

Peter R. Wilton
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EDUCATION

Harvard University Cambridge, MA
PhD, Organismic and Evolutionary Biology August 2011 – May 2016
Dissertation:
Frontiers in coalescent theory: pedigrees, identity-by-descent, and sequentially Markov coalescent models

Carleton College Northfield, MN
BA, *summa cum laude*, Biology, Phi Beta Kappa Sept 2006 – June 2010
Thesis, with distinction: Polyandry and the evolution of selfish genetic elements

RESEARCH

University of California, Berkeley Berkeley, CA
Postdoctoral Researcher – Advisor: Rasmus Nielsen July 2016 – April 2019
Cell-lineage population genetics of mitochondrial heteroplasmy in humans
Detecting low-frequency somatic mosaicism and heteroplasmy by jointly estimating allele frequency and sequencing error spectra
Global epistasis and non-additivity across quantitative traits in the UK Biobank data

Harvard University Cambridge, MA
Graduate student – Advisor: John Wakeley 2011 – 2016
Effects of population pedigree on coalescence in structured populations
Two-locus properties of sequentially Markov coalescent models, with an exploration of consistency and bias in the SMC and SMC'
(*in collaboration with Shai Carmi and Pier Palamara*)
Theory of IBD segment lengths and mutational mismatches on IBD segments
(*in collaboration with Frank Rheindt*)
Phylogeography and introgression in *Zimmerius* flycatchers and *Rhipidura* fantails (class: Aves)

Peter R. Wilton

(in collaboration with Maurine Neiman)

Population genomics of reproductive mode in sexual and asexual *Potamopyrgus* snails

University of Iowa Iowa City, IA

Research technician with Maurine Neiman and Andrew Forbes

2010 – 2011

Evolution of reproductive mode in sexual and asexual *Potamopyrgus* snails

Speciation across trophic levels in tephritid flies and parasitoid wasps

PUBLICATIONS (* EQUAL AUTHOR CONTRIBUTION)

Zaidi, A.*, **Wilton, P.R.***, Su, M.S.*, Paul, I.M., Anthony, K., Nekrutenko, A., Nielsen, R., and Makova, K. (2019). The germline bottleneck, mother's age, and selection modulate the transmission dynamics of mtDNA heteroplasmies in human pedigrees. *In review*.

Barrett, A.*, Arbeithuber, B.*, Zaidi, A., **Wilton, P.R.**, Paul, I., Nielsen, R., Makova, K. Pronounced somatic bottleneck in mitochondrial DNA of human hair (2019) *Philosophical Transactions B*, *accepted*.

Stern, A., **Wilton, P.R.**, Nielsen, R. (2019) An approximate full-likelihood method for inferring selection and allele frequency trajectories from DNA sequence data. *PLOS Genetics* 15: e1008384.

Garg, K.M., Chattopadhyay, B., **Wilton, P.R.**, Malia Prawiradilaga, D., and Rheindt, F.E. (2018). Pleistocene land bridges act as semipermeable agents of avian gene flow in Wallacea. *Molecular Phylogenetics and Evolution* 125, 196–203.

Wilton, P.R., Zaidi, A., Makova, K., and Nielsen, R. (2018) A population phylogeny view of mitochondrial heteroplasmy. *Genetics*, 208, 1261–1274.

Ng, N.S.R., **Wilton, P.R.**, Prawiradilaga, D.M., Tay, Y.C., Indrawan, M., Garg, K.M., and Rheindt, F.E. (2017) The effects of Pleistocene climate change on biotic differentiation in a montane songbird clade from Wallacea. *Molecular Phylogenetics and Evolution*, 114, 353–366.

Wilton, P.R., Baduel, P., Landon, M.M., and Wakeley, J. (2017) Population structure and coalescence in pedigrees: comparisons to the structured coalescent and a framework for inference. *Theoretical Population Biology*, 115, 1–12.

Wakeley, J., King, L., and **Wilton, P.R.** (2016) Effects of the population pedigree on genetic signatures of historical demographic events. *PNAS*, 113, 7994–8001.

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Palamara, P.F., Francioli, L., **Wilton, P.**, Genovese, G., Gusev, A., Finucane, H., Sankararaman, S., Sunyaev, S., Debakker, P., Wakeley, J., et al. (2015). Leveraging distant relatedness to quantify human mutation and gene conversion rates. *American Journal of Human Genetics* *97*, 775–789.

Wilton, P.R., Carmi, S.*, and Hobolth, A*. (2015). The SMC' is a highly accurate approximation to the ancestral recombination graph. *Genetics* *200*, 343–355.

