

Curriculum Vitae

Daniel R. Schrider

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PROFESSIONAL EXPERIENCE

Assistant Professor, Department of Genetics, University of North Carolina at Chapel Hill (2018 – Present)

Analyst, Cincinnati Children’s Hospital Medical Center, Dept. of Biomedical Informatics (2007)

EDUCATION

2013 – 2018 Postdoctoral Associate, Department of Genetics
Rutgers University, Piscataway, NJ
Advisor: Andrew Kern

2007 – 2012 Ph.D., Informatics; Evolution, Ecology, and Behavior
Indiana University, Bloomington, IN
Advisor: Matthew Hahn

2003 – 2007 B.S., Computer Science (Honors)
Indiana University, Bloomington, IN

HONORS/AWARDS/SCHOLARSHIPS

Fall 2007 – Spring 2008 Barwise Scholarship (IU School of Informatics and Computing)
Fall 2003 – Spring 2007 Honors Balfour Scholarship (IU Honors College)
Fall 2003 – Spring 2007 Faculty Award (IU College of Arts and Sciences)

BIBLIOGRAPHY

REFEREED RESEARCH ARTICLES

1. Xue, A, **Schrider, DR**, Kern, AD, Ag1000G Consortium (2020). Discovery of ongoing

selective sweeps within *Anopheles* mosquito populations using deep learning. *Molecular Biology and Evolution*. 38:1168–1183.

2. **Schrider, DR.** (2020). Background selection does not mimic the patterns of genetic diversity produced by selective sweeps. *Genetics*. 216:499–519.
3. *Anopheles gambiae* 1000 Genomes Consortium (2020). Genome variation and population structure among 1142 mosquitoes of the African malaria vector species *Anopheles gambiae* and *Anopheles coluzzii*. *Genome Res*. 30:1533–1546

For this paper my role is ‘Partner working group member’ rather than ‘Author’. This paper uses data and analyses contributed by a consortium whose participant names are expanded in the PubMed record.

4. Adrion, JR, Cole, CB, Dukler, N, Galloway, JG, Gladstein, AL, Gower, G, Kyriazis, CC, Ragsdale, AP, Tsambos, G, Baumdicker, F, Carlson, J, Cartwright, RA, Durvasula, A, Gronau, I, Kim, BY, McKenzie, P, Messer, PW, Noskova, E, Ortega-Del Vecchyo, D, Racimo, F, Struck, TJ, Gravel, S, Gutenkunst, RN, Lohmueller, KE, Ralph, PL, **Schrider, DR**, Siepel, A, Kelleher, J, Kern, AD (2020). A community-maintained standard library of population genetic models. *eLife*. 9: e54967
5. Suvorov, A, Hochuli, J, and **Schrider, DR.** (2020). Accurate inference of tree topologies from multiple sequence alignments using deep learning. *Systematic Biology*. 69: 221–233
6. Flagel, L, Brandvain, Y, and **Schrider, DR.** (2019). The unreasonable effectiveness of convolutional neural networks in population genetic inference. *Molecular Biology and Evolution*. 36: 220–238.
7. Price, N, Moyers, BT, Lopez, L, Lasky, JR, Monroe, JG, Mullen, JL, Oakley, CG, Lin, J, Ågren, J, **Schrider, DR**, Kern, AD, McKay, JK (2018). Combining population genomics and fitness QTLs to identify the genetics of local adaptation in *Arabidopsis thaliana*. *PNAS*. 115: 5028–5033.
8. **Schrider, DR**, Ayroles, J, Matute, DR, and Kern, AD (2018). Supervised machine learning reveals introgressed loci in the genomes of *Drosophila simulans* and *D. sechellia*. *PLoS Genetics*. 14: e1007341.
9. Kern AD, and **Schrider, DR** (2018). diploS/HIC: An updated approach to classifying selective sweeps. *G3: Genes, Genomes, Genetics*. 8: 1959–1970.
10. *Anopheles gambiae* 1000 Genomes Consortium (2017). Genetic diversity of the African malaria vector *Anopheles gambiae*. *Nature*. 552: 96–100.

My role in this study: the estimation of migration rates among different *Anopheles* populations, and assistance with inferring population size changes over time.

