Jeffrey D. Jensen

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PROFESSIONAL EXPERIENCE

2016-present	**Professor** Arizona State Univ (US), School of Life Sciences Center for Evolution & Medicine, Center for Mechanisms of Evolution
2024	**Sabbatical Fellow** Univ of Oxford (UK), Merton College
2011-2017	**Assistant / Associate Professor** Swiss Federal Institute of Technology (CH), School of Life Sciences
2009-2011	**Assistant Professor** Univ of Massachusetts Medical School (US), Bioinformatics Program
2007-2009	**NSF Biological Informatics Postdoctoral Fellow** UC Berkeley / UC San Diego (US), Dept of Integrative Biology Advisors: Doris Bachtrog, Peter Andolfatto, Rasmus Nielsen
2001	**BRAVO Undergraduate Research Abroad Fellow** Univ of Edinburgh (UK), Institute of Evolutionary Biology Advisor: Brian Charlesworth

EDUCATION

2002-2006	**Ph.D.**	Cornell Univ (US), Molecular Biology & Genetics Advisors: Charles Aquadro, Carlos Bustamante
1998-2002	**B.S./B.A.**	Univ of Arizona (US), Evolutionary Biology / Anthro. Advisor: Michael Nachman

PROFESSIONAL INTERESTS

population genetics, evolutionary genomics

PROFESSIONAL SERVICE

Societies: American Association for the Advancement of Science (AAAS), Genetics Society of America (GSA), Society for the Study of Evolution (SSE), Society for Molecular Biology and Evolution (SMBE)

Review (journal): *Am J Hum Genet, Ann Hum Genet, Arch Virol, Bioinformatics, Biol Rev, BMC Evol Biol, Cell, Cell Genom, Ecol Evol, Evolution, Evol Lett, Front Genet, G3, Genetics, Genet Res, Genet Sel Evol, Genome Biol, Genome Biol Evol, Genome Res, Heredity, J Evol Biol, J Mol Evol, Mol Biol Evol, Mol Ecol, Mol Ecol Res, Nature, Nat Commun, Nat Ecol Evol, Nat Rev Genet, Nucleic Acids Res, Philos Trans R Soc B, Proc R Soc, PNAS, PLoS Biol, PLoS Comput Biol, PLoS Genet, PLoS One, Science, Sci Adv, Sci Rep, J Stat Phys*

Review (funding): Austrian Science Fund, European Research Council, European Science Foundation, French National Research Agency, German Science Foundation, Human Frontier Science Program, Israeli Science Foundation, MacArthur Fellows Program, Polish National Science Centre, Swiss National Science Foundation, UK Biotech & Bio Sci Research Council, UK Natl Environ Research Council, US National Institutes of Health, US National Science Foundation

Editorial:

2016-2023	*Evolution*, Associate Editor
2014-2018	*Journal of Evolutionary Biology*, Board Member
2014-2015	*Molecular Ecology*, Associate Editor
2014-2015	*PLoS Computational Biology*, Guest Editor
2012-2015	*PLoS Genetics*, Guest Editor
2011-2015	*Frontiers*, Associate Editor

Committees:

elected member of ASU's Graduate Faculty Mentor Academy (GFMA) (2022-present)
AZPopGroup organizer (US, 2016-present)
SOLS Research Initiatives (RI) Committee (ASU) (2023-2024)
Faculty Search Committee: Mechanisms of Evolution (ASU) (2018-19)
Faculty Search Committee: Mechanisms of Evolution (ASU) (2017-18)
Research Committee: Center for Evolution & Medicine (ASU) (2016-18)
‘Clinically Relevant Population Genetics’ workshop organizer (US, 2017)
German Science Foundation, Rapid Evolutionary Adaptation Grant Panel (2015-16)
‘Theoretical & Empirical Evidence of Adaptation’ workshop organizer (CH, 2015)
European Society for Evolutionary Biology Conference organizer (CH, 2015)
‘Systems Genetics & Evolution’ workshop organizer (CH, 2015)
Serbian Genetics Society, Scientific Advisor (2015)
Graduate Admissions Committee: Life Sciences (EPFL) (2013-15)
National Academy of Finland, Scientific Advisor (2013)
‘Bridging Theoretical & Experimental Evolution’ workshop organizer (CH, 2013)
Faculty Search Committee: Ecology of Infectious Disease (ETH) (2013-14)

