Curriculum Vitae

Peter Beerli

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Professional Preparation

1994 Doctor of Philosophy, Universität Zürich, Switzerland. Major: Biological Sciences. Zoology. Supervisors: Vincent Ziswiler, Thomas Uzzell, Robert Martin. *With distinction* [highest degree at University of Zurich].

Peter Beerli (1994). *Genetic isolation and calibration of an average protein clock in western Palearctic water frogs of the Aegean region. Dissertation Universität Zürich 1994. 90 pp*. (Doctoral dissertation, Universität Zürich, Switzerland). `http://people.sc.fsu.edu/∼pbeerli/ownpapers/phd-thesis-beerli-1994.pdf`.

1986 Master of Science, Universität Zürich, Switzerland. Major: Zoology. Ecological genetics. Supervisor: Hansjürg Hotz, Vincent Ziswiler.

Peter Beerli (1986). *Seefrösche in einer Tümpelfrosch-Wasserfrosch-Population in einem anthropogen beeinflussten Habitat. Diploma thesis, Universität Zürich: VII + 40 pp*. Master's thesis, Universität Zürich, Switzerland.

1979 Diploma, Lehrerseminar Kreuzlingen, Switzerland. Major: Education.

Nondegree Education and Training

1994–1996 Postdoctoral Study with Joseph Felsenstein, Genome Sciences, University of Washington, Seattle WA.

Professional Credential(s)

1979 – present Permission and Certification to Teach, Kanton Thurgau, Switzerland.

Professional Experience

2014–present	Full Professor, Department of Scientific Computing, Florida State University,Tallahassee.
2009–2014	Associate Professor, Scientific Computing, Florida State University.
2003–2009	Assistant Professor, Biological Sciences and School of Computational Science, Florida State University. Responsible for teaching and research in Computational Biology.
2000–2003	Research Assistant Professor, Genomics, University of Washington, Seattle WA. Responsible for research and teaching in Computational Population Genetics.
1996–1999	Research Associate, Genomics, University of Washington, Seattle WA. Responsible for research in Computational Population Genetics.
1985–1994	Co-owner, Kaden and Partner – Ecological Consulting. Acquisition, Organization, Execution of ecological studies contracted by the regional and state government in Switzerland.

Language Proficiency

French - advanced in speaking, reading, and writing.
German - native in speaking, reading, and writing.

Honors, Awards, and Prizes

2019-present	Fellow of the American Association for the Advancement of Science
2016-present	Member of the Faculty of 1000 (F1000 Faculty).
2014-present	Honorary member, Sociedad Chilena de Evolucion.
1994	Dissertation with Honors, University of Zürich, Switzerland.
1989	Award of the Fonds für Kunst und Wissenschaft [Fund for Art and Science] of the Teacher's College of Canton Thurgau for the research of the fauna in the Canton Thurgau, Switzerland.

Fellowship(s)

1994-1996	Swiss National Science Foundation Fellowship.

Current Membership in Professional Organizations

American Association for the Advancement of Science
American Genetic Association
American Society for Genetics
Sociedad Chilena de Evolucion
Society for Systematic Biology
Society for the Study of Evolution

RESEARCH

Statistics: Google Scholar (February 20, 2020)

	All	Since 2015
Citations	12403	4144
h-index	38	28
i10-index	54	44

Computer Software Development

Since 1999 I develop, distribute, and maintain an open-source inference program called MIGRATE. It allows biologists to estimate parameters of population genetics models, for example parameters such as population size and gene flow. The software is available from the websites `https://peterbeerli.com/migrate` or `http://popgen.sc.fsu.edu`. In addition to the software, the websites contain a manual, tutorials, and the source and binary executables to download. A help community is maintained through the google-group migrate-support.

Publications

[All publications were refereed, except when marked [u] (7 out of 68)]

68. Beerli, P., Mashayekhi, S., Sadeghi, M., Khodaei, M., & Shaw, K. (2019). Population genetic inference with MIGRATE. *Current Protocols in Bioinformatics*, e87. doi: 10.1002/cpbi.87
67. Mashayekhi, S., & Beerli, P. (2019). The fractional coalescent. *Proceedings of the National Academy of Sciences*: 1-6 [`https://www.pnas.org/content/early/2019/03/12/1810239116`]
66. Beerli, P., Ashki, H., Mashayekhi, S., & Palczewski, M. (2019). Population divergence time estimation using individual lineage label switching. *Biorxiv: http://biorxiv.org/cgi/content/short/587832v1*, 1-20 pages. [u]
65. Baco, A., Etter, R., Ribeiro, P. A., van der Heyden, S., Beerli, P., & Kinlan, B. P. (2016). A synthesis of genetic connectivity in deep-sea fauna and implications for marine reserve design. *Molecular Ecology*, *25*, 3276–3298. doi:10.1111/mec.13689
64. Beerli, P. (2016). Gene flow. In *Oxford Press Online Dictionary*. Oxford Press.
63. Çilingir, F., Akın Pekşen, Ambarlı, H., Beerli, P., & Bilgin, C. (2016). Exceptional maternal lineage diversity in brown bears (*Ursus arctos*) from Turkey. *Zoological Journal of the Linnean Society*, *176(2)*, 463-477.
62. Liu, P., Ye, M., Beerli, P., Zeng, X., Lu, D., & Tao, Y. (2016). Evaluating Bayesian Model Probabilities Using Markov Chain Monte Carlo with Thermodynamic Integration. *Water Resources Research*, *1944*, 1-29.
61. Plata Stapper, A., Beerli, P., & Levitan, D. (2015). Assortative Mating Drives Linkage-Disequilibrium between Sperm and Egg Recognition Protein loci in the Sea Urchin Strongylocentrotus purpuratus. *Molecular Biology and Evolution*, 1-45.
60. Chi, H., & Beerli, P. (2014). Quasi-Monte Carlo method in population genetics parameter estimation. *Mathematics and Computers in Simulation*, *103*, 33–38.
59. Jackson, J. A., Steel, D. J., Beerli, P., Congdon, B. C., Olavarria, C., Leslie, M. S., Pomilla, C., Rosenbaum, H., & Baker, C. S. (2014). Global diversity and oceanic divergence of humpback

whales (Megaptera novaeangliae). *Proceedings of the Royal Society, B Biological Sciences*, *281*, 20133222.

