

Curriculum Vitae

GORDON LUIKART

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CURRENT APPOINTMENTS:

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

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Visiting Senior Scientist, Center for Investigation of Biodiversity and Genetic Resources (CIBIO),
University of Porto, Portugal, 4485-661 Vairão, Portugal. <http://cibio.up.pt/>

BIRTH/FAMILY: Born 30 October, 1964; Sioux City, Iowa, USA; American citizen; France residency card;
married, two children, 3.5 horses

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

POSTDOCTORAL:

Research Fellow, Population Genetics and Demographic History, 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
Nationale Recherche Agriculture, Montpellier, France).
European Postdoc Fellow, Conservation & Evolutionary Genetics, Université Joseph Fourier, 1997-1998.

RESEARCH INTERESTS: Conservation Biology, Ecology, Evolution, 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-current, Senior Research (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 Recherche Scientifique), France
(Officially on leave without pay until 2015)
2000-2001, CNRS, Research Fellow, Statistical and Population Genetics, France
1991-1992, Teaching Assistantships, Biological Station, U. of Montana (Aquatic Botany, Mammal Ecology)
1989-1995, Teaching Assistantships, U. of Montana (Genetics & Evolution, Conservation
Genetics, Mammalogy, Ecology, Anatomy & Physiology),
1987, Research and Teaching Assistant, Sumilon University, Philippines (SCUBA diving & Marine Biology)
1986, Field Research Assistant, Virginia Polytech Institute (trapping & banding passerine birds)
1985-1986, Iowa Department of Natural Resources (gill-netting, radio-telemetry of fish, grouse, & otters)

ACADEMIC HONORS:

Named one of "The World's Most Influential Scientific Minds in 2014", by Thomson Reuters as one of the
most highly cited researchers publishing scientific papers between 2003 and 2013.
Adjunct Professor, Wildlife 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)
Scholarship: top 5% of graduate students in research at The University of Montana, 1991, 1994
Phi Beta Kappa National Honors Society Award (top 5% of liberal arts students in USA), 1988

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

TEACHING: 2014-current, 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)
www.popgen.net/congen2013; <http://www.umt.edu/sell/cps/congen/>
2007-current, Population Genetics Seminar, 1 credit (undergrad and grad students)
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
Ecological Society of America
Society for Conservation Biology
Wildlife Disease Association
Wildlife 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* [Second Edition]. Wiley-Blackwell. Pp. 642. [3rd edition commissioned for 2016/2017]

BOOK CHAPTERS:

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*. Lindenmayer, DB; Pierson, JC and Barton P. (Eds.) 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. Huetteman. 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): (*students)

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

*Garner B.A, B.K. Hand, *B. Addis, S. 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**. 2015. Genomics in conservation: case studies for bridging the gap between data and application. *Trends in Ecology and Evolution*, in press.
Kovach, R., C.C. Muhlfeld, B.K. Hand, D. Whited, A.A. Wade, P.W. DeHaan, R. Al-Chokhachy, and **G. Luikart**. 2015. Climatic and habitat variation is related to genetic diversity in bull trout: implications for vulnerability to climate change. *Global Change Biology*, doi: 10.1111/gcb.12850
Hand, B.K., W.H. Lowe, R.P. Kovach, C.C. Muhlfeld, and **G. Luikart**. 2015. Landscape community genomics: understanding eco-evolutionary processes in complex environments. *Trends in Ecology and Evolution*, 30:161–168.
Hand, B.K., T.D. Hether, R.P. Kovach, C.C. Muhlfeld, S.J. Amish, M.C. Boyer, S.M. O'Rourke, M.R. Miller, W.H. Lowe, P.A. Hohenlohe, and **G. Luikart**. 2015. Genomics of introgression: discovery and mapping of thousands of species-diagnostic SNPs using RAD sequencing in trout. Invited paper for special edition on hybridization, *Current Zoology*, In press.

