



Newsletter August 2016

Welcome to the 10th edition of the PopGen ALUMNI newsletter!

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Recent events

July 2016: Evolution explained to kids

Two of our students (Anna Langmüller and Olga Paulouskaya) joined the "Kinderuni" as teachers in July 2016 to bring the complex topic of evolution into the spotlight during a workshop with 25 school kids aged 10-12. The kids actively engaged in a lecture about the principles of DNA, organisms and evolution. In the following practical session they were fascinated to see DNA being extracted from Strawberries, and to observe fruit flies and mutants under the microscope.



Anna and Olga teaching the Kinderuni kids

July 2016: PhD defense

Polina Novikova (Nordborg group) successfully defended her thesis "Speciation in the Arabidopsis genus" at the GMI. Polina presented her work on aspects of non-bifurcating speciation in Arabidopsis, as well as a special case of instant speciation - the origin of the allotetraploid *Arabidopsis suecica*.

June 2016: PhD defense

Tom Hill (Betancourt group) successfully defended his thesis "Hybrid dysgenesis in *Drosophila simulans*, caused by a rapid global invasion of the P-element". Tom will soon move to Kansas, USA, to accept a postdoc position.



April 2016: Mini-Symposium: Frontiers of Population Genetics III

The yearly Scientific Advisory Board (SAB) meeting was concluded by a Mini-Symposium on April 27, featuring talks by Nick Barton, Brian Charlesworth, Jean-Michel Gibert and Andy Clark.

Alumni lab portraits

We feature a brief report about one of PopGen's graduate and faculty alumni in every Newsletter. This time, PopGen Vienna alumnus **Christian Huber** tells us about his research in sunny California:

"Since December 2014 I am a postdoc at UCLA in Los Angeles in the group of Kirk Lohmueller. I work on the distribution of fitness effects of new mutations. Highly deleterious mutations are segregating at lower frequencies than neutral mutations because of their negative effect on survival or offspring number. Using the genome-wide distribution of allele frequencies of protein-changing mutations, we can infer how deleterious these mutations are. By looking at several different species, we try to find the factors that cause mutations to be more deleterious in some species than in others. Knowing such factors can be relevant for many other fields, like conservation genetics or medical genomics. I am also involved in a number of other collaborative projects that range from spatial genetics in humans to beak size evolution in African birds.

I live with my wife and my (almost) three-year-old son in the University Village, an apartment complex close to the campus that is provided for PhD students and postdocs with their families. Since these postdocs experience similar problems and challenges, there is a strong sense of community, and we quickly found new friends. What I enjoy most about living in Los Angeles is the sunny weather and the beach. Our apartment is only 15 minutes away from Santa Monica beach, and we go there almost every weekend. Although I miss some aspects of living in Vienna (public transport!), I am more than glad that we took up the challenge of moving to another country."



Our favorite location: at the beach.



Visiting Grand Canyon. There is a strange cold substance on the floor. The natives call it "snow".

Breaking news: *Christian just became a daddy, again: Congrats to the Huber family on the arrival of Lori Addison!*

Out of sight, out of mind?

Experiences of our students abroad

Many of our students choose to spend 3 months in foreign labs during their study time.

Agnes Jonas (advisors Carolin Kosiol, Andreas Futschik, Christian Schlötterer) was hosted by the Department of Genetics, Univ. of Cambridge, by the group of Chris Illingworth (November 2015 - March 2016). Agi shares her impressions:

"Last semester I visited Chris Illingworth at Department of Genetics, University of Cambridge (UK). With Chris, we were working on a method for estimating recombination rate in influenza data.

Viral populations undergo rapid evolution partly because of their large population size and high mutation rate, but for some type of viruses, such as HIV, recombination also contributes significantly to genetic diversity and can give rise to novel forms that may become part of a global epidemic. In influenza, however, homologous recombination seems to play a little role. So, I was pretty excited to have the opportunity to work on this challenging problem. Time-resolved sequence data give a great power for identifying recombinant sequences, however, viral populations, because of their high mutation rate,

need special treatment. To disentangle the effect of recombination from that of mutation and sequencing noise, we made use of the fact that only recombination depends strongly on the distance between the two sites under consideration, and developed a maximum likelihood method to estimate rates of recombination from time series viral sequence data.