58. Palczewski, M., & Beerli, P. (2014). Population model comparison using multiple-locus datasets. In Ming-Hui Chen, Lynn Kuo, & Paul O Lewis (Eds.), *Bayesian Phylogenetics: Methods, Algorithms, and Applications* (pp. 187-200). CRC Press.

57. Bouzid, W., Stefka, J., Bahri-Sfar, I., Beerli, P., Loot, G., Lek, S., Haddaoui, N., Hypsa, V., Scholz, T., & Dkhil-Abbes, T. (2013). Pathways of cryptic invasion in a fish parasite traced using coalescent analysis and epidemiological survey. *Biological Invasions*, *15*, 1-17.

56. Hotz, H., Beerli, P., Uzzell, T., Guex, G.-D., Pruvost, N., Schreiber, R., & Plötner, J. (2013). Balancing a Cline by Influx of Migrants: A Genetic Transition in Water Frogs of Eastern Greece. *Journal of Heredity*, *104*, 57-71.

55. Palczewski, M., & Beerli, P. (2013). A Continuous Method for Gene Flow. *Genetics*, *194*, 687-696.

54. Qiu, F., Kitchen, A., Beerli, P., & Miyamoto, M. (2013). A possible explanation for the population size discrepancy in tuna (genus Thunnus) estimated from mitochondrial DNA and microsatellite data. *Molecular Phylogenetics and Evolution*, *66*, 463-468.

53. Ayres, D. L., Darling, A., Zwickl, D. J., Beerli, P., Holder, M. T., Lewis, P. O., Huelsenbeck, J. P., Ronquist, F., Swofford, D. L., Cummings, M. P., Rambaut, A., & Suchard, M. A. (2012). BEAGLE: an application programming interface and high-performance computing library for statistical phylogenetics. *Systematic Biology*, *61*, 170-173.

52. Bradic, M., Beerli, P., Garcia-de Leon, F. J., Esquivel-Bobadilla, S., & Borowsky, R. L. (2012). Gene flow and population structure in the Mexican blind cavefish complex (Astyanax mexicanus). *BMC Evolutionary Biology*, *12(1)*, 1-9.

51. Plötner, J., Baier, F., Akın, C., Mazepa, G., Schreiber, R., Beerli, P., Litvinchuk, S., Bilgin, C., Borkin, L., & Uzzell, T. (2012). Genetic data reveal that water frogs of Cyprus (genus Pelophylax) are an endemic species of Messinian origin. *Zoosystematics and Evolution*, *88*, 261–283.

50. Roshier, D., Heinsohn, R., Adcock, G., Beerli, P., & Joseph, L. (2012). Biogeographic models of gene flow in two waterfowl of the Australo-Papuan tropics. *Ecology and Evolution*, *2*, 2803–2814.

49. Akın, &., Bilgin, C. C. C., Beerli, P., Westaway, R., Ohst, T., Litvinchuk, S. N., Uzzell, T., Bilgin, M., Hotz, H., Guex, G.-D., & Plötner, J. (2010). Phylogeographic patterns of genetic diversity in eastern Mediterranean water frogs are shaped by past geologic events and cyclic climate changes. *Journal of Biogeography*, *37(11)*, 2111-2124.

48. Beaumont, M. A., Nielsen, R., Robert, C., Hey, J., Gaggiotti, O., Knowles, L., Estoup, A., Panchal, M., Corander, J., Hickerson, M., & others. (2010). In defence of model-based inference in phylogeography. *Molecular Ecology*, *19(3)*, 436-446.

47. Bedford, T., Cobey, S., Beerli, P., & Pascual, M. (2010). Global Migration Dynamics Underlie Evolution and Persistence of Human Influenza A (H3N2). *PLoS Pathogens*, *6(5)*, e1000918.

46. Beerli, P., & Palczewski, M. (2010). Unified Framework to Evaluate Panmixia and Migration Direction Among Multiple Sampling Locations. *Genetics*, *185*, 313-326.

45. Boykin, L. M., Shatters, R. G., Jr., Hall, D. G., Dean, D., & Beerli, P. (2010). Genetic variation of Anastrepha suspensa (Diptera: Tephritidae) in Florida and the Caribbean using Microsatellite DNA markers. *Journal of economic entomology*, *103(6)*, 2214-2222.

44. Plötner, J., Uzzell, T., Beerli, P., Akin, &., Bilgin, C. C., Haefeli, C., Ohst, T., Köhler, F., Schreiber, R., & Guex, G.-D. (2010). Genetic divergence and evolution of reproductive isolation in eastern Mediterranean water frogs. In M. Glaubrecht, & H. Schneider (Eds.), *Evolution in Action. Case studies in adaptive radiation and the origin of biodiversity* (pp. 373-404). Heidelberg, Springer.

43. Akın, C., Bilgin, C. C., Hotz, H., Beerli, P., Westaway, R., Ohst, T., Guex, G.-D., Litvinchuk, S. N., Uzzell, T., & Plötner, J. (2009). Summary of *Use of genetic divergence in water frogs to constrain geodynamics and landscape development in the eastern Mediterranean Region*. International Workshop on Active Tectonic Studies and Earthquake Hazard Assessment in Syria and Neighboring Countries, Arab School of Science and Technology Damascus Syria.

