

Curriculum vitae

GORDON LUIKART

Sept. 2022

CURRENT APPOINTMENTS:

Professor in Wildlife Biology and Systems Ecology
Flathead Lake Biological Station
The University of Montana
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Polson, MT, 59860, USA

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EDUCATION:

Ph.D., University of Montana, 1997, Organismal Biology and Ecology
Supervisor: Dr. Fred Allendorf; Field supervisor: Dr. J. T. Hogg
M.S., University of Montana, 1992, Zoology
B.S., Iowa State University, 1988, General Biology, minor in Animal Ecology

POST-DOCTORAL:

Research Fellow, Population Genetics and Demography, CNRS, Grenoble, France, 1999-2000.
NSF-NATO Postdoc Fellowship, Conservation Biology and Population Genetics, France, 1998-1999
Advisors: P. Taberlet (Université Joseph Fourier, CNRS, Grenoble, France), J.-M. Cornuet
(Institut National de la Recherche Agronomique, Montpellier, France).
European Postdoc Fellow, Conservation & Evolutionary Genetics, Université Joseph Fourier, 1997-1998.

RESEARCH INTERESTS: Conservation Biology, Evolutionary Ecology, Population/Landscape Genomics

EMPLOYMENT:

2014-current, Professor, Flathead Lake Biological Station, Division of Biological Sciences, University of Montana, USA
2010-2014, Associate Professor, Flathead Lake Biological Station, University of Montana, USA
2005-2010, Research Associate Professor, Organismal Biology and Ecology, University of Montana, USA
2005-2015, Senior Researcher (or Visiting) Scientist, Centro de Investigação em Biodiversidade e Recursos Genéticos (CIBIO), University of Porto, Vairão, Portugal
2003-2005, Faculty Affiliate, University of Montana, USA
2004-2005, Research Scientist, Montana Conservation Science Institute (MOCSI), USA
2001-2005, Research Scientist (CR1), CNRS (Centre National de Recherche Scientifique), France
2000-2001, CNRS, Research Fellow, Statistical and Population Genetics, France
1991-1992, Teaching Assistantships, Flathead Lake Biological Station, U. of Montana (Botany, Mammalogy)
1989-1995, Teaching Assistantships, U. of Montana (Genetics & Evolution, Conservation Genetics, Mammalogy, Ecology, Anatomy & Physiology),

ACADEMIC HONORS:

Named one of "The World's Most Influential Scientific Minds" in 2014-2016 & 2018 by Thomson Reuters for publishing highly-cited papers during the past 10 years (e.g., see: <http://sciencewatch.com/sites/sw/files/sw-article/media/worlds-most-influential-scientific-minds-2014.pdf>)
Adjunct Professor Department of Integrative Biology at Michigan State University, 2019-current
Professor, Wildlife Biology Program and Systems Ecology Program, University of Montana, 2010-current
Bronze medal, a top scientist in France CNRS (Centre Nationale de la Recherche Scientifique), 2004-2005
Doctoral Research Fellowship, University of Montana, 1996
Fulbright Fellow, La Trobe Univ., Melbourne, Australia, 1994-95 (Genetics of endangered marsupials)

PROFESSIONAL ACTIVITIES:

2001-2004, Journal editorial board member for *Conservation Biology*
2003-2006, Journal associate editor for *Molecular Ecology Resources*
2009-2011, Associate editor for *Journal of Heredity*
2010-current, Member Swan Ecosystem Center Native Fish Committee
2010-current, Member IUCN Conservation Genetics Specialist Group
2018- current, Member GEO BON Genetics Composition working group

TEACHING:

2018-current, Advanced Population Genetics, 3 credits (advanced undergrads, grad students)
2014-2017, Conservation Genetics, 3 credits (advanced undergrads and graduate students)
2010-current, Conservation Ecology, 3 credits (advanced undergrads), field course
.....2006-current, Population Genetic Data Analysis, 3 credits (grad students & postdocs)

<http://www.umt.edu/sell/cps/congen2018/>; www.popgen.net/congen2013

2007-current, Population Genetics Seminar, 1 credit (undergrad and grad students)

2019-current, Seminars in Ecology & Resource Management, 1 credit, undergrads & grads)

2007-2010, Genetics and Evolution, 3 credits (team-taught, graduate students in NSF-IGERT)

2006, 2010, Frontiers in Conservation Genetics, 2 credits (team taught)

SOCIETIES (Last five years): American Fisheries Society
American Genetic Association
Ecological Society of America
Society for Conservation Biology
Wildlife Society
Freshwater Mollusk Conservation Society

BOOKS:

Allendorf, F.W. and **G. Luikart**. 2007. *Conservation and the Genetics of Populations*. Wiley-Blackwell. Pp. 642.

