Eric C. Anderson

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EDUCATION

Ph.D. (Quant. Ecol. & Res. Mgmt.)	2001	University of Washington, Seattle, WA
M.S. (Fisheries)	1998	University of Washington, Seattle, WA
B.A. (Human Biology)	1993	Stanford University, Stanford, CA
—	1990–91	Prescott College, Prescott, AZ
High School Diploma	1988	The Thacher School, Ojai, CA

GRANTS AND FELLOWSHIPS

2013–17 Co-PI. National Science Foundation Division of Ocean Sciences Award #1260693. *Integrative evaluation of larval dispersal and delivery in kelp rockfish using intergenerational genetic tagging, demography and oceanography* (PI: Mark Carr, UCSC) $878,770

2012–13 PI. Pacific Salmon Commission Chinook Technical Committee (US Section) Grant Funded under the 2008 Letter of Agreement: *Simultaneous inference of parentage and population origin to estimate abundance and escapement of Pacific salmon.* $78,378.

2008–9 PI. Pacific Salmon Commission Chinook Technical Committee (US Section) Grant Funded under the 2008 Letter of Agreement: *Computational algorithms and user-friendly software for parentage-based tagging of Pacific salmonids.* $49,803.

2005–06 Co-PI. Pacific Salmon Commission Chinook Technical Committee-Funded Grant: *Power Analysis of the Chinook salmon DNA baseline developed by the Genetic Analysis of Pacific Salmon (GAPS) group.* ≈$10,000.

1999–01 Designated Research Assistant, National Science Foundation Grant #BIR-9807747, *Computational Methods for Inference of Population Parameters*, (PI: E.A. Thompson).

1996–99 Trainee, National Science Foundation Mathematical Biology Training Grant #BIR-9256532, University of Washington. (PIs: G.M Odell and T.L. Daniel)

1998 Fellow, Program in Mathematics and Molecular Biology, Burroughs Wellcome Fund, University of Washington.

1994–96 Fellow, H. Mason Keeler Endowment for Excellence. School of Fisheries, University of Washington.

HONORS AND AWARDS

2000 First Prize, Western North American Region Student Papers Competition, International Biometrics Society Conference, July, 2000, Berkeley, CA, for talk titled "Bayesian analysis of genetic mixture and admixture."

1993 Phi Beta Kappa and graduation "With Distinction," Stanford University.

EMPLOYMENT

2008–12 Assistant Adjunct Professor, Department of Applied Mathematics and Statistics, University of California, Santa Cruz.

2003– Research Molecular Geneticist, National Marine Fisheries Service, Southwest Fisheries Science Center, Santa Cruz Lab, Santa Cruz, California.

2001–03	Postdoctoral Researcher, National Institutes of Health Grant #GM-40282 to Montgomery Slatkin, "Models of Complex Genetic Systems." Department of Integrative Biology, University of California, Berkeley.
1999–01	Research Assistant, NSF Grant #BIR-9807747 to Elizabeth A. Thompson, "Computational Methods for Inference of Population Parameters." Department of Statistics, University of Washington, Seattle.
1999	Pre-Doctoral Lecturer. Prepared syllabus and lectured for the first four weeks of Biology 472, Advanced Undergraduate Ecology. Summer. University of Washington, Seattle.
1997	Graduate Assistant, Curriculum development, Department of Statistics, University of Washington, Seattle
1994–98	Research Assistant, Center for Streamside Studies, School of Fisheries, Quantitative Ecology and Resource Management, and Department of Statistics, University of Washington, Seattle.

