

University of Oregon
Institute of Ecology and Evolution
Departments of Mathematics and Biology
Fenton Hall, Eugene, OR 97403

Phone: (707) 502-5854
Email: plr@uoregon.edu
<https://kr-colab.github.io>

Research field: The study of populations and evolution with genomic data, especially spatially explicit models of adaptation and inheritance; development of stochastic models and statistical inference methods for population genetics/genomics.

Work Experience

- **Associate Professor**, Departments of Mathematics and Biology, University of Oregon, May 2020 –
- **Assistant Professor**, Departments of Mathematics and Biology, University of Oregon, June 2016 – April 2020
- **Assistant Professor**, Molecular and Computational Biology, University of Southern California, January 2013 – May 2016.
- **Postdoctoral Researcher**, Department of Evolution and Ecology, UC Davis, with Graham Coop and Sebastian Schreiber, 2009–2011.
- **Lecturer**, Department of Statistics, UC Berkeley (one-third time), Fall semester 2010.

Grants

Pending:

- co-PI on NSF *BII:Scaling biodiversity and ecological function from genes to biogeographic regions:an integrative institute across temperate rainforests*; 1/2024–12/2029; led by collaborators at OSU.

Awarded:

- PI on NIH/NHGRI R01 for Investigator Initiated Research: **Scaling up computational genomics with tree sequences**, 6/2023 – 5/2028.
- PI on NIH/NHGRI R56: **Scaling up computational genomics with tree sequences**, 7/2021 – 12/2022.
- co-I on NSF *CSSI: CANDY: Cyberinfrastructure for Accelerating Innovation in Network Dynamics*, 8/2021–8/2023; led by Boyana Norris
- Co-I on NIH/NHGRI R01 HG010774-01A1: **Deep learning for population genetics**, 4/2020 – 3/2025.
- **Incubating Interdisciplinary Initiatives (I3)** award: internal University of Oregon competition, 6/2019.
- **Alfred P. Sloan Research Fellowship** in Computational & Evolutionary Molecular Biology, 3/4/2015.

- NSF Advances in Biological Informatics grant #1262645, “**Visualization and Statistics for Spatial Population Genomic Analysis**”, 3/2013-8/2018.
- **Ruth L. Kirschstein National Research Service Award** (NIH), postdoctoral study 2011–2013, with Graham Coop and Charles Langley, sponsors.

Education and Awards

- **PhD, Statistics**, advisor Steven N. Evans, UC Berkeley, 2003–2009
- **Citation in Probability**, Department of Statistics, for PhD thesis, May 2009
- **Bernard Friedman Prize in Applied Mathematics**, Department of Mathematics, for PhD thesis, May 2009
- **AB, Applied Mathematics**, UC Berkeley, 1997–2002

Preprints: *(note: all are currently in review or revision)*

Alison M Etheridge, Thomas G Kurtz, Ian Letter, Peter L Ralph, and Terence Tsui Ho Lung. Looking forwards and backwards: dynamics and genealogies of locally regulated populations. (preprint at arXiv:2305.14488) *(authors alphabetical)*

Todd Parsons and Peter L Ralph Large effects and the infinitesimal model. (preprint at bioRxiv:2023.07.20.549972)

Clara T Rehmann, Peter L Ralph and Andrew D Kern. Evaluating evidence for co-geography in the Anopheles Plasmodium host-parasite system. (preprint at bioRxiv:2023.07.17.549405)

Murillo Fernando Rodrigues, Andrew D Kern, and Peter L Ralph (2023). *Shared evolutionary processes shape landscapes of genomic variation in the great apes*. (preprint at bioRxiv:2023.02.07.527547v1)

Martin Petr, Benjamin C Haller, Peter L Ralph, and Fernando Racimo (2022). *slendr: a framework for spatio-temporal population genomic simulations on geographic landscapes*. (preprint at bioRxiv:2022.03.20.485041v3)

Peer-reviewed publications: *(* denotes all authors contributed equally)*

Chris CR Smith, Silas Tittes, Peter L Ralph, and Andrew D Kern (2022). *Dispersal inference from population genetic variation using a convolutional neural network*. Genetics 224 (2).

