CURRICULUM VITAE **AUGUST 2020**

MARY K. KUHNER, PhD

1. PERSONAL DATA

Home Address	1611 NE 63rd St, Seattle, WA 98115
Work Address	Department of Genome Sciences, University of Washington Box 355065, Seattle, WA 98195-5065
Date of Birth	July 6, 1963
Birthplace	Seattle, WA
Citizenship	USA

2. EDUCATION

1980-1982	AAS, Computer Information Systems, Anchorage Community College
1983-1985	BS, Cell and Molecular Biology, University of Washington
1985-1991	PhD, Genetics, University of California Berkeley

3. POSTGRADUATE TRAINING

1991-1996	Postdoctoral Fellow, Department of Genetics, University of Washington

4. FACULTY POSITIONS HELD

1996-2002	Research Assistant Professor, Department of Genetics/Genome Sciences, University of Washington
2003-2015	Research Associate Professor, Department of Genome Sciences, University of Washington
2015-2020	Research Professor, Department of Genome Sciences, University of Washington
2020-	Research Scientist, Department of Biology, University of Washingon

5. HOSPITAL POSITIONS HELD

Not Applicable

6. CURRENT EMPLOYMENT (WWAMI only)

Not Applicable

7. HONORS

Not Applicable

8. BOARD CERTIFICATION

Not Applicable

9. CURRENT LICENSE TO PRACTICE

Not Applicable

10. PROFESSIONAL ORGANIZATIONS

Member, Brotman Baty Institute for Precision Medicine

11. TEACHING RESPONSIBILITIES

(a) Courses taught

1999	General Studies 197 “Freshman Seminar” (sole instructor 1 term)
2001-2017	Genetics/Genome 453 “Evolutionary Genetics” (sole instructor 8 terms, co-instructor 2 terms)
2003	Genetics/Genome 490 “Undergraduate Seminar” (sole instructor 1 term)
2008-2010	Genome 371 “Introductory Genetics” (sole instructor 1 term, co-instructor 2 terms, course coordinator 2 terms)
2008-2010	Genome 559 “Introduction to Statistical and Computational Genomics” (co-instructor 3 terms)
2012	Genome 361 “Fundamentals of Genetics and Genomics” (co-instructor 1 term)
2019	Genome 562 “Population Genetics” (sole instructor 1 term)

(b) Students supervised

Undergraduate	Wang Yi
Graduate Commitee	Charla Lambert (committee co-chair), Arindam Roy Choudhury, Chul Joo Kang, Rumen Kostadinov (U Pennsylvania)
Graduate Rotation	Heather Lindloff, Elain Fu, Maria Malzone, Jennifer Gogarten, Divya Bhat, Sayer Herin
Postdoctoral	Lucian Smith, Brendan O'Fallon

12. EDITORIAL RESPONSIBILITIES

Not Applicable

13. SPECIAL NATIONAL AND INTERNATIONAL RESPONSIBILITIES

1998-2011	Faculty, Workshop on Molecular Evolution
2001-2008	Faculty, International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology
2009-2013	Faculty, European Workshop on Molecular Evolution
2011-2015	Advisory Board, European Workshop on Molecular Evolution
2013, 2016, 2017	Grant Review Panelist, NSF DEB

14. SPECIAL LOCAL RESPONSIBILITIES

2001-present	Faculty Member, Program in Computational Biology
2002-06	Admissions Committee Head, Program in Computational Molecular Biology

2003-06, 2017-18	Faculty Senator, University of Washington
2006-2009	Director, Program in Computational Molecular Biology
2006	External Advisory Board, Seattle Barrett's Esophagus Project, Fred Hutchinson Cancer Research Center
2007-2014	Faculty, Summer Institutes in Statistical Genetics
2018	Instructor, “Genome Hackers” girls' camp
2018-	Member, Brotman Baty Institute
2018-2019	Science Fair project mentor, Diya Basu and Nitisha Gautam, Tesla STEM High School

