

Curriculum Vitae  
Yun-Xin Fu  
October 18, 2024

Address

Yun-Xin Fu, Ph.D.  
Director, Computational Genomics Section  
Human Genetics Center and Division of Biostatistics  
School of Public Health  
The University of Texas at Houston  
1200 Herman Pressler Drive, Room E541  
Houston, Texas 77030

Phone: 713-500-9813  
Fax: 713-500-0900  
E-mail: Yunxin.Fu@uth.tmc.edu

Education

INSTITUTION AND LOCATION	DEGREE	YEAR CONFERRED	FIELD OF STUDY
Zhongshan University, China	BS.C.	1978-82	Mathematics and statistics
University of Reading, England	Ph.D.	1984-88	Statistics
Nat. Inst. for Med. Res. London	Postdoc.	1988-89	Sequence alignment
University of Georgia, Athens	Postdoc.	1989-90	Population genetics
University of Texas, Houston	Postdoc.	1990	Molecular evolution

PhD thesis

Change point theory and its application to the prediction of protein secondary structure,  
Department of Applied Statistics, University of Reading, England

PhD supervisor

Robert N. Curnow, Ph.D.

Postdoctoral supervisors

Tom Kirkwood, Ph.D. (London)  
Jonathan Arnold, Ph.D. (Georgia)  
Wen-Hsiung Li, Ph.D. (Houston)

## Professional Appointments

Guest Professor, Yunnan University, China, Sept. 2003 - Aug. 2010

Guest Professor, University of Sun Yet-sen, China, Sept. 2003 - Aug. 2012

Betty Wheless Trotter professorship, School of Public Health (SPH) The University of Texas at Houston, Jan. 2002 - 2016

Director, Computational Genomics Section, Human Genetics Center, SPH, The University of Texas at Houston, Oct. 2001 - present

Full Professor with tenure, Human Genetics Center, SPH, The University of Texas at Houston, Sept. 2001 - present

Associate Professor with tenure, Human Genetics Center, SPH, The University of Texas at Houston, Sept. 1996 - Aug. 2001

Assistant Professor (tenure-track), Human Genetics Center, SPH, The University of Texas at Houston, Oct. 1994 - Aug. 1996

Assistant Professor (tenure-track), Center for Demographic and Population Genetics, Graduate School of Biomedical Sciences (GSBS), The University of Texas at Houston, Oct. 1991 - Aug. 1994

Research Assistant Professor, Center for Demographic and Population Genetics, GSBS, The University of Texas at Houston, Jan. 1991 - Sept. 1991

Faculty Associate, Center for Demographic and Population Genetics, GSBS, The University of Texas at Houston, Sept. 1990 - Dec. 1990

Assistant Lecturer, Department of Basic Sciences, South China College of Tropical Crops, China. Mar. 1982 - Aug. 1984

## Research Area and Interests

Human population history and human genome diversity

Population and quantitative genetics, conservation biology

Coalescent theory and its applications

Statistics/Mathematics

Evolution of infectious disease

Phylogenetic reconstruction and molecular evolution

Computational biology, comparative genomics and functional genomics

## Honors

Overseas Research Student Award (by British Council of Education) 1985-1988

Outstanding Research Student Award (Reading University, England) 1986-1988

Short-term visiting Professorship, Japan Society for Promotion of Science (JSPS) (1998)

Visiting Professorship, Japan Institute of Genetics (2018-2022)

## Memberships and Service

The Society for the Study of Evolution

The Society for Molecular Biology and Evolution

Webmaster for the Society of Molecular Biology (1995-1999) and Evolution, and for the journal Molecular

## Biology and Evolution

Associate Editor for Molecular Biology and Evolution, Oct. 1998-Oct. 2001

Associate Editor for Genetics, Dec. 1998-2010

Member of the NIH Study Section (ad hoc member), Oct. 1998, Oct. 2004, Feb. 2006, Mar. 2005

Panel member of the NIEHS site visit to University of Southern California, Dec. 2001

Member of the NIH Genetics Study Section (ad hoc member), Feb. 1998

Member of the NIH Genetics Study Section, Oct. 1999-2004

Member of the Membership committee of the Society of Chinese Bioscientists in America, 1999-present

Member of the NIH Genetic Variation and Evolution Study Section committee (ad hoc member), 2004-2010

Member of the NIH Genetic Variation and Evolution Study Section committee, 2011-present

Member of the advisory committee, Schull Institute, 2017-present

## Teaching Experience

2000 - present: Lecturer of GSBS and SPH course "Introduction to Genomics and Bioinformatics" (two credit hours)

2001 - 2013: Lecturer of GSBS and SPH course "Evolution of Protein and DNA sequences" (two credit hours)

2014 - present: Course Coordinator and Lecturer of GSBS and SPH course "Evolution of DNA and Protein Sequences" (three credit hours)

1991 - present: Course Coordinator and Lecturer (sole lecturer in most years) of GSBS and SPH course "Population Genetics" (three credit hours)

2002 - 2020: Course Coordinator and Lecturer of GSBS and SPH course "Introduction to Statistical Genetics" (three credit hours)

2006 Fall: Lecturer for SPH course "Monte Carlo Approach in Statistics and Genetics" (two credit hours)

2009 Fall, 2010 Fall: Lecturer for GSBS course "Ethical Dimensions of Biomedical Sciences" (one credit hours)

2010 Summer : Lecturer of SPH course PH1610 "Biostatistics I" (four credit hours)

2010 Fall - present : Course Director for SPH course PH1690 "Foundations of Biostatistics" (four credit hours)

2010 Fall - present : Course Coordinator for SPH course PH1690 "Foundations of Biostatistics" (four credit hours)

2016 Fall - 2018 Spring: Course Coordinator for SPH course PH1988 "Biostatistics Seminar" (one credit hours)

2018 Spring - present: Course Coordinator for SPH course PH1970 "Intermediate Biostatistics" (three credit hours)

2021 Fall - present: Course Coordinator for SPH/GSBS course PH1982 "Introduction to Statistical Genetics and Bioinformatics" (three credit hours)

2022 Fall - present: Course Coordinator for SPH/GSBS course PH1986 "Evolution of DNA and Protein

sequences” (three credit hours)

Note: GSBS – Graduate School of Biomedical Sciences, SPH – School of Public Health