M Elise Lauterbur, Mariz Izabel A Cavassim, Ariella L Gladstein, Graham Gower, Nathaniel S Pope, Georgia Tsambos, Jeffrey Adrion, Saurabh Belsare, Arjun Biddanda, Victoria Caudill, Jean Cury, Ignacio Echevarria, Benjamin C Haller, Ahmed R Hasan, Xin Huang, Leonardo Nicola Martin Iasi, Ekaterina Noskova, Jana Obšteter, Vitor Antonio Corrêa Pavinato, Alice Pearson, David Peede, Manolo F Perez, Murillo F Rodrigues, Chris CR Smith, Jeffrey P Spence, Anastasia Teterina, Silas Tittes, Per Unneberg, Juan Manuel Vazquez, Ryan K Waples, Anthony Wilder Wohms, Yan Wong, Franz

- Baumdicker, Reed A Cartwright, Gregor Gorjanc, Ryan N Gutenkunst, Jerome Kelleher, Andrew D Kern, Aaron P Ragsdale, Peter L Ralph, Daniel R Schrider, and Ilan Gronau (2023). *Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations*. eLife 12:RP84874. (*I am a co-senior author on this paper.*)
- Erick Matsen and Peter Ralph (2022). *Enabling inference for context-dependent models of mutation by bounding the propagation of dependency*. Journal of Computational Biology 29 (8), 802-824.
- C. John Ralph, Carlo P Ralph, Pedro Martins and Peter L Ralph. A New Zealand island in change: 38 years of landbird populations affected by habitat restoration and invasive mammalian predator control. Notornis 69 (4), 211-227 .
- Josh Schiffman and Peter Ralph (2022). *System drift and speciation*. Evolution (76) 2, 236-251.
- Franz Baumdicker, Gertjan Bisschop, Daniel Goldstein, Graham Gower, Aaron P Ragsdale, Georgia Tsambos, Sha Zhu, Bjarki Eldon, Castedo E Ellerman, Jared G Galloway, Ariella L Gladstein, Gregor Gorjanc, Bing Guo, Ben Jeffery, Warren W Kretzschmar, Konrad Lohse, Michael Matschiner, Dominic Nelson, Nathaniel S Pope, Consuelo D Quinto-Cortés, Murillo F Rodrigues, Kumar Saunack, Thibaut Sellinger, Kevin Thornton, Hugo van Kemenade, Anthony W Wohms, Yan Wong, Simon Gravel, Andrew D Kern, Jere Koskela, Peter L Ralph, and Jerome Kelleher (2021). *Efficient ancestry and mutation simulation with msprime 1.0*. Genetics 220 (3), iyab229.
- Katja Kasimatis, Abin Abraham, Peter Ralph, Andy Kern, John Capra, and Patrick Phillips (2021). *Evaluating human autosomal loci for sexually antagonistic viability selection in two large biobanks*. Genetics 217 (1), 1-10.
- Jeff Adrion, Chris Cole, Noah Dukler, Jared Galloway, Ariella Gladstein, Graham Gower, Christopher Kyriazis, Aaron Ragsdale, Georgia Tsambos, Franz Baumdicker, Jedidiah Carlson, Reed Cartwright, Arun Durvasula, Ilan Gronau, Bernard Kim, Patrick McKenzie, Philipp Messer, Ekaterina Noskova, Diego Ortega-Del Vecchyo, Fernando Racimo, Travis Struck, Simon Gravel, Ryan Gutenkunst, Kirk Lohmueller, Peter Ralph, Daniel Schrider, Adam Siepel, Jerome Kelleher, and Andrew Kern (2020). *A community-maintained standard library of population genetic models*. Elife 9, e54967.
- CJ Battey, Peter Ralph, and Andy Kern (2020). *Predicting geographic location from genetic variation with deep neural networks*. ELife 9, e54507.
- CJ Battey, Peter Ralph, and Andy Kern (2020). *Space is the place: Effects of continuous spatial structure on analysis of population genetic data*. Genetics 215 (1), 193-214.
- Peter Ralph, Kevin Thornton, and Jerome Kelleher (2020). *Efficiently summarizing relationships in large samples: a general duality between statistics of genealogies and genomes*. Genetics 215 (3), 779-797.
- Sean Stankowski, Madeline Chase, Alison Fuiten, Murillo Rodrigues, Peter Ralph, and Matt Streisfeld (2019). *Widespread selection and gene flow shape the genomic landscape during a radiation of monkeyflowers*. PLOS Biology 17(7): e3000391.
- Jared Galloway, William Cresko, and Peter Ralph (2019). *A few stickleback suffice for the*

