

Paul A. Maier, Ph.D.

Population and Statistical Geneticist

Senior Population Geneticist

FamilyTreeDNA / Gene by Gene

1445 N Loop W, Houston, TX 77008

Email: paulm@genebygene.comwww.paulmaierresearch.comwww.linkedin.com/in/paul-maier**PROFESSIONAL SUMMARY**

Population and statistical geneticist with eight years of industry research experience analyzing population-scale human genomic data and turning the results into popular tools and peer-reviewed publications. At FamilyTreeDNA I work daily with one of the largest human genomic databases held outside a national biobank: roughly 330,000 complete mitochondrial genomes, more than 90,000 whole-Y sequences, and autosomal data for about 1.5 million genotyped individuals spanning SNP arrays and 30× whole-genome sequencing. My work covers variant calling and QC across sequencing and array platforms, ancestry and relatedness inference, single-variant association and outlier scans, phylogenetic and coalescent modeling, simulation-based method validation, and age estimation for lineages and founder mutations. I traced the origin of a founder mutation causing recessive dystrophic epidermolysis bullosa using local ancestry methods, and contributed human genetics analyses to ancient DNA studies of Ludwig van Beethoven and two Holy Roman Emperors. I spent years building predictive models with machine learning and deep learning before large language models existed, and I now develop population genetic, phylogenetic and ancestry inference with Claude Opus 5 in VS Code, while all scientific ideas, hypothesis-testing, and validation were directed by myself. Python was my first language and carries most new pipeline work; R carries the phylogenetics and statistical modeling. Across human and wildlife systems the problem has been the same: infer history and adaptation from genomes at scale, then make the answer usable by people who have to act on it. Human disease genetics is one area I want to take that next.

SELECTED PROJECTS**Mitotree: universal human mitochondrial reference phylogeny** | *Project lead, 2021 to present*

- Built the largest human phylogeny described to date from 331,221 complete mitogenomes (177,196 unique haplotypes), resolving 53,588 haplogroups, roughly ten times the resolution of PhyloTree v17, the previous reference standard.
- Designed the full analysis stack: an automated NGS pipeline adapted from GATK Best Practices for mitochondrial short variant discovery (GATK 4.6, BWA-MEM, BCFtools), sample and variant QC rules for heteroplasmy, ambiguity, reference bias and post-mortem damage, alignment normalization, and data-driven marker weighting.
- Invented a recursive divide-and-conquer weighted-parsimony framework that runs heuristic searches on 175,000 haplotypes, 3.5 times the largest previously benchmarked dataset, with a three-part node support metric separating character sampling variance, search variance, and mutational consistency.
- Validated the pipeline against simulated phylogenies with known ground truth across 10 replicates, reporting a 3.5% false negative and 1.0% false positive branch recovery rate, and benchmarked it against FastTree2, the only alternative that scales comparably.
- Estimated times to most recent common ancestor for every branch under a relaxed clock (LSD, calibrated with BEAST), integrating 3,206 radiocarbon-dated ancient DNA samples as age constraints.
- Released the tree publicly through HaploGrep v3 plugins so that external groups can assign haplogroups without changing their existing pipelines. Higher resolution supports finer mtDNA haplogroup association testing in biobank-scale cohorts.

Archaic Origins: genome-wide archaic ancestry across the customer base | *Project lead, 2026*

- Designed and built a three-arm pipeline reporting Neanderthal, Denisovan and ghost-archaic ancestry as calibrated percentages and per-chromosome segments. Runs across 1000 Genomes, SGDP and a customer cohort in the hundreds of thousands, on a tiered output layout with 11x BCF compaction so the cache scales. Release is planned on the FamilyTreeDNA Discover platform.
- Neanderthal detection uses IBDmix against Vindija 33.19. Denisovan detection uses SPrime discovery with a two-tier screened marker set. The ghost arm matches customer haplotypes against a 19,239-locus catalogue derived from TRACE, scoring each window by its distance to carriers minus its distance to non-carriers. Normalizing by the window's own diversity cancels population ancestry out of both terms.
- Anchored calibration to published f4 and conditional random field estimates rather than to the detection method itself, which would have calibrated the pipeline against its own known underestimate. Validation against published population ranges across six ancestry groups placed 12 of 13 cells in range, including held-out populations the constants were never fitted to.
- Traced and removed two sources of false positives that let West Africans assemble Denisovan tracts they should not carry. Adding an African allele-frequency screen and a Denisovan-specificity screen also tightened European Denisovan estimates

from an implausibly wide range into a narrow one consistent with published values. A segment-level audit identified overlapping tracts being counted twice; correcting this and refitting the calibration constants improved accuracy across all three arms.