FUNDING & AWARDS

2025-2030	U.S. National Institutes of Health, NIGMS, R35 (renewal) PI: *On differentiating selective and neutral evolutionary processes*
2025	Elected Fellow, American Assoc for the Advancement of Science (AAAS) - in recognition of contributions to the field of population genetics
2021-2025	U.S. National Institutes of Health, NIGMS, R35 PI: *On differentiating selective and neutral evolutionary processes*
2022	Outstanding Postdoctoral Mentor of the Year Award - Awarded annually by ASU in recognition of contributions to mentorship
2019-2024	U.S. National Institutes of Health, NIAID, P01 co-I: *Immunologic and virologic determinants of CMV transmission*
2022-2023	U.S. National Institutes of Health, NIGMS, P30 Consultant: *Surveillance resequencing to detect SARS-CoV-2 variants*
2019-2022	U.S. National Institutes of Health, NIGMS/DMS, R01 PI: *Novel coalescent approaches for the study of virus evolution*
2015-2020	U.S. Department of the Army, DARPA co-I: *Anticipating influenza resistance evolution*
2017-2018	Illumina Innovative Investigators program co-I: *Characterizing HCMV infections in native Bolivian populations*
2015-2018	Swiss National Science Foundation PI: *The population genetics of adaptation* (renewal)
2013-2018	European Research Council, Starting Grant PI: *Theoretical, empirical, & computational tools in evolution*
2012-2015	Swiss National Science Foundation PI: *The population genetics of adaptation*
2012-2015	Swiss National Science Foundation co-I: *Genetic basis of adaptive change in camouflaged deer mice*
2011-2014	DARPA co-I: *Algorithms to limit viral epidemics*
2011	AAAS Newcomb Cleveland Prize - Awarded for Outstanding Paper of the Year in *Science*

2010-2011	U.S. National Science Foundation PI: *The population genetics of adaptation*
2010-2011	Worcester Foundation for Biomedical Research PI: *Method developments: searching for selection*
2006-2008	U.S. National Science Foundation - Biological Informatics Postdoc Fellowship

INVITED LECTURES

2020-present	Cornell (US); U.Pittsburgh (US); Virginia Tech (US); FSU (US); U.Chicago (US); U.Bern (CH); 'Precision Medicine 2.0' symposium (US); OSU (US); U.Edinburgh (UK)
2015-2019	UW-Madison (US); 'Evolutionary Genetics of Infectious Disease' symposium (CA); MidwesternU. (US); Cornell (US); MPI Plant Breeding (DE); U.Arizona (US); U.Montana (US); AZPopGroup (US); ‘Clinically Relevant Population Genetics’ workshop (US); SIB symposium (CH); U.Basel (CH); MPI Human History (DE); Mathematical Evolutionary Biology Conf (FR); EMBO Conf (DE); MPI Plant Breeding (DE); USC (US); ASU (US); SSE Conf (BR); ‘Theoretical & Empirical Evidence of Adaptation’ workshop (CH); U.Zurich (CH); EAWAG (CH); MPI Plant Breeding (DE); LMU-Munich (DE); VetMedUni (AT); IST (AT); PopGenomics workshop (DE)
2010-2014	Systems Genetics & Evolution Conf (CH); U.Arizona (US); Natl Academy of Finland (FI); SMBE Conf (US); IGC (PT); ‘Population Genetic Models' workshop (DE); U.Konstanz (DE); MakerereU. (UG); ‘Landscape Genomics’ workshop (CH); U.Edinburgh (UK); Konrad Lorenz Institute (AT); U.Vienna (AT); Heidelberg Institute for Theoretical Studies (DE); SIB PopGen Summer School (CH); Lausanne Genomics Day (CH); U.Basel (CH); U.Lausanne (CH); ‘Evolutionary Innovations’ workshop (DE); SMBE Conf (JP); ESEB Conf (DE); Harvard (US); Oxford (UK); USC (US); EPFL (CH); U.Idaho (US)
2005-2009	Brandeis (US); ‘Mathematical Challenges from Genetics’ workshop (CA); Neandertal Genome Consortium Conf (US); Neandertal Genome Consortium Conf (HR); Harvard (US); NCSU (US); UNC (US); LMU-Munich (DE); MPI Evolutionary Anthropology (DE); Sanger Institute (UK); ‘Statistical Inference of Selection’ workshop (AT); Cornell (US); J.Monod Conf in Evolutionary Genetics (FR); U.Arizona (US); U.Vienna (AT); U.Maryland (US); UCSD (US); SMBE Conf (ES); U.Chicago (US); SMBE Conf (US)

