Name: Iker Rivas-González
Date of birth: 24/11/1996
Nationality: Spanish
Email: iker_rivas_gonzalez@eva.mpg.de
ORCID: https://orcid.org/0000-0002-0515-0628
Google Scholar: https://scholar.google.com/citations?user=dwAn44IAAAAJ&hl=en
GitHub: https://github.com/rivasiker
Webpage: https://rivasiker.github.io
Languages: English (C2), Spanish (native), Basque (C2), Danish (B2), German (B1)
Keywords: population genetics, bioinformatics, phylogenomics, incomplete lineage sorting (ILS)

I am a computational biologist with broad interests in **evolutionary and population genetics**. I have a strong background in **biology, population genetics, mathematics, and statistics**, which has allowed me both to **develop novel methods** and to **draw biological inferences from real data**. During my PhD, I analyzed **hundreds of primate genomes**, reconstructing the primate tree of life, while inferring the ancestral history of species at the base-pair level. Such a comprehensive view of primate evolution allowed me to link genome-wide estimates of gene tree incongruences and variation in the height of gene trees to other genomic covariates (e.g., recombination) and ancestral selective processes. This work exemplifies my interest in **integrating conventionally disparate data types** to understand **natural selection across different timescales**. While I am mainly focused on primate genomics, the methods I develop are not restricted to specific taxa, and during my PhD I also applied them to birds and marsupials, showing the **versatility and broad applicability** of my models. During my current work as a Postdoctoral Researcher, I study a natural population of baboons, connecting genomic data with long-term field observations, including behavioral and demographic data.

Education

01/02/2020 – 25/09/2023	**PhD in Bioinformatics** *Bioinformatics Research Center (BiRC), Aarhus University (DK)* - Note that the beginning of my PhD overlaps with the end of my MSc, following the typical structure of the “4+4” program at Aarhus University
01/09/2018 – 01/07/2021	**MSc in Bioinformatics** *Aarhus University (Denmark)*
01/09/2014 – 01/07/2018	**BSc in Biochemistry and Molecular Biology** *University of the Basque Country (Spain)* - Including **Erasmus Exchange Program** (01/09/2017 – 01/07/2018) *Aarhus University (DK)*

Research experience

04/11/2023 – present	**Postdoctoral Researcher** *Department. of Primate Behavior and Evolution,* *Max Planck Institute for Evolutionary Anthropology, Leipzig (DE)* - ***Advisor:*** Prof. Dr. Jenny Tung
01/02/2020 – 25/09/2023	**PhD Thesis** *Bioinformatics Research Center (BiRC), Aarhus University (DK)* - ***Title:*** “Ancestral multi-species population genomics” - ***Advisor:*** Prof. Dr. Mikkel Heide Schierup - ***Award date:*** 25/09/2023
01/09/2022 – 01/02/2023	**Research experience abroad during PhD** *Department of Organismic and Evolutionary Biology and* *Department of Human Evolutionary Biology,* *Harvard University (USA)* - ***Advisors:*** Prof. Dr. John Wakeley and Prof. Dr. David Reich

01/09/2018 – 01/07/2021 **Master’s Thesis**
Bioinformatics Research Center (BiRC), Aarhus University (DK)
- ***Title:*** “Pervasive incomplete lineage sorting in primates and its genomic and functional determinants”
- ***Advisor:*** Prof. Dr. Mikkel Heide Schierup

01/02/2019 – 01/07/2019 **Project in Bioinformatics**
Bioinformatics Research Center (BiRC), Aarhus University (DK)
- ***Title:*** “A composite of multiple signals reveals signatures of positive selection in the 3p21.31 region of East Asians”
- ***Advisor:*** Dr. Kasper Munch

01/09/2018 – 01/02/2019 **Project in Bioinformatics**
Bioinformatics Research Center (BiRC), Aarhus University (DK)
- ***Title:*** “Analysis of the human epigenome using an interpretable deep convolutional neural network”
- ***Advisor:*** Dr. Lasse Maretty