#### Postdoctoral Fellows trained

Hongwen Deng, 1995-1996, supported by grant R29 GM50428

Daniel C. Vasco, 1997-1998, supported by grant R29GM50428

Haiying Huai, 1998-2004, supported by grant R29 GM50428

David de Lorenzo, 1998-2001, supported by grant DEB-9707567

Yuande Tan, 2000-2001, supported by grant HL51021

Haipeng Li, 2000-2004, supported by grant GM50428

Zanhua Xie, 2006-2011, supported by state funds

#### Visiting Scholars

Dr. Long-Zhen Tong, 1994-1995

Dr. Lindan Ji, 2015-2016

Nan Yaoi, 2017-2017

## Graduated Students

- Li Jin, Ph.D. student, graduated in 1994. Served on Supervisory Committee. Currently Professor in Fudan University, China.
- Benny Chang, Ph.D. student, graduated in 1995. Served on both Examining and Supervisory Committees. Currently Assistant Professor, Baylor College of Medicine.
- Xun Gu, Ph.D. student, graduated in 1996. Served on Advisory, Examining and Supervisory Committees. Currently Associate Professor, University of Iowa.
- Julia Krushkal, Ph.D. student, graduated in 1996. Served on Advisory, Examining and Supervisory Committees. Currently Computational Biologist, Biometric Research Branch, National Institutes of Health, Bethesda, MD.
- George Li, Ph.D. student, graduated in 1996. Served on Supervisory Committee. Currently a Senior Statistician in a biotechnology company, California.
- Grier Page, MSc. student, graduated in 1997. Served on Examining Committee. Currently Senior Statistical Geneticist, RTI international, Atlanta, GA.
- Andrew Rodin, Ph.D. student, graduated in 1999. Served as on-site Supervisory Professor. Dissertation: New Algorithms for Automated Phylogenetic Reconstruction Using Artificial Intelligence and Data Mining Techniques. Currently Dr. Susumo Ohno Chair in Theoretical Biology; Associate Professor, Diabetes and Metabolic Diseases Research, City of Hope, Duarte, CA.
- Zhongming Zhao, Ph.D. student, graduated in 2000. Served as on-site Supervisory Professor. Dissertation: Global patterns of DNA Polymorphism in Noncoding Regions in Human Populations. Currently Assistant Professor, Dept. Psychiatry, Center for the Study of Biological Complexity, Virginia Commonwealth University, Richmond, VA.
- Qiqing Huang, Ph.D. student graduated in 2002. Served as Supervisor. Dissertation: Single Nucleotide Polymorphism (SNP) Selection for Genotype-Phenotype Association Studies. Currently a Research Scientist in Johnson's and Johnson's, VA.
- Hongyan Xu, Ph.D. student, graduated in 2003. Served as supervisor. Dissertation: Detecting the Signature of Natural Selection with Micro-satellites. Currently Assistant Professor, Dept. of Biostatistics, Medical College of Georgia, Augusta, GA
- Haipeng Li, Ph.D. student, graduated in 2002 and Postdoc. (2000-2003). Served as Supervisor. Principal Investigator, Institute of Computational Biology, Chinese Academy Science, Shanghai, China.
- Feng Zhan, Ph.D. student, graduated in 2004. Thesis Advisor. Dissertation: Statistical Methods for Estimating Mutation Rate and Effect Population Size from Samples of DNA Sequence. Currently a Research Statistician, US Oncology, Houston, Tx.
- Rafael Gonzalez, M.S. (2005) Visiting Ph.D. student from Mexico.
- Xiaoming Liu, Ph.D. student, graduated in 2006. Served as Supervisor. Dissertation: Analyzing Pathogen Populations-New Model, New Methods and Application. Currently Assistant Professor, Human Genetics Center, School of Public Health, The University of Texas, Houston, Tx.
- Hui Zhao, Ph.D. student, graduated in 2007. Served as Dissertation Advisor. Dissertation: A coalescent analysis for modeling the mutation process in colorectal cancer. Currently Senior Data Analyst Department of Breast Medical Oncology, The University of Texas M. D. Anderson Cancer Center, Houston, Tx.
- Degang Wang, Ph.D. (2003). M.S. student, graduated in 2008. Advisor. Thesis: Performance evaluation in Bayesian adaptive randomization. Currently at the Veterans Hospital, Houston, TX.
- Shut-ye Jessica Yeung, MPH student, graduated in 2010. Advisor. Thesis: Performance Recovery from

Exercise: A Review from a Statistical Point of View.

- Yaji Xu, Ph.D. student, graduated in 2010. Advisor. Dissertation: Genome-wide algorithm for detecting CNV associations with diseases. Currently Visiting Professor, Department of Statistics, The George Washington University, Washington, D.C.
- Yuande Tan, Ph.D. (1996) M.S. student, graduated 2010. Advisor and Research Supervisor. Thesis: Statistical methods for differential expressions of genes detected in multiple-condition experiment of microarray. Currently Research Associate, Institute for Personalized Medicine, Penn State College of Medicine, Hershey, PA
- Jiangong Niu, Ph.D. (2004) M.S. student, graduated in 2011. Advisor and Research Supervisor. Thesis: Comparison of two statistical methods for rare variant association analysis. Currently Senior Data Analyst, MD Anderson.
- Yefei Zhang, M.S. student, graduated 2012. Advisor and Research Supervisor. Thesis: Impact of donor-recipient gender and race mismatching on patient survival in patients with end-stage liver diseases undergoing liver transplantation. Currently Ph.D. student Advisor until 2013 when changed advisor. Currently Ph.D. student in Biostatistics.
- Hong Wei Tang, Ph.D. student, graduated 2012. Advisor. Dissertation: Interaction of genes and pathways with BMI, diabetes during development of pancreatic cancer. Currently Postdoc, Department Gastro-Intestinal Medical Oncology, UTMDACC.
- Xiao Su, M.S. student, graduated 2012. Advisor and Research Supervisor. Currently Ph.D. student in Biostatistics.
- Vinu Jyoti, MPH student, graduated 2012. Advisor and Research Supervisor. Changed Advisors.
- Nga T. Nguyen, Currently Ph.D. student. Advisor and Research Supervisor.
- Nianxiang Zhang, Ph.D. (1999) Currently Ph.D. student. Thesis Advisor.
- Shaojie Zhang, Ph.D. (2000) M.S. student graduated 2013. Advisor and Research Supervisor. Dissertation: Optimal DNA methylation biomarkers for differentiating normal and renal cancer samples. Currently Research Associate, Dept. of Molecular Virology and Microbiology, Baylor College of Medicine.
- Huzhang Mao, M.S. student, graduated 2013. Student Advisor and Research Supervisor. PhD Student, Advisor until 2014 when changed Advisor.
- Wei Guo, Ph.D. (2002) M.S. student, graduated 2013. Advisor and Research Supervisor. Dissertation: Optimal DNA methylation biomarkers for characterizing triple negative breast cancer. Currently Instructor, Dept. Systems Biology, UTMDACC.
- Duong Trung Tran, Ph.D. student, graduated 2013. Advisor. Dissertation: Partial mouth-periodontal examination protocol for estimation of prevalence, severity and extent of periodontitis. Currently Postdoctoral Research Fellow, Diagnostic Sciences, UT School of Dentistry, Houston, TX.
- Yue Song, M.S. student, graduated 2013. Student Advisor and Research Supervisor. Thesis: Modified 3+3 design for phase I clinical trials. Currently Ph.D. Student.
- Renke Zhou, M.S. (2007) Ph.D. student, graduated 2014. Advisor. Dissertation: A Semi-parametric joining model for semi-competing risks data with missing cause of informative terminal events. Currently Senior Biostatistician, Cancer Prevention and Population Sciences, Duncan Cancer Center, Baylor College of Medicine, Houston, TX.
- Jia Sun, MPH student, graduated in 2009. Advisor. Ph.D. Student, graduated 2015. Advisor and Research Supervisor. Dissertation: A hierarchical model of mutations with genotyping errors and maximum likelihood estimation of the male-to-female mutation rate ratio. Currently Statistical Analyst, UT MD Anderson, Houston, Tx.
- Qi Yu, M.S. student, graduated 2016. Student Advisor. Thesis: Spatial Statistical Analysis of Childhood Blood Lead Exposure in Texas. Currently Department of Public Health, City of Houston, Houston,

TX.

Shiyun Ling, M.S. student, graduated 2017. Advisor. Thesis: Removing Batch Effects in mRNA Data with Empirical Bayes Based Methods and Replicates. Currently Postdoctoral Fellow Department Bioinformatics and Computational biology, UT MDAnderson, Houston, TX.

Weiwei Shan, Ph.D. (2007) M.S. student, graduated 2018. Advisor. Thesis: Utilization of Propensity Score Weighting and Targeted Maximum Likelihood Estimation in the Post Hoc Analysis of a Randomized controlled Trial for the Treatment of Cocaine Dependence (NIDA-MDS-MODAFINIL-0001). Currently

Xiao Li, Ph.D. student, graduated 2018. Advisor until changed advisors Sept. 2016.

Andrew R. Aschenbrenner, Currently Ph.D. student. Advisor.

Katarzyna Latkowska, Currently Ph.D. student, University of Houston. Advisor.

Ross Harrison, Currently MPH student. Advisor.

## University or School Committees Served

Academic Computing Committee of the Health Science Center at Houston (1993-1996)  
Admission Committee of Genetics Program, GSBS (1992-1996)  
Admission Committee, Disease Control module, SPH (1999-2003)  
Admission Committee, Biological Sciences, SPH (2000-2005)  
Scientific Review Committee, UT Health Science Center (2001-2005)  
Faculty Council, Member, SPH (2006-2009)  
Search Committee for Hideki Innan, Member, SPH (2002-2003)  
Search Committee for Biostatistics Division Chair, Member SPH (2006-2006)  
Search Committee for Xioming Liu, Member, SPH (2006-2007)  
Search Committee for Biostatistics Division Faculty, Member SPH (2008-current),  
Academic Council, Member SPH (2008-2010)  
Research Council, Member SPH (2011-Present)  
Committee for the Development of PH1690, Chair SPH (2010-current)  
Mentor Committee, Member SPH for Dr. Momiao Xiong (2001-2009)  
Mentor Committee, Chairman SPH for Dr. Andrei Rodin (2003-2012)  
Mentor Committee, Chairman SPH for Dr. Xiaoming Liu (2007-2018)  
Mentor Committee, Member SPH for Dr. Taylor Maxwell (2007-2013)  
Mentor Committee, Member SPH for Dr. Wei Peng (2009-2016)  
Committee for Preliminary Examination, Chair BADS (2015-)  
Faculty Council, Member SPH (2019-) and Chair for 2020-2021  
Inter-Faculty Council, Member UTSHC (2021-)