Allendorf, F.W., **G. Luikart**, and S. Aitken. 2013. *Conservation and the Genetics of Populations* [2nd Edition]. Wiley-Blackwell. Pp. 642.

Allendorf, F.W., W.C. Funk, S.N. Aitken, M. Byrne, **G. Luikart**. 2022. *Conservation and the Genomics of Populations*. [3rd Edition]. Oxford University Press.

BOOK CHAPTERS:

Scribner, K., M. Kardos, **G. Luikart**, R.S. Waples, N. Sard, J. Homola, J. Kanefsky, and S. Smith. Application of genetic data and theory in fisheries management. Chapter 20 in *Analysis and Interpretation of Freshwater Fisheries Data*. 2nd ed. Eds: Guy, Brown, and Brenden. In review.

Luikart, G., B.K. Hand, M. Kardos, O.P. Rajora, S. Aitkin, P. Hohenlohe. 2018. Population genomics: Advancing understanding of nature. *In Population Genomics Concepts, Approaches and Applications*. Ed: Om P. Rajora.

Hohenlohe, P., M. Kardos, B. Hand, K. Andrews, **G. Luikart**. 2018. Population genomics revolutionizes ecology and evolution. *In Population Genomics Concepts, Approaches and Applications*. Editor: Om P. Rajora. DOI: 10.1007/13836_2018_20

Pierson, J.C., **G. Luikart**, and M.K. Schwartz. 2015. The application of genetic indicators in wild populations: potential and pitfalls for genetic monitoring. *In Surrogates and Indicators in Ecology, Conservation and Environmental Management*. Eds: Lindenmayer, D.B., J.C. Pierson, and P. Barton. CSIRO Publishing, Melbourne. CRC Press, London.

Schwartz, M.K., **G. Luikart**, K.S. McKelvey, and S. Cushman. 2009. Landscape genomics: a brief perspective. Chapter 19 in *Spatial Complexity, Informatics and Animal Conservation*, Eds: S.A. Cushman and F. Huettman. Springer, Tokyo.

Geffen, E., **G. Luikart**, and R.S. Waples. 2006. Impacts of modern molecular techniques on conservation biology. Chapter 4 In: *Key Topics in Conservation Biology*, Eds: D.W. Macdonald and K. Service, Blackwell Publishing.

Luikart, G., H. Fernandez, M. Mashkour, P.R. England, and P. Taberlet. 2006. Origins and diffusion of domestic goats inferred from DNA markers: example analyses of mtDNA, Y-chromosome and microsatellites. In: *Documenting Domestication*, Eds: M. Zeder, B. Smith, and D. Bradley, Smithsonian Press, USA.

Taberlet, P., **G. Luikart**, and E. Geffen. 2001. Novel approaches for obtaining and analyzing genetic data for conserving wild carnivore populations, In: *Carnivore Conservation*, Eds: Gittleman, J.L., Funk, S.M., Macdonald, D., and Wayne, R. Cambridge University Press.

PUBLICATIONS (in peer-reviewed journals): (*my students, ^students helped, **postdocs)

For some see: <http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=search&term=Luikart%20G>

Nagarajan, R.P., M. Bedwell, A.E. Holmes, T. Sanches, S. Acuña, M. Baerwald, M.A. Barnes, S. Blankenship, R.E. Connon, K. Deiner, D. Gille, C.S. Goldberg, M.E. Hunter, C.L. Jerde, **G. Luikart**, R.S. Meyer, A. Watts, and A. Schreier. 2022. Environmental DNA methods for ecological monitoring and biodiversity assessment in estuaries. *Estuaries and Coasts*, in press. doi.org/10.1007/s12237-022-01080-y

van Rees, C.B., B.K. Hand, C. Barger, T.J. Cline, W. Daniel, J.A. Ferrante, K. Gaddis, M.E. Hunter, C.S. Jarnevich, M.A. McGeoch, J. Morissette, M. Neilson, C. Rees, A. Sepulveda, R.D. Wallace, D. Whited, T. Wilcox, J. Kimball, and **G. Luikart. 2022. Alien invasive species management needs methodological integration. *Biological Reviews*, 97: 1712–1735.

