Current Biology*, **31**:R193–R214.

2. Jones, C.T. **Susko, E.** and Bielawski, J.P. (2019). Chapter 14. Looking for Darwin in genomic sequences: validity and success depends on the relationship between model and data. pp399–426, In Evolutionary Genomics. Methods in Molecular Biology, **1910**:399–426.

3. **Susko, E**. (2016). Tree Support Measures. In Kliman, R.M. (ed.), Encyclopedia of Evolutionary Biology. vol. 4, pp. 256–260. Oxford: Academic Press.

4. **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.

5. 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).

6. 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.

7. **Susko, E.** (1999). Comment on 'Integrated Likelihood Methods for Eliminating Nuisance Parameters'. *Statistical Science*, **14**:1–28.

8. **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 Pourhmadi, Editors, **31**, 432-438.

9. **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. Janovicek, K., Wang, H., McDonald, I., Sulik, J., **Susko, E.** and Nasielski, J. (2024). Effect of soil sample handling and storage on inorganic nitrogen determination: implications for the pre-sidedress nitrate test. *Under Revision for Soil Science Society of America 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

EDITORIAL ACTIVITIES

2010–2020 Associate Editor, Systematic Biology
2007–2019 Associate Editor, Canadian Journal of Statistics

REVIEW RESPONSIBILITIES

American Naturalist (1)
Annals of Statistics (1)
Annals of Applied Statistics (1)
Bioinformatics (14)
Biometrics (2)
Biometrika (1)
BMC Bioinformatics (5)
BMC Biology (1)
BMC Ecology and Evolution (1)
BMC Evolutionary Biology (9)
BMC Genomics (1)
Canadian Journal of Statistics (7)
Clinical Cancer Research (1)
Computational Statistics and Data Analysis (2)
Current Biology (2)
Data (1)
Discrete Applied Mathematics (1)
Evolutionary Bioinformatics (2)
Evolutionary Biology Online (1)
FEBS Letters (1)
Frontiers in Neuroinformatics (1)
Genes (1)
Genome (1)
Genome Biology and Evolution (9)
IEEE/ACM Transactions on Computational Biology and Bioinformatics (1)
International Statistical Review (1)
Journal of Applied Probability (1)
Journal of Mathematical Biology (1)
Journal of Medical Virology (1)

Journal of Molecular Evolution (3)
Journal of Multivariate Analysis (1)
Journal of Theoretical Biology (5)
Methods in Ecology and Evolution (1)
Molecular Biology and Evolution (40)
Molecular Phylogenetics and Evolution (3)
Nature (2)
Nature Biotechnology (1)
Nature Communications (2)
Nature Methods (1)
Philosophical Transactions of the Royal Society, Series B: Biological Sciences (1)
PLoS Biology (2)
PloS One (2)
Probability Theory and Related Fields (1)
Proceedings of Mathematics of Evolution and Phylogenetics (1)
Proceedings of the National Academy of Sciences (1)
Recomb-2005 (2)
Science (2)
Statistics and Probability Letters (1)
Statistical Science (1)
Statistica Sinica (1)
Systematic Biology (29)
Trends in Ecology and Evolution (2)
Theoretical Population Biology (1)
Zoology (1)

Operating Grant Reviewer, NSERC (18)
Swedish Research Council Grant Reviewer
Marsden Fund Grant Reviewer, New Zealand (2)
New Frontiers in Research Fund Reviewer, Canada
NSF Reviewer, Systematic Biology Panel (2)
US-Israel BSF Reviewer (1)
Tenure Reviewer (8)
Promotion Reviewer (3)

COMMITTEE MEMBERSHIP

2020–2022	SSC/CJS Award Committee
2016–2019	SSC/CRM Award Committee
2016–2019	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

EVENT ADMINISTRATION

2015–2016	SSC 2016 Program Chair
2011–2015	SSC 2015 Local Arrangements Chair
2013	Program Committee Member for ISMB 2013
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	Program Committee Member for ISMB 2005

SELECTED PRESENTATIONS

1. Woods Hole, Massachusetts, June 2023. Bootstrap & Topology Tests. Workshop on Molecular Biology and Evolution.

2. Woods Hole, Massachusetts, June 2022. Amino Acid Models & Topology Tests. Workshop on Molecular Biology and Evolution.