TEACHING

2017	Case Studies in Reproducible Research. Seminar in Ecology and Evolutionary Biology Dept., UCSC. Spring. Course website: `http://eriqande.github.io/rep-res-eeb-2017/`
2015	Guest lecturer. Delivered the lecture "Uses of genetic markers in conservation of Pacific salmon." to the Marine Sciences 341 class (Marine Population and Evolutionary Genetics) at CSU Monterey Bay. Autumn.
2014	Reproducible Research. Informal 11 week course given to colleagues at NMFS, UCSC graduate students, and local high school students. Autumn. Course website: `http://eriqande.github.io/rep-res-web/`.
2012	Practical Computing for Biologists and Scientists. Informal 15 week course given to colleagues at NMFS and 6 local high school students. Autumn.
2010	Guest Lecturer. Delivered the lecture "Salmon in the Ocean: Where are they Coming From? How Many are Out There?" to undergraduate students at Beam Reach Science School, Friday Harbor, WA. September
2010	Lecturer. As adjunct professor I developed the one-quarter course, "Applications of Bayesian nonparametric methods in statistical genetics," taught as AMS 291— Advanced Topics in Bayesian Inference. Spring Quarter 2010 at UCSC. [Course Website].
2009-12	Lecturer. Prepared syllabus, wrote lecture notes, and delivered roughly 10 hours of lectures on "Inference of relationships and relatedness from genetic data" at the Summer Institute for Statistical Genetics at the University of Washington, Department of Biostatistics (09–12), and at the European Institute for Statistical Genetics in Edinburgh (2012). Co-taught with Elizabeth A. Thompson.
2007	Guest Lecturer. Delivered a lecture on "The Wright-Fisher model and the coalescent," for Biological Sciences 107. Population Genetics. University of California, Santa Cruz. January.
2004–14	Lecturer. Prepared syllabus, wrote lecture notes, and delivered roughly 10 hours of lectures on "Markov chain Monte Carlo for Geneticists" at the Summer Institute for Statistical Genetics at North Carolina State University, Bioinformatics Research Center (04 and 05) and University of Washington, Department of Biostatistics (06,08).

2004	Lecturer. Delivered lectures on Bayesian data analysis and the program *structure* at the "Recent Advances in Conservation Genetics" course at the Smithsonian Institution's Conservation & Research Center. August. Front Royal, VA.
1999	Pre-Doctoral Lecturer. Prepared syllabus, delivered all lectures, maintained course web site, wrote exams and problem sets, for the first half of Biology 472, Advanced Undergraduate Ecology. Summer. Department of Biology, University of Washington, Seattle.
1999	Guest Lecturer. Delivered guest lectures on random walks and renewal processes for the undergraduate level stochastic processes course Statistics 396, and a guest lecture on the Monte Carlo method and importance sampling for the graduate-level statistical genetics course, Statistics 578C. My Lecture Notes from this have been widely circulated over the Web. Department of Statistics, University of Washington, Seattle.
1997–98	Paid Tutor for students in Statistics 512 and 513 (graduate mathematical statistics), University of Washington.
1995	Teaching Assistant, University of San Francisco Wildlands Study Program. Assisted Dr. John McLaughlin on a three-week summer course studying carnivores and conservation in the North Cascades, Washington.

Students Advised/Mentored

Thomas Ng, UCSC, Biomolecular Engineering. I am currently the supervisor of Thomas' committee. Advanced to Ph.D. candidacy in February 2016.

Benjamin Moran, Northeastern University Hollings Scholar. Benjamin completed a summer internship wiht me developing the R package `rubias`. Summer 2016.

Elena Venable, Brown University Hollings Scholar. Elena completed a summer internship with me developing a statistical method for identifying contaminated genetic samples from SNP data. Summer 2014.

Anthony Clemento, UCSC, Ocean Sciences, Ph.D. completed December 2013. Member of supervisory committee.

Josh Israel, UC Davis, Ecology, Ph.D. completed June 2007. "Conservation genetics of North American green sturgeon: advances for precautionary management and population monitoring." Member of supervisory committee.

Jazz Pouls. High-school junior at Pacific Collegiate School. I advised him on his science fair project: a bioinformatic analysis of next generation sequencing data from the Swainson's thrush. His work won top honors at the county level, and he was a co-author on Ruegg et al. (2014b) for his role in the analysis.

Veronica Mayorga, UCSC, former Ph.D. student in Computer Science and Applied Math and Statistics. I mentored Veronica in a one year graduate student research assistantship (2008/2009) implementing software for parentage inference.

Kevin K. Dunham, undergraduate intern from Cabrillo College. Kevin worked with me for a year in 2004/5 learning to do Unix scripting, simulation of genetic models, plotting in R, and typesetting with LaTeX, leading to three publications.

Chizu Kawamoto, outstanding high school student at Pacific Collegiate School. I mentored her in an independent study in probability and statistics and advised her on a senior science project investigating the use of genetic data to improve salmon fishery forecasts off the coast of California. Her project one top honors in the senior division of the Santa Cruz County Science Fair.