- Kovach, R., C.C. Muhlfeld, M.C. Boyer, W. Lowe, F.W. Allendorf, and **G. Luikart** et al. 2015. Dispersal and selection mediate hybridization between a native and invasive species. *Proceedings of the Royal Society B*. <http://dx.doi.org/10.1098/rspb.2014.2454>.
- *Kardos, M., **G. Luikart**, R. Bunch, S. Dewey, W. Edwards, S. McWilliam, J. Stephenson, F.W. Allendorf, J.T. Hogg, and J. Kijas. 2015. Genome sequencing reveals selective sweeps for horn size and other traits in bighorn sheep. In press. *Molecular Ecology*.
- Schoenecker, K.A., M.K. Watry, L.E. Ellison, M.K. Schwartz, and **G. Luikart**. 2015. Bighorn sheep abundance determined using non-invasive sampling in a national park wilderness area *Western North American Naturalist*, In press.
- Muhlfeld C.C., R.P. Kovach, *L.A. Jones, M.C. Boyer, R.F. Leary, W.H. Lowe, **G. Luikart**, and F.W. Allendorf. 2014. Invasive hybridization in a threatened species is accelerated by climate change. *Nature Climate Change*, 4:620-624. DOI: 10.1038/nclimate2252.
- Landguth, E.L., C.C. Muhlfeld, R.S. Waples, *L.A. Jones, W.H. Lowe, D. Whited, J. Lucotch, H. Neville, and **G. Luikart**. 2014. Combining demographic and genetic factors to assess population vulnerability in stream species. *Ecological Applications*, <http://dx.doi.org/10.1890/13-0499.1>.
- Andrews, K.R., P.A. Hohenlohe, M.R. Miller, J.E. Seeb, and **G. Luikart**. 2014. Trade-offs and utility of alternative RADseq methods. *Molecular Ecology*, 23:1661–1667. doi: 10.1111/mec.12964.
- *Kardos, M., **G. Luikart**, and F.W. Allendorf. 2014. Measuring individual inbreeding in the age of genomics: marker-based measures are better than pedigrees. *Molecular Ecology Resources*, 14:519-30. doi: 10.1111/1755-0998.
- Giersch, J.J., S. Jordan, **G. Luikart**, *L.A. Jones, F.R. Hauer, and C.C. Muhlfeld. 2014. Range contraction of a rare alpine stonefly, *Zapada glacier*, under climate change. *Freshwater Science*, in press. DOI: 10.1086/679490
- Andrews, K.R., and **G. Luikart**. 2014. Recent novel approaches for population genomics data analysis. *Molecular Ecology*, 23:1661-7. doi: 10.1111/mec.12686.
- Waples, R.A., T. Antao, and **G. Luikart**. 2014. Effects of overlapping generations on linkage disequilibrium estimates of effective population size. *Genetics*, 197: 769–780.
- *Cosart, T., A. Beja-Pereira, J. Johnson, and **G. Luikart**. 2014. ExonSampler: A computer program for genome-wide sequence sampling to facilitate new generation sequencing. *Molecular Ecology Resources*, 14:1296-301. DOI: 10.1111/1755-0998.12267.
- Benavides, J.A., P.C. Cross, S. Creel, and **G. Luikart**. 2014. Limitations to estimating bacterial cross-species transmission using genetic and genomic markers: inferences from simulation modeling. *Evolutionary Applications*, DOI: 10.1111/eva.12173.
- *Roffler, G.H., S.L. Talbot, **G. Luikart**, G.K. Sage, K.L. Pilgrim, L.G. Adams, and M.K. Schwartz. 2014. Lack of sex-biased dispersal promotes fine-scale genetic structure in alpine ungulates. *Conservation Genetics*, DOI 10.1007/s10592-014-0583-2.
- *Hand, B.K., S. Chen, N. Anderson, A. Beja-Pereira, P. Cross, M. Ebinger, H. Edwards, B. Garrett, M. Kardos, H. Edwards, M. Kauffman, E.L. Landguth, A. Middleton, B. Scurlock, P.J. White, P. Zager, M. Schwartz, and **G. Luikart**. 2013. Sex-biased gene flow among elk in the Greater Yellowstone Ecosystem. *Journal of Fish and Wildlife Management*, 5:124-132. <http://dx.doi.org/10.3996/022012-JFWM-017>
- Lane-deGraaf, K.E., S.J. Amish, *F. Gardipee, A. Jolles, **G. Luikart**, and V.O. Ezenwa. 2014. Signatures of natural and unnatural selection: evidence from an immune system gene in African buffalo. *Conservation Genetics*, In press.
- *Kardos, M., **G. Luikart**, and F.W. Allendorf. 2014. Evaluating the role of inbreeding depression in heterozygosity-fitness correlation: how useful are tests of identity disequilibrium? *Molecular Ecology Resources*, 14, 519-530.
- Colli, L., S. Joost, R. Negrini, L. Nicoloso, P. Crepald, P. Ajmone-Marsan, and ECONOGENE Consortium. 2014. Assessing the spatial dependence of adaptive loci in 43 European and Western Asian goat breeds using AFLP markers. *PLoS One*, 9:e86668.
- Hohenlohe, P.A., M.D. Day, S.J. Amish, M.R. Miller, *N. Kamps-Hughes, M.C. Boyer, C.C. Muhlfeld, F.W. Allendorf, E.A. Johnson, and **G. Luikart**. 2013. Genomic patterns of introgression in rainbow and westslope cutthroat trout illuminated by overlapping paired-end RAD sequencing. Invited paper on next generation sequencing. *Molecular Ecology*, 22:3002–3013.
- Waples, R.A., **G. Luikart**, D.A. Tallmon, and J. Faulkner. 2013. Simple life history traits explain key effective population size ratios across diverse taxa. *Proceedings of Royal Society B*. 280: 20131339 doi:10.1098/rspb.2013.1339.
- Cross, P.C., E. Maichak, *A. Brennan, M.R. Ebinger, B.M. Scurlock, J. Henningsen, and **G. Luikart**. 2013. An ecological perspective on the changing face of *Brucella abortus* in the western United States. Invited review, *OIE Revue Scientifique*. 32:79-87.
- Campbell, N.R., S.A. Amish, V. Pritchard, K. McKelvey, M. Young, M.K. Schwartz, J.C. Garza, **G. Luikart**, and S. Narum. 2012. Development and evaluation of 200 novel SNP assays for

