

EDWARD STALLKNECHT RICE

Computational biologist with expertise in genome assembly and single-cell methods
Located in Munich, Germany

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EDUCATION

Doctor of Philosophy in Bioinformatics, University of California, Santa Cruz, June 2018
Adviser: Richard (Ed) Green, Department of Biomolecular Engineering
Dissertation title: “Long-range assembly and transcriptomics elucidate the regulatory architecture of three vertebrate genomes”

Bachelor of Arts in Computer Science, Brown University, May 2012
Academic/Research Adviser: Ben Raphael, Center for Computational Molecular Biology

Thomas Jefferson High School for Science and Technology, Alexandria, Virginia, June 2008
Senior research mentor: Alejandro Schäffer, National Center for Biotechnology Information

RESEARCH

June 2019 - present	Senior Research Scientist in lab of Prof. Wes Warren University of Missouri
August 2018 - May 2019	Postdoctoral Research Associate in lab of Prof. Jessica Petersen University of Nebraska - Lincoln
January 2014 - June 2018	Ph.D. student in lab of Prof. Richard (Ed) Green University of California, Santa Cruz
November 2013 - January 2014	Rotation student in lab of Prof. David Haussler, UC Santa Cruz
September - November 2013	Rotation student in lab of Prof. Josh Stuart, UC Santa Cruz
July 2012 - July 2013	Post-baccalaureate fellow in lab of Dr. Richa Agarwala National Center for Biotechnology Information
Summer 2009 - Spring 2012	Research assistant to Prof. Ben Raphael Brown University Center for Computational Molecular Biology
Summer 2007 - Spring 2008	Research assistant to Dr. Alejandro Schäffer National Center for Biotechnology Information
Summer 2006	Research assistant to Dr. Alejandro Schäffer National Center for Biotechnology Information

TEACHING

Teaching assistant for The Human Genome
UC Santa Cruz Dept. of Biomolecular Engineering; Spring 2017

Teaching assistant and guest lecturer, Technical Writing and Communication in Computer Science
UC Santa Cruz Dept. of Computer Science; Winter 2017

Teaching assistant and guest lecturer, Bioinformatics Models and Algorithms
UC Santa Cruz Dept. of Biomolecular Engineering; Fall 2016

Teaching assistant for The Human Genome
UC Santa Cruz Dept. of Biomolecular Engineering; Spring 2016

Teaching assistant for The Human Genome
UC Santa Cruz Dept. of Biomolecular Engineering; Winter 2016

Teaching assistant for The Human Genome
UC Santa Cruz Dept. of Biomolecular Engineering; Fall 2015

Head teaching assistant for Computational Molecular Biology
Brown University Department of Computer Science; Spring 2012

Head teaching assistant for Computational Molecular Biology
Brown University Department of Computer Science; Fall 2010

AWARDS

Horse Genome Coordinators' Travel Award, Plant and Animal Genome Conference, 2018
ARCS Foundation Scholarship, 2017-2018
Baskin Dissertation Year Fellowship, 2017-2018
Genome 10K Conference Presenter's Fellowship, 2015
UC Santa Cruz Chancellor's Fellowship, 2013
NIH Intramural Research Training Award, 2012
Karen T. Romer Undergraduate Teaching and Research Award, 2009

PUBLICATIONS

Carroll, R. A., **Rice, E. S.**, Lyons, L. A., Coghill, L., Swanson, W. F., Terio, K. A., Boyd, T., & Warren, W. C. (in submission). "A novel fishing cat reference genome for the evaluation of potential germline risk variants." *bioRxiv*, 2022.11.17.516921.

Lu, Y., **Rice, E. S.**, Du, K., Kneitz, S., Naville, M., Dechaud, C., Volff, J., Boswell, M., Boswell, W., Hillier, L., Tomlinson, C., Kremitzki, M., Walter, R., Scharl, M., & Warren, W. C. (2023).

“High resolution genomes of multiple Xiphophorus species provide new insight into microevolution, hybrid incompatibility, epistasis and disease.” *Genome Research*, in press.