I found it inspiring to work at one of the oldest universities in the world with such a great history and many notable alumni, such as Charles Darwin or Ronald A. Fisher. I had the chance to try several things that are unique to Cambridge. For example, I tried the famous DNA beer at the Eagle pub, where, according to the anecdote, James Watson and Francis Crick first announced, that they discovered the double helix structure of DNA. I went to two formal halls, which are special events held in university colleges, where students and fellows put on formal wear, often gowns to dine. On one of these occasions, I had the opportunity to dine at the high table with the college fellows and drank coffee with them in the senior common room after dinner. While running along the river Cam, I witnessed several rowing races, even some special ones, where the crew was wearing Santa and reindeer costumes around Christmas.

I also had some time for travelling; I spent an entire day in the Natural History Museum in London and also visited the historic cathedral in Canterbury with other PopGen alumni. The picture shows us in the centre of Canterbury.”



PopGen conquered Canterbury: Florian Clemente, Agnes Jonas, Susanne Franssen, Daniel Fabian

Upcoming events

With the arrival of new PopGen Vienna students, the yearly **Introductory Course** is coming up. This year we will have 14 participants, including international students from Germany, Portugal, the Netherlands and the Czech Republic.

This year's **retreat** will be held from October 7-9 at the Hagan Lodge in Altaussee after last year's return to Feuerkogel. We're expecting 35 participants for a weekend of seminars, socialising and hiking.

Registration for attendance of the **5th Mind the Gap** meeting, organised by our students in Vienna, is still possible. Please spread the word around your colleagues, too. Details about speakers and registration: <http://www.popgen-vienna.at/news/mind-the-gap-5.html>

Upcoming seminars

The schedule for the Winter Term is under construction and will feature seminar visits by Nicolas Gompel, Harmit Malik, Martin Lascoux, Mark Siegal, Benoit Pujol, Fyodor Kondrashov, Richard Neher, PopGen Vienna faculty alumnus Thomas Flatt, and Claude Becker.

Publications of our students this year

Agnes Jonas, Thomas Taus, C. Kosiol, C. Schlötterer and Andreas Futschik: Estimating the effective population size from temporal allele frequency changes in experimental evolution. *Genetics* (accepted)

R. Kofler, **Daniel Gomez-Sanchez** and C. Schlötterer: PoPoolationTE2: comparative population genomics of transposable elements using Pool-Seq. *Mol Biol Evol* doi: 10.1093/molbev/msw137 (2016)

Ana Marija Jakšić and C. Schlötterer: The interplay of temperature and genotype on patterns of alternative splicing in *Drosophila melanogaster*. *Genetics* PubMed PMID: 27440867 (2016)

Polina Y. Novikova, N. Hohmann, V. Nizhynska, T. Tsuchimatsu, J. Ali, G. Muir, A. Guggisberg, T. Paape, K. Schmid, O.M. Fedorenko, S. Holm, T. Säll, C. Schlötterer, K. Marhold, A. Widmer, J. Sese, K.K. Shimizu, D. Weigel, U. Krämer, M.A. Koch and M. Nordborg: Sequencing of the genus *Arabidopsis* identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. *Nature Genetics* doi:10.1038/ng.3617 (2016)

Dominik Schrempf, B.Q. Minh, **Nicola De Maio**, A. von Haeseler and C. Kosiol: Reversible Polymorphism-Aware Phylogenetic Models and their Application to Tree Inference. *J Theor Biol* 407:362-370. (2016)

Tom Hill, C. Schlötterer and A.J. Betancourt: Hybrid Dysgenesis in *Drosophila simulans* Associated with a Rapid Invasion of the P-Element. *PLoS Genet* 12(5):e1006058. (2016)

Kerstin Gärtner and A. Futschik: Improved Versions of Common Estimators of the Recombination Rate. *J Comp Biol* PMID: 27409412 (2016)

C. Vogl and **Juraj Bergman**: Computation of the Likelihood of Joint Site Frequency Spectra Using Orthogonal Polynomials. *Computation* 4(1), 6; doi:10.3390/computation4010006 (2016)

A.O. Bergland, **Raymond Tobler**, J. González, P. Schmidt and D. Petrov: Secondary contact and local adaptation contribute to genome-wide patterns of clinal variation in *Drosophila melanogaster*. *Mol Ecol.* 25(5):1157-74 (2016)

C. Huber, M. DeGiorgio, I. Hellmann and R. Nielsen: Detecting recent selective sweeps while controlling for mutation rate and background selection. *Mol Ecol* 25(1):142-56 (2016)

See all publications [here](#)

Have a nice Autumn!