11. **Schrider, DR**, and Kern, AD (2017). Soft sweeps are the dominant mode of adaptation in the human genome. *Molecular Biology and Evolution*. 35: 1863–1877.
12. Adrion, JR, Song, M, **Schrider, DR**, Hahn, MW, and Schaack, S. (2017) Genome-wide estimates of transposable element insertion and deletion rates in *Drosophila melanogaster*. *Genome Biology and Evolution*. 9: 1329–1340.
13. **Schrider, DR***, Shanku, AG*, and Kern, AD. (2016) Effects of linked selective sweeps on demographic inference and model selection. *Genetics*. 204: 1207–1223.
14. Kern, AD, and **Schrider, DR**. (2016). discoal: flexible coalescent simulations with selection. *Bioinformatics*. 32: 3839–3841.
15. **Schrider, DR**, and Kern, AD. (2016). S/HIC: Robust identification of soft and hard sweeps using machine learning. *PLoS Genetics*. 12: e1005928.
16. **Schrider, DR**, Hahn, MW, and Begun, DJ. (2016) Parallel Evolution of Copy-Number Variation Across Continents in *Drosophila melanogaster*. *Molecular Biology and Evolution*. 33: 1308–1316.
17. Fletcher, RS, Herrmann, D, Mullen, JL, Li, Q, **Schrider, DR**, Price, N, Lin, J, Grogan, K, Kern, AD, and McKay, JK. (2016) Identification of Polymorphisms Associated with Drought Adaptation QTL in *Brassica napus* by Resequencing. *G3*. 6: 793–803.
18. Keith, N, Tucker, AE, Jackson, CE, Sung, W, Lucas Lledó, JI, **Schrider, DR**, Schaack, S, Dudycha, JL, Ackerman, MS, Younge, AJ, Shaw, JR, and Lynch, M. (2016) High mutational rates of large-scale duplication and deletion in *Daphnia pulex*. *Genome Research*. 26: 60–69.
19. **Schrider, DR**, and Kern, AD. (2015) Inferring selective constraint from population genomic data suggests recent regulatory turnover in the human brain. *Genome Biology and Evolution*. 7: 3511–3528.
20. **Schrider, DR**, Mendes, FK, Hahn, MW, and Kern, AD. (2015) Soft shoulders ahead: spurious signatures of soft and partial selective sweeps result from linked hard sweeps. *Genetics*. 200: 267–284.
21. **Schrider, DR**, and Kern, AD. (2014) Discovering Functional DNA Elements Using Population Genomic Information: A Proof of Concept Using Human mtDNA. *Genome Biology and Evolution*. 6: 1542–1548.
22. Denton, JF, Lugo-Martinez, J, Tucker, AE, **Schrider, DR**, Warren, WC, and Hahn, MW. (2014) Extensive error in the number of genes inferred from draft genome assemblies. *PLoS Comput Biol*. 10: e1003998
23. Marmoset Genome Sequencing and Analysis Consortium. (2014) The common

marmoset genome provides insight into primate biology and evolution. *Nature Genetics*. 46: 850–857.

My role in this study: investigating patterns of retrotransposition, which we found to be far more prevalent in the marmoset genome than in other primates.

24. **Schrider, DR**, Houle, D, Lynch, M, and Hahn, MW. (2013) Rates and consequences of spontaneous mutational events in *Drosophila melanogaster*. *Genetics*. 194:937–954
25. **Schrider, DR***, Navarro FCP*, Galante, PAF, Parmigiani, RB, Camargo, AA, Hahn, MW, and de Souza, SJ. (2013) Gene copy-number polymorphism caused by retrotransposition in humans. *PLoS Genetics*. 9:e1003242
26. **Schrider, DR**, Begun, DJ, and Hahn MW (2013) Detecting highly differentiated copy-number variants from pooled population sequencing. *Pacific Symposium on Biocomputing*. 18:344–355
27. Langley, CH, Stevens, KS, Cardeno, C, Lee, YCG, **Schrider, DR**, Pool, JE, Langley, SA, Suarez, C, Detig-Corbett, R, Kolaczowski, B, Fang, S, Nista, PM, Holloway, AK, Kern, AD, Dewey, CN, Song, YS, Hahn, MW, and Begun, DJ (2012) Genomic variation in natural populations of *Drosophila melanogaster*. *Genetics*. 192:533–598
28. **Schrider, DR**, Stevens, K, Cardeño, CM, Langley, CH, and Hahn, MW (2011). Genome-wide analysis of retrogene polymorphisms in *Drosophila melanogaster*. *Genome Research*. 21:2087–95
29. **Schrider, DR**, Gout, JF, and Hahn, MW (2011) Very few RNA and DNA sequence differences in the human transcriptome. *PLoS ONE*. 6:e25842
30. **Schrider, DR**, Hourmozdi, JN, and Hahn, MW (2011) Pervasive multi-nucleotide mutational events in eukaryotes. *Current Biology*. 21:1051–1054.
31. Locke, DP, Hillier, LW, Warren, WC, Worley, KC, Nazareth, LV, Muzny, DM, Yang, SP, Wang, Z, Chinwalla, AT, Minx, P, Mitreva, M, Cook, L, Delehaunty, KD, Fronick, C, Schmidt, H, Fulton, LA, Fulton, RS, Nelson, JO, Magrini, V, Pohl, C, Graves, TA, Markovic, C, Cree, A, Dinh, HH, Hume, J, Kovar, CL, Fowler, GR, Lunter, G, Meader, S, Heger, A, Ponting, CP, Marques-Bonet, T, Alkan, C, Chen, L, Cheng, Z, Kidd, JM, Eichler, EE, White, S, Searle, S, Vilella, AJ, Chen, Y, Flicek, P, Ma, J, Raney, B, Suh, B, Burhans, R, Herrero, J, Haussler, D, Faria, R, Fernando, O, Darré, F, Farré, D, Gazave, E, Oliva, M, Navarro, A, Roberto, R, Capozzi, O, Archidiacono, N, Della Valle, G, Purgato, S, Rocchi, M, Konkel, MK, Walker, JA, Ullmer, B, Batzer, MA, Smit, AF, Hubley, R, Casola, C, **Schrider, DR**, Hahn, MW, Quesada, V, Puente, XS, Ordoñez, GR, López-Otín, C, Vinar, T, Brejova, B, Ratan, A, Harris, RS, Miller, W, Kosiol, C, Lawson, HA, Taliwal, V, Martins, AL, Siepel, A, Roychoudhury, A, Ma, X, Degenhardt, J, Bustamante, CD, Gutenkunst, RN, Mailund, T, Dutheil, JY, Hobolth, A, Schierup, MH, Ryder, OA, Yoshinaga, Y, de Jong, PJ, Weinstock, GM, Rogers, J, Mardis, ER, Gibbs, RA, Wilson, RK (2011) Comparative