*Howard, L., **C.B. van Rees, B.K. Hand, and **G. Luikart**. 2022. A review of invasive species reporting

- apps for citizen science and opportunities for innovation. *NeoBiota*, In press.
- ^Carter, S., **C.B. van Rees, B.K. Hand, C. Muhlfeld, and **G. Luikart**, J.S. Kimball. 2022. Aquatic invasive species target screening: a case study using machine learning species distribution models on an invasive trout. *Frontiers in Big Data*, 4:734990. doi:10.3389/fdata.2021.734990.
- ^Smith, S.R., E. Normandeau, H. Djambazian, P.M. Nawarathna, P. Berube, A.M. Muir, J. Ragoussis, C.M. Penney, K.T. Scribner, **G. Luikart**, C.C. Wilson, and L. Bernatchez. 2021. A chromosome-anchored genome assembly for lake trout (*Salvelinus namaycush*). *Molecular Ecology Resources*, 2:679-694. <https://doi.org/10.1111/1755-0998.13483>
- **Kardos, M., and **G. Luikart**. 2021. The genomic architecture of fitness drives population viability in changing environments. *American Naturalist*, 197:511–525. doi.org/10.1086/713469
- Myers, B.J.E. S.R. Weiskopf, A.N. Shiklomanov, S. Ferrier, E. Weng, K.A. Casey, M. Harfoot, S.T. Jackson, A.K. Leidner, T.M. Lenton, **G. Luikart**, H. Matsuda, N. Pettoirelli, I.M.D. Rosa, A.C. Ruane, G.B. Senay, S.P. Serbin, D.P. Tittensor, and T.D. Beard. 2021. A new approach to evaluate and reduce uncertainty of model-based biodiversity projections for conservation policy formulation. *Biosciences*, 71:1261–1273. <https://doi.org/10.1093/biosci/biab094>
- Leigh, D.M. C.B. **van Rees, K.L. Millette et al. 2021. Opportunities and challenges of macrogenetic studies. *Nature Reviews Genetics*, 22:791–807. <https://doi.org/10.1038/s41576-021-00394-0>
- Schweizer, R.M., N. Saarman, K.M. Ramstad, B.R. Forester, J.L. Kelley, B.K. Hand, R.L. Malison, A.S. Ackiss, M. Watsa, T.C. Nelson, A. Beja-Pereira, R.S. Waples, W.C. Funk, and **G. Luikart**. 2021. Big data in conservation genomics: boosting skills, hedging bets, and staying current in the field, *Journal of Heredity*, 112:313-327. doi.org/10.1093/jhered/esab019
- *Strait, J. et al. 2020. Hybridization alters growth and migratory life history expression of native trout. *Evolutionary Applications*, 8:821-833. doi.org/10.1111/eva.13163
- Ezenwa, V.O., S.A. Budischak, P. Buss, M. Seguel, and **G. Luikart**, A.E. Jolles, and K. Sakamoto. 2021. Natural resistance to worms exacerbates bovine tuberculosis severity independently of worm coinfection. *Proceedings of the National Academy of Sciences, USA*, 118 (3) e201508011. <https://doi.org/10.1073/pnas.2015080118>
- ^Robinson, Z., ^Bell, D., *Dhendup, T., **Luikart, G.**, Whiteley, A., and **Kardos, M. 2021. Evaluating genetic rescue attempts in the Anthropocene. *Conservation Biology*, 35: 666-677. doi.org/10.1111/cobi.13596
