

Review (journal): *American Journal of Human Genetics, Annals of Human Genetics, Archives of Virology, Bioinformatics, BMC Evolutionary Biology, Evolution, Evolution Letters, Frontiers in Genetics, G3, Genetics, Genetics Research, Genetics Selection Evolution, Genome Biology, Genome Biology & Evolution, Genome Research, Heredity, Journal of Evolutionary Biology, Journal of Molecular Evolution, Molecular Biology & Evolution, Molecular Ecology, Molecular Ecology Resources, Nature, Nature Communications, Nature Ecology & Evolution, Nature Reviews Genetics, Nucleic Acids Research, Philosophical Transactions of the Royal Society B, Proceedings of the Royal Society, PNAS, PLoS Biology, PLoS Computational Biology, PLoS Genetics, PLoS One, Science, Science Advances, Scientific Reports, Statistical Physics*

Committees:

Search:

Faculty Search Committee: Mechanisms of Evolution (ASU) (2018-19)
Faculty Search Committee: Mechanisms of Evolution (ASU) (2017-18)
Faculty Search Committee: Ecology of Infectious Disease (ETH) (2013-14)
Faculty Search Committee: Integrative Biology (UMass Med School) (2010-11)

Advisory:

Research Committee: Center for Evolution & Medicine (ASU) (2016-2018)
Graduate Admissions Committee: Life Sciences (EPFL) (2013-2015)
German Science Foundation, Rapid Evolutionary Adaptation Grant Panel (2015-16)
Serbian Genetics Society, Scientific Advisor (2015)
National Academy of Finland, Scientific Advisor (2013)

Organizing:

Arizona PopGroup (USA, 2016-present)
'Clinically Relevant Population Genetics' workshop (USA, 2017)
'Theoretical & Empirical Evidence of Adaptation' workshop (Switzerland, 2015)
European Society for Evolutionary Biology Conference (Switzerland 2015)
'Systems Genetics & Evolution' workshop (Switzerland, 2015)
'Bridging Theoretical & Experimental Evolution' workshop (Switzerland, 2013)

Thesis:

Kevin Leempoel (Golay Lab, EPFL), Pierre-Yves Helleboid (Trono Lab, EPFL), Ana Bittencourt (Fellay Lab, EPFL), Pedro Refinetti (Morgenthaler Lab, EPFL), Sebastian Waszak (Deplancke Lab, EPFL), Andreas Massouras (Deplancke Lab, EPFL), Benjamin Zoller (Naef Lab, EPFL), Dominique Monteil (Wurm Lab, EPFL), Niecee Srivastava (Fasshauer Lab, Uni Lausanne), Ryan Hietpas (Bolon Lab, UMass Med), Alex Panzierra (Bertorelle Lab, Uni Ferrara), Adele Crane (Stone Lab, ASU), Mario Apata (Wilson Lab, ASU), Gaurav Bilolikar (Geiler-Samerotte Lab, ASU), Cyril Versoza (Pfeifer Lab, ASU), Man Lin (Lynch Lab, ASU), Mark Milhaven (Pfeifer Lab, ASU)

TEACHING

F/S, 2017 - current	<i>Population Genetics Reading Group (BIO 498/591), ASU</i>
F, 2017 - 2020	<i>Research Areas of Evolution (EVO 610), Guest Lecturer, ASU</i>
S, 2018	<i>Evolution (BIO 345), ASU</i>
S, 2012-2016	<i>Statistical Population Genetics (BIO 366), EPFL</i>
F, 2014-2015	<i>Scientific Literature Analysis (BIO 371), EPFL</i>
S, 2014-2015	<i>A History of Evolutionary Thought (BIO 672), EPFL</i>
F, 2012-2014	<i>Projects in Genomics & Bioinformatics (BIO 466), EPFL</i>
F, 2010-2011	<i>Population Genetics Journal Club (BBS 741), UMass Med</i>
F, 2010-2011	<i>Molecular Evolution (BBS 705), UMass Med</i>

ADVISING

Postdoctoral	2021 -	Vivak Soni
	2018 -	Parul Johri
	2019 - 2021	Susanna Sabin (<i>Government (CDC), USA</i>)
	2018 - 2020	Ana Morales-Arce (<i>Postdoc, Uni Berne</i>)
	2019 - 2020	João Santos (<i>Industry, Portugal</i>)
	2019 - 2020	Matt Jones (<i>Government (USGS), USA</i>)
	2017 - 2019	Rebecca Harris (<i>Industry, USA</i>)
	2017 - 2019	Andrew Sackman (<i>Faculty, Washington & Lee</i>)
	2015 - 2017	Sebastian Matuszewski (<i>Industry, Austria</i>)
	2014 - 2017	Stefan Laurent (<i>Faculty, Max Planck-Koln</i>)
	2015 - 2017	Severine Vuilleumier (<i>Faculty, HES-SO</i>)
	2011 - 2016	Nicholas Renzette (<i>Industry, USA</i>)
	2015 - 2016	Valeria Montano (<i>Postdoc, Uni St. Andrews</i>)
	2013 - 2015	Greg Ewing (<i>Industry, New Zealand</i>)
	2012 - 2015	Claudia Bank (<i>Faculty, Uni Berne</i>)
	2013 - 2015	Anna Ferrer Admettla (<i>Industry, Spain</i>)
	2012 - 2014	Matthieu Foll (<i>Faculty, WHO-Lyon</i>)
	2010 - 2014	Yu-Ping Poh (<i>Industry, USA</i>)
	2013 - 2014	Cornelia Pokalyuk (<i>Faculty, Uni Magdeburg</i>)
	2012 - 2013	Lisha Mathew (<i>Industry, Germany</i>)
	2012 - 2013	Daniel Wegmann (<i>Faculty, Uni Fribourg</i>)
Graduate (Ph.D.)	2013 - 2018	Mado Kapopoulou (<i>Bioinformatician, Uni Berne</i>)
	2012 - 2017	Louise Ormond (<i>Postdoc, UCL</i>)
	2009 - 2014	Alfred Simkin (<i>Faculty, UMass Medical School</i>)
	2009 - 2013	Jessica Crisci (<i>Industry, USA</i>)
Graduate (M.S.)	2016 - 2017	Marcel Hildebrandt (<i>Industry, Germany</i>)
	2016 - 2017	Stefano Tartini (<i>Industry, Switzerland</i>)
	2012 - 2014	Hyunjin Shim (<i>Postdoc, UC Berkeley</i>)
	2011 - 2013	Priyanka Sinha (<i>Postdoc, Otago Univ</i>)

