

## Newsletter January 2024

Welcome to the 30<sup>th</sup> edition of the PopGen ALUMNI newsletter!

Follow us on Social Media
<a href="https://twitter.com/PopGenViennaPhD">https://twitter.com/PopGenViennaPhD</a>
<a href="https://www.youtube.com/channel/UCAdGx2zyQNyVti9Cr1muhUq">https://www.youtube.com/channel/UCAdGx2zyQNyVti9Cr1muhUq</a>

Join our Tuesday webinars: <a href="https://www.popgen-vienna.at/news/seminars/">https://www.popgen-vienna.at/news/seminars/</a>

#### HAPPY NEW YEAR!

### Recent events and news

### **December 2023: Experimental Evolution course**

Also this year our students organised the international practical course "Experimental evolution: Exploring evolutionary forces in controlled environments" from Nov 27 to Dec 1, 2023 at the Vetmeduni. Our students planned the entire course, invited speakers for the morning sessions, screened applications from around the world and taught and tutored all practical sessions for the 25 participants to train on real data.

Link to course website: https://www.popgen-vienna.at/training/experimental-evolution-course/



### November, December 2023: PopGen Xmas

We enjoyed a Xmas dinner to celebrate a successful year soon coming to an end. Ice skating had been planned as our team activity but was was postponed to December due to bad weather (see proof below).

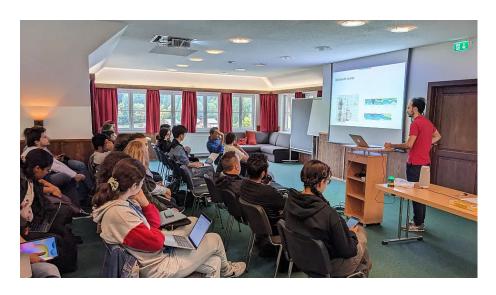




#### October 2023: retreat

31 PhD students and faculty joined this year's retreat at the beautiful surroundings of Altaussee. We had great weather at the foot of the Loser mountain and listened to exciting talks with plenty of discussion opportunities, had a free afternoon for hikes and relaxing and enjoyed traditional food, good company and a night walk.

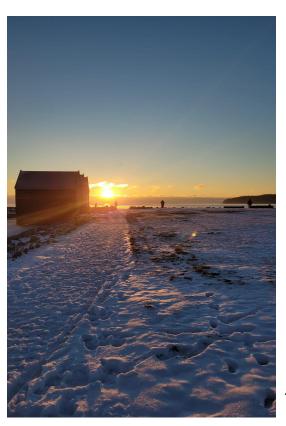




## Alumni portraits

We feature a brief report about one of PopGen's graduate and faculty alumni in the Newsletter. This time, PopGen Vienna graduate alumna **Marta Pelizzola** (former PhD student of the Futschik group) gives us some insight into her postdoc research in Denmark:

"My name is Marta. I finished my PhD at Popgen under the supervision of Andreas Futschik in February 2022. Despite COVID, I did my stay abroad during the PhD at Popgen, and this is how I got to know Asger Hobolth and his group at Aarhus University. After the end of my PhD, I started a postdoc with Asger.



Within my postdoc, I have several projects with different collaborators at the Department of Bioinformatics and at Aarhus University Hospital. My main projects consist in developing methods for 1. discovering mutational signatures from the mutational counts data from cancer patients and 2. predicting the treatment burden after radio-chemotherapy for cancer patients in different treatment arms. It has been very exciting to work on a different research area and I have been learning a lot about these applications.

Within my second project, I am working with a team of medical physicists and medical doctors at the hospital which is a new experience compared to the PhD. Everyone is very involved with the patients and patients contribute to our research in different ways and it is extremely fascinating for me.

I still have two more years of postdoc to go. Right now, I've begun to think about what to do and where to apply for my next position and we are starting a new collaboration, so I will start some new popgen projects soon as well ""



The snowy landscape above is a picture from the beach in Aarhus (January 8, 2024). And this is a group picture from last year's summer retreat with the Department of Bioinformatics.

# Out of sight, out of mind? Experiences of our students abroad

Many of our students choose to spend three to six months abroad during their study time. **Howard Chen** (advisor Andreas Futschik) spent 6 months at the University of Bremen, hosted by Werner Brannath.

"Last year, I had the privilege of joining the research group led by Werner Brannath at the University of Bremen for half a year through an opportunity offered by PopGen Vienna. The research group, unlike the one at the graduate school in Vienna, was mathematically oriented and focused on applications in clinical trials. This distinct environment gave me a diverse and enriching experience, as I not only found myself in another country but also worked with individuals from different fields.

The research seminars they offered were particularly interesting, where people talked about their previous work. The subject matter provided me with new knowledge and invaluable insights. My project there started with something theoretical, where we aimed to reduce the conservativeness of a subset selection test. With the overarching goal of establishing connections between population genetics and clinical trials, we hope to apply our proposed method in both fields. Thanks to countless suggestions from researchers in the group, this became much more achievable.