- Built the archaic trait layer: 137 curated variants across 109 loci, covering eye colour, fear of heights, chronotype, mosquito bite reaction, and EPAS1, the Denisovan variant behind high-altitude adaptation in Tibetans. A call requires both tract overlap and an allele match on the same haplotype. Dropped 644 of 839 candidate rows where the archaic allele was the ancestral one and would have returned a confident positive for nearly every customer.
- Measured the ghost arm against held-out data: within-population AUC 0.837 against a 0.499 null, segment precision and recall of 0.45 and 0.43 at the medium-confidence tier, 0.82 and 0.12 at the high-confidence tier. Per-person error exceeds real between-person variance, so we present it as a population-level estimate rather than an individual measurement.
- Tested and ruled out an African-archaic arm based on the introgression reported by Durvasula and Sankararaman (2020), and retired two of three candidate ghost-detection routes, documenting the supporting measurements in each case.
- Built the pipeline end to end with Claude Opus 5 in Microsoft VS Code across several working sessions, each closed with a written handoff covering what was measured and what was refuted. The method decisions, calibration design and validation standards were mine; Claude helped with fast implementation and hypothesis-testing.

Founder mutation origin in a rare Mendelian disease | *Statistical genetics lead for ancestry analysis, 2019 to 2025*

- Determined the population origin of COL7A1 c.6527insC, the most prevalent mutation causing recessive dystrophic epidermolysis bullosa in Hispanic populations, by combining local ancestry inference, identity-by-descent haplotype analysis, and genome-wide array data from patients across Spain, Argentina, Chile and Mexico.
- Showed that carriers share a Sephardic Jewish haplotype background, which reframed the mutation as a single crypto-Jewish founder event carried to the New World rather than several independent origins. Published in the Journal of Medical Genetics (2025) and the American Journal of Medical Genetics (2021).
- Worked with a cross-functional group of dermatologists, clinical geneticists, and population geneticists across seven countries, and translated the genetic findings for a clinical audience.

myOrigins 3.0: joint global and local ancestry inference | *Method inventor and first author, 2019 to 2021*

- Invented a method that estimates global ancestry proportions and per-chromosome local ancestry jointly rather than in sequence, which improved consistency between the two and allowed reference panel expansion from 24 to 90 populations.
- Assembled and curated reference panels from public and proprietary genotype resources, ran the QC, and set the population definitions and hierarchy used to report results.
- Shipped to the full customer base with a chromosome painting feature, and authored the public white paper and a three-part video series explaining method and interpretation.

Y-chromosome age estimation and Discover | *Method inventor, 2019 to 2023*

- Built the age estimation (TMRCA) method for the largest Y-DNA phylogeny yet constructed, over 90,000 Big Y whole-Y sequences, accounting for variable coverage across the callable Y region and for uncertainty in mutation rate.
- Method underpins the public Y-DNA Discover tool and the FTDNATiP relationship report.

Family Finder Matching 5.0: relatedness estimation | *Co-author, 2020 to 2021*

- Contributed to an autosomal matching and relationship prediction algorithm that corrects for endogamy, a systematic source of inflated relatedness estimates in founder populations, and co-authored the white paper describing it.

Ancient DNA case studies | *Population genetics contributor, 2021 to present*

- Inferred the biogeographic origin of Ludwig van Beethoven from hair-derived ancient DNA using a geo-genetic triangulation method I developed, as part of an international study published in Current Biology (2023) and covered by the New York Times.
- Contributed lineage and ancestry analyses to genomic studies of Holy Roman Emperors Otto I and Henry II, an Iron Age Finnish burial, Ötzi the Iceman, and Abraham Lincoln.

Population-scale and controlled-access cohort data | *2018 to present*

- Primary analyst on one of the largest human genomic databases held outside a national biobank: over 330,000 complete mitogenomes, more than 90,000 whole-Y sequences, and autosomal data for roughly 1.5 million genotyped individuals across SNP arrays and 30× whole-genome sequencing. A resource that size carries its own schema, access control and QC burden.
- Held All of Us Researcher Workbench access for a Y-chromosome phylogeny project. Loaded the curated FamilyTreeDNA Y-DNA tree and its branch-defining mutations into the Workbench, assigned participant sequences to that tree, and recorded derived and ancestral calls at prehistoric branch mutations. The aim was resolving the order of evolutionarily equivalent variants across hundreds of thousands of diverse Y chromosomes.

- Designed that analysis to be privacy-preserving by construction: only tree branches older than roughly 1,000 years were in scope, and participant-private variants capable of pointing to a specific family or surname lineage were excluded before analysis.
- Harmonized public reference resources against internal data as routine practice, including 1000 Genomes, HGDP, SGDP, GGVP, GenBank and gnomAD, under consistent QC and ancestry-aware filtering.
- Built the QC framework used across projects: contamination and heteroplasmy thresholds, depth and ambiguity filters, reference-bias screens that exclude whole studies showing systematic artifacts, and post-mortem damage correction for degraded samples.

