Liangqun Lu

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Education

University of Memphis   **Memphis, T**N
MS Program in Computer Science (Main Advisor: Dr. Vasile Rus)   *2017 - 2019*
Thesis area: Machine Learning, Deep Learning, Natural Language
Processing, Information Retrieval, Dialogue System and
AutoTutor
Current GPA: 3.64

University of Memphis   **Memphis, T**N
PhD Program in Biology Department (Main Advisor: Dr. Bernie Daigle, Jr.)   *2016 - 2019*
Dissertation area: Machine Learning, Biomarker Discovery and
Bioinformatics, Biomedical Image Processing
Current GPA: 3.64

University of Hawaii at manoa
MS in Molecular Biosciences and Bioengineering (Main Advisor: Dr. Lana Garmire)   **Honolulu, H**I
Thesis area: Bioinformatics, Cancer Genomics and Data   *2014 - 2016*
Integration
Thesis title: Multi-omic data integration to stratify population in hepatocellular
carcinoma
GPA: 3.60

China Agricultural University   **Beijing, Chin**a
MS in Bioinformatics   *2010 - 2013*
Thesis area: Bioinformatics, database construction and plant
genomics
Thesis title: Functional database construction on Carbohydrate-active enzymes
GPA: 3.41

China Agricultural University   **Beijing, Chin**a
BS in Biological Science   *2006 - 2010*
Thesis title: FK506 research as an adjuvant treatment of EAE in mice
GPA: 3.56

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.

Generative Adversarial Network
Research Experience in GAN, including DCGAN, WGAN and EBGAN. In "GAN-based ECG simulation to enhance AF classification", made use of GANs to generate single beat and generate long segments using magnitude and phase.

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.

Natural Language Processing
Formal training in information retrieval and natural language processing, involved in projects to build a information retrieval system and generate dialogue systems using RNN.

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++. Practiced leetcode algorithm questions using JAVA.

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), had experience on Ruby on Rails and JAVA Spring MVC.

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   **Memphis, T**N
Research Assistant   *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 Integrative
Analysis of Histopathological Images and Genomic Data Predicts Hepatocellular
Carcinoma Prognosis.

Division of Imaging, Diagnostics, and Software Reliability, OSEL/CDRH/FDA   **Silver Spring, MD**
Summer Intern / ORISE Fellow   *2018 Summer*
Worked on 'Generating Synthetic Electrocardiograms (ECGs) for Training Arrhythmia
Detection Algorithms', in which I tried DCGAN/EBGAN/BEGAN/WGAN to generate single
beats and segments in ECG signals.

Institute for Intelligent Systems, University of Memphis   **Memphis, T**N
Summer Intern   *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   **Memphis, T**N
Teaching Assistant   *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   **Honolulu, H**I
Research Assistant   *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   **Beijing, China**
Bioinformatics Engineer   *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   **Beijing, China**
Research Assistant   *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   **Beijing, China**
Teaching Assistant   *2011*
Helped instruct the course Bioinformatics, and answered questions from students

Publications

Manuscripts in preparation

1. Liangqun Lu, Kevin Townsend, Bernie Daigle, Jr. . Large-scale Microarray Data Based Feature Selection For Improved Molecular Classification
2. Liangqun Lu, Bernie Daigle, Jr. . Prognostic Analysis of Histopathological Images Using Pre-Trained Convolutional Networks
3. Liangqun Lu, Bernie Daigle, Jr. . Clinical Subgroup-Specific PTSD Classification and Biomarker Discovery
4. Liangqun Lu, Bernie Daigle, Jr. . Multi-omic data integration to discover subgroups of PTSD

Peer reviewed journal articles

1. Chaudhary Kumardeep *, Olivier B. Poirion **, Liangqun Lu**, Sijia Huang, Travers Ching, and Lana X. Garmire. 2018. "Multi-Modal Meta-Analysis of 1494 Hepatocellular Carcinoma Samples Reveals Significant Impact of Consensus Driver Genes on Phenotypes." Clinical Cancer Research: An Official Journal of the American Association for Cancer Research, September.
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. Prognostic Analysis of Histopathological Images Using Pre-Trained Convolutional Networks, Birmingham, AL, March 28 – 30, 2019
2. Generating ECG signals with Generative Adversarial Networks, Silver Spring, MD, August 01, 2018
3. Clinical Subgroup-Specific PTSD Classification and Biomarker Identification. Big Data in Precision Health 2018, Stanford, CA, May 23 - 24, 2018
4. Large-scale Microarray Data Based Feature Selection For Improved Molecular Classification. 16th annual UT-KBRIN Bioinformatics Summit 2017, Burns, TN, April 21-23, 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