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| **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 interested in studying cancer or clinical data using bioinformatics, ML and DL. |

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| **EDUCATION** |
| **Carnegie Mellon University Aug 2016 – May 2021**  **Ph.D. in Computational Biology (Mentor: Dr. Russell Schwartz) (**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 existing 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  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**  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., Schӓffer, 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.  **Lei, H.**, Gertz, E. M., Schäffer, A. A., Fu, X., Tao, Y., Heselmeyer-Haddad, K., … and Schwartz, R. (2020). Tumor  heterogeneity assessed by sequencing and fluorescence in situ hybridization (FISH) data.  *bioRxiv*  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.  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., Schӓffer, 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., Schӓffer, A. A., & 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. Conference on Intelligent System for Molecular Biology (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. |