Machine learning and AI-assisted method development | 2012 to present

- Built classification and prediction models from genetic data using hidden Markov models, random forests, support vector machines and neural networks, including the classifier behind local ancestry assignment in myOrigins 3.0 and a prototype genomic age predictor.
- Develop production tooling with Claude Opus 5 in Microsoft VS Code as a standard part of the loop, covering implementation, refactoring, test construction and documentation across the population genetics, phylogenetics and autosomal ancestry codebases. This cut the time from method idea to testable prototype sharply.
- Hold AI-generated code to the same bar as hand-written code: validation against simulated data with known ground truth, regression against previously published releases, and review before any result is trusted downstream.

TECHNICAL SKILLS

Human genomics: variant calling and QC for WGS, targeted sequencing and array genotyping; GATK Best Practices workflows; sample-level and variant-level QC; contamination, heteroplasmy and reference-bias filtering; single-variant association and outlier scans across genome-wide SNP data; haplogroup assignment; relatedness and IBD estimation; global and local ancestry inference; founder mutation dating; ancient DNA handling and post-mortem damage correction

Reference resources: All of Us Researcher Workbench, 1000 Genomes, HGDP, SGDP, GGVP, CNCB, GenBank, gnomAD, PhyloTree, HaploGrep, AmtDB

Statistics: GLM, GLMM and GAM; linear and generalized mixed models; Bayesian inference including approximate Bayesian computation; maximum likelihood and weighted parsimony; bootstrap and resampling; relaxed molecular clocks; coalescent theory and site frequency spectra; time series; spatial statistics and kriging; graph and network models; power analysis and simulation-based validation

Machine learning: hidden Markov models, random forests, support vector machines, neural networks and deep learning, dimension reduction; predictive model construction, tuning and out-of-sample validation

Programming: Python (first language, and the primary language for new pipeline and tool development) and R (expert, used for phylogenetics, statistical modeling and the Mitotree pipeline); Unix and shell, C, C++, Java, Perl, SQL

Tools and pipelines: GATK, BWA-MEM, BCFtools, PLINK, STACKS, ipyrad, Bioconductor, MUSCLE, TNT, IQ-TREE2, BEAST, LSD, ape, phytools, phangorn, git and GitHub, high-performance compute clusters

Released code: Mitotree tree files and haplogroup definitions (github.com/genebygene/mitotree); fasta2genotype.py, a RAD-to-genotype converter that uses whole haplotypes rather than one SNP per locus (github.com/paulmaier); data and analysis scripts archived at Dryad under [10.5061/dryad.xsj3tx99h](https://doi.org/10.5061/dryad.xsj3tx99h), [10.5061/dryad.pg4f4qrvj](https://doi.org/10.5061/dryad.pg4f4qrvj) and [10.5061/dryad.6m905qg3r](https://doi.org/10.5061/dryad.6m905qg3r); raw reads at NCBI BioProjects [PRJNA558546](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA558546) and [PRJNA574353](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA574353)

AI-assisted development: Claude Opus 5 in Microsoft VS Code as a standard part of the development loop for population genetic, phylogenetic and autosomal ancestry tooling, spanning implementation, refactoring, test construction and documentation, with generated code validated against simulated ground truth and prior releases before any downstream use

Laboratory: DNA and RNA extraction, PCR (basic, touchdown, gradient, emulsion), quantification (Bioanalyzer, Qubit, Nanodrop), library preparation (digestion and ligation, Pippin Prep, combinatorial barcoding, cDNA synthesis), sequencing on Illumina HiSeq and Roche 454

GIS and other: ESRI ArcGIS, QGIS, geospatial modeling, network analysis, cartography; Adobe Photoshop, Lightroom and Illustrator; Spanish at intermediate fluency

EMPLOYMENT and RESEARCH EXPERIENCE

Senior Population Geneticist, FamilyTreeDNA / Gene by Gene | Houston, Texas, Oct. 2018 to present

- Led statistical genetics research across mitochondrial, Y-chromosome and autosomal data for a database of roughly 1.5 million genotyped individuals and hundreds of thousands of sequenced genomes, taking methods from concept through validation, release and public explanation.

- Designed and maintained automated NGS pipelines for alignment, variant calling, QC and annotation. Full reanalyses rerun without supervision as new data arrive.
- Invented a joint global and local ancestry estimation method (myOrigins 3.0) and a phylogenetic method behind the largest mitochondrial tree yet built (Mitotree).
- Invented the age estimation method for the largest human Y-DNA tree constructed, more than 90,000 whole-Y sequences.
- Improved autosomal matching and relationship estimation to account for endogamy, a known source of bias in founder populations.
- Applied local ancestry methods to identify the Sephardic origin of a founder mutation causing a rare Mendelian skin disease, working with clinicians and clinical geneticists across seven countries.
- Applied population genetic theory, machine learning and hidden Markov models to DNA classification problems, and used coalescent approaches, Mendelian genetics and site frequency spectra throughout.
- Built and engineered analysis pipelines with Claude Opus 5 in VS Code as part of the normal development loop. All scientific ideas, hypothesis-testing, and validation were directed by myself.
- Used phylogeographic and landscape genetic methods to reconstruct prehistoric human movement, released to the public as the Globetrekker tool.
- Communicated results to cross-functional partners including laboratory, engineering, product, marketing and executive teams, and to external audiences through conference talks, white papers, peer-reviewed papers and press interviews.
- Mentored colleagues in population genetics, and spoke for the company on scientific questions in public forums.