## Completed Grants

NIH FIRST AWARD (R29 GM50428)  
Title: "Coalescent theory and analysis of DNA polymorphisms"  
Total Cost: \$499,000  
Period: Aug. 1994 - July 2000  
Position: Principle Investigator

NIH Supplement grant (R29 GM50428)  
Title: "Coalescent theory and analysis of DNA polymorphisms"  
Total Cost: \$24,000  
Period: Sept. 1998 - July 2000  
Position: Principle Investigator

NSF Grant (DEB-9707567)  
Title: "Estimating the age of the common ancestor of a population"  
Total Cost: \$120,000  
Period: Sept. 15, 1997 - Sept. 14, 2000 (no-cost extension to August 31, 2001)



Position: Principle Investigator

NIH grant (R01 HG01708)

Title: "Statistical methods for studying disease gene history"

Total Cost: \$377,074

Period: Sept. 30, 1997 - Sept. 29, 2000 (no cost extension to August 31, 2001)

Position: Principle Investigator

NIH grant (R01 GM55759 subcontract)

Title: "Human DNA polymorphism and evolution"

Total Cost: \$189,855

Period: Jan. 1, 1998 - Dec. 31, 2002

Position: Principle Investigator

NIH grant (HL51021)

Title: "Molecular epidemiology of essential hypertension"

Total Cost: \$5,297,411

Period: June 1999 - May 2004

Position: Co-investigator (5%) (PI: Eric Boerwinkle)

NIH grant (R25 CA57730 subcontract)

Title: "Supplement in genetic epidemiology education"

Total Cost: \$505,967

Period: Sept. 1999 - Aug. 2004

Position: Co-investigator (10%) (PI: Eric Boerwinkle)

NIH grant R01 GM50428-06A1

Title: "Coalescent theory and analysis of DNA polymorphism"

Period: Aug. 1, 2000 - July 31, 2005

Total Cost: \$737,479

Position: Principle Investigator

Chinese NSF grant

Title: "Award for outstanding Chinese scientist abroad"

Period: Jan. 1, 2001 - Dec. 31, 2003

Total Cost: 400,000 yen (about \$50,000)

Position: Principle Investigator (Dr. Yaping Zhang as host)

Chinese NSF grant 30570248

Title: "Mutation screening for *Drosophila Melanogaster*"

Period: Jan. 1, 2005 - Dec. 31, 2008

Total Cost: 400,000 yen (about \$60,000)

Position: Principle Investigator (Yunnan University as host)

NIH grant R01 GM5060777-04

Title: "Statistical methods for studying infectious disease"

Period: Sept. 1, 2001 - June 30, 2006

Total Cost: \$382,365

Position: Principle Investigator

NIH grant 4R37HL51021-11 “Molecular epidemiology of essential hypertension”

Total Cost: \$3,912,381 + indirect cost

Period: Aug. 15, 2004 - June 30, 2010

Position: : Co-investigator (5%) (PI: Eric Boerwinkle)

NIH grant R01 A1061385-01A2 “Molecular epidemiology of CA-MRSA”

Total Cost: \$39,800 + indirect cost

Period: Mar. 1, 2006 - Feb. 29, 2010

Position: PI Subcontract (PI: S. Skukla)

Framingham Heart Study Project No. 2005-3 “Patterns of mutation at microsatellite loci in the Framingham Heart Study Population” no cost

Period: May 11, 2006 - May 10, 2010

Position: Principle Investigator

NIH grant T32 GM074902-01A1 “Training program in Biostatistics at UTHSC-SPH ”

Total Cost: \$587,660 For student expenses only. No funds for faculty/administrative salaries or faculty/administrative expenses

Period: July 14, 2006 - June 30, 2012

Position: Investigator (PI Robert Hardy)

USDHHS, CDC 200-2001-00088 “Tuberculosis Epidemiology Studies Consortium (TBESC) assessing QFT as an initial screening tool for U.S.-bound applicants for immigration and feasibility of follow-up in U.S. immigrants”

Total Cost: \$17,665 + indirect cost

Period: Apr. 01, 2010 - Mar. 31, 2012

Position: PI Subcontract (PI Edward Graviss)

NIH R01 1U01HG005728 “Detecting natural selection for the 1000 Genomes Dataset ”

Total Cost: \$521,537 + indirect cost

Period: Apr. 01, 2010 - Oct. 31, 2013 (no cost extension)

Position: Principle Investigator

Chinese NSF 91231120 “Modeling and Analysis of Drosophila Experimental Data”

Total Cost: \$1,000,000 yuan (about \$150,000)

Period: Jan. 01, 2013 - Dec. 31, 2017

Position: Principle Investigator (Hosted by Yunnan University)

NIH 2 U54 HG003273-09 “The Human Genome Sequencing Center at Baylor College of Medicine”

Total Cost: \$1,094,626 + indirect cost

Period: Nov. 01, 2011 - Oct. 31, 2015

Position: Co-Investigator of subcontract (PI Richard Gibbs)

NIH/NHLBI/ROC Univ. Washington 5U01HL077863-10 “Data Coordinating Center for the Prospective, Randomized Optimal Platelet and Plasma Ratios (PROPPR)”

Total Cost: \$5,331,045 (Total budget) + indirect

Period: Oct. 1, 2010 - Dec. 31, 2015

Position: Co-Investigator (20%) (PI Barbara Tilley)

UT Dental School/US Academy of Osseointegration HSC-DB-13-0786 “Survival of Dental Implants Placed in a Grafted and Non-grafted Bone: A Retrospective Study in a University Setting ”

Period: Mar. 27, 2014 - Mar. 15, 2015

Position: Consultant (PI Isabel Gay)

NIH/NIGM 5T 32 GM074902-09A1 “Training Grant Program in Biostatistics at UTHSC-SPH ”

Total Cost: \$149,904. Student expenses only. No funds for faculty/administrative salaries or faculty/administrative expenses

Period: July 1, 2012 - June 30, 2017 NCE

Position: Investigator (PI Barbara Tilley)

NIH R01HG009524 ”Accurately Inferring Demographic Histories of Human Populations Using Large Whole Genome Sequence Data”

Total Cost: \$1,528,968

Period: Aug. 30, 2018 - May 31, 2021

Position: Co-Investigator

NIH/NIGM 5T 32 GM074902 “Training Grant Program in Biostatistics at UTHSC-SPH”

Total Cost: \$449,712. Student expenses only. No funds for faculty/administrative salaries or faculty/administrative expenses

Period: July 1, 2016 - June 30, 2020

Position: Investigator (PI Stacia M. DeSantis)

MD Anderson Cancer Center/CPRIT “Collaborative Training of a New Cadre of Innovative Cancer Prevention Researchers”. Student expenses only. No funds for faculty/administrative salaries or faculty/administrative expenses \$1,661,213 (Total budget) + indirect

Period: Mar. 1, 2016 - Feb. 28, 2021

Position: Mentor (PI Shine Chang and Sanjay Shete)

## Active Grants

## Pending Grants

NIH ”Coalescent theory and methods for inferring the history of multiple populations”

Total Cost: \$2,288,340 - Apr. 1, 2025 – Mar. 31,2030

Position: Principle Investigator.

NIH ”Understanding how antifouling coatings affect biofilm formation and bacterial interference against CAUTI”

Total Cost: \$2,531,185 - July 1, 2023 – June 30,2028

Position: Principle Investigator of subcontract.