15. RESEARCH FUNDING

A. Current

B. Past

1995-2002	Sponsor: NIH Title: Likelihood of Sequences with Recombination and Selection R01 GM51929 Total Costs: $992,867 PI: Joseph Felsenstein Role on Project: Co-investigator
1999-2002	Sponsor: NIH Title: Linkage Disequilibrium Mapping Using the Coalescent R01 HG01989 Total Costs: ~$500,000 PI: Joseph Felsenstein Role on Project: Co-investigator
2003-2007	Sponsor: NIH Selection and Association in Coalescent Genealogies R01 GM51929. Total Costs: $1,887,350 PI: Mary Kuhner Role on Project: PI
2008-2010	Sponsor: NSF Title: Estimating natural selection in population pairs locally adapted to contrasting environments

DEB-0814322
Total Costs: $530,000
PIs: Kevin McCracken (UAF) and Mary Kuhner
Role on Project: co-PI

2009-2011
Sponsor: NIH
Title: Scaling up linkage disequilibrium mapping
R01 HG004839
Total Costs: $1,287,024
PI: Mary Kuhner
Role on Project: PI

2012-2017
Sponsor: NIH
Project Title: Statistical and Quantitative Genetics
Subproject Title: Resolving Complex Traits Through Inferred Co-Ancestry
P01 GM099568
Total Costs: $7,296,079
Project PI: Bruce Weir
Subproject PI: Elizabeth Thompson
Role on Project: Co-investigator

2013-2016
Sponsor: NSF
Title: Distance, consensus and query algorithms for recombinant genealogies
DEB-1256731
Total costs: $213,481
PI: Mary Kuhner
Role on Project: PI

2014-2019
Sponsor: NIH
Title: Modeling Neoplastic Progression in Barrett's Esophagus
R01 CA140657
Subaward Costs: $58,913
PI: Carlo Maley
Role on Project: Consultant

2014-2019
Sponsor: NIH
Title: Barrett's Esophagus: Predictors of Progression
P01 CA91955

Subaward Costs: $210,070
PI: Brian Reid, FHCRC
Role on Project: Subproject PI

16. BIBLIOGRAPHY

a) Publications in Refereed Journals

1. Thomson G, WP Robinson, **MK Kuhner,** S Joe, MJ MacDonald, JL Gottschall, J Barbosa, SS Rich, J Bertrams, MP Baur, J Partanen, B Tait, E Schober, WR Mayr, J Ludvigsson, B Lindblom, NR Farid, C Thompson, I Deschamps (1988). Genetic heterogeneity, modes of inheritance and risk estimates for a joint study of Caucasians with insulin dependent diabetes mellitus. American Journal of Human Genetics 43: 799-816. [original work]
2. Motro, U, G Thomson, **MK Kuhner,** WP Robinson (1989). Affected sib pair IBS methods: detection of linkage and genetic models. Prog Clin Biol Res 329: 105-110. [original work]
3. Thomson, G, WP Robinson, **MK Kuhner,** S Joe, W Klitz (1989). HLA and insulin gene associations with IDDM. Genetic Epidemiology 6: 155-160. [original work]
4. Klitz, W, **MK Kuhner,** WP Robinson, M Esposito, G Thomson (1989). Clues to IDDM pathogenesis from genetic and serological traits. Genetic Epidemiology 6: 117-122. [original work]
5. **Kuhner, MK,** RS Goodenow (1989) DNA sequences of mouse H-2 and Qa genes. Immunogenetics 30(6): 458-464. [data compilation]
6. **Kuhner, MK,** S Watts, W Klitz, G Thomson, RS Goodenow (1990). Gene conversion in the evolution of both the H-2 and Qa class I genes of the murine major histocompatibility complex. Genetics 126: 1115-1126. [original work]
7. **Kuhner, MK**, DA Lawlor, PD Ennis, P Parham (1991). Gene conversion in the evolution of the human and chimpanzee MHC class I loci. Tissue Antigens 38: 152-164. [original work]
8. **Kuhner, MK,** MJ Peterson (1992). Genetic exchange in the evolution of the human MHC class II loci. Tissue Antigens 39: 209-215. [original work]
9. **Kuhner, MK,** J Felsenstein (1994). A simulation comparison of phylogeny algorithms under equal and unequal evolutionary rates. Molecular Biology and Evolution 11: 459-468. [original work]
10. **Kuhner, MK**, J Yamato, J Felsenstein (1995). Estimating effective population size and mutation rate from sequence data using Metropolis-Hastings sampling. Genetics 140: 1421-1430. [original work]
11. **Kuhner, MK,** J Yamato, J Felsenstein (1998). Maximum likelihood estimates of population growth rates based on the coalescent. Genetics 149: 429-434. [original work]
12. Felsenstein, J, **MK Kuhner,** J Yamato, P Beerli (1999). Likelihoods on coalescents: a Monte

