



## ***Newsletter December 2016***

Welcome to the 11<sup>th</sup> edition of the PopGen ALUMNI newsletter!

*Follow us on Twitter @PopGenViennaPhD*

**Call for PhD students is open – please help us spread the word!**  
**([Flyer for download](#) on the website)**

### ***Recent events***

#### **December 2016: Christmas Event**

We had a great time at this year's PopGen Vienna Xmas party: we met on a chilly winter evening in a studio in the 9th district to paint ceramic mugs. Everyone acted as Secret Santa painter for a colleague. After the painting we enjoyed burgers and craft beer at the Beaver Brewing Company just around the corner.

We'll swap the creative and beautiful mugs during a get-together before the Christmas break.



#### **November 2016: Mind The Gap Meeting**

On October 31 and November 1 our students hosted the 5th MIND THE GAP meeting at the autumn-colored campus of the University of Veterinary Medicine in Vienna. Like at previous meetings of the series, MIND THE GAP brought together theoretical and empirical population geneticists. Nearly 80 international participants attended the conference in 2016. Previous meetings were organised in Freiburg (2009), Plön (2010), Cologne (2011) and Vienna (2013).



### October 2016: PhD defense

Congratulations to Agi Jónás of the Kosiol group! She successfully defended her thesis "Inferring evolutionary trajectories from time series data" on October 25 at the Vetmeduni Vienna.



### October 2016: PhD retreat

We spent a fun, social weekend with seminar talks and a workshop at the Hagan Lodge in Altaussee, at the foot of the Styrian Loser plateau. As opposed to previous years, the weather wasn't very pleasant but we managed a few short hikes after discussing recent research results and e.g. how to exploit social media for science. Thirty participants (PhD students, postdocs, faculty and associated guests) enjoyed brainstorming together, discussing and of course some partying!



## September 2016

We're sad to see group leader Andrea Betancourt leave Vienna but we wish her all the best for her next career step at the Institute of Integrative Biology at University of Liverpool! We threw a surprise BBQ party for Andrea on one of the last warm days of the year.



## September 2016: Introductory course for PhD students

We're happy that also this year our introductory course was noted internationally. We welcomed our new cohort of students along with several external PhD students to PopGen Vienna's intense, 1-month course covering basic and advanced concepts in population genetics, *Drosophila* genetics, statistics, biomathematics, phylogenetics and bioinformatics.



*International attendants of the introductory course, alongside our new students.*

Early Stage Researchers of the BINGO training network joined us from the Netherlands and the Czech Republic, and PhD students of Universities in Germany, Portugal and Greece.

**Our new PhD students:** Lauri Törmä from Finland worked with PopGen Vienna alumnus Alistair McGregor at Oxford Brookes. He started his project with our new group leader Kirsten-Andre Senti. Robert Kofler, also new group leader, hired two students: Divya Selvaraju from India and Christos Vlachos from Greece. Also the Kosiol group welcomes a new PhD student: Manuela Geiß from Germany. We will introduce the new students and their projects on the website, soon.

## ***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 **Ray Tobler** tells us about his research down under:

*"I am currently the lead postdoctoral researcher on the Aboriginal Heritage Project, a collaboration between the Australian Centre of Ancient DNA (ACAD) and the South Australian Museum (SAM), which aims to reconstruct the genetic history of Aboriginal Australia.*

*SAM is the custodian of 5000+ hair samples collected from Aboriginal Australians during the past 100 years, along with extensive biometric, cultural and genealogical data. By combining ancient DNA from the hair samples with information on ancestral residence patterns dating back hundreds of years, this unique dataset makes it possible to build the first phylogenetic map of Aboriginal Australia as it was prior to European colonisation.*

*Early results using mtDNA markers suggest that there was a deep phylo-geographical structure across Australia that coincides with the initial settling of the continent >50K years ago.*

*I was recently awarded an Indigenous Discovery Fellowship that will enable us to extend our surveys to the nuclear genome, adding much more power to the phylogenetic analyses and also making possible studies of paleo-demography and adaptation."*

## ***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.

**Dominik Schrempf** (advisors Carolin Kosiol, Arndt von Haeseler, Claus Vogl) was hosted by the Bioinformatics Research Center (BiRC) in the group of Asger Hobolth in Denmark (March - June 2016). Dominik received an Aarhus University visiting grant for his research stay.