01/02/2018 – 01/07/2018 **Bachelor’s Thesis**
Dpt. of Molecular Biology and Genetics, Aarhus University (DK)
- ***Title:*** “Deciphering the role of intrinsically disordered proteins in the regulation of PSDs: towards crystallization of a phosphomimetic PSD-95–NR2b chimeric construct”
- ***Advisor:*** Dr. Magnus Kjærgaard

01/06/2016 – 31/07/2016 **Lab Assistant at Molecular Genetics Lab**
Araba University Hospital, Vitoria-Gasteiz (ES)
- ***Advisor:*** Dr. Guiomar Perez de Nanclares Leal

Teaching and mentoring experience

01/09/2025 – present **Mentoring of Master Student**, Willi Thomas at Leipzig University
- Guidance with coding and data processing

01/11/2023 – present **Mentoring of PhD Student**, Carlota F. Galán-Plana at MPI-EVA
- Guidance with data processing and analysis and overall scientific direction

01/11/2023 – 01/09/2025 **Mentoring of Master Student**, David Martín Pestaña at Aarhus University
- Guidance with math, coding and algorithmic engineering

Guest Lecturer *Leipzig University and MPI-EVA (Germany)*
- Molecular Anthropology course

01/09/2020 – 01/06/2022 **Teaching Assistant** *Aarhus University (Denmark)*
- ***Courses from the MSc in Bioinformatics:***
  - Data Science in Bioinformatics (Fall of 2020 and 2021)
  - Statistical and Machine Learning in Bioinformatics (Spring of 2020, 2021 and 2022)

01/09/2018 – 25/09/2023 **Student Ambassador** *Aarhus University (Denmark)*
- Helping and advising prospective Master and PhD students

Scientific publications

My published work has focused on modeling evolutionary dynamics across multiple species, with a particular emphasis on incomplete lineage sorting (ILS), natural selection, and the multi-species ancestral recombination graph. To date, I have published 12 papers, five of which I led as the first author. My work has gathered a total of 1008 citations (2022-2026), and I have an h-index of 9 (Google Scholar).

Peer-reviewed publications (* indicates equal contribution):

1. **Rivas-González, I.**, Mirarab, S., & Braun, E. L. (2026). Phylogenomics beyond the ‘bag-of-genes’ model. *Trends in Genetics* (in press, published online). https://doi.org/10.1016/j.tig.2026.05.003.

Significance: This paper highlights the lack of existing methods in phylogenomics that include positional, recombination-aware information, even though it might reveal interesting and valuable insight in phylogenomic reconstruction. **Contribution:** I conceptualized and co-wrote the review.

2. Southworth, C. A.*, Winans, J. C.*, Gordon, J. B., Learn, N. H., … **Rivas-González, I.**, … Tung, J. (2026). Demographic, behavioral, and ecological data from a long-term field study of wild baboons in Amboseli, Kenya. *Scientific Data*, *13*(1), 311. https://doi.org/10.1038/s41597-026-06741-2

   Significance: This paper presents over 50 years of longitudinal data collected for the Amboseli Baboon Research Project, including demographic, behavioral and environmental data. **Contribution:** I processed and visualized behavioral data on diet, showing monthly and yearly variation in diet composition.

3. Yoo, D., Rhie, A., Hebbar, P., Antonacci, F., Logsdon, G. A., Solar, S. J., Antipov, D., Pickett, B. D., Safonova, Y., Montinaro, F., Luo, Y., Malukiewicz, J., Storer, J. M., Lin, J., Sequeira, A. N., Mangan, R. J., Hickey, G., Anez, G. M., … **Rivas-González, I.**, … Eichler, E. E. (2025). Complete sequencing of ape genomes. *Nature, 641*, 401-418. https://doi.org/10.1038/s41586-025-08816-3.