3. 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.

4. Halifax, Nova Scotia, October 2017. Bayes Factor Biases for Non-nested Models and Corrections. Mathematics and Statistics Colloquium, Dalhousie University.

5. Waterloo, Ontario, July 2017. Bayes Factor Biases for Non-nested Models and Corrections. Celebrating 50 years of Statistics and Actuarial Science. Invited Speaker.

6. Wolfville, Nova Sctoia, October 2015. Phylogenetic Estimation and Inference. The Atlantic Universities Mathematics, Statistics and Computer Science Conference. Plenary Speaker.

7. Boston, Massachusetts, August 2014. Tests for Two Trees using Likelihood Methods. Joint Statistical Meetings (JSM). Invited Speaker.

8. Centre de recherches mathematiques (CRM), Montreal, Canada, September 2013. Tests for Two Trees using Likelihood Methods. Workshop on Mathematics of Sequence Evolution: Biological Models and Applications. Invited Speaker.

9. Ann Arbor, Michigan, September 2012. Likelihood Ratio Tests with Boundary Constraints. Symposium in Honor of Jack Kalbfleisch. Invited Speaker.

10. Montpellier, France, June 2012. Testing Phylogenies. Mathematical and Computational Evolutionary Biology 2012. Keynote Speaker.

11. Waterloo, Ontario, December 2011. Properties of Measures of Uncertainty in Phylogenetic Inference. Department of Statistics, University of Waterloo. Invited Talk.

12. Antigonish, Nova Scotia, October 2011. Properties of Measures of Uncertainty in Phylogenetic Inference Keynote address at the AARMS Special Session on high-dimensional data.

13. Centre de Recherches de Mathémathiques, Université de Montréal, September 2011. Properties of Bayesian Posteriors and Bootstrap Support in Phylogenetic Inference. Invited Talk.

14. 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.

15. Halifax, Nova Scotia, May 2009. The Star Tree Paradox, Posterior Probabilities and Bootstrap Support. Invited talk. Canadian Society for Ecology and Evolution Annual Meeting.

16. Halifax, Nova Scotia, June 2007. On Reduced Amino Acid Alphabets for Phylogenetic Inference. Invited talk. CIFAR Evolutionary Biology Program. 19th Annual Meeting.

17. Seattle, Washington, August, 2006. Using bootstrap support for splits to construct confidence regions for trees. Invited talk. Joint Statistical Meetings.

18. 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.

19. Toronto, Ontario, September 2003. Organizer and discussant of phylogenetics session of National Program in Complex Data Sets (NPCDS) inaugural workshop in Statistical Genomics.

20. Harrison Hot Springs, British Columbia, October 2002. Inconsistency of distance methods under model mis-specification. Invited talk, CIAR Evolutionary Biology Program. 16th Annual Meeting.

21. 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.

22. Hamilton, Ontario, May 2002. Testing for rate variation in phylogenetic subtrees. Invited talk, Annual Meeting of the Statistical Society of Canada.

23. Val-David, Quebec, October 2001. Models for Rate Variation. Invited Talk. CIAR Evolutionary Biology Program. 15th Annual Meeting.

24. Hamburg, Germany, July 2001. Diagnostics for Mixture Models and Weighted Homogeneity Tests. Invited talk, Mixtures 2001, Hamburg, Germany.

25. Dalhousie University, September 2000. Issues in the Analysis of Microarray Data.

26. Schaumburg, Illinois, June 1999. Computational Methods for Mixture Estimation. Invited talk, Proceedings of the 31st Symposium of the Interface between Computing Science and Statistics.