- Luikart, G.**, T. Antao, B.K. Hand, C.C. Muhlfeld, M.C. Boyer, T. Cosart, ^B. Trethewey, R. Al-Chockhachy, R. Waples. 2021. Detecting population declines via estimating the effective number of breeders (N_b). *Molecular Ecology Resources*. 21: 379-393. doi.org/10.1111/1755-0998.13251
- Paz-Vinas I., E. Jensen, L. Bertola, M. Breed, B.K. Hand, M.E. Hunter, F. Kershaw D.M. Leigh, **G. Luikart**, J. Mergeay, J.M. Miller, **C.B. Van rees, G. Segelbacher, S. Hoban. 2020. Macro-genetic studies must not ignore limitations of genetic markers and scale. *Ecology Letters*, 24:1282-1284.
- Antao, T., Cosart, T., ^B. Trethway, R.S. Waples, M.W. Ackerman, **G. Luikart**, and B.K. Hand. 2020. AgeStruc N_b : Software for simulating and detecting changes in the effective number of breeders (N_b). *Journal of Heredity*, 111:491–497.
- *Garner, B.A., S. Hoban, and **G. Luikart**. 2020. IUCN red list and the value of integrating genetics. *Conservation Genetics*, 21:795–801.
- Sepulveda, A., N. Nelson, C. Jerde, and **G. Luikart**. 2020. Are environmental DNA methods ready for aquatic invasive species management? *Trends in Ecology and Evolution*, 35:668-678.
- Malison, R.L., A. DelVecchia, A. Woods, B.K. Hand, **G. Luikart**, and J.A. Stanford. 2020. Tolerance of aquifer stoneflies to repeated hypoxia exposure and oxygen dynamics in an alluvial aquifer. *Journal of Experimental Biology*, <https://doi.org/10.1242/jeb.225623>
- Malison, R.L., B.K. Ellis, A.G. DelVecchia, H.N. Jacobson, B.K. Hand, **G. Luikart**, H.A. Woods, M. Gamboa, K. Watanabe, and J.A. Stanford. 2020. Remarkable anoxia tolerance by stoneflies from a floodplain aquifer. *Ecology* 101: e03127. 10.1002/ecy.312
- Smith, S., S.A. Amish, L. Bernatchez, J. Le Luyer, C. Wilson, O. Boeberitz, **G. Luikart**, and K. Scribner. 2020. Mapping of adaptive traits enabled by a high-density linkage map for lake trout. *Genes Genomes and Genetics*, in press.
- Schabacker J., S.J. Amish, A. Sepulveda, B. Gardner, D. Miller, Y. Wang, and **G. Luikart**. 2020. Sensitive eDNA detection using large volume water samples and seasonal sampling. *Environmental DNA*, 2: 244-251.
- Stahlke A, D.B., T. Dhendup, B. Kern, S. Pannoni, Z. Robinson, J. Strait, S. Smith, B.K. Hand, P.A. Hohenlohe, and **G. Luikart**. 2020. Population genomics training for the next generation of conservation geneticists: ConGen 2018 Workshop. *J Heredity*, 111: 227–236, <https://doi.org/10.1093/jhered/esaa001>
- Jordan, S., B.K. Hand, S. Hotaling, ^A. DelVecchia, R. Malison, C. Nissley, J. Stanford, and **G. Luikart**. 2019. Genomic data reveal similar genetic differentiation in aquifer species with