   Significance: This study presents haplotype-resolved telomere-to-telomere (T2T) assemblies for six ape species. These state-of-the-art genomes improve insight into sequence divergence, speciation times, ILS, selection, epigenetics, and previously inaccessible regions such as telomeres and centromeres. **Contribution:** I conceptualized and coordinated the analysis of ILS, contributed to data visualization and coding, and wrote and edited the manuscript.

4. **Rivas-González, I.**, Schierup, M. H., Wakeley, J., & Hobolth, A. (2024). TRAILS: Tree reconstruction of ancestry using incomplete lineage sorting. *PLOS Genetics, 20*(2), e1010836. https://doi.org/10.1371/journal.pgen.1010836.

   Significance: This paper reports novel algorithms to more accurately compute ILS. It presents a general framework for inferring the multi-species ancestral recombination graph, which can be extended to model more complex speciation scenarios, including introgression. **Contribution:** As first author, I conceptualized and executed the work, developed the software, and led manuscript writing and editing.

5. Stiller, J., Feng, S., Chowdhury, A.-A., **Rivas-González, I.**, Duchêne, D. A., Fang, Q., Deng, Y., Kozlov, A., Stamatakis, A., Claramunt, S., Nguyen, J. M. T., Ho, S. Y. W., Faircloth, B. C., Haag, J., Houde, P., Cracraft, J., Balaban, M., Mai, U., Chen, G., … Zhang, G. (2024). Complexity of avian evolution revealed by family-level genomes. *Nature, 629*(8013), 851–860. https://doi.org/10.1038/s41586-024-07323-1.

   Significance: This paper analyzed the latest release of the Bird 10,000 Genomes project, representing the most extensive phylogenomic analysis of birds to date. **Contribution:** I led the analysis of phylogenetic nodes and taxa that were previously difficult to place within the avian phylogeny by accounting for high levels of ILS.

6. Mirarab, S., **Rivas-González, I.**, Feng, S., Stiller, J., Fang, Q., Mai, U., Hickey, G., Chen, G., Brajuka, N., Fedrigo, O., Formenti, G., Wolf, J. B. W., Howe, K., Antunes, A., Schierup, M. H., Paten, B., Jarvis, E. D., Zhang, G., & Braun, E. L. (2024). A region of suppressed recombination misleads neoavian phylogenomics. *Proceedings of the National Academy of Sciences, 121*(15), e2319506121. https://doi.org/10.1073/pnas.2319506121.

   Significance: This study characterizes a large region in an avian chromosome that exhibits a distinct gene tree topology compared to the rest of the genome, presumably by impeding normal recombination. We show that failure to account for this region can result in misleading phylogenetic reconstructions. **Contribution:** I performed conceptualization, quantification of ILS, analysis of synteny, and manuscript writing and editing.

7. **Rivas-González, I.**, & Tung, J. (2024). A multi-million-year natural experiment: Comparative genomics on a massive scale and its implications for human health. *Evolution, Medicine, and Public Health, 12*(1), 67–70. https://doi.org/10.1093/emph/eoae006.

Significance: This review paper summarizes recent advancements in primate phylogenomics and evolution, with a particular emphasis on their relevance for human health. **Contribution:** I co-led all aspects of conceptualization, data visualization, and writing.

8. Hobolth, A., **Rivas-González, I.**, Bladt, M., & Futschik, A. (2024). Phase-type distributions in mathematical population genetics: An emerging framework. *Theoretical Population Biology, 157*, 14–32. https://doi.org/10.1016/j.tpb.2024.03.001.

   Significance: This paper introduces phase-type distributions as a novel framework for modeling population genetics parameters. By incorporating coding examples as well as typical review material, it offers a comprehensive guide for researchers to get familiar with phase-type distributions. **Contribution:** I led the coding, data analysis and visualization efforts, wrote major parts of the manuscript, and reviewed and edited the content.

