

# 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

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. (in submission). "A second unveiling: haplotig masking of the eastern oyster genome improves population-level inference." *bioRxiv*, 2022.08.29.505626.

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. (in review). “The immune cell landscape and response of Marek’s disease resistant and susceptible chickens infected with Marek’s disease virus.” *Research Square* (preprint). rs.3.rs-1858513.
- 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), giaa029.
- 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

“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 Genome 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](https://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