Curriculum Vitae

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Education

Sep 2011 – Jun 2018 **Ph.D.** in Computational Biology.
Chinese Academy of Sciences–Max Planck Society Partner Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Shanghai, China.
University of Chinese Academy of Sciences, Beijing, China.

Sep 2007 – Jun 2011 **B.Sc.** in Biochemistry and Molecular Biology (With Distinction).
South China Agricultural University, Guangzhou, China.

Positions

Aug 2021 – present **Postdoctoral Researcher.**
Department of Evolutionary Anthropology. University of Vienna, Vienna, Austria.

Nov 2019 – Jun 2021 **Postdoctoral Research Associate.**
Department of Molecular and Cellular Biology. University of Arizona, Tucson, United States.

Sep 2018 – Jul 2019 **Senior Scientist.**
Department of Research Service and Translational Medicine. WuXi NextCODE Genomics (Shanghai) Co. Ltd., Shanghai, China.

Research interests

My major research interest is developing and applying computational tools for population genetic inference. I have led or participated in projects for various population genetics problems, including detecting signals of natural selection, estimating the strength of natural selection, quantifying the distribution of fitness effects, and inferring ghost introgressed fragments. I am exploring population genetics with different methodologies, especially with machine learning or deep learning algorithms. I am also interested in implementing computational approaches into software and applying them for analyzing large-scale genomic datasets from various species, such as humans and great apes.

Academic publications

* Corresponding author

† Co-first author

Peer-reviewed publications

2024 **Huang X***, Rymbekova A, Dolgova O, Lao O*, Kuhlwilm M*. Harnessing deep learning for population genetic inference. *Nature Reviews Genetics* **25**: 61–78. PMID: 37666948. DOI: 10.1038/s41576-023-00636-3

2023 Pawar H, Rymbekova A, Cuadros S, **Huang X**, de Manuel M, van der Valk T, Lobon I, Alvarez-Estape M, Haber M, Dolgova O, Han S, Esteller-Cucala P, Juan D, Ayub Q, Bautista R, Kelly JL, Cornejo OE, Lao O, Andrés AM, Guschanski K, Ssebide B, Cranfield M, Tyler-Smith C, Xue Y, Prado-Martinez J, Marques-Bonet T*, Kuhlwilm M*. Ghost admixture in eastern gorillas. *Nature Ecology & Evolution* **7**: 1503–1514. PMID: 37500909. DOI: 10.1038/s41559-023-02145-2

2023 Lauterbur ME*, Cavassim MIA, Gladstein AL, Gower G, Pope NS, Tsambos G, Adrion J, Belsare S, Biddanda A, Caudill V, Cury J, Echevarria I, Haller BC, Hasan AR, **Huang X**, Iasi LNM, Ekaterina Noskova, Obšteter J, Pavinato VAC, Pearson A, Peede D, Perez MF, Rodrigues MF, Smith CCR, Spence JP, Teterina A, Tittes S, Unneberg P, Vazquez JM, Waples RK, Wohns AW, Wong Y, Baumdicker F, Cartwright RA, Gorjanc G, Perregor, Gutenkunst RN, Kelleher J, Kern AD, Ragsdale AP, Ralph PL, Schrider DR, Gronau I*. Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations. *eLife* **12**: RP84874. PMID: 37342968. DOI: 10.7554/eLife.84874

2022 **Huang X***, Kruisz P, Kuhlwilm M*. sstar: A Python package for detecting archaic introgression from population genetic data with *S**. *Molecular Biology and Evolution* **39**: msac212. PMID: 36181428. DOI: 10.1093/molbev/msac212

- Highlighted in a special 40th anniversary perspective on human diversification for the founding of *Molecular Biology and Evolution* by Hünemeier (2024). DOI: 10.1093/molbev/msae029

2021 **Huang X**, Fortier AL, Coffman AJ, Struck TJ, Irby MN, James JE, León-Burguete JE, Ragsdale AP, Gutenkunst RN*. Inferring genome-wide correlations of mutation fitness effects between populations. *Molecular Biology and Evolution* **38**: 4588–4602. PMID: 34043790. DOI: 10.1093/molbev/msab162