- transport of alleles to new lakes*. G3: Genes—Genomes—Genetics; 10 (2), 505-514.
- Katja R Kasimatis, Peter L Ralph, and Patrick C Phillips (2019). *Limits to Genomic Divergence Under Sexually Antagonistic Selection*. G3: Genes—Genomes—Genetics; 9(11) 3813–3824.
- Gideon Bradburd and Peter Ralph (2019). *Spatial Population Genetics: It's About Time*. Annual Review of Ecology, Evolution, and Systematics; 50:427–449.
- Erik Lundgren and Peter Ralph (2019). *Are populations like a circuit? The relationship between isolation by distance and isolation by resistance*. Molecular Ecology Resources; 19(6) 1388–1406.
- Peter Ralph (2019). *An empirical approach to demographic inference with genomic data*. Theoretical Population Biology; 127:91–101.
- Ben Haller, Jared Galloway, Jerome Kelleher, Phillip Messer, and Peter Ralph (2019). *Tree-sequence recording in SLiM opens new horizons for forward-time simulation of whole genomes*. Molecular Ecology Resources; 19:552–566.
- Jerome Kelleher, Kevin Thornton, Jaime Ashander, and Peter Ralph (2018). *Efficient pedigree recording for fast population genetics simulation*. PLoS Computational Biology 14 (11), e1006581.
- Han Li and Peter Ralph (2018). *Local PCA shows how the effect of population structure differs along the genome*. Genetics 211 (1) 289-304.
- Gideon Bradburd, Graham Coop and Peter Ralph (2018). *Inferring continuous and discrete population genetic structure across space*. Genetics 210 (1) 33-52.
- Rachael A Bay, Noah Rose, Rowan Barrett, Louis Bernatchez, Cameron K Ghalambor, Jesse R Lasky, Rachel B Brem, Stephen R Palumbi, and Peter Ralph (2017). *Predicting responses to contemporary environmental change using evolutionary response architectures*. The American Naturalist 189 (5) 463-473.
- Alisa Sedghifar, Yaniv Brandvain, and Peter Ralph (2016). *Beyond clines: lineages and haplotype blocks in hybrid zones*. Molecular Ecology 25 (11) 2559-2576.
- Jessica Crisci, Matt Dean, and Peter Ralph (2016). *Adaptation in isolated populations: when does it happen and when can we tell?*. Molecular Ecology 25 (16) 3901-3911.
- Charleston W.K. Chiang, Peter Ralph, and John Novembre (2016). *Conflation of short identity-by-descent segments can bias their inferred length distribution*. G3: Genes, Genomes, Genetics g3.116.027581.
- Peter Ralph and Graham Coop (2015). *Convergent evolution during local adaptation to patchy landscapes*. PLoS Genetics 11 (11) e1005630.
- Peter Ralph and Graham Coop (2015). *The role of standing variation in geographic convergent adaptation*. American Naturalist 186 (S1) S5-S23.
- Alisa Sedghifar, Yaniv Brandvain, Peter Ralph, and Graham Coop (2015). *The spatial mixing of genomes in secondary contact zones*. Genetics 201 (1) 243-261.
- Shohei Takuno, Peter Ralph, Kelly Swarts, Rob J Elshire, Jeffrey C Glaubitz, Edward

