

Newsletter October 2021

Welcome to the 24th edition of the PopGen ALUMNI newsletter!

Follow us on Social Media
https://twitter.com/PopGenViennaPhD
https://www.youtube.com/channel/UCAdGx2zyQNyVti9Cr1muhUq

Join our Tuesday webinars: https://www.popgen-vienna.at/news/seminars/

Do you know of suitable candidates for PopGen Vienna?

Our call for PhD students 2022 is open – please help us spread the word!

Application deadline: December 12, 2021

Flyer for download on the website: https://www.popgen-vienna.at/media/popgenviennaflyertopics_4.pdf

https://www.popgen-vienna.at/application/procedure/

Recent events and news

October 2021: PhD retreat

After the pandemic forced us to skip last year's retreat, we decided to cease the 100% vaccination status and free PCR testing in Vienna to spend two days at the huts of Feuerkogel (Upper Austria). We had small group workshops, enjoyed some hiking (despite very uninviting weather) and comforting mountain food at 1600m elevation. It was great to catch up on research and friendships after the long break - finally face to face!











September 2021: PhD defense

Congratulations to **Anna Maria Langmüller** (Schlötterer group) on successfully defending her thesis "The detection of temperature-dependent fitness effects with Evolve and Resequence experiments".



September 2021: PopGen Hike

We enjoyed a **hike** among the "Vienna Woods" with wonderful weather. After a long time with no social activities due to the pandemic, it was a special treat to spend time together! **Dr. Sam Yeaman** (Univ. of Calgary, currently on sabbatical) joined us and it was great to discuss latest research in person instead of zoom.



July 2021: Outreach

PhD students **Dagny Runarsdottir** and **Lara Radovic** reach out to young researchers at Children's University to explain how populations evolve.



July 2021: Alumni News

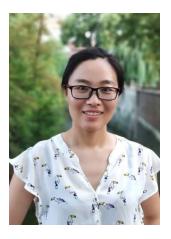
Congratulations to alumna **Ana Marija Jaksic** for having been selected as a runner-up for the prestigious best student paper award for papers published in MBE during 2020 with the paper "Neuronal Function and Dopamine Signaling Evolve at High Temperature in *Drosophila*".

June 2021: Competition winner

Congratulations to Lara Radovic (Wallner group), winner of the student competition (genetics) at the Equine Science Society Virtual Symposium!

June 2021: PhD defense

Congratulations to **Huying Shang** on successfully defending her thesis "Genomics of the speciation continuum in Eurasian *Populus* species".



May 2021: Faculty meeting

The faculty met online on 20th of May, 2021.

May 2021: SAB meeting

Also this year's **SAB meeting** had to be carried out online from May 17th to 20th. We enjoyed four afternoons of student presentations, discussions and informal interactions with our board members.



April 2021: PhD defense

Congratulations to **Emmanouil Lyrakis** (Schlötterer group) on the highest exam grade for his PhD zoom defense "The physiological and genetic basis of reproductive dormancy in *Drosophila* fruit flies".



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. **Marta Pelizzola** (advisor Andreas Futschik) was hosted by Asger Hobolth at Aarhus Univ. (DK) as a guest researcher for 5 months.

"Despite some delays due to COVID-19, I began my semester abroad in May 2021. I spent 5 months at the Department of Mathematics of Aarhus University collaborating with Asger Hobolth's research group. Here, I worked with Asger, Ragnhild (Ph.D. student), Kim, and Ida (master students). When I left Austria, the pandemic was still affecting our daily life in Vienna. However, most of the restrictions had just been lifted in Denmark when I arrived. This allowed me to go to the office, meet everyone in person, and join the activities of the department from the very beginning. Additionally, Asger helped me a lot with settling in Aarhus, thus I immediately felt very welcome both in the department and in the city.

The aim of my stay was to work on a model for mutational signatures in cancer data to account for overdispersion. Given a collection of mutational profiles from several patients, mutational signatures are derived using non-negative matrix factorization. However, to apply this factorization to mutational counts data, we need to know the number of mutational signatures to be used in the factorization. Thus, we also worked on a rigorous model selection procedure to determine the number of mutational signatures. As a statistician, it has been very valuable for me to work on a new application and gain experience in this research area. We are now continuing our collaboration to finish up the manuscript we have drafted during my stay.

I would like to thank Asger, Andreas, and the graduate school for this opportunity and I would like to recommend it to everyone. Below, a picture of me and my colleague Ragnhild in the Mols Bjerge National Park from our retreat with the Bioinformatics department and a picture of one of the beaches in Aarhus © "



Upcoming seminars

Our Tuesday seminars have gone virtual, so you can join us from all over the world!

Sign up here to receive reminders and links for the upcoming webinars by Kerstin Lindblad-Toh, Florian Schwarz, Kathryn Elmer, Eugene Koonin, Amaury Lambert, Jianzhi Zhang, Aglaia Szukala, Torsten Günther, Bart Nieuwenhuis and John Kelly.

https://forms.gle/r88bEbanC8HRpmLz6

Enjoy Autumn, stay healthy and have a successful rest of the year!