- population genetic studies of westslope cutthroat trout and genetic identification of related taxa. *Molecular Ecology Resources*, 12:942-9.
- Amish, S.J., P.A. Hohenlohe, R.F. Leary, C. Muhlfeld, F.W. Allendorf, and **G. Luikart**. 2012. Next-generation RAD sequencing to develop species-diagnostic SNPs chips: An example from westslope cutthroat and rainbow trout. *Molecular Ecology Resources*. 12:653–660. doi: 10.1111/j.1755-0998.2012.03157.x
- Pérez-Figueroa, A., R. Wallen, T. Antao, *J. Coombs, M.K. Schwartz, P.J. White and **G. Luikart**. 2012. Conserving genetic variability in large mammals: Effect of population fluctuations and variance in male reproductive success on genome-wide variation in Yellowstone bison. *Biological Conservation*, 150:159-166.
- *See W., H. Edwards, *C. Almendra, *M. Kardos, J. Lowell, R. Wallen, S. Cain, B. Holben, and **G. Luikart**. 2012. *Yersinia enterocolitica*: an unlikely cause of positive brucellosis tests in greater Yellowstone ecosystem bison. *Journal of Wildlife Diseases*, 3:537-41.
- Landguth, E.L., C.C. Muhlfeld, and **G. Luikart**. 2011. CDFISH: an individual-based, spatially-explicit, landscape genetics simulator for aquatic species in complex riverscapes. *Conservation Genetics Resources*, 4:133–136.
- Ferreira, A.C., *C. Almendra, R. Cardoso, M.S. Pereira, A. Beja-Pereira, **G. Luikart**, and M.I.C. de Sá. 2012. Development and evaluation of a selective medium for improved isolation of *Brucella suis*. *Research in Veterinary Science*, 93:565-567.
- *Cosart, T., A. Beja-Pereira, S. Chen, J. Shendure, and **G. Luikart**. 2011. Exome-wide DNA capture and next generation sequencing in domestic and wild species. *BMC Genomics*, 12:347-355.
- Muhlfeld, C.C. J.J. Giersch, F.R. Hauer, G.T. Pederson, **G. Luikart**, D.P. Peterson, C.C. Downs, and D.B. Fagre. 2011. Climate change links fate of glaciers and a rare alpine invertebrate. *Climate Change Letters*, 106:327-345.
- Luikart, G.**, S. Amish, J. Winnie, R. Godinho, A. Beja-Pereira, F.W. Allendorf, and R.B. Harris. 2011. High connectivity among Argali from Afghanistan and adjacent countries: Assessment using neutral and candidate gene microsatellites. *Conservation Genetics*, 12:921-931.
- Hohenlohe, P., Amish, S.J., J. Catchen, F.W. Allendorf, and **G. Luikart**. 2011. RAD sequencing identifies thousands of SNPs for assessing hybridization in rainbow and westslope cutthroat trout. Invited paper, *Molecular Ecology Resources*, 11:117–122.
- *Johnson, H.E., L.S. Mills, J.D. Wehausen, T.R. Stephenson, and **G. Luikart**. 2011. Translating effects of inbreeding depression on component vital rates to overall population growth in endangered bighorn sheep. *Conservation Biology*, 25:1240-1249.
- *Short Bull, R.A, R. Mace, S.A. Cushman, *E.L Landguth, T. Chilton, K. Kendall, M.K. Schwartz, K.S. McKelvey, F.W. Allendorf, and **G. Luikart**. 2011. Why replication is important in landscape genetics: Case of the American black bear in the Rocky Mountains. *Molecular Ecology*, 6: 1092–1107.
- Allendorf, F.W., P. Hohenlohe, and **G. Luikart**. 2010. Genomics and the future of conservation. Invited Review, *Nature Reviews Genetics*, 11:697-709.
- *Antao, T., A. Pérez-Figueroa, and **G. Luikart**. 2010. Detecting population declines: High power of genetic monitoring using effective population size estimators. *Evolutionary Applications*, 4:144–154.
- *Landguth, E.L., S.A. Cushman, M. Murphy, and **G. Luikart**. 2010. Quantifying landscape connectivity: Assessing lag time until barrier signals are detectable. *Molecular Ecology Resources*, 19:4179–4191.
- England, P.R., **G. Luikart**, and R.S. Waples. 2010. Early detection of population fragmentation using linkage disequilibrium estimation of effective population size. *Conservation Genetics*, 11:2425–2430.
- Landguth, E.L., S.A. Cushman, M.K. Schwartz, K.S. McKelvey, M. Murphy, and **G. Luikart**. 2010. Relationships between migration rates and landscape resistance assessed using individual-based simulations. *Molecular Ecology Resources*, 10:854-862.
- Luikart, G.**, N. Ryman, D.A. Tallmon, M.K. Schwartz, and F.W. Allendorf. 2010. Estimating census and effective population sizes: Increasing usefulness of genetic methods. Invited Review, *Conservation Genetics*, 11: 355-373.
- Ezenwa V.O., R.S. Etienne, **G. Luikart**, A. Beja-Pereira, *F. Gardipee, and A. E. Jolles. 2010. Hidden consequences of living in a wormy world: nematode-induced immune-suppression facilitates tuberculosis invasion in African buffalo. *American Naturalist*, 176:613–624.
- Harris, R.B., J. Winnie, JR., S. Amish, A. Beja-Pereira, R. Godinho, and **G. Luikart**. 2010. Population estimation of argali (*Ovis ammon*) in the Afghan Pamir using capture-recapture modeling from fecal DNA. *Journal of Wildlife Management*, 74:668–677.
- Cross, P.C., E.K. Cole, A.P. Dobson, W.H. Edwards, K.L. Hamlin, **G. Luikart**, A. Middleton, B.M. Scurlock, and P.J. White. 2010. Probable causes of increasing elk brucellosis in the Greater Yellowstone Ecosystem. *Ecological Applications*, 20:278-288.