Carlo sampling approach to inferring parameters from population samples of molecular data. Lecture Notes - Monograph Series, Institute of Mathematical Statistics 33: 163-185. [review]

13. **Kuhner, MK**, P Beerli, J Yamato, J Felsenstein (2000). Usefulness of single nucleotide polymorphism data for estimating population parameters. Genetics 156: 439-447. [original work]
14. **Kuhner, MK,** J Yamato, J Felsenstein (2000). Maximum likelihood estimation of recombination rates from population data. Genetics 156: 1393-1401. [original work]
15. **Kuhner, MK,** J Felsenstein (2000). Sampling among haplotype resolutions in a coalescent-based genealogy sampler. Genetic Epidemiology 19 (Suppl. 1): S15-S21. [original work]
16. **Kuhner, MK** (2006). LAMARC 2.0: maximum likelihood and Bayesian estimation of population parameters. Bioinformatics 22: 768-770. [original work]
17. **Kuhner, MK** (2006). Robustness of coalescent estimators to between-lineage mutation rate variation. Mol. Biol. Evol. 23: 2355-2360. [original work]
18. **Kuhner, MK,** LP Smith (2007). Comparing likelihood and Bayesian coalescent estimation of population parameters. Genetics 175: 155-165. [original work]
19. Smith, LP, **MK Kuhner** (2009). The limits of fine-scale mapping. Genetic Epidemiology 33: 344-356. [original work]
20. **Kuhner, MK** (2009). Coalescent genealogy samplers: windows into population history. Trends in Ecology and Evolution 24: 86-93. [review]
21. McCracken, KG, M Bulgarella, KP Johnson, **MK Kuhner,** J Trucco, TH Valqui, RE Wilson, JL Peters (2009). Gene flow in the face of countervailing selection: adaptation to high-altitude hypoxia in the beta-A hemoglobin subunit of yellow-billed pintails in the Andes. Mol Biol Evol 26: 815-827. [original work]
22. McCracken, KG, CP Barger, M Bulgarella, KP Johnson, **MK Kuhner,** AV Moore, JL Peters, J Trucco, TH Valqui, K Winkler, RE Wilson (2010). Signatures of high-altitude adaptation in the major hemoglobin of five species of Andean dabbling ducks. Am Nat 174: 631-650. [original work]
23. McGill, JR, E Walkup, **MK Kuhner** (2013). Correcting coalescent analyses for panel-based SNP ascertainment. Genetics 193(4): 1185-1196. doi: 10.1534/genetics.112.146738. [original work]
24. Kostadinov, RL, **MK Kuhner,** CA Sanchez, PC Gallipeau, TG Paulson, X Li, CL Sather, A Srivastava, RD Odze, PL Blount, TL Vaughan, BJ Reid, CC Maley (2013). NSAIDs modulate clonal evolution in Barrett's Esophagus. PLoS Genetics 9(6): e1003553. doi: 10.1371/journal.pgen. 1003553. [original work]
25. McGill, JR, EA Walkup, **MK Kuhner** (2013). GraphML specializations to codify ancestral recombination graphs. Frontiers in Evol. and Pop. Genetics 4, doi=10.3389/fgene.2013.00146. [original work]
26. Li, X, PC Galipeau, TG Paulson, CA Sanchez, J Arnaudo, K Liu, CL Sather, RL Kostadinov, RD

Odze, **MK Kuhner,** CC Maley, SG Self, TL Vaughan, PL Blount, BJ Reid (2014). Temporal and spatial evolution of somatic chromosomal alterations: A case-cohort study of Barrett's esophagus. Cancer Prevention Research 7(1): 114-127. [original work]