Dominik shares his impressions:

*"Early spring in Aarhus, Denmark, is a cloudy, foggy and surprisingly cold and wet experience. It would even be a little bit depressing, if it weren't for all those happy faces cycling around the streets, smiling at you and helping you out when you do not find your way around; or if it wasn't for the student housing that was buzzing with internationals up for*

adventure; or for the sea that comforts you and washes up winter swimmers onto the beaches; or for those tiny blossoms that fight their way through in one of the numerous large parks that the city has.

All in all, experiencing the arrival of spring and growing days in Aarhus at that time while being part of a very stimulating research environment was extraordinary in many ways. The Bioinformatics Research Center (BiRC) is a meeting place for motivated researchers that specialize on molecular evolution, molecular population genetics, and statistical and algorithmic approaches to bioinformatics. Often, freshly developed models are applied to a country-wide DNA sequence database — a valuable tool to test interesting hypotheses.

In particular, my supervisor in Aarhus, Asger Hobolth, was of great help in finding analytical solutions to models in population genetics. We can now use our findings to improve phylogenetic inference by employing the site frequency spectrum of the populations under consideration. Also, my office mates, Svend, Dan and Maria, did their best to maximize our creative output by numerous discussions about science and closely related topics (e.g., Minetest).

I want to thank Asger, Svend, Dan, Maria, and all other researchers at the BiRC for making my stay a valuable and beautiful memory.”



### ***Upcoming events***

The 2017 SAB meeting will take place from April 19 to 21.

### ***Upcoming seminars***

Our next seminar speakers also include a PopGen Vienna alumnus: Thomas Flatt will visit us, and also Fyodor Kondrashov, Alexander Stark, Richard, Patricia Gibert and Claude Becker.

***Merry Xmas and a Happy New Year to you all!***

## ***Publications of our students so far in 2016***

**B. Horvath** and A.T. Kalinka: Effects of larval crowding on quantitative variation for development time and viability in *Drosophila melanogaster*. *Evol Evol* DOI: 10.1002/ece3.2552 (2016)

**B. Horvath**, A.J. Betancourt and A.T. Kalinka: A novel method for quantifying the rate of embryogenesis uncovers considerable genetic variation for the duration of embryonic development in *Drosophila melanogaster*. *BMC Evolutionary Biology* 16(1):200 (2016)

R. Kofler, **A.M. Langmüller**, P. Nouhaud, K.A. Otte and C. Schlötterer: Suitability of Different Mapping Algorithms for Genome-wide Polymorphism Scans with Pool-Seq Data. *G3* (Bethesda). pii: g3.116.034488. (2016)

P. Nouhaud, **R. Tobler**, V. Nolte and C. Schlötterer: Ancestral population reconstitution from isofemale lines as a tool for experimental evolution. *Ecol Evol* 6: 7169–7175 (2016)

**A. Jonas**, **T. Taus**, C. Kosiol, C. Schlötterer and A. Futschik: Estimating the effective population size from temporal allele frequency changes in experimental evolution. *Genetics* doi: 10.1534/genetics.116.191197 (2016)

R. Kofler, **D. Gomez-Sanchez** and C. Schlötterer: PoPoolationTE2: comparative population genomics of transposable elements using Pool-Seq. *Mol Biol Evol* 33(10):2759-64 (2016)

**A.M. Jakšić** and C. Schlötterer: The interplay of temperature and genotype on patterns of alternative splicing in *Drosophila melanogaster*. *Genetics* 204(1):315-25 (2016)

**P.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* 48(9):1077-82 (2016)

**D. Schrempf**, B.Q. Minh, **N. 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)

**T. 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)

**K. Gärtner** and A. Futschik: Improved Versions of Common Estimators of the Recombination Rate. *J Comp Biol* 23(9):756-68. (2016)

C. Vogl and **J. 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, **R. 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)

See all publications [here](#)