EDWARD S. RICEMEYER

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EDUCATION

2025-	Habilitand in Genomics Faculty of Veterinary Medicine, Ludwig-Maximilians-Universität
2018	Ph.D. in Bioinformatics Department of Biomolecular Engineering, University of California, Santa Cruz
2012	A.B. in Computer Science Department of Computer Science, Brown University

PROFESSIONAL APPOINTMENTS

2023-	Visiting Scientist Faculty of Veterinary Medicine, Ludwig-Maximilians-Universität
2019-	Senior Research Scientist Bond Life Sciences Center, University of Missouri
2018-19	Postdoctoral Research Associate University of Nebraska - Lincoln

PUBLICATIONS

(note birth name Rice)
† co-first authorship

Hennelly, L. M., **Ricemeyer, E. S**., Bougiouri, K., Scarsbrook, L., Martins, N. F. G., Balboa, R., Satander, C. G., Gaubert, P., Rueness, E. K., Sacks, B. N., Armstrong, E. E., Mooney, J. A., Quinn, N., Careym S. B., Harkess, A., Lanigan, L. T., Gilbert, M. T. P., Larson, G., Songsasen, N., Koepfli, K., Gopalakrishnan, S., Sinding, M. S., & Frantz, L. A. F. (in revision). "Tracking the evolutionary history of aseasonal reproduction in dogs."

Sculley, E. R.†, **Ricemeyer, E. S.**†, Carroll, R. A., Driver, J., Smith, J., Kaufman, J., Hearn, C., Balic, A., Chen, P., Lamont, S., Kramer, S., Drechsler, Y, Cheng, H., & Warren, W .C. (in submission). "A single-nucleus census of immune and non-immune cell types for the major immune organ systems of chicken." Preprint: *bioRxiv* 2024.08.05.606414.

Ricemeyer, E. S. †, Schaefer, N. K. †, Du, K., da Cruz, I., Kneitz, S., Acemel, R. D., Lupiáñez, D. G., Carroll, R. A., Drinkwater, R., Schartl, M., & Warren, W. C. (in press). "Gene conversion empowers natural selection in a clonal fish species." *Nature.*

Naumann, I., **Ricemeyer, E. S.**, Elleder, D., Plachy, J., von La Roche, D., Vučinić, K., Göbel, T. W., Kaspers, B., Früh, S. P., & Härtle, S. (2025). "Beyond FoxP3 – Identification of a chicken regulatory T cell signature." *European Journal of Immunology*, 55(12), e70106.

Carroll, R. A., **Ricemeyer, E. S.**, Hillier, L. W., DaCosta, J. M., Osipova, E., Smith, S., Joardar, V., Jamie, G., Martinez Suarez, J. G., Marques-Bonet, T., Manthey, J. D., Fuxjager, M. J., Lynch, K. S., Jarvis, E., Joarder, V., Thibaud-Nissen, F., Spottiswoode, C. N., Sackton, T. B., Balakrishnan, C. N., Sorenson, M. D., & Warren, W. C. (2025). "Genomic resources for comparative analyses of obligate avian brood parasitism." *Journal of Heredity*, esaf087.

Nussbaum, Y. I., Bryan, J. N., Li, G., Rodney, A., Culp, W. T. N., Dickinson, P. J., Koutoulas, A., Megquier, K., An, H., Kramer, S. T., **Ricemeyer, E. S.**, Mitchem, J. B., & Warren, W. C. (2025). "Comparative multi-omics evaluation of the tumor microenvironment in canine and human hepatocellular carcinoma." *Veterinary Oncology*, 2, 25.

Treffer, L. K., Schroeder, R. L., **Ricemeyer, E. S.**, Kalbfleisch, T., Fuller, A. M., & Petersen, J. L. (2025). "Mitochondrial introgression with potential functional effects in North American yak." *Ecology and Evolution*, 15(10), e72362.

Ricemeyer, E. S., Carroll, R. A., & Warren, W. C. (2025). "Agptools: a utility suite for editing genome assemblies." *Bioinformatics*, 41(7), btaf388.

Warren, W. C., **Rice, E. S.**, X, M., Roback, E., Keene, A., Smith, F., Ogeh, D., Haggerty, L., Carroll, R. A., McGaugh, S., & Rohner, N. (2024). "Astyanax mexicanus surface and cavefish chromosome-scale assemblies for trait variation discovery." *G3: Genes, Genomes, Genetics*, 14(8).