- Hausssler, D. et al. 2009. Genome 10K: A proposal to obtain whole-genome sequence for 10,000 vertebrate species. *Journal of Heredity*, 100:659-674.
- *Gebremedhin, B., G.F. Ficetola, *S. Naderi, *H.-R. Rezaei, *C. Maudet, D. Rioux, **G. Luikart**, Ø. Flagstad, W. Thuiller, and P. Taberlet. 2009. Frontiers in identifying conservation units: from neutral markers to adaptive genetic variation. Invited commentary, *Animal Conservation*, 12:107-109.
- Beja-Pereira, A., *R. Oliveira, P.C. Alves, M.K. Schwartz, and **G. Luikart**. 2009. Advancing ecological understanding through technological transformations in noninvasive genetics. Invited Review, *Molecular Ecology Resources*, 9:1279-1301.
- Archie, E.A., **G. Luikart**, and V. Ezenwa. 2009. Infecting epidemiology with genetics: A new frontier in disease ecology. *Trends in Ecology and Evolution*, 24:21-30.
- Beja-Pereira, A., B.J. Bricker, S. Chen, *C. Almendra, P.J. White, and **G. Luikart**. 2009. DNA genotyping suggests recent brucellosis outbreaks near Yellowstone National Park originate from elk. *Journal of Wildlife Diseases*, 45:1174-1177.
- *Oliveira, R., D. Castro, R. Godinho, **G. Luikart**, and P. C. Alves. 2009. Species identification using analysis of a nuclear gene: application to sympatric wild carnivores of Southwest Europe. *Conservation Genetics*, 11:1023-1032.
- Chen, A. et al. 2009. Zebu cattle are an exclusive legacy of the South Asia Neolithic. *Molecular Biology and Evolution*, 27:1-6.
- *Gebremedhin, B., *S. Naderi, *H.-R. Rezaei, *C. Maudet, G.F. Ficetola, D. Rioux, **G. Luikart**, Ø. Flagstad, W. Thuiller, and P. Taberlet. 2009. Conservation status of the critically endangered Walia ibex (*Capra walie*): evidence from genetic data and environmental parameters. *Animal Conservation*, 12:89-100.
- Pariset, L., A. Cuteri, C. Ligda, P. Ajmone-Marsan, A. Valentini, and the Econogene Consortium. 2009. Geographical patterning of sixteen goat breeds from Italy, Albania and Greece assessed by Single Nucleotide Polymorphisms. *BMC Ecology*, 9:20 (doi: 10.1186/1472-6785-9-20).
- Pariset L., S. Joost, P.A. Marsan, A. Valentini, and the Econogene Consortium. 2009. Landscape genomics and biased F_{ST} approaches reveal single nucleotide polymorphisms under selection in goat breeds of North-East Mediterranean. *BMC Genetics*, 10:7 (doi: 10.1186/1471-2156-10-7).
- *Da Silva, A., J.-M. Gaillard, N.G. Yoccoz, A.J.M. Hewison, M. Galan, T. Coulson, D. Allainé, *L. Vial, D. Delorme, G. Van Laere, F. Klein, and **G. Luikart**. 2009. Heterozygosity-fitness correlations revealed by neutral and candidate gene markers in roe deer from a long-term study. *Evolution*, 63:403-417.
- Luikart, G.**, K. Pilgrim, J. Vistry, V.O. Ezenwa, and M.K. Schwartz. 2008. Candidate gene microsatellite variation is associated with parasitism in wild bighorn sheep. *Biology Letters*, 4:228-231.
- *Antao, T., A. Lopes, R.J. Lopes, A. Beja-Pereira, and **G. Luikart**. 2008. LOSITAN: A workbench to detect molecular adaptation based on an F_{ST} -outlier method. *BMC Bioinformatics*, 9:323.
- *Almendra, C., *T.L. Silva, A. Beja-Pereira, A.C. Ferreira, L. Ferrão-Beck, M. I. Sá, B.J. Bricker, and **G. Luikart**. 2008. "HOOF-Print" VNTR genotyping and haplotype inference discriminates among *Brucella* spp isolates. *Infection, Genetics and Evolution*, 9:104-107.
- Allendorf, F.W., P.R. England, **G. Luikart**, G.A. Ritchie, and N. Ryman. 2008. Genetic effects of harvest on wild animal populations. *Trends in Ecology and Evolution*, 6:327-337.
- Luikart, G.**, S., Zundel, D. Rioux, C. Miquel, K.A. Keating, J. T. Hogg, B. Steele, K. Foresman, and P. Taberlet. 2008. Low genotyping error rates for microsatellite multiplexes and noninvasive fecal DNA samples from bighorn sheep. *Journal of Wildlife Management*, 72:299-304.
- Tallmon, D., A. Koyuk, **G. Luikart**, and M. Beaumont. 2008. OneSamp: a program to estimate effective population size using approximate Bayesian computation. *Molecular Ecology Resources*, 8:299-301.
- Chen, S., *V. Costa, V., M. Azevedo, **G. Luikart**, and A. Beja-Pereira. 2008. New alleles of the bovine kappa-casein gene revealed by re-sequencing and haplotype inference analysis. *J. Dairy Science*, 91:3682-3686.
- Manel, S., F. Berthoud, *E. Bellemain, M. Gaudeul, **G. Luikart**, J.E. Swenson, L.P. Waits, and P. Taberlet. 2007. A new individual-based spatial approach for identifying genetic discontinuities in natural populations: example application in brown bears. *Molecular Ecology*, 16:2031-2043.
- *Antao, T., A. Beja-Pereira, and **G. Luikart**. 2007. MODELER4SIMCOAL2: A user-friendly, extensible modeler of demography and linked loci for coalescent simulations. *Bioinformatics*, 23:1848-50.
- Schwartz, M.K., **G. Luikart**, and R.S. Waples. 2007. Genetic monitoring as a promising tool for conservation and management. *Trends in Ecology and Evolution*, 22:25-33.