ADVISING (*with current positions indicated for lab alumni*)

Postdoctoral Scholars

2025-	Gabriella Spatola
2025-	Erangi Heenkenda
2025-	Takahiro Maruki
2022-	John Terbot II
2021-	Vivak Soni
2024-2025	Adriana Calahorra-Oliart (*Research Fellow, INECOL, MX*)
2018-2023	Parul Johri (*Asst Professor, Dept of Genetics, UNC-Chapel Hill, US*)
2019-2021	Susanna Sabin (*Staff Biologist, CDC, US*)
2018-2020	Ana Morales-Arce (*Research Fellow, IZSVe, IT*)
2019-2020	João Santos (*Research Consultant, INSA, PT*)
2019-2020	Matt Jones **(***Hospice Chaplain, US*)
2017-2019	Rebecca Harris (*Senior Manager of Comp Bio, Adaptive Biotech, US*)
2017-2019	Andrew Sackman (*Asst Professor, Virginia Commonwealth Univ, US*)
2015-2017	Sebastian Matuszewski (*Data Engineering Manager, Accenture, AT*)
2014-2017	Stefan Laurent (*Associate Director of Bioinformatics, BioNTech, DE*)
2015-2017	Severine Vuilleumier (*Professor & Vice-Dean, La Source (HES-SO), CH*)
2011-2016	Nicholas Renzette (*Director of Bioinformatics, Essex Management, US*)
2015-2016	Valeria Montano (*Research Scientist, James Hutton Inst (BioSS), UK*)
2013-2015	Greg Ewing (*Test Engineer, Rocket Lab, NZ*)
2012-2015	Claudia Bank (*Professor & Director, Inst Ecol Evol, Univ of Bern, CH*)
2013-2015	Anna Ferrer Admettla (*General Director, Naccari Ravà Foundation, ES*)
2012-2014	Matthieu Foll (*Bioinformatics Group Leader, IARC-WHO, FR*)
2010-2014	Yu-Ping Poh (*Research Scientist, ASU, US*)
2013-2014	Cornelia Pokalyuk (*Professor, Inst of Mathematics, Univ of Lübeck, DE*)
2012-2013	Lisha Mathew (*Bioinformatician, CeGaT, DE*)
2012-2013	Daniel Wegmann (*Professor, Dept of Biology, Univ of Fribourg, CH*)

Graduate Students (Ph.D.)

2013-2018	Mado Kapopoulou (*Bioinformatician, Inst Ecol Evol, Univ of Bern, CH*)
2012-2017	Louise Ormond (*Research Scientist, Univ of Lausanne Hospital, CH*)
2009-2014	Alfred Simkin (*Research Professor, Dept of Pathology, Brown Univ, US*)
2009-2013	Jessica Crisci (*freelance artist, US*)

Graduate Students (M.S.)

2016-2017	Marcel Hildebrandt (*Research Scientist, Siemens, DE*)
2016-2017	Stefano Tartini (*Project Manager, SBB CFF FFS, CH*)
2012-2014	Hyunjin Shim (*Asst Professor, College of Science, Cal State - Fresno, US*)
2011-2013	Priyanka Sinha (*Lead Consultant for Data Science, Capgemeni, NZ*)

Staff Members

2019-2021	Kellen Riall (*PhD student, Univ of Chicago, US*)
2014-2017	Kristen Irwin (*Head of International Funding, EPFL, CH*)
2012-2013	Shivani Mahajan (*Head of Computational Science, Helio Genomics, US)*

Sabbatical & Study Abroad Visitors

2016 Matt Jones (while a PhD Student, Univ of Montana), Study Abroad
2014 Derek Setter (while a PhD Student, Univ of Vienna), Study Abroad
2012 Daniel Bolon (while a Professor, UMass Med School), Sabbatical

Undergraduate Researchers

P. DeSmet, D. Shah, E. Howell, K. Riall, D. Mollet, S. Tartini, A. Dussuet, L. Cêtre, A. Haget, T. Rossy, M. Malier, P. Reiff, G. Thurre, L. Aeberli, C. Finelli, F. Philippe, L. Alter, M. Quinodoz, F. Widmer, R. Küng, D. Virgil, G. Xu, A. Dincer, H. Chen

