

CURRICULUM VITAE – DANIEL WEGMANN, PHD

PERSONAL INFORMATION

Affiliation Department of Ecology and Evolutionary Biology
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Date of Birth May 1st 1980

Nationality Swiss

Language skills German – fluent (mother tongue)
English – fluent
French – fluent
Russian – basic skills

EDUCATION

- 2009 – Postdoctoral training with John Novembre, Department of Ecology and Evolutionary Biology, University of California, Los Angeles, USA
- 2005 – 2009 PhD thesis in Computational Population Genetics with Laurent Excoffier, Institute of Ecology and Evolution, University of Bern, Switzerland
Title: *Understanding the Past: New Methodologies to estimate Forces shaping Genetic Diversity*
- 2003 – 2004 Master thesis in Computational Population Genetics with Laurent Excoffier, Institute of Ecology and Evolution, University of Bern, Switzerland
Title: *Molecular Diversity after a Range Expansion in Heterogeneous Environments*
- 2000 – 2003 Undergraduate studies in Zoology at the University of Bern, Switzerland
- 1995 – 2000 Matura Typus C, Mathematics and Sciences, Gymnasium Bern-Neufeld, Switzerland

AWARDS AND GRANTS

- 2010 Faculty-Award from the Faculty of Sciences, University of Bern, for the Dissertation “Understanding the Past: New Methodologies to estimate Forces shaping Genetic Diversity”
- 2009 Kugelpyramide-Award of the Swiss Association of Science Olympiads for a distinguished Engagement for Science and the Youth
- 2007 Travel Grant of the Swiss Zoological Society to attend the ESEB conference in Uppsala, Sweden
- 2006 Töggeli-Award of the Institute of Ecology and Evolution, University of Bern, for the best Presentation of a Student at an international Conference

PUBLICATIONS

- 2011
- Stahl EA, **Wegmann D**, Kraft P, Chen R, Kallberg HJ, Kurreeman FAS, Gregersen PK, Alfredsson L, Siminovitch KA, Worthington J, de Bakker PIW, Raychaudhuri S and Plenge RM (2011) Polygenic modeling of genome-wide association study data reveals hidden heritability of rheumatoid arthritis risk. *Nat Genet* (revision in review)

- Slater GJ, Harmon LJ, **Wegmann D**, Joyce P, Revell LJ and Alfaro ME (2011) Using Approximate Bayesian Computation to fit models of continuous trait evolution to incompletely sampled comparative data. *Evolution* (in press)
 - Veeramah KR, **Wegmann D**, Woerner A, Mendez FL, Watkins JC, Destro-Bisol G, Soodyall H, Louie L and Hammer MF (2011) An early divergence of KhoeSan ancestors from those of other modern humans is supported by an ABC-based analysis of autosomal re-sequencing data. *Mol Biol Evol* (in press)
 - **Wegmann D**, Kessner D, Veeramah KR, Mathias RA, Nicolae DL, Yanek LR, Sun YV, Torgerson DG, Rafaels N, Mosley T, Becker LC, Ruczinski I, Beaty TH, Kardia SLR, Meyers DA, Barnes KC, Becker DM, Freimer N and Novembre J (2011) Recombination rates in admixed individuals identified by ancestry-based inference. *Nat Genet* 43:9 847-853
 - Veeramah KR, Tönjes A, Kovacs P, Gross A, **Wegmann D**, Geary P, Gasperikova D, Klimes I, Scholz M, Novembre J and Stumvoll M (2011) Genetic variation in the Sorbs of eastern Germany in the context of broader European genetic diversity. *Eur J Human Genet* (in press)
 - Thalmann O*, **Wegmann D***, Spitzner M, Arandjelovic M, Guschanski K, Leuenberger C, Bergl RA and Vigilant L (2011) Historical sampling reveals dramatic demographic changes in western gorilla populations. *BMC Evol Biol* 11: 85
- 2010
- Peter B, **Wegmann D** and Excoffier L (2010) Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. *Mol Ecol* 19 (21): 4648-4660.
 - Ray N, **Wegmann D**, Fagundes NJR, Wang S, Ruiz-Linares A, and Excoffier L (2010) A Statistical Evaluation of Models for the Initial Settlement of the American Continent Emphasizes the Importance of Gene Flow with Asia. *Mol Biol Evol* 27 (2): 337-345.
 - **Wegmann D** and Excoffier L (2010) Bayesian Inference of the Demographic History of Chimpanzees. *Mol Biol Evol* 27 (6): 1425-1435.
 - **Wegmann D**, Leuenberger C, Neuenschwander S and Excoffier L (2010) ABC-toolbox: a versatile toolkit for approximate Bayesian computations. *BMC Bioinformatics* 11: 116.
- 2009
- Leuenberger C* and **Wegmann D*** (2010) Bayesian Computation and Model Selection Without Likelihoods. *Genetics* 184 (1): 243-252.
 - **Wegmann D**, Leuenberger C and Excoffier L (2009) Efficient Approximate Bayesian Computation Coupled With Markov Chain Monte Carlo Without Likelihood. *Genetics* 182 (4): 1207-1218.
 - Hofer T, Ray N, **Wegmann D** and Excoffier L (2009) Large allele frequency differences between human continental groups are more likely to have occurred by drift during range expansions than by selection. *Ann Hum Genet* 73 (1): 95-108.
- 2008
- **Wegmann D**, Dupanloup I and Excoffier L (2008) Width of Gene Expression Profile Drives Alternative Splicing. *PLoS One* 3 (10): e3587.
- 2006
- **Wegmann D**, Currat M and Excoffier L (2006) Molecular Diversity After a Range Expansion in Heterogeneous Environments. *Genetics* 174 (4): 2009-2020.
- * order of authorship is arbitrary
the five most important publications are highlighted