Publications:

1. Fu, Y.X. and R.N. Curnow (1990) Locating a changed segment in a sequence of Bernoulli variables. *Biometrika* 77:295-304.
2. Fu, Y.X. and R.N. Curnow (1990) Maximum likelihood estimate of multiple change points. *Biometrika* 77:563-573.
3. Fu, Y.X. and J. Arnold (1991) On the association of restriction fragment length polymorphisms across species boundaries. *Proc. Natl. Acad. Sci.* 88:3967-3971. PMID: PMC51574
4. Fu, Y.X. and W.H. Li (1991) Necessary and sufficient conditions for the existence of certain quadratic invariants under a phylogenetic tree. *Math. Biosci.* 105:229-238.
5. Fu, Y.X. and J. Arnold (1992) Dynamics of cytonuclear disequilibria in finite populations and comparison with a two-locus nuclear system. *Theor. Popul. Biol.* 41:1-25.
6. Fu, Y.X. and W.H. Li (1992) Necessary and sufficient conditions for the existence of linear invariants in phylogenetic inference. *Math. Biosci.* 108:203-218.
7. Fu, Y.X. and W.H. Li (1992) Construction of linear invariants in phylogenetic inference. *Math. Biosci.* 109:201-228.
8. Fu, Y.X., W.E. Timberlake and J. Arnold (1992) On the design of genome mapping experiments using short synthetic oligonucleotides. *Biometrics* 48:337-359.
9. Fu, Y.X. and J. Arnold (1992) A table of exact sample sizes for the use with Fisher's exact test for 2X2 tables. *Biometrics* 48:1103-1112.
10. Li, W.H. and Y.X. Fu (1992) Method of linear invariants for phylogenetic reconstruction. In: *Modeling and Computer Methods in Molecular Biology and Genetics*. Ratner V.A., Kolchanov N.A. (eds.). NY: Nova Science Publishers, Inc. pp. 379-389.
11. Fu, Y.X. and W.H. Li (1993) Statistical tests of neutrality of mutations. *Genetics* 133:693-709. PMID: PMC1205353
12. Fu, Y.X. and W.H. Li (1993) Maximum likelihood estimate of population parameters. *Genetics* 134:1261-1270. PMID: PMC1205593
13. Fu, Y.X. (1994) An phylogenetic estimator of effective population size or mutation rate. *Genetics* 136:685-692. PMID: PMC1205817
14. Li, W.H. and Y.X. Fu (1994) Estimation of population parameters and detection of natural selection from DNA sequences. In: *Non-neutral Evolution: Theories and Molecular Data*. Golding, B.(ed.). NY: Chapman and Hall, pp. 112-125.
15. Fu, Y.X. (1994) Estimating effective population size or mutation rate using the frequencies of mutations of various classes in a sample of DNA sequences. *Genetics* 138:1375-1386. PMID: PMC1206273
16. Fu, Y.X. (1995) Linear invariants with Jukes' and Cantor's one-parameter model, *J. Theor. Biol.* 173:339-352.
17. Steel, M.A. and Y.X. Fu (1995) Classifying and counting linear phylogenetic invariants for Jukes-Cantor model. *J. Computational Biol.* 2:39-47.
18. Fu, Y.X. (1995) Statistical properties of segregating sites. *Theor. Popul. Biol.* 48:172-197.

19. Gu, X., Y.X. Fu and W.H. Li (1995) Maximum likelihood estimation of heterogeneity of substitution rate among nucleotide sites. *Mol. Biol. Evol.* 12:546-557.
20. Fu, Y.X. (1996) New statistical tests of neutrality for DNA samples from a population. *Genetics* 143:557-570. PMID: PMC1207287
21. Fu, Y.X. and W.H. Li (1996) Estimating the age of the common ancestor of men from the ZFY intron. *Science* 272:1356-1357. PMID: PMC1207573
22. Datta, S., Y.X. Fu and J. Arnold (1996) Dynamics and equilibrium behavior of cytonuclear disequilibrium under genetic drift, mutation and migration. *Theor. Popul. Biol.* 50:298-824.
23. Fu, Y.X. (1996) Estimating the age of the common ancestor of a DNA sample using the number of segregating sites. *Genetics* 144:829-838.
24. Deng, H.W. and Y.X. Fu (1996) The effects of variable mutation rates across sites on the phylogenetic estimation of effective population size or mutation rate of DNA sequences. *Genetics* 144:1271-1281. PMID: PMC1207618
25. Fu, Y.X. and W.H. Li (1997) Estimating the age of the common ancestor of a sample of DNA sequences. *Mol. Biol. Evol.* 14:195-199.
26. Fu, Y.X. (1997) Coalescent theory for a partially selfing population. *Genetics* 146:1489-1499. PMID: PMC1208091
27. Fu, Y.X. (1997) Statistical tests of neutrality of mutations against population growth, hitchhiking and background selection. *Genetics* 147:915-925. PMID: PMC1208208
28. Huang, W., Y.X. Fu, B.H.J. Chang, X. Gu, L.B. Jorde and W.H. Li (1998) Sequence variation in ZFX introns in human populations. *Mol. Biol. Evol.* 15:138-142.
29. Deng, H.W. and Y.X. Fu (1998) Conditions for positive and negative correlations between fitness and heterozygosity in equilibrium populations. *Genetics* 148:1333-1340. PMID: PMC1460038
30. Stockbauer, K.E., D. Grigsby, X. Pan, Y.X. Fu, L.M. Perea-Mejia, A. Cravioto and J.M. Musser (1998) Hypervariability generated by natural selection in an extracellular complement inhibiting protein of serotype M1 strains of group A streptococcus. *Proc. Natl. Acad. Sci. USA* 95:3128-3133. PMID: PMC19706
31. Fu, Y.X. (1998) Probability of a segregating pattern in a sample of DNA sequences. *Theor. Popul. Biol.* 54:1-10.
32. Deng, H.W. and Y.X. Fu (1998) Parsimonious counting of mutations and estimating mutation rate heterogeneity within a DNA sequence. In: *Proceeding of the Trinational Workshop on Human Evolution*. Uyenoyama, M.K. and von Haeseler, A. (eds.). University of Munich, Munich, Germany, June 5-7, 1997. Durham, NC: Duke University Publishing Group, pp. 57-72.
33. Deng, H.W. and Y.X. Fu (1998) On the three methods for estimating deleterious genomic mutation parameters. *Genet. Res.* 71:223-236.
34. Deng, H.W., Y.X. Fu and M. Lynch (1998) Inferring the major genomic mode of dominance and overdominance. *Genetica* 102/103:559-567.
35. Fu, Y.X. and R. Chakraborty (1998) Simultaneous estimation of all the parameters in a step-wise mutation model. *Genetics* 150:487-497. PMID: PMC1460324
36. Li, W.H. and Y.X. Fu (1999) Coalescent theory and its applications in population genetics. In: *Statistics in Genetics*. Halloran, M.E. and Geisser, S. (eds.). NY:Springer-Verlag, pp. 45-79.

37. Fu, Y.X. and W.H. Li (1999) Coalescing into the 21st century: An overview and prospects of coalescent theory. *Theor. Popul. Biol.* 56:1-10.
38. Hoe, N.P, K. Nakashima, S. Lukomski, D. Grigsby, M. Liu, P. Kordari, S.J. Dou, X. Pan, J. Vuopio-Varkila, S. Salmelinn, A. McGeer, D.E. Low, B. Schwartz, A. Schuchat, S. Naidich, D. De Lorenzo, Y.X. Fu and J.M. Musser (1999) Rapid selection of complement-inhibiting protein variants of Group A Streptococcus epidemic waves. *Nature Med.* 5:924-929.
39. Fu, Y.X. (2000) Measures of genetic variation. In *Encyclopedia of Life Sciences*, Stockton Press.
40. Deng, H.W. and Y.X. Fu (2000) Counting mutations by parsimony and estimation of mutation rate variation across nucleotide sites. *Math. Comput. Modeling* 32:83-95.
41. Vasco, D.A., K.A. Crandle and Y.X. Fu (2000) Molecular population genetics: coalescent methods using summary statistics. In *Computational and Evolutionary Analysis of HIV Molecular Sequences*. Rodrigo, A.G. and Learn, G.H. (eds.). Boston, MA: Kluwer Academic Publishers, pp. 175-218.
42. Fu, Y.X. (2000) Neutrality and selection in molecular evolution: Statistical tests. In *Encyclopedia of Life Sciences*. Stockton Press.
43. Fu, Y.X. (2000) Interpreting DNA evidence. *Theor. Popul. Biol.* 57:399-400.
44. Zhao, Z., L. Jin, Y.X. Fu , M. Ramsay, T. Jenkins, E. Leskinen, P. Pamilo, M. Trexler, L. Patthy, L.B. Jorde, S. Ramos-Onsins, N. Yu and W.H. Li (2000) Worldwide DNA sequence variation in a 10 kb noncoding region on human chromosome 22. *Proc. Natl. Acad. Sci. USA* 97:11354-11358. PMID: PMC17204
45. Ding, Y.C., S. Wooding, H.C. Harpending, H.C. Chi, H.P. Li, Y.X. Fu , J.F. Pang, Y.G. Yao, J.G. Xiang-Yu, R. Moyzis and Y. Zhang (2000) Population structure and history in East Asia. *Proc. Natl. Acad. Sci. USA* 97:14003-14006. PMID: PMC17690
46. Fu, Y.X. (2001) Estimating mutation rate and generation time from longitudinal samples of DNA sequences. *Mol. Biol. Evol.* 18:620-626.
47. Yu, N., Z. Zhao, Y.X. Fu , N. Sambuughin, M. Ramsay, T. Jenkins, E. Leskinen, L. Patthy, L.B. Jorde, T. Kuromori and W.H. Li (2001) Global patterns of human DNA sequence variation in a 10-kb region on chromosome 1. *Mol. Biol. Evol.* 18:214-222.
48. Hoe N.P., J. Vuopio-Varkila, M. Vaara, D. Grigsby, D. De Lorenzo, Y.X. Fu , S.J. Dou, X. Pan, K. Nakashima and J.M. Musser (2001) Distribution of streptococcal inhibitor of complement variants in pharyngitis and invasive isolates in an epidemic of serotype M1 group A Streptococcus infection. *J. Infect. Dis.* 183:633-639.
49. Su, B., Y.X. Fu , Y. Wang, L. Jin and R. Chakraborty (2001) Genetic diversity and population history in Red Pandas (*Ailurus fulgens*) as inferred from mitochondrial DNA sequence variations. *Mol. Biol. Evol.* 18:1070-1076.
50. Yao Y.G., L. Nie, H. Harpending, Y.X. Fu , Z.G. Yuan and Y.P. Zhang (2002) Genetic relationship of Chinese ethnic populations revealed by mtDNA sequence diversity. *Am. J. Phy. Anthropol.* 118:63-76.
51. Yu, N., Y.X. Fu and W.H. Li (2002) DNA polymorphism in a world-wide sample of human X chromosomes. *Mol. Biol. Evol.* 19:2131-2141.
52. Lu, X.M., Y.X. Fu and Y.P. Zhang (2002) Evolution of mitochondrial cytochrome b pseudogene in genus *Nycticebus*. *Mol. Biol. Evol.* 19:2237-2341.
53. Li, H., Y. Zhang, Y.P. Zhang and Y.X. Fu (2003) Neutrality tests using DNA polymorphism from multiple samples. *Genetics* 163:1147-1151. PMID: PMC1462489