Staff 2019 - 2021	Kellen Riall (<i>PhD student, Univ. of Chicago</i>)
2014 - 2017	Kristen Irwin (<i>Grants Administration, EPFL</i>)
2012 - 2013	Shivani Mahajan (<i>Industry, USA</i>)

Bachelor Projects:

UMass (2009-11): Aslihan Dincer, Daniel Virgil, Guang Xu
EPFL (2011-17): Luc Aeberli, Laurent Alter, Laure Cetre, Edouard Deckersberg, Anna Dussuet, Philippe Fabrice, Christopher Finelli, Anais Haget, Roger Kung, Marie Malier, Dariush Mollet, Mathieu Quinodoz, Pauline Reiff, Tamara Rossy, Stefano Tartini, Gaelle Thurre, Florian Widmer
ASU (2017-current): Kellen Riall, Emma Howell, Andrew Hopkins

Sabbatical & Study Abroad Visitors

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

FUNDING & AWARDS

2021-2026 U.S. National Institutes of Health, NIGMS, R35
'Established Investigator MIRA'
PI
On differentiating selective and neutral evolutionary processes

2019-2024 U.S. National Institutes of Health, NIAID, P01
co-I (with: S. Permar, T. Kowalik, A. Kaur, P. Barry, S. Pfeifer)
Immunologic and virologic determinants of CMV transmission

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 (with: R. Finberg, C. Schiffer, D. Bolon, T. Kowalik, J. Wang)
Anticipating influenza resistance evolution

2017-2018 Illumina Innovative Investigators program
co-I (with: T. Kowalik, S. Pfeifer, B. Trumble)
Characterizing HCMV infections in native Bolivian populations

2017-2018 Center for Evolution & Medicine, Venture Fund
co-I (with: S. Pfeifer, B. Trumble)
The evolutionary history of HCMV in native Americans

- 2015-2018 Swiss National Science Foundation
PI
The population genetics of adaptation (renewal)
- 2013-2018 European Research Council
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 (with: H. Hoekstra, L. Excoffier)
Genetic basis of adaptive change in camouflaged deer mice
- 2011-2014 DARPA
co-I (with: R. Finberg, J. Wang, T. Kowalik, D. Bolon, C. Schiffer)
Algorithms to limit viral epidemics
- 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
Identifying cis-acting binding sites for dosage compensation

INVITED LECTURES

- 2021 University of Berne (Switzerland)
- 2020 Ohio State University (USA); University of Edinburgh (UK)
- 2019 University of Wisconsin - Madison (USA); 'Evolutionary Genetics of Infectious Disease' symposium (Canada); Midwestern University, College of Veterinary Medicine (USA)
- 2018 Cornell University (USA); Max Planck Institute for Plant Breeding Research (Germany)

- 2017 University of Arizona, Quantitative Biology Colloquium (USA); University of Montana (USA); Arizona PopGroup (USA); ‘Clinically Relevant Population Genetics’ workshop (USA)
- 2016 Swiss Institute of Bioinformatics Symposium (Switzerland); University of Basel (Switzerland); Max Planck Institute for the Science of Human History (Germany); Mathematical and Computational Evolutionary Biology Conference (France); EMBO Conference (Germany); Max Planck Institute for Plant Breeding Research (Germany)
- 2015 University of Southern California (USA); Arizona State University (USA); Society for the Study of Evolution Conference (Brazil); ‘Theoretical & Empirical Evidence of Adaptation’ workshop (Switzerland); Univ of Zurich Next Generation Sequencing Retreat (Switzerland); Swiss Federal Institute of Aquatic Sciences (Switzerland); Max Planck Institute for Plant Breeding Research (Germany); University of Munich (Germany); University of Veterinary Medicine (Austria); Institute of Science & Technology (Austria); ‘Population Genomics: the Footprint of Wolfgang Stephan’ workshop (Germany)
- 2014 Systems Genetics & Evolution Conference (Switzerland); University of Arizona (USA)
- 2013 National Academy of Finland (Finland); Society for Molecular Biology & Evolution Conference (USA); Instituto Gulbenkian Ciencia (Portugal); ‘Population Genetics Models Including Selection’ workshop (Germany); University of Konstanz (Germany); Makerere University (Uganda)
- 2012 ‘Landscape Genomics’ workshop (Switzerland); University of Edinburgh (UK); Konrad Lorenz Institute for Evolution & Cognition Research (Austria); University of Vienna (Austria); Heidelberg Institute for Theoretical Studies (Germany); SIB Population Genetics Summer School (Switzerland); Lausanne Genomics Day (Switzerland); University of Basel (Switzerland); University of Lausanne (Switzerland)
- 2011 ‘Evolutionary Innovations’ workshop (Germany); Society for Molecular Biology & Evolution Conference (Japan); European Society for Evolutionary Biology Conference (Germany); Harvard University (USA); Oxford University (UK); University of Southern California (USA); Swiss Federal Institute of Technology (Switzerland); University of Idaho (USA)
- 2010 Brandeis University (USA)
- 2009 ‘Mathematical Challenges from Genetics’ workshop (Canada); Neandertal Genome Consortium Conference (USA); Neandertal Genome Consortium Conference (Croatia)

