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Gender: Male
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Profile: I am a self-motivated and reliable person with extensive scientific data analysis experience. I am able to work well both in a team as well as using own initiative, with good communication ability. I am keen to learn new knowledge and skills and willing to solve scientific questions, and also to seek for responsibilities in my research scope.

Education:

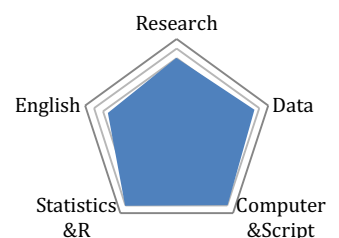
- **Ph.D.** in Computational Biology 2010.09~2017.07
Partner Institute for **C**omputational **B**iology (PICB)
Shanghai Institutes for Biological Sciences
Chinese Academy of Sciences
(Supervisor: Dr. Shuhua Xu)
- **Bachelor D.** in Horticulture 2006.09~2010.06
Jilin University (China's Project 211/985)

Research Interests:

- Genetic diversity of Copy Number Variation/Structural Variation (CNV/SV) in populations.
- CNV/SV in human genetic diseases and evolution.
- Metagenomic diversity in host populations and the association between host genome and metagenome.
- Human population history.

Research skills:

- Proficient **English** in reading, writing and communication.
- Familiar with sorts of genomic data and data formats, including both array chip and **NGS** data and corresponding **pipelines** and **tools**.
- Proficient computer skills, especially with **Linux** and clusters.
- Extensive experience in programming languages, including **Shell**, **Perl** and **Python**.
- Skilled in **statistics** and using **R** software.



Research Experience:

- Build pipelines for **CNV/SV** data processing
Build several pipelines for CNV/SV data analysis based on different detecting platforms, including SNP array, aCGH, and NGS, by integrating distinct popular and robust methods/tools. Two of the advantages of the pipelines are that they are optimized by real data processing experience and can be applied to large population data. I accomplished the major work.
- Build a **CNV** map of Han Chinese
Use aCGH, partly along with NGS, to build a representative CNV map of Han Chinese, with hundreds of individuals, and find some regional specific CNVs. I accomplished the major work of the data analysis.
- Build a **CNV** map of Peninsular Malaysia (PM) populations
Build a comprehensive CNV map of PM populations, including Orange Asli ("indigenous people"), taking advantages of Affymetrix SNP 6.0 chip, and investigate their genetic diversity. Find population specific CNVs and genes underlying natural selection. I was responsible for this project.
- Differentiated **CNV** detect and TED found in Tibetan (*published*)
Devise WinXPCNVer to detect population differentiated CNV, using array probe intensity. Apply it in Tibetan population and find TED (Tibetan-enriched deletions) that is associated with high-altitude adaptation. I was responsible for development of WinXPCNVer and part work of data analysis.
- Dissect gut **metagenomic** variation in Han Chinese and Muslim population
Demonstrate genetic differentiation between enterotypes, as well as among populations in gut microbiome, investigated the metagenomic diversity and differentiated selection pressures from food on metagenome, and find associations between gut microbiome and host genome. I finished the most part of the data analysis.

Publication:

1. Lu J, Lou H, **Fu R**, Lu D, Zhang F, Wu Z, et al. Assessing genome-wide copy number variation in the Han Chinese population. **J Med Genet [Internet]. 2017 Jul 13 (co-first)**
2. Haiyi Lou, Yan Lu, Dongsheng Lu, **Ruiqing Fu**, Xiaoji Wang, Qidi Feng, Sijie Wu, Yajun Yang, Shilin Li, Longli Kang, Yaquin Guan, Boon-Peng Hoh, Yeun-Jun Chung, Li Jin, Bing Su, Shuhua Xu*. **2015. A 3.4-kb Copy-Number Deletion near EPAS1 Is Significantly Enriched in High-Altitude Tibetans but Absent from the Denisovan Sequence. Am.J.Hum.Genet. 97(1):54-66. (co-first)**
3. Haiyi Lou, Shilin Li, Wenfei Jin, **Ruiqing Fu**, Dongsheng Lu, Xinwei Pan, Huaigu Zhou, Yuan Ping, Li Jin and Shuhua Xu*. **2015. Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. European Journal of Human Genetics. 23:536-542.**
4. Lian Deng, Boon Peng Hoh, Dongsheng Lu, **Ruiqing Fu**, Maude E. Phipps, Shilin Li, Ab Rajab Nur-Shafawati, Wan Isa Hatin, Endom Ismail, Siti Shuhada Mokhtar, Li Jin, Bin Alwi Zilfalil, Christian R. Marshall, Stephen W. Scherer, Fahd Al-Mulla, Shuhua Xu*. **2014. The population genomic landscape of human genetic structure, admixture history and local adaptation in Peninsular Malaysia. Hum Genet. 133(9):1169-1185**