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Education

- Ph.D., 1997, University of Montana, Organismal Biology and Ecology
- M.S., 1992, University of Montana, Zoology
- B.S., 1988, Iowa State University, General Biology with minor in Animal Ecology

Research Interests

My general research interests are in conservation biology, population genetics, and ecology (**view CV**). My primary research applies genetics to the conservation of natural and managed populations (**video**). I work at FLBS and in the **Montana Conservation Genomics Laboratory** (MCGL) at the University of Montana (UM) with colleagues, **Fred Allendorf**, Steve Amish, Leif Howard, Brian Hand, Ryan Kovach, and others. Our research applies principles and tools of population genetics/omics to fish, wildlife, and a variety of other taxa, including invasive species and parasites that are threatening native ecosystems and regional economies (**AIS video**). We have established exchange programs and collaborations between the University of Montana and the University of Porto in Portugal (CIBIO-UP) with Portuguese colleagues (e.g., Albano Beja-Pereira) to promote international education, research, and conservation. We also established an exchange with South Africa's National Biodiversity Institute (SANBI) and zoological gardens (e.g., Prof Antoinette Kotze). We have exciting projects with Montana Fish Wildlife and Parks (e.g., Matt Boyer), US Geological Survey (Clint Muhlfeld, Adam Sepulveda), National Marine Fisheries Service (Robin Waples), and the US Forest Service (Mike Schwartz, Beth Gardner). We develop and apply novel field sampling methods, DNA typing techniques, and data analysis approaches to understand landscape connectivity, adaptation to climate change, invasive species control (including pathogens), and the negative effects of inbreeding depression and hybridization on individual fitness and population viability. Current work includes predicting adaptive gene flow rates and population persistence in species challenged by climate warming.

Publications

Google Scholar page

Books:

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

Book chapters (selected):

- 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. **(link)**
- 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. (link)

Publications (selected): (*student) (^postdoc)

- van Rees, C.B., B.K. Hand, C. Bargeron, T.J. Cline, W. Daniel, J.A. Ferrante, K. Gaddis, M.E. Hunter, C.S. Jarnevich, M.A. McGeoch, J. Morisette, 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. **https://doi.org/10.1111/brv.12859**
- ^Kardos, M., and G. Luikart. 2021. The genomic architecture of fitness drives population viability in changing environments. *American Naturalist*, 197**:511–525. org/10.1086/713469**
- *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
- 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., L.A. Eby, R.P. Kovach, C.C. Muhlfeld, M.C. Boyer, S.J. Amish, S. Smith, W.H. Lowe, and **G. Luikart**. 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, **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., D. Bell, *T. Dhendup, **G. Luikart,** A. Whiteley, and ^M. Kardos. 2021. Evaluating genetic rescue attempts in the Anthropocene. *Conservation Biology*, 35: 666-677.*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, and 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
- *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.
- 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.
- *Beja-Pereira, A., ^P.R. England, N. Ferrand, A. Bakheit, M.A. Abdalla, M. Mashkour, J. Jordana, P. Taberlet, and **G. Luikart**. 2004. African origins of the domestic donkey. *Science*, 304:1781.
- **Luikart G.**, ^P.R. England, ^D. Tallmon, ^S. Jordan, and P. Taberlet. 2003. The power and promise of population genomics: from genotyping to genome typing. *Nature Reviews Genetics*, 4:981-994. **(link)**

Teaching (selected)

- 2006-current, Population Genetic Data Analysis, 3 credits (advanced undergrads, grad students, postdocs, government scientists, faculty, with participants from >10 countries) **https://www.umt.edu/ces/conferences/congen/**;
- 2010-current, Conservation Ecology, 3 credits (undergrads, grad students), field course involving camping, sampling, and researching in Glacier National Park area with expert biologists from multiple agencies
- 2018, Advanced Population Genetics, 3 credits