# CURRICULUM VITAE

## WEIHAO MAI (麦伟浩)

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## EDUCATION

**Zhejiang University, Hangzhou, China**

*MRes. in Neurobiology*, GPA: 83.9/100 **Sep 2016 - present**

Supervisors: Dr. Shumin Duan (段树民) and Dr. Zhihua Gao (高志华)

**South China Normal University, Guangzhou, China**

*B.S. in biotechnology*, GPA: 86.9/100, ranking: 4/20 **Sep 2012 - June 2016**

## SUMMER / WINTER SCHOOLS

**Peking University, Beijing, China**

*Tutorial in Neuroscience and Artificial Neural Network* **July 2018**

- Understanding of modeling and statistical physics approach focusing on the information processing of neural circuits and networks

*Summer school on data science*, School of Mathematical Sciences **July 2017**

- Recent developments of graphical theory, reinforcement learning and applied mathematics in high performance data analysis

*Cognitive and neuroscience summer school*, Center for Life Sciences **July 2013**

- Understanding basic knowledges of modern neurobiology and cognitive neuroscience through lectures and laboratory touring

**Shanghai Jiao Tong University, Shanghai, China**

*Computational Neuroscience winter school*, Institute of Natural Sciences **Dec 2017**

- Introduction of modeling and experimental studies focusing on the information processing properties of individual neurons, neural circuits and networks, and systems
- Computer lab class: implementing Hodgkin–Huxley model in matlab

## RESEARCH EXPERIENCE

**Zhejiang University, Hangzhou, China** **Sep 2016 - present**

<u>Microglial specific metabolic gene expression feature</u>

- Purpose: data mining of RNA-seq data to better understand the metabolism function of microglia
- Methods:

- identified metabolic differences among microglia and other types of brain cells by spearman's rank correlation and principal component analysis (PCA)
- analyzed metabolic gene expression in microglial development data using the Markov clustering algorithm (MCL)

- Results & conclusion:
  - microglia possesses a unique metabolic gene expression feature among other brain cell types
  - microglial specific metabolic genes associated with glycolysis and increasingly expressed during development

Feature selection of disease specific microglial gene expression

- Purpose: determine biomarkers which regulate the microglial activation in Alzheimer's disease (AD)
- Methods: utilized machine learning (ML) methods to analyze two single cell data set from published articles of AD and neurodegeneration
  - applied t-Distributed Stochastic Neighbor Embedding (t-SNE) technique to determine specific microglia clusters in single cell RNA-seq data
  - performed feature selection using elastic net logistic regression with stability selection
  - assessed classification performance of feature selection by support vector machine (SVM) model
  - unravel the biological functions of biomarkers by Gene Ontology (GO) enrichment analysis
  - validation of selected genes expression in bulk RNA-seq neurodegeneration data sets
- Results & conclusion:
  - Key genes in activated microglia in AD or neurodegeneration are defense response related
  - ML-selected gene set exhibited microglia-specific expression pattern while there was no apparent difference in neuron and astrocyte
  - The expression pattern of the key genes were consistent among other bulk RNA-seq data
  - The analysis provided a new direction for determining biomarkers in scRNA-seq data and a new insight to uncover neurodegeneration mechanism

**China National GeneBank-Shenzhen, BGI-Shenzhen, Shenzhen, China** Mar 2015 – July 2016

*Joint training student*

Clopidogrel pharmacogenomics study

- Investigated single-nucleotide polymorphisms (SNPs) in over 1,800 patients treated by percutaneous coronary interventions (PCI)
- Applied PCA, logistic regression and survival analysis to detect SNPs associated with clopidogrel pharmacodynamic effects

## PUBLICATIONS

ZG Zhu, QQ Ma, HB Yang, L Miao, JT Wu, SJ Hao, S Lin, **WH Mai**, YZ Hao, N M. Shah, YQ Yu and SM Duan. The Substantia Innominata Acts as a Rage Nucleus in Mice. in preparation

F Meng, ZG Guo, YL Hu, **WH Mai**, ZJ Zhang, B Zhang, QQ Ge, HF Lou, JF Chen, SM Duan and ZH Gao. Restricting ecto-5'-nucleotidase-derived adenosine attenuates neuroinflammation and protects neuronal loss in Parkinson's disease models. ***Brain***, accepted

XM Liu, HS Xu, HQ Xu, QS Geng, **WH Mak**, Z Su, F Yang, T Zhang, R Gao, PP Jiang, HM Yang, J Wang, XQ Zhang, X Xu, XY Li, JY Chen, X Liu and SL Zhong. New genetic predispositions underlying cardiovascular outcomes among patients treated with clopidogrel and aspirin after percutaneous coronary intervention. ***Scientific Reports***, submitted

## HONORS AND AWARDS

- **Zhejiang University** Outstanding Graduate Student **2018**
- **Zhejiang University** Academic Scholarship **2016**
- **Zhejiang University** Outstanding Camper **2015**
- **South China Normal University** Extracurricular Research Certificate **2014**
- **South China Normal University** School Study Activist **2013**

## SKILLS

Computer: R (packages: ggplot2, caret, Seurat), Python (packages: scikit-learn, scipy, numpy), bash shell

Language: Chinese (native), English (TOEFL score: 98)