54. Li, H., S.J. Meng, Z.M. Men, Y.X. Fu and Y.P. Zhang (2003) Genetic diversity and population history of golden monkeys (*Rhinopithecus roxellana*). *Genetics* 164:269-275. PMID: PMC1462553
55. Fu, Y.X. and H.Y. Huai (2003) Estimating mutation rate: how to count mutations. *Genetics* 164:797-805. PMID: PMC1462584
56. Zhao, Z., Y.X. Fu, D. Hewett-Emmett and E. Boerwinkle (2003) Investigating single nucleotide polymorphism (SNP) density in the human genome and its implications for molecular evolution. *Gene* 312:207-213.
57. Huang, Q., Y.X. Fu and E. Boerwinkle (2003) Comparison of strategies for selecting single nucleotide polymorphisms for case/control association studies. *Hum. Genet.* 113:253-357.
58. Xu, H.Y. and Y.X. Fu (2004) Estimating effective population size or mutation rate with microsatellites. *Genetics* 166:555-563. PMID: PMC1470688
59. Choudhary, M., Y.X. Fu, C. Mackenzie and S. Kaplan (2004) DNA sequence duplication in *Rhodobacter sphaeroides* 2.4.1: Evidence of an ancient partnership between chromosomes I and II. *J. Bacteriol.* 186:2019-2027. PMID: PMC374402
60. Zhao, Z., H. Li, X. Wu, Y. Zhong, K. Zhang, Y.P. Zhang, E. Boerwinkle and Y.X. Fu (2004) Moderate mutation rate in the SARS coronavirus genome and its implications. *BMC Evol. Biol.* 4:21. PMID: PMC446188
61. Graviss, E.A., X. Ma and Y.X. Fu (2004) IL-8 polymorphism is not associated with pulmonary tuberculosis in the Gambia and to original article: Association between interleukin-8 gene alleles and human susceptibility to tuberculosis disease. A rebuttal. *J. Infect. Dis.* 189:1545-1546.
62. Shi, S., Y. Huang, K. Zeng, F. Tan, H. He, J. Huang and Y.X. Fu (2005) Molecular phylogenetic analysis of mangroves: independent evolutionary origins of vivipary and salt secretion. *Mol. Phylogenet. Evol.* 34:159-166. PMID: PMC15579389
63. Xu, H., R. Chakraborty and Y.X. Fu (2005) Mutation rate variation at human dinucleotide microsatellites. *Genetics* 170:305-312. PMID: PMC1449715
64. Pan, D., Y. Li, H.X. Hu, S.J. Meng, Z.M. Men, Y.X. Fu, Y.P. Zhang (2005) Microsatellite polymorphisms of Sichuan golden monkeys. *Chinese Sci. Bull.* 50(24):2850-55.
65. Fu, Y.X. (2006) Exact coalescent for the Wright-Fisher model. *Theor. Popul. Biol.* 69(4):385-394.
66. Lynch, H.T., A. de la Chapelle, H. Hampel, A. Wagner, R. Fodde, J.F. Lynch, R. Okimoto, M.B. Clark, S. Coronel, A. Trownou, Y.X. Fu, G.R. Haynatzki and G. Gong (2006) American founder mutation for Lynch syndrome: prevalence estimates and implications. *Cancer* 106(2):448-452.
67. Chen, J.H., D. Pan, C. Groves, Y.X. Wang, E. Narushima, H. Fitch-Snyder, P. Crow, V. Ngoc Thanh, O. Ryder, H.W. Zhang, Y.X. Fu and Y.P. Zhang (2006) Molecular phylogeny of *Nycticebus* inferred from mitochondrial genes. *Int. J. Primatol.* 27(4):1187-1200.
68. Pan, D., Y.X. Fu and Y.P. Zhang (2006) Population genetics of *Rhinopithecus bieti*: A study of the mitochondrial control region. *Yi Chuan* 28(4):432-436 (in Chinese).
69. Gong, G., G. Haynatzki, V. Haynatzka, S. Kosoko-Lasaki, R. Howell, Y.X. Fu, J.C. Gallaher and M.R. Wilson (2006) Bone mineral density of recent African immigrants in the United States. *J. Natl. Med. Assoc.* 98(5):746-752.
70. Gong, G., G. Haynatzki, V. Haynatzka, R. Howell, S. Kosoko-Lasaki, Y.X. Fu, F. Yu, J.C. Gallaher and M.R. Wilson (2006) Bone mineral density-affecting genes in Africans. *J. Natl. Med. Assoc.* 98(7):1102-1108.

