Newsletter May 2023

Welcome to the 28th edition of the PopGen ALUMNI newsletter!

Follow us on Social Media
https://twitter.com/PopGenViennaPhD
https://www.youtube.com/channel/UCAdGx2zyQNyVti9Cr1muhUg

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

Do you know of suitable candidates for the
brand-new SFB "Polygenic Adaptation"
and PopGen Vienna?

Our call for Postdocs and PhD students 2023 is open –
please help us spread the word!

Application deadline: June 04, 2023

Details:

https://www.vetmeduni.ac.at/sfb-polygenic-adaptation/open-positions

https://www.popgen-vienna.at/media/popgenviennaflyer.pdf

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

Recent events and news

May 2023: Final Symposium
More than 50 former and current members of the Vienna Graduate School of Population Genetics met to celebrate the conclusion of 12 successful years of the FWF-funded DK. Two full days of exciting talks by alumni, current students and SAB members were part of the Final Symposium from May 15-17 at Hirschwang/Reichenau a.d. Rax. An extra day for hiking, networking and team games was only slightly spoilt by intense rain – we generated plenty of sunshine ourselves and had a great time talking about projects, experiences and learnings of the past decade.


Fort, PNAS 2012

May 2023: PhD defense

Congratulations to **Wei-Yun Lai** (Schlötterer group) on successfully defending her PhD thesis entitled "The role of polygenic adaptation and genetic redundancy in gene expression evolution".

Alumni portraits

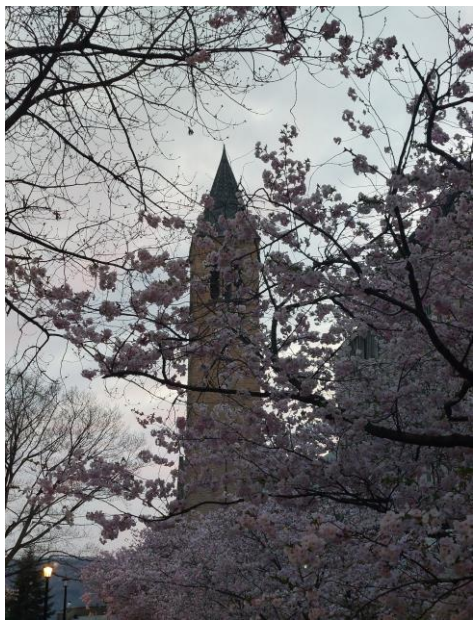
We feature a brief report about one of PopGen's graduate and faculty alumni in the Newsletter. This time, PopGen Vienna graduate alumna **Anna Maria Langmüller** (former PhD student of the Schlötterer group) gives us some insight into her work environment at the *Cornell University (US)*:

"Hi! My name is Anna, and I am currently a postdoc in the Messer lab at Cornell University. I finished my PhD under the supervision of Christian Schlötterer in September 2021, and moved to Ithaca, NY in December 2021. There, I swapped fruit flies for (simulated) mosquitoes and have been studying the effect of population structure on host-pathogen dynamics in mosquito-transmitted diseases ever since.

Mosquito-transmitted diseases continue to wreak havoc, affecting millions of individuals worldwide each year. Despite recent strides in computational advancements, agent-based models often fall short in disease forecasting when compared to their idealized mathematical counterparts. This might be caused by a lack in our fundamental understanding of how spatial dynamics need to be appropriately modeled. In my research, funded by the Marie Skłodowska-Curie Actions program, I leverage the power of Gaussian processes, a sophisticated statistical framework, to significantly advance sensitivity analysis for agent-based models, which will further our understanding of how spatial structure impacts the intricate dynamics between hosts and pathogens. Consequently, our efforts will not only enhance disease forecasting but also enable a more thorough evaluation of proposed intervention strategies.

In the last couple of months, I have developed a keen interest into spatial population genetics, which I hope to pursue during my 1-year return phase to Vienna where I will be working with Joachim Hermisson … stay tuned. Until then - lovely greetings from Ithaca & the Messer lab, which has become a second (academic) home to me.

Sunset on Campus (Cayuga lake in the background).