- Highlighted in a special 40th anniversary perspective on inferential methods for the founding of *Molecular Biology and Evolution* by Russo et al (2024). DOI: 10.1093/molbev/msad264

2021 **Huang X***, Wang S, Jin L*, He Y*. Dissecting dynamics and differences of selective pressures in the evolution of human pigmentation**.** *Biology Open* **10**: bio056523. PMID: 33495209. DOI: 10.1242/bio.056523

2019 **Huang X***, Jin L, He Y. SeleDiff: A fast and scalable tool for testing and estimating selection differences between populations**.** *The Journal of Open Source Software* **4**: 1545. DOI: 10.21105/joss.01545

2015 He Y*, Wang M, **Huang X**, Li R, Xu H, Xu S, Jin L*. A probabilistic method for testing and estimating

selection differences between populations. *Genome Research* **25**: 1903–1909. PMID: 26463656. DOI: 10.1101/gr.192336.115

2015 Zhou B, Dong H, He Y, Sun J, Jin W, Xie Q, Fan R, Wang M, Li R, Chen Y, Xie S, Shen Y, **Huang X**, Wang S, Lu F, Jia J, Zhuang H, Locarnini S, Zhao G, Jin L, Hou J. Composition and interactions of hepatitis B virus quasispecies defined the virological response during telbivudine therapy. *Scientific Reports* **5**: 17123. PMID: 26599443. DOI: https://doi.org/10.1038/srep17123

2014 Wang M, **Huang X**, Li R, Xu H, Jin L*, He Y*. Detecting recent positive selection with high accuracy and reliability by conditional coalescent tree. *Molecular Biology and Evolution* **31**: 3068–3080. PMID: 25135945. DOI: 10.1093/molbev/msu244

Preprints and under reviews

2023 Gelabert P*, Bickle P, Hofmann D, Teschler-Nicola M, Anders A, **Huang X**, Olalde I, Fournier R, Ringbauer H, Akbari A, Cheronet O, Lazaridis I, Broomandkhoshbacht N, Fernandes DM, Sawyer S, Schattke C, Buttinger K, Callan K, Candilio F, Bravo G, Curtis E, Ferry M, Keating D, Freilich S, Kearns A, Harney É, Lawson AM, Mandl K, Michel M, Oberreiter V, Oppenheimer J, Sawyer S, Schattke C, Ozdogan KT, Hämmerle M, Qiu L, Workman N, Zalzala F, Mallick S, Mah M, Micco A, Pieler F, Pavuk J, Lazar C, Paluch T, Škrivanko MK, Šlaus M, Bedić Ž, Novotny F, Szabó LD, Cserpák-Laczi O, Hága T, Hajdú Z, Mirea P, Nagy EG, Virág ZM, Horváth AM, Horváth LA, Biró KT, Domboróczki L, Szeniczey T, Jakucs J, Szelekovszky M, Zoltán F, Sztáncsuj S, Tóth K, Csengeri P, Pap I, Patay R, Putica A, Vasov B, Havasi B, Sebők K, Raczky P, Lovász G, Tvrdý Z, Rohland M, Novak M, Ruttkay M, Boric D, Dani J, Kulhwilm M, Palmara PF, Hajdu T, Pinhasi R*, Reich D*. Social and genetic diversity among the first farmers of Central Europe. bioRixv. DOI: 10.1101/2023.07.07.548126

2023 **Huang X**†*, Struck TJ†, Davey SW, Gutenkunst RN*. dadi-cli: Automated and distributed population genetic model inference from allele frequency spectra. bioRixv. DOI: 10.1101/2023.06.15.545182

Additional research achievements

Journal reviewer

Archives of Virology (1), *Gene* (1), *Genetica* (1), *Genetics* (1), *Genome Biology and Evolution* (1), *Genomics* (1), *Molecular Biology and Evolution* (2), *Molecular Ecology Resources* (1), *Proceedings of the Royal Society B: Biological Sciences* (1), *The Journal of Open Source Software* (3).

Software

2021 – present **sstar:** https://github.com/xin-huang/sstar

A Python package for detecting archaic introgression from population genetic data with S.*

2020 – present **dadi-cli:** https://github.com/xin-huang/dadi-cli

Automated and distributed model-based inference from population genomic data.