- Warren, W. C., Fedrigo, O., Tracey, A., Mason, A. S., Formenti, G., Perini, F., Wu, Z., Murphy, T., Schneider, V., Stiers, K., **Rice, E. S.**, Coghill, L. M., Anthony, N., Okimoto, R., Carroll, R. A., Mountcastle, J., Balacco, J., Haase, B., Yang, C., Zhang, G., Smith, J., Drechsler, Y, Cheng, H., Howe, K., & Jarvis, E. (2023). “Multiple chicken (*Gallus gallus*) genome references to advance genetic variation studies.” *Cytogenetic and Genome Research*, in press.
doi://10.1159/000529376.
- Puritz, J. B., Guo, X., Hare, M., He, Y., Hillier, L., Jin, S., Liu, M., Lotterhos, K., Minx, P., Modak, T., Proestou, D., **Rice, E. S.**, Tomlison, C., Warren, W. C., Witkop, E., Zhao, H., & Gomez-Chiarri, M. (2023). “A second unveiling: haplotig masking of the eastern oyster genome improves population-level inference.” *Molecular Ecology Resources*, 2023(00):1-18.
- Warren, W. C., **Rice, E. S.**, Meyer, A., Hearn, C. J., Steep, A., Hunt, H. D., Monson, M. S., Lamont, & S. J, Cheng, H. H. (2023). “The immune cell landscape and response of Marek’s disease resistant and susceptible chickens infected with Marek’s disease virus.” *Scientific Reports*, 13:5355.
- Potts, H. G., Lemieux, M. E., **Rice, E. S.**, Warren, W.C., Choudhury, R. P., & Mommersteeg, M. T. M. (2022). “Discordant genome assemblies drastically alter the interpretation of single cell RNA sequencing data which can be mitigated by a novel integration method.” *Cells*, 11, 608.
- Edwards, R. J., Field, M. A., Ferguson, J. M., Dudchenko, O., Keilwagen, J., Rosen, B. D., Johnson, G. S., **Rice, E. S.**, Hillier, L., Hammond, J. M., Towarnicki, S. G., Omer, A., Skvortsova, K., Bogdanovic, O., Zammit, R. A., Lieberman Aiden, E., Warren, W. C., & Ballard, J. W. O. (2021). “Chromosome-length genome assembly and structural variations of the primal Basenji dog (*Canis lupus familiaris*) genome.” *BMC Genomics*, 22, 188.
- Warren, W. C., Boggs, T. E., Borowsky, R., Carlson, B. M., Ferrufino, E., Gross, J. B., Hillier, L., Hu, Z., Keene, A. C., Kenzior, A., Kowalko, J. E., Tomlinson, C., Kremitzki, M., Lemieux, M. E., Graves-Lindsay, T., McGaugh, S. E., Miller, J. T., Mommersteeg, M., Moran, R. L., Peuß, R., **Rice, E. S.**, Riddle, M. R., Sifuentes-Romero, I., Stanhope, B. A., Tabin, C. J., Thakur, S., Yoshiyuki, Y. & Rohner, N. (2021). “A chromosome-level genome of *Astyanax mexicanus* surface fish for comparing population-specific genetic differences contributing to trait evolution.” *Nature Communications*, 12, 1447.
- Trujillo, C. A., **Rice, E. S.**, Schaefer, N. K., Chaim, I. A., Wheeler, E. C., Madrigal, A. A., Buchanan, J., Preissl, S., Wang, A., Negraes, P. D., Szeto, R., Herai, R. H., Huseynov, A., Ferraz, M. S. A., da S. Borges, F., Kihara, A. H., Byrne, A., Marin, M., Vollmers, C., Brooks, A. N., Lautz, J. D., Semendeferi, K., Shapiro, B. A., Yeo, G. W., Smith, S. E. P., Green, R. E., & Muotri, A. R. (2021). “Reintroduction of the archaic variant of NOVA1 in cortical organoids alters neurodevelopment.” *Science*, 371(6530), eaax2537.

