

## Curriculum Vitae

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GitHub: <https://github.com/xin-huang>

Hugging Face: <https://huggingface.co/xin-huang>

### Education

- Sep 2011–Jun 2018    **PhD** 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    **BSc** in Biochemistry and Molecular Biology (With Distinction).  
College of Life Sciences, 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 primary research interest lies in developing and applying advanced computational methods, such as machine learning and deep learning, to enable rigorous population genetic inference. I aim to uncover how evolutionary forces—mutation, genetic drift, gene flow, and natural selection—shape genetic diversity across species, with broad implications for understanding gene adaptation, biodiversity conservation, and evolutionary history. In addition, I am committed to integrating heterogeneous computational approaches into cohesive, reproducible pipelines, enabling efficient analysis of large-scale genomic datasets. Ultimately, my research seeks to bridge algorithmic innovation and biological discovery, advancing both the theoretical foundations and practical applications of evolutionary genomics.

## Academic Publications

\* Corresponding author

† Co-first author

### Peer-reviewed Publications

- 2025 **Huang X\***, Chen S, Hackl J, Kuhlwilm M. SAI: A Python package for statistics for adaptive introgression. Accepted by *Molecular Biology and Evolution*.
- 2025 Han S, Riyahi S, **Huang X**, Kuhlwilm M\*. A curated dataset of great ape genome diversity. Accepted by *Scientific Data*.
- 2025 Gower G†, Pope NS†, Rodrigues MF†, Tittes S†, Tran LN†, Alam O, Cavassim MIA, Fields PD, Haller BC, **Huang X**, Jeffrey B, Korfmann K, Kyriazis CC, Min J, Rebollo I, Rehmann C, Small ST, Smith CC, Tsambos G, Wong Y, Zhang Y, Huber CD, Gorjanc G, Ragsdale AP, Gronau I, Gutenkunst RN, Kelleher J, Lohmueller KE, Schrider DR, Ralph PL, Kern AD\*. Accessible, realistic genome simulation with selection using stdpopsim. *Molecular Biology and Evolution* **42**: msaf236. PMID: 40166307. DOI: [10.1093/molbev/msaf236](https://doi.org/10.1093/molbev/msaf236).
- 2025 **Huang X\***, Hackl J, Kuhlwilm M\*. Decoding genomic landscapes of introgression. *Trends in Genetics*. PMID: 40707291. DOI: [10.1016/j.tig.2025.07.001](https://doi.org/10.1016/j.tig.2025.07.001).
- 2025 Gelabert P\*, Bickle P, Hofmann D, Teschler-Nicola M, Anders A, **Huang X**, Hämmerle M, Olalde I, Fournier R, Ringbauer H, Akbari A, Cheronet O, Lazaridis I, Broomandkhoshbacht N, Fernandes DM, Buttinger K, Callan K, Candilio F, Morante BG, Curtis E, Ferry M, Keating D, Freilich S, Kearns A, Harney É, Lawson AM, Mandl K, Michel M, Oberreiter V, Zagorc B, Oppenheimer J, Sawyer S, Schattke C, Özdoğan KT, Qiu L, Workman JN, Zalzala F, Mallick S, Mah M, Micco A, Pieler F, Pavuk J, Šefčáková A, Lazar C, Starović A, Djuric M, Škrivanko MK, Šlaus M, Bedić Ž, Novotny F, Szabó LD, Cserpák-Laczi O, Hága T, Szolnoki L, Hajdú Z, Mirea P, Nagy EG, Virág ZM, Horváth AM, Horváth LA, Biró KT, Domboróczki L, Szeniczey T, Jakucs J, Szelekowszky M, Zoltán F, Sztáncsuj SJ, Tóth K, Csengeri P, Pap I, Patay R, Putica A, Vasov B, Havasi B, Sebők K, Raczkay P, Lovász G, Tvrđy Z, Rohland N, Novak M, Ruttkay M, Krošlaková M, Bátor J, Paluch T, Boric D, Dani J, Kuhlwilm M, Palamara PF, Hajdu T, Pinhasi R\*, Reich D\*. Social and genetic diversity in the first farmers of Central Europe. *Nature Human Behavior* **9**: 53–64. PMID: 39613963. DOI: [10.1038/s41562-024-02034-z](https://doi.org/10.1038/s41562-024-02034-z).
- 2025 Hackl J, **Huang X\***. Revisiting adaptive introgression at the HLA genes in Lithuanian genomes with machine learning. *Infection, Genetics and Evolution* **127**: 105708. PMID: 39732272. DOI: [10.1016/j.meegid.2024.105708](https://doi.org/10.1016/j.meegid.2024.105708).
- 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](https://doi.org/10.1038/s41576-023-00636-3).

- Inspired the cover image featured on [Nature Reviews Genetics, Volume 25, Issue 1](#).
  - Highlighted in a collection on [Machine Learning in Genomics](#) by *Nature Reviews Genetics*.
- 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](https://doi.org/10.1038/s41559-023-02145-2).
- 2023 Lauterbur ME\*, Cavassim MIA, Gladstein AL, Gower G, Pope NS, Tsambos G, Adrión 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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. *Journal of Open Source Software* **4**: 1545. DOI: [10.21105/joss.01545](https://doi.org/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](https://doi.org/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: [10.1038/srep17123](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](https://doi.org/10.1093/molbev/msu244).