PUBLICATIONS

Peer-Reviewed Journal Articles

Anderson, EC, TC Ng, ED Crandall, and JC Garza (2017). Genetic and individual assignment of tetraploid green sturgeon with SNP assay data. *Conservation Genetics* 1–12. DOI: `https://doi.org/10.1007/s10592-017-0963-5`.

Ruegg, KC, EC Anderson, RJ Harrigan, KL Paxton, JF Kelly, F Moore, and TB Smith (2017). Genetic assignment with isotopes and habitat suitability (GAIAH), a Migratory Bird Case Study. *Methods in Ecology and Evolution*. DOI: `10.1111/2041-210X.12800`.

Steinhorst, K, T Copeland, MW Ackerman, WC Schrader, and EC Anderson (2017). Abundance estimates and confidence intervals for the run composition of returning salmonids. *Fishery Bulletin* **115**:1–12.

Waples, RS and EC Anderson (2017). Purging putative siblings from population genetic data sets: a cautionary view. *Molecular Ecology* **26**:1211–1224.

Wringe, BF, RR Stanley, NW Jeffery, EC Anderson, and IR Bradbury (2017). parallelnewhybrid: an R package for the parallelization of hybrid detection using NEWHYBRIDS. *Molecular Ecology Resources* **17**:91–95.

Bravington, MV, HJ Skaug, EC Anderson, et al. (2016). Close-kin mark-recapture. *Statistical Science* **31**:259–274.

Anderson, EC and PD Barry (2015). Interpreting the flock algorithm from a statistical perspective. *Molecular Ecology Resources* **15**:1020–1030. ISSN: 1755-0998. DOI: `10.1111/1755-0998.12417`. URL: `http://dx.doi.org/10.1111/1755-0998.12417`.

Anderson, EC and TC Ng (2015). Bayesian pedigree inference with small numbers of single nucleotide polymorphisms via a factor-graph representation. *Theoretical Population Biology*. DOI: `http://dx.doi.org/10.1016/j.tpb.2015.09.005`.

Ciancio, JE, CR Rossi, M Pascual, E Anderson, and JC Garza (2015). The invasion of an Atlantic Ocean river basin in Patagonia by Chinook salmon: new insights from SNPs. *Biological Invasions* **17**:2989–2998.

Hagenlund, M, K Østbye, K Langdal, M Hassve, RA Pettersen, E Anderson, F Gregersen, and K Præbel (2015). Fauna crime: elucidating the potential source and introduction history of European smelt (*Osmerus eperlanus* L.) into Lake Storsjøen, Norway. *Conservation Genetics* 1–14.

Hasselman, DJ, EC Anderson, EE Argo, ND Bethoney, SR Gephard, DM Post, BP Schondelmeier, TF Schultz, TV Willis, and EP Palkovacs (2015). Genetic stock composition of marine bycatch

reveals disproportional impacts on depleted river herring genetic stocks. *Canadian Journal of Fisheries and Aquatic Sciences* **73**:951–963.

Satterthwaite, WH, J Ciancio, E Crandall, ML Palmer-Zwahlen, AM Grover, MR O'Farrell, EC Anderson, MS Mohr, and JC Garza (2015a). Stock composition and ocean spatial distribution inference from California recreational Chinook salmon fisheries using genetic stock identification. *Fisheries Research* **170**:166–178.

Anderson, EC and TC Ng (2014). Comment on 'Bayesian parentage analysis with systematic accountability of genotyping error, missing data and false matching'. *Bioinformatics (Oxford, England)* **30**:743–745.

Anderson, EC, HJ Skaug, and DJ Barshis (2014). Next-generation sequencing for molecular ecology: a caveat regarding pooled samples. *Molecular ecology* **23**:502–512.

Clemento, AJ, ED Crandall, JC Garza, and EC Anderson (2014). Evaluation of a single nucleotide polymorphism baseline for genetic stock identi cation of Chinook Salmon (Oncorhynchus tshawytscha) in the California Current large marine ecosystem. *Fishery Bulletin* **112**:

Garza, JC, EA Gilbert-Horvath, BC Spence, TH Williams, H Fish, SA Gough, JH Anderson, D Hamm, and EC Anderson (2014). Population Structure of Steelhead in Coastal California. *Transactions of the American Fisheries Society* **143**:134–152.