The visit to Bremen coincided with the summer months, which at the time in Bremen was known to be one of the hottest summers ever recorded in history. Fortunately, being a coastal city, the



temperature wasn't too unbearable thanks to the refreshing sea breeze. A visit to the harbour, part of an activity at the MCP conference, also made the stay more enjoyable. The conference, which I had the fascinating opportunity to both attend and contribute to its organization, was also a wonderful experience. It also allowed the opportunity to present previous work done in Vienna to a broader audience.

It was a great experience having spent my time in Bremen, and I would recommend everyone to seize the opportunity of going for a research stay abroad whenever possible."

Foto: A landmark structure at Uni Bremen: The Bremen Drop Tower at the Center of Applied Space Technology and Microgravity.

## **Upcoming seminars**

Our Tuesday seminars are arranged as hybrid (or online) seminars, so you can join us from all over the world! The list of guests is growing and includes C. Baer, R. Nielsen, B. Blackman, D. Obbard, C. Landry, N. Galtier, T. Lenormand, N. Chen, O. X. Cordero during the Summer term!

Sign up here to receive reminders and Zoom links: https://forms.gle/eE7ZoaUL326TCX4M6

## Have a successful and healthy 2024!

## **Publications of our students 2023**

**Xiao** C, **Duarri-Redondo** S, **Thorhölludottir DAV**, **Chen Y** and Schlötterer C. Non-additive effects between genotypes: Implications for competitive fitness assays. Ecol. Evol. 13(11), e10713. (2023) doi: 10.1002/ece3.10713 <a href="https://onlinelibrary.wiley.com/doi/10.1002/ece3.10713">https://onlinelibrary.wiley.com/doi/10.1002/ece3.10713</a>

Buchner S, **Hsu S-K**, Nolte V, Otte KA and Schlötterer C. Effects of larval crowding on the transcriptome of *Drosophila simulans*. Evol. Appl. (2023) in print. doi: 10.1111/eva.13592 <a href="https://onlinelibrary.wiley.com/doi/10.1111/eva.13592">https://onlinelibrary.wiley.com/doi/10.1111/eva.13592</a>

**Pianezza R, Scarpa A**, Narayanan P, Signor S and Kofler R. Spoink, a LTR retrotransposon, invaded *D. melanogaster* populations in the 1990s. bioRxiv 2023.10.30.564725. (2023) doi: 10.1101/2023.10.30.564725 https://www.biorxiv.org/content/10.1101/2023.10.30.564725v2

**Wierzbicki F** and Kofler R. The composition of piRNA clusters in *Drosophila melanogaster* deviates from expectations under the trap model. BMC Biol. 21(224). (2023) doi: 10.1101/2023.02.14.528490 https://bmcbiol.biomedcentral.com/articles/10.1186/s12915-023-01727-7

**Scarpa A** and Kofler R. The impact of paramutations on the invasion dynamics of transposable elements. Genetics iyad181, 2023.03.14.532580. (2023) doi: 10.1101/2023.03.14.532580 https://academic.oup.com/genetics/advance-article/doi/10.1093/genetics/iyad181/7306651

Signor S, Vedanayagam J, Kim BY, **Wierzbicki F**, Kofler R and Lai EC. Rapid evolutionary diversification of the flamenco locus across simulans clade *Drosophila species*. PLoS Genet. 19(8), e1010914. (2023) doi: 10.1371/journal.pgen.1010914

https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1010914

Chen H, Pelizzola M and Futschik A. Haplotype based testing for a better understanding of the selective architecture. BMC Bioinformatics 24(1), 322. (2023) doi: 10.1186/s12859-023-05437-3 <a href="https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-023-05437-3">https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-023-05437-3</a>

**Yıldırım B** and Vogl C. Purifying selection against spurious splicing signals contributes to the base composition evolution of the polypyrimidine tract. J. Evol. Biol. n/a(n/a). (2023) doi: 10.1111/jeb.14205 <a href="https://onlinelibrary.wiley.com/doi/10.1111/jeb.14205">https://onlinelibrary.wiley.com/doi/10.1111/jeb.14205</a>

**Langmüller AM**, Nolte V, Dolezal M and Schlötterer C. The genomic distribution of transposable elements is driven by spatially variable purifying selection. Nucleic Acids Res. gkad635. (2023) doi: 10.1093/nar/gkad635 <a href="https://academic.oup.com/nar/advance-article/doi/10.1093/nar/gkad635/7240371">https://academic.oup.com/nar/advance-article/doi/10.1093/nar/gkad635/7240371</a>