Population Geneticist (Contractor), USDA El Dorado National Forest | Placerville, California, Jun. 2023 to Dec. 2024

- Developed a diagnostic SNP panel to quantify hybridization between Yosemite toads (*Anaxyrus canorus*) and western toads (*Anaxyrus boreas*), using ddRADseq library preparation and analysis methods from my dissertation.
- Estimated hybrid ancestry proportions for individuals of uncertain status and delivered a final report to the US Forest Service that informed management decisions.

Joint Doctoral Research, Bohonak Lab, San Diego State University and UC Riverside | San Diego and Riverside, California, Aug. 2012 to Jul. 2018

Advisers: Andrew Bohonak (SDSU), Leonard Nunney (UCR), Amy Vandergast (USGS)

- Generated and analyzed genome-wide SNP data (thousands of single-copy nuclear loci) and a complete transcriptome to reconstruct population history and detect signatures of local adaptation.
- Built a genetic network model using spatial statistics, mixed models and graph theory to estimate environmentally mediated migration, and used it to project future connectivity under climate scenarios.
- Identified putatively adaptive markers in pure and admixed lineages and modeled admixture outcomes, work that produced five peer-reviewed papers.
- Taught five semesters of university laboratory courses and mentored 12 graduate and 6 undergraduate students.

Biologist GS-05/07 Lead, US Geological Survey | Oakhurst and San Diego, California, Feb. 2010 to Mar. 2017

- Led field crews for a multi-year census of amphibian, reptile, mammal and plant populations across the western United States, including a census of all Yosemite toad meadows in Yosemite and Kings Canyon National Parks.
- Designed sampling protocols, managed tabular and spatial data, produced summary reports, and contributed statistical analysis.

Director and Adviser of Science and GIS, The Biodiversity Group (501(c)(3)) | Ecuador, Jun. 2009 to 2016

- Ran amphibian and reptile field research in lowland and montane Ecuador, built a habitat-based model of species detectability from transect data, and set the organization research and GIS direction.

Earlier positions: Independent Contractor, Conservation Science (2011); Research Assistant, Florida International University, Costa Rica (2009); Research Assistant, Institute for Conservation Research, San Diego Zoo, Dominica (2009); Research Assistant, Marine Science Institute, UC Santa Barbara (2008 to 2009); Biological Science Technician GS-05 and GS-04, US Forest Service (2006, 2008). Details available on request.

EDUCATION

Ph.D. in Evolutionary Biology, 2018. GPA 4.0

San Diego State University and University of California Riverside, joint doctoral program, California

Dissertation: Evolutionary past, present, and future of the Yosemite toad (*Anaxyrus canorus*): a total evidence approach to delineating conservation units