Carmi, S., **Wilton, P.R.**, Wakeley, J., and Pe'er, I. (2014). A renewal theory approach to IBD sharing. *Theoretical Population Biology* *97*, 35–48.

Rheindt, F.E., Fujita, M.K., **Wilton, P.R.**, and Edwards, S.V. (2014). Introgression and Phenotypic Assimilation in *Zimmerius* Flycatchers (Tyrannidae): Population Genetic and Phylogenetic Inferences from Genome-Wide SNPs. *Systematic Biology* *63*, 134–152.

Wilton, P.R., Sloan, D.B., Logsdon Jr, J.M., Doddapaneni, H., and Neiman, M. (2013). Characterization of transcriptomes from sexual and asexual lineages of a New Zealand snail (*Potamopyrgus antipodarum*). *Molecular Ecology Resources* *13*, 289–294.

Neiman, M., Larkin, K., Thompson, A.R., and **Wilton, P.** (2012). Male offspring production by asexual *Potamopyrgus antipodarum*, a New Zealand snail. *Heredity* *109*, 57–62.

Willacker, J.J., Von Hippel, F.A., **Wilton, P.R.**, and Walton, K.M. (2010). Classification of threespine stickleback along the benthic–limnetic axis. *Biological Journal of the Linnean Society* *101*, 595–608.

BOOK CHAPTERS

Wakeley J., **Wilton P.R.** Coalescent and models of identity by descent. In: *Encyclopedia of Evolutionary Biology*. Vol 1. Academic Press, Oxford, 2016: pp. 287-292.

TEACHING

University of California, Berkeley

Guest Lecturer, Human Genetics and Genomics

Guest Lecturer, Statistics for Data Science

Berkeley, CA

Fall 2017

Spring 2018

Harvard University

Teaching Fellow, Coalescent Theory

Cambridge, MA

Fall 2015, Fall 2012

Peter R. Wilton

- Awarded Certificate of Teaching Excellence
Teaching Fellow, Statistics for Biologists
- Awarded Certificate of Teaching Excellence Fall 2014
- Led weekly section, giving review and prospective lectures
- Designed, implemented, and led introduction to the R statistical programming language for biologists, available on [GitHub](#)

Carleton College	Northfield, MN
Teaching Assistant, Population Ecology	Spring 2010
Teaching Assistant, Evolutionary Biology	Fall 2009
Prefect, Population Ecology	Spring 2009

AWARDS

Smith Family Graduate Science and Engineering Fellowship
Harvard University

Phi Beta Kappa Honor Society
Carleton College

SELECTED ORAL PRESENTATIONS

- A population phylogeny approach to understanding mitochondrial heteroplasmy
Biology of Genomes 2017, Cold Spring Harbor Laboratory, Laurel Hollow, NY, USA
- Joint inference of sample pedigrees, admixture proportions, and migration rates
Probabilistic Modeling in Genomics,
Cold Spring Harbor Laboratory, October 2015
- Theory of identity-by-descent and sequentially Markov coalescent models
Evolution 2014, Raleigh, NC, USA
- The effect of selective sweeps on genetic variation at unlinked sites
Evolution 2012, Ottawa, Ontario, CAN

SELECTED POSTER PRESENTATIONS

- A population phylogeny approach to understanding mitochondrial heteroplasmy
SMBE meetings 2017, Austin, TX
- Clarifying the approximations inherent in sequentially Markov coalescent models
SMBE meetings 2015, Vienna, Austria
- Introgression and phenotypic assimilation in *Zimmerius* flycatchers: population genetic and phylogenetic inferences from genome-wide SNPs

Peter R. Wilton

American Ornithological Union meetings 2013, Chicago, IL

TECHNICAL SKILLS

Statistical inference, probabilistic modeling, and stochastic processes

Next-generation sequencing and large-scale genotype data

Scientific programming and software development

Daily-use familiarity with

Python (numpy, pandas, cython, matplotlib, h5py, etc.), C, R, Git, Linux coreutils,
Awk, BASH, SLURM clusters

Some familiarity with

Tensorflow, LSF clusters, SQL

GitHub user: @ammodramus

REFERENCES

Rasmus Nielsen

Professor

Departments of Integrative Biology and Statistics

University of California, Berkeley

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Berkeley, CA 94720-3140 USA

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John Wakeley

Professor

Department of Organismic and Evolutionary Biology

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Biological Laboratories Rm 4096

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Kateryna Makova

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