Chenkai Lv

MS candidate, School of life Science, East China Normal University, Shanghai, China
Email : lvchenkai0812@gmail.com
Tel : +86-18916838506

Objective

A highly motivated individual, trained in both **mathematics** and **biology**, with good programming and problem solving abilities, has an intense interest in exploring the **cause and treatment of cancer**. Focuses on learning **statistical methods** and developing **bioinformatics algorithms** for genotype-phenotype correlation analysis and **multi-omics** data integration-based cancer subtyping.

Education

M.S. Candidate, East China Normal University   **2016-present**
Major: Biomedical Engineering   **Advisor: Prof. Tieliu Shi**
Courses: Biochemical and Molecular Biology   Bioinformatics   Multivariate Statistics

B.S, Huazhong Agricultural University   **2012-2016**
Major: Bioinformatics   **Advisor: Prof. Feng Li & Prof. Guoliang Li**
Courses: Linear Algebra   Biochemistry   Discrete Mathematics   Mathematical Modeling
          Biostatistics   Biophysics   Molecular Biology   Bioinformatics   Chemoinformatics

Research Experience

Multi-omics data integration-based high risk neuroblastoma subtyping   **2018**

- Applied **autoencoder** method to integrate multi-omics(**gene expression and CNVs**) data to identify new subtypes in **high risk neuroblastoma** and validated robustness of our model with a supervised classifier in independent datasets.

- Compare several methods like **SVM**, **logistic regression**, **XGBoost** and **naive Bayes** to make our model get the best performance.

- Contributed to the study design, model conduct and manuscript draft.

Correlation analysis between structural variation genotype and phenotype   **2017-2018**

- Developed **BioSV**, a novel tool to call Structural Variations(SVs) from WGS data with high sensitivity, precision and resolution. Moreover, a **Bayesian model** was applied to comprehensively genotype SVs.

- Incorporated two methods, **XGBoost** and **Deep Neural Networks**, to build a scoring algorithm to evaluate the pathogenicity of CNVs based on twenty features such as **minor allele frequency**, **length** and **variation type**.

- Contributed to feature selection, programming and manuscript draft.

Integrative analysis uncovers regulatory relationships between multi-types of RNAs responsible for HCC tumorigenesis and candidate biomarkers   **2016-2018**

- Transcriptome profiling of **hepatocellular carcinoma** by jointly analyzing multi-types of RNAs, including mRNAs, lncRNAs, circRNAs and miRNAs to uncover the regulatory relationships(**ceRNA network**) responsible for tumorigenesis.

- Integrative analysis with blood and liver tissue samples to identify **circulating miRNAs** and candidate biomarkers for **biopsy**, moreover, we linked this to therapy and gave a list of drugs which could be beneficial to HCC prognosis.

- Contributed to study design, sequence data pre-progressing, data analysis and manuscript draft.

The next and the third generation sequencing data based genome assembly   2015-2016

- Integrated the **next generation** and the **third generation** whole genome DNA sequencing data to assemble *Ralstonia solanacearum* genome. This project involved extensive use of Perl programming language, several assembly softwares and some wet experiments.

Internship Experience

Roche Pharma Product Development

- Text mined the clinical trial management system records and extracted s**emantic predications** from them using Natural Language Processing.

- Built some **shiny apps** and **web servers** to help visualize clinical trial data and analysis clinical test schedule of patients

- Use different Machine Learning and statistical methods to optimize **investigation site selection**.

Jiaofu Scientific Research

- Established the pipelines of raw sequencing data analysis, such as ATAC-seq, ChIP-seq, RNA-seq, RIP-seq, etc.

Skills

Programming languages: Proficient in **R, Python, Shell, Awk, Perl,** Matlab.

Bioinformatics/ Data science: Expertise in processing and analysis of array and NGS-based transcriptomic data using standard statistical analysis. Experience in the usage of machine learning and deep learning algorithms. Experience in text mining and nature language processing skills.

Web server and database: Expertise in building web servers/pages by shiny or PHP. Familiar with SQL based databases.

Others: Cluster management and maintenance, GitHub(**https://github.com/Tening**)

Academic Conference Attended

2016.7   **Bioinformatics** Summer Training in Shirley Xiaole Liu's Lab, Shanghai, China

2017.8   Dragon Course **Bioinformatics** Training, Harbin, China

2018.2   **Oral presentation** in GSCG(Gold standard of Chinese Genome)

2018.3   Advanced Analyses for Understanding Rare Diseases

Publication

Published
- Zhang, L., **Lv, C.**, Jin, Y., Cheng, G., Fu, Y., Yuan, D., Tao, Yi., et al. (2018) Deep learning-based multi-omics data integration reveals two prognostic subtypes in high-risk neuroblastoma. *Frontiers in Genetics.(PMID:30405689)*
- Zhang, L., Jin, Y., Zheng, K., Wang, H., Yang, S., **Lv, C.**, Han, W., Yu, Y., Yang, Y., Geng, D., Yang, H., Shi, T., et al.(2018) Whole-Genome Sequencing Identifies a Novel Variation of WAS Gene Coordinating With Heterozygous Germline Mutation of APC to Enhance Hepatoblastoma Oncogenesis. *(PMID:30619485)*

On-going
- (Submitted) Zhang, L., Ding, W., **Lv, C.**, Liu, W., Shi, Y., Hou, C., Christopher E. Mason, et al. BioSV: an accurate structural variation caller and genotyper with high resolution.
- (Submitted) Zhang, L., Wang, C., **Lv, C.**, Lu, X., Xu, X., Shi, T., et al. Transcriptome profiling of hepatocellular carcinoma uncovers multi-types of dysregulated ncRNAs.
- Mechanistic biomarker discovery in Hepatocellular Carcinoma(**first author**)

Honors and Awards

- **International Taoist Medicine Certificate**   **2018.09**

- **National Scholarship Awards Candidate**   **2018.10**

- **Mathematical Modeling in central China, First Prize**   **2015.12**

Paper title: The reconstruction of the gene regulation networks and pathogenic mechanism of virus infection

- **Interdisciplinary Mathematical Contest in Modeling, Second Prize**   **2014.10**

Paper title: The prediction of metabolic concentration in cell

- **Merit student Award**   **2014.9**

- **College Taekwondo Competition in Hubei Province, Champion**   **2013.10**