27. Zheng, C, **MK Kuhner,** EA Thompson (2014). Joint inference of identity by descent along multiple chromosomes from population samples. J. Comp. Biol. 21: 185-200. [original work]
28. Zheng, C, **MK Kuhner,** EA Thompson (2014). Bayesian inference of local trees along chromosomes by the sequential Markov coalescent. J Mol Evol 78: 279-292. PMCID PMC4104301. [original work]
29. **Kuhner, MK,** and JA Yamato (2014) Practical performance of tree comparison metrics. Systematic Biology 64(2): 205-214. [original work]
30. **Kuhner, MK**, and JR McGill (2014) Correcting for sequencing error in maximum likelihood phylogeny inference. G3 4(12): 2545-2552. [original work]
31. **Kuhner, MK,** and J Yamato (2015) Assessing differences between ancestral recombination graphs. J Mol Evol 80(5-6): 258-264. https://doi.org/10.1007/s00239-015-9676-x. [original work]
32. Li, X, TG Paulson, PC Galipeau, CA Sanchez, K Liu, **MK Kuhner,** CC Maley, SG Self, TL Vaughn, BJ Reid, PL Blount (2015). Assessment of esophageal adenocarcinoma risk using somatic chromosome alterations in longitudinal samples in Barrett's esophagus. Cancer Prev Prev Res 8 (9): 845-856. [original work]
33. Kostadinov, R, CC Maley, **MK Kuhner** (2015). Bulk genotyping of biopsies can create spurious evidence for heterogeneity in mutation content. PLOS Comp Biol 12(4): e1004413. [original work]
34. **Kuhner, MK**, R Kostadinov, BJ Reid (2016) Limitations of the driver/passenger model in cancer prevention. Cancer Prev Res 9 (5): 335-338. [review]
35. **Kuhner, MK**, and J Yamato (2017) A consensus method for ancestral recombination graphs. J Mol Evol 84(2-3): 335-338. [original work]
36. Martinez, P, D Mallo, TG Paulson, X Li, CA Sanchez, BJ Reid, TA Graham, **MK Kuhner,** CC Maley (2018) Evolution of Barrett's esophagus through space and time at single-crypt and whole-biopsy levels. Nat Comm 9(1): 794. [original work]
37. Galipeau, PC, KM Oman, TG Paulson, CA Sanchez, Q Zhang, JA Marty, JJ Delrow, **MK Kuhner,** TL Vaughan, BJ Reid, X Li (2018) NSAID use and somatic exomic mutations in Barrett's esophagus. Genome Med 10(1): 17. https://doi.org/10.1186/s13073-018-0520-y. [original work]
38. Smith, LP, JA Yamato, **MK Kuhner** (2019) CNValidator: validating somatic copy-number inference. Bioinformatics, bty1022, https://doi.org/10.1093/bioinformatics/bty1022. [original work]
39. Hadi, K, X Yao, JM Behr, A Deshpande, C Xanthopoulakis, et al. (2019) Novel patterns of complex structural variation revealed across thousands of cancer genome graphs. bioRxiv

836296.

40. Smith, LP, JA Yamato, PC Galipeau, TG Paulson, X Li, CA Sanchez, BJ Reid, MK Kuhner (2020) Within-patient phylogenetic reconstruction reveals early events in Barrett's Esophagus. Evolutionary Applications, in press.