- 2008 Harvard University (USA); NC State University (USA); University of North Carolina (USA); University of Munich (Germany); Max Planck Institute for Evolutionary Anthropology (Germany); Sanger Institute (UK)
- 2007 ‘Statistical Inference of Selection’ workshop (Austria); Cornell University Probability Symposium (USA); Monod Conference in Evolutionary Genetics (France); University of Arizona (USA)
- 2006 University of Vienna (Austria); University of Maryland (USA); University of California, San Diego (USA); Society for Molecular Biology & Evolution Conference (Spain); University of Chicago (USA)
- 2005 Society for Molecular Biology & Evolution Conference (USA)

PUBLICATIONS

(lab members indicated)

2021

- 117) Morales-Arce, A.*, P. Johri*, and J.D. Jensen. 2021. Inferring the distribution of fitness effects in patient-sampled and experimental virus populations: two case studies. In review.
* authors contributed equally
- 116) Wang, H.-Y., S. Valencia, S.P. Pfeifer, J.D. Jensen, T.F. Kowalik, and S.R. Permar. 2021. Common polymorphisms in the glycoproteins of human cytomegalovirus and associated strain-specific immunity. In review.
- 115) Jiang, L., N. Samant, M. Somasundaran, J.D. Jensen, T.F. Kowalik, W. Marasco, C. Schiffer, R. Finberg, J. Wang, and D.N. Bolon. 2021. Identification of a permissive secondary mutation that restores the enzymatic activity of oseltamivir resistance mutation H275Y. In revision.
- 114) Hager, E.R., O. Harringmeyer, T.B. Wooldridge, S. Theingi, J. Gable, S. McFadden, B. Neugeboren, K. Turner, J.D. Jensen, and H.E. Hoekstra. 2021. A chromosomal inversion drives evolution of multiple adaptive traits in deer mice. In revision.
- 113) Johri, P.*, B. Charlesworth*, E. Howell, M. Lynch, and J.D. Jensen. 2021. Revisiting the notion of deleterious sweeps. In revision.
* authors contributed equally
- 112) Charlesworth, B., and J.D. Jensen. 2021. Population genetics. Forthcoming in the *Encyclopedia of Biodiversity*, 3rd ed. Elsevier Ltd.

- 111) Charlesworth, B., and J.D. Jensen. 2021. The effects of selection at linked sites on patterns of genetic variability. In press, *Annual Review of Ecology, Evolution, and Systematics*.
- 110) Johri, P., K. Riall, H. Becher, L. Excoffier, B. Charlesworth, and J.D. Jensen. 2021. The impact of purifying and background selection on the inference of population history: problems and prospects. In press, *Molecular Biology & Evolution*.
- 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. (in press).
- 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, and C. Papageorgopoulou. 2021. The genomic history of the Aegean palatial civilizations. In press, *Cell*.
- 107) Morales-Arce, A., S. Sabin, A. Stone, and 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, and M. Lynch. 2020. Imposed mutational meltdown as an antiviral strategy. *Evolution* 74: 2549-59.
- 105) Jones, M., L.S. Mills, J.D. Jensen, and 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, and 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. and 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, and J.D. Jensen. 2020. Evaluating the contributions of purifying selection and progeny-skew in dictating within-host *Mycobacterium tuberculosis* evolution. *Evolution* 74: 992-1001.

- 101) Johri, P., B. Charlesworth, and J.D. Jensen. 2020. Towards an evolutionarily appropriate null model: jointly inferring demography and purifying selection. *Genetics* 215: 173-92.
- 100) Jensen, J.D., and M. Lynch. 2020. Considering mutational meltdown as a potential SARS-CoV-2 treatment strategy. *Heredity* 124: 619-20.
- 99) Harris, R., K. Irwin, M. Jones, S. Laurent, R. Barrett, M. Nachman, J. Good, C. Linnen, J.D. Jensen, and S.P. Pfeifer. 2020. The population genetics of crypsis in vertebrates: recent insights from mice, hares, and lizards. *Heredity* 124: 1-14.
- 98) Jensen, J.D., and T.F. Kowalik. 2020. A consideration of within-host human cytomegalovirus (HCMV) genetic diversity. *PNAS* 117: 816-7.

2019

- 97) Sackman, A., R. Harris, and J.D. Jensen. 2019. Inferring demography and selection in organisms characterized by skewed offspring distributions. *Genetics* 211: 1019-28.
- 96) Barrett, R. *, S. Laurent*, R. Mallorino*, S.P. Pfeifer, C. Xu, M. Foll, K. Wakamatsu, J. Duke-Cohan, J.D. Jensen, and H.E. Hoekstra. 2019. Linking a mutation to survival in wild mice. *Science* 363: 499-504.
* authors contributed equally
- 95) Jensen, J.D., B. Payseur, W. Stephan, C. Aquadro, M. Lynch, D. Charlesworth, and B. Charlesworth. 2019. The importance of the Neutral Theory in 1968 and 50 years on: a reply to Kern & Hahn 2018. *Evolution* 73: 111-14.
- 94) Prachanronarong, K., A.S. Canale, P. Liu, M. Somasundaran, S. Hou, Y.-P. Poh, T. Han, Q. Zhu, N. Renzette, K. Zeldovich, T.F. Kowalik, N. Kurt-Yilmaz, J.D. Jensen, D.N. Bolon, W.A. Marasco, R.W. Finberg, C.A. Schiffer, and J.P. Wang. 2019. Mutations in influenza A virus neuraminidase and hemagglutinin confer resistance against a broadly neutralizing hemagglutinin stem antibody. *Journal of Virology* 93(2): e01639.