Carroll, R. A., **Rice, E. S.**, Lyons, L. A., Coghill, L., Swanson, W. F., Terio, K. A., Boyd, T., & Warren, W. C. (2024). "A chromosome-scale fishing cat reference genome for the evaluation of potential germline risk variants." *Scientific Reports*, 14, 8073.

Rice, E. S., Alberdi, A., Alfieri, J., Athrey, G., Balacco, J. R., Bardou, P., Blackmon, H., Fedrigo, O., Fiddaman, S. R., Formenti, G., Frantz, L., Gilbert, M. T. P., Hearn, C. J., Jarvis, E. D., Klopp, C., Marcos, S., Velez-Irizarry, D., Xu, L., & Warren, W. C. (2023). "A pangenome graph reference of 30 chicken genomes allows genotyping of large and complex structural variants." *BMC Biology*, 21, 267.

Bredemeyer, K. R., Hillier, L., Harris, A. J., Hughes, G. M., Foley, N. M., Lawless, C., Carroll, R. A., Storer, J. M., Batzer, M. A., **Rice, E. S.**, Davis, B. W., Raudsepp, T., O'Brien, S. J., Lyons, L. A., Warren, W. C., & Murphy, W. J. (2023) "Single-haplotype comparative genomics reveals the role of structural innovations during cat evolution." *Nature Genetics*, 55, 1953-1963.

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., Schartl, M., & Warren, W. C. (2023). "High resolution genomes of multiple Xiphophorus species provide new insight into microevolution, hybrid incompatibility, epistasis and disease." *Genome Research*, 33, 557-571.

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.

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*, 162, 8-9.

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.

AWARDS

2026	Deutsche Forschungsgemeinschaft (DFG) Individual Research Grant “A pangenome of worldwide chicken diversity to discover structural variants impacting health, sustainability, breeding, and domestication.” € 495,119
2024	SuperMUC-NG Regular Project Grant, Leibniz Supercomputing Center “Leveraging genome assemblies to establish the impact of structural variation on domestic animals,” 6M CPU-hours (ca. € 375,000 value)
2018	Horse Genome Coordinators’ Travel Award, $1,000
2017	ARCS Foundation Scholarship, $11,000
2017	Baskin Dissertation Year Fellowship, $39,267
2015	Genome 10K Conference Presenter’s Fellowship
2013	UC Santa Cruz Chancellor’s Fellowship, $55,278
2012	National Institutes of Health Intramural Research Training Award, $30,000
2009	Karen T. Romer Undergraduate Teaching and Research Award, $3,000

INVITED SEMINARS

UC Davis; University of Münster

CONFERENCE TALKS

(selection)

2025	Plant and Animal Genomes, San Diego, CA, USA
	European Cavefish Meeting, Wettringen, Germany
2024	Astyanax International Meeting, Fort Lauderdale, FL, USA
	AnimalFarm, Naples, Italy
2023	Plant and Animal Genomes, San Diego, CA, USA
	EvoGenMunich, Munich, Germany
2022	Astyanax International Meeting, San Antonio, TX, USA
	Plant and Animal Genomes, online
2019	Advances in Genome Biology and Technology, Marco Island, FL, USA
2018	Plant and Animal Genomes, San Diego, CA, USA

TEACHING

As instructor

Introduction to Programming, Ludwig-Maximilians-Universität (1 term, 2025)

As guest lecturer

Introduction to Evolutionary Biology, Ludwig-Maximilians-Universität (2 terms, 2023-2024)

As teaching assistant

The Human Genome, UC Santa Cruz (4 quarters, Fall 2015 - Spring 2017)
Technical Writing and Communication in Computer Science, UC Santa Cruz (Winter 2017)
Bioinformatics Models and Algorithms, UC Santa Cruz (Fall 2016)

ACADEMIC SERVICE

Journal Reviews

Animal Genetics; BMC Genomics; British Poultry Science; Genetics Selection Evolution; GigaScience; Heredity; Integrative & Comparative Biology; Molecular Biology and Evolution; Molecular Ecology Resources; Nature; Nature Communications; Scientific Data

SKILLS

Technical

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

Languages

English (native), German (basic proficiency)