Benjamin Robert Evans

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Education

Yale University, New Haven, CT (08/2012 – 12/2016)
PhD Ecology and Evolutionary Biology
Thesis Title: "Population Genomics in *Aedes aegypti*", *Advisor*: Jeffrey Powell
Honors/Awards: Ruth L. Kirschstein National Research Service Award,
Dillon and Mary Ripley Graduate Fellowship, Robert W. Carle Scholarship
NIH 5T32AI007404 Training in Parasitology and Vector Biology

Lehigh University, Bethlehem, PA (09/2005 – 05/2009)
BA Biology, minor in Computer Science
Honors/Awards: Dean's List, Phi Eta Sigma, Dean's Scholarship,
Donald & Dorothy Stabler scholarship, Lehigh University Grant, Patricia Battin Scholarship

Related Experience

Software Engineer, GeneDx, Gaithersburg, MD (01/2023-present)
Production Bioinformatics
- Manage/develop/run HIPAA compliant HPC and Azure Cloud native bioinformatics pipelines
- Engineer ETL tasks that run on TiB of data per day

Data Scientist III, Sema4 Genomics, Stamford, CT (01/2022-01/2023)
Production Bioinformatics
- Manage/develop/run HIPAA compliant AWS Cloud native bioinformatics pipelines
- Update and maintain metadata database used to orchestrate pipelines

Sr. Computational Research Support Analyst, Yale University, New Haven, CT (10/2016-12/2021)
Yale Center for Research Computing
- Computational research consulting for life & biomedical Sciences: 4 HPC Clusters ~1000 Researchers
- Cloud+local hybrid computing engineering and support
- Develop and give workshops and tutorials
- XSEDE Campus Champion: national community engagement
- Researcher collaboration: genomics, phylogenetics, epidemiology models, IoT freezer monitoring

Research Assistant II, Caccone Lab, Yale University, New Haven, CT (08/2009-08/2012)
DNA Analysis Facility On Science Hill

Skills & Abilities

AWS/Azure: S3/Blob, EC2/AzureVM, Lambda/Functions, ECR/ACR, Batch/Batch,
Aurora/Azure SQL, SQS+SNS/QueueStorage+ServiceBus,
SDLC: Agile/Scrum, GitHub & GitHub Actions, Jira, Confluence
Linux/HPC: Coreutils & Linux CLI, Git, Docker/Singularity, *S*lurm, Lmod, EasyBuild
Languages: Bash, Python, R, SQL
Bioinformatics: Sequence analysis (QC/alignment), variant calling (GATK etc),
pipeline development (NextFlow, custom scripts, etc)

Publications

Kortright KE, Chan BK, Evans BR, Turner PE Arms race and fluctuating selection dynamics in Pseudomonas aeruginosa bacteria coevolving with phage OMKO1. J Evol Biol. doi:10.1111/jeb.14095 (2022)

Li W, Shen X, Evans BR, Dunn CW, Rokas A Rooting the Animal Tree of Life. Mol. Biol doi:10.1093/molbev/msab170 (2021)

Evans BR, Kotsakiozi P, Costa-da-Silva AL, Ioshino RS, Garziera L et al. Transgenic Aedes aegypti mosquitoes transfer genes into a natural population. Sci. Rep. doi:10.1038/s41598-019-49660-6 (2019)

Quesada V, Freitas-Rodríguez S, Miller J, Pérez-Silva JG, et al. Giant tortoise genomes provide insights into longevity and age-related disease. Nat Ecol Evol. doi:10.1038/s41559-018-0733-x (2019)

Orr AR, Quagraine JE, Suwondo P, George S, Harrison LM, et al. Genetic Markers of Benzimidazole Resistance among Human Hookworms (*Necator americanus*) in Kintampo North Municipality, Ghana. Am J Trop Med Hyg. doi:10.4269/ajtmh.18-0727 (2019)

Publications (continued)

Kotsakiozi P, Evans BR, Gloria-Soria A, Kamgang B, et al. Population structure of a vector of human diseases: *Aedes aegypti* in its ancestral range, Africa. Ecol Evol. doi:10.1002/ece3.4278 (2018)

Matthews BJ, Dudchenko O, Kingan SB, Koren S, Antoshechkin I, et al. Improved reference genome of *Aedes aegypti* informs arbovirus vector control. Nature. doi:10.1038/s41586-018-0692-z (2018)

Pless E, Gloria-Soria A, Evans BR, Kramer, V, Bolling BG, et al. Multiple Introductions of the Dengue Vector, *Aedes aegypti*, into California. PloS NTD, doi:10.1371/journal.pntd.0005653 (2017)

Kotsakiozi P, Gloria-Soria A, Caccone A, Evans B, Schama R, et al. Tracking the return of *Aedes aegypti* to Brazil, the major vector of the dengue, chikungunya and Zika viruses. PloS NTD, doi:10.1371/journal.pntd.0005653 (2017)

Saarman NP, Gloria-Soria A, Anderson EC, Evans BR, Pless E, et al. Effective population sizes of a major vector of human diseases, *Aedes aegypti*. Evol Appl. doi:10.1111/eva.12508 (2017)

Powell JR, Evans B. How Much Does Inbreeding Reduce Heterozygosity? Empirical Results from *Aedes aegypti*. Am J Trop Med Hyg. doi:10.4269/ajtmh.16-0693 (2017)

Walter K, Carpi G, Evans B, Caccone A, Diuk-Wasser M. Vectors as Epidemiological Sentinels: Patterns of Within-Tick *Borrelia burgdorferi* Diversity. PLoS Pathogens. doi:10.1371/journal.ppat.1005759 (2016)

Gloria-Soria A, Dunn W, Telleria E, Evans B, Okedi L, et al. Patterns of Genome-Wide Variation in *Glossina fuscipes fuscipes* Tsetse Flies from Uganda. G3 Genes|Genomes|Genetics. doi:10.1534/g3.116.027235 (2016)

Richardson JB, Evans B, Pyana PP, Reet N Van, Sistrom M. Whole genome sequencing shows sleeping sickness relapse is due to parasite regrowth and not reinfection. Evol Appl. doi:10.1111/eva.12338 (2016)

Sistrom M, Evans B, Benoit J, Balmer O, Aksoy S, Caccone A. De Novo Genome Assembly Shows Genome Wide Similarity between *Trypanosoma brucei brucei* and *Trypanosoma brucei rhodesiense*. PLoS One. doi:10.1371/journal.pone.0147660 (2016)

Evans BR, Gloria-Soria A, Hou L, McBride C, Bonizzoni M, Zhao H, et al. A Multipurpose High Throughput SNP Chip for the Dengue and Yellow Fever Mosquito, *Aedes aegypti*. G3 Genes|Genomes|Genetics. doi:10.1534/g3.114.016196 (2015)

Eytan RI, Evans BR, Dornburg A, Lemmon AR, Lemmon EM, Wainwright PC, et al. Are 100 enough? Inferring acanthomorph teleost phylogeny using Anchored Hybrid Enrichment. BMC Evol Biol. doi:10.1186/s12862-015-0415-0 (2015)

Sistrom M, Evans B, Bjornson R, Gibson W, Balmer O, Mäser P, et al. Comparative genomics reveals multiple genetic backgrounds of human pathogenicity in the *Trypanosoma brucei* complex. Genome Biol Evol. doi:10.1093/gbe/evu222 (2014)

Brown JE, Evans BR, Zheng W, Obas V, Barrera-Martinez L, et al. Human impacts have shaped historical and recent evolution in *Aedes aegypti*, the dengue and yellow fever mosquito. Evolution. doi:10.1111/evo.12281 (2013)