B.S. in Aquatic Biology / Ecology and Evolution, 2008. GPA 3.7

University of California Santa Barbara, Santa Barbara, California

PEER-REVIEWED PUBLICATIONS and REPORTS

- Wood D.A., Smith J.G., Jones J.L., Pawlicki A., DeNardo D.F., **Maier P.A.**, Rognan C., Hromada S.J., Nussear K.E., Stalker J.B., Stratton C.S., Gienger C.M., Vandergast A.G. (2026). Population structure and genomic diversity of the Gila monster reflect ecoregional patterns. Cooperator Report prepared for the Desert Conservation Program, Clark County, Nevada. U.S. Geological Survey.
- Levy-Toledano R., Penninx W., Waas M., Runfeldt G., Sager M., **Maier P.**, Brown A. (2026). Patrilineal genetic ancestry of Moroccan Jews. *Genealogy*, 10(2), 66. <https://doi.org/10.3390/genealogy10020066>
- Davranoglou L.-R., Kofinakos A.P., Mariolis A.D., Runfeldt G., **Maier P.A.**, Sager M., Soulioti P., Mariolis-Sapsakos T., Heraclides A. (2026). Uniparental analysis of Deep Maniot Greeks reveals genetic continuity from the pre-Medieval era. *Communications Biology*, 9, 157. <https://doi.org/10.1038/s42003-026-09597-9>
- Warshauer E., **Maier P.A.**, Runfeldt G., Fuentes I., Escámez M.J., Valinotto L., Natale M., Manzur G., Illera N., García M., del Río M., Mencia Á., Larcher F., Hellenthal G., Brown A., Consuegra L., Rivera C., Nogueiro I., Tang J., Oro A., Marinkovich P., Palisson F., Titeux M., Hovnanian A., Sprecher E., Skorecki K., Norris D., Bruckner A., Kogut I., Bilousova G., Roop D. (2025). Sephardic origins revealed for rare skin disorder, recessive dystrophic epidermolysis bullosa, in individuals carrying the unique c.6527insC mutation. *Journal of Medical Genetics*, 63(1), 40–49. <https://doi.org/10.1136/img-2025-110967>
- Maier P.A.**, Mabe J.A., Hale J.L., Herman A.E., Kantz B.P. (2024). Hybridization between *Anaxyrus boreas* × *canorus* within Eldorado National Forest: the first genomic assessment. Final Report to US Forest Service, Eldorado National Forest, Placerville, CA. <https://doi.org/10.13140/RG.2.2.26918.28488>
- Maier P.A.**, Vandergast A.G., Bohonak A.J. (2024). Yosemite toad (*Anaxyrus canorus*) transcriptome reveals interplay between speciation genes and adaptive introgression. *Molecular Ecology*, 33(8), e17317. <https://doi.org/10.1111/mec.17317>
- Warshauer E.M., **Maier P.**, Runfeldt G., Fuentes I., Escámez M., Hellenthal G., Brown A., Valinotto L., Hovnanian A., Sprecher E., Skorecki K., Roop D. (2023). Crypto-Jewish origins revealed in recessive dystrophic epidermolysis bullosa individuals carrying the prevalent c.6527insC mutation associated with Sephardic ancestry [abstract]. *Journal of Investigative Dermatology*, 143(5), S147. <https://doi.org/10.1016/j.jid.2023.03.867>
- Begg T.J.A., Schmidt A., Kocher A., Larmuseau M.H.D., Runfeldt G., **Maier P.A.**, Wilson J.D., Barquera R., Maj C., Szolek A., Sager M., Clayton S., Peltzer A., Hui R., Ronge J., Reiter E., Freund C., Burri M., Aron F., Tiliakou A., Osborn J., Behar D.M., Boecker M., Brandt G., Cleynen I., Strassburg C., Prüfer K., Kühnert D., Meredith W.R., Noethen M., Attenborough R.D., Kivisild T., Krause J. (2023). Genomic analyses of hair from Ludwig van Beethoven. *Current Biology*, 33, 1–17. <https://doi.org/10.1016/j.cub.2023.02.041>
- Maier P.A.**, Vandergast A.G., Bohonak A.J. (2023). Using landscape genomics to delineate future adaptive potential for climate change in the Yosemite toad (*Anaxyrus canorus*). *Evolutionary Applications*, 16(1), 74–97. <https://doi.org/10.1111/eva.13511>
- Warshauer E.M., **Maier P.**, Fuentes I., Runfeldt G., Escámez M., Valinotto L., Brown A., Palisson F., Hovnanian A., Roop D. (2022). Sephardic ancestry in recessive dystrophic epidermolysis bullosa individuals carrying the prevalent c.6527insC mutation [abstract]. *Journal of Investigative Dermatology*, 142(12), S232. <https://doi.org/10.1016/j.jid.2022.09.316>
- Maier P.A.**, Vandergast A.G., Ostojia S.M., Aguilar A., Bohonak A.J. (2022). Landscape genetics of a sub-alpine toad: climate change predicted to induce upward range shifts via asymmetrical migration corridors. *Heredity*, 129(5), 257–272. <https://doi.org/10.1038/s41437-022-00561-x>
- Maier P.A.**, Runfeldt G., Estes R.J., Vilar M.G. (2022). African mitochondrial haplogroup L7: a 100,000-year-old maternal human lineage discovered through reassessment and new sequencing. *Scientific Reports*, 12(1), 10747. <https://doi.org/10.1038/s41598-022-13856-0>
- Maier P.A.**, Vandergast A.G., Ostojia S.M., Aguilar A., Bohonak A.J. (2022). Gene pool boundaries for the Yosemite toad (*Anaxyrus canorus*) reveal asymmetrical migration within meadow neighborhoods. *Frontiers in Conservation Science*, 3, 851676. <https://doi.org/10.3389/fcsc.2022.851676>
- Maier P.A.**, Hu R., Runfeldt G., Giniebra D., Frichot E. (2021). myOrigins 3.0: combining global and local methods for determining population ancestry. FamilyTreeDNA White Paper 2021-08-18. <https://doi.org/10.13140/RG.2.2.30398.00328>
- Hu R., **Maier P.A.**, Runfeldt G., Estes R., Rocha E., Walker A., Baur P., Ty L. (2021). Family Finder Matching 5.0: matching algorithm and relationship estimation. FamilyTreeDNA White Paper 2021-08-18. <https://doi.org/10.13140/RG.2.2.13620.78720>
- Warshauer E., Brown A., Fuentes I., Shortt J., Gignoux C., Montinaro F., Metspalu M., Youssefian L., Vahidnezhad H., Jacków J., Christiano A.M., Uitto J., Fajardo-Ramírez Ó.R., Salas-Alanis J.C., McGrath J.A., Consuegra L., Rivera C., **Maier P.A.**, Runfeldt G., Behar D.M., Skorecki K., Sprecher E., Palisson F., Norris D.A., Bruckner A.L., Kogut I., Bilousova G., Roop D.R. (2021). Ancestral patterns of recessive dystrophic epidermolysis bullosa mutations in Hispanic populations suggest Sephardic ancestry. *American Journal of Medical Genetics Part A*, 185(11), 3390–3400. <https://doi.org/10.1002/ajmg.a.62456>