Ph.D. Thesis Committees

K. Leempoel (Golay Lab, EPFL), P. Helleboid (Trono Lab, EPFL), A. Bittencourt (Fellay Lab, EPFL), P. Refinetti (Morgenthaler Lab, EPFL), S. Waszak (Deplancke Lab, EPFL), A. Massouras (Deplancke Lab, EPFL), B. Zoller (Naef Lab, EPFL), D. Monteil (Wurm Lab, EPFL), N. Srivastava (Fasshauer Lab, Uni Lausanne), R. Hietpas (Bolon Lab, UMassMed), A. Panzierra (Bertorelle Lab, Uni Ferrara), A. Crane (Stone Lab, ASU), G. Bilolikar (Geiler-Samerotte Lab, ASU), A. Howell (Pfeifer Lab, ASU), M. Apata (Wilson Lab, ASU), C. Versoza (Pfeifer Lab, ASU), M. Lin (Lynch Lab, ASU), M. Milhaven (Pfeifer Lab, ASU)

TEACHING

2023-present	*Principles of Human Genetics* BIO 446/546, ASM 446; ASU
2017-2025	*Population Genetics Reading Group* BIO 498/591; ASU
2017-2024	*Research Areas of Evolution*, Guest Lecturer EVO 610; ASU
2018	*Evolution* BIO 345; ASU
2012-2016	*Statistical Population Genetics* BIO 366; EPFL
2013-2015	*A History of Evolutionary Thought* BIO 672; EPFL
2012-2014	*Projects in Genomics & Bioinformatics* BIO 466; EPFL
2010-2011	*Molecular Evolution* BBS 705; UMass Med

PUBLICATIONS

lab members indicated; * authors contributed equally; # co-corresponding authors

Books

Jensen, J.D., Charlesworth, B. (Eds.), 2027. *Population genetic inference: theory and practice*. Elsevier, Amsterdam. (*Forthcoming*)

Pfeifer, S.P., Jensen, J.D. (Eds.), 2027. *Evolutionary genomics of non-human primates*. Elsevier, Amsterdam. (*Forthcoming*)

Articles

in review / revision

157) Soni, V., C. Versoza, J. Terbot, G. Spatola, K. Bales, S.P. Pfeifer#, and J.D. Jensen#. 2026. Inferring patterns of purifying, positive, and balancing selection in the coppery titi monkey (*Plecturocebus cupreus*) utilizing a well-fit evolutionary baseline model. In review.

156) Terbot, J., V. Soni, C. Versoza, K. Bales, S.P. Pfeifer#, J.D. Jensen#. 2026. Inferring the demographic history of coppery titi monkeys (*Plecturocebus cupreus*) from high-quality, whole-genome, population-level data. In review.

155) Soni, V. *, C. Versoza*, J. Terbot, G. Spatola, K. Bales, J.D. Jensen#, S.P. Pfeifer#. 2026. Inferring fine-scale rates of mutation and recombination in the coppery titi monkey (*Plecturocebus cupreus*). In review.

154) Versoza, C., K. Bales, J.D. Jensen, S.P. Pfeifer. 2026. Sex-specific landscapes of crossover and non-crossover recombination in coppery titi monkeys (*Plecturocebus cupreus*). In review.

153) Versoza, C., K. Bales, J.D. Jensen, S.P. Pfeifer. 2026. The landscape of structural variation in coppery titi monkeys (*Plecturocebus cupreus*). In review.

152) Soni, V. *, C. Versoza*, J.D. Jensen#, S.P. Pfeifer#. 2026. Inferring the landscapes of mutation and recombination in the common marmoset (*Callithrix jacchus*) in the presence of twinning and hematopoietic chimerism. In review.

151) Versoza, C., K. Bales, J.D. Jensen, S.P. Pfeifer. 2026. Characterization of *de novo* germline mutations suggests a strong male mutation bias in coppery titi monkeys (*Plecturocebus cupreus*). In revision.

2025

150) Soni, V., S.P. Pfeifer[#], J.D. Jensen[#]. 2025. Recent insights into the evolutionary genomics of the critically endangered aye-aye (*Daubentonia madagascariensis*). *American Journal of Primatology* 87: e70105.