- S Buckler, Matthew B Hufford, and Jeff Ross-Ibarra (2015). *Independent molecular basis of convergent highland adaptation in maize*. *Genetics* 200 (4) 1297-1312.
- Gideon Bradburd, Peter L Ralph, and Graham Coop (2015). *A spatial framework for understanding population structure and admixture*. *PLoS Genetics* 12 (1) e1005703.
- Jim Dines, Erik Otárola-Castillo, Peter Ralph, Jesse Alas, Tim Daley, Andrew Smith, and Matt Dean (2014). *Sexual selection targets cetacean pelvic bones*. *Evolution* 68 (11) 3296-3306.
- Gideon Bradburd, Peter Ralph, and Graham Coop (2013). *Disentangling the effects of geographic and ecological isolation on genetic differentiation*. *Evolution*, 67 (11) 3248-3273.
- Peter Ralph and Graham Coop (2013). *The geography of recent genetic ancestry across Europe*. *PLoS Biology* 11(5) e1001555.
- Steven Evans*, Peter Ralph*, Sebastian Schreiber*, and Arnab Sen* (2013). *Stochastic population growth in spatially heterogeneous environments*. **Journal of Mathematical Biology** 66 (3) 423-476.
- Graham Coop and Peter Ralph (2012). *Patterns of neutral diversity under general models of selective sweeps*. **Genetics** 192 (1) 205-224.
- Carl Boettiger, Graham Coop, and Peter Ralph (2012). *Is your phylogeny informative? Measuring the power of comparative methods*. **Evolution** 66 (7) 2240-2251.
- Alistair Boettiger*, Steven Evans* and Peter Ralph* (2011). *Transcriptional regulation: Effects of promoter proximal pausing on speed, synchrony and reliability*. **PLoS Computational Biology** 7 (5) e1001136.
- Peter Ralph and Graham Coop (2010). *Parallel adaptation: One or many waves of advance of an advantageous allele?* **Genetics** 186 (2) 647-668.
- Steven Evans* and Peter Ralph* (2010). *Dynamics of the time to the most recent common ancestor in a large branching population*. **Annals of Applied Probability** 20 (1), 1-25.
- Peter Ralph (2008). *Seed dispersal kernel estimation without fecundities*. **Molecular Ecology** 17 (8) 1881-1882.
- Shankar Bhamidi*, Steve Evans*, Ron Peled* and Peter Ralph* (2008). *Brownian motion on disconnected sets, basic hypergeometric functions, and some continued fractions of Ramanujan*. in **Essays in Honor of David A. Freedman**, Institute of Mathematical Statistics Collections in Probability and Statistics 2 42-75.
- Brian Sullivan, Marshall Iliff, Peter Ralph, C.J. Ralph, and Steven Kelling (2008). *A Lesser Frigatebird (Fregata ariel) in California: a first for the state and a fourth for North America*. in **North American Birds**, 61 (4) 540-545.
- Anita Pearson, Oliver Pearson, and Peter Ralph (2006). *Growth and Activity Patterns in a Backyard Population of the Banana Slug, Ariolimax columbianus*. *The Veliger* 48 (3) 143-150.

Technical reports:

Evan McCartney-Melstad, Peter Ralph, Jannet Vu, and H. Bradley Shaffer (2016). *Desert Tortoises in the genomic age: Population genetics and the landscape*. report to the California Department of Fish & Wildlife. (bioRxiv:195743)

Selected invited seminars and workshops:

- Gave the *Computational Biology Seminar* at Cornell, September, 2023.
- Gave the *Statistics Department Seminar* at the University of Michigan, February 2022.
- Invited speaker at *Probability and Biological Evolution* conference, CIRM, Luminy, France, June 2021.
- Gave the *Center for Genome Research and Biocomputing* seminar, Oregon State University, May 2021.
- Gave the *Ecology, Evolution & Conservation Biology* seminar, UIUC, February 2021.
- Talked in the *Empirical Research Workshop Series* at Reed College, August 2020.
- Gave the *EvoLunch* seminar at IST Austria, October 2020.
- Invited speaker at *Mutation and Speciation* symposium, Collège de France, May 2019.
- Gave the *Bioinformatics and Computational Biology* seminar, University of Idaho, Moscow, March 2019.
- Talk at the *ProbGen meeting*, Cold Springs Harbor, November 2018.
- Gave the *Genetics seminar*, UW-Madison, September 2018.
- Gave the *Broad Institute* research seminar, March 2018.
- Talk at the *Evolution* meetings, Portland, June 2017.
- Talk at the *Evolution* meetings, Austin, June 2016.
- Symposium speaker at *American Society of Naturalists* meeting, January 2016.
- Talk at the *American Mathematical Society* Western Regional Meeting, Fullerton, October 2015.
- Talk in the *Math-Bio Seminar*, University of Pennsylvania, September 2015.
- Talk at *phyloseminar.org*, January, 2015.
- Talk at the *Center for Bioinformatics Research* seminar, Indiana University, September, 2014.
- Talk at the *Biological Sequence Analysis and Probabilistic Models* workshop, University of Oxford, July, 2014.
- Talk at the *New Directions in Probabilistic Models of Evolution* workshop, Simons Institute, UC Berkeley, May 2014.
- Gave the *Ecology & Evolutionary Biology Seminar*, UC Irvine, April, 2014.