CONFERENCE CONTRIBUTIONS AND INVITED TALKS

- 2011
- Invited talk “Deep re-sequencing reveals the abundance and geographic structure of rare variant diversity in humans” on December 6 at the Department of Ecology and Evolution, University of Bern, Switzerland
 - Talk “Deep re-sequencing reveals the abundance and geographic structure of rare variant diversity in humans” at the 13th ESEB congress, August 20-25 in Tübingen, Germany

- Invited talk “Recombination Rates in Admixed Individuals Revealed by Ancestry-based Inference” on July 7 at the Department of Life Sciences, National Taiwan Normal University, Taiwan
- 2010

 - Talk “Inferring recombination rates in recently admixed human populations” at the annual meeting of the American Society of Human Genetics (ASHG), November 2-6 in Washington DC, USA
 - Poster “Inferring Recombination Rates in recently admixed Human Populations” at the annual meeting of the Society for Molecular Biology and Evolution (SMBE), July 4-8 in Lyon, France
- 2008

 - Talk “Approximate Bayesian Computation and Markov Chain Monte Carlo” at the meeting of the French GDR (GDR CNRS 1928 Génomique des populations), Octobre 15–17 in Sète, France
 - Poster “Approximate Bayesian Computation and Markov Chain Monte Carlo” at the annual meeting of the Swiss Zoological, Botanical and Mycological Societies, February 16-17 in Lausanne, Switzerland
- 2007

 - Poster “Approximate Bayesian Computation and Markov Chain Monte Carlo” at the 11th ESEB congress, August 20-25 in Uppsala, Sweden
 - Talk “Approximate Bayesian Computation and Markov Chain Monte Carlo” at the La Fouly 2005 Meeting “Estimating Demographic Parameters from Genetic Data”, September 14–17 in La Fouly, Switzerland
 - Poster “Approximate Bayesian Computation and Markov Chain Monte Carlo at the Jacques Monod conference “Evolutionary genomics”, May 2-6 in Roscoff (Brittany), France
- 2006

 - Talk “Range Expansions in Heterogeneous Environments” at the meeting of the French GDR (GDR CNRS 1928 Génomique des populations), March 16–17 in Banyuls, France
 - Talk “Range Expansions in Heterogeneous Environments” at the annual meeting of the Swiss Zoological, Botanical and Mycological Societies, February 16-17 in Geneva, Switzerland
- 2005

 - Talk “Range Expansions in Heterogeneous Environments” at the La Fouly 2005 Meeting “Demogenetics of Fragmented Populations”, September 14-17 in La Fouly, Switzerland
 - Poster “Range Expansions in Heterogeneous Environments” at the annual meeting of the Swiss Zoological, Botanical and Mycological Societies, February 24–25 in Basel, Switzerland

PROFESSIONAL SERVICE

Membership	European Society of Evolutionary Biology ESEB American Society of Human Genetics ASHG Swiss Zoological Society
Reviewing for	Molecular Biology and Evolution Molecular Ecology Heredity BMC Bioinformatics BMC Evolutionary Biology Theoretical Biology and Medical Modelling PLoS One

TEACHING EXPERIENCE

- 2011 Guest lecture “Inferring Demographic Histories from Genetic Data” in the course “Population Genomics” for graduate students, 10 hours
- 2011 Guest lecture “Genetic Drift” in the course “Introduction to Population Genetics”

	for undergraduate students, 2 hours
2010 – 2011	Guest lecture “Human Genetic History” in the course “Genes, Peoples and Cuisines” for undergraduate students, 2 hours per course
2006 – 2009	Assisting the practical course “Molecular Population Genetics practicals, part Data Analysis” for advanced graduate students, 20 hours per course
2004 – 2009	Lecture “Introduction to Molecular Biology and Genetics” for high school students participating in the Swiss Biology Olympiad, 10 hours per course
2000 – 2009	Preparing theoretical and practical exams for high school students participating in the Swiss and International Biology Olympiads
2006 – 2008	Assisting the practical course “Population Genetics” for undergraduate students, 10 hours per course
2001 – 2008	Lecture “Introduction to Evolutionary Biology” for high school students participating in the Swiss Biology Olympiad, 5 hours per course
2007	General Biology course at the High School Gymnasium Bern-Neufeld, 16 hours
2001 – 2007	Lecture “Introduction to Cell biology” for high school students participating in the Swiss Biology Olympiad, 12 hours per course
2001 – 2007	Lecture “Introduction to Plant Physiology” for high school students participating in the Swiss Biology Olympiad, 5 hours per course

COMMUNITY OUTREACH

2002 – 2011	Member of the Jury of the International Biology Olympiads
2000 – 2009	Head of the Swiss Biology Olympiad
2004 – 2008	Head of the Swiss Association of Science Olympiads