9. **Rivas-González, I.***, Rousselle, M.*, Li, F.*, Zhou, L., Dutheil, J. Y., Munch, K., Shao, Y., Wu, D., Schierup, M. H., & Zhang, G. (2023). Pervasive incomplete lineage sorting illuminates speciation and selection in primates. *Science, 380*(6648), eabn4409. https://doi.org/10.1126/science.abn4409.

   Significance: I led the primary analyses in this paper, which represents the largest investigation of ILS to date, allowing to link the phylogenetic history of primates with ancestral selective processes. **Contribution:** I developed the pipeline for modeling primate ILS, reconstructed the species tree, computed per-base-pair estimates of ILS, and investigated selective correlates of genome-wide ILS. I also led the data visualization, writing, and editing of the manuscript.

10. Shao, Y., Zhou, L., Li, F., Zhao, L., Zhang, B.-L., Shao, F., Chen, J.-W., Chen, C.-Y., Bi, X., Zhuang, X.-L., Zhu, H.-L., Hu, J., Sun, Z., Li, X., Wang, D., **Rivas-González, I.**, Wang, S., Wang, Y.-M., Chen, W., … Wu, D.-D. (2023). Phylogenomic analyses provide insights into primate evolution. *Science, 380*(6648), 913–924. https://doi.org/10.1126/science.abn6919.

    Significance: This study uses 50 primate genome assemblies, including 27 newly reported ones, to reconstruct the primate phylogeny, infer chromosomal rearrangements in the primate ancestors, and identify candidate targets of primate-specific adaptation. **Contribution:** I analyzed phylogenetic discordance in the gibbon lineage using ILS, solving its placement within the primate phylogeny. I also contributed to writing and editing of the manuscript.

11. **Rivas-González, I.**, Andersen, L. N., & Hobolth, A. (2023). PhaseTypeR: An R package for phase-type distributions in population genetics. *Journal of Open Source Software, 8*(82), 5054. https://doi.org/10.21105/joss.05054.

    Significance: This paper introduces user-friendly, extensible, and flexible software for modeling phase-type distributions, with special emphasis in population genetics. **Contribution:** I conceptualized, wrote, and developed the software; I led the data visualization, writing, and editing of the manuscript; and I am the maintainer of the package.

12. Feng, S., Bai, M., **Rivas-González, I.**, Li, C., Liu, S., Tong, Y., Yang, H., Chen, G., Xie, D., Sears, K. E., Franco, L. M., Gaitan-Espitia, J. D., Nespolo, R. F., Johnson, W. E., Yang, H., Brandies, P. A., Hogg, C. J., Belov, K., Renfree, M. B., … Zhang, G. (2022). Incomplete lineage sorting and phenotypic evolution in marsupials. *Cell, 185*(10), 1646-1660.e18. https://doi.org/10.1016/j.cell.2022.03.034.

    Significance: This study analyzes the genome of the South American marsupial monito del monte and successfully resolves its phylogenetic position within marsupials. It also demonstrates the functional importance of ILS by showing that some discrepancies between the species tree and the marsupial skeleton of marsupials are due to ILS. **Contribution:** I calculated ILS in all of the marsupial nodes, identifying candidate locations for phylogenomic incongruences that were then confirmed using transgenic mice. I also wrote and edited the manuscript.