27. Dalhousie University, July 1998. Residual Diagnostics for Normal Mixture Models.

28. Dalhousie University, January 1998. The Estimation of T_2 Distributions in Magnetic Resonance Imaging.

29. New Brunswick, June 1996. Nonparametric Maximum Likelihood Estimation for Mixture Models. Pierre Robillard Lecture, Annual Meeting of the Statistical Society of Canada.

30. University of Toronto, February 1997. Nonparametric Maximum Likelihood for Mixture Models.

31. University of Toronto, Department of Computer Science, October 1996. Computational approaches for Mixture Estimation.

32. McMaster University, December 1995. Constrained Maximum Likelihood Estimation for Mixture Models.

33. 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.

34. Waterloo, May 1994. Mixture Models. Hidden Markov Model Seminar Series.

35. Banff, Alberta, May 1994. The Asymptotic Distribution of the Likelihood Ratio Statistic in Mixture Models. Annual Meeting of Statistical Society of Canada.

36. 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

Postdoctoral Fellows

2021–	Charley McCarthy (Co-supervisor with A.J. Roger) New Phylogenomic Models and Methods to Resolve The Prokaryote to Eukaryote Transition
2021–2023	Charith Bhagya Karunarathna (Co-supervisor with Lam Ho) Change Point Models for Epidemics
2021–2023	Hector Baños (Co-supervisor with A.J. Roger) New Phylogenomic Models and Methods to Resolve The Prokaryote to Eukaryote Transition
2004-2017	Huaichun Wang (Co-supervisor with A.J. Roger) Statistical Issues in Phylogenetics
2004-2006	Matthew Spencer (Co-supervisor with A.J. Roger) Gene Content Models

PhD Students

2021-2023	Jingyu Li (Co-supervisor with L. Ho) Time-varying Compartmental Epidemic Models with Bubbles
2010-2021	Joey Mingrone (Co-supervisor with J.P. Bielawski) Assessing and Improving The Reliability of Models of Molecular Evolution
2016-2021	Noor Youssef (Biology Co-supervisor with J.P. Bielawski) Evolutionary Dynamics under A Stability-Constrained Model
2014-2019	Chris Jones (Co-supervisor with J.P. Bielawski) On Models for Detecting Evidence of Molecular Adaptation in Homologous Sequences of Protein Coding Genes
2005-2011	Liwen Zou (Co-supervisor with C. Field and A.J. Roger) Construction of Amino Acid Rate Matrices and Extensions of The Barry And Hartigan Model for Phylogenetic Inference
2006-2010	Jihua Wu Distance Method Adjustments and A Test for General Heterotachy in Phylogenetic Estimation

MSc Students

2021-	Bailey Drew Missing Data Adjustments for Frequency Models in Phylogenetics
2021-2023	Jingyu Li (Co-supervisor with L. Ho) Effects of Subpopulation Structure in Epidemic Models
2017-2022	Ziwei Jin A Nonparametric Bootstrap Likelihood Ratio Test for Quantile Regression
2019-2021	Ebrahim Adeeb (Co-supervisor with L. Ho) Cross-validation Adjustment for Model Selection with Correlated Data
2017-2021	Etai Markowski A Comparison of Methods for Constructing Confidence Sets of Phylogenetic Trees using Maximum Likelihood
2008-2009	He Gao Corrected Log Det Evolutionary Distance Estimation
2007-2008	Yifei Hu Testing for a Genomic Clock
2005-2006	Paul Sheridan Generalized Least Squares Methods in Phylogenetics
2004-2006	Leah Gerber (Co-supervisor with R. Myers) Overdispersion and Fisheries Models
2005	Jihua Wu A Random Branch Length Model for Rate Heterogeneity in Phylogenetics
2004-2005	Liwen Zou (Co-supervisor with C. Field) Estimation of Rate Matrices from Sequence Data
2002	Wei Xu (Co-supervisor with C. Field) Covarion Models in Molecular Evolution
2001	Bo Lin Maximum Likelihood Estimation of Phylogenetic Trees