42. Beerli, P. (2009). How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use? In Bertorelle, Giorgio, Bruford, M W, Hauffe, Heidi C, Rizzoli, A, & Vernesi, C (Eds.), *Population Genetics for Animal Conservation* (pp. 42-79). Cambridge University Press, Cambridge UK.

41. Plötner, J., Köhler, F., Uzzell, T., Beerli, P., Schreiber, R., Guex, Gaston-Denis, & Hotz, H. (2009). Evolution of serum albumin intron-1 is shaped by a 5' truncated non-long terminal repeat retrotransposon in western Palearctic water frogs (Neobatrachia). *Mol Phylogenetics and Evolution*, *53(3)*, 784-91.

40. Douhan, G. W., Smith, M. E., Huyrn, K. L., Westbrook, A., Beerli, P., & Fisher, A. J. (2008). Multigene analysis suggests ecological speciation in the fungal pathogen Claviceps purpurea. *Molecular Ecology*, *17(9)*, 2276-86.

39. Plötner, J., Uzzell, T., Beerli, P., Spolsky, C., & OHST, T. (2008). Widespread unidirectional transfer of mitochondrial DNA: a case in western Palaearctic water frogs. *Journal of Evolutionary Biology*, *21*, 668–681.

38. Gonzalez, E. G., Beerli, P., & Zardoya, R. (2008). Genetic structuring and migration patterns of Atlantic bigeye tuna, Thunnus obesus (Lowe, 1839). *BMC Evolutionary Biology*, *8*, 252 (14 pages).

37. Hotz, H., Guex, G. D., Beerli, P., Semlitsch, R., & Pruvost, N. (2008). Hemiclone diversity in the hybridogenetic frog Rana esculenta outside the area of clone formation: the view from protein electrophoresis. *Journal of Zoological Systematics and Evolutionary Research*, *46(1)*, 56-62.

36. Beerli, P. (2007). Estimation of the population scaled mutation rate from microsatellite data. *Genetics*, *177(3)*, 1967-1968.

35. Plötner, J., Köhler, F., Uzzell, T., Beerli, P., & Spolsky, C. (2007). Molecular Systematics of Amphibians. In Harold Heatwole, & Michael Tyler (Eds.), *Amphibian Biology* (pp. 2672-2756). Surrey Beatty and Sons.

34. Beerli, P. (2006). Comparison of Bayesian and maximum likelihood inference of population genetic parameters. *Bioinformatics*, *22(3)*, 341-345.

33. Beerli, P. (2006). Book review: Statistical methods in (molecular) evolution. *Evolution*, *60*, 421-423. [u]

32. Chi, H., Beerli, P., & Evans, D. (2005). On the Scrambled Sobol Sequences. *Lecture Notes in Computer Science*, *3615*, 775-784.

31. Mu, J., Joy, D. A., Duan, J., Huang, Y., Carlton, J., Walker, J., Barnwell, J., Beerli, P., Charleston, M. A., Pybus, O. G., & Su, X. Z. (2005). Host Switch Leads to Emergence of Plasmodium vivax Malaria in Humans. *Molecular Biology and Evolution*, *2(8)*, 1686-1693.

30. Beerli, P. (2004). Effect of unsampled populations on the estimation of population sizes and migration rates between sampled populations. *Molecular Ecology*, *13*, 827-836.

29. Brumfield, R. T., Beerli, P., Nickerson, D. A., & Edwards, S. V. (2003). The utility of single nucleotide polymorphisms in inferences of population history. *Trends in Ecology & Evolution*, *18(5)*, 249-256.

28. Joy, D. A., Feng, X., Mu, J., Furuya, T., Chotivanich, K., Krettli, A. U., Ho, M., Wang, A., White, N. J., Suh, E., Beerli, P., & Su, Xin-Zhuan. (2003). Early origin and recent expansion of Plasmodium falciparum. *Science*, *300(5617)*, 318-321.

27. Arbogast, B. S., Edwards, S. V., Wakeley, J., Beerli, P., & Slowinski, J. B. (2002). Estimating divergence times from molecular data on phylogenetic and population genetic timescales. *Annual Review of Ecology and Systematics*, *33*, 707-740.

26. Beerli, P., & Edwards, S. V. (2002). When did Neanderthals and modern humans diverge? *Evolutionary Anthropology*, *11*, 60-63. [u]

25. Beerli, P., & Felsenstein, J. (2001). Maximum likelihood estimation of a migration matrix and effective population sizes in n subpopulations by using a coalescent approach. *Proceedings of the National Academy of Sciences of the United States of America*, *98(8)*, 4563-4568.

24. Guex, G. D., Hotz, H., Uzzell, T., Semlitsch, R. D., Beerli, P., & Pascolini, R. (2001). Developmental disturbances in Rana esculenta tadpoles and metamorphs. *Zoosystematics and Evolution*, *77(1)*, 79-86.

23. Hoekstra, H. E., Hoekstra, J. M., Berrigan, D., Vignieri, S. N., Hoang, A., Hill, C. E., Beerli, P., & Kingsolver, J. G. (2001). Strength and tempo of directional selection in the wild. *Proceedings of the National Academy of Sciences*, *98(16)*, 9157-9160.

22. Hotz, H., Uzzell, T., Guex, G. D., Alpers, D., Semlitsch, R. D., & Beerli, P. (2001). Microsatellites: a tool for evolutionary genetic studies of western Palearctic water frogs. *Zoosystematics and Evolution*, *77(1)*, 43-50.

21. Kingsolver, J. G., Hoekstra, H. E., Hoekstra, J. M., Berrigan, D., Vignieri, S. N., Hill, C., Hoang, A., Gibert, P., & Beerli, P. (2001). The strength of phenotypic selection in natural populations. *The American Naturalist*, *157(3)*, 245-261.