- *von Hardenberg, A., B. Bassano, M. Festa-Bianchet, **G. Luikart**, P. Lanfranchi, and D. Coltman. 2007. Age-dependent genetic effects on a secondary sexual trait in male Alpine ibex *Capra ibex*. *Molecular Ecology*, 16:1969–1980.
- England, J.-M. Cornuet, *P. Berthier, D.A. Tallmon and **G. Luikart**. 2006. Estimating effective population size from linkage disequilibrium: severe bias using small samples. *Conservation Genetics*, 7:303-308.
- Hogg, J.T., S.H. Forbes, B.M. Steele, and **G. Luikart**. 2006. Genetic rescue of an insular population of large mammals. *Proceedings of the Royal Society*, 273:1491-1499.
- Jordan, S., C. Miquel, P. Taberlet, and **G. Luikart**. 2006. Sequencing primers and SNPs for five rapidly evolving reproductive loci in endangered ibex and their kin (Bovidae, *Capra spp.*), *Molecular Ecology Notes*, 6:776-779.
- Liu, Y-P., G-S. Wu, Y-G. Yao, Y-W Miao, **G. Luikart**, *M. Baig, A. Beja-Pereira, Z-L. Ding, M G. Palanichamy, and Y-P. Zhang. 2006. Multiple maternal origins of chickens: Out of the Asian jungles. *Molecular Phylogenetics and Evolution*, 38:12-19.
- Beja-Pereira, A., **G. Luikart** et al. 2006. Genetic evidence for multiple origins of European cattle in Near-East, Africa, and Europe. *Proceedings of the National Academy of Sciences, USA*, 103:8113-8118.
- *Valière, N., C. Bonenfant, C. Toigo, **G. Luikart**, J.-M. Gaillard, and F. Klein. 2006. Importance of a pilot study for non-invasive genetic sampling: genotyping errors and population size estimation in red deer.
- Fernández, H., G. Hodgins, C. Miquel, C. Hänni, **G. Luikart**, and P. Taberlet. 2006. Divergent mtDNA lineages of goats in an early Neolithic site, far from the initial domestication areas. *Proceedings of the National Academy of Sciences, USA*, 103:15375-15379.
- *Da Silva, A., **G. Luikart**, N.G. Yoccoz, A. Cohas, and D. Allainé. 2005. Genetic diversity-fitness correlation revealed by microsatellite analyses in European Alpine marmots (*Marmota marmota*). *Conservation Genetics*, 7:371-382.
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PUBLICATIONS (selected papers in review/prep): (*students)