71. Tan, Y.D. and Y.X. Fu (2006) A novel method for estimating linkage maps. *Genetics* 173(4):2383-2390.
72. Shi, P., L. Yu, Y.X. Fu, J.F. Huang, K.Q. Zhang and Y.P. Zhang (2006) Evolutionary implications of Avian Infectious Bronchitis Virus (AIBV) analysis. *Cell Res.* 16(3):323-327.
73. Zhao, Z., N. Yu, Y.X. Fu and W.H. Li (2006) Nucleotide variation and haplotype diversity in a 10-kb noncoding region in three continental human populations. *Genetics* 174:399-409. PMID: PMC1569808
74. Gonzalez, R., A. Revol, D. Esquivel, G. Corrales, I. Rodriguez, V. Gonzalez, G. Davila, Q. Cao, P. de Jong, Y.X. Fu and H.A. Barrera (2006) Growth hormone locus expands and diverges after the separation of New and Old World monkeys. *Gene* 380:38-45.
75. Zeng, K., Y.X. Fu, S. Shi and C.I. Wu (2006) Statistical tests for detecting positive selection by utilizing high frequency variants. *Genetics* 174:1431-1439. PMID: PMC1667063
76. Tan, Y.D., M. Fornage and Y.X. Fu (2006) Ranking analysis of microarray data: A powerful method for identifying differentially expressed genes. *Genomics* 88:846-855.
77. Liu, X., M.M. Gutacker, J.M. Musser and Y.X. Fu (2006) Evidence for recombination in *Mycobacterium tuberculosis*. *J. Bacteriol.* 88:8169-8177. PMID: PMC1698211
78. Liu, S.Q., C.Q. Liu and Y.X. Fu (2007) Molecular motions in HIV-1 gp120 mutants reveal their preferences for different conformations. *J. Mol. Graph. Model.* 26(1):306-318.
79. Choudhary, M., X. Zanhua, Y.X. Fu and S. Kaplan (2007) Genome analyses of three strains of "Rhodobacter sphaeroides": Evidence of rapid evolution of chromosome II. *J. Bacteriol.* 189:1914-1921. PMID: PMC1855717
80. Tan, Y.D. and Y.X. Fu (2007) A new strategy for estimating recombination fractions between dominant markers from an F2 population. *Genetics* 175(2):923-931. PMID: PMC1800593
81. Liu, S.Q., Z.H. Meng, J.K. Yang, Y.X. Fu and K.Q. Zhang (2007) Characterizing structural features of cuticle-degrading proteases from fungi by molecular modeling. *BMC Struct. Biol.* 7:33. PMID: PMC1890553
82. Liu, X. and Y.X. Fu (2007) Test of genetical isochronism for longitudinal samples of DNA sequences. *Genetics* 176(1):327-342. PMID: PMC1893063
83. Liu, S.Q., S.X. Liu and Y.X. Fu (2007) Dynamic domains and geometrical properties of HIV-1 gp120 during conformational changes induced by CD4 binding. *J. Mol. Model.* 13(3):411-424.
84. Romeo, S., L.A. Pennacchio, Y.X. Fu, E. Boerwinkle, A. Tybjaerg-Hansen, H.H. Hobbs and J.C. Cohen (2007) Population-based resequencing of ANGPTL4 uncovers variations that reduce triglycerides and increase HDL. *Nat. Genet.* 39(4):513-516. PMID: PMC2762948
85. Pan, D., J.H. Chen, C. Groves, Y.X. Wang, E. Narushima, H. Fitch-Synder, P. Crow, X. Jinggong, V. Ngoc Thanh, O. Ryder, L. Chemnick, H.W. Zhang, Y.X. Fu and Y.P. Zhang (2007) Mitochondrial control regions and population genetic patterns of *Nycticebus bengalensis* and *N. pygmaeus*. *Int. J. Primatol.* 28:791-799.
86. Liu, S.Q., Y.X. Fu, C.Q. Liu (2007) Molecular motions and conformational transition between different conformational states of HIV-1 gp120 envelope glycoprotein. *Chinese Sci. Bull.* 52(22):3074-3088.
87. Liu, X. and Y.X. Fu (2008) Algorithms to estimate the lower bounds of recombination with or without recurrent mutations. *BMC Genomics* 9(Suppl 1):S24. PMID: PMC2386066
88. Liu, S.Q., S.X. Liu and Y.X. Fu (2008) Molecular motions of human HIV-1 gp120 envelope glycopro-



- teins. *J. Mol. Model.* 14(9):857-870. [Not NIH funded]
89. Liu, X. and Y.X. Fu (2008) Summary statistics of neutral mutations in longitudinal DNA samples. *Theor. Popul. Biol.* 74:56-67. PMID: PMC3060710
  90. Zhang, W., W.W. Cai, W.P. Zhou, H.P. Li, L. Li, W. Yan, Q.K. Deng, Y.P. Zhang, Y.X. Fu and X.M. Xu (2008) Evidence of gene conversion in the evolutionary process of the codon 41/42 (-CTTT) mutation causing beta-Thalassemia in Southern China. *J. Mol. Evol.* 66:436-445. [Not NIH funded]
  91. Xue, C. and Y. Fu (2009) Preservation of duplicate genes by originalization. *Genetica* 136(1):69-78. [Not NIH funded]
  92. Xue, C. and Y. Fu (2009) Mean time to resolution of gene duplication. *Genetica* 136(1):119-126. [Not NIH funded]
  93. Liu, X., T.J. Maxwell, E. Boerwinkle and Y.X. Fu (2009) Inferring population mutation rate and sequencing error rate using the SNP frequency spectrum in a sample of DNA sequences. *Mol. Biol. Evol.* 26(7):1479-1490. PMID: PMC 2734145
  94. Pan, D., H.X. Hu, S.J. Meng, Z.M. Men, Y.X. Fu and Z.P. Zhang (2009) A high polymorphism level in *Rhinopithecus roxella*. *Int. J. Primatol.* 30:337-351. [not NIH funded]
  95. Fu, Y.X. and X. Liu (2010) Statistical methods for detecting the presence of natural selection in bacterial populations. In: *Bacterial Population Genetics in Infectious Disease*. Robinson D.A., Falush, D. and Feil E.J. (eds.) Hoboken, NJ: John Wiley & Sons, Inc., pp. 87-101.
  96. Liu, X., Y.X. Fu, T.J. Maxwell and E. Boerwinkle E. (2010) Estimating population genetic parameters and comparing model goodness-of-fit using DNA sequences with error. *Genome Res.* 20(1):101-9. PMID: PMC2798822
  97. Xue, C., R. Huang, T.J. Maxwell and Y.X. Fu (2010) Genome changes after gene duplication: haploidy versus diploidy. *Genetics* 186:287-294. PMID: PMC2940293
  98. Zhang, Z.X., Y. Yang, F. P. Ye, Q.S. Fan, D.J. Li, X. Zhang, Y.X. Fu and Y. Zheng (2010) Epitope analysis of cDNA sequences of *Deinagkistrodon acutus* snake venom metalloproteinases and observation of their immune protective effects. *Academic J. Second Military Med. Univ.* 31(4):364-368. [not NIH funded]
  99. Xue, C., R. Huang, S.Q. Liu and Y.X. Fu (2010) Recombination facilitates neofunctionalization of duplicate genes via originalization. *BMC Genet.* 11:46. PMID: PMC2906408
  100. Liu, S.Q., Z.H. Meng, Y.X. Fu and K.Q. Zhang (2010) Insights derived from molecular dynamics simulation into the molecular motions of serine protease proteinase K. *J. Mol. Model.* 16(1):17-28. [Not NIH funded]
  101. Liu, S.Q., L.M. Liang, T Yan, L.Q. Yang, X.L. Ji, J.K. Yang, Y.X. Fu and K.Q. Zhang (2011) Structural and dynamic basis of serine proteases from nematophagous fungi for cuticle degradation. In: Stoytcheva M (ed). *Pesticides in the Modern World – Pests Control and Pesticides Exposure and Toxicity Assessment*. Intech Open Access Publisher. pp.333-356.
  102. Xu, Y., B. Peng, Y. Fu and C.I. Amos (2011) Genome-wide algorithm for detecting CNV associations with diseases. *BMC Bioinformatics* 12:331. PMID: PMC3173460
  103. Gao, J.J., X.R. Pan, J. Hu, L. Ma, J.M. Wu, Y.L. Shao, S.A. Barton, R.C. Woodruff, Y.P. Zhang and Y.X. Fu (2011) Highly variable recessive lethal or nearly lethal mutation rates during germline development of male *Drosophila melanogaster*. *Proc. Natl. Acad. Sci. USA* 108(38):15914-15919. PMID: PMC3179084
-