20. Beerli, P., Grassly, N., Kuhner, M. K., Nickle, D., Pybus, O., Rain, M., Rambaut, A., Rodrigo, A. G., & Wang, Y. (2000). Population genetics of HIV: parameter estimation using genealogy-based methods. Computational and Evolutionary Analysis of HIV Molecular Sequences. In Rodrigo, Allen G, & Learn, Gerald H (Eds.), *Computational and Evolutionary Analysis of HIV Molecular Sequences* (pp. 217-252). Kluwer Academic Publishers, Boston.

19. Edwards, S. V., & Beerli, P. (2000). Perspective: gene divergence, population divergence, and the variance in coalescence time in phylogeographic studies. *Evolution*, *54(6)*, 1839-1854.

18. Kuhner, M. K., Beerli, P., Yamato, J., & Felsenstein, J. (2000). Usefulness of single nucleotide polymorphism data for estimating population parameters. *Genetics*, *156(1)*, 439-447.

17. Wilson, L., Stephens, D. A., Harding, R. M., Griffiths, B., Joyce, P., Edwards, A. W. F., Fearnhead, P., Ewens, W. J., Beaumont, M. A., Kuhner, M. K., Beerli, P., Brooks, S., Gelman, A., Chen, Y. G., Liu, J. S., Emond, M., Raftery, A. E., Steele, R., Felsenstein, J., Larget, B., Markovtsova, L., Marjoram, P., Tavare, S., Mau, B., Meng, X. L., Thompson, E. A., & Ventura, V. (2000). Inference in molecular population genetics - Discussion. *Journal of the Royal Statistical Society Series B-Statistical Methodology*, *62*, 636-655.

16. Beerli, P., & Felsenstein, J. (1999). Maximum-likelihood estimation of migration rates and effective population numbers in two populations using a coalescent approach. *Genetics*, *152(2)*, 763-773.

15. Felsenstein, J., Kuhner, M. K., Yamato, J., & Beerli, P. (1999). Likelihoods on coalescents: a Monte Carlo sampling approach to inferring parameters from population samples of molecular data. In Françoise Seillier-Moiseiwitsch (Eds.), *Statistics in molecular biology and genetics: Selected proceedings of the Joint AMS-IMS-SIAM Summer Conference on Statistics in Molecular Biology held in Seattle, WA, June 22–26, 1997* (pp. 163-185). Hayward, CA: Institute of Mathematical Statistics, 1999.

14. Hotz, H., Semlitsch, R. D., Gutmann, E., Guex, G. D., & Beerli, P. (1999). Spontaneous heterosis in larval life-history traits of hemiclonal frog hybrids. *Proceedings of the National Academy of Sciences*, *96(5)*, 2171-2176.

13. Beerli, P. (1998). Estimation of Migration Rates and Population Sizes in Geographically Structured Populations. In Carvalho, Gary R (Ed.), *Advances in Molecular Ecology* (pp. 39-53). Amsterdam: ISO Press.

12. Schnabel, A., Beerli, P., Estoup, A., & Hillis, D. (1998). A Guide to Software Packages for Data Analysis in Molecular Ecology. In Carvalho, Gary R (Ed.), *Advances in Molecular Ecology* (pp. 291-303). Amsterdam: ISO Press.

11. Beerli, P. (1997). Statistical analyses of population genetic data. *Trends in Ecology & Evolution*, *12(12)*, 488-488.

10. Beerli, P., Hotz, H., & Uzzell, T. (1996). Geologically dated sea barriers calibrate a protein clock for Aegean water frogs. *Evolution*, *50(4)*, 1676-1687.

9. Hotz, H., Uzzell, T., Beerli, P., & Guex, G.-D. (1996). Are hybrid clonals species? A case for enlightened anarchy. *Amphibia-Reptilia*, *17(4)*, 315-320.

8. Semlitsch, R. S., Schmiedehausen, S., Hotz, H., & Beerli, P. (1996). Genetic compatibility between sexual and clonal genomes in local populations of the hybridogenetic \it Rana esculenta complex. *Evolutionary Ecology*, *10(5)*, 531-543.

7. Beerli, P. (1995). Amphibien in der Umgebung des Nussbaumer Sees. In A. Schläfli (Eds.), Die Nussbaumer Seen [Monograph]. *Ittinger Schriftenreihe*, *5*, 1-9. [u]

6. Beerli, P., Hotz, H., Tunner, H. G., Heppich, S., & Uzzell, T. (1994). Two new water frog species from the Aegean islands Crete and Karpathos (Amphibia, Salientia, Ranidae). *Notulae Naturae, Academy of Natural Sciences of Philadelphia*, *470*, 1-9.

5. Beerli, P. (1993). Amphibien des Hudelmoos. *Mitteilungen der thurgauischen naturforschenden Gesellschaft*, *51*, 257-260. [u]

4. Kaden, D., & Beerli, P. (1993). Heuschrecken des Hudelmoos. *Mitteilungen der thurgauischen naturforschenden Gesellschaft*, *51*, 207-213.[u]

3. Hotz, H., Beerli, P., & Spolsky, C. (1992). Mitochondrial DNA reveals formation of nonhybrid frogs by natural matings between hemiclonal hybrids. *Molecular Biology and Evolution*, *9(4)*, 610-620.

2. Beerli, P., Billing, H., & Schätti, B. (1986). Taxonomischer Status von Vipera latasti monticola Saint Girons, 1953. *Salamandra*, *22(2/3)*, 101-104.

