**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: [www.cs.cmu.edu/~haoyunl/](http://www.cs.cmu.edu/~haoyunl/)

|  |
| --- |
| **SUMMARY** |
| I design algorithm of optimization to study cancer genetics, inferring phylogeny for tumor evolution from multiple types of genomic data. I also work on interdisciplinary projects of machine learning (ML) and deep learning (DL), and their applications to cancer genomics. I am looking for a full-time job related to Bioinformatics, Computational Biology, ML and DL, etc. |

|  |
| --- |
| **EDUCATION** |
| **Carnegie Mellon University (USA) Aug 2016 - May 2022**  **Ph.D. in Computational Biology (Mentor: Dr. Russell Schwartz) (**expected)  Computational Biology Department, School of Computer Science  **M.Sc in Machine Learning,** Machine Learning Department, School of Computer ScienceAug 2020 - Dec 2021    **Huazhong University of Science and Technology (China) 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 * 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** * Recovered CNVs with a weaker signal in a very small panel of targets with over **94%** in sensitivity and **90%**  in specificity |
| **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 **tumor evolution** problem using **bulk** and **single-cell sequencing** data * Developed an efficient **coordinate descent algorithm** to solve the DNA and RNA deconvolution problem in **Python** * Designed a **Mixed Integer Linear Programming Model** with the popular optimization solvers of **Gurobi** and **SCIP** * Designed a comprehensive simulator for multiple types of mutations in DNA-seq data with phylogenetic progress   Function Specific Representational Similarity Inference in the Brain (PyTorch) Spring 2021   * Designed **probabilistic graphical model** for brain fMRI data * Developed neurons-independent and neurons-dependent network to study function-specific representational similarity * Recovered similar structure in correlated functional areas in the brain   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  Model Gene Regulatory Network by combining **Boolean network** and **Ordinary Differential Equation** models Fall 2016 |
| **TEACHING EXPERIENCE** |
| **Algorithm and Advanced Data Structure Aug 2019 - Dec 2019**  **Algorithms: Breadth-first Search, Depth-first Search, Binary Search, Quick Sort, Merge Sort etc.**  Data Structure: Linked List, Graph, Tree, Stack, Queue, Heap, ArrayList, Hash Table etc.  Concepts: Recursion, Dynamic Programming, Time and Space Complexity, NP-problem etc.  **Laboratory Methods for Computational Biologists** Aug 2018 - Apr 2019  Designed a faster pipeline combining multiple new analysis tools to detect differentially expressed genes in RNA-seq data |
| **PUBLICATIONS & TALKS** |
| **Articles**  **Lei, H.**,Guo, A. X., Tao, T., Ding, K., Fu, X., Oesterreich, S., Lee, V. A. and Schwartz, R. (2022) Semi-deconvolution of  bulk and single-cell RNA-seq data with application to metastatic progression in breast cancer. (*Submitted to ISMB 2022*)  Fu, X., **Lei, H.**, Tao, Y., and Schwartz, R. (2022). Reconstructing clonal lineage trees incorporating single nucleotide  variants (SNVs), copy number alterations (CNAs), and structural variations (SVs). (*Submitted to ISMB 2022*)  **Lei, H.**, Gertz, E. M., Schäffer, A. A., Fu, X., Tao, Y., Heselmeyer-Haddad, K., ..., and Schwartz, R. (2021). Tumor  heterogeneity assessed by sequencing and fluorescence in situ hybridization (FISH) data.  *Bioinformatics 37 (24)*, 4704-4711  Fu, X., **Lei, H.**, Tao, Y., Heselmeyer-Haddad, K., Li, G., Shi, X., Xu, L., Torres, I., Hou, Y., Wu, K., Dean, M., Ried, T.,  and Schwartz, R. (2021). Joint clustering of single cell sequencing and fluorescence in situ hybridization data to infer  tumor copy number phylogenies.  *Journal of Computational Biology 28 (11)*, 1035-1051  Tao, Y., **Lei, H.**, Fu, X., Lee, A. V., Ma, J., and Schwartz, R. (2020). Robust and accurate deconvolution of tumor  populations uncovers evolutionary mechanisms of breast cancer metastasis.  ISMB2020, *Bioinformatics, 36,* i407-i416,  **Lei, H**., Lyu, B., Gertz, E., Schäffer, A. A., Shi, X., Wu, K., Li, G., Xu, L., Hou, Y., Dean, M., and Schwartz, R. (2020).  Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data.  RECOMB 2019, *Journal of Computational Biology, 27(4)* 565-598.  Tao, Y., **Lei, H.**, Lee, A. V., Ma, J., and Schwartz, R. (2020). Neural Network Deconvolution Method for Resolving  Pathway-Level Progression of Tumor Clonal Expression Programs with Application to Breast Cancer Brain Metastases.  *Frontiers in Physiology, 11*, 1055.  Tao, Y., **Lei, H.**, Lee, A. V., Ma, J., and Schwartz, R. (2019). Phylogenies derived from matched transcriptome reveal the  evolution of cell populations and temporal order of perturbed pathways in breast cancer brain metastases.  ISMCO 2019 *(pp. 3-28). Springer, Cham*.  **Abstracts & Talks**  **Lei, H.**, Gertz, E. M., Schäffer, A. A., Fu, X., Tao, Y., Heselmeyer-Haddad, K., … and Schwartz, R. (2020, July). Tumor  heterogeneity assessed by sequencing and fluorescence in situ hybridization (FISH) data.  Conference on Intelligent System for Molecular Biology (ISMB), virtual  Fu, X., **Lei, H.**, and Schwartz, R. (2020, July). Joint Clustering of single cell sequencing and fluorescence in situ  hybridization data to infer tumor copy number phylogenies. ISMB, virtual.  **Lei, H**., Lyu, B., Gertz, E., Schäffer, A. A., Shi, X., Wu, K., Li, G., Xu, L, Hou, Y., Dean, M., and Schwartz, R. (2019,  May). Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. International Conference  on Research in Computational Molecular Biology (RECOMB), Washington, DC.  **Lei, H**., Lyu, B., Gertz, E. M., Schäffer, A. A., and Schwartz, R. (2018, October). Tumor Copy Number Data  Deconvolution Integrating Bulk and Single-cell Sequencing Data. In *2018 IEEE 8th International Conference on*  *Computational Advances in Bio and Medical Sciences (ICCABS)*, Las Vegas, NV.  **Lei, H.,** Roman, T., Eaton, J., and Schwartz, R. (2018, July). Deconvolution of tumor copy number data using bulk and  single-cell sequencing data. ISMB, Chicago, IL.  **Lei, H.,** Roman, T., Eaton, J., and Schwartz, R. (2018, April). New directions in deconvolving genomics mixtures of copy  number variation data. SIAM Conference on Discrete Mathematics, Denver, CO. |