- different dispersal capabilities and life histories. *Biological Journal of the Linnean Society*, 129:315–322.
- Kotzé, A., [^]R.M. Smith, Y. Moodley, **G. Luikart**, C. Birss, A.M. Van Wyk, J.P. Grobler, and D.L. Dalton. 2019. Lessons for conservation management: Monitoring temporal changes in genetic diversity of Cape mountain zebra (*Equus zebra zebra*). *PloS one* 14 (7), e0220331
- Haines, M.L., **G. Luikart**, S.J. Amish, ^{*}S. Smith, and E.K. Latch. 2019. Evidence for adaptive introgression of exons across a hybrid swarm in deer. *BMC Evolutionary Biology*, 19:199- . doi.org/10.1186/s12862-019-1497-x
- Sepulveda, A., S.A. Amish. ^{*}J. Schabacker, ^{*}D. Miller, and **G. Luikart**. 2019. Improved detection of rare, endangered and invasive trout in using a new large-volume sampling method for eDNA capture. *Environmental DNA*, 1: 227–237. DOI: 10.1002/edn3.23
- Grummer, J., L.B. Beheregaray, L. Bernatchez, B.K. Hand, **G. Luikart**, S.R. Narum, and E.B. Taylor. 2019. Aquatic landscape genomics and environmental effects on genetic variation. *Trends in Ecology and Evolution*, 34:641-654.
- Hand, B.K., C.G. Flint, C. Frissell, C.C. Muhlfeld, S. Devlin, B. Kennedy, R. Crabtree, A. McKee, **G. Luikart**, and J.A. Stanford. 2019. Challenges in Columbia River fisheries conservation. *Frontiers in Ecology and the Environment*, 17: 11-13. doi:10.1002/fee.1990
- [^]Hendricks, S., E. Anderson, T. Antao, L. Bernatchez, B. Forester, ^{*}B.A. Garner, B. Hand, P. Hohenlohe, M. Kardos, L.B. Koop, R. Waples, and **G. Luikart**. 2018. Recent advances in population genomics data analysis: Improving bioinformatics and computational approaches. *Evolutionary Applications*, 11:1197–1211. doi.org/10.1111/eva.12659
- Hand, B.K., C.G. Flint, C. Frissell, C.C. Muhlfeld, S. Devlin, B. Kennedy, R. Crabtree, A. McKee, **G. Luikart**, and J.A. Stanford. 2018. Social-ecological systems approach for riverscape sustainability in the Columbia River Basin. *Frontiers in Ecology and the Environment*, S23-S33. doi.org/10.1002/fee.1752
- Amish, S.J., [^]A.O. Ali, M. Peacock, M. Miller, M. Robinson, ^{*}S. Smith, **G. Luikart**, and H. Neville. 2018. Assessing thermal adaptation using family-based association and F_{ST} -outlier tests in a threatened trout. *Molecular Ecology*, 28:2573-2593.
- [^]Cross, P.R., B.N. Sacks, **G. Luikart**, M.K. Schwartz, K.W. Van Etten, and R.L. Crabtree. 2018. Red fox ancestry and connectivity assessments reveal minimal fur farm introgression in the Greater Yellowstone Ecosystem. *Journal of Fisheries and Wildlife Management*, 9:519-30. DOI: 10.3996/092017-JFWM-073
- ^{**}Kardos, M., **G. Luikart**, and F.W. Allendorf. 2018. Predicting the evolutionary effects of hunting requires an understanding of genetics. *Journal of Wildlife Management and Wildlife Monographs*. 82: 889-891. doi.org/10.1002/jwmg.21475
- [^]Harrison, K.A., S. Amish, A. Pavlova, S. Narum, M. Telonis-Scott, M.L. Rourke, J. Lyon, Z. Tonkin, D. Gilligan, B. Ingram, M. Lintermans, H.M. Gan, C.M. Austin, **G. Luikart**, and P. Sunnucks. 2017. Signatures of polygenic adaptation associated with climate across the range of an Australian freshwater fish species. *Molecular Ecology*, 28: 6253-6269. DOI: 10.1111/mec.14368
- [^]Hotaling, S., C.C. Muhlfeld, J.J. Giersch, [^]O.A. Ali, S. Jordan, M.R. Miller, **G. Luikart**, and D.W. Weisrock. 2018. Demographic modelling reveals a history of divergence with gene flow for a glacially tied stonefly in a changing post-Pleistocene landscape. *J of Biogeography*, 45: 304-317. DOI: 10.1111/jbi.13125.
- Kovach, R., C.C. Muhlfeld, R. Al-Chokhachy, S.J. Amish, J.L. Kershner, R.F. Leary, W.H. Lowe, **G. Luikart**, P. Matson, D.A. Schmetterling, B.B. Shepard, P.A.H. Westley, D. Whited, A. Whiteley, and F.W. Allendorf. 2017. No evidence for ecological segregation protecting native trout from invasive hybridization. *Global Change Biology*, e11-12. DOI: 10.1111/gcb.13825
- Muhlfeld C.C., R.P. Kovach, R. Al-Chokhachy, S.J. Amish, J.L. Kershner, R.F. Leary, W.H. Lowe, **G. Luikart**, P. Matson, D.A. Schmetterling, B.B. Shepard, P.A.H. Westley, D. Whited, A. Whiteley, and F.W. Allendorf. 2017. Legacy introductions and climatic variation explain spatiotemporal patterns of invasive hybridization in a native trout. *Global Change Biology*, 23: 4663-4674. DOI: 10.1111/gcb.13681
- ^{**}Kovach, R., B.K. Hand, P. Hohenlohe, T. Cosart, M. Boyer, H. Neville, C. Muhlfeld, S. Amish, K. Carim, S. Narum, W. Lowe, F.W. Allendorf, and **G. Luikart**. 2016. Vive la résistance: genome-wide selection against introduced alleles in invasive hybrid zones of trout. *Proceedings of the Royal Society*, 283: 4663-4674.
- Wade A.A., B.K. Hand, ^{**}R.P. Kovach, C.C. Mulhfeld, R. Waples, and **G. Luikart**. 2017. Assessments of species' vulnerability to climate change: from pseudo to science. *Biodiversity and Conservation*, 26: 223–229.
- [^]Rezaeia, H.R., **G. Luikart**, et al. 2016. Corrigendum to “Evolution and taxonomy of the wild species of the genus *Ovis* (Mammalia, Artiodactyla, Bovidae). *Molec. Phylogenet. Evol.* 54:315–326.