1. Beerli, P. (1985). Amphibieninventar des Kantons Thurgau. *Mitteilungen der thurgauischen naturforschenden Gesellschaft*, *46*, 7-51. [u]

Presentations

Invited Keynote and Plenary Lectures

Beerli, P. (presented 2017, July). Everything you wanted to know about Frogs, Computers, and Population genetics. Plenary presentation in M. Turelli, M. Slatkin (Chair), *Symposium to honor Joe Felsenstein's Scientific Achievements*. Symposium conducted at the meeting of Evolution 2017 meeting, Portland OR. (International)

Beerli, P. (presented 2014, November). *Structured populations: from landscape genetics to assortative mating*. Keynote presentation at Yearly Conference of the Sociedad Chilena de Evolucion, Sociedad Chilena de Evolucion, Puerto Varas, Chile. (National)

Beerli, P. (presented 2002). Effective population and the coalescent. In M. Hare (Chair), *Mini-Symposium: Effective population size and conservation*. Presentation at the meeting of University of Maryland, College Park MA. (International)

Beerli, P. (presented 2000). Subdivided Populations: Parameter Estimation and other Complications. Plenary presentation in P. Oefner (Chair), *DNA 2000: International Symposium on the State-of-the-Art in Genetic Analsysis*. Symposium conducted at the meeting of California Separation Science Society, Boston, MA. (International)

Beerli, P. (presented 1999). When did the Neanderthals and modern humans diverge? Plenary presentation in *Centennial Anniversary of the Anthropological Institute of the University of Zurich*. Symposium conducted at the meeting of Anthropologisches Institut, Universität Zürich, Zürich, Switzerland. (International)

Refereed Presentations at Conferences

Beerli, P., Ashki, H., Mashayekhi, S., & Palzcewski, M. (presented 2018, August). *Estimation of divergence time using lineage label switching*. Poster presentation at II Joint Congress on Evolutionary Biology – Montpellier 2018, Systematic Bioloogists, Society for Evolution, Society of American naturalists, Montpellier. (International)

Beerli, P., & Mashayekhi, S. (presented 2018, August). *The fractional coalescent*. Presentation at II Joint Congress on Evolutionary Biology – Montpellier 2018, Systematic Biologists, Society for Evolution, Society of American naturalists, Montpellier France. (International)

Beerli, P. (presented 2017). *Population divergence time estimation*. Presentation at Mathematical and Computational Evolutionary Biology, University of Montpellier, France, Porquerolles, France. (International)

Nonrefereed Presentations at Conferences

Beerli, P. (presented 2014). *MIGRATE 4.0: (many loci), divergence , and assignment*. Presentation at Evolution 2014, Society for the Study of Evolution, the Society of Systematic Biologists, and American Society of Naturalists, Raleigh NC. (International)

Beerli, P. (presented 2013). *Genomics, Recombination, and parameter estimation or "too much, too little, just right"*. Presentation at Evolution 2013, Society for the Study of Evolution, the Society of Systematic Biologists, and American Society of Naturalists, Snowbird UT. (International)

Beerli, P. (presented 2012). *Recombination affects inference of population parameters, but how much?* Presentation at SEPEEG – Southeast Population, Ecology and Evolutionary Genetics Group meeting, Southeast Population, Ecology and Evolutionary Genetics Group, Clemson SC. (Regional)

Invited Workshops

Beerli, P. (2019, September). *Population genetic estimation in the context of Epidemiology*. Workshop “Eponge 2.0" in Arequipa, Peru, organized by the Global Health Institute in Antwerpen, Belgium.

Beerli, P. (2019, August). *Molecular Evolution*. Workshop delivered at Marine Biology Laboratory, Woods Hole MA. (International)

Beerli, P. (2018, July). *Molecular Evolution*. Workshop delivered at Marine Biology Laboratory, Woods Hole MA. (International)

Beerli, P. (2018, April). *Learning how to compare models with the program Migrate 4.x*. Workshop delivered at Smithsonian Institutions, Washington DC. (Regional)

Beerli, P. (2017, October). *Migrate 4.0*. Workshop delivered at Harvard University, Harvard MA. (State)

Beerli, P. (2017, July). *Molecular Evolution*. Workshop delivered at Marine Biology Laboratory, Woods Hole MA. (International)

Beerli, P. (2017, April). *Learning how to compare models with the program Migrate 4.x*. Workshop delivered at Smithsonian Institutions, Washington DC. (Regional)

Beerli, P. (2017, February). *Migrate 4.0*. Workshop delivered at Ohio State University, Columbus OH. (State)

Beerli, P. (2016, October). *EPONGE: Epidemiology meets Population Genetics*. Workshop delivered at Global Health Institute, University of Antwerp (Belgium), Universidad Peruana Cayetano Heredia, Lima (Peru), and Universidad Nacional de Amazonia Peruana (Peru), Lima, Peru. (International)

Beerli, P. (2016, July). *Molecular Evolution*. Workshop delivered at Marine Biology Laboratory, Woods Hole MA. (International)

Beerli, P. (2016, April). *Learning how to compare models with the program Migrate 4.x*. Workshop delivered at Smithsonian Institutions, Washington DC. (Regional)

Beerli, P. (2015, July). *Molecular Evolution*. Workshop delivered at Marine Biology Laboratory, Woods Hole MA. (International)

Beerli, P. (2015, April). *Migrate 4.0*. Workshop delivered at Smithsonian Institutions, Washington DC. (Regional)

Beerli, P. (2015, February). *Molecular Evolution Europe*. Workshop delivered at Solis LTD, Cesky Krumlov, Czech Republic. (International)

Beerli, P. (2014, December). *Migrate 4.0*. Workshop delivered at Sociedad Chilena de Evolucion, Universidad de Chile, Santiago de Chile. (National)

Beerli, P. (2014). *Divergence models with MIGRATE*. Workshop delivered at Smithsonian Institution Conservation Genetics, Washington DC. (Regional)

Beerli, P. (2014). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2013). *Biogeography, Models, Migrate, oh my!* Workshop delivered at Evolution 2013, Snowbird UT. (International)

