



Newsletter September 2019

Welcome to the 19th edition of the PopGen ALUMNI newsletter!

Follow us on Twitter @PopGenViennaPhD

Do you know suitable PhD candidates for PopGen Vienna?

Our call for PhD students is open – please help us spread the word!

Application deadline: September 29, 2019

[\(Flyer for download on the website\)](#)

PopGen Vienna students are organising the course
"Experimental evolution: bringing theory and practice together"
at Vetmeduni Vienna, **December 2-6, 2019.**

Applications are accepted until the end of September 2019

[Link to details](#)

Recent events and news

July 2019: travel awards

Aglaiia Szukala and **Mimmi Eriksson** received travel awards by ÖFG (Austrian Research Community) to present their projects at the 2019 Evolution meeting in Rhode Island (USA).

July 2019: visiting student

Chaimae Belmouaden is a BSc student in biology and computer sciences at the University of Poitiers in France. During her internship, Chaimae spends 3 months at the Vienna Graduate School of Population Genetics, interacting with PhD students of the Schlötterer lab.

May 2019: SAB meeting

This years' **Scientific Advisory Board (SAB) meeting** took place from May 13 to 15. Our new board member **Virginie Courtier-Orgogozo** visited for the first time. The students reported their progress in front of Advisory Board, the faculty and peers. After the busy daily presentation schedules and the invaluable feedback by the SAB, the students further interacted with the board members in more relaxed settings over drinks and dinner.

May 2019: Faculty meeting

The faculty met on 15th of May, 2019.

Alumni lab portraits

We feature a brief report about one of PopGen's graduate and faculty alumni in the Newsletter. This time, PopGen Vienna alumnus **Dominik Schrempf** gives us some insight into his postdoc experience at Eötvös Lóránd University (Hungary):

"The next research (or work) destination is always a little bit of a lottery. Personal interests and available opportunities have to be combined with possible constraints. In my case, after my PhD at the Vetmeduni, I wanted to continue working in phylogenetics. Additionally, I had started a family, and, for this reason, wanted to stay at least close to home and the grandparents (it is amazing to have grandparents available, not only for the parents and the grandparents, but especially for the child). I was lucky, because a good postdoc position, which fit very well into my research interests, opened up in Budapest, and so I am here, at the ELTE, the Eötvös Lóránd University. You may already guess, languages can be a barrier.

Here, I work on phylogenetic questions involving the transfer of genetic material across species, and the inference of trees from distantly related species, for example from data sets that include eukaryotes and archaea. I am part of the Biophysics Institute, and so, we have seminars together with researchers working on the evolution of somatic tissue to model the emergence of cancer, but also with astrophysicists talking about gravitational fields. I really enjoy this inter-disciplinary environment. Figure 1 shows the participants of an in-house conference held in May 2019, which included talks about the collective motion of birds as well as drones controlled by a computer (which is programmed by a human).



Fig. 1. Group picture of the participants of an in-house conference at the Eötvös Lóránd University in Budapest (May, 2019).

As a scientist being part of the local community, I also feel obliged to write some sentences about the impacts of the political situation in Hungary, which is mediocre at the very best. We scientists are always vulnerable to political decisions, a fact that is usually not apparent, at least in countries with stable politics and good funding opportunities. However, in the last two years, politics has repeatedly interfered with scientific institutions here in Hungary. The Central European University (CEU) was forced to move away from Budapest because it is not allowed anymore to issue US-American degrees within Hungary. The Hungarian Academy of Science has been stripped off of all research institutes which have been put under ministry control¹. The respective funding is now controlled by a committee including politicians. These political decisions affect us scientists and our families. I know a family where the parents have now jobs in different cities (one in Budapest and one in Vienna, where the CEU has moved to). I believe that it is ever more important that we stay informed and remain united so that we can advocate our needs in a coordinated manner.

Luckily, I am not personally affected by these problems. I enjoy excellent funding because I am paid through an ERC grant, and work together with a lively and stimulating research group. In fact, our research group has access to a private high performance cluster, which constitutes the best computational environment I have ever had. Naturally, a private cluster also comes with some (interesting and fun) obligations (see Figure 2; we had just added a few more computing nodes).



Fig. 1. Mario Perez Jimenez, a Mexican PhD student, and I in front of the high performance cluster available to our group (July 2019)

The city Budapest itself has a thriving night life and people are impressing me with their mix of melancholic happiness (yes, that's how it is) and kindness. In summary, the atmosphere is very relaxing which is truly beneficial to thinking deeply about the numerous interesting problems that we are trying to solve.”

¹ [Hungarian government takes control of research institutes despite outcry](#)

Out of sight, out of mind?

