**Haoyun Lei** E-mail: [haoyunl@andrew.cmu.edu](http://haoyunl@andrew.cmu.edu) **|** Phone: +1(412)969-3798

LinkedIn: [linkedin.com/in/haoyunlei/](https://www.linkedin.com/in/haoyunlei/)  **|**  Website: [cs.cmu.edu/~haoyunl/](http://www.cs.cmu.edu/~haoyunl/)

|  |
| --- |
| **EDUCATION** |
| **Carnegie Mellon University Aug 2016 – May 2021**  **Ph.D. in Computational Biology (**expected)  Joint Carnegie Mellon-University of Pittsburgh Ph.D. Program in Computational Biology  Computational Biology Department, School of Computer Science  **Huazhong University of Science and Technology Sep 2008 – Jun 2012**  **B.S. in Biological Science**  College of Life Science and Technology |
| **SKILLS** |
| **Programming Languages: Python (proficient), R (fluent), MATLAB (fluent), Shell (fluent), Java (familiar)** **Technical Skills and Tools: Machine Learning (scikit-learn), Deep Learning (PyTorch, TensorFlow), Bioinformatics** **(GATK, SAMtools, bedtools CNVkit etc.), Data Analysis (Numpy, Scipy, Pandas), Data Visualization (Matplotlib,** **Seaborn), Combinatorial Optimization (Gurobi, SCIP), Cloud Computing (AWS), Web Development (HTML/CSS/JS)** **WORK EXPERIENCE** |
| **Laboratory Corporation of America Holdings (LabCorp)** May 2020 – Jul 2020**Bioinformatics Summer Intern Westborough, MA** Converting Free-text Patient Data to ICD Codes using Natural Language Processing (PyTorch, TensorFlow)   * Explored language tools (**BioBERT**, **medaCy**) to annotate and chunk the important information in medical text * Fine-tuned **BERT** model on ICD-10 code classification at chapter and block (first three characters) level * Designed a **two-step BERT** model to predict multiple ICD-10 codes in LabCorp’s patient medical text * Managed to work on a small dataset and reached **84%** on multi-label clarification at chapter level   Benchmarking CNV Detection Tools (Python, R, Perl)   * Tested and compared public CNV detection tools for calling CNVs in targeted NGS data with a very small panel * Explored combinations of parameters of tools to increase true positive detection in **CNVkit**, **DECoN** & **CoNVaDING** * Designed algorithms to rescue and recover CNVs with a weaker signal in a very small panel of targets * Reached over **94%** in sensitivity while kept specificity around **90%** |
| **RESEARCH EXPERIENCE** |
| **Ph.D. Thesis:** Integrating Multiple Data Types to Infer Tumor Evolution (Python, R, MATLAB)May 2017 - Present   * Created a mixed membership model for the **Non-negative Matrix Factorization (NMF)** problem * Developed an efficient **coordinate descent algorithm** to solve the NMF problem in **Python** * Designed a **Mixed Integer Linear Programming Model** with the popular optimization solvers of **Gurobi** and **SCIP** * Reached **~95% accuracy**, surpassing exisiting methods     Detection of Cancer Types and Relevant Features using Deep Learning with RNA-seq Data (PyTorch) Spring 2020   * Designed and fine-tuned **1D CNN**, **2D CNN** and a **hybrid CNN** models to detect cancer types * Designed a **Stacked Denoising Autoencoder Classifier** to improve the detections (**~96% accuracy**) * Applied **embedding** method to find implicit relationships between cancer samples and genes   Footprint Match and Pattern Detection using Machine Learning (scikit-learn)Spring 2017   * Classified ~ 10,000 footprint images with **Neural Network** and **SVM** using **scikit-learn (~95% accuracy)** * Applied the **Scale-invariant feature transform (SIFT)** algorithm to the match of saved and new images * Extracted the image patterns with **K-Means** and **Gaussian Mixture Model**   Predict Proto Genes using **Logistic Regression, Naïve Bayes Classifier** and **Decision Tree** Spring 2017  Copy Number Extraction from DNA Sequencing Data with **Numpy**, **Scipy** and **Regular Expression**  Fall 2016  Model Gene Regulatory Network by combining **Boolean network** and **Ordinary Differential Equation** models Fall 2016 |