Beerli, P. (2013). *Differentiation of population models with MIGRATE*. Workshop delivered at Smithsonian Institution Conservation Genetics, Washington DC. (Regional)

Beerli, P. (2013). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2013). *Molecular Evolution Europe*. Workshop delivered at Solis LTD, Cesky Krumlov, Czech Republic. (International)

Beerli, P. (2012). *Differentiation of population models with MIGRATE*. Workshop delivered at Smithsonian Institution Conservation Genetics, Washington DC. (Regional)

Beerli, P. (2012). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2012). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2011). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2011). *Molecular Evolution Europe*. Workshop delivered at Solis LTD, Cesky Krumlov, Czech Republic. (International)

Beerli, P. (2011). *Workshop on how to improve the program BEAST*. Workshop delivered at National Evolutionary Synthesis Center, Durham NC. (International)

Beerli, P. (2010). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods

Hole, MA. (International)

Beerli, P. (2010). *Molecular Evolution Europe*. Workshop delivered at Solis LTD, Cesky Krumlov, Czech Republic. (International)

Beerli, P. (2010). *Recent Advances in Conservation Genetics 2010*. Workshop delivered at NCI, Smithsonian Institutions, White Oak Conservation Center near Jacksonville FL. (International)

Beerli, P. (2010). *Workshop on how to improve the program BEAST*. Workshop delivered at National Evolutionary Synthesis Center, Durham NC. (International)

Beerli, P. (2009). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2009). *Molecular Evolution Europe*. Workshop delivered at Solis LTD, Cesky Krumlov, Czech Republic. (International)

Beerli, P. (2009). *Workshop and forming of working group for phylogenetic maximum likelihood library to use fast computer hardware, such as GPU and cluster architectures*. Workshop delivered at M. Cummings, University of Maryland, University of Maryland. (International)

Beerli, P. (2009). *Workshop on how to improve the program BEAST*. Workshop delivered at National Evolutionary Synthesis Center, Durham NC. (International)

Beerli, P. (2008). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2007). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2007). *Population Genetics applied to Conservation Biology*. Workshop delivered at Centro di Ecologia Alpina, Trento, Italy, Trento, Italy. (International)

Beerli, P. (2006). *Conservation Genetics Data Analysis Course*. Workshop delivered at Center for Investigation of Biodiversity and Genetic Resources at the University of Porto, Portugal, and University of Montana, Porto. Portugal. (International)

Beerli, P. (2006). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2006). *NESCENT Catalysis meeting: Historical perspectives on the distribution of biodiversity in Madagascar*. Workshop delivered at NESCENT – National Evolutionary Synthesis Center, Durham, NC. (International)

Beerli, P. (2006). *Workshop on Markov Chain Monte Carlo*. Workshop delivered at Harvard University, Cambridge, MA. (International)

Beerli, P. (2005). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2005). *Molecular Evolution, Biodiversity, and Bioinformatics*. Workshop delivered at Korean Oceanography and Development Institute, Jangmok, South Korea. (International)

Beerli, P. (2005). *Phylogeography and Phylogenetics*. Workshop delivered at Mathematical Biosciences Institute at Ohio University, Columbus OH. (International)

Beerli, P. (2004). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2003). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods

Hole, MA. (International)

Beerli, P. (2003). *Molecular Evolution, Biodiversity, and Bioinformatics*. Workshop delivered at Korean Oceanography and Development Institute, Jangmok, South Korea. (International)

Beerli, P. (2003). *Population Genetics applied to Conservation Biology*. Workshop delivered at Centro di Ecologia Alpina, Trento, Italy, Centro di Ecologia Alpina, Trento, Italy. (International)

Beerli, P. (2003). *Testing of Spatial Structure Models Workshop*. Workshop delivered at International Whaling Commission and Scripps Institute of Oceanography, La Jolla, CA. (International)

Beerli, P. (2003). *Workshop on Coalescence and Plant Genetics*. Workshop delivered at Eidgenössische Technische Hochschule (ETH), Zürich, Switzerland. (International)

Beerli, P. (2002). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2001). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (2000). *Molecular Evolution*. Workshop delivered at Marine Biology Institute, Woods Hole, MA. (International)

Beerli, P. (1998). *NATO-ASI workshop "Molecular Ecology": population genetics*. Workshop delivered at NATO-ASI, Erice, Italy. (International)

Invited Lectures Beerli, P. (2019). *The fractional Coalescent*. Delivered at Smithsonian Institution, Department of Conservation Genomics. (Regional)

Beerli, P. (2019). *Population divergence time estimation using individual lineage label switching*. Delivered at Florida State University, Florida State University. (Local)

Beerli, P. (2018). *All models are good but only some are useful*. Delivered at Smithsonian Institution, Department of Conservation Genomics. (Regional)

Beerli, P. (2018). *All models arre good, but only some are useful*. Delivered at Florida State University, Department of Statistics. (Local)

Beerli, P. (2018). *Phylogenetics and some of its application*. Delivered at Florida State University, Department of Scientific Computing. (Local)

Beerli, P. (2017, October). *All models are good, but only some are useful*. Delivered at Harvard University, Harvard MA. (Local)

Beerli, P. (2017, February). *All models are good, but only some are useful*. Delivered at Ohio State University, Columbus OH. (Regional)

Beerli, P. (2016, February). *Fun with population models or Goldilock's principle*. Delivered at University of California, Berkeley, Berkeley, CA. (Regional)

Beerli, P. (2015, November). *Structured populations or divergence versus migration and other complications*. Delivered at Department of Biology, Temple University, Temple University, Philadelphia PA. (Local)

Beerli, P. (2015, September). *Structured populations or divergence versus migration and other complications*. Delivered at Department of Biology, University of Connecticut, University of Connecticut. (Local)