- Khalyfa, A., Warren, W. C., Andrade, J., Bottoms, C. A., **Rice, E. S.**, Cortese, R., Kheirandish-Gozal, L., & Gozal, D. (2021). “Transcriptomic Changes of Murine Visceral Fat Exposed to Intermittent Hypoxia at Single Cell Resolution.” *Int. J. Mol. Sci*, 22, 261.
- Rice, E. S.**, Koren, S., Rhie, A., Heaton, M. P., Kalbfleisch, T. S., Hardy, T., Hackett, P. H., Bickhart, D. M., Rosen, B. D., Vander Ley, B., Maurer, N. W., Green, R. E., Phillippy, A. M., Petersen, J. L., & Smith, T. P. L. (2020). “Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle.” *GigaScience*, 9(4), gaaa029.
- Rice, E. S.** & Green, R. E (2019). “New approaches for genome assembly and scaffolding.” *Annual Review of Animal Biosciences*, 7, 17-40.
- Kalbfleisch, T.S.†, **Rice, E. S.**†, DePriest, Jr., M. S., Walenz, B. P., Hestand, M. S., Vermeesch, J. R., O’Connell, B.L, Fiddes, I. T., Vershinina, A. O., Saremi, N. F., Petersen, J. L., Finno, C. J., Bellone, R. R., McCue, M. E., Brooks, S. A., Bailey, E., Orlando, L., Green, R. E., Miller, D. C., Antczak, D. F., & MacLeod, J. N. (2018). “Improved reference genome for the domestic horse increases assembly contiguity and composition.” *Communications Biology*, 1(1), 197.
- Murray, G. G. R., Soares, A. E. R., Novak, B. J., Schaefer, N. K., Cahill, J. A., Baker, A. J., Demboski, J. R., Doll, A., Fonseca, R. R. D., Fulton, T. L., Gilbert, M. T. P., Heintzman, P. D., Letts, B., McIntosh, G., O’Connell, B., Peck, M., Pipes, M., **Rice, E. S.**, Santos, K. M., Sohrweide, A. G., Vohr, S. H., Corbett-Detig, R. B., Green, R. E., & Shapiro, B. (2017). “Natural selection shaped the rise and fall of passenger pigeon genomic diversity.” *Science*, 358(6365), 951-954.
- Rice, E. S.**, Kohno, S., St. John, J., Pham, S., Howard, J., Lareau, L. F., O’Connell, B. L., Hickey, G., Armstrong, J., Deran, A., Fiddes, I. T., Platt, R. N., Gresham, C., McCarthy, F., Kern, C., Haan, D., Phan, T., Schmidt, C., Sanford, J. R., Ray, D. A., Paten, B., Guillette, L. J. & Green, R.E. (2017). “Improved genome assembly of American alligator genome reveals conserved architecture of estrogen signaling.” *Genome Research*, 27(5), 686-696.
- Raudsepp, T., Gustafson-Seabury, A., Durkin, K., Wagner, M. L., Goh, G., Seabury, C. M., Brinkmeyer-Langford, C., Lee, E. J., Agarwala, R., **Rice, E. S.**, Schäffer, A. A., Skow, L. C., Tozaki, T., Yasue, H., Penedo, M. C., Lyons, L. A., Khazanehdari, K. A., Binns, M. M., MacLeod, J. N., Distl, O., Guérin, G., Leeb, T., Mickelson, J. R., & Chowdhary, B. P. (2008). “A 4,103 marker integrated physical and comparative map of the horse genome.” *Cytogenetic and Genome Research*, 122(1), 28-36.
- Schäffer, A. A., **Rice, E. S.**, Cook, W., & Agarwala, R. (2007). “rh_tsp_map 3.0: end-to-end radiation hybrid mapping with improved speed and quality control.” *Bioinformatics*, 23(9), 1156-1158.

† These authors contributed equally to this work.

PRESENTATIONS

“Creation and use of a chicken pangenome reference.”

Plant and Animal Genomes Conference, 2023

“The evolution of structural change along a surface to cavefish genome trajectory.”
Astyanax International Meeting, 2022

“The chicken immune cell atlas: A resource to advance knowledge of the avian immune response.”
Plant and Animal Genomes Conference, 2022

“Chromosome-Length Haplotigs for Cattle and Yak from Trio Binning Assembly of an F1 Hybrid”
Advances in Genome Biology and Technology, 2019

“EquCab3: A New Horse Reference Genome Assembled Using First-, Second-, and Third-Generation Sequencing Data”
Plant and Animal Genome Conference, 2018

“Sex-biased genes and temperature-dependent sex determination in the American alligator.”
Genome 10K Conference, 2015

SKILLS

15+ years programming experience in Python, R, C/C++ (github.com/esrice)
Proficient with Unix environments and standard bioinformatics databases, file formats, and software

VOLUNTEERING

Naturalist Docent, Natural Bridges State Beach, 2014-2019
County Correctional Facility outreach program, Santa Cruz Public Library, 2018-2020