

# Chenkai Lv

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## Objective

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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

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**M.S. Candidate, East China Normal University** **2016-present**

**Major: Biomedical Engineering** **Advisor: Prof. Tielu 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

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**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**

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### **Roche Pharma Product Development**

- Text mined the clinical trial management system records and extracted **semantic 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**

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**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

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- 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

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### 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

- (Under Revision) Zhang, L., Ding, W., **Lv, C.**, Liu, W., Shi, Y., Hou, C., Christopher E. Mason, et al. (2018) BioSV: an accurate structural variation caller and genotyper with high resolution. *Nucleic acids research*.
- (Submitted) Zhang, L., Wang, C., **Lv, C.**, Lu, X., Xu, X., Shi, T., et al. (2018) Transcriptome profiling of hepatocellular carcinoma uncovers multi-types of dysregulated ncRNAs. *EBiomedicine*.
- Mechanistic biomarker discovery in Hepatocellular Carcinoma(**first author**)

## Honors and Awards

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- **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**