- ^Ackerman, M.W., B.K. Hand, R.K. Waples, **G. Luikart**, R.S. Waples, C. Steele, *B.A. Garner, J. McCane, N. Vu, and M. Campbell. 2017. Effective number of breeders estimated from sibship reconstruction: empirical evaluations using hatchery steelhead. *Evolutionary Applications*, 10: 146–160.
- *O'Brien, M.P., A. Beja-Pereira, N. Anderson, R.M. Ceballos, H. Edwards, B. Harris, R. Wallen, and **G. Luikart**. 2017. Brucellosis transmission among wildlife and livestock in the Greater Yellowstone Ecosystem: Inferences from DNA genotyping. *J. of Wildlife Diseases*, 53:339-343.
- **Kardos, M., H. Taylor, H. Ellegren, **G. Luikart**, and F.W. Allendorf. 2016. Genomics advances the study of inbreeding depression in the wild. *Evolutionary Applications*. 9: 1205-1218.
- Wade, A.A., B.K. Hand, C.C. Muhlfeld, **R.P. Kovach, D.C. Whited, J. Kimball, and **G. Luikart**. 2016. Accounting for adaptive capacity and uncertainty in species' climate change vulnerability assessments. *Conservation Biology*, 31: 136-149. DOI: 10.1111/cobi.12764
- Muhlfeld, C.C., V.S. D'Angelo, C. Downs, J. Powel, A. Amish, **G. Luikart**, **R. Kovach M. Boyer, and S. Kalinowski. 2016. Genetic status and conservation of westslope cutthroat trout in Glacier National Park. *Transactions of the American Fisheries Society*, 145: 1093-1109.
- ^Benestan, L., ^A.L. Ferchaud P. Hohenlohe, *B.A. Garner, G. Naylor, I. Baums, and **G. Luikart**. 2016. Conservation genomics of natural and managed populations: building a conceptual and practical framework for genomicist. *Molecular Ecology* 25:2967-77. doi: 10.1111/mec.13647.
- *Della Croce, P.P., G.C. Poole, and **G. Luikart**. 2016. Simplifying assumptions yield overconfidence in detecting and quantifying introgression in hybridized populations. *Molecular Ecology Resources*, 16: 1287–1302. DOI: 10.1111/1755-0998.12520
- *Roffler, G.H., M.K. Schwartz, K. Pilgrim, S.L. Talbot, G.K. Sage, L.G. Adams, and **G. Luikart**. 2016. Identification of landscape features influencing gene flow: how useful are habitat selection models? *Evolutionary Applications*, 9: 805–817
- Powell, J., S.J. Amish, G. Haynes, **G. Luikart**, and E. Latch. 2016. Identifying SNPs and candidate genes associated with lineage divergence: use of next-generation targeted re-sequencing in mule deer (*Odocoileus hemionus*). *Molecular Ecology Resources*, 16:1165-1172
- *Stetz, J.B., *S. Smith, M.A. Sawaya, A.B. Ramsey, S.J. Amish. M.K. Schwartz, and **G. Luikart**. 2016. Discovery of 20,000 RAD–SNPs and development of a 52-SNP array for monitoring river otters. *Conservation Genetics Resources*, 8: 299–302. doi:10.1007/s12686-016-0558-3.
- *Roffler, G.H., S.J. Amish, *S. Smith, T. Cosart, *M. Kardos, M.K. Schwartz, and **G. Luikart**. 2016. SNP discovery in candidate adaptive genes using exon capture in a free-ranging alpine ungulate. *Molecular Ecology Resources*, 16:1147–1164.
- Jordan, S., J.J. Giersch, C.C. Muhlfeld, *S. Hotaling, L. Fanning, and **G. Luikart**. 2016. Loss of genetic diversity and increased subdivision in an endemic alpine stonefly threatened by climate change. *PLOS ONE*, e0157386. doi:10.1371/journal.pone.0157386.
- Kamath, P.L., J.T. Foster, K.P. Drees, **G. Luikart**, C. Quance, N.J. Anderson, P.R. Clarke, E.K. Cole, M.L. Drew, W.H. Edwards, J.C. Rhyhan, J.J. Treanor, R.L. Wallen, P.J. White, S. Robbe-Austerman, and P.C. Cross. 2016. Genomics reveals historic and contemporary transmission dynamics of a bacterial disease among wildlife and livestock. *Nature Communications*, 7:11448.
- Hand, B.K., C.C. Muhlfeld, A.A. Wade, R.P. Kovach, D.C. Whited, S.R. Narum, A.P. Matala, M.W. Ackerman, *B.A. Garner, J.S. Kimball. J.A. Stanford, and **G. Luikart**. 2016. Climate variables explain neutral and adaptive variation within salmonid metapopulations: the importance of replication in landscape genetics. *Molecular Ecology*, 25:689–705.
- *Ali, O.A., S.M. O'Rourke, S.J. Amish, M.H. Meek, **G. Luikart**, C. Jefferys, and M.R. Miller. 2016. RAD Capture (Rapture): Flexible and efficient sequence-based genotyping. *BioRxiv preprint* doi: <http://dx.doi.org/10.1101/028837>. *Genetics*, 202:389–400.
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- Kamath, P.L., M.A. Haroldson, **G. Luikart**, D. Paetkau, C. Whitman, and F.T. van Manen. 2015. Multiple estimates of effective population size for monitoring a long-lived vertebrate: an application to Yellowstone grizzly bears. *Molecular Ecology*, 24:5507–5521.
- *Garner, B.A, B.K. Hand, *B. Addis, S.J. Amish, L. Bernatchez, J.T. Foster, K.M. Miller, P.A. Morin, S.R. Narum, S.J. O'Brien, *G. Roffler, J. Seeb, L. Seeb, W.D. Templin, P. Sunnucks, *J. Strait, K.I. Warheit, T.R. Seamons, J. Wenburg, J. Olsen, and **G. Luikart**. 2016. Genomics in conservation: case studies for bridging the gap between data and application. *Trends in Ecology and Evolution*, 31:81–83.
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PUBLICATIONS in review or revision: (*students, ^postdocs)

