

Liangqun Lu

(808) 232-6356 | liangqunlu@gmail.com | <http://liangqunlu.github.io/liangqun.github.io/>

Education

University of Memphis

MS student in Computer Science (Main Advisor: Vasile Rus)

Thesis area: Machine Learning, Deep Learning, Natural Language Processing, Information Retrieval, Dialogue System and AutoTutor

Current GPA: 3.73

Memphis, TN

2017 - Present

University of Memphis

PhD student in Biology Department (Main Advisor: Dr. Bernie Daigle)

Dissertation area: Machine Learning, Biomarker Discovery and Bioinformatics, Biomedical Image Processing

Current GPA: 3.73

Memphis, TN

2016 - Present

University of Hawaii at manoa

M.S. in Molecular Biosciences and Bioengineering (Main Advisor: Lana Garmire)

Thesis area: Bioinformatics, Cancer Genomics and Data Integration

Thesis title: Multi-omic data integration to stratify population in hepatocellular carcinoma

GPA: 3.60

Honolulu, HI

2014 - 2016

China Agricultural University

M.S. in Bioinformatics

Thesis area: Bioinformatics, database construction and plant genomics

Thesis title: Functional database construction on Carbohydrate-active enzymes

GPA: 3.41

Beijing, China

2010 - 2013

China Agricultural University

B.S. in Biological Science

Thesis title: FK506 research as an adjuvant treatment of EAE in mice

GPA: 3.56

Beijing, China

2006 - 2010

Skills

Machine Learning / Deep Learning

Formal training in various aspects of machine learning, including feature reduction, regression, classification, clustering, bayesian network, recommendation system, reinforcement learning.

Be familiar with Deep Learning framework TensorFlow and Keras. Used deep learning architectures autoencoder and DNN in cancer datasets. Used Neural Network language model, Generative Adversarial Network and Reinforcement Learning in research projects..

Bioinformatics / Computational Biology and Cancer Bioinformatics

Formal training in bioinformatics, NGS and microarray analysis. Processed the cancer data from TCGA, ICGC and cBioPortal. And involved in driver gene research and cancer evolution.

Programming Languages

Extensive programming experience in my previous projects. Being familiar with R (Limma, ggplot2, caret, CMA) and Python (sklearn, pandas, tensorflow, keras). And have finished projects using perl, php, matlab and C++.

Web Development

Used ASP.NET MVC to build a new interface for CohMetrix webtool (<http://tool.cohmetrix.com/>). In 2017 HackMemphis, used Python Django to build a demon one-stop convenience website (<https://github.com/LiangqunLu/HackMemphis>), Ruby on Rails

Microbiology and Molecular Biology

Being familiar with the basic microbiology skills from instructing introductory microbiology course. Exposed to the RT-PCR, ELISA experiments and microarray chips in undergraduate training.

Experience

Bioinformatics Program, University of Memphis

Research Assistant

Memphis, TN

2017 - Present

Research on Large-scale Microarray Data Based Feature Selection For Improved Molecular Classification, Clinical Subgroup-Specific PTSD Classification and Biomarker Identification, Multi-omic data integration to discover subgroups at PTSD and Use of deep learning to predict survival in cancer.

Division of Imaging, Diagnostics, and Software Reliability, OSEL/CDRH/FDA

Summer Intern / ORISE Fellow

Silver Spring, MD

2018 Summer

Worked on 'Generating Synthetic Electrocardiograms (ECGs) for Training Arrhythmia Detection Algorithms', in which I tried DCGAN/EBGAN/BEGAN/WGAN to generate single beat or segments in ECG signals.

Institute for Intelligent Systems, University of Memphis

Summer Intern

Memphis, TN

2017 Summer

Summer internship on using ASP.NET MVC (Model-View-Controller, C#) structure to build a new interface for CohMetrix webtool (<http://tool.cohmetrix.com/>), including recaptchas implementation and Socket IP connection.

