Chieh (Jessica) Lin

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Education

- **Carnegie Mellon University** — Pittsburgh, PA
  PhD Candidate in Machine Learning — *Sept. 2015 - May 2020 (expected)*
  Advisor: Ziv Bar-Joseph
  GPA 3.97/4.0

- **National Taiwan University** — Taipei, Taiwan
  M.S. in Computer Science — *Sept. 2013 - June 2014*
  Advisor: Yufeng Jane Tseng
  GPA 3.98/4.0

- **National Taiwan University** — Taipei, Taiwan
  B.S. in Computer Science — *Sept. 2009 - June 2013*
  Rank 1/141
  GPA 3.97/4.0
  Student Representative of graduation work and certificate reception

Professional Experience

- **Healthcare Predictive Analytics Research Intern** — Cambridge, MA
  Summer Internship in Philips — *June 2017 - Aug. 2017*
  Developed logistic regression and LSTM model for mortality/sepsis prediction for ICU patient data (including clinical data, gene expression data, protein data)

- **Research Assistant** — Taipei, Taiwan
  Supervisor: Prof. Yufeng Jane Tseng — *Sept. 2014 - June 2015*
  Participate in the P450 Project (rule-based classification models) and Breathomic Database project (text-mining)

- **Part-Time Research Assistant** — Taipei, Taiwan
  Supervisor: Dr. Tsan-sheng Hsu — *Oct. 2012 - Mar. 2013*
  Help to prepare the teaching material for course Theory of Computer Games (about designing AI for 2-player competitive games

- **Programmer** — Taipei, Taiwan
  Summer Internship in Nexcom corporation — *July 2010*
  Helped to complete keyboard mapping project using VB.NET.

Research Projects

- **Single-cell Lineage Tracing with mutations and expression Data** Pittsburgh, PA
  Advisor: Ziv Bar-Joseph *Aug. 2018 - Aug. 2019*

  We reconstruct single-cell lineage trees with both expression data and CRISPR-Cas9 mutation data. We showed that using both types of data together could help improve the understanding of cell differentiation process and resulting in better cell lineage reconstruction. Manuscript under review in Nature Communications.

- **Cell lineage inference from SNP and scRNA-Seq data** Pittsburgh, PA
  Advisor: Ziv Bar-Joseph *Mar. 2018 - Aug. 2018*

  We develop a method to detect significant, cell type specific, sequence mutations from scRNA-Seq data. We showed that integrating mutations data with expression data further improves the accuracy of the reconstructed models for distinguishing cell types. Manuscript accepted by Nucleic Acid Research .

- **Continuous Assignment of scRNA-Seq Data by CS-HMM** Pittsburgh, PA
  Advisor: Ziv Bar-Joseph *Nov. 2016 - June 2018*

  We develop a Continuous-State Hidden Markov Model (CS-HMM) for analyzing single-cell RNA-Seq mouse lung differentiation data. Assign cell continuously on each differentiation path and perform biological analysis on the differential expressed genes on each path to study cell lineage differentiation. This model is further extended to detect TF activation time. For application, we collaborate with Darrell Kotton's lab from Boston University to improve differentiation protocal of lung cell types. 1 manuscript accepted by Bioinformatics, 1 manuscript under revision by Cell Stem Cell, and 1 manuscript under revision by PLOS Computational Biology

- **Single-Cell RNA-Seq data analysis with Neural Networks** Pittsburgh, PA
  Advisor: Ziv Bar-Joseph *Mar. 2016 to July 2017*

  We design new Neural Network architectures for dimensionality reduction (learning embeddings) of scRNA-Seq data by using domain knowledge of protein-protein interaction (PPI) and transcrition factor-target (TF-target) relationships. We verify the performance by performing clustering and retrieval on the reduced dimension. We also perform functional analysis on the top-weighted genes of neural networks. Manuscript published in Nucleic Acids Research

- **Drug Synergy Predication Challenge** Pittsburgh, PA
  Advisor: Ziv Bar-Joseph *Sep. 2015 to Mar. 2016*

  We develop a machine learning model to predict the drug synergy effect and optimize it with proximal coordinate descent. We participate in AstraZeneca-Sanger Drug Combination Predication DREAM Challenge. Consortium paper has been published on Nature Communications.

- **Breathomic Database** Taipei, Taiwan
  Advisor: Yufeng Jane Tseng *Feb. 2015 to June 2015*

  We build a breathomics database for doctors to look up information for exhaled molecules and breath diseases. We perform text-mining to look for the study design information from abstracts of breathomics publications. Manuscript under review by DATABASE

- **P450 Project**   Taipei, Taiwan
  Advisor: Yufeng Jane Tseng   *Nov. 2014 to Feb. 2015*

  Rule-based machine learning models are built to predict the inhibitors for P450 isomers. Models achieve better accuracy and sensitivity than previous models. 2 manuscript accepted (Journal of Chemical Information and Bioinformatics)

- **PolymerName2Structure project**   Taipei, Taiwan
  Advisor: Yufeng Jane Tseng   *July 2013 to June 2014*

  We convert polymer names to unique repeating units by using machine learning methods to predict the polymerization method. Used invented algorithms for simulating process of synthesizing monomers into polymers. System can accurately predict simple polymer structures with ¿ 0.9 accuracy. Process incorporates data mining, text mining, and computer-aided material design in the brand new polymer informatics field. Manuscript in preparation.