- ^Moreno, N., *L. Howard, S. Relyea, J. Dunnigan, M. Boyer, M. Kardos, S. Glaberman, **G. Luikart**, and Y. Chiari. In review. Gene expression estimates: Influence of sequencing library, sampling methods, tissue type, and harvest time in native fish. *Authorea*. In revision. DOI: 10.22541/au.161142130.04599849/v1
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- Her, C., H-R. Rezaei, S. Hughes, S. Naderi, M. Duffraisie, M. Mashkour, H-R. Naghash, A. Bălăşescu, **G. Luikart**, S. Jordan, D. Özüt, A. Kence, M.W. Bruford, A. Tresset, J-D. Vigne, P. Taberlet, C. Hänni, F. Pompanon. In review. Extensive maternal origin of domestic sheep in Anatolia and the Zagros. In review.
- Scribner, K., M. Kardos, **G. Luikart**, R.S. Waples, N. Sard, J. Homola, J. Kanefsky, and S. Smith. Application of Genetic Data and Theory in Fisheries Management. Chapter 20 in *Analysis and Interpretation of Freshwater Fisheries Data*. 2nd ed. Eds: Guy, Brown, and Brenden. In review.
- Amish, S.J., S. Bernall, P. DeHaan, M. Miller, S. O'Rourke, M.C. Boyer, C. Muhlfeld, S. Painter, R.F. Leary, and **G. Luikart**. Improved relatedness estimation, hybrid detection, and sex identification using a SNP-chip developed from next-generation RAD sequencing in threatened bull trout. *In revision*.