- Gave the *Bioinformatics Seminar*, UCLA, October, 2013.
- Talk at the *American Society of Human Genetics*, San Francisco, November 2012.
- Talk at the *Probability, Population Genetics and Evolution* workshop, Centre International de Rencontres Mathématiques, Marseille-Luminy, June 2012.
- Gave the *Center for Population Biology Seminar*, UC Davis, March 29, 2011.
- Gave the *Probability Seminar*, Cornell University, January 26, 2009.

Other activities:

- Associate editor for *Genetics* (since 2022).
- Core organizer and developer with the *tskit* group (<https://tskit.dev>), an international group of 8–15 researchers developing open-source software tools and methods for working with tree sequences, that is increasingly built on by other software.
- Core organizer and developer with the *PopSim Consortium*, a group of 10–20 researchers worldwide developing open-source tools for reproducible simulation in population genetics research.
- Co-organizer for the fifth annual *Probabilistic Modeling in Genomics* meeting, Oxford, September 2016 (attended by ~150 people).
- Co-organizer of the twice-yearly Southern California Evolutionary Genetics & Genomics meetings, hosted at USC in March 2014 and February 2015 (attended by ~75 people).
- Active journal reviewer, including for: *Molecular Ecology*, *Genetics*, *PLoS Computational Biology*, *Current Biology*, *Journal of Mathematical Biology*, *Bioinformatics*, *Evolutionary Ecology*, *Molecular Biology and Evolution*, *BMC Genomics*, *PLoS Genetics*, *American Journal of Human Genetics*, *Biometrika*, *PLoS One*, *Annals of Applied Probability*.
- Grant review panelist for NSF; Swiss National Science Foundation (ad hoc); Icelandic Centre for Research (ad hoc); Vienna Science and Technology Fund (ad hoc).

Selected teaching experience:

- *Probability and Statistics for Data Science* (undergraduate, 29 students), instructor, Fall 2022 and Spring 2023, University of Oregon. (slides and material: <https://uodsci.github.io/dsci345>)
- *Probability Theory* (graduate, 6 students), instructor, Spring 2021, University of Oregon. (slides and material: https://petrelharp.github.io/probability_theory)
- *Advanced Biological Statistics* (graduate, 27 students), instructor, most recently Fall 2022, University of Oregon. (slides and material: https://uo-biostats.github.io/UO_ABS)

- *Applied Stochastic Processes* (graduate, 12 students), instructor, Fall 2019, University of Oregon. (slides and material: https://uo-applied-math.github.io/applied_math/pages/winter.html)
- *Statistical Methods* (grad/undergrad, 30 students), instructor, Fall 2016 & Winter 2017, University of Oregon.
- *Introduction to Statistics for Biologists* (undergraduate, 40 students), coinstructor, Fall 2013, Spring 2015, and Fall 2015, USC. (slides: <https://github.com/petrelharp/bisc305>)
- *Computational Molecular Biology* (graduate, 8 students), coinstructor, Fall 2014 and Fall 2015, USC.
- *Narrowing the brain-publication barrier with R+markdown*, short course, Spring 2015, USC. (slides: <https://github.com/petrelharp/r-markdown-tutorial>)
- *Visualizing geographic structure and demographic history*, short course, Spring 2015, La Kretz Workshop in Conservation Genomics. (slides: <https://github.com/petrelharp/popgen-visualization-course>)
- *Introduction to Coalescent Theory* (graduate, 10 students), Spring 2014, USC.
- *Introduction to Computational Biology and Bioinformatics* (undergraduate, 10 students), coinstructor Spring 2014, USC.
- *Probability for Applications* (graduate course, 15 students), Fall 2010, UC Berkeley.
- *Concepts in Probability* (upper division undergraduate, 80 students), Summer 2008, UC Berkeley.