2018

- 93) Harris, R. *, A. Sackman*, and J.D. Jensen. 2018. On the unfounded enthusiasm for soft selective sweeps II: examining recent evidence from humans, flies and viruses. *PLoS Genetics* 14(12): e1007859.
* authors contributed equally
- 92) Fragata, I. *, S. Matuszewski*, M. Schmitz, T. Bataillon, J.D. Jensen, and C. Bank. 2018. The fitness landscape of the codon table across environments. *Heredity* 121: 422-37.
* authors contributed equally

- 91) Kapopoulou, A., S.P. Pfeifer, J.D. Jensen, and S. Laurent. 2018. The demographic history of African *Drosophila melanogaster*. *Genome Biology & Evolution* 10(9): 2338-42.
- 90) Jones, M.R., L. S. Mills, P.C. Alves, C.M. Callahan, J. Alves, D.J.R. Lafferty, F.M. Jiggins, J.D. Jensen, J. Melo-Ferreira, and J.M. Good. 2018. Adaptive introgression underlies polymorphic seasonal camouflage in Snowshoe Hares. *Science* 360(6395): 1355-58.
- 89) Canale, A., S. Venev, T. Whitfield, D. Caffrey, W. Marasco, C. Schiffer, T. Kowalik, J.D. Jensen, R. Finberg, K. Zeldovich, J. Wang, and D. Bolon. 2018. Synonymous mutations at the beginning of the influenza A virus hemagglutinin gene impact experimental fitness. *Journal of Molecular Biology* 430: 1098-1115.
- 88) Pfeifer, S.^{*}, S. Laurent^{*}, V. Sousa^{*}, C. Linnen^{*}, M. Foll, L. Excoffier[#], H.E. Hoekstra[#], and J.D. Jensen[#]. 2018. The evolutionary history of Nebraska deer mice: local adaptation in the face of strong gene flow. *Molecular Biology & Evolution* 35: 792-806.
^{*} authors contributed equally; [#] co-corresponding authors
- 87) Sackman, A.M., S.P. Pfeifer, T.F. Kowalik, and J.D. Jensen. 2018. On the demographic and selective forces shaping patterns of human cytomegalovirus variation within hosts. *Pathogens* 7: 16.
- 86) Matuszewski, M., M. Hildebrandt, G. Achaz, and J.D. Jensen. 2018. Coalescent processes with skewed offspring distributions and non-equilibrium demography. *Genetics* 208: 323-38.
- 2017**
- 85) Avnir, Y., K. Prachanronarong, Z. Zhang, S. Hou, E. Peterson, J. Sui, H. Zayed, V. Kurella, A. McGuire, L. Stamatatos, B. Hilbert, M. Bohn, K. Zeldovich, T. Kowalik, J.D. Jensen, D. Bolon, R. Finberg, J. Wang, R. Jefferis, Q. Zhu, N. Yilmaz, C. Schiffer, and W. Marasco. 2017. Structural determination of the broadly reactive anti-IGHV1-69 anti-idiotypic antibody G6 and its idiotope. *Cell Reports* 21: 3243-3255.
- 84) Carratala, A., H. Shim, Q. Zhong, V. Bachmann, J.D. Jensen, and T. Kohn. 2017. Experimental adaptation of human echovirus 11 to ultraviolet radiation leads to resistance to disinfection and ribavirin. *Virus Evolution* 3(2): 1-11.

- 83) Crawford, N., D. Kelley, M. Hansen, M.H. Beltrame, S. Fan, S.L. Bowman, E. Jewett, A. Ranciaro, S. Thompson, Y. Lo, S.P. Pfeifer, J.D. Jensen, M. Campbell, W. Beggs, E. Hormozdiari, S.W. Mpoloka, G. Mokone, T. Nyambo, D. Meskel, G. Belay, J. Haut, NISC Comparative Sequencing Program, H. Rothschild, L. Zon, Y. Zhou, M. Kovacs, M. Xu, T. Zhang, K. Bishop, J. Sinclair, C. Rivas, E. Elliot, J. Choi, S. Li, B. Hicks, S. Burgess, C. Abnet, D. Watkins-Chow, E. Oceana, Y. Song, E. Eskin, K.M. Brown, M.S. Marks, S.K. Loftus, W.J. Pavan, M. Yeager, S. Chancock, and S. Tishkoff. 2017. Loci associated with skin pigmentation identified in African populations. *Science* 358(6365).
- 82) Ma, L., J.I. Boucher, J. Paulsen, S. Matuszewski, C.A. Eide, J. Ou, G. Eickelberg, R.D. Press, L.J. Zhu, B.J. Druker, S. Branford, S.A. Wolfe, J.D. Jensen, C.A. Schiffer, M.R. Green, and D.N. Bolon. 2017. CRISPR-Cas9 mediated saturated mutagenesis screen predicts clinical drug resistance with improved accuracy. *PNAS* 114: 11751-56.
- 81) Zhong, Q., A. Carratala, H. Shim, V. Bachmann, J.D. Jensen, and T. Kohn. 2017. Resistance of echovirus 11 to ClO₂ is associated with enhanced host receptor use, altered entry routes and high fitness. *Environmental Science & Technology* 51: 10746-55.
- 80) Ormond, L., P. Liu, S. Matuszewski, N. Renzette, C. Bank, K. Zeldovich, D.N. Bolon, T.F. Kowalik, R.W. Finberg, J.D. Jensen[#], and J.P. Wang[#]. 2017. The combined effect of oseltamivir and favipiravir on influenza A virus evolution. *Genome Biology & Evolution* 9: 1913-24.
[#] co-corresponding authors
- 79) Pokalyuk, C., N. Renzette, K. Irwin, S. Pfeifer, L. Gibson, W.J. Britt, A.Y. Yamamoto, M.M. Mussi-Pinhata, T.F. Kowalik[#], and J.D. Jensen[#]. 2017. Characterizing human cytomegalovirus reinfection in congenitally infected infants: an evolutionary perspective. *Molecular Ecology* 26: 1980-90.
[#] co-corresponding authors
- 78) Matuszewski, S., L. Ormond, C. Bank, and J.D. Jensen. 2017. Two sides of the same coin: a population genetics perspective on lethal mutagenesis and mutational meltdown. *Virus Evolution* 3(1): 1-5.
- 77) Renzette, N., S.P. Pfeifer, S. Matuszewski, T.F. Kowalik, and J.D. Jensen. 2017. On the analysis of intra-host and inter-host viral populations: human cytomegalovirus as a case study of pitfalls and expectations. *Journal of Virology* 91(5): e01976-16.