Ruegg, KC, EC Anderson, KL Paxton, V Apkenas, S Lao, RB Siegel, DF DeSante, F Moore, and TB Smith (2014a). Mapping migration in a songbird using high-resolution genetic markers. *Molecular ecology* **23**:5726–5739.

Ruegg, K, EC Anderson, J Boone, J Pouls, and TB Smith (2014b). A role for migration-linked genes and genomic islands in divergence of a songbird. *Molecular ecology* **23**:4757–4769.

Satterthwaite, WH, MS Mohr, MR O'Farrell, EC Anderson, MA Banks, SJ Bates, MR Bellinger, LA Borgerson, ED Crandall, JC Garza, et al. (2014). Use of Genetic Stock Identification Data for Comparison of the Ocean Spatial Distribution, Size at Age, and Fishery Exposure of an Untagged Stock and Its Indicator: California Coastal versus Klamath River Chinook Salmon. *Transactions of the American Fisheries Society* **143**:117–133.

Abadía-Cardoso, A, EC Anderson, DE Pearse, and J Carlos Garza (2013). Large-scale parentage analysis reveals reproductive patterns and heritability of spawn timing in a hatchery population of steelhead (*Oncorhynchus mykiss*). *Molecular Ecology* **22**:4733–4746.

Ruegg, KC, HC Rosenbaum, EC Anderson, M Engel, A Rothschild, CS Baker, and SR Palumbi (2013). Long-term population size of the North Atlantic humpback whale within the context of worldwide population structure. *Conservation Genetics* **14**:103–114.

Steele, CA, EC Anderson, MW Ackerman, MA Hess, NR Campbell, SR Narum, MR Campbell, and J Grant (2013). A validation of parentage-based tagging using hatchery steelhead in the Snake River basin. *Canadian Journal of Fisheries and Aquatic Sciences* **70**:1046–1054.

Almudevar, A and EC Anderson (2012). A new version of PRT software for sibling groups reconstruction with comments regarding several issues in the sibling reconstruction problem. *Molecular Ecology Resources* **12**:164–178.

Anderson, EC (2012). Large-scale parentage inference with SNPs: an efficient algorithm for statistical confidence of parent pair allocations. *Statistical Applications in Genetics and Molecular Biology* **11**:

Ruegg, KC, EC Anderson, and H Slabbekoorn (2012). Differences in timing of migration and response to sexual signalling drive asymmetric hybridization across a migratory divide. *Journal of Evolutionary Biology* **25**:1741–1750.

Finger, AJ, EC Anderson, MR Stephens, BP May, and E Taylor (2011). Application of a method for estimating effective population size and admixture using diagnostic single nucleotide polymorphisms (SNPs): implications for conservation of threatened Paiute cutthroat trout *(Oncorhynchus clarkii seleniris)* in Silver King Creek, California. *Canadian Journal of Fisheries and Aquatic Sciences* **68**:1369–1386.

Kinziger, AP, RJ Nakamoto, EC Anderson, and BC Harvey (2011). Small founding number and low genetic diversity in an introduced species exhibiting limited invasion success (speckled dace, *Rhinichthys osculus*). *Ecology and Evolution* **1**:73–84.

Anderson, EC (2010a). Assessing the power of informative subsets of loci for population assignment: standard methods are upwardly biased. *Molecular Ecology Resources* **10**:701–10.

Ruegg, KC, EC Anderson, C Scott Baker, M Vant, JA Jackson, and SR Palumbi (2010). Are Antarctic minke whales unusually abundant because of 20th century whaling? *Molecular Ecology* **19**:281–291.

Clemento, AJ, EC Anderson, D Boughton, D Girman, and JC Garza (2009). Population genetic structure and ancestry of *Oncorhynchus mykiss* populations above and below dams in south-central California. *Conservation Genetics* **10**:1321–1336.

Israel, JA, KJ Bando, EC Anderson, and B May (2009). Polyploid microsatellite data reveal stock complexity among estuarine North American green sturgeon (*Acipenser medirostris*). *Canadian Journal of Fisheries and Aquatic Sciences* **66**:1491–1504.

Pearse, DE and EC Anderson (2009). Multiple paternity increases effective population size. *Molecular Ecology* **18**:3124–3127.