104. Xue, C., Y.X. Fu, Y. Zhao, Y. Gong and X. Liu (2011) Smaller genetic risk in catabolic process explains lower energy expenditure, more athletic capability and higher prevalence of obesity in Africans. *PLoS One* 6(10):e26027. PMID: PMC3189926
105. Liu, S.Q., Y. Tao, Z.H. Meng, Y.X. Fu and K.Q. Zhang (2011) The effect of calciums on molecular motions of proteinase K. *J. Mol. Model.* 17:289-300. [not NIH funded]
106. Wei, P., X. Liu and Y.X. Fu (2011) Incorporating predicted functions of nonsynonymous variants into gene-based analysis of exome sequencing data: a comparative study. *BMC Proc.* 2011 Nov 29;5 Suppl 9:S20. PMID: PMC3287855
107. 1000 Genomes Project Consortium, G.R. Abecasis, A. Auton, L.D. Brooks, M.A. DePristo, R.M. Durbin, R.E. Handsaker, H.M. Kang, G.T. Marth, and G.A. McVean (2012) An integrated map of genetic variation from 1,092 human genomes. *Nature* 491(7422):56-65. PMID: PMC3498066
108. Clarke, L., X. Zheng-Bradley, R. Smith, E. Kulesha, C. Xiao, I. Toneva, B. Vaughan, D. Preuss, R. Leinonen, M. Shumway, S. Sherry, P. Flicek; 1000 Genomes Project Consortium (2012) The 1000 Genomes Project: data management and community access. *Nat. Methods* 9(5):459-62. PMID: PMC3498066
109. Liu, S-Q., X-L. Ji, Y. Tao, D-Y. Tan, K-Q. Zhang and Y.X. Fu (2012) Protein folding, binding and energy landscape: A Synthesis. In: Kaumaya PTP (ed). *Protein Engineering*. InTech Open Access Publisher. pp. 207-252.
110. Hu, Z., Y.X. Fu, A.J. Greenberg, C.I. Wu and W.W. Zhai (2013) Age-dependent transition from cell-level to population-level control in murine intestinal homeostasis revealed by coalescence analysis. *PLoS Genet.* 9(2):e1003326. PMID: PMC3585040
111. Fu, Y.X. (2013) Statistical methods for analyzing *Drosophila* germline mutation rates. *Genetics* 194:927-936. PMID: PMC3730920
112. Xue, C., X. Liu, Y. Gong, Y. Zhao and Y.X. Fu (2013) Significantly fewer protein functional changing variants for lipid metabolism in Africans than in Europeans. *J. Transl. Med.* 11:67. PMID: PMC3610238
113. Tran, D.T., I.C. Gay, X.L. Du, Y.X. Fu, R.D. Bebermeyer, A.S. Neumann, C. Streckfus, W. Chan, and M.F. Walji (2013) Assessing periodontitis in populations: A systematic review of the validity of partial mouth examination protocols. *J. Clin. Periodont.* 40(12):1064-1071. PMID: PMC3859863
114. Khurana, E, Y. Fu, V. Colonna, X.J. Mu, H.M. Kang, T. Lappalainen, A. Sboner, L. Lochovsky, J. Chen, A. Harman, J. Das, A. Abyzov, S. Balasubramanian, K. Beal, D. Chakravarty, D. Challis, Y. Chen, D. Clarke, L. Clarke, F. Cunningham, U.S. Evan, P. Flicek, P. R. Fragoza, E. Garrison, R. Gibbs, Z.H. Gümüs, J. Herrero, N. Kitabayash, Y. Kong, K. Lage, V. Liliashvili, S.M. Lipkin, D.G. MacArthur, G. Marth, D. Muzny, T.H. Pers, G.R. Ritchie, J.A. Rosenfeld, C. Sisu, X. Wei, M. Wilson, Y. Xue, F Yu; 1000 Genomes Project Consortium, E.T. Dermitzakis, H. Yu, M.A. Rubin, C. Tyler-Smith, and M. Gerstein (2013) Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science* 342(6154):1235587. PMID: PMC3947637
115. Yang, L.Q., P. Sang, Y. Tao, Y.X. Fu, K-Q. Zhang, Y.H. Xie and S-Q. Liu (2014) Protein dynamics and motions in relation to their functions: Several case studies and the underlying mechanisms. *J. Biomol. Struct. Dyn.* 32(3):372-93. PMID: PMC3919177
116. Delaneau, O., J. Marchini; 1000 Genomes Project Consortium; 1000 Genomes Project Consortium (2014) Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. *Nat. Commun.* 5:3934. PMID: PMC4338501
117. Colonna, V., Q. Ayub, Y. Chen, L. Pagan, P. Luisi, M. Pybus, E. Garrison, Y. Xue, C. Tyler-

- Smith; 1000 Genomes Project Consortium, G.R. Abecasis, A. Auton, L.D. Brooks, M.A. DePristo, R.M. Durbin, R.E. Handsaker, H.M. Kang, G.T. Marth, and G.A. McVean (2014) Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. *Genome Biol.* 15(6):R88. PMID: PMC4197830
118. Walter, N.D., J. Painter, M. Parker, P. Lowenthal, J. Flood, Y.X. Fu , R. Asis, and R. Reves (2014) Persistent latent tuberculosis reactivation risk in US immigrants. *Am. J. Respir. Crit. Care Med.* 189(1):88-95. PMID: PMC3919127
119. Gao, J-J., X-R. Pan, J. Hu, L. Ma, J-M. Wu, Y-L. Shao, S. Ai, S. Liu, S.A. Barton, R.C. Woodruff, Y-P. Zhang, and Y.X. Fu (2014) Pattern of mutation rates in the germline of *Drosophila melanogaster* males from a large-scale mutation screening experiment. *G3: Genes l Genomes l Genetics* 4(8):1503-1514. PMID: PMC4132180
120. Fu, Y.X. (2014) An efficient estimator of mutation parameter and analysis of the polymorphism from the 1000 Genomes Project. *Genes* 5(3):561-575. PMID: PMC4198917
121. Sang, P., L.Q. Yang, X.L. Ji, Y.X. Fu , and S.Q. Liu (2014) Insight derived from molecular dynamics simulations into molecular motions, thermodynamics and kinetics of HIV-1 gp120. *PLoS One* 9(8):e104714. PMID: PMC4126740
122. Tran, D.T., I. Gay, X.L. Du, Y.X. Fu , R.D. Bebermeyer, A.S. Neumann, C. Stereckfus, W. Chan, and M.R. Walji (2014) Assessment of partial-mouth periodontal examination protocols for periodontitis surveillance. *J. Clin. Periodontol.* 41(9):846-52. PMID: PMC4318801
123. Baraniuk, S., B.C. Tilley, D.J. del Junco, E.E. Fox, G. van Belle, C.E. Wade, J.M. Podbielski, A.M. Beeler, J.R. Hess, E.M. Bulger, M.A. Schreiber, K. Inaba, T.C. Fabian, J.D. Kerby, M.J. Cohen, C.N. Miller, S. Rizoli, T.M. Scalea, T. O’Keeffe, K.J. Brasel, B.A. Cotton, P. Muskat, J.B. Holcomb; PROPPR Study Group (2014) Pragmatic Randomized Optimal Platelet and Plasma Ratios (PROPPR) Trial: design, rationale and implementation. *Injury* 45(9):1287-95. PMID: PMC4137462
124. Liu, X. and Y.X. Fu (2015) Exploring population size changes using SNP frequency spectra. *Nat. Genet.* 47(5):555-559. PMID: PMC4414822
125. Ai, S-M., J-J. Gao, S-Q. Liu, and Y.X. Fu (2015) Efficient estimation of mutation rates during individual development by minimization of chi-square. *PLoS One* 10(8):e0135398. PMID: PMC4534375
126. Aiona, K., P. Lowenthal, J. Painter, R. Reves, J. Flood, M. Parker, Y.X. Fu , K. Wall, and N. Walter. (2015) Transnational record linkage for tuberculosis surveillance and program evaluation. *Public Health Rep.* 130(5):475-484. PMID: PMC4529832
127. Holcomb, J.B., B.C. Tilley, S. Baraniuk, E.E. Fox, C.E. Wade, J.M. Podbielsk, D.J. del Junco, K.J. Brase, E.M. Bulger, R.A. Callcut, M.J. Cohen, B.A. Cotton, T.C. Fabian, K. Inaba, J.D. Kerby, P. Muskat, T. O’Keeffe, S. Rizoli, B.R. Robinson, T.M. Scalea, M.A. Schreiber, D.M. Stein, J.A. Weinberg, J.L. Callum, J.R. Hess, N. Matijevic, C.N. Miller, J.F. Pittet, D.B. Hoyt, G.D. Pearson, B. Leroux, G. van Belle G; PROPPR Study Group (2015) Transfusion of plasma, platelets, and red blood cells in a 1:1:1 vs a 1:1:2 ratio and mortality in patients with severe trauma: the PROPPR randomized clinical trial. *JAMA* 313(5):471-82. PMID: PMC4374744
128. 1000 Genomes Project Consortium (2015) A global reference for human genetic variation. *Nature* 526(7571):68-74. PMID: PMC4750478
129. Gay, I.C., D.T. Tran, R. Weltman, K. Parthasarathy, J. Diaz-Rodriguez, M. Walji, Y.X. Fu , and L. Friedman L (2016). Role of supportive maintenance therapy on implant survival: A university-based 17 years retrospective analysis. *J. Dent. Hyg.* 2015 Dec 22. doi: 10.1111/idh.12188. [Not NIH funded]
130. Lin, R., Y. Zhang, D. Yan, X. Liao, G. Gong, J. Hu, Y.X. Fu , and W. Cai (2016) Lack of association

