

## Jingru Shi

Female. MS degree candidate  
School of life Science, East China Normal University.  
500 Dongchuan Road, Shanghai, China, 200241  
Email: jingrushijane@gmail.com  
Tel : +86-18019230617



### Objective

A highly motivated individual, trained in both **mathematics** and **biology**, with good programming skills and problem solving abilities. Focusing on the causative gene identification and genotype-phenotype correlation analysis for rare diseases with **statistical methods** and **bioinformatics algorithms**, **clinical data standardization** and **multi-omics data** integration-based cancer classification. A member of “China and France jointly train graduate programs” **co-operated** by East China Normal University, École normale supérieure (ENS), ENS de Lyon, ENS de Cachan and ENS de Rennes.

### Education

**M.S. Candidate, East China Normal University** **2017-present**

**Research field: Bioinformatics** **Advisor: Prof. Tielu Shi**

Courses: Biochemical and Molecular Biology, Bioinformatics, Multivariate Statistics

**B.S, Shanghai University** **2013-2017**

**Major: Biomedical Engineering** **Advisor: Jiehui Jiang**

Courses: Linear algebra, Programming (C language), Complex Function and Integral Transformation, Probability and Random Processes, Data Structure and Fundamentals of Algorithm, Object-Oriented Programming A(C++), Biomedical Informatics A

### Research Experience

#### On-going Projects:

#### 1. Investigating rare disease mechanism based on multi-omics data integration and network Analysis

- Involved in constructing a standardized knowledge base of rare diseases by **multi-omics data** integration and large scale of text mining of rare disease-manifestation associations from **nearly 10 million** PubMed abstracts and **~ 1 million** full text articles from PMC (PubMed Central).
- Exploring the underlying mechanisms of rare diseases by gene-based disease network and phenotype based disease network analyses.

#### 2. Establishing a standardized knowledge base of birth defects

- Constructing a database of birth defects by multi-omics data integration and text mining from published literature and **over 100 million** electronic health records (**EHR**) (co-operated with Beijing Children`s Hospital), including associations between birth defect-manifestation, genotype frequency, pathogenic factors, prenatal diagnosis methods etc.
- In charge of the data standardization and text-mining.

### **3. Participating in the development of a function-based HPO (human phenotype ontology) system and an enhanced HPO system**

- Quantifying the similarity between disease phenotypes and gene molecular functions based on gene ontology.
- Conducting **text-mining** and standardizing phenotype terms.
- Mapping the **eHPO** to EHR for **EHR standardization** and data mining.

### **4. Classifying triple negative breast cancer (TNBC) based on multi-omics data integration**

- Exploring the effective methodology of multi-omics integration for TNBC classification.
- Revealing the difference of molecular functions between different TNBC subtypes and identifying the features and potential **therapeutic targets** for different TNBC subtypes.

### **Finished Projects:**

#### **1. Exploring the new pathogenic factors for Osteogenesis imperfecta disease based on genotype-phenotype association analysis**

- Identifying new pathogenic variations in causative genes of **Osteogenesis imperfecta rare disease**.
- Predicting novel pathogenic candidate genes based on protein-protein interaction, genotype-phenotype correlation and gene expression pattern. Manuscript is under review.

#### **2. Exploring novel pathogenic sites and novel pathogenic candidate genes for Berardinelli-Seip congenital lipodystrophy**

- Identifying new pathogenic variations in causative genes of **Berardinelli-Seip congenital lipodystrophy rare disease**.
- Predicting novel pathogenic candidate genes based on protein-protein interaction, genotype-phenotype association and gene expression pattern. Manuscript is under second around review.

#### **3. Text processing for Adult Attachment Interview (AAI)** 2018.7.1-2018.7.29

- A project in the summer school (La Rochelle University and Institut National de Recherche en Informatique et en Automatique (INRIA)) supported by **Campus France**.
- Taking courses about **“Document Analysis”**, “Document Understanding: Natural Language Processing and Information Retrieval”, “Data Science”, “GATE”, **“Natural Language Processing (NLP)”** in this summer school.
- Classifying the content of an AAI document into two categories: Interviewer and interviewee by using **a combination data processing algorithm**.

### **Skills**

- **Languages:** Chinese, English, French (basic)
- **Programming languages:** **R, Python, Shell** (basic)
- **Bioinformatics/ Data science:** Expertise in text mining. Experienced in processing and analysis of Gene Expression Data.

## **Publications**

- **Shi, J.**, Ren, M., Jia, J., Tang, M., Guo Y., Ni X. and Shi, T. Genotype-Phenotype association analysis reveals new pathogenic factors for Osteogenesis imperfecta disease. *Frontiers in pharmacology*. (Under review)
- Ren, M.<sup>#</sup>, **Shi, J.**<sup>#</sup>, Jia, J., Guo Y., Ni X. and Shi, T. Genotype-Phenotype correlations of Berardinelli-Seip congenital lipodystrophy and novel candidate genes prediction. *Frontiers in pharmacology*. (Co-first author), (Under second round review)

## **Honors and Awards (Recent 5 Years)**

- The Excellence Award in the 2019 APEC Voices of the Future Preliminary 2019
- Excellent Member of Academic Section 2017-2018
- First Academic Scholarship 2015-2016
- Innovation and Entrepreneurship Scholarship 2015-2016
- Excellent Student 2015-2016
- Second Academic Scholarship 2014-2015