- Lindauer A.L., **Maier P.A.**, Voyles J. (2020). Daily fluctuating temperatures decrease growth and reproduction rate of a lethal amphibian fungal pathogen in culture. *BMC Ecology*, 20(18), 1–9. <https://doi.org/10.1186/s12898-020-00286-7>
- Jia K.-H., Zhao W., **Maier P.A.**, Hu X.-G., Jin Y., Zhaou S.-S., Jiao S.-Q., El-Kassaby Y.A., Wang T., Wang X.-R., Mao J.-F. (2020). Landscape genomics predicts climate change vulnerability for a forest tree: a case from a widespread conifer, *Platycladus orientalis*. *Evolutionary Applications*, 13(4), 665–676. <https://doi.org/10.1111/eva.12891>
- Maier P.A.**, Vandergast A.G., Ostoja S.M., Aguilar A., Bohonak A.J. (2019). Pleistocene glacial cycles drove lineage diversification and fusion in the Yosemite toad (*Anaxyrus canorus*). *Evolution*, 73(12), 2476–2496. <https://doi.org/10.1111/evo.13868>
- Maier P.A.** (2019). *Anaxyrus canorus* (Yosemite toad) larval diet. *Herpetological Review*, 50(1), 111–112.
- Maier P.A.** (2018). *Anaxyrus canorus* (Yosemite toad) breeding behavior. *Herpetological Review*, 49(4), 727–728.
- Maier P.A.** (2018). Evolutionary past, present, and future of the Yosemite toad (*Anaxyrus canorus*): a total evidence approach to delineating conservation units. Ph.D. dissertation, University of California Riverside and San Diego State University, San Diego, CA. <https://escholarship.org/uc/item/7jf3x4kg>
- Maier P.A.**, Ostoja S.M., Aguilar A., Bohonak A.J. (2016). Conservation genomics of the Yosemite toad: implications of deep divergence and limitations to meadow connectivity. USGS Cooperator's Report to the National Park Service, San Diego State University, San Diego, CA. <https://doi.org/10.13140/RG.2.2.10270.41281>
- Klinger R., Cleaver M., Anderson S., **Maier P.**, Clark J. (2015). Implications of scale-dependent habitat specialization on persistence of a rare small mammal. *Global Ecology and Conservation*, 3, 100–114. <https://doi.org/10.1016/j.gecco.2014.10.003>
- Klinger R., Cleaver M., Anderson S., **Maier P.**, Clark J. (2013). Short-term population dynamics, demography, and habitat selection by the Amargosa vole. USGS Final Report to the Bureau of Land Management, USGS Bishop Field Station, Bishop, CA.