Published software

- **TRAILS:** python package for running the algorithm for inferring ILS described in Rivas-González et al. 2024. The implementation of this software is optimized for running in parallel using several cores and can perform parameter optimization of population parameters and subsequent posterior decoding of alternative tree states through easy-to-use python functions. The package can be installed from pip (https://pypi.org/project/trails-rivasiker/), and the source code, together with a tutorial on its basic functionality, is available on GitHub (https://github.com/rivasiker/trails).
- **PhaseTypeR:** user-friendly, easily customizable R package for obtaining descriptive statistics of phase-type distributions. I wrote the code, extensive documentation, and several tutorials that explain the full functionality of the package (https://rivasiker.github.io/PhaseTypeR/). The package can easily be installed from CRAN (https://cran.r-project.org/package=PhaseTypeR), and the source code is publicly available on GitHub (https://github.com/rivasiker/PhaseTypeR). Number of downloads: >7,500 from CRAN.
- **autoCoalHMM:** fully automated bioinformatics pipeline that runs the CoalHMM algorithm (Dutheil et al. 2009, *Genetics* 183, 259–274) in chunks along the genome, jointly computing population genetics parameters and an incomplete lineage sorting map at the base-pair level. The code is freely available on GitHub together with a tutorial on how to run it (https://github.com/rivasiker/autocoalhmm).
- **ggHoriPlot:** R package for building horizon plots in ggplot2. The package contains several vignettes that show the overall functionality of the package and several examples using real datasets, including whole-genome data (https://rivasiker.github.io/ggHoriPlot/). ggHoriPlot is available on CRAN (https://cloud.r-project.org/package=ggHoriPlot), and its source code can be browsed on GitHub (https://github.com/rivasiker/ggHoriPlot/). Number of downloads: >12,000 from CRAN, > 7,000 from conda.

Skills

Throughout my academic career, I have developed a diverse set of **personal and technical skills**, making me a **balanced and versatile** researcher. I have led several international research projects, showcasing my abilities in **teamwork, leadership, and management**. My participation in group meetings, seminars, and conferences highlights my capacity for effective **communication and dissemination** across various scientific levels. I frequently leverage my **creativity** for problem-solving, and my ability to **think outside the box** has enabled me to integrate different data sources. Additionally, I value **empathy and emotional intelligence**, which have helped me build a healthy network of professional relationships. My **technical skills** include:

- **Programming languages**: *R* (expert), *python* (expert), *bash* (advanced)
- **Data wrangling and statistics**: *dplyr* (expert), *pandas* (advanced), *numpy* (advanced), *scipy* (advanced)
- **Data visualization**: *ggplot2* (expert), *Inkscape* (advanced)
- **Text editing and processing**: *Microsoft Office* (expert), *Markdown* (expert), *RStudio* (expert), *Jupyter Notebook* (expert), *Visual Studio Code* (advanced), *LaTeX* (advanced), *awk* (advanced), *regex* (advanced)
- **Advanced computational skills**: high-performance computing using *slurm* (expert), workflow management using *gwf* (expert), parallelization using *ray* (advanced)
- **Other tools and programs**: *SLiM*, *msprime* and *tskit* for genomic simulations (expert), *GATK* for sequencing data (advanced), *IGV* for genome-wide visualizations (intermediate), *Zotero* for scientific references (advanced), *git* for version control (advanced).

Service and outreach

04/2023 **Conference Co-Organizer** *University of Copenhagen (DK)*

My tasks included applying for funding, coordinating invited speakers, and moderating discussions

- ***Title:*** "Phase-Type Distributions in Population Genomics"
- ***Co-organizer:*** Prof. Dr. Asger Hobolth

07/2023 **Symposium Co-Organizer**

Society for Molecular Biology and Evolution (SMBE) Meeting, Ferrara (IT)

My tasks included searching for invited speakers, selecting contributed talks, budgeting, and coordinating expenses

- ***Title:*** "Modeling the genomic, social, and ecological drivers of speciation"
- ***Invited speakers:*** Prof. Dr. Guojie Zhang and Prof. Dr. Tomas Marques-Bonet
- ***Co-organizer:*** Dr. Arun Durvasula

07/2023 **Media Coverage**

Upon publishing in *Science*, I was interviewed by several Spanish and Basque media outlets:

- ***Live radio interview:*** Faktoria (Euskadi Irratia)
- ***Interviews for newspapers:*** El País, El Mundo, El Correo, El Confidencial

03/2022 **Three Minute Thesis (3MT) Competition Finalist** *Aarhus (DK)*

The 3MT competition is an academic contest where PhD students present their research in just three minutes using a single slide, aiming to make their work understandable and engaging to a non-specialist audience.