Department of Biology, University of Memphis

Teaching Assistant

Memphis, TN

2016

Instructed the introductory Microbiology. Educated students to know aseptic techniques, use of microscope, bacteria identification and functions of antibiotics

Epidemiology Program, University of Hawaii Cancer Center
Research Assistant

Honolulu, HI
2014 - 2016

Worked on Time Series miRNA-mRNA integrated analysis reveals critical miRNAs and targets in macrophage polarization, and integrated RNA-seq, miRNA-seq and Methylation datasets to classify patients in liver cancer, and deciphering the impact of driver genes on transcriptions and survival

Department of Computational Biology, Beijing Computing Center
Bioinformatics Engineer

Beijing, China
2013 - 2014

Being responsible for RNA-seq analysis, including pipeline management and customer service. Finished analysis projects, such as on rice, cows and pigs. Instructed RNA-seq analysis in the next-generation sequencing workshop.

Bioinformatics Program, China Agricultural University
Research Assistant

Beijing, China
2010 - 2013

Built the database of carbohydrate-active enzymes in plants using PHP and Mysql. Analyzed the conservative domains in five main categories of carbohydrate-active enzymes and predicted new members and visualized the information Gene Ontology, KEGG pathways, location and function.

Department of Plant Science, China Agricultural University
Teaching Assistant

Beijing, China
2011

Helped instruct the course Bioinformatics, and answered questions from students

Publications

Peer reviewed journal articles

1. Chaudhary Kumardeep *, Olivier B. Poirion *, **Liangqun Lu**, Travers Ching, and Lana X. Garmire. 2017. "Multi-modal meta-analysis of 1494 hepatocellular carcinoma samples reveals vast impacts of consensus driver genes on phenotypes", American Association for Cancer Research. (In press)
2. Chaudhary Kumardeep *, Olivier B. Poirion *, **Liangqun Lu**, and Lana X. Garmire. 2017. "Deep Learning Based Multi-Omics Integration Robustly Predicts Survival in Liver Cancer." Clinical Cancer Research: An Official Journal of the American Association for Cancer Research, January. American Association for Cancer Research, clincanres.0853.2017.
3. **Liangqun Lu** *, Sara McCurdy *, Sijia Huang, Xun Zhu, Karolina Peplowska, Maarit Tiirikainen, William A. Boisvert, and Lana X. Garmire. 2016. "Time Series miRNA-mRNA Integrated Analysis Reveals Critical miRNAs and Targets in Macrophage Polarization." Scientific Reports 6 (December): 37446.

Conference abstracts/posters

1. Clinical Subgroup-Specific PTSD Classification and Biomarker Identification. Big Data in Precision Health 2018, Stanford, CA, May 23 - 24, 2018
2. Clinical Subgroup-Specific PTSD Classification and Biomarker Identification. MCBIOS 2018, Starkville, MS, March 29 - 31, 2018

3. Large-scale Microarray Data Based Feature Selection For Improved Molecular Classification. 16th annual UT-KBRIN Bioinformatics Summit 2017, Burns, TN, April 21-23, 2017
4. Large-scale Microarray Data Based Feature Selection For Improved Molecular Classification. MCBIOS 2017, Little Rock, AR, Mar. 23-25, 2017
5. Association analysis of driver genes of hepatocellular carcinoma with cancer hallmarks. 13th Rocky Mountain Bioinformatics Conference, Aspen, CO, Dec.10-13, 2015
6. Integrative analysis of RNA-seq and miRNA-seq revealed functional miRNAs in the macrophage. Jabsom Symposium, Honolulu, HI, Apr. 15, 2015
7. Pan-cancer analysis based on transcriptional response reveals similarity among different human cancers. The sixth National Conference on Bioinformatics and Systems Biology and International Workshop on Advanced Bioinformatics, Nanjing, China, Oct.06-09, 2014

Other activities

2015 Volunteer at Humane Society, Honolulu