b) Book chapters

1. Motro, U, G Thomson, **MK Kuhner,** WP Robinson (1989). Affected sib pair IBS methods: detection of linkage and genetic models. In: Multipoint Mapping and Linkage Based Upon Affected Pedigree Members: Genetic Analysis Workshop 6, eds. Elston RC, Spence MA, Hodge SE, MacCluer JW. Alan R. Liss, New York, pp. 105-110.
2. Hedrick, PW, W Klitz, WP Robinson, **MK Kuhner,** G Thomson (1991). Population genetics of HLA. In: Evolution at the Molecular Level, eds. RK Selander, AG Clark, TS Whittam. Sinauer Associates, pp. 248-271.
3. **Kuhner, MK,** J Yamato, J Felsenstein (1997). Applications of Metropolis-Hastings genealogy sampling. Pp 183-192 in Progress in Population Genetics and Human Evolution, ed. P Donnelly and S Tavere. IMA Volumes in Mathematics and Its Applications, vol. 87.
4. Beerli, P, NC Grassly, **MK Kuhner,** D Nickle, O Pybus, M Rain, A Rambaut, AG Rodrigo, Y Wang (2001). Population genetics of HIV: parameter estimation using genealogy-based methods. Chapter 10 in Computational and Evolutionary Analysis of HIV Molecular Sequences, ed. Rodrigo AG and Learn, GH. Kluwer Academic Publishers, Norwell, Massachusetts.
5. **Kuhner, MK**. (2003). LAMARC: estimating population genetic parameters from molecular data. Pp. 378-398 in The phylogenetic handbook: a practical approach to DNA and protein phylogeny. M. Salemi and A-M Vandamme, eds. Cambridge University Press, Cambridge, UK.
6. **Kuhner, MK** (2009). LAMARC: estimating population genetic parameters from molecular data. Pp. 378-398 in The phylogenetic handbook: a practical approach to phylogenetic analysis and hypothesis testing, 2nd edition. Lemey P, Salemi M, and Vandamme A-M, eds. Cambridge University Press, Cambridge, UK.
7. **Kuhner, MK** (2014). Bayesian methods in the presence of recombination. Chapter in Bayesian Phylogenetics: Methods, Algorithms, and Applications. Chen M-H, Kuo L, Lewis P (editors). Chapman and Hall/CRC Press.

c) Published Software

1. NEIGHBOR: neighbor-joining phylogeny inference program (PHYLIP package) (1994). http://evolution.gs.washington.edu/ phylip.html.

2. LAMARC Package: At least 237 studies have been conducted using LAMARC package programs (this does not include citations for reasons other than use of the software). http://evolution.gs.washington.edu/lamarc.html.
   a) COALESCE: coalescent inference of population size (1995).
   b) FLUCTUATE: coalescent inference of population growth rate (1998).
   c) RECOMBINE: coalescent inference of recombination rate (2000).
   d) LAMARC: coalescent inference of multiple population parameters (2001-2013).
3. "Exploring Human Prehistory through Genome Sequencing" (2016). Interactive educational module for advanced undergraduates and graduate students.
   http://evolution.gs.washington.edu/module1/

d) Other Publications

1. Zheng, C, **MK Kuhner,** EA Thompson (2013). Joint inference of identity by descent along multiple chromosomes from population samples. Technical Report 621, Department of Biostatistics, University of Washington.
2. Mallo, D, R Kostadinov, L Cisneros, MK Kuhner, CC Maley (2018) Cryptsim: modeling the evolutionary dynamics of the progression of Barrett's esophagus to esophageal adenocarcinoma. BioRxiv doi: https://doi.org/10.1101/323485

e) Abstracts

1. **Kuhner, MK,** J Yamato, J Felsenstein (2001). Markov chain Monte Carlo simulation for linkage disequilibrium mapping. Abstract for the 10th Conference of the International Genetic Epidemiology Society, Garmisch-Partenkirchen, Germany.
2. Kostadinov, R, R Kosoff, **MK Kuhner,** P Galipeau, P Rabinovitch, B Reid, CC Maley (2006). Genome-wide case study of clonal evolution over 16 years in Barrett's Esophagus. Abstract for the 5th AACR International Conference on Frontiers in Cancer Prevention, USA.
3. Thompson, EA, **MK Kuhner** (2014). Inferring identity by descent in admixed populations. Abstract for the XXVII International Biometric Society meeting, Italy.

17. OTHER

A. Invited presentations:

1996	Society for Molecular Biology and Evolution Coalescent Workshop, invited talk
2003	University of Gothenburg, invited talk
2005	Decatur High School, invited talk

2005, 2007	University of Ohio, invited talks
2006, 2013	University of Alaska Fairbanks, invited talks
2013	International Biannual Evolution and Cancer Conference, invited talk
2014	Wednesday Evenings at the Genome public lecture
2015	Canadian Human and Statistical Genetics meeting, invited talk
2017	Symposium in honor of Joseph Felsenstein, Evolution Meeting, invited talk
2019	Evolutionary Dynamics in Cancer, Ohio State University, invited talk