Hansen Han

hansen.h97@gmail.com | (718) 578-2122
https://github.com/hansenrhan| https://github.com/hhan-schrodinger

EDUCATION

Skidmore College **2015 - 2019**
Saratoga Springs, NY Cumulative GPA: 3.7 / 4.0
B.A. Molecular Biology & Genetics (*Honors*), *Cum Laude* Major GPA: 3.8 / 4.0

EXPERIENCE

Data Engineer I, Drug Discovery Informatics **2022 - Current**
Schrödinger Inc., New York NY *10 Months*

- Collaborated with scientific teams to support build out and integration of data management and visualization solutions to support drug discovery target validation and target tracking efforts
- Wrote and modified code in Javascript, Python, R, Java, and SQL, performed code reviews, version control, software quality assurance testing, and usability testing

Research Associate II, Computational Biology **2020 - 2022**
RAPT Therapeutics Inc., South San Francisco CA *1 Year, 7 Months*

- Contributed to the biomarker analysis of Phase I/II clinical trial data for FLX475, a C-C chemokine receptor 4 (CCR4) antagonist, by analyzing patient metadata, transcriptomic, and genomic data to identify predictive biomarkers and changes in the tumor microenvironment post-treatment, and utilizing immunohistochemistry (IHC) data to investigate protein expression and localization within the tumor
- Designed and implemented a data collection and preparation pipeline utilizing public databases (e.g., ChEMBL, PubChem) for an in-house machine learning tool to predict compound toxicity
- Conducted a comprehensive literature review to identify relevant gene expression data for oncology and immune diseases, and systematically collected and curated data from various public repositories. Utilized machine learning methods such as Support Vector Machine, Random Forest, and Elastic-net regression to analyze the data and identify robust and clinically relevant biomarkers for disease diagnosis and prognosis

Data Science Intern **2020**
Stochastic Inc., Harvard Innovation Labs, Cambridge MA *7 Months*

- Utilized Natural Language Processing (NLP) techniques such as sentiment analysis and topic modeling, leveraging Python libraries including NLTK, spaCy, and Gensim, to process and model large text datasets

- Created pipelines to scrape and handle real-time data from 200+ news and social media sites
- Developed Python tool for cell-type clustering and visualization of single-cell RNAseq data using Latent Dirichlet Allocation (LDA)

Summer Undergraduate Research Fellow **2018**

Hanes Laboratory, SUNY Upstate Medical University 3 *Months*

- Joined laboratory studying Ess1 and Pin1 (genes responsible for regulating cell growth in fungi and humans, respectively) as potential targets for anti-fungal and anti-cancer therapeutics
- Completed ten-week project on Ess1 in cold-adapted fungal species using molecular cloning techniques

SKILLS

Coding Python, R, Javascript, SQL, HTML, CSS

Tools Git/Github, Flask, Jupyter, sklearn, Pandas, Numpy SciPy, Matplotlib, Plotly, Seaborn, Flask, Tidyverse, Shiny, MySQL, SQLite, Bootstrap, Docker, Linux, Cloud Computing (AWS), Bioinformatics Tools (Kallisto, Bioconductor, QIIME, DESeq2, EdgeR, limma, Seurat, BLAST+, HMMER, etc.) Django

Other Strong Attention to Detail, Time Management, Teamwork, Written & Verbal Communication Skills, Public Speaking, Problem Solving & Analytical Skills, Wire-framing, Statistical Analysis, Machine Learning, Data Visualization

PUBLICATIONS & PRESENTATIONS

---

1. Hegge, M. , **Han, H**. , Akaryan, A. , Ophel, L., Edelstein, G. and Possidente, B. (2020). Skeleton photoperiods shed light on sex-differences in *Drosophila* circadian activity patterns in wild-type and *radish* mutant strains. *Drosophila Information Service* , Vol. 102, in press.
2. Hou, Y., Ji, N., Zhang, H., Shi, X., **Han, H.** and Lin, S. (2019), Genome size-dependent pcna gene copy number in dinoflagellates and molecular evidence of retroposition as a major evolutionary mechanism. *Journal of Phycology*, 55: 37-46. doi:10.1111/jpy.12815.
3. **Han, H.** , Hegge, M. , and Possidente, B. (2019), The *radish* anesthesia-resistant long-term memory mutation in *Drosophila* increases daytime activity only in the absence of light. Poster session presented at the 2019 NEURON Conference at Quinnipiac University on February 24th, 2019.