MANUSCRIPTS IN REVIEW and IN PREPARATION

- Maier P.A.**, Runfeldt G., Estes R.J., Goloboff P.A., Detsikas J., Burke A.J., Sager M.T., Vilar M.G. Mitotree: the universal human mitochondrial reference phylogeny at 10× the resolution. *Cladistics*, in review. <https://doi.org/10.64898/2026.05.28.728540>
- Goloboff P.A., **Maier P.A.** Phylogenetic tree searches under topological constraints. *Cladistics*, in review.
- Lipson J., Bohrer S.G., Cohen-Weinstein S., Cooper L., Revivo D., Staetsky D., **Maier P.A.**, Runfeldt G., Skorecki K. Revisiting the lineages of the Cohanim using data from next-generation sequencing. *Rambam Maimonides Medical Journal*, in review. <https://doi.org/10.64898/2025.12.08.692646>
- Yardumian A., Sahakyan H., Carlin M., Askapuli A., Bryant R., Ilumäe A.-M., Reidla M., Runfeldt G., **Maier P.**, Vilar M. Phylogeographic analyses of mitochondrial DNA haplogroup W offer insights into dispersals of women in Eurasia from the Early Neolithic through the Iron Age. *Communications Biology*, in review.
- Ivarsson-Aalders M., Krzewińska M., Varela R.R., Yaka R., Burke A., Sager M., **Maier P.**, Runfeldt G., Kjellström A., Götherström A. Between kin and community: biological relatedness and belonging at Viking Age Ihre, Gotland. *Proceedings of the National Academy of Sciences*, in review.
- Götherström A., Vicente M., Pochon Z., Kjellström A., Sager M., **Maier P.**, Runfeldt G., Storå J. The sword man from Janakkala: a genomic analysis of his ancestry. *Fennoscandia Archaeologica*, in review.
- Lee S.R., Ostoja S.M., **Maier P.A.**, Matchett J.R., Knapp R.A., McKenny H., Brooks M.L., Danielle N., Berlow E.L. Distribution and spatiotemporal variation of Yosemite toad populations across Sierra Nevada national parks. *Herpetological Conservation and Biology*, in review.
- Ringbauer H., Wozniak T., Feuchter J., Runfeldt G., Bianco R.A., Zhang G., Prüfer K., Orschiedt J., Simm A., **Maier P.**, Sager M., Dresely V., Krause J., Meller H., Wehner D. Reconstructing their genomes confirms the historically attested genealogy of the two medieval emperors Otto I (the Great) and Heinrich II (Saint Henry). In preparation. <https://doi.org/10.64898/2026.03.18.712637>
- Maier P.A.** Larval development evolution among pure and admixed lineages of *Anaxyrus canorus*. In preparation.
- Shoop R.K., Smith B.P., **Maier P.A.**, Derkarabetian S., Hedin M.C., Bohonak A.J. Phylogenomic methods uncover unexpected relationships in North American subgenus *Micruracrus* (Acari: Hydrachnidiae: Arrenuridae: *Arrenurus*) water mites. In preparation.

SELECTED PRESENTATIONS

- Maier P.A.** (2026). Mitotree: the frontier of mitochondrial DNA research. Genetic Genealogy Research Network, Strathclyde Institute for Genealogical Studies, University of Strathclyde. Sept. 8, 2026. • [Video](#)
- Maier P.A.** (2025). Behind the scenes: Mitotree and Mito Discover, an AMA with the experts (invited panel). Professional Management Conference, Association of Professional Genealogists. Sept. 19, 2025. • [Program](#)

Maier P.A. (2025). Mitochondrial DNA and the Mitotree. Genetic Genealogy Research Network, hosted by the North of Ireland Family History Society with the University of Strathclyde. Sept. 4, 2025. · [Event](#)

Maier P.A., Runfeldt G., Estes R.J., Detsikas J.O., Sager M., Vilar M.G. (2025). Mitotree: the frontier of human phylogenetic research. 42nd Annual Willi Hennig Society Meeting, The Chinese University of Hong Kong, Hong Kong.

Maier P.A. (2025). Mitotree Discover demo: a year of breakthroughs in maternal lineages and historical connections. RootsTech International Conference, Salt Lake City, UT.

Maier P.A. (2024). Ten years of evolutionary research on the Yosemite toad (*Anaxyrus canorus*) (invited talk). Tucson Herpetological Society, Tucson, AZ. · [Video](#)

Maier P.A. (2023). Big Y: march of the ages. 15th International Conference on Genetic Genealogy, Houston, TX. · [Video](#)

Maier P.A. (2023). Beethoven's first DNA test (invited talk). FamilyTreeDNA Town Hall, Houston, TX. · [Video](#)

Maier P.A. (2023). A taste of population genetics: the sampler platter (invited technical talk). Gene by Gene Ltd. Laboratory, Houston, TX. · [Video](#)

Maier P.A., Vandergast A.G., Bohonak A.J. (2023). Ten years of evolutionary research on the Yosemite toad (*Anaxyrus canorus*). Amphibian Population Task Force, Sebastopol, CA. · [Slides](#)

Vandergast A.G., Wood D.A., **Maier P.A.** (2022). Applying genetics to inform the three Rs for conservation of California's herpetofauna. American Society of Ichthyologists and Herpetologists Conference, Spokane, WA.

Maier P.A. (2022). Unraveling your population history with myOrigins 3.0. East Coast Genetic Genealogy Conference, Baltimore, MD. · [Video](#)

Maier P.A., Vilar M.G., Estes R.J. (2022). Mitochondrial DNA Academy. East Coast Genetic Genealogy Conference, Baltimore, MD.

Maier P.A. (2022). Innovator session (invited): the tree of mankind age estimates. RootsTech International Conference, Salt Lake City, UT. · [Video](#)

Maier P.A. (2022). The Million Mito Project: growing the tree of womankind. RootsTech International Conference, Salt Lake City, UT. · [Video](#)

Maier P.A., Vilar M.G., Estes R.J. (2021). Everything you wanted to know about mitochondrial DNA. Genealogical Forum of Oregon, Portland, OR. · [Video](#)

Maier P.A. (2021). Family Finder's myOrigins 3.0 explained, parts 1 to 3 (overview, methodology, interpretation). Product launch and white paper support, Houston, TX. · [Part 1](#) · [Part 2](#) · [Part 3](#)

Maier P.A. (2020). A taste of population genetics: the sampler platter. RootsTech International Conference, Salt Lake City, UT. · [Slides](#)

Maier P.A. (2019). A taste of population genetics: the sampler platter. 14th International Conference on Genetic Genealogy, Houston, TX.