2016

- 76) Bank, C. *, S. Matuszewski*, R.T. Hietpas, and J.D. Jensen. 2016. On the (un)predictability of a large intragenic fitness landscape. *PNAS* 113(49): 14085-90.
* authors contributed equally
- 75) Prachanronarong, K, A. Ozen, K. Thayer, S. Yilmaz, K. Zeldovich, D. Bolon, T. Kowalik, J.D. Jensen, R. Finberg, J. Wang, N. Kurt-Yilmaz, and C. Schiffer. 2016. Molecular basis for differential patterns of drug resistance in influenza N1 and N2 neuraminidase. *Journal of Chemical Theory & Computation* 12: 6098-6108.
- 74) Irwin, K.K., S. Laurent, S. Matuszewski, S. Vuilleumier, L. Ormond, H. Shim, C. Bank, and J.D. Jensen. 2016. On the importance of skewed offspring distributions and background selection in virus population genetics. *Heredity* 117: 393-99
- 73) Pfeifer, S.P., and J.D. Jensen. 2016. The impact of linked selection in chimpanzees: a comparative study. *Genome Biology & Evolution* 8: 3202-8.
- 72) Bank, C., N. Renzette, P. Liu, S. Matuszewski, H. Shim, M. Foll, D.N. Bolon, T.F. Kowalik, R.W. Finberg, J.P. Wang, and J.D. Jensen. 2016. An experimental evaluation of drug-induced mutational meltdown as an antiviral treatment strategy. *Evolution* 70: 2470-84.
- 71) Matuszewski, S., M.E. Hildebrandt, A. Ghenu, J.D. Jensen, and C. Bank. 2016. A statistical guide to the design of deep mutational scanning experiments. *Genetics* 204: 77-87.
- 70) Irwin, K.K., N. Renzette, T.F. Kowalik, and J.D. Jensen. 2016. Antiviral drug resistance as an adaptive process. *Virus Evolution* 2(1): 1-10.
- 69) Ferrer-Admetlla, A., C. Leuenberger, J.D. Jensen, and D. Wegmann. 2016. An approximate Markov model for the Wright-Fisher diffusion and its application to time series data. *Genetics* 203:831-46.
- 68) Shim, H., S. Laurent, S. Matuszewski, M. Foll, and J.D. Jensen. 2016. Detecting and quantifying changing selection intensities from time-sampled polymorphism data. *G3: Genes, Genomes, Genetics* 6: 893-904.
- 67) Jiang, L., P. Liu, C. Bank, N. Renzette, K. Prachanronarong, L. Yilmaz, D.R. Caffrey, K.B. Zeldovich, C.A. Schiffer, T.F. Kowalik, J.D. Jensen, R.W. Finberg, J.P. Wang and D.N. Bolon. 2016. A balance between inhibitor binding and substrate processing confers influenza drug resistance. *Journal of Molecular Biology* 428: 538-53.

- 66) Alcala, N., J.D. Jensen, A. Telenti, and S. Vuilleumier. 2016. The genomic signature of population reconnection following isolation: from theory to HIV. *G3: Genes, Genomes, Genetics* 6: 107-20.
- 65) Kapopoulou, A., L. Mathew, A. Wong, D. Trono, and J.D. Jensen. 2016. The evolution of gene expression and binding specificity of the largest transcription factor family in primates. *Evolution* 70: 167-80.
- 64) Jensen, J.D., M. Foll, and L. Bernatchez. 2016. Introduction: the past, present, and future of genomic scans for selection. *Molecular Ecology* 25(1): 1-4.
- 63) Ormond, L., M. Foll, G. Ewing, S. Pfeifer, and J.D. Jensen, 2016. Inferring the age of a fixed beneficial allele. *Molecular Ecology* 25(1): 157-9.
- 62) Ewing, G. and J.D. Jensen, 2016. The consequences of not accounting for background selection in demographic inference. *Molecular Ecology* 25(1): 135-141.
- 61) Laurent, S.*, S. Pfeifer*, M. Settles, S. Hunter, K. Hardwick, L. Ormond, V. Sousa, J.D. Jensen#, and E.B. Rosenblum#, 2016. The population genomics of rapid adaptation: disentangling signatures of selection and demography in White Sands lizards. *Molecular Ecology* 25(1): 306-23.
* authors contributed equally, # co-corresponding authors
- 60) Renzette, N., T.F. Kowalik, and J.D. Jensen, 2016. On the relative roles of background selection and genetic hitchhiking in shaping human cytomegalovirus diversity. *Molecular Ecology* 25(1): 403-13.