149) Terbot, J., V. Soni, C. Versoza, M. Milhaven, A. Calahorra-Oliart, D. Shah, S.P. Pfeifer[#], J.D. Jensen[#]. 2025. Interpreting patterns of X chromosomal relative to autosomal diversity in aye-ayes (*Daubentonia madagascariensis*). *American Journal of Primatology* 87: e70091.

148) Soni, V., C. Versoza, S.P. Pfeifer[#], J.D. Jensen[#]. 2025. Investigating the effects of chimerism on the inference of selection: quantifying genomic targets of purifying, positive, and balancing selection in common marmosets (*Callithrix jacchus*). *Heredity* 134: 645-657.

147) Terbot, J. [*], A. Calahorra-Oliart[*], C. Versoza[*], D. Shah, V. Soni, S.P. Pfeifer[#], J.D. Jensen[#]. 2025. Re-evaluating the demographic history of, and inferring the fine-scale recombination landscape for, wild Chinese rhesus macaques (*Macaca mulatta*). *American Journal of Primatology* 87: e70088.

146) Soni, V. [*], C. Versoza[*], J. Terbot, J.D. Jensen[#], S.P. Pfeifer[#]. 2025. Inferring fine-scale mutation and recombination rate maps in aye-ayes (*Daubentonia madagascariensis*). *Ecology and Evolution* 15: e72314.

145) Versoza, C., J.D. Jensen, S.P. Pfeifer. 2025. The landscape of structural variation in aye-ayes (*Daubentonia madagascariensis*). *Genome Biology & Evolution* 17: evaf167.

144) Soni, V., C. Versoza, S.P. Pfeifer[#], J.D. Jensen[#]. 2025. Estimating the distribution of fitness effects in aye-ayes (*Daubentonia madagascariensis*), accounting for population history as well as mutation and recombination rate heterogeneity. *American Journal of Primatology* 87: e70058.

143) Soni, V., C. Versoza, E. Vallender, J.D. Jensen[#], S.P. Pfeifer[#]. 2025. Accounting for chimerism in demographic inference: reconstructing the history of common marmosets (*Callithrix jacchus*) from high-quality, whole-genome, population-level data. *Molecular Biology & Evolution* 42: msaf119.

142) Versoza, C. [*], Lloret-Villas, A. [*], J.D. Jensen, S.P. Pfeifer. 2025. A pedigree- based map of crossovers and non-crossovers in aye-ayes (*Daubentonia madagascariensis*). *Genome Biology & Evolution* 17: evaf072.

141) Soni, V., J. Terbot, C. Versoza, S.P. Pfeifer[#], J.D. Jensen[#]. 2025. A whole-genome scan for evidence of recent positive and balancing selection in aye-ayes (*Daubentonia madagascariensis*) utilizing a well-fit evolutionary baseline model. *G3* 15: jkaf078.

140) Soni, V., J.D. Jensen. 2025. Inferring demographic and selective histories from population genomic data using a two-step approach in species with coding-sparse genomes: an application to human data. *G3* 15: jkaf019.

139) Versoza, C., E. Ehmke, J.D. Jensen, S.P. Pfeifer. 2025. Characterizing the rates and patterns of *de novo* germline mutations in the aye-aye (*Daubentonia madagascariensis*). *Molecular Biology & Evolution* 42: msaf034.

138) Terbot, J., V. Soni, C. Versoza, S.P. Pfeifer[#], J.D. Jensen[#]. 2025. Inferring the demographic history of aye-ayes (*Daubentonia madagascariensis*) from high-quality, whole-genome, population-level data. *Genome Biology & Evolution* 17: evae281.

2024

137) Soni, V., J.D. Jensen. 2024. Temporal challenges in detecting balancing selection from population genomic data. *G3* 14: jkae069.

136) Soni, V., J. Terbot, J.D. Jensen. 2024. Population genetic considerations regarding the interpretation of within-patient SARS-CoV-2 polymorphism data. *Nature Communications* 15: 3240.

135) Soni, V., S.P. Pfeifer, J.D. Jensen. 2024. The effects of mutation and recombination rate heterogeneity on the inference of demography and the distribution of fitness effects. *Genome Biology & Evolution* 16: evae004.

134) Versoza, C., S. Weiss, R. Johal, B. La Rosa, J.D. Jensen, S.P. Pfeifer. 2024. Novel insights into the landscape of crossover and non-crossover events in rhesus macaques. *Genome Biology & Evolution* 16: evad223.

