

Faculty Search Committee Chenlu Di, Ph.D.

Department of XXX Ecology and Evolutionary Biology

University of XXX 4207 Life Science Building

Los Angeles, California 90024

Mobile: (520)-223-0807

Email: chenludi6@gmail.com

Website: https://chenludi.github.io/

XXX, 2025

Dear Search Committee Members,

It is with great pleasure that I apply for the position of Assistant Professor position in the Department of XXX at the University of XXX. I am currently a postdoctoral researcher at the University of California, Los Angeles, under the guidance of Dr. Kirk Lohmueller. Previously, I earned my PhD in the Department of Ecology and Evolutionary Biology at the University of Arizona, where I was advised by Dr. David Enard.

My research investigates how natural selection shapes human health and disease. I combine evolutionary theory, model-based, statistical and machine-learning computational methods, and genomic, protein structure, transcription and epigenomic data to answer two questions: 1) how natural selection affects human infectious diseases, particularly on how humans adapt to viruses 2) how natural selection affects human chronic diseases. Particularly on natural selection on various non-coding genomic regions and its impact on chronic diseases.

In my previous work, I demonstrated that protein stability is a key mechanism of viral adaptation in human proteins ([preprint](http://doi.org/10.1101/2022.12.01.518739) at *bioRxiv*, under review at *Molecular Biology and Evolution*). I estimated the distribution of fitness effects of putatively functional noncoding mutations in human genomes, revealing that top conserved genomic regions only include a small proportion of deleterious mutations ([preprint](http://doi.org/10.1101/2025.05.14.654124) at *bioRxiv*). I also discovered that Mendelian disease genes show slower recent adaptation, highlighting how a lag in evolutionary response to environmental change may underlie human genetic disease (published in [*eLife*](https://elifesciences.org/articles/69026), old model).

My previous work has uncovered important adaptive mechanism to viruses in proteins, but the genetic mechanism of adaptation remains an open question. The adaptation against viruses may be dominated by large-effect mutations or polygenic adaptation. Moreover, the role of noncoding elements in adaptation to viruses is also unclear. My future research aims explore these questions by investigating when and how did humans adapt to viruses and by inferring selection of putative regulatory elements in response to viruses. These results would shed light on the evolution of human immunity and health.

Building on my method for estimating the distribution of fitness effects of human noncoding mutations, I will investigate how selection on putatively functional noncoding elements differs across human populations. I will also investigate which human traits, particularly chronic diseases such as schizophrenia, are connect to transitions in natural selection in primates or more recent time. In addition, I will develop a publicly accessible database of evolutionary statistics that integrates modern inference methods. Together, these projects will reveal how population history and lineage-specific selection shape vulnerability to chronic diseases, while providing resources that connect evolutionary genomics with biomedical research.

I am enthusiastic about contributing to the Department of Molecular Genetics and Genome Sciences. My expertise in population genetics, coupled with my research on host adaptation to viruses and the evolutionary mechanisms underlying complex diseases, aligns closely with the Department’s focus on **computational genomics** and **translational bioinformatics** for **complex diseases**. By framing human health challenges through the lens of evolutionary medicine, I offer a distinctive perspective that connects **biomedical data science**, **genotype–phenotype mapping**, and **evolutionary** principles. This broad scope enables me to uncover fundamental mechanisms of human evolution while translating them into insights relevant to chronic disease vulnerability, providing a unique complement to the Department’s mission of integrating genomics with human health. Moreover, the Department’s setting within a medical school offers rich opportunities for collaborative studies, particularly on the immune system, where my expertise in host–virus interactions can connect directly with clinical and biomedical research.

As a STEM educator, I create interactive and inclusive classrooms that foster inquiry and critical thinking. With over four years of experience teaching evolution and genetics, I have developed a student-centered approach that adapts to diverse learning needs. At XXX, I would be excited to teach Population Genetics, Genetics, Evolutionary Medicine, and Evolution as well as develop an upper-division course on **machine learning in biology** with hands-on computational labs. These offerings would strengthen the new graduate program in genetics and genome sciences and align with the Department’s emphasis on computational genomics and biomedical data science.

I am equally dedicated to mentoring, having guided both graduate and undergraduate students through projects now resulting in manuscripts. I tailor mentorship to individual strengths while fostering collaboration within and beyond the lab, and I welcome opportunities for co-mentoring. I am eager to contribute to XXX’s mission by training the next generation of scientists who can bridge genomics, computation, and medicine.

I am actively engaged in scientific communities, having organized and chaired over 40 symposia and webinars, many during the lockdown to foster connection and support. I have also led population genetics study groups with graduate students and would be eager to establish a journal club on evolutionary medicine within the department. In addition, I mentor undergraduate students and help them gain exposure through international conferences.

Given the unique focus and path of my research and shared interests with faculties in the department, I am excited about the opportunity to continue my research and service at XXX. Thank you for considering my application.

Sincerely,

Chenlu Di

University of California, Los Angeles