2015

- 59) Mathew, L. and J.D. Jensen, 2015. Evaluating the ability of the pairwise joint site frequency spectrum to co-estimate selection and demography. *Front. Genet.* 6: 268.
- 58) Renzette, N., C. Pokalyuk, L. Gibson, M.R. Schleiss, K. Hamprecht, M. Mussi-Pinhata, A.Y. Yamamoto, W.J. Britt, J.D. Jensen#, and T.F. Kowalik#, 2015. Limits and patterns of cytomegalovirus genomic diversity in humans. *PNAS* 112: E4120-28.
co-corresponding authors
- 57) Montano, V., X. Didelot, M. Foll, B. Linz, Y. Moodley#, and J.D. Jensen#, 2015. Worldwide population structure, long term demography, and local adaptation of *Helicobacter pylori*. *Genetics* 200: 947-63.
co-corresponding authors

- 56) Mahajan, S., J. Crisci, A. Wong, S. Akbarian, M. Foll[#], and J.D. Jensen[#], 2015. Quantifying polymorphism and divergence from epigenetic data: a framework for inferring the action of selection. *Front. Genet.* 6: 190.
[#] co-corresponding authors
- 55) Ewing, G., P. Reiff, and J.D. Jensen, 2015. PopPlanner: Visually constructing demographic models for simulation. *Front. Genet.* 6: 150.
- 54) Zeldovich, K.B., P. Liu, N. Renzette, M. Foll, S.T. Pham, S.V. Venev, D.N. Bolon, E.A. Kurt-Jones, G.R. Gallagher, J.D. Jensen, D.R. Caffrey, C.A. Schiffer, T.F. Kowalik, J.P. Wang, and R.W. Finberg, 2015. Positive selection drives preferred segment combinations during influenza virus reassortment. *Molecular Biology & Evolution* 32: 1519-32.
- 53) Bank, C., R.T. Hietpas, J.D. Jensen, and D.N. Bolon, 2015. A systematic survey of an intragenic epistatic landscape. *Molecular Biology & Evolution* 32: 229-38.
- 52) Foll, M.* , H. Shim* , and J.D. Jensen, 2015. A Wright-Fisher ABC-based approach for inferring per-site effective population sizes and selection coefficients from time-sampled data. *Molecular Ecology Res* 15: 87-98.
* authors contributed equally

2014

- 51) Malaspinas, A.-S., O. Lao, H. Schroeder, M. Rasmussen, M. Raghavan, I. Moltke, P.F. Campos, V.F. Goncalves, S. Rasmussen, F. Santana Sagredo, A. Albrechtsen, M.E. Allentoft, P.L.F. Johnson, M. Li, S. Reis, D.V. Bernardo, A.T. Duggan, M. Bastos, E. Hodges, G.J. Hannon, M. DeGiorgio, Y. Wang, J. Stenderup, S. Brunak, T. Sicheritz-Ponten, L. Orlando, T.D. Price, J.D. Jensen, R. Nielsen, J. Heinemeier, J. Olsen, C. Rodrigues-Carvalho, M. Mirazon Lahr, W. Neves, M. Kayser, T. Higham, M. Stoneking, S.D.J. Pena, and E. Willerslev, 2014. Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudo of Brazil. *Current Biology* 24(21): R1035-7.
- 50) Bank, C., M. Foll, A. Ferrer-Admetlla, G. Ewing, and J.D. Jensen, 2014. Thinking too positive? Revisiting current methods in population genetic selection inference. *Trends in Genetics* 30(12): 540-6.
- 49) Poh, Y.-P., V. Domingues, H.E. Hoekstra, and J.D. Jensen, 2014. On the prospect of identifying adaptive loci in recently bottlenecked populations. *PLOS One* 9(11): e110579.
- 48) Jensen, J.D., 2014. On the unfounded enthusiasm for soft selective sweeps. *Nature Communications* 5: 5281.

- 47) Renzette, N., L. Gibson J.D. Jensen, and T.F. Kowalik, 2014. Human cytomegalovirus intrahost evolution – a new avenue for understanding and controlling herpesvirus infections. *Curr. Opin. in Virol.* 8C: 109-115.
- 46) Simkin, A., J. Bailey, B. Theurkauf, F.-B. Gao, and J.D. Jensen, 2014. Inferring the evolutionary history of primate miRNA binding sites: overcoming motif counting biases. *Molecular Biology & Evolution* 31: 1894-1901.
- 45) Bank, C., R.T. Hietpas, A. Wong, D.N.A. Bolon[#], and J.D. Jensen[#], 2014. A Bayesian MCMC approach to assess the complete distribution of fitness effects of new mutations: uncovering the potential for adaptive walks in challenging environments. *Genetics* 196: 841-52.
[#] co-corresponding authors
- 44) Foll, M.*, Y.-P. Poh*, N. Renzette, A. Ferrer-Admetlla, H. Shim, A.-S. Malaspinas, G. Ewing, C. Bank, P. Liu, D. Wegmann, D. R. Caffrey, K.B. Zeldovich, D.N.A. Bolon, J. Wang, T.F. Kowalik, C.A. Schiffer, R.W. Finberg, and J.D. Jensen, 2014. Influenza virus drug resistance: a time-sampled population genetics perspective. *PLOS Genetics* 10(2): e1004185.
^{*} authors contributed equally
- 43) Ewing, G., and J.D. Jensen, 2014. Distinguishing neutral from deleterious mutations in growing populations. *Front. Genet.* 5: 7.
- 42) Renzette, N., D.R. Caffrey, K.B. Zeldovich, P. Liu, G.R. Gallagher, D. Aiello, A.J. Porter, E.A. Kurt-Jones, D.N. Bolon, Y.-P. Poh, J.D. Jensen, C.A. Schiffer, T.F. Kowalik, R.W. Finberg, and J.P. Wang, 2014. Evolution of the influenza A virus genome during development of oseltamivir resistance in vitro. *Journal of Virology* 88: 272-81.
- 2013**
- 41) Hietpas, R.T.* , C. Bank*, J.D. Jensen[#], and D.N. Bolon[#], 2013. Shifting fitness landscapes in response to altered environments. *Evolution* 67: 3512-22.
^{*} authors contributed equally; [#] co-corresponding authors
- 40) Crisci, J., Y.-P. Poh, S. Mahajan, and J.D. Jensen, 2013. The impact of equilibrium assumptions on tests of selection. *Front. Genet.* 4: 235.
- 39) Renzette, N., L. Gibson, B. Bhattacharjee, D. Fisher, M.R. Schleiss, J.D. Jensen[#], and T. F. Kowalik[#], 2013. Rapid intrahost evolution of human cytomegalovirus is shaped by demography and positive selection. *PLOS Genetics* 9(9): e1003735.
[#] co-corresponding authors