Undergraduate Students

2024 Zirui Dong (Co-supervisor with C. Feng)
Arsenic Contamination in Nova Scotia's Domestic Well Water: A Spatial-temporal Statistical Analysis
2024 Jiayang He (Co-supervisor with C. Feng)
Survival Analysis of SEER Breast Cancer Data
2023 Jingyi Wang
Universal Inference Procedures
2023 Jinlei Xu
Extensions of the Mann-Whitney Test
2021 Jingyu Li
Clustering Analysis of Surgeons from Surgical Data
2021 Ziwei Wang
Stochastic Models for Epidemics
2020 Xuran Feng
Classification Methods to Predict Taxonomic Groups from Amino Acid Compositions
2020 Fatma Sarhan
Bootstrapping with Censored Data
2020 Zhixian Yang
Cross-validation in Phylogenetic Estimation
2020 Xiaohang Zhou
An Investigation of Binning Strategies in Goodness of Fit Testing
2016 Léa Lincker (Research Internship (France) Co-supervisor with A.J. Roger)
Frequency Mixture Models
2015 Benjamin Potter
Computing Transition Probabilities for The General Birth-Death Process
2014 Moyan Mei
Least squares Methods in Phylogenetics
2011 Malcolm Cameron
Outliers and Influence in Phylogenetics Through Least Squares Methods
2005 Isabelle Nadeau (Summer Student - Co-supervisor with A.J. Roger)
Site-specific Models of Evolution
2001 Sofia Mosesova
Handwritten Digit Recognition

THESIS COMMITTEE MEMBERSHIP

2023– Wensha Zhang PhD
2023– Leticia Magpali PhD (Biol)
2021– Fatemah Tofighi PhD
2021– Wensha Zhang PhD
2023 Claire Cui MSc
2021-2023 Son Luu MSc
2021-2022 Yun Cai PhD
2020 Mia Parentau MSc
2020 Vishal Sood MSc

2019	Junqiu Gao MSc
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	Francesco 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 Loredo-Osti PhD

EXTERNAL EXAMINATIONS

2019	D. Shepherd (Auckland)	PhD
2016	Y. Zhai (British Columbia)	PhD
2011	A. Rea (Auckland)	PhD
2006	Erica Nahm (Acadia)	MSc

ADMINISTRATIVE RESPONSIBILITIES

2019–	Undergraduate and Honours Coordinator, Statistics Division Department of Mathematics and Statistics, Dalhousie University
2016–	Director, Statistical Consulting Service Department of Mathematics and Statistics, Dalhousie University
2023	Member, Hiring Committee Department of Mathematics and Statistics, Dalhousie University
2022	Member, Adjudications Panel Ontario Genomics-CANSSI Ontario Postdoctoral Fellowship in Genome Data Science
2021-2022	Chair, Hiring Committee