- ***Title:*** "A journey into the past to decipher primate evolution"
- ***Recording:*** https://www.youtube.com/watch?v=CEt9OAg_nuk

I have contributed to the scientific community as a peer reviewer for several journals, including *Nature Communications*, *Nature Ecology & Evolution*, *Genome Biology*, *Genome Biology and Evolution*, *Nature Reviews Biodiversity*, *Systematic Biology, Communications Biology, Molecular Biology and Evolution*, and *Peer Community In Mathematical and Computational Biology.*

Invited and contributed talks and presentations

Oral presentations (submitted abstract chosen for a talk)

07/2026 **Flash talk, Society for Molecular Biology and Evolution (SMBE) Meeting** *Copenhagen (DK)*
09/2024 **Flash talk, EMBO | EMBL Symposium, Reconstructing the Human Past: Using Ancient and Modern Genomics** *Heidelberg (DE)*
04/2024 **Probabilistic Modelling in Genomics** *Vienna (AT)*
08/2023 **Evolution and Population Genetics in Denmark: EPIC-DK** *Copenhagen (DK)*
04/2023 **Phase-Type Distributions in Population Genomics** *Copenhagen (DK)*
03/2023 **Probabilistic Modelling in Genomics** *Cold Spring Harbor Laboratory (US)*
09/2022 **Society for Molecular Biology and Evolution (SMBE) Everywhere GS4: Using ARGs to Infer Evolutionary Processes** *virtual*
05/2022 **The Biology of Genomes** *Cold Spring Harbor Laboratory (US)*
03/2022 **Probabilistic Modelling in Genomics** *Oxford (UK)*
03/2022 **Three Minute Thesis Competition** *Aarhus (DK)*

Poster presentations

05/2025 **The Biology of Genomes** *Cold Spring Harbor Laboratory (US)*
09/2024 **EMBO | EMBL Symposium, Reconstructing the Human Past: Using Ancient and Modern Genomics** *Heidelberg (DE)*
07/2023 **Society for Molecular Biology and Evolution (SMBE) Meeting** *Ferrara (IT)*
11/2021 **Annual Danish Bioinformatics Conference** *Aalborg (DK)*
07/2021 **Society for Molecular Biology and Evolution Meeting** *virtual*

Invited talks

06/2026 **Department of Statistics, University of Oxford** *Oxford (UK)*

Grants and awards

10/04/2024 – 12/04/2024 **Best postdoc talk**
Probabilistic Modelling in Genomics meeting, *Vienna (AT)*
20/04/2023 – 21/04/2023 **Danish Data Science Academy (DDSA) funding for conference**
Phase-Type Distributions in Population Genomics, *Copenhagen (DK)*
01/09/2022 – 01/02/2023 **STIBOFONDEN's IT travel grant for PhD students**
01/09/2022 – 01/02/2023 **Aarhus University Graduate School of Natural Sciences mobility grant**
01/09/2017 – 01/07/2018 **Travel grants for Erasmus**

- Basque Government scholarship for international mobility
- Kutxabank Erasmus scholarship

01/09/2014 – 01/07/2018 **Extraordinary Prize**

Awarded to the student with the highest academic record in the BSc in Biochemistry and Molecular Biology graduating in the 2017/2018 academic year

Workshops and training

13/05/2024 – 17/05/2024	**SLiM Workshop** hosted by Ben Haller *University of Copenhagen (DK)*
01/03/2022 – 01/04/2022	**Three Minute Thesis Competition Training** hosted by Linda Greve *Aarhus University (DK)*
01/11/2020 – 30/11/2020	**Science Teaching Course** *Aarhus University (DK)*