- 38) Joost, S., S. Vuilleumier, J.D. Jensen, S. Schoville, K. Leempoel, S. Stucki, C. Melo de Lima, J. Rolland, I. Widmer, and S. Manel, 2013. Uncovering the genetic basis of adaptive change: on the intersection of landscape genomics and theoretical population genetics. *Molecular Ecology* 22(14): 3659-3665.
- 37) Simkin, A., A. Wong, Y.-P. Poh, B. Theurkauf, and J.D. Jensen, 2013. Recurrent and recent selective sweeps in the piRNA pathway. *Evolution* 67: 1081-90.
- 36) Linnen, C.R., Y.-P. Poh, B. Peterson, R. Barrett, J. Larson, J.D. Jensen, and H.E. Hoekstra, 2013. Adaptive evolution of multiple traits through multiple mutations at a single gene. *Science* 339: 1312-1316.
- 35) Singh, N.D., J.D. Jensen, A. G. Clark, and C.F. Aquadro, 2013. Inferences of demography and selection in an African population of *Drosophila melanogaster*. *Genetics* 193(1): 215-28.

2012

- 34) Massouras, A., S.M. Waszak, M. Albarca, K. hens, W. Westphal, J.F. Ayroles, E.T. Dermitzakis, E.A. Stone, J.D. Jensen, T.F.C. Mackay, and B. Deplancke, 2012. Genomic variation and its impact on gene expression in *Drosophila melanogaster*. *PLOS Genetics* 8(11): e1003055.
- 33) Shulha, H. *, J. Crisci*, D. Reshetov*, J.S. Tushir, I. Cheung, R. Bharadwaj, H.J. Chou, I. Houston, C.J. Peter, A.C. Mitchell, W-D. Yao, R.H. Myers, J-F. Chen, T. Preuss, E. RogaeV, J.D. Jensen[#], Z. Weng[#], and S. Akbarian[#], 2012. Human-specific histone methylation signatures at transcription start sites in prefrontal neurons. *PLOS Biology*. 10(11): e1001427.
* authors contributed equally; # co-corresponding authors
- 32) Pavlidis, P., J.D. Jensen, W. Stephan, A. Stamatakis, 2012. A critical assessment of story-telling: GO categories and the importance of validating genomic scans. *Molecular Biology & Evolution* 29(10): 3237-48.
- 31) Domingues, V., Y.-P. Poh, B. Peterson, P. Pennings, J.D. Jensen, and H.E. Hoekstra, 2012. Evidence of adaptation from ancestral variation in young populations of beach mice. *Evolution* 66: 3209-23.
- 30) Crisci, J., and J.D. Jensen, 2012. Evolution of the human genome: adaptive changes. *eLS*, John Wiley & Sons.
- 29) Crisci, J., Y.-P. Poh, A. Bean, A. Simkin, and J.D. Jensen, 2012. Recent progress in polymorphism-based population genetic inference. *Journal of Heredity* 103: 287-96.

2011

- 28) Xu, X. *, S. Ge *, J.D. Jensen *, R. Gutenkunst *, J. Li *, X. Li *, L. Fang, L. Huang, K. Ye, W. He, G. Zhang, X. Zheng, F. Zhang, F. Hu, Y. Li, C. Yu, Y. Guo, D. Li, K. Kristiansen, X. Zhang, J. Wang, R. Nielsen, J. Wang, and W. Wang, 2011. Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. *Nature Biotech* 30: 105-11.
*authors contributed equally
- 27) Sinha, P., A. Dincer, D. Virgil, G. Xu, Y.-P. Poh, and J.D. Jensen, 2011. On detecting selective sweeps using single genomes. *Front. Genet.* 2: 85-90.
- 26) Crisci, J., A. Wong, J. Good, and J.D. Jensen, 2011. On characterizing adaptive events unique to modern humans. *Genome Biology & Evolution* 3: 791-798.
- 25) Albert, F.W., E. Hodges, J.D. Jensen, F. Besnier, Z. Xuan, M. Rooks, A. Bhattacharjee, L. Brizuela, J.M. Good, R. E. Green, H. Burbano, I.Z. Plyusnina, L. Trut, L. Andersson, T. Schoneberg, O. Carlborg, G.J. Hannon, and S. Paabo, 2011. Targeted resequencing of a genomic region influencing tameness and aggression reveals multiple signals of positive selection. *Heredity* 107: 205-14.
- 24) Jensen, J.D. and D. Bachtrog, 2011. Characterizing the influence of effective population size on the rate of adaptation: Gillespie's Darwin Domain. *Genome Biology & Evolution* 3: 687-701.
- 23) Renzette, N., B. Bhattacharjee, J.D. Jensen, L. Gibson, and T.F. Kowalik, 2011. Extensive genome-wide variability of human cytomegalovirus in congenitally infected infants. *PLOS Pathogens* 7(5): e1001344.
- 22) Hietpas, R.T., J.D. Jensen, and D.N.A. Bolon, 2011. Experimental illumination of a fitness landscape. *PNAS* 108: 7896-901.

2010

- 21) Cutler, D.J. and J.D. Jensen. 2010. To pool, or not to pool. *Genetics* 186: 41-3.
- 20) Pavlidis, P., J.D. Jensen, and W. Stephan. 2010. Searching for footprints of positive selection in whole-genome SNP data from non-equilibrium populations. *Genetics* 185: 907-22.
- 19) Jensen, J.D., and O.J. Rando. 2010. Recent evidence for pervasive adaptation targeting gene expression attributable to population size change. *PNAS* 107: E109-110.