**Szukala A**, Bertel C, Frajman B, Schönswetter P and Paun O. Parallel adaptation to lower altitudes is associated with enhanced plasticity in *Heliosperma pusillum* (*Caryophyllaceae*). Plant J. early online. (2023) doi: 10.1111/tpj.16342 <a href="https://onlinelibrary.wiley.com/doi/10.1111/tpj.16342">https://onlinelibrary.wiley.com/doi/10.1111/tpj.16342</a>

**Scarpa A**, **Pianezza R**, **Wierzbicki F** and Kofler R. Genomes of historical specimens reveal multiple invasions of LTR retrotransposons in *Drosophila melanogaster* populations during the 19th century. bioRxiv 2023.06.06.543830. (2023) doi: 10.1101/2023.06.06.543830

https://www.biorxiv.org/content/10.1101/2023.06.06.543830v1

**Bozlak E, Radovic L**, Remer V, Rigler D, Allen L, Brem G, Stalder G, Castaneda C, Cothran G, Raudsepp T, Okuda Y, Moe KK, Moe HH, Kounnavongsa B, Keonouchanh S, Van NH, Vu VH, ... Wallner B. Refining the evolutionary tree of the horse Y chromosome. Sci. Rep. 13(1), 8954. (2023) doi: 10.1038/s41598-023-35539-0 <a href="https://rdcu.be/ddALX">https://rdcu.be/ddALX</a>

**Lai W-Y**, Otte KA and Schlötterer C. Evolution of metabolome and transcriptome support a hierarchical organization of adaptive traits. Genome Biol. Evol. evad098. (2023) doi: 10.1093/gbe/evad098 https://academic.oup.com/gbe/advance-article/doi/10.1093/gbe/evad098/7180075

**Pisupati R**, Nizhynska V, Mollá Morales A and Nordborg M. On the causes of gene-body methylation variation in *Arabidopsis thaliana*. PLoS Genet. 19(5), e1010728. (2023) doi: 10.1371/journal.pgen.1010728 <a href="https://pubmed.ncbi.nlm.nih.gov/37141384/">https://pubmed.ncbi.nlm.nih.gov/37141384/</a>

**Höllinger I**, **Wölfl B** and Hermisson J. A theory of oligogenic adaptation of a quantitative trait. Genetics, iyad139. (2023) doi: 10.1101/2023.04.20.537719

https://academic.oup.com/genetics/advance-article/doi/10.1093/genetics/iyad139/7238502

Barghi N and **Ramirez-Lanzas** C. A high throughput method for egg size measurement in *Drosophila*. Sci. Rep. 13(1), 3791. (2023) doi: 10.1038/s41598-023-30472-8 https://www.nature.com/articles/s41598-023-30472-8

**Kotari I**, Kosiol C and Borges R. The patterns of codon usage between chordates and arthropods are different but coevolving with mutational biases. bioRxiv 2023.03.30.534958. (2023) doi: 10.1101/2023.03.30.534958 https://www.biorxiv.org/content/10.1101/2023.03.30.534958v1

**Scarpa A** and Kofler R. The impact of paramutations on the invasion dynamics of transposable elements. bioRxiv 2023.03.14.532580. (2023) doi: 10.1101/2023.03.14.532580 https://www.biorxiv.org/content/10.1101/2023.03.14.532580v1

**Götsch H** and Bürger R. Evolution of quantitative traits under directional selection: Selective sweeps or small allele-frequency changes? bioRxiv 2023.02.23.529647. (2023) doi: 10.1101/2023.02.23.529647 https://www.biorxiv.org/content/10.1101/2023.02.23.529647v1

Crego CG, Hess J, Yardeni G, Harpe M de La, Beclin F, Cauz-Santos LA, Saadain S, Barbará T, Temsch EM, Weiss-Schneeweiss H, Barfuss MHJ, Till W, Heyduk K, Lexer C, Paun O and Leroy T. Short structural variation fuelled CAM evolution within an explosive bromeliad radiation. bioRxiv 2023.02.01.526631. (2023) doi: 10.1101/2023.02.01.526631 <a href="https://www.biorxiv.org/content/10.1101/2023.02.01.526631v1">https://www.biorxiv.org/content/10.1101/2023.02.01.526631v1</a>

**Wierzbicki** F and Kofler R. The composition of piRNA clusters in *Drosophila melanogaster* deviates from expectations under the trap model. bioRxiv 2023.02.14.528490. (2023) doi: 10.1101/2023.02.14.528490 <a href="https://www.biorxiv.org/content/10.1101/2023.02.14.528490v1">https://www.biorxiv.org/content/10.1101/2023.02.14.528490v1</a>

Borges R, **Kotari I**, **Bergman J**, Chase MA, Mugal CF and Kosiol C. Traditional phylogenetic models fail to account for variations in the effective population size. bioRxiv 2022.09.26.509598. (2023) doi: 10.1101/2022.09.26.509598 https://www.biorxiv.org/content/10.1101/2022.09.26.509598v2

See all publications <u>here</u>