Pearse, DE, SA Hayes, MH Bond, CV Hanson, EC Anderson, RB Macfarlane, and JC Garza (2009). Over the falls? Rapid evolution of ecotypic differentiation in steelhead/rainbow trout (*Oncorhynchus mykiss*). *Journal of Heredity* **100**:515–525.

Anderson, EC and KK Dunham (2008). The influence of family groups on inferences made with the program Structure. *Molecular Ecology Resources* **8**:1219–1229.

Anderson, EC (2008). Bayesian inference of species hybrids using multilocus dominant genetic markers. *Philosophical Transactions of the Royal Society B: Biological Sciences* **363**:2841–2850.

Anderson, EC, RS Waples, and ST Kalinowski (2008). An improved method for predicting the accuracy of genetic stock identification. *Canadian Journal of Fisheries and Aquatic Sciences* **65**:1475–1486.

Hayes, SA, MH Bond, CV Hanson, EV Freund, JJ Smith, EC Anderson, AJ Ammann, and RB Mac-Farlane (2008). Steelhead growth in a small central California watershed: upstream and estuarine rearing patterns. *Transactions of the American Fisheries Society* **137**:114–128.

Kinziger, AP, EJ Loudenslager, DG Hankin, EC Anderson, and JC Garza (2008). Hybridization between spring-and fall-run Chinook salmon returning to the Trinity River, California. *North American Journal of Fisheries Management* **28**:1426–1438.

Sogard, SM, E Gilbert-Horvath, EC Anderson, R Fisher, SA Berkeley, and JC Garza (2008). Multiple paternity in viviparous kelp rockfish, Sebastes atrovirens. *Environmental Biology of Fishes* **81**:7–13.

Anderson, EC and M Slatkin (2007). Estimation of the number of individuals founding colonized populations. *Evolution* **61**:972–983.

Spies, IB, EC Anderson, K Naish, and P Bentzen (2007). Evidence for the existence of a native population of sockeye salmon (Oncorhynchus nerka) and subsequent introgression with introduced populations in a Pacific Northwest watershed. *Canadian Journal of Fisheries and Aquatic Sciences* **64**:1209–1221.

Anderson, EC and JC Garza (2006). The power of single nucleotide polymorphisms for large-scale parentage inference. *Genetics* **172**:2567–2582.

Anderson, EC (2005). An efficient Monte Carlo method for estimating Ne from temporally spaced samples using a coalescent-based likelihood. *Genetics* **170**:955–967.

Anderson, EC and K Dunham (2005). spip 1.0: a program for simulating pedigrees and genetic data in age-structured populations. *Molecular Ecology Notes* **5**:459–461.

Palsbøll, P, M Bérubé, EC Anderson, and K Dunham (2005). High levels of statistical uncertainty in 'gametic'recapture estimates of male abundance in humpback whales. *Marine Ecology Progress Series* **295**:305–307.

Anderson, EC and M Slatkin (2004). Population-genetic basis of haplotype blocks in the 5q31 region. *The American Journal of Human Genetics* **74**:40–49.

Anderson, EC and J Novembre (2003). Finding haplotype block boundaries by using the minimum-description-length principle. *The American Journal of Human Genetics* **73**:336–354.

Anderson, EC and M Slatkin (2003). Orr's quantitative trait loci sign test under conditions of trait ascertainment. *Genetics* **165**:445–446.

Anderson, EC and E Thompson (2002). A model-based method for identifying species hybrids using multilocus genetic data. *Genetics* **160**:1217–1229.

Anderson, EC and PA Scheet (2001). Improving the estimation of bacterial allele frequencies. *Genetics* **158**:1383–1386.

Anderson, EC, EG Williamson, and EA Thompson (2000). Monte Carlo evaluation of the likelihood for Ne from temporally spaced samples. *Genetics* **156**:2109–2118.

Peer-Reviewed Book Chapters

Anderson, EC (2009). Statistical methods for identifying hybrids and groups. In: *Population Genetics and Animal Conservation*. Ed. by G Bertorelle, M Bruford, H Hauffe, A Rizzoli, and C Vernesi. New York: Cambridge University Press. pp. 25–41.

Naiman, RJ and EC Anderson (1997). Streams and rivers: their physical and biological variability. In: *The rain forests of home: profile of a North American bioregion. Island Press, Washington, DC, USA*. pp. 131–148.