- 18) Green, R.E., J. Krause, A.W. Briggs, T. Maricic, U. Stenzel, M. Kircher, N. Patterson, H. Li, W. Zhai, M. H-Y. Fritz, N. Hansen, E.Y. Durand, A.-S. Malaspinas, J.D. Jensen, T. Marques-Bonet, C. Alkan, M. Meyer, K. Prufer, H.A. Burbano, J.M. Good, R. Schultz, A. Aximu-Petri, A. Butthof, B. Hober, B. Hoffner, M. Siegemund, A. Weihmann, C. Nusbaum, E.S. Lander, C. Russ, N. Novod, J. Affourtit, M. Egholm, P. Rudan, D. Brajkovic, Z. Kucan, I. Gusic, V.B. Doronichev, L.V. Golovanova, C. Lalueza-Fox, M. de la Rasilla, J. Fortea, A. Rosas, R. Schmitz, P. Johnson, E.E. Eichler, D. Flash, E. Birney, J.C. Mullikin, M. Slatkin, R. Nielsen, J. Kelso, M. Lachmann, D. Reich, and S. Paabo. 2010. A draft sequence of the Neandertal genome. *Science* 328: 710-722.
- 17) Jensen, J.D. and D. Bachtrog. 2010. Characterizing recurrent positive selection at fast evolving genes in *Drosophila miranda* and *Drosophila pseudoobscura*. *Genome Biology & Evolution* 2: 371-8.
- 16) Pool, J. E., I. Hellmann, J.D. Jensen, and R. Nielsen. 2010. Population genetic inference from genomic sequence variation. *Genome Research* 20: 291-300.
- 2009**
- 15) Jensen, J.D., 2009. On reconciling single and recurrent hitchhiking models. *Genome Biology & Evolution* 1: 320-4.
- 14) Xia, Q., Y. Guo, Z. Zheng, D. Li, Z. Xuan, Z. Li, F. Dai, Y. Li, D. Cheng, R. Li, T. Cheng, T. Jiang, C. Becquet, X. Xu, C. liu, X. Zha, W. Fan, Y. Lin, Y. Shen, L. Jiang, J.D. Jensen, I. Hellmann, S. Tang, P. Zhao, H. Xu, C. Yu, G. Zhang, J. Li, J. Cao, S. Liu, N. He, Y. Zhou, H. Liu, J. Zhao, C. Ye, C. Du, G. Pan, A. Zhao, H. Shao, W. Zeng, P. Wu, C. Li, M. Pan, J. Li, X. Yin, D. Li, J. Wang, H. Zheng, W. Wang, X. Zhang, S. Li, H. Yang, C. Lu, R. Nielsen, Z. Zhou, J. Wang, Z. Xiang, and J. Wang. 2009. Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (*Bombyx*). *Science* 326 (5951): 433-6.
- 13) Linnen, C.R., E. P. Kingsley, J.D. Jensen, and H.E. Hoekstra. 2009. On the origin and spread of an adaptive allele in deer mice. *Science* 325 (5944): 1095-1098.
- 12) Bachtrog, D., J.D. Jensen, and Z. Zhang, 2009. Accelerated adaptive evolution on a newly formed X chromosome. *PLOS Biology* 7(4): e1000082.
- 2008**
- 11) Jensen, J.D., K.R. Thornton, and P. Andolfatto, 2008. An approximate Bayesian estimator suggests strong, recurrent selective sweeps in *Drosophila*. *PLOS Genetics* 4(9): e1000198.
- 10) Jensen, J.D., K.R. Thornton, and C.F. Aquadro, 2008. Inferring selection in partially sequenced regions. *Molecular Biology & Evolution* 25: 438-46.

2007

- 9) Singh, N.D., J.M. Macpherson, J.D. Jensen, and D.A. Petrov, 2007. Similar levels of X-linked and autosomal nucleotide variation in African and non-African populations of *Drosophila melanogaster*. *BMC Evolutionary Biology* 7: 202-210.
- 8) Jensen, J.D., K.R. Thornton, C.D. Bustamante, and C.F. Aquadro, 2007. On the utility of linkage disequilibrium as a statistic for identifying targets of positive selection in non-equilibrium populations. *Genetics* 176: 2371-2379.
- 7) Jensen, J.D., V. Bauer DuMont, A.B. Ashmore, A. Gutierrez and C.F. Aquadro, 2007. Patterns of variability and divergence at the diminutive gene region of *Drosophila melanogaster*: a complex patterns suggests an ancestral selective sweep. *Genetics* 177: 832-840.
- 6) Jensen, J.D., A. Wong, and C.F. Aquadro, 2007. Approaches for identifying targets of positive selection. *Trends in Genetics* 23: 484-491.
- 5) Thornton, K.R. and J.D. Jensen, 2007. Controlling the false positive rate in multi-locus genome scans for selection. *Genetics* 175: 737-750.
- 4) Wong, A.W., J.D. Jensen, J.E. Pool and C.F. Aquadro, 2007. Phylogenetic incongruence in the *Drosophila melanogaster* species group. *Molecular Phylogenetics and Evolution* 43: 1138-50.
- 3) Thornton, K.R., J.D. Jensen, C. Bequet and P. Andolfatto, 2007. Progress and prospects in mapping recent selection in the genome. *Heredity* 98: 340-8.

2006

- 2) Casa, A.M., S.E. Mitchell, J.D. Jensen, M.T. Hamblin, A.H. Paterson, C.F. Aquadro, and S. Kresovich, 2006. Evidence for a selective sweep on chromosome 1 of cultivated sorghum. *Crop Science* 46: S15-S26.

2005

- 1) Jensen, J.D., Y. Kim, V. Bauer DuMont, C.F. Aquadro, and C.D. Bustamante, 2005. Distinguishing between selective sweeps and demography using DNA polymorphism data. *Genetics* 170: 1401-1410.