### Preprints

- 2025 **Huang X\***, Chen S, Han S, Kuhlwilm M\*. Genomic landscapes of natural selection in great apes. bioRxiv. DOI: [10.1101/2025.08.29.673040](https://doi.org/10.1101/2025.08.29.673040).
- 2024 **Huang X\***. Developing machine learning applications for population genetic inference: Ensuring precise terminology and robust implementation. EcoEvoRixv. DOI: [10.32942/X2N90M](https://doi.org/10.32942/X2N90M).
- 2023 **Huang X†\***, Struck TJ†, Davey SW, Gutenkunst RN\*. dadi-cli: Automated and distributed population genetic model inference from allele frequency spectra. bioRxiv. DOI: [10.1101/2023.06.15.545182](https://doi.org/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), *Journal of Open Source Software* (5), *Molecular Biology and Evolution* (2), *Molecular Ecology Resources* (1), *Nature Communications* (1), *Nucleic Acid Research* (1), *PeerJ* (1), *Proceedings of the Royal Society B: Biological Sciences* (1), *STAR Protocols* (1).

#### Software

- 2025–present **selscape**: <https://github.com/xin-huang/selscape>.  
*Snakemake Workflow for Investigating Genomic Landscapes of Natural Selection.*
- 2024–present **SAI**: <https://github.com/xin-huang/sai>.  
*Python Package for Statistics for Adaptive Introgression.*
- 2024–present **introscape**: <https://github.com/xin-huang/introscape>.  
*Snakemake Workflow for Investigating Genomic Landscapes of Introgression.*
- 2022–present **GAISHI**: <https://github.com/xin-huang/gaishi>.  
*Python Package for Genomic Analysis of Introgressed-Site and -Haplotype Identification.*
- 2021–present **sstar**: <https://github.com/xin-huang/sstar>.  
*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>.  
*Community-driven Effort to Standardize Population Genetics.*

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

### **Research Grants as Principal Investigator**

- Jul 2024–Jun 2025      **Postdoctoral Researcher Seed Grant: 4,000.00 EUR.**  
Funder: *Faculty of Life Sciences, University of Vienna*.  
Project: Detecting Introgressed Alleles in Genomes with Supervised Deep Learning.
- Apr 2024–Mar 2025      **EuroHPC Development Access Call: 4,500 Node Computing Hours.**  
Funder: *European High Performance Computing Joint Undertaking*.  
Project: Detecting Ghost Introgressed Fragments with Supervised Learning.  
Co-PI: Prof. Martin Kuhlwilm.  
Grant number: EHPC-DEV-2024D04-011.
- Jan 2024–Jul 2024      **Funding for Research with Azure Services: 2,000.00 EUR.**  
Funder: *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–Jun 2023      **HEAS Seed Grant: 2,840.00 EUR.**  
Funder: *Human Evolution & Archaeological Sciences, University of Vienna*.  
Project: dbHAP: A Database for Understanding and Visualizing Genomic Diversity with Human Ancestral Populations.
- Jun 2021–Sep 2021      **Talente: Karriere-Grants 2021: 2,000.00 EUR.**  
Funder: *Austrian Research Promotion Agency (FFG)*.  
Grant number: 890029.

### **Invited Talks**

- 2025 Deep learning for population genetic inference. *Seminar at the Division of Epidemiology, Department of Medicine, Vanderbilt University Medical Center.* Virtual.

### **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**

- 2025 Machine Learning in Population Genetics.  
Lecturer. University of Vienna, Vienna, Austria.

URL: <https://ufind.univie.ac.at/en/course.html?lv=300005&semester=2025S>.

Materials: <https://github.com/xin-huang/pgml>.

2024 Machine Learning in Genetics.

Lecturer. University of Vienna, Vienna, Austria.

URL: <https://ufind.univie.ac.at/en/course.html?lv=300052&semester=2024S>.

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 Paleogenomic 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.

URL: <https://ufind.univie.ac.at/en/course.html?lv=300177&semester=2022S>.

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

## Research Supervision

### Master's Theses

Jul 2025–present Alexander Stöckl.  
Project: A Reinforcement Learning Framework for Phylogenetic Reconstruction Analysis.

Co-mentor with Prof. Martin Kuhlwilm.

Mar 2023–Oct 2024 Josef Hackl.  
Project: Performance Benchmarking of Methods for Detecting Genetic Introgression from Unsampled Lineages.

- First-author publication in *Infection, Genetics and Evolution*.

Co-mentor with Prof. Martin Kuhlwilm.

### Undergraduate Projects

Dec 2024–Jan 2025 Simon Chen.  
Project: The Genomic Landscape of Natural Selection in Great Apes.

- Co-authored manuscript currently under review

Co-mentor with Prof. Martin Kuhlwilm.

### Non-thesis Projects

Sep 2025–present Andrea Koca.

Project: A Python-Native Tool for Detecting Archaic Introgression from Population Genetic Data with  $S^*$ .

Feb 2025–present      Simon Chen.

Project: A Snakemake Workflow for Investigating Genomic Landscapes of Natural Selection.

- First-author manuscript currently in preparation.

### ***Academic Competitions***

Sep 2025–Nov 2025      Xmon team (Simon Chen, Xin Huang).

*Genomic History Inference Strategies Tournament (GHIST) 2025.*