Reports (not Peer-Reviewed)

Satterthwaite, W, E Anderson, M Campbell, JC Garza, M Mohr, S Narum, and C Speir (2015b). *Multidisciplinary evaluation of the feasibility of parentage-based genetic tagging (PBT) for management of Pacific salmon*. Tech. rep.

Anderson, EC (2010b). *Computational algorithms and user-friendly software for parentage-based tagging of Pacific salmonids*. Final report submitted to the Pacific Salmon Commission's Chinook Technical Committee (US Section). 46 p.

Anderson, EC and JC Garza (2009). *Estimation of population size with molecular genetic data*. U.S. Department of Commerce, NOAA Technical Memorandum NOAA-TM-NMFS-SWFSC-448. 57 p.

Manoukis, NC and EC Anderson (2008). *GuiLiner: A Configurable and Extensible Graphical User Interface for Scientific Analysis and Simulation Software*. arXiv preprint arXiv:0806.0314.

Boughton, DA, PB Adams, EC Anderson, C Fusaro, EA Keller, E Kelley, LD Lentsch, JL Nielsen, K Perry, H Regan, et al. (2007). *Viability criteria for steelhead of the south-central and southern California coast*. U.S. Department of Commerce, NOAA Technical Memorandum NMFS, NOAA-TM-NMFS-SWFSC-407, 33 p.

Garza, JC and EC Anderson (2007). *Large scale parentage inference as an alternative to coded-wire tags for salmon fishery management*. In: PSC Genetic Stock Identification Workshop (May, September 2007): Logistics Workgroup final report, and recommendations, p. 48-55. Pacific Salmon Commission, Vancouver, British Columbia, Canada.pp. 48–55.

Boughton, DA, PB Adams, E Anderson, C Fusaro, E Keller, E Kelley, LD Lentsch, JL Nielsen, K Perry, H Regan, et al. (2006). *Steelhead of the south-central/southern California coast: population characterization for recovery planning*. U.S. Department of Commerce, NOAA Technical Memorandum NMFS, NOAA-TM-NMFS-SWFSC-394, 116 p.

Anderson, EC and JC Garza (2005). *A description of full parental genotyping*. Report submitted to the Pacific Salmon Commission, Vancouver, British Columbia. 11 p.

Conference Proceedings (not Peer-Reviewed)

Anderson, EC and EA Thompson (1999). MCMC likelihoods for population genetics. In: *Proceedings of the 52nd Session of the International Statistical Institute*. Vol. 3pp. 347–348.

THESES AND DISSERTATIONS

ANDERSON, E.C. (2001) Monte Carlo methods for inference in population genetic models. Ph.D. Dissertation, University of Washington (Advisor: Dr. Elizabeth Thompson).

ANDERSON, E.C. (1998) Inferring the ancestral origin of sockeye salmon, *Oncorhynchus nerka*, in the Lake Washington basin: A statistical method in theory and application. Master's Thesis. University of Washington (Advisor: Dr. Thomas Sibley).

SOFTWARE AUTHORED

`SNPPIT`: A program for performing fast and accurate, likelihood-based, parentage inference with single nucleotide polymorphisms (SNPs). Described in report provided with the software.

`nfCoNe`: Computes the likelihood of the number of founding lineages using the computational machinery of `CoNe`. Described in Anderson & Slatkin (2007).

`CoNe`: Computes the likelihood of N_e given data on two temporally spaced genetic samples using a coalescent based likelihood model. Described in Anderson (2005).

`spip`: **S**imulate **P**edigrees **i**n **P**opulations. An application written in C for simulating pedigrees and genetic data in age-structured populations. Described in Anderson and Dunham (2005)

`MDBlocks`: Minimum Description Length Blocks. An application co-authored in C with John Novembre and distributed for free. It implements the minimum description length model selection procedure and dynamic programming algorithm described in Anderson and Novembre (2003) to delineate haplotype blocks in samples of phased SNP data.

`NewHybrids`: Program written in C and distributed for free, implementing a Gibbs sampler to estimate the posterior probability that genetically sampled individuals fall into each of a set of user-defined hybrid categories. Described in Anderson, E.C. and Thompson, E.A. (2002).

`GF(MC)`^{2}: GLUT for Markov Chain Monte Carlo. A small application programming interface written in C and distributed freely for using the OpenGL Utilities Toolkit to render real-time pictures of Markov Chain Monte Carlo simulations.