SELECTED GRANTS AND CONTRACTS AWARDED (RECENTLY):

- NASA-ROSES: Predicting the Spread of Aquatic Invasive Species Using Remote Sensing, Genetics, and Climate Modeling. \$740k. 2019-2022.
- NASA-ROSES (Ecological forecasting for conservation): Projecting effects of climate change on river habitats and salmonid fishes. \$750k. 2014-2018.
- NSF-DoB: (Dimensions of Biodiversity) - Predicting Biodiversity Vulnerability to Climate Change: Integrating Phylogenetic, Genomic, and Function Diversity in River Floodplains. \$2M. 2016-20.
- NSF-DEB: Evolutionary mechanisms influencing the spread of hybridization: genomics, fitness, and dispersal. \$600k. 2013-2017.
- MREDI (Montana University System): Development of autonomous chemical and biological instrumentation for environmental and industrial monitoring. M. DeGrandpre (PI), O. Berryman, C. Palmer, S. Amish, G. Luikart. \$1.4M, 2015-2017

SYNERGISTIC ACTIVITIES & OUTREACH:

- **Development of young scientists** – I have mentored >50 undergrad and grad students (& published with >30), mentored >6 postdocs, and helped occasional high school students in research projects. With collaborators, we mentored 15 university undergrads from Montana and nationwide working on aquatic ecology projects for 2-20 weeks per student per summer in 2013-current. I teach primary or high school students yearly about science, ecology, & conservation.
- **Organizing courses** - Population Genetic Data Analysis for graduate students, Portugal, 2006, 2008; for MS, Ph.D., postdocs, and faculty, Montana, 2007, 2009, 2011, 2013-2022; e.g.

www.popgen.net/congen2013; <http://www.umt.edu/ces/conferences/congen/>. Workshop/courses on invasive species detection with representatives from US Forest Service, US Geological Survey, Montana Fish Wildlife and Parks, and County Weed Districts.

- **Development of educational and fundraising videos (with collaborators)** – on "Conservation Genetics" <https://www.youtube.com/watch?v=MlaQnjibMq0>; and "Aquatic invasive species" prevention and eDNA detection <https://www.youtube.com/watch?v=ONXV2hhTp44&feature=youtu.be> ; and citizen science "sampling of trout" training video: <https://www.youtube.com/watch?v=ymETcLLm5QY>; and on sampling wildlife to understand and control disease transmission <http://vimeo.com/33527913>; <http://www.gyeburcellosis.net/index.php>. **See Brittany Garner's CV (videographer).**
- **Advising managers, agencies & specialist groups** (selected examples) – Montana Fish Wildlife and Parks cutthroat trout conservation committee; expert witness and consultant on hatcheries and wild salmon for NGOs and law firms 2011-present; Swan Valley Trout Restoration Program advisor; co-authored sections of MFWP bighorn sheep conservation action plan. IUCN Caprinae Specialists Group, taxonomy working group, 2001–2012. IUCN Genetics Specialist Group. GEO BON Species Populations working group.
- **Formal exchange program agreements** – Established between The University of Montana and The University of Porto, Portugal, 2007, 2009-present; and also the National Zoological Gardens of South Africa (SANBI) 2018-present; Obtained funding for students and faculty from Montana to travel to or collaborate with Portugal, 2006-present; and with South Africa 2018-present.
- **Reviewer** – for the US National Science Foundation (proposals and panels), Genome Canada, and journals and agencies including: Nature Reviews Genetics, Proceedings of the Royal Society B, Science, Trends in Ecology & Evolution, Science. Advisory board member for the Journal Environmental DNA.