and demographic analysis of orang-utan genomes. *Nature*. 469:529–533.

32. **Schrider, DR**, and Hahn, MW (2010) Lower linkage disequilibrium at CNVs is due to both recurrent mutation and transposing duplications. *Molecular Biology and Evolution*. 27:103–111.
33. **Schrider, DR**, Costello, JC, and Hahn, MW (2009) All human-specific gene losses are present in the genome as pseudogenes. *Journal of Computational Biology*. 16:1419–1427.
34. Costello JC, **Schrider, DR**, Gehlhausen J, and Dalkilic M (2009) Data driven ontologies. *Pacific Symposium on Biocomputing*. 14:15–26.

REVIEWS

1. **Schrider, DR**, and Kern, AD (2018). Supervised Machine Learning for Population Genetics: A New Paradigm. *Trends in Genetics*. 34: 301–312.
2. **Schrider, DR**, and Hahn, MW (2010) Gene copy-number polymorphism in nature. *Proceedings of the Royal Society B*. 277:3213-3221.

SUBMITTED MANUSCRIPTS AND PREPRINTS

1. Suvorov, A, Kim, BY, Wang, J, Armstrong, E, Peede, D, D’agostino, ERR, Price, DK, Lang, M, Courtier-Orgozozo, V, David, JR, Petrov, D, Matute, DR*, **Schrider, DR***, and Comeault A*. Widespread introgression across a phylogeny of 155 *Drosophila* genomes (2021) *Submitted to eLife*. doi: <https://doi.org/10.1101/2020.12.14.422758> (31 pages).
2. Suvorov, A, Scornavacca, C, Fujimoto, MS, Bodily, P, Clement, M, Crandall, KA, Whiting, MF, **Schrider DR***, and Bybee, SM*. Deep ancestral introgression shapes evolutionary history of dragonflies and damselflies (2020) *Submitted to Systematic Biology*. doi: <https://doi.org/10.1101/2020.06.25.172619> (37 pages).

*Denotes equal contribution.

PRESENTATIONS

1. Invited seminar, Department of Biological Sciences, Vanderbilt University, 2021
2. Invited seminar, Department of Biology, University of Florida, 2021
3. Invited seminar, Department of Scientific Computing, Florida State University, 2021
4. Invited seminar, Evolutionary Anthropology Department, Duke University, 2020
5. Invited seminar, Biology Department, University of Arizona, 2019