- between polymorphisms in the SIRT6 gene and longevity in a Chinese population *Mol. Cell. Probes* 30(2):79-82. [not NIH funded]
131. Lin, R., Y. Zhang, D. Yan, X. Liao, G. Gong, J. Hu, Y.X. Fu , and W. Cai (2016) Association of common variants in TOMM40/APOE/APOC1 region with human longevity in a Chinese population. *J. Hum. Genet.* 61(4):323-8. [not NIH funded]
  132. Lin, R., D. Yan, Y. Zhang, X. Liao, G. Gong, J. Hu, Y.X. Fu , and W. Cai (2016) Common variants in SIRT1 and human longevity in a Chinese population. *BMC Med. Genet.* 17:31. PMID: PMC483616
  133. Tran, D.T., I. Gay, X.L. Du, Y.X. Fu , R.D. Bebermeyer, A.S. Neumann, C. Stereckfus, W. Chan, and M.R. Walji (2016) Partial-mouth periodontal examination protocols for estimating periodontitis extent and severity in a US population. *Clin. Exp. Dent. Res.* 2(1):73-79. doi: 10.1002/cre2.24 [not NIH funded]
  134. Sang, P., Q. Yang, X. Du, N. Yang, L.Q. Yang, X.L. Ji, Y.X. Fu , Z.H. Meng, and S.Q. Liui (2016) Effect of the solvent temperatures on dynamics of serine protease proteinase K. *Int. J. Mol. Sci.* 17(2):254. PMID: PMC4783983
  135. Li, H., J. Xiang-Yu, G. Dai, Z. Gu, C. Ming, Z. Yang, O.A. Ryder, W.H. Li, Y.X. Fu and Y.P. Zhang (2016) Large numbers of vertebrates began rapid population decline in the late 19th century. *Proc. Nat. Acad. Sci. USA* 113(49):14079-14084. PMID: PMC5150392
  136. Lin, R., Y. Zhang, D. Yan, X. Liao, X. Wang, Y.X. Fu and W. Cai (2016) Geneti association analysis of common variants in FOXO3 related to longevity in a Chinese population. *PloS One* 11(12):e0167918. PMID: PMC5148017.
  137. Du, X., P. Sang, Y.L. Xia, Y. Li, J. Liang, S.M. Ai, X.L. Ji, Y.X. Fu and S.Q. Liu (2017) Comparative thermal unfolding study of psychrophilic and mesophilic substilism-like serine proteases by molecular dynamics simulations. *J. Biomol. Struct. Dyn.* 35(7):1400-1417. [Not NIH funded]
  138. Yu, D., L. Dong, F. Yan, H. Mu B. Tang B, X. Yang, T. Zeng, Q. Zhou, F. Gao, Z. Wang, Z. Hao, H. Kang, Y. Zheng, H. Huang, Y. Wei, W. Pan, Y. Xu, J. Zhu, S. Zhao, C. Wang, P. Wang, L. Dai, M. Li, L. Lan, Y. Wang, H. Chen, Y. Li, Y.X. Fu , Z. Shao, Y. Bao, F. Zhao, L. Chen, G-Q. Zhang, W. Zhao, H. Li (2019) eGPS 1.0: comprehensive software for multi-omic and evolutionary analyses. *Natl Sci Rev* 0:1-4. doi: 10.1093/nsr/nwz079 Advance access publication 18 June 2019. [Not NIH funded]
  139. Li, Y, L. Deng, S.M. Ai, P. Sang , J. Yang, Y.L. Xia, Z. B. Zhang, Y.X. Fu , and S.Q. Liu. (2018) Insights into the molecular mechanism underlying CD4-dependency and neutralization sensitivity of HIV-1: a comparative molecular dynamics study on gp120s from isolates with different phenotypes. *RSC Adv* 8(26): 14355-14368. [Not NIH funded]
  140. Xia, Y.L., J.H. Sun, S.M. Ai, Y. Li, X. Du, P. Sang P, L.Q. Yang, Y.X. Fu , and S.Q. Liu. (2018). Insights into the role of electrostatics in temperature adaptation: a comparative study of psychrophilic, mesophilic, and thermophilic subtilisin-like serine proteases. *RSC Adv* 8(52): 29698-29713. [Not NIH funded]
  141. Liu, Q.Y., J.H. Wei, Y.W. Li, M. Wang, J. Su, Y.H. Lu, M. G. Lopez, X.Q. Qian, Z.Q. Zhu, H.Y. Wang, M.Y. Gan, J. Qi, Y.X. Fu , H.E. Takiff, N. Comas, F. Li, X.M. Lu, S.M. fortune and Q. Gao (2020) Mycobacterium tuberculosis clinical isolates carry mutational signatures of host immune environments. *Science Advances* 6:22, eaba4901 DOI: 10.1126/sciadv.aba4901
  142. Li, Y., L. Deng, J. Liang, G. H. Dong, Y. L. Xia, Y.X. Fu and S. Q. Liu (2020) Molecular dynamics simulations reveal distinct differences in conformational dynamics and thermodynamics between the unliganded and CD4-bound states of HIV-1 gp120. *Phys. Chem. Chem. Phys.*, 2020,22, 5548-5560.
  143. Wang, G.Y., K. Chen, J. Zhang, S. Deng, J. Xiong, X. L. He, Y.X. Fu and Miao, W. Drivers of

- mating type composition in *Tetrahymena thermophila*. *Genome Biology and Evolution*, 12(12):28-2343, <https://doi.org/10.1093/gbe/evaa197>.
144. Xia, Y.L., Y.P. Li, Y.X. Fu, and S.Q. Liu (2020). The Energetic Origin of Different Catalytic Activities in Temperature-Adapted Trypsins. *ACS Omega*, 5(39): 25077–25086. DOI: 10.1021/acsomega.0c02401
  145. Wang, G.Y., L. Fu, J. Xiong, K. Mochizuki, Y.X. Fu and W. Miao (2020) Identification and Characterization of Base-Substitution Mutations in the Macronuclear Genome of the Ciliate *Tetrahymena thermophila*. *Genome Biology and Evolution*, 13(1):1–8. doi:10.1093/gbe/evaa232
  146. Liu, X. and Y.X. Fu (2020) Stairway Plot 2: demographic history inference with folded SNP frequency spectra. *Genome Biology*, 21:280
  147. Zhang, Z.B., Xia Y.L., Dong G.H., Y.X. Fu and S.Q. Liu (2021) Exploring the Cold-Adaptation Mechanism of Serine Hydroxymethyltransferase by Comparative Molecular Dynamics Simulations. *Int J Mol Sci*. Feb 11;22(4):1781. doi: 10.3390/ijms22041781.
  148. Xia, Y. L., W. Li, Y. Li, X. L. Ji, Y. X. Fu and S. Q. Liu (2021) A Deep Learning Approach for Predicting Antigenic Variation of Influenza A H3N2. *Computational and Mathematical Methods in Medicine*, V2021, ID 9997669, <https://doi.org/10.1155/2021/9997669>
  149. Fu, Y.X., Wang, G., Chen, K., Ma. X., Liu, S.Q. and Miao, W. (2022) Amitosis as a strategy of cell division—Insight from the proliferation of *Tetrahymena thermophila* macronuclei. *Theor. Pop. Biol.* 145: 52–62.
  150. Fu, Y.X. (2022) Variances and covariances of linear summary statistics of segregating sites. *Theor. Pop. Biol.* 145: 95–108.
  151. Zhang, Z.B., Xia, Y.L., Shen, J.X., Du, W.W., Y.X. Fu and Liu, S.Q. (2022) Mechanistic Origin of Different Binding Affinities of SARS-CoV and SARS-CoV-2 Spike RBDs to Human ACE2. *Cells*, 11,1274.
  152. Shen J-X, Du W-W, Xia Y-L, Zhang Z-B, Yu Z-F, Fu Y-X, Liu S-Q. (2023) Identification of and Mechanistic Insights into SARS-CoV-2 Main Protease Non-Covalent Inhibitors: An In-Silico Study. *International Journal of Molecular Sciences*. 24(4):4237.
  153. Hu, W.J., Hao, Z.Q., Du, P.Y., Vincenzo, F. D., Manzi, G., Cui, J.L., Fu, Y.X., Pan, Y.H. and Li, H.P. (2023) Genomic inference of a severe human bottleneck during the Early to Middle Pleistocene transition. *Science*, 331:979–984.
  154. Xia, Y.L., Du, W.W., Li, Y.P., Tao, Y., Zhang, Z.B., Liu, S.M, Fu, Y.X., Zhang, K.Q., and Liu, S.Q. (2024) Computational Insights into SARS-CoV-2 Main Protease Mutations and Nirmatrelvir Efficacy: The Effects of P132H and P132H-A173V. *J. Chem. Inf. Model.* 64, 5207–5218