`MCLEEPS`: Monte Carlo Likelihood for Estimation of Effective Population Size. Program written in C and distributed for free. Implements the importance sampling algorithm described in Anderson et al. (2000) to estimate a population's genetically effective population size from temporally spaced samples.

SELECTED INVITED TALKS

ANDERSON, E.C. (2017) "Next-generation genetic technologies for studying marine larval dispersal: Microhaplotypes and kelp rockfish." Department of Marine and Environmental Biology, University of Southern California, Los Angeles, invited seminar, February.

ANDERSON, E.C. (2014) "A pseudo-Gibbs sampler for computationally efficient pedigree inference from SNPs in molecular ecology applications," International Centre for Mathematical Sciences, Edinburgh, Scotland. Invited participant at the workshop, "Statistical and computational methods for relatedness and relationship inference from genetic marker data," September.

ANDERSON, E.C. (2013) UCSF Biostatistics: "Computational aspects of pedigree reconstruction in large problems," University of California, San Francisco, Dept. of Biostatistics, invited seminar, December.

ANDERSON, E.C. (2011) "Parentage-based tagging of Pacific Salmon: Statistical challenges and opportunities for evolutionary research," University of Idaho, Departments of Statistics, Mathematics, and Biology, and the Initiative For Bioinformatics and Evolutionary Studies, invited seminar, March.

ANDERSON, E.C. (2010) "Parentage-based tagging: an up-and-coming fishery-management tool with benefits for hatchery managers," USFWS Pacific Region Hatchery Management Workshop. Pasco. WA. November.

ANDERSON, E.C. (2010) "Statistical and Computational Aspects of Parentage-Based Tagging of Salmon", Humboldt State University Mathematics Department Colloquium. February.

ANDERSON, E.C. (2009) "Statistical and computational advances for intergenerational genetic tagging of Pacic salmon", CSTAR Group Seminar, UCSC. February.

ANDERSON, E.C. (2009) "Parentage-based tagging of Pacific salmon with single nucleotide polymorphisms," invited to the International Workshop on Kinship-based Genetic Methods for Marine Resource Management. Institute for Marine Research, Bergen, Norway. April.

ANDERSON, E.C. (2008) "Genetic methods for ocean monitoring and harvest management of Pacific salmon," invited departmental seminars at Monterey Bay Aquarium Research Institute and Stanford University Hopkins Marine Station. Moss Landing/Pacific Grove, CA, October.

ANDERSON, E.C. (2007) "On the statistical power of single nucleotide polymorphisms for conservation-genetic applications," invited to the International Workshop on Population Genetics for Animal Conservation–II, Monte Bondone, Trento, Italy, September.

ANDERSON, E.C. (2007) "Computational and statistical methods for large-scale parentage inference," University of Michigan Bioinformatics Seminar. (Quicktime movie available from http://treehouse.ctaalliance.org/).

ANDERSON, E.C., Finger, A, Stephens, M (2007) "Joint estimation of N_e and admixture proportions in golden trout, with a coalescent likelihood", Genomic Variation Laboratory Seminar, UC Davis. December.

ANDERSON, E.C. (2006) "Model-based statistical inference and hybridization," invited keynote lecture at the Symposium on Hybridization in Animals—Extent, Processes, and Evolutionary Impact. Johann Wolfgang Goethe University, Frakfurt Main, Germany, October.

ANDERSON, E.C. (2006) "Computational and statistical algorithms for parentage inference with single nucleotide polymorphisms," invited to session on Statistical Methods in Computational Biology. Joint Statistical Meetings. Seattle, WA, August.

ANDERSON, E.C. (2005) "Efficient computations on the coalescent for estimating N_e from two temporally-spaced samples," University of California at Santa Cruz, Applied Math and Statistics Seminar. April.

ANDERSON E.C. and Garza, J.C. (2005) "Genetic Technologies for Monitoring of Central Valley Chinook: Genetic Stock Identication (GSI) and Full Parental Genotyping (FPG)" at the

CALFED Science Program and U.S. Fish and Wildlife Service's Workshop on Monitoring Central Valley Chinook salmon and steelhead populations. Tiburon Center, August.