McGraw Tower in Spring '23

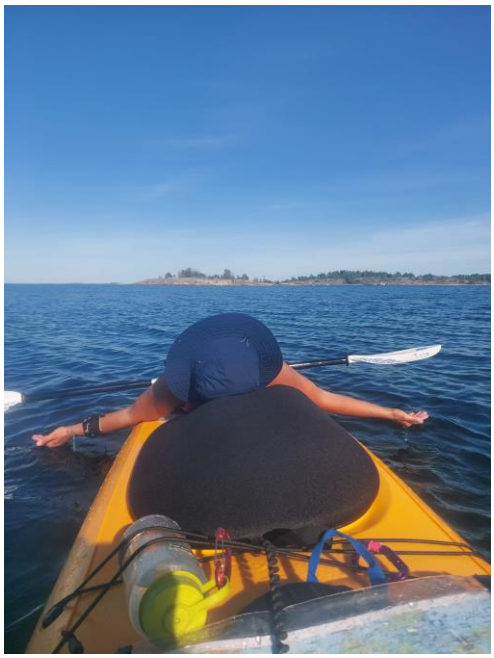
Out of sight, out of mind?

Experiences of our students abroad

Many of our students choose to spend three to six months abroad during their study time. **Elif Bozlak** (advisor Barbara Wallner) spent 6 months at the University of Stockholm, hosted by Love Dalen.

"During my third year of doctoral studies at the Vienna Graduate School of Population Genetics, I had the opportunity to pursue a six-month study abroad program. I joined Prof. Love Dalén's group at the Center for Paleogenetics at University of Stockholm, from May to October 2022, which was also supported by an EMBO Scientific Exchange Grant.

Working with the international research team at the Center for Paleogenetics was an incredible experience. I collaborated with talented researchers, which helped me understand the importance of various scientific approaches. The decision to join their team was driven by my deep admiration for ancient DNA studies. Witnessing their thorough process, from sample collection to data analysis and interpretation, was both impressive and instructive. Besides engaging in fruitful scientific discussions, I also learned a lot about how larger research groups operate.



Beyond the scientific aspects, my time in Sweden was personally enriching. Exploring the Swedish Archipelago was a must-do experience. I stayed on a nearby island where I occasionally needed to row back home. This allowed me to fully immerse myself in the beautiful surroundings and meet wonderful people. I also had the chance to explore the Swedish mountains and hike through the wilderness. The Swedish culture's appreciation for nature and outdoor activities left a strong impression on me.

Overall, this entire experience has been amazing, and I am thankful for everyone who supported the process. I highly recommend it to all students at the Vienna Graduate School of Population Genetics. "

Elif Bozlak and Burcin Yildirim (group Vogl, see Alumni News edition 27) during their abroad stays in Sweden.

Upcoming seminars

Our Tuesday seminars are arranged as hybrid (or online) seminars, so you can join us from all over the world! Join us for seminars by Stephen Dorus (Syracuse Univ., US), Emilie Brasset (Univ. Clermont Auvergne, FR), Dolph Schluter (Univ. of British Columbia, CA)and Elif Bozlak (Vetmeduni, AT) before we resume with the winter term seminars in October.

Sign up here to receive reminders and links for the remaining term's webinars:
https://forms.gle/jvgbtz5pa7Ewz1Hj6

Have a great summer!

Publications of our students since the last newsletter

Höllinger I, **Wölfl B** and Hermisson J. A theory of oligogenic adaptation of a quantitative trait. bioRxiv 2023.04.20.537719. (2023) doi: 10.1101/2023.04.20.537719
https://www.biorxiv.org/content/10.1101/2023.04.20.537719v1

Kotari I, Kosiol C and Borges R. The patterns of codon usage between chordates and arthropods are different but co-evolving 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

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
https://www.biorxiv.org/content/10.1101/2023.02.14.528490v1

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

Langmüller AM, Champer J, Lapinska S, Xie L, Metzloff M, Champer SE, Liu J, Xu Y, Du J, Clark AG and Messer PW. Fitness effects of CRISPR endonucleases in *Drosophila melanogaster* populations. Elife 11, e71809. (2022) doi: 10.7554/eLife.71809
https://elifesciences.org/articles/71809

Selvaraju D, **Wierzbicki F** and Kofler R. P-element invasions in *Drosophila erecta* shed light on the establishment of host control over a transposable element. bioRxiv 2022.12.22.521571. (2022) doi: 10.1101/2022.12.22.521571
https://www.biorxiv.org/content/10.1101/2022.12.22.521571v1

Chen H, **Pelizzola M** and Futschik A. Haplotype based testing for a better understanding of the selective architecture. *bioRxiv* 2022.07.18.500395. (2022) doi: 10.1101/2022.07.18.500395
https://www.biorxiv.org/content/10.1101/2022.07.18.500395v1

See all publications here