Publications of our students so far in 2021

Burny C, Nolte V, Dolezal M and Schlötterer C. Highly parallel genomic selection response in replicated Drosophila melanogaster populations with reduced genetic variation. *Genome Biol. Evol.* evab239. (2021) doi: 10.1101/2021.04.06.438598

https://academic.oup.com/gbe/advance-article/doi/10.1093/gbe/evab239/6409861?login=true

Yardeni G, Viruel J, Paris M, Hess J, **Groot Crego C**, de La Harpe M, Rivera N, Barfuss MHJ, Till W, Guzmán-Jacob V, Krömer T, Lexer C, Paun O and Leroy T. Taxon-specific or universal? Using target capture to study the evolutionary history of a rapid radiation. *Mol. Ecol. Resour.* 00, 1–19. (2021) doi: 10.1101/2021.05.20.444989

https://onlinelibrary.wiley.com/doi/10.1111/1755-0998.13523

Wolfe TM, Balao F, Trucchi E, Bachmann G, Gu W, Baar J, Hedren M, Weckwerth W, Leitch AR and Paun O. Recurrent allopolyploidization events diversify eco-physiological traits in marsh orchids. *bioRxiv* 2021.08.28.458039. (2021) doi: 10.1101/2021.08.28.458039 https://www.biorxiv.org/content/10.1101/2021.08.28.458039v1

Shang H, Rendón-Anaya M, Paun O, Field DL, Hess J, Vogl C, Liu J, Ingvarsson PK, Lexer C and Leroy T. Conserved genomic landscapes of differentiation across *Populus* speciation continuum. *bioRxiv* 2021.08.26.457771. (2021) doi: 10.1101/2021.08.26.457771 https://www.biorxiv.org/content/10.1101/2021.08.26.457771v1

Wierzbicki F, Kofler R and Signor S. Evolutionary dynamics of piRNA clusters in *Drosophila*. *bioRxiv* 2021.08.20.457083. (2021) doi: 10.1101/2021.08.20.457083 https://www.biorxiv.org/content/10.1101/2021.08.20.457083v1

Szukala A, Lovegrove-Walsh J, Luqman H, Fior S, **Wolfe TM**, Frajman B, Schoenswetter P and Paun O. Polygenic routes lead to parallel altitudinal adaptation in *Heliosperma pusillum* (*Caryophyllaceae*). *bioRxiv* 2021.07.05.451094. (2021) doi: 10.1101/2021.07.05.451094 https://www.biorxiv.org/content/10.1101/2021.07.05.451094v2

Wierzbicki F*, **Schwarz** F*, Cannalonga O and Kofler R. Novel quality metrics allow identifying and generating high-quality assemblies of piRNA clusters. *Mol Ecol Res* (2021) accepted https://onlinelibrary.wiley.com/doi/abs/10.1111/1755-0998.13455

Yang E, Metzloff M, Langmüller AM, Clark AG, Messer PW and Champer J. A homing suppression gene drive with multiplexed gRNAs maintains high drive conversion efficiency and avoids functional resistance alleles. *bioRxiv* 2021.05.27.446071. (2021) doi: 10.1101/2021.05.27.446071

https://www.biorxiv.org/content/10.1101/2021.05.27.446071v1

Langmüller AM, Champer J, Lapinska S, Xie L, Metzloff M, Liu J, Xu Y, Clark AG and Messer PW. Fitness effects of CRISPR endonucleases in *Drosophila melanogaster* populations. *bioRxiv* 2021.05.13.444039. (2021) doi: 10.1101/2021.05.13.444039 https://www.biorxiv.org/content/10.1101/2021.05.13.444039v1

Wölfl B, te Rietmole H, Salvioli M, Kaznatcheev A, Thuijsman F, Brown JS, Burgering B and Staňková K. The contribution of evolutionary game theory to understanding and treating cancer. *medRxiv* 2020.12.02.20241703. (2021) doi: 10.1101/2020.12.02.20241703 https://www.medrxiv.org/content/10.1101/2020.12.02.20241703v3

Johnson KD, Beiglböck M, Eder M, Grass A, Hermisson J, Pammer G, Polechová J, Toneian D and **Wölfl B**. Disease momentum: Estimating the reproduction number in the presence of superspreading. *Infect. Dis. Model.* (2021) doi: 10.1016/j.idm.2021.03.006. https://www.sciencedirect.com/science/article/pii/S2468042721000270?via%3Dihub

Bayle V, Fiche J-B, **Burny** C, Platre MP, Nollmann M, Martinière A and Jaillais Y. Single-particle tracking photoactivated localization microscopy of membrane proteins in living plant tissues. *Nat. Protoc.* (2021) doi: 10.1038/s41596-020-00471-4 https://www.nature.com/articles/s41596-020-00471-4

Langmüller AM, Dolezal M and Schlötterer C. Fine mapping without phenotyping: Identification of selection targets in secondary Evolve and Resequence experiments. *Genome Biol. Evol.* evab154. (2021) doi: 10.1093/gbe/evab154

https://academic.oup.com/gbe/advance-article/doi/10.1093/gbe/evab154/6311659

Lai W-Y, Nolte V, **Jakšić AM** and Schlötterer C. Evolution of phenotypic variance provides insights into the genetic basis of adaption. *bioRxiv* 2021.01.19.427260. (2021) doi: 10.1101/2021.01.19.427260

https://www.biorxiv.org/content/10.1101/2021.01.19.427260v1

Lai W-Y and Schlötterer C. Evolution of gene expression variance during adaptation to high temperature in *Drosophila*. *bioRxiv* 2021.01.19.427270. (2021) doi: 10.1101/2021.01.19.427270 https://www.biorxiv.org/content/10.1101/2021.01.19.427270v1

Hsu SK, Belmouaden C, Nolte V, Schlötterer C. Parallel gene expression evolution in natural and laboratory evolved populations. *Mol Ecol* 30: 884–894. (2021) doi: 10.1111/Mec.15649 https://onlinelibrary.wiley.com/doi/full/10.1111/mec.15649

See all publications <u>here</u>