- Hand, B.K., Kovach, R., C.C. Muhlfeld, D. Whited, and **G. Luikart**. Climate variables explain genetic differentiation within metapopulations of steelhead trout: The Importance of Replication and Uncertainty Assessments in Landscape Genetics. *Molecular Ecology*, Accepted pending revisions.
- Scribner K.T. et al. Applications of genetic data to improve management and conservation of river fishes and their habitats. *Fisheries*, In Review.
- *Hand, B.K., D.W. Raiford, W.H. Lowe, P.C. Cross, N.J. Anderson, S. Chen, and **G. Luikart**. Confronting uncertainty in landscape genetics: a case study of elk connectivity in the Greater Yellowstone Ecosystem. *J. Heredity*, In review.
- *Antao, T., I.M. Hastings, **G. Luikart**, and M.J. Donnelly. Estimating effective population size in disease vectors: a critical assessment of applications and performance. In review.
- Luikart, G.**, T. Antao, M.C. Boyer, C.C. Muhlfeld, R. Waples, et al. Estimating the effective number of breeders (N_b): Effects of life history and sampling strategy on performance of the LDNe one-sample method. In prep.
- Andrews, K.R., P.A. Hohenlohe, M.R. Miller, J. Good, G. Luikart. Harnessing the power of RADseq for ecological and evolutionary genomics. Invited review, *Nature Review Genetics*, In Prep.