Maier P.A. (2018). Evolutionary past, present, and future of the Yosemite toad (*Anaxyrus canorus*). Exit seminar, San Diego State University, San Diego, CA.

Maier P.A., Vandergast A.G., Ostojia S.M., Aguilar A., Bohonak A.J. (2014). Influences of habitat variation and geography on genomic diversity in the Yosemite toad (invited talk, Special Genomics Session). 21st Annual Wildlife Society Meeting, Pittsburgh, PA.

Additional conference presentations from 2012 to 2017 and four posters available on request or at paulmaierresearch.com.

TEACHING and MENTORING

2017 – 2018 Teaching Associate: Organismal Biology, San Diego State University

2016 – 2017 Invited Guest Lecturer: Population Genetics, San Diego State University. Designed a population genomics workshop for graduate students.

2016 – 2017 Teaching Associate: Herpetology, San Diego State University

2014 – 2016 Teaching Associate: Genetics and Evolution, San Diego State University (two years)

2010 – 2014 Crew Lead, United States Geological Survey

Mentored 12 graduate and 6 undergraduate students. Student evaluations available on request.

AWARDS and HONORS

2017 – 2018 Jordan D. Covin Memorial Scholarship (\$600)

2015 – 2018 ARCS Scholarship (\$7,500 per year, three years)

2014 – 2015 Jordan D. Covin Memorial Scholarship (\$900)

2013 – 2014 Harold and June Grant Memorial Scholarship (\$2,400)
2012 – 2014 USGS Conservation Genetics Assistantship (\$111,100)
2012 – 2013 Eugene Cota-Robles Fellowship (\$53,616, declined)

PROFESSIONAL ACTIVITIES and MEMBERSHIPS

Peer reviewer (2017 to present): Evolution, Heredity, Molecular Ecology, Conservation Genetics, Scientific Reports, Molecular Biology and Evolution, Herpetological Conservation and Biology

Memberships: Society for the Study of Evolution; Society for Molecular Biology and Evolution; Phi Kappa Phi Honor Society

Service: Student job search committees for Quantitative Biology and Genomics faculty searches (chair, 2013 to 2014), San Diego State University; President, SDSU Natural History Club (2016 to 2017); co-organizer, R workshop for graduate students (2015 to 2016)

TRAINING and CERTIFICATIONS

Next Generation Data Analysis with R, Institute for Integrative Genome Biology (2013). Workshop in Conservation Genomics, UCLA La Kretz Center (2013). Genomics Data Analysis Workshop, USGS San Diego Field Station (2013). Spatial Statistics Workshop, USGS Western Ecological Research Center (2012). Private Pilot License, Riverside Flight Academy (2015). Wilderness First Responder, Wilderness Medical Associates (2010, recertified 2013 and 2016).

FIELD RESEARCH EXPERIENCE

Roughly 3,240 hours of field research on Yosemite toads (*Anaxyrus canorus*) across eight seasons between 2006 and 2016, spanning Yosemite and Kings Canyon National Parks and four national forests. Led a census covering 185 of 224 toad meadows (83%) in Yosemite National Park and 30 of 32 (94%) in Kings Canyon National Park. Observed and handled 181 (50 handled) adults, 4,500 (1,224) subadults, 126,000 (3,755) tadpoles, and 41,200 eggs, with no animals killed or harmed. Previously authorized under a 10(a) (1)(A) permit. Field methods include mark-recapture with PIT and VIE tags, Bd swabbing, morphometrics, radio telemetry, and standard survey protocols for amphibians, reptiles, small mammals, birds, fish, insects and plants. Observed or handled 60 amphibian species in the United States and 190 species across Ecuador, Costa Rica, Belize, Dominica and Mexico.

OTHER ACTIVITIES

Private pilot, single engine land (2015 to 2018). Collegiate rower, UC Santa Barbara (2004 to 2008). Distance runner, second place Lake Tahoe Marathon. Wildlife photographer, several first place awards. Percussionist across many genres.

REFERENCES

Göran Runfeldt, Head of R&D, FamilyTreeDNA / Gene by Gene
Andrew Bohonak, Ph.D., Professor of Biology, San Diego State University
Amy Vandergast, Ph.D., Geneticist, USGS Western Ecological Research Center
Steve Ostojka, Ph.D., Director, USDA California Climate Hub
Robert Klinger, Ph.D., Ecologist, USGS Western Ecological Research Center
Contact details available on request.