133) Charlesworth, B., J.D. Jensen. 2024. Population genetics. *Encyclopedia of Biodiversity, 3rd ed.* Elsevier Ltd. Vol. 7: 467-483.

2023

132) Terbot, J., B. Cooper, J. Good, J.D. Jensen. 2023. A simulation framework for modeling the within-patient evolutionary dynamics of SARS-CoV-2. *Genome Biology & Evolution* 15: evad204.

131) Moström, M., S. Yu, D. Tran, F. Saccoccio, C. Versoza, D. Malouli, A. Mirza, S. Valencia, M. Gilbert, R. Blair, S. Hansen, P. Barry, K. Fruh, J.D. Jensen, S.P. Pfeifer, T. Kowalik, S. Permar, A. Kaur. 2023. Protective effect of pre-existing natural immunity in a nonhuman primate reinfection model of congenital cytomegalovirus infection. *PLoS Pathogens* 19: e1011646.

130) Soni, V., P. Johri, J.D. Jensen. 2023. Evaluating power to detect recurrent selective sweeps under increasingly realistic evolutionary null models. *Evolution* 77: 2113-2127.

129) Johri, P., S.P. Pfeifer, J.D. Jensen. 2023. Developing an evolutionary baseline model for humans: jointly inferring purifying selection with population history. *Molecular Biology & Evolution* 40: msad100.

128) Howell, A.A., J. Terbot, V. Soni, P. Johri, J.D. Jensen, S.P. Pfeifer. 2023. Developing an appropriate evolutionary baseline model for the study of human cytomegalovirus. *Genome Biology & Evolution* 15: evad059.

127) Terbot, J., P. Johri, S. Liphardt, V. Soni, S.P. Pfeifer, B.S. Cooper[#], J.M. Good[#], J.D. Jensen[#]. 2023. Developing an appropriate evolutionary baseline model for the study of SARS-CoV-2 patient samples. *PLoS Pathogens* 19: e1011265.

126) Freund, F., E. Kerdoncuff, S. Matuszewski, M. Lapierre, M. Hildebrandt, J.D. Jensen, L. Ferretti, A. Lambert, T. Sackton, G. Achaz. 2023. Interpreting the pervasive observation of U-shaped site frequency spectra. *PLoS Genetics* 19: e1010677.

125) Ghafoor, S., J. Santos, C.J. Versoza, J.D. Jensen, S.P. Pfeifer. 2023. The impact of sample size and population history on observed mutational spectra: a case study in human and chimpanzee populations. *Genome Biology & Evolution* 15: evad019.

124) Charlesworth, B., J.D. Jensen. 2023. Population genetic considerations regarding evidence of biased mutation rates in *Arabidopsis thaliana*. *Molecular Biology & Evolution* 40: msac275.

123) Jensen, J.D. 2023. Population genetic concerns related to the interpretation of empirical outliers and the neglect of common evolutionary processes. *Heredity* 130: 109-110.

2022

122) Charlesworth, B., J.D. Jensen. 2022. Some complexities in interpreting apparent effects of hitchhiking: a commentary on Gompert *et al.* 2022. *Molecular Ecology* 31: 4440-4443.

121) Hager, E.R., O. Harringmeyer, T.B. Wooldridge, S. Theingi, J. Gable, S. McFadden, B. Neugeboren, K. Turner, J.D. Jensen, H.E. Hoekstra. 2022. A chromosomal inversion contributes to divergence in multiple traits between deer mouse ecotypes. *Science* 377: 399-405.

120) Charlesworth, B., J.D. Jensen. 2022. How can we resolve Lewontin's paradox? *Genome Biology & Evolution* 14(7): evac096.

119) Johri, P., A. Eyre-Walker, R. Gutenkunst, K. Lohmueller, J.D. Jensen. 2022. On the prospect of achieving accurate joint estimation of selection with population history. *Genome Biology & Evolution* 14(7): evac088.

118) Johri, P., C.F. Aquadro, M. Beaumont, B. Charlesworth, L. Excoffier, A. Eyre-Walker, P. Keightley, M. Lynch, G. McVean, B.A. Payseur, S.P. Pfeifer, W. Stephan, J.D. Jensen. 2022. Recommendations for improving statistical inference in population genomics. *PLoS Biology* 20(5): e3001669.