SELECTED GRANTS AND CONTRACTS AWARDED: (selected examples)

- NASA-ROSES (Ecological forecasting for conservation): Projecting effects of climate change on river habitats and salmonid fishes. 2014-2018.
- NSF-DEB: Evolutionary mechanisms influencing the spread of hybridization: genomics, fitness, and dispersal. 2013-2017.
- NSF-EID (Ecology of infectious diseases): Effects of land-use and predation risk on wildlife contact networks and *Brucella* transmission in the Yellowstone Ecosystem. 2010-2014.
- NSF-EID: Microparasite-Macroparasite Interactions: Dynamics of Co-infection and Implications for Disease Control. Co-PI with V. Ezenwa, A. Jolles, E. Nunn. 2007-2011.
- NSF-IGERT: Montana Ecology of Infectious Diseases: Integrative Graduate Training on Multi-scalar Computational, Mathematical and Empirical Approaches to Complex Biological Problems. Added as co-PI with Bill Holben, Jesse Johnson, Jonathan Graham. 2006-2013.
- USGS-PNW Climate center: Predicting Climate Change Impacts on River Ecosystems and Salmonids across the Pacific Northwest: Combining Vulnerability Modeling, Landscape Genomics, and Economic Evaluations for Conservation. 2012-2015.
- ARC (Australian Research Council) Linkage grant funding for a research project entitled "Genomics for persistence of Australia freshwater fish". P. Sunnucks et al. 2010-2015
- USFWS, USGS, and NPS: Estimating the number of breeders in lake trout and bull trout following suppression of lake trout. 2012-2015.

SYNERGISTIC ACTIVITIES & OUTREACH:

- **Development of Young Scientists** – I have mentored >50 university students (& published with >30), mentored >6 postdocs, and helped occasional high school students in research projects. My lab group and I mentored 8 university undergrads from Montana and nationwide working on aquatic ecology projects for 2-20 weeks per student in 2013-2014. I also teach several primary school classes each year about science, aquatic ecology, & conservation biology.
- **Organizing international courses** on Population Genetic Data Analysis for graduate students, Portugal, 2006, 2008; for MS, PhD, postdocs and faculty, Montana, 2007, 2009, 2011, 2013; e.g. www.popgen.net/congen2013. Workshop/course on invasive species detection with represents from US Forest Service, US Geological Survey, Montana Fish Wildlife and Parks, and the Missoula County Weed District.
- **Development of educational and fundraising videos** – on "Conservation Genetics" <https://www.youtube.com/watch?v=MlaQnjibMq0>; and "Aquatic invasive species" prevention and eDNA detection <https://www.youtube.com/watch?v=Fx-CcXHdlIc&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.gyebrucellosis.net/index.php>.

- **Advising managers and conservation agencies** (selected examples) – Montana Fish Wildlife and Parks cutthroat trout conservation committee; expert witness and consultant on hatcheries and wild salmon for Wild Fish Conservancy (WFC), Oregon and Washington state 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, 2001–2011
- **Formal exchange program agreements** – Established between The University of Montana and The University of Porto, Portugal, 2007, 2009-present; Obtained funding for 6 students and 3 faculty from Montana to travel to and research in Portugal, 2006-present.
- **Reviewer** (for numerous journals and agencies) – Examples: Nature Reviews Genetics, Proceedings of the Royal Society B, Science, Trends in Ecology & Evolution, Science, NSF-EID panel member, and NSF proposal reviewer.