2021 – 2023 **PopSim Consortium:** https://github.com/popsim-consortium

A community-driven effort to standardize population genetics.

2015 – 2018 **SeleDiff:** https://github.com/xin-huang/SeleDiff

A fast and scalable tool for estimating and testing selection differences between populations.

Honors and awards

Jul 2017 **Student Poster Prize.**

Evolution of Complex Traits Symposium, Annual Meeting of the Society for Molecular Biology and Evolution 2017, Company of Biologists.

Sep 2011 – Jun 2018 **Graduate Student Fellowship.**

Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences.

Jun 2010 **Best Prize of Experiment Operation and Second Prize of Experiment Design.**

The Sixth Biochemistry Experiment Skills Competition, Department of Education of Guangdong Province and Department of Science and Technology of Guangdong Province.

Project: Detecting genetically modified papayas sold in supermarkets.

Fundings

Jan 2024 **Funding for Research with Azure Services: 2,000 EUR.**

Vienna University Computer Center, University of Vienna.

Project: selscape: Automated and distributed pipelines for investigating the landscape of natural selection from large-scale genomic datasets.

May 2022 **HEAS Seed Grant: 2,840 EUR.**

Human Evolution & Archaeological Sciences, University of Vienna.

Project: dbHAP: A database for understanding and visualizing genomic diversity with human ancestral populations.

Jun 2021 **Talente: Karriere-Grants 2021: 2,000 EUR.**

Austrian Research Promotion Agency (FFG).

Grant number: 890029.

Conference talks

2021 Inferring genome-wide correlations of fitness effects between populations. *Joint Annual Meeting of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists 2021*. Virtual.

2020 Genome-wide correlation in fitness effects between populations. *AZ PopGroup 2020*. Virtual.

2018 Dissecting historical changes of selective pressures in the evolution of human pigmentation. *The Sixth Youth Forum for Mathematics, Computer Sciences and Life Sciences*. Beijing, China.

Conference posters

2024 PGML notes: Interactive Jupyter notebooks for an introduction to population genetics with machine learning. *Probabilistic Modeling in Genomics 2024*. Vienna, Austria.

2023 A comprehensive benchmarking for ghost introgression tract analysis with supervised learning. *Annual Meeting of the Society for Molecular Biology and Evolution 2023*. Ferrara, Italy.

2022 dadi-cli: Automated and distributed computational inference of demographic history and distributions of fitness effects from population genetic data. *Probabilistic Modeling in Genomics 2022*. Oxford, United Kingdom.

2022 sstar: A Python package for detecting archaic introgression from population genetic data with *S**. *Probabilistic Modeling in Genomics 2022*. Oxford, United Kingdom.

2021 Inferring genome-wide correlations of fitness effects between populations. *Probabilistic Modeling in Genomics 2021*. Virtual.

2018 Quantification of selective pressures on human pigmentation between populations and over epochs. *Annual Meeting of the American Society of Human Genetics 2018*. San Diego, United States.

2018 SeleDiff: A fast and scalable tool for testing and estimating selection differences between populations. *Annual Meeting of the Society for Molecular Biology and Evolution 2018*. Yokohama, Japan.

2017 Dissecting historical changes of selective pressures: Learning the evolution of human pigmentation. *Annual Meeting of the Society for Molecular Biology and Evolution 2017*. Austin, United States.

Teaching experience

2024 An introduction to population genetics with machine learning.
Lecturer. University of Vienna, Vienna, Austria.
Materials: https://github.com/xin-huang/pgml

2023 Paleogenomics: From sampling and data collection to multidisciplinary analyses.
Trainer. CA19141 iNEAL Training School, Vienna, Austria.

2022 Introduction to Neanderthal palaeogenomic analyses for non-geneticists.
Trainer. CA19141 iNEAL Training School, Vienna, Austria.
Materials: https://github.com/admixVIE/iNEAL

2022 Computational methods in evolutionary genomics.
Lecturer. University of Vienna, Vienna, Austria.

Materials: https://github.com/admixVIE/appladmix

Thesis supervision

Mar 2023 – present	Josef Hackl. Level: Master. Project: Detecting ghost introgressed fragments with supervised learning. Co-mentor: Dr. Martin Kuhlwilm.