Experiences of our students abroad

Many of our students choose to spend three to six months in foreign labs during their study time. **Martin Pontz** (advisor Reinhard Bürger) was hosted by Simon Aeschbacher at University of Zurich as guest researcher from September to December 2018:

“Almost a year ago, I had the opportunity to do a second research stay abroad after my 3 months at Stanford. This time it was much closer to home, at the University of Zurich, where I was hosted by Simon Aeschbacher in the lab of Lukas Keller. Simon finished his PhD with Nick Barton in Vienna and then did a post-doc with Reinhard Bürger. So he is very familiar with the evolvienna community. Now, he is a junior group leader closely associated with the lab of Lukas Keller. The Keller lab is leading the research on alpine ibex genomics and many discussions at lab meetings and throughout the day were connected to this.

During my stay, Simon and I expanded the range of questions which can be asked in the realm of my main PhD-project. We discussed a lot about theoretical approaches to shed some light on the questions and made significant progress. This was facilitated in parts by the fact that I could share an office with him and that he saved much time for advising me. Right in the first weeks, he also arranged that I could participate in a retreat of a large evolution-working group. From the talks, presented by PhD students, I gained a lot of insight into the various interesting projects of evolutionary biologists.

During the semester, they also run two very nice seminar series. PopGen Vienna alumnus Martin Kapun was one of the invited speakers and presented his work on *Drosophila*. Near the end of my stay, I also had the opportunity to present my results during the “Behaviour, Ecology, Environment and Evolution” Seminar.

While the whole stay was academically very satisfying and productive, also the town of Zurich was very beautiful in the Fall. For the first month of my stay, also my family could join me and we had a wonderful time exploring the close-by mountains and enjoying the views on the alps. After this month, my daughter started Kindergarten and they had to go back to Vienna.

Again, I can't recommend it highly enough to spend some time during the PhD abroad to get to know people and labs.”



Upcoming events

This year's edition of the **Introductory Course** started on September 2nd and runs until October 08th. Several external students are taking part alongside our ten (!) new PopGen students.

The yearly **retreat** with 37 participants takes place from October 10 to 12 at the Hagan Lodge in Altaussee. The program will feature talks, ample time for discussion and brainstorming, and of course we'll plan for hiking/climbing/relaxing and most probably for some party ☺

PopGen Vienna students are organising the course "**Experimental evolution: bringing theory and practice together**" at Vetmeduni Vienna, December 2-6, 2019. Applications are accepted until the end of September 2019. [Link to details](#)

Upcoming seminars

The Winter Term seminars are in preparation, we invited e.g. Grace Lee, Matt Robinson, Peter Visscher, Ludovic Orlando, Bruce Walsh, Roger Butlin, Konrad Lohse, Bart Deplancke, Elly Tanaka, Howard Rundle, Scott Waddell, Bart Pannebakker.

New: We're planning to record seminars and make them available online, visit our website for updates! <https://www.popgen-vienna.at/news/seminars/>

Wishing you a good start of the Winter term!

Publications of our students so far in 2019

Vlachos C, Burny C, Pelizzola M, Borges R, Futschik A, Kofler R and Schlötterer C. Benchmarking software tools for detecting and quantifying selection in evolve and resequencing studies. *Genome Biol.* 20(1), 169. (2019) doi: 10.1186/s13059-019-1770-8
<https://genomebiology.biomedcentral.com/articles/10.1186/s13059-019-1770-8>

Vlachos C and Kofler R. Optimizing the power to identify the genetic basis of complex traits with Evolve and Resequence studies. *Mol. Biol. Evol.* (2019) doi: 10.1093/molbev/msz183
<https://academic.oup.com/mbe/advance-article/doi/10.1093/molbev/msz183/5545983>

Weilguny L, **Vlachos C, Selvaraju D** and Kofler R. Reconstructing the invasion route of DNA transposons using extant population samples. *BioRxiv* 729889. (2019) doi: 10.1101/729889
<https://www.biorxiv.org/content/10.1101/729889v1>

Burny C, Nolte V, Nouhaud P, Dolezal M and Schlötterer C. Secondary evolve and re-sequencing: an experimental confirmation of putative selection targets without phenotyping. *bioRxiv* 722488. (2019) doi: 10.1101/722488
<https://www.biorxiv.org/content/10.1101/722488v1>

Christodoulaki E, Barghi N and Schlötterer C. Distance to trait optimum is a crucial factor determining the genomic signature of polygenic adaptation. *bioRxiv* 721340. (2019) doi:

10.1101/721340

<https://www.biorxiv.org/content/10.1101/721340v1>

Lirakis M and Magalhães S. Does experimental evolution produce better biological control agents? A critical review of the evidence. *Entomol. Exp. Appl.* 167(7), eea.12815. (2019) doi: 10.1111/eea.12815

<https://onlinelibrary.wiley.com/doi/10.1111/eea.12815>

Setter D, Mousset S, Cheng X, Nielsen R, DeGiorgio M and Hermisson J. VolcanoFinder: genomic scans for adaptive introgression. *bioRxiv* 697987. (2019) doi: 10.1101/697987

