

## *Curriculum vitae*

### **Duo Xu, Ph.D.**

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### **CURRENT POSITION**

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**Research associate**, Dec 2020 - now

Institute of Computational Biomedicine, Weill Cornell Medical College, New York, NY

### **EDUCATION and PAST POSITIONS**

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**Post-doctoral associate**, June 2018 - Nov 2020

Institute of Computational Biomedicine, Weill Cornell Medical College, New York, NY

**Ph.D. in Biology** (Major in Biological Sciences, general), May 2015 - June 2018

the State University of New York, University at Buffalo, Buffalo, NY

**M.S. in Biology** (Major in Biological Sciences, general), Aug 2013 – May 2015

the State University of New York, University at Buffalo, Buffalo, NY

**B.S. in Biology** (Major in Biological Sciences, general), Sep 2009 – Jun 2013

Fudan University, Shanghai, China

### **PUBLICATIONS**

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**Xu D**, Pavlidis P, Flanagan C, Blekhman R, Ruhl S, Gokcumen O. Archaic hominin introgression in Africa contributes to functional salivary MUC7 genetic variation. *Molecular Biology and Evolution*. 2017 Oct 1;34(10):2704-2715. **[First author]**

-- Featured in *Sciencemag.org*, *Futurity*, *theGuardian*, among others. Altmetric Score: 525 (99<sup>th</sup> percentile).

**Xu D**, Pavlidis P, Thamadilok S, Redwood E, Fox S, Blekhman R, Ruhl S, Gokcumen O. Recent evolution of the salivary mucin MUC7. *Scientific Reports*. 2016 Aug 25;6:31791. **[First author]**

-- Featured in *Futurity*, *Popular Science*, *Technology.org*, among others. Altmetric Score: 139 (98<sup>th</sup> percentile).

**Xu D**, Jaber Y, Pavlidis P, Gokcumen O. **VCFtoTree**: A user-friendly tool to construct locus-specific alignments and phylogenies from thousands of anthropologically relevant genome sequences. *BMC Bioinformatics*. 2017 Sep 26;18(1):426. **[First author]**

**Xu D**, Gokcumen O, Khurana E. Loss-of-function tolerance of enhancers in the human genome. *PLoS Genetics*. 2020 Apr 3;16(4):e1008663. **[First author]**

Eaaswarkhanth M\*, **Xu D\***, Flanagan C, Rzhetskaya M, Hayes G, Blekhman R, Jablonski N, Gokcumen O. Atopic Dermatitis Susceptibility Variants In Filaggrin Hitchhike Hornerin Selective Sweep. *Genome Biology and Evolution*. 2016 Nov 11;8(10):3240-3255. **[\*Co-first author]**

Pajic P, Lin YL, **Xu D**, Gokcumen O. The psoriasis-associated deletion of late cornified envelope genes LCE3B and LCE3C has been maintained under balancing selection since Human Denisovan divergence. *BMC Evol Biol*. 2016 Dec 5;16(1):265. **[Co-author]**

Resendez SD, Bradley JR, **Xu D**, Gokcumen O. (2018) Structural Variants in Ancient Genomes. *Paleogenomics*. Springer, Cham **[Co-author, part of the *Population Genomics* book series]**

Saitou M, Gaylord EA, **Xu D**, May AJ, Neznanova L, Nathan S, Grawe A, Chang J, Ryan W, Ruhl S, Knox SM, Gokcumen O. Functional Specialization of Human Salivary Glands and Origins of Proteins Intrinsic to Human Saliva. *Cell Rep*. 2020 Nov 17;33(7):108402. **[Co-author]**

Earlier (undergraduate work at Fudan University)

Zeng L, Yin Y, You C, Pan Q, **Xu D**, Jin T, Zhang B, Ma H. Evolution and protein interactions of AP2 proteins in Brassicaceae: Evidence linking development and environmental responses. *J Integr Plant Biol*. 2016 Jun;58(6):549-63. **[Co-author]**

## SKILLS & RESEARCH EXPERIENCE

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### Proficient in Python, Unix, R programming

- Developed Python/Unix based bioinformatic pipelines from scratch to construct haplotype structure for thousands of individuals from 1000 Genomes.
- Compiled it into a macOS app, **VCFtoTree**, with a user-friendly interface that can be used by audiences without knowledge of programming. (Xu et al. 2017)
- Simulated the evolution of copy number variation in both Python and R to reveal the recurrent evolution of *MUC7* tandem repeats. (Xu et al. 2016)
- Analyzed RNA sequencing data for gene differential expression in human salivary glands.
- Built machine learning models to predict the function of enhancers in human genomes. (Xu et al. 2020)

- Built machine learning models to predict the interaction between transcription factors and target genes and build patient-specific regulatory networks.

### **Proficient in bioinformatics tools and handling big genomics datasets**

- Proficient in Next Generation Sequencing tools: Bowtie, TopHat, SAMTools, BCFtools, bedtools, VCFtools, Plink, GATK, BWA, Kallisto, DESeq, etc.
- Familiar with population genetics simulation tool MSMS.
- Worked with a combination of PacBio and Illumina data to study the structural variants in *C. albicans*.

## **CONFERENCE**

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**Duo Xu**, Ekta Khurana. (2019) Loss-of-function tolerance of enhancers in the human genome.  
*- Network Biology at CSHL, 2019, poster*

**Duo Xu**, Pavlos Pavlidis, Recep Ozgur Taskent, Nikos Alachiotis, Colin Flanagan, Ran Blekhman, Stefan Ruhl, Omer Gokcumen. (2017) Archaic hominin introgression in Africa contributes to functional salivary *MUC7* genetic variation.  
*- The 86th Annual Meeting of the American Association of Physical Anthropologists (2017) Podium presentation.*

**Duo Xu**, Pavlos Pavlidis, Colin Flanagan, Supaporn Thamadilok, Emilie Redwood, Sara Fox, Ran Blekhman, Stefan Ruhl, Omer Gokcumen. (2016) Evolution of *MUC7*: Insights into human salivary adaptation.  
*- The 85th Annual Meeting of the American Association of Physical Anthropologists (2016) Poster.*

**Duo Xu**, Pavlos Pavlidis, Colin Flanagan, Supaporn Thamadilok, Emilie Redwood, Sara Fox, Ran Blekhman, Stefan Ruhl, Omer Gokcumen. The recent evolution of the salivary mucin *MUC7* in primates.  
*- Northeastern Evolutionary Primatologists 2nd Conference (2016) Poster*

## **FUNDS AND AWARDS**

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### Graduate

2017 Dissertation Fellowship from College of Arts and Sciences, University at Buffalo  
 2016 GSA Conference Travel Fund for the 2016 AAPA meeting at Atlanta

### Undergraduate

2013 Second-class People's Scholarship (Top 15%)  
 2012 Silver Medal and the Special Prize "Safety Commendation" in Asian Regional Jamboree of iGEM  
 2012 School's Professional Scholarship  
 2010 School's Professional Scholarship  
 2010 Third-class People's Scholarship (Top 30%)