	Department of Mathematics and Statistics (Statistics), Dalhousie University
2020-2022	Member, Canadian Journal of Statistics Award Committee
	Statistical Society of Canada
2020	Chair, Tenure and Promotion Subcommittee
	Department of Mathematics and Statistics (Statistics), Dalhousie University
2020	Chair, Gray-Doolittle Award Committee
	Institute for Comparative Genomics and Evolutionary Bioinformatics
	Dalhousie University
2019-2020	Member, Hiring Committee
	Department of Mathematics and Statistics (Statistics), Dalhousie University
2016-2019	Member, SSC/CRM Award Committee
	Statistical Society of Canada
2016-2019	Member, 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)
	Department of Mathematics and Statistics (Statistics), Dalhousie University
2015-2016	Program Chair
	2016 Annual Meeting of the Statistical Society of Canada
2012-2016	Member, Program Committee
	Statistical Society of Canada Annual Meeting
2011-2015	Chair, Local Arrangements Committee
	2015 Annual Meeting of the Statistical Society of Canada
2014	Member, Tenure and Promotion Subcommittee
	Department of Mathematics and Statistics (Statistics), Dalhousie University
2014	Chair, Math Director Search Committee
	Department of Mathematics and Statistics, Dalhousie University
2012–2014	Member, SSC Research Committee
	Statistical Society of Canada
2012–2014	Atlantic Regional Representative
	Statistical Society of Canada
2013	Member, Hiring Committee
	Department of Mathematics and Statistics (Statistics), Dalhousie University
2012	Member, Hiring Committee
	Department of Mathematics and Statistics (Statistics), Dalhousie University
2011–2012	Senator
	Dalhousie University
2010	Member, Chair Advisory Committee (Physics)
	Faculty of Science, Dalhousie University
2006-2010	Member, Executive Committee
	Computational Biology and Bioinformatics Program, Dalhousie University
2005–2010	Graduate Coordinator, Statistics Division
	Department of Mathematics and Statistics, Dalhousie University
2002–2009	Member, Scientific Committee
	National Program on Complex Data Structures
2007	Member, Reappointment Committee
	Department of Mathematics and Statistics (Statistics), Dalhousie University

2007	Member, Tenure Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2007	Member, Tenure Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2007	Chair, Pierre Robillard Award Committee Statistical Society of Canada
2006–2007	Member, Organizing Committee 2007 Annual Meeting for the Society of Molecular Biology and Evolution
2006–2007	Member, Chair Advisory Committee (Chemistry) Faculty of Science, Dalhousie University
2006	Member, Tenure Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2006	Chair, Appointments Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2006	Member, Appointments Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2005-2007	Member, Pierre Robillard Award Committee Statistical Society of Canada
2005	Member, Tenure Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2005	Chair, Promotion Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2005	Member, Program Committee 2005 Annual Meeting, Intelligent Systems for Molecular Biology
2003–2005	Chair, Computing Resources Committee Department of Mathematics and Statistics, Dalhousie University
2002	Member, Computing Resources Committee Department of Mathematics and Statistics, Dalhousie University
2002	Member, Hiring Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2002	Coordinator, Statistics Seminar Series Department of Mathematics and Statistics (Statistics), Dalhousie University
2000–2002	Atlantic Regional Representative Statistical Society of Canada
2001	Member, Math Director Search Committee Department of Mathematics and Statistics, Dalhousie University
2000–2001	Member, Hiring Committee Department of Mathematics and Statistics (Statistics), Dalhousie University
2000	Member, Education Committee Atlantic Genomics Centre
1999	Member, Hiring Committee Department of Mathematics and Statistics (Statistics), Dalhousie University

CONSULTING

2016–	Director, Statistical Consulting Service, Dalhousie University
2009	Consultant, 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 otilith data
2000-	Consultant, Health Canada
	Bayesian methods for predictive microbiology
1998–2000	Consulant, 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. `chkl.idx.k`, `gapc`, `heatmap.d` and `heatmap.nod`: R functions for the methods described in **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.

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.

GRANTS

2021-2023	**$375,000/yr**	NSERC Emerging Infectious Disease Modelling Statistical methods for managing emerging infectious diseases Bogoch, I., Brown, P. (*PI*), Cowen, L., Dean, C., Deardon, R., Feng, C. Gustafson, P., Ho, L., Jha, P. Moodie, E., Schmidt, A., Stephens, D., Susko, E., Torabi, M. and Yi, G.
2020-2023	**$364,032/yr**	Moore-Simons Project New phylogenomic models and methods to resolve the prokaryote to eukaryote transition

		Bui, M., Eme, L., Roger A.J. (*PI*) and Susko, E.
2019-2024	**$20,000/yr**	NSERC Discovery Grant Statistical methods for molecular evolution Susko, E.
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. (*PI*), 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. (*PI*), Susko, E.
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.
2006-2009	**$141,917/yr**	CIHR Operating Grant Integron metagenomics Doolittle, W.F. (*PI*), 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. (*PI*), 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.

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