<https://www.biorxiv.org/content/10.1101/697987v1.full>

Felkel S, Vogl C, Rigler D, Dobretsberger V, Chowdhary BP, Distl O, Fries R, Jagannathan V, Janečka JE, Leeb T, Lindgren G, McCue M, Metzger J, Neuditschko M, Rattei T, Raudsepp T, Rieder S, ... Wallner B. The horse Y chromosome as an informative marker for tracing sire lines. *Sci. Rep.* 9(1), 6095. (2019) doi: 10.1038/s41598-019-42640-w

<https://www.nature.com/articles/s41598-019-42640-w>

Durmaz E, Rajpurohit S, Betancourt N, **Fabian DK**, Kapun M, Schmidt P and Flatt T. A clinal polymorphism in the insulin signaling transcription factor *foxo* contributes to life-history adaptation in *Drosophila*. *Evolution* evo.13759. (2019) doi: 10.1111/evo.13759

<https://onlinelibrary.wiley.com/doi/abs/10.1111/evo.13759>

Felkel S, Wallner B, Chuluunbat B, Yadamsuren A, Faye B, Brem G, Walzer C and Burger PA. A first Y-chromosomal haplotype network to investigate male-driven population dynamics in domestic and wild Bactrian camels. *Front. Genet.* 10, 423. (2019) doi: 10.3389/fgene.2019.00423

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6537670/>

Fages A, ... **Felkel S**, Wallner B, ... Orlando L. Tracking five millennia of horse management with extensive ancient genome time series. *Cell* 177(6), 1419-1435.e31. (2019) doi: 10.1016/j.cell.2019.03.049

[https://www.cell.com/cell/fulltext/S0092-8674\(19\)30384-8](https://www.cell.com/cell/fulltext/S0092-8674(19)30384-8)

Howie JM, Mazzucco R, **Taus T**, Nolte V and Schlötterer C. DNA motifs are not general predictors of recombination in two *Drosophila* sister species. *Genome Biol. Evol.* 11(4), 1345–1357. (2019) doi: 10.1093/gbe/evz082

<https://academic.oup.com/gbe/advance-article/doi/10.1093/gbe/evz082/5454723>

Höllinger I, Pennings PS and Hermisson J. Polygenic adaptation: From sweeps to subtle frequency shifts. *PLoS Genet.* 15(3), e1008035. (2019) doi: 10.1371/journal.pgen.1008035

<https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1008035>

Spitzer K, **Pelizzola M** and Futschik A. Modifying the Chi-square and the CMH test for population genetic inference: adapting to over-dispersion. *arXiv* (2019) arXiv:1902.08127

<https://arxiv.org/pdf/1902.08127.pdf>

Jakšić AM, Karner J, Nolte V, **Hsu S-K**, Barghi N, Mallard F, Otte KA, Svečnjak L, Senti KA and Schlötterer C. Neuronal function and dopamine signaling evolve at high temperature in *Drosophila*. *bioRxiv* 585422. (2019) doi: 10.1101/585422

<https://www.biorxiv.org/content/10.1101/585422v1.full>

Bergman J and Eyre-Walker A. Does adaptive protein evolution proceed by large or small steps at the amino acid level? *Mol. Biol. Evol.* (2019) doi: 10.1093/molbev/msz033
<https://academic.oup.com/mbe/advance-article/doi/10.1093/molbev/msz033/5319976?guestAccessKey=fa3fff8d-08a6-40e9-a3e3-cc25065b22ec>

Barghi N, **Tobler R**, Nolte V, **Jakšić AM**, Mallard F, Otte KA, Dolezal M, **Taus T**, Kofler R and Schlötterer C. Genetic redundancy fuels polygenic adaptation in *Drosophila*. *PLoS Biol.* 17(2), e3000128. (2019) doi: 10.1371/journal.pbio.3000128
<https://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.3000128>

Hsu S-K, **Jakšić AM**, Nolte V, Barghi N, Mallard F, Otte KA, Schlötterer C. A 24 h age difference causes twice as much gene expression divergence as 100 generations of adaptation to a novel environment. *Genes* 10(2), 89. (2019) doi: 10.3390/genes10020089
<https://www.mdpi.com/2073-4425/10/2/89>

Rogers J, Raveendran M, Harris RA, Mailund T, Leppälä K, Athanasiadis G, Schierup MH, Cheng J, Munch K, Walker JA, Konkel MK, Jordan V, Steely CJ, Beckstrom TO, Bergey C, Burrell A, **Schrempf D**, ... Consortium BGA. The comparative genomics and complex population history of *Papio* baboons. *Sci. Adv.* 5(1), eaau6947. (2019) doi: 10.1126/sciadv.aau6947
<http://advances.sciencemag.org/content/5/1/eaau6947>

Liu J, Champer J, **Langmüller AM**, Liu C, Chung J, Reeves R, Luthra A, Lee YL, Vaughn AH, Clark AG and Messer PW. Maximum likelihood estimation of fitness components in experimental evolution. *Genetics* genetics.301893.2018. (2019) doi: 10.1534/genetics.118.301893
<http://www.genetics.org/content/early/2019/01/24/genetics.118.301893>

See all publications [here](#)