Beerli, P. (2015, April). *Population Structure: from Landscape Genetics to Assortative Mating*. Delivered at Smithsonian Institutions, Washington DC. (Regional)

Beerli, P. (2008). *Model comparison using Bayes factors*. Delivered at University of New Orleans, New Orleans, LA. (National)

Beerli, P. (2007). *Science on the Edge Series: Population genetics inference and Computers: an embarrassingly parallel development*. Delivered at Michigan State University, East Lansing, MI. (National)

Beerli, P. (2006). *Comparison of maximum likelihood and Bayesian inference in population genetics*. Delivered at Harvard University, Cambridge, MA. (International)

Beerli, P. (2006). *Comparison of maximum likelihood and Bayesian inference in population genetics*. Delivered at Zologisches Institut, Universität Zürich. (International)

Beerli, P. (2005). *Comparison of maximum likelihood and Bayesian inference in population genetics*. Delivered at University of Florida, Gainesville FL. (National)

Beerli, P. (2005). *Population genetics: Or why I loved to learn to use (slightly) wrong models*. Delivered at New York University, New York, NY. (National)

Beerli, P. (2004). *Gene flow: probability and parameter estimation*. Delivered at Organismal biology and Evolution, Harvard University, Cambridge MA. (National)

Beerli, P. (2004). *On population genetics models, probability, and parameters estimation (BEES lecture series)*. Delivered at Department of Biology, University of Maryland, College Park, MA. (National)

Beerli, P. (2003). *Inference of population genetic parameters using the coalescent*. Delivered at Department of Medical Genetics, University of Alberta, Edmonton, Canada. (International)

Beerli, P. (2003). *Introduction to the Coalescent*. Delivered at Florida State University, Tallahassee, FL. (Local)

Beerli, P. (2003). *Measuring population size using genetic samples obtained today*. Delivered at Biologisches Institut, Universität Zürich, Zürich, Switzerland. (International)

Beerli, P. (2002). *Introduction to the Coalescent*. Delivered at Florida State University, Tallahassee, FL. (Local)

Beerli, P. (2000). *Maximum likelihood estimation of population parameters using the coalescent*. Delivered at Stanford University, Stanford, CA. (State)

Beerli, P. (1999). *Maximum likelihood estimation of migration rates and related population parameters*. Delivered at University of Nevada, Reno, NV. (State)

Beerli, P. (1999). *Population genetics in the 21st century*. Delivered at Max Planck Institut für evolutionäre Anthropologie, Leipzig, Germany. (International)

Beerli, P. (1998). *Maximum likelihood estimation of migration rates*. Delivered at Rutgers University, Newark, NJ. (Local)

Beerli, P. (1998). *Maximum likelihood estimation of migration rates*. Delivered at Academy of Natural Sciences Philadelphia, Philadelphia PA. (Local)

Beerli, P. (1998). *Maximum likelihood estimation of migration using the coalescent*. Delivered at Newton Institute, University of Cambridge, Cambridge, United Kingdom. (International)

Beerli, P. (1998). *The coalescence and migration rate estimation*. Delivered at Universität Zürich, Zürich, Switzerland. (International)

Contracts and Grants

Beerli, P. (2019). *COFRS: Genetic ancestry and Population assignment*. Total award $14,000.

Beerli, Peter (PI). (May 2016–Apr 2020). *ABI Innovation: Coalescence-Based Inference Of Adaption*. Funded by National Science Foundation. (1564822). Total award $757,717.

Beerli, Peter (PI). (May 2015–Aug 2015). *COFRS: Simulating Deep Sea Shark Populations, Explorations to Improve Population Genetic Inference From Genomic Data*. Funded by FSU CRC. Total award $14,000.

Beerli, Peter (PI). (Jan 2012–Dec 2015). *Model Inference, Comparison, and Averaging for Genetically Structured Populations*. Funded by National Science Foundation. (1145999). Total award $327,000.

Levitan, Don (PI), & Beerli, Peter (Co-PI). (Jul 2008–Sep 2014). *The Consequences of Sperm Availability to the Evolution of Gamete Recognition Proteins*. Funded by National Science Foundation. (0822626). Total award $700,000.

Beerli, Peter (PI). (May 2006–Apr 2011). *Improving population genetics parameter estimation based on SNPs*. Funded by National Institute of General Medical Sciences. (5R01GM078985). Total award $418,333.

Beerli, Peter (PI). (May 2004–Aug 2004). *FYAP - Exploration and Improvement of Parallel Execution of the program MIGRATE*. Funded by FSU CRC. Total award $13,000.

ADVISING AND TEACHING

Postdoctoral Supervision

2016-2019	Somayeh Mashayekhi	Assistant Professor, Kennesaw University, Kennesaw GA [Fall 2019]
2005-2008	Koffi Y. Sampson	Statistician Quebec, Canada
2004	Hongmei Chi	Associate Professor for Computer Science, Florida Agricultural and Mechanical University, Tallahassee FL

Doctoral Committee Chair

Ashki, Haleh (2015); Palczewski, Michael (2013); Shaw , Kyle; Sadeghi, Marjan; Khodaie Tara; Ben Pomidor, Stephen Alex Townsend.

