

# LONG WANG

[longw@andrew.cmu.edu](mailto:longw@andrew.cmu.edu) | (412) 880-9374 | [Linkedin](#)

## EDUCATION

<b>Carnegie Mellon University (CMU)</b> Pittsburgh, PA	May 2018(expected)
Master of Science in Computational Biology	
<b>Huazhong Agricultural University (HZAU)</b> Wuhan, China	Jul 2015
Bachelor of Science in Bioinformatics, Valedictorian	

## WORK EXPERIENCE

<b>SemanticMD, Inc.</b> Houston, TX.	May 2017–Aug 2017
<i>Deep Learning R&amp;D Intern</i>	
<ul style="list-style-type: none"><li>Preprocessed on images and videos to filter out essential features using computer vision algorithms</li><li>Developed and implemented machine learning pipelines to 1. detect sperm cells from cell cluster images and recognize their classes; 2. identify diabetic retinopathy and glaucoma patients using optical coherence tomography images; 3. classify two-chambers vs. four-chambers ultrasound videos.</li></ul>	
<b>Jianbing Yan's Lab</b> <i>National Key Laboratory of Crop Genetic Improvement.</i> Wuhan, China.	Aug 2014–Jul 2015
<i>Research Assistant</i>	
<ul style="list-style-type: none"><li>Developed a tree-based ensemble method to detect SNP associations with rare variants in maize</li><li>Participated in maize genomes assembly (hybrid PacBio and Illumina sequencing data)</li></ul> <p>Have published one paper as a participating author in <i>Nature Communication</i>.</p>	
<b>Lingling Chen's Lab</b> <i>College of Informatics, HZAU.</i> Wuhan, China.	Jul 2013–Jun 2016
<i>Research Assistant</i>	
<ul style="list-style-type: none"><li>Developed an ensemble model to infer transcriptional regulation using RNA-seq in Prokaryotes.</li><li>Developed a computational method to predict protein-protein interaction network; constructed the protein-protein pipeline of <i>Bacillus licheniformis</i> WX-02; analyzed network features.</li><li>Updated sequence and annotation of <i>Bacillus licheniformis</i> WX-02; analyzed asRNAs regulation under salt condition.</li></ul> <p>Have published two papers as a participating author in <i>FEBS Letters</i> and <i>Scientific Reports</i>, respectively and a paper as the first author has been accepted in <i>Current Bioinformatics</i>.</p>	

## SELECTED COURSE PROJECTS

<b>3D Structure Reconstruction of Human Chromosomes from Hi-C data</b> (Python   Group)
<ul style="list-style-type: none"><li>• Extracted interaction frequency information from Hi-C data</li><li>• Estimated the 3D position for each nucleosome bead by posing the distance information to a constraint convex problem (solved two objective functions via gradient descent)</li><li>• Visualized 3D structure results in PYMOL</li></ul>
<b>Machine learning in Large datasets</b> (Independent)
<ul style="list-style-type: none"><li>• Applied sequential analysis on one-month Wikipedia data (set filters and MapReduce pipeline)</li><li>• Design an efficient way to run regularized logistic regression on stochastic gradient descent</li><li>• Implemented automatic reverse-mode differentiation for multilayer perceptron and long short term memory (LSTM) on large datasets</li></ul>
<b>Retrieval Algorithms for Search Engine</b> (Java   Independent)
<ul style="list-style-type: none"><li>• Implemented Boolean retrieval, BM25 and Indri ranking, and learning-to-rank capabilities.</li><li>• Implemented query expansion capabilities(pseudo-feedback) and diversification (PM-2 and xQuAD).</li><li>• Evaluate performance by calculating and comparing different metrics.</li></ul>

## SKILLS

**Programming:** Java, Python, R, Perl, Bash, Matlab, Golang, C.  
**Tools:** Git, Hadoop, Spark, Scikit-learn, OpenCV, Tensorflow, Weka, GATK.

## ACADEMIC HONORS AND AWARDS

<b>MSCB Merit Fellowship</b> , <i>Computational Biology Department. CMU, USA.</i>	Aug 2017
<b>Honorable Mention, Interdisciplinary Contest in Modeling</b> , <i>Comap Inc. USA.</i>	Apr 2014
<b>First Prize, Chinese Undergraduate Mathematical Contest in Modeling</b> , <i>Ministry of Education, CN.</i>	Nov 2013
<b>National Scholarship</b> , <i>Ministry of Education, China. (for top 0.5% students)</i>	May 2012