Jinru Shi

Female. MS degree candidate
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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. Tieliu 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 Programing A(VC++), 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.

• 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 lipodystroph

• 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. (2018) Genotype-Phenotype association analysis reveals new pathogenic factors for Osteogenesis imperfecta disease. Frontiers in pharmacology. (Under review)

• Ren, M.[#], **Shi, J.**[#], Jia, J., Guo Y., Ni X. and Shi, T. (2018) 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