117) Sabin, S., A. Morales-Arce, S.P. Pfeifer, J.D. Jensen. 2022. The impact of frequently neglected model violations on bacterial recombination rate estimation: a case study in *Mycobacterium canettii* and *Mycobacterium tuberculosis*. *G3* 12(5): jkac055.

116) Jiang, L., N. Samant, P. Liu, M. Somasundaran, J.D. Jensen, W. Marasco, C. Schiffer, R. Finberg, J. Wang, T.F. Kowalik, D.N. Bolon. 2022. Identification of a permissive secondary mutation that restores the enzymatic activity of oseltamivir resistance mutation H275Y. *Journal of Virology* 96: e0198221.

115) Morales-Arce, A.*, P. Johri*, J.D. Jensen. 2022. Inferring the distribution of fitness effects in patient-sampled and experimental virus populations: two case studies. *Heredity* 128: 79-87.

114) Johri, P., W. Stephan, J.D. Jensen. 2022. Soft selective sweeps: addressing new definitions, evaluating competing models, and interpreting empirical outliers. *PLoS Genetics* 18(2): e1010022.

2021

113) Johri, P. *, B. Charlesworth*, E. Howell, M. Lynch, J.D. Jensen. 2021. Revisiting the notion of deleterious sweeps. *Genetics* 219: iyab094.

112) Charlesworth, B., J.D. Jensen. 2021. Effects of selection at linked sites on patterns of genetic variability. *Annual Review of Ecology, Evolution, and Systematics* 52: 177-197.

111) Johri, P., K. Riall, H. Becher, L. Excoffier, B. Charlesworth, J.D. Jensen. 2021. The impact of purifying and background selection on the inference of population history: problems and prospects. *Molecular Biology & Evolution* 38: 2986-3003.

110) Wang, H.-Y., S. Valencia, S.P. Pfeifer, J.D. Jensen, T.F. Kowalik, S.R. Permar. 2021. Common polymorphisms in the glycoproteins of human cytomegalovirus and associated strain-specific immunity. *Viruses* 13: 1106.

109) Jensen, J.D. 2021. Studying population genetic processes in viruses: from drug-resistance evolution to patient infection dynamics. In the *Encyclopedia of Virology, 4th ed.* Elsevier Ltd., Vol. 5: pgs. 227-232.

108) Clemente, F., M. Unterlander, O. Dolgova, C. Amorim, F. Coroado-Santos, S. Neunschwander, E. Ganiatsou, D. Cruz Davalos, L. Anchieri, F. Michaud, L. Winkelbach, J. Blocher, Y. Cardenas, B. Sousa de Mota, E. Kalliga, A. Souleles, I. Kontopoulos, G. Karamitrou-Mendessidi, O. Philaniotou, A. Sampson, D. Theodorou, M. Tsipopoulou, I. Akamatis, P. Halstead, K. Kotsakis, D. Urem-Kotsou, D. Panagiotopoulous, C. Ziota, S. Triantaphyllou, O. Delaneau, J.D. Jensen, J. Moreno-Mayar, J. Burger, V.C. Sousa, O. Lao, A-S. Malaspinas, C. Papageorgopoulou. 2021. The genomic history of the Aegean palatial civilizations. *Cell* 184: 2565-2586.

107) Morales-Arce, A, S. Sabin, A. Stone, J.D. Jensen. 2021. Recent insights in to the population genomics of within-host tuberculosis. *Heredity* 126: 1-9.

2020

106) Jensen, J.D., R.A. Stikeleather, T.F. Kowalik, M. Lynch. 2020. Imposed mutational meltdown as an antiviral strategy. *Evolution* 74: 2549-59.

105) Jones, M., L.S. Mills, J.D. Jensen, J.M. Good. 2020. Convergent evolution of seasonal camouflage in response to reduced snow cover across the snowshoe hare range. *Evolution* 74: 2033-45.

104) Jones, M., L.S. Mills, J.D. Jensen, J.M. Good. 2020. The origin and spread of locally adaptive seasonal camouflage in snowshoe hares. *The American Naturalist* 196: 316-32.

103) Harris, R., J.D. Jensen. 2020. Considering genomic scans for selection as coalescent model choice. *Genome Biology & Evolution* 12: 871-877.

102) Morales-Arce, A.Y., R. Harris, A.C. Stone, J.D. Jensen. 2020. Evaluating the contributions of purifying selection and progeny-skew in dictating within-host *Mycobacterium tuberculosis* evolution. *Evolution* 74: 992-1001.

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