- **Computer-aided drug design projects**   Taipei, Taiwan
  Advisor: Yufeng Jane Tseng   *Sep. 2012 to June 2013*

  We propose candidate molecules that could be new drugs for cancer and schizophrenia drugs by performing computational techniques including fragment docking, virtual screening, LeadOp, LeadOp+R. Target proteins are Topoisomerase II and D-amino acide oxidase (DAO) proteins. The top-ranked molecules have been confirmed more effective by wet-lab experiments.

Selected Publications

- Hamim Zafar*, <u>**Chieh Lin**</u>*, Ziv Bar-Joseph, **Single-cell Lineage Tracing by Integrating CRISPR-Cas9 Mutations with Transcriptomic Data** (* equally-contributed, order determined by coin flip), under review in Nature Communications, 2019

- Killian Hurley, Jun Ding, ... , <u>**Chieh Lin**</u>, ... , Ziv Bar-Joseph, and Darrell N Kotton, **Single-cell time-series mapping of cell fate trajectories reveals an expanded developmental potential for human PSC-derived distal lung progenitors**, under review in Cell Stem Cell, 2019

- <u>**Chieh Lin**</u>, Jun Ding, Ziv Bar-Joseph, **Inferring TF activation order in time series scRNA-Seq studies**, under revision in PLOS Computational Biology, 2019

- Jun Ding, <u>**Chieh Lin**</u>, Ziv Bar-Joseph, **Cell lineage inference from SNP and scRNA-Seq data**, Nucleic Acids Research, 2019

- <u>**Chieh Lin**</u>, Ziv Bar-Joseph, **Continuous State HMMs for Modeling Time Series Single Cell RNA-Seq Data**, Bioinformatics, 2019

- <u>**Chieh Lin**</u>, Siddhartha Jain, Hannah Kim, Ziv Bar-Joseph, **Using neural networks for reducing the dimensions of single-cell RNA-Seq data**, Nucleic Acids Research, 2017

Other Publications

- Bo-Han Su, ... , **Chieh Lin**, ... , Yufeng J. Tseng, **Human Breathomics Database**, under revision in DATABASE, 2019

- Killian Hurley, Anjali Jacob, Jun Ding, ... , **Chieh Lin**, ... , Ziv Bar-Joseph, and Darrell N Kotton, **Single-Cell Transcriptomic Analysis of Type 2 Alveolar Epithelial Cell Differentiation from Induced Pluripotent Stem Cells: An Emerging Tool to Model Interstitial Lung Diseases.**, American Thoracic Society, C28. PATHWAYS OF LUNG MORPHOGENESIS abstract 2019

- Hamim Zafar, **Chieh Lin**, Ziv Bar-Joseph, **Single-cell Lineage Tracing by Integrating CRISPR-Cas9 Mutations with Transcriptomic Data**, ISMB/ECCB abstract, 2019

- Bo-Han Su, ... , **Chieh Lin**, ... , Yufeng J. Tseng, **An efficient computer-aided structural elucidation strategy for mixtures using an iterative dynamic programming algorithm.** , Journal of Cheminformatics, 2017

- Bo-Han Su, Yi-shu Tu, **Chieh Lin**, Chi-Yu Shao, Olivia A Lin, Yufeng J. Tseng, **Rule-based Cytochrome P450 Inhibition Prediction Models.**, Journal of Chemical Information and Modeling, 2015

- Chi-Yu Shao, Bo-Han Su, Yi-Shu Tu, **Chieh Lin**, Olivia A. Lin, Yufeng J. Tseng, **CypRules: A rule-based P450 inhibition prediction server**, Bioinformatics, 2015

Honors and Distinctions

- GARMIN corporation Fellowship 2014
- Presidential Award from NTU (7 times) 2010, 2011, 2012, 2013
- Honorable Member of The Phi Tau Phi Scholastic Honor Society 2013
- NTU Alumni Association Fellowship 2012
- NTU Dean's List Award (3 times) 2010, 2011
- Outstanding Award in Service Learning Education from NTU 2011

Miscellaneous

- Teaching Assistant

    - Machine Learning Department, Carnegie Mellon University
    - Introduction to Machine Learning course (PhD level A.I.) 2016, 2017

- Reviewer

    - **Journal:** Nucleic Acids Research

- Master Admission Committee

    - Machine Learning Department, Carnegie Mellon University
    - Reviewing the applications of Machine Learning Master's Program