Doctoral Committee Member or University Representatitve

Ebadi, S. (2018). Tahmassebi, A. (2018). Cheung, J. (2018). Pomidor, B. J. (2018). Mechtley, A. C. (2018). Kosman, E. T. (2018) Pearson, V. M.(2017). Sackman, A. M. (2017). Wesolowski, S. J. (2017). Soda, K. J. (2017). Margres, M. J. (2016). Barrow, L. N. (2016). Stahala, C. (2016). Walker, C. S.(2016). Warwick, A. (2016). Stoyanova, D. K. (2015). Takeh, A. (2014). Kuchera, M. P. (2014). Wray, K. P. (2013). Plata Stapper, A. C. (2013). Lu, D. (2012). Lotterhos, K. E. (2011). Oakley, C. G. (2011). Lakner, C. (2011). Fierst, J. L. (2010). Jue, N. K. (2010). Tomaiuolo, M. (2008). Sevim, V., (2008). Conry, M. T.; Crock, N. D.; Morgan, N. B.; Olsen, K. C.; Scherer, B. P.; Shi, L.; Torrence, K. G.; Dye, M. L.; Hogan, M. P.; Hoover, D.A.; Zhao, P. A.;

Master's Committee Chair

Bricker, J. T. (2015). Ashki, H. (2012). Joshi, S. (2007).

Master's Committee Member Ficara, Cody (2019) Conry, M. T. (2018). Boren, S. B. (2017). Tahmassebi, A. (2017). Ehtemami, A. (2016). Ralicki, H. F. (2015). Pomidor, B. J. (2013). Kuchera, M. P. (2012). Michelsohn, M. J. (2012). Nye, J. M. (2011). Takeh, A. (2011). Schwinn, S. J. (2010). Shi, Y., graduate. (2007). Townsend, S. A. Zheng, X.

Bachelor's Committee Member

Rebecca Falter (2012).

Courses Taught

Programming for Science Applications (ISC4304C)
Symbolic and Numerical Computations (ISC3222)
Programming for Scientific Computing (ISC5935)
Computational Evolutionary Biology (ISC5317)
Introduction to Scientific Computing (ISC3313)
Practical Genetic Inference (ISC5907)
Discrete Algorithms for Science Applications (ISC4221C)
Markov Chain Monte Carlo in Praxis (ISC5939)
Conservation Biology (BSC3052)
Programming Skills for Computation Biology and Bioinformatics (ISC5306)
UNIX-RX: Short summer workshop for Python for Beginners (2011-2017)

SERVICE

Florida State University

Co-Director, Computational Biology program (2016–present).
Senator, Faculty Senate (2019–present).
Alternate senator, Faculty Senate (2013–2019).
Member, High Performance Computing Advisory Committee (2007–present).
Senator, Faculty Senate (2007-2008, 2011–2013).
Member, Arts and Sciences Policy Committee (2017–present).
Member, Graduate Policy Subcommittee for the College of Medicine (2018).
Member, Graduate Policy Subcommittee for the Department of Biological Sciences (2017).

Chair, Undergraduate committee (2019-).
Member/Chair, Executive Committee (2009-2011,2012–2019).
Chair, Publications committee (2014–2015).
Member, Graduate curriculum committee (2011–2013).
Member, Search committee for a microbiologist [Biological Sciences] (2007–2008).
Member, Executive committee [Biological Sciences] (2006–2007).
Member, Search committee for a computational biologist (2006).
Member, Search committee for a computational chemist (2006).
Member, Election Committee (2005–2006).
Member, Evaluation study committee (2005–2006).
Member, Search committee for a microbiologist [Biological sciences] (2005–2006).
Member, Academic affairs committee (2004–2005).
Member, Publications committee (2004–2005).

The Profession

Co-director Workshop on Molecular Evolution at the Marine Biology Laboratory, Woods Hole MA (2019-2021)

Editorial Board Membership(s): *PEERJ* (2015–present), *Evolutionary Bioinformatics* (2003–present).

Advisory Boards: *Advisory Board for Workshop on Molecular Evolution in Europe at Cesky Krumlov, Czech Republic. Lead: S. Handley. St. Louis*. Workshop on Molecular Evolution. (2011–2013);

Steering committee for the Molecular Evolution workshop at the Marine Biology Laboratory, Woods Hole MA. Marine Biology Institute Woods Hole MA. (2010-)

Reviewer for refereed Journals: *American Naturalist* , *Bioinformatics*, *Biological Journal of the Linnean Society*, *Carnivore Conservation*, *Conservation Genetics*, *Copeia*, *Current Biology*, *Evolutionary Bioinformatics Online*, *Ecology Letters* , *Ecological Modelling*, *Evolution* , *Genetics*, *Human Genetics*, *Journal of Biogeography*, *Journal of Evolutionary Biology*, *Journal of Fish Biology* , *Journal of Mammalogy*, *Journal of Molecular Evolution*, *Marine Biology* , *Molecular Ecology*, *Molecular Biology and Evolution*, *Molecular Phylogenetics and Evolution*, *Nature Review Genetics* , *PLoS Biology*, *PLoS One*, *Proceedings of the Royal Society B: Biological Sciences*, *Proceedings of the National Academy of Sciences USA* , *Science* , *Statistical Genetics*, *Systematic Biology* , *Theoretical Population Biology*, *Trends in Ecology and Evolution*.

Reviewer for Textbooks: *Phylogenetics* (2017). *Conservation Biology* (2015). *Model Based Inference in the Life Sciences: A Primer on Evidence* (2007). *New Mathematical Models for Evolution*

(2005). *Molecular Ecology* (2003).

Reviewer or Panelist for Grant Applications: European Research Council. Natural Sciences and Engineering Research Council of Canada. National Science Foundation. Marsden Fund (New Zealand) Schweizer Nationalfond. NIH/NSF (mathematical biology). IUCN Red List.

Interviews

Zachary Boehm: "New computational tool could change how we study pathogens, FSU researchers say". Online news cast at news.fsu.edu: https://news.fsu.edu/news/science-technology/2019/03/22/new-computational-tool-could-change-how-we-study-pathogens-fsu-researchers-say/

Kathleen Haughney. (2015, June). Genomics revolution: Cutting-edge research could lead to breakthroughs. *Across the Spectrum*. http://artsandsciences.fsu.edu/content/download/259029/1956567/file/SPECTRUM_2015-spring-summer.pdf