ANDERSON, E.C., Garza, J.C. (2005) "Large Scale Parentage Analysis a.k.a. 'Full Parental Genotyping' as an Alternative or Complement to Coded Wire Tagging," invited to the Salmonid Restoration Federation Conference (Genetics Section), Fortuna, CA. April.

ANDERSON, E.C. (2003) "Bayesian methods for inferring population structure, hybridization, and migration using multilocus genetic data," invited to the International Workshop on Population Genetics for Animal Conservation, Monte Bondone, Trento, Italy, September.

ANDERSON, E.C. (2002) "Statistical identification of hybrid individuals using genetic markers." University of Caifornia, Berkeley, Museum of Vertebrate Zoology Seminar. October.

ANDERSON, E.C. (2001) "Bayesian Analysis of Population-Genetic Mixture and Admixture," USC Program in Molecular and Computational Biology, Departmental Seminar. Los Angeles. May.

ANDERSON, E.C. (2001) "Bayesian methods for inference in populations of hybridizing fish," invited to session on Statistics in Fisheries I. Joint meetings of the Statistics Society of Canada, Western North American Region of the International Biometrics Society, and International Mathematics Society. Burnaby, Canada, July.

ANDERSON, E.C. (2000) "Salmon, genetics, and Monte Carlo," invited departmental seminar, Department of Mathematics and Statistics, Simon Fraser University. Burnaby, Canada, April.

SELECTED CONTRIBUTED TALKS

ANDERSON, E.C. (2010) "Single Nucleotide Polymorphisms for Intergenerational Tagging", SNP Workshop III: Applications of SNP Genotyping in Non-Model Organisms. Blaine, Washington. March.

ANDERSON, E.C. (2008) "Further adventures in biasing the predicted accuracy of GSI: 'high-grading' loci and 'beeng-up' your baseline," Coastwide Salmonid Genetics Meeting, Olympia, Washington. June.

ANDERSON, E.C. (2006) "SNPs for genetic stock identification: how many? Insights from neutral-evolution simulations." Coastwide Salmonid Genetics Meeting, Santa Cruz, CA. June.

ANDERSON, E.C. (2004) "Efficient Monte Carlo computations on the coalescent for estimating Ne from two temporally-spaced samples," Evolution 2004. Fort Collins, CO. June.

ANDERSON, E.C. (2002) "Identifying species hybrids using multilocus genetic data," Evolution 2002. Urbana-Champaign, June.

ANDERSON, E.C. and Pritchard, J. K. (2000) "Bayesian analysis of population mixture and admixture," International Biometrics Conference, Berkeley, July.

ANDERSON, E.C. (1999) "Analyzing genetic mixtures using reversible jump Markov chain Monte Carlo," informal seminar to the Department of Statistics while visiting the Mathematical Genetics Group, Department of Statistics, University of Oxford, UK, November.

Anderson, E.C., Thompson, E.A., and Williamson, E.G. (1999) "Importance sampling for Monte Carlo evaluation of the likelihood for effective population size," Western North American Region of the International Biometrics Society conference, Seattle, June.

Anderson, E.C. (1997) "The origins of Lake Washington sockeye salmon: What can genetic data tell us?" presented at the multi-agency Lake Washington Workshop, December.

POSTERS

Anderson, E.C. and Novembre, J. (2002) "Haplotype block inference using the minimum description length principle," DIMACS/RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotype Inference, Rutgers University, Piscataway, November 21–22.

EDITORIAL DUTIES

Associate Editor for *Conservation Genetics.* 2007–2010.

COMMITTEE SERVICE

Co-Chair, Coastal California Distinct Population Segment Boundary Biological Review Team. 2010–.

Member, Technical Oversight Committee for Alaska Dept of Fish and Game-sponsored Auke Creek Sockeye Supplementation Parentage Project. 2008–.

Member, Information Technology Committee at FED, SWFSC. 2005–.

Member, Southern California and South-Central California Steelhead Technical Recovery Team. 2003–.

REFEREE FOR JOURNALS

American Journal of Human Genetics
Bioinformatics
BioMed Central Bioinformatics
Canadian Journal of Fisheries and Aquatic Sciences
Candollea
Conservation Genetics
Evolution
Genetical Research
Genetics
Journal of Fish Biology (UK)
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Molecular Ecology
Molecular Ecology Resources
Nature Reviews Genetics
North American Journal of Fisheries Management
Oikos
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Theoretical Population Biology