Chenkai Lv

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Objective

A highly motivated individual, trained in both **informatics** and **biology**, with good programming and problem solving skills, has an intense interest in the field of **personalized healthcare**. Hoping to finding new insights of exploring the biomedical problems from the perspective of **data science**.

Education

M.S, East China Normal University   **2016-2019**
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   **2018-2019**

- Applied **autoencoder** method to integrate multi-omics(**gene expression and CNVs**) data to identify new subtypes in **high risk neuroblastoma** and validated robustness.

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

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

- Identify different types of SVs and evaluate the **pathogenicity** of each SV by **ML** methods

Integrative analysis of HCC RNA-Seq data   **2016-2018**

- Transcriptome profiling of **hepatocellular carcinoma** in mRNAs, lncRNAs, circRNAs and miRNAs to uncover the regulatory relationships responsible for tumorigenesis and to identify potential biomarkers for biopsy by finding candidate **circulating miRNAs**.

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

Work Experience

Jiaofu Scientific Research   **Intern**

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

Roche   **Statistical Programming Analyst**

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

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

- R End to End Project from SDTM data to ADaM data then to outputs(table listing graphs)

- Automated Clinical Study Report(CSR) generating system to support fast filing purpose

- Attending PrecisionFDA challenge to develop a ML model to predict the prognosis of Glioma

- Perform subgroup analysis of Herception global trial data to support China filing

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/Teninq**)

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 Conference

2019.9   Roche Advanced Analytics Network

2019.10   China Data Science Network

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)*
- Jin, Y., Guo, W., Hu, X., Liu, M., Xu, X., Hu, F., Lan, Y., **Lv, C.**, Fang, Y., Liu, M., Shi, T., Huang, J., et al.(2019) Static magnetic field regulates Arabidopsis root growth via auxin signaling. *(PMID:31591431)*

Honors and Awards

- **Outstanding Graduates of East China Normal University.**   **2019.05**

- **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**