6. Background selection does not mimic the patterns of genetic diversity produced by selective sweeps, *Evolution* 2019, Providence, RI, 2019
7. Invited seminar, Biology Department, University of North Carolina at Greensboro, 2019
8. Keynote lecture, 2nd Annual Genomic Sciences and Biomathematics Joint Symposium, North Carolina State University, 2019.
9. Invited talk. Microbial and Plant Genomics Fall 2018 Symposium, University of Minnesota, 2018
10. The unreasonable effectiveness of convolutional neural networks in population genetic inference. Population, Evolutionary, and Quantitative Genetics Conference, 2018
11. The unreasonable effectiveness of convolutional neural networks in population genetic inference. New York Area Population Genomics Workshop, 2018
12. Elucidating recent gene flow across *Drosophila* species using a novel machine learning approach. 58th Annual *Drosophila* Research Conference, 2017
13. Soft sweeps are the dominant mode of adaptation in the human genome. New York Area Population Genomics Workshop, 2017
14. Hard sweeps, soft shoulders, and using machine learning to accurately detect positive selection. International Symposium of Molecular Populations Genetics and Evolution: Genes, Genomes, and Models (In Honor of Chuck Langley's Contribution to Science), 2015
15. Invited talk. Soft shoulders ahead: roadblocks and detours on the road to detecting recent adaptation from population genetic data. Department of Biology, University of Pennsylvania, 2014
16. Soft shoulders ahead: spurious signatures of soft and partial selective sweeps result from linked hard sweeps. *Evolution*, 2014.
17. Inferring selective constraint from population genetic data. *Evolution*, 2013.
18. Parallel selection on copy-number variants across continents and species in *Drosophila*. *Drosophila* Research Conference, 2013.
19. Genomic variation in natural populations of *Drosophila melanogaster*. Pacific Symposium on Biocomputing, 2013.
20. Mutational inflation of the *Drosophila melanogaster* genome is countered by strong selection. Annual Meeting of the Society for Molecular Biology and Evolution, 2012.

21. Pervasive multi-nucleotide mutation events in *Drosophila* and other organisms. *Drosophila* Research Conference, 2011.
22. Retrotransposition and Gene Copy Number Polymorphism in Humans and *Drosophila*. Keystone Symposia: Functional Consequences of Structural Variation in the Genome, 2011.

TEACHING EXPERIENCE

CLASSROOM TEACHING AT UNC

- Fall, 2018 – 2020 Course Director & Instructor – BCB 722 – Topics in Population Genetics
- 5 week module taught each Fall semester (10 lectures)
 - ~15 students per term on average (ranged from 10 to 20)
 - ~17.5 student contact hours per term

PAST CLASSROOM TEACHING EXPERIENCE (AT INDIANA UNIVERSITY)

- Fall 2011 Associate Instructor – BIOL Z620 – Evolutionary Genetics
Fall 2010 Associate Instructor – INFO I590 – SNP Discovery and Population Genet.
Fall 2007 Associate Instructor – INFO I211 – Information Infrastructure II

MENTORING

Postdoctoral researchers

- Will Booker January 2021 – Present
Rebecca Love December 2020 – Present
Anton Suvorov May 2018 – Present
Ariella Gladstein September 2018 – December 2021 (Current position: Research Scientist at Embark)

Graduate students

- Logan Whitehouse Summer 2020 – Present
Amjad Dabi Summer 2021 – Present

Rotation students

- Amjad Dabi Spring 2021

Polygenic risk scores and health disparities: the role of blood cells, immune response, and evolutionary adaptation
\$56,384 annual Direct Costs; 20% effort

Completed support

2020 – 2025	NIH NIGMS R01 (Co-I; PI: Bobay); rescinded due to R35 Investigating the impact and patterns of homologous recombination and adaptive evolution on bacterial genomes \$64,589 annual Direct Costs; 10% effort
2016 – 2021	NIH NHGRI K99/R00 Pathway to Independence Award Inferring selection from human population genomic data K99 Phase: \$159,188 cumulative Direct Costs; 100% effort R00 Phase: \$747,000 cumulative Total Costs; 32% effort
2013 – 2016 Fall 2012 Fall 2010 – Spring 2012	NIH National Research Service Award Postdoctoral Fellowship Don Brown Fellowship (IU School of Informatics and Computing) Fellow, Genetics, Cellular & Molecular Sciences Training Grant (NIH T32 to Indiana University Department of Biology)

PROFESSIONAL SERVICE

To Discipline

Manuscript reviews for journals:

BMC Biology

eLife

Evolution

G3: Genes, Genomes, Genetics

Genes

Genetics

Genome Biology

Genome Biology and Evolution

Molecular Biology and Evolution

Molecular Ecology

Molecular Ecology Resources

Nature Methods

PLoS Genetics

PLoS Computational Biology

Proceedings of the National Academy of Sciences
Science
Scientific Reports

Within UNC

Genetics Advisory Committee	Fall 2018 – Present
BBSP Graduate Student Admissions Committee	Fall 2018 – Present
BBSP Written Exam Committee	Spring 2019 – Present

Membership in Professional Societies

2013 – Present	Society for the Study of Evolution
2012 – Present	Society for Molecular Biology and Evolution
2009 – Present	Genetics Society of America

Other Activities

2008 & 2009 Instructor, Jim Holland Summer Enrichment Program (summer educational program in Biology for underrepresented minority high school students)