Meghan M. Thommes

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Summary

Creative and skilled data scientist with a passion for developing robust analytical pipelines, processing and integrating large-scale experimental datasets, and communicating complex results clearly and effectively. Experienced in collaborating with software engineers, wet-lab scientists, and computational biologists to generate innovative solutions in fast-paced environments. Seeking a position that offers opportunities for growth, fosters collaboration, and makes a tangible impact.

Skills

Languages:	Python, SQL, Bash/Shell, R
Python Packages:	pandas, sqlalchemy, pydantic, pytest, scikit-learn, statsmodels, numpy, scipy, seaborn, matplotlib
Techniques:	Object-Oriented Programming, Unit Testing, Data Modeling (conceptual), Regression (multivariate, linear, logistic), Random Forest, Clustering/Dimensionality Reduction (PCA, t-SNE, k-means)
Tools:	GitHub, VSCode, Jupyter Notebook, Google Colab, Linux

Education

PhD Biomedical Engineering, Boston University   **May 2020**

    Thesis: *Strategies for Engineering Microbial Communities*

BS Biomedical Engineering, Case Western Reserve University   **May 2013**

Experience

Dyno Therapeutics   Watertown, MA
Scientist I, Computational Biology   **Oct. 2021 – March 2024**

- Developed data analysis pipelines in Python using SQLAlchemy, Pydantic models, and Matplotlib/Seaborn figures to process, QC, and contextualize high-throughput viral screens of engineered AAV capsids, enhancing data quality and research efficiency

- Distilled complex, large-scale NGS datasets into clear, actionable, and standardized visual representations and reports that informed decision-making and advanced project goals

- Partnered with wet-lab scientists to design experiments, develop new data generation methods, and produce reports, driving strategic decisions for internal stakeholders

- Collaborated with software engineers to design and improve analysis frameworks, standardizing data access and workflows across the computational biology team, leading to improved efficiency and consistency

Joyn Bio   Boston, MA
Data Scientist   **June 2020 – Sept. 2021**
- Evaluated and predicted translation from *in vitro* to *in planta* biological performance of engineered microbes by developing modeling frameworks (linear regression, random forest) in Python and R
- Built data integration pipelines and packages in Python and R to clean, standardize, and consolidate data across departments; developed interactive dashboards in Tableau
- Created conceptual data models to inform modeling efforts, create data templates, and organize data in a centralized location so they can easily be queried and imported into databases
- Collaborated with scientists to design schemas for LIMS and ELN implementation in Benchling; tested API in Python to import existing data; queried PostgreSQL database to generate example dashboards

Insight, *Health Data Science*   Boston, MA
Fellow   **Jan. 2020 – April 2020**
- Created "NoveList", a web app that predicts a Goodreads user's want-to-read book ratings, enabling them to prioritize what to read next
- Built, trained, and evaluated a collaborative filtering recommender system in Jupyter Notebooks with scikit-surprise, pandas, numpy, and seaborn
- Deployed "NoveList" using streamlit and Heroku

Publications and Presentations

Meghan Thommes, Taiyao Wang, Qi Zhao, Ioannis Ch. Paschalidis, Daniel Segrè. Designing metabolic division of labor in microbial communities. *mSystems* (2019). doi: 10.1128/mSystems.00263-18 (Editor's Choice)

Konrad Herbst, Elena J. Forchielli, Taiyao Wang, **Meghan Thommes**, Ioannis Ch. Paschalidis, Daniel Segrè. Multi-Attribute Subset Selection enables prediction of representative phenotypes across microbial populations. *Communications Biology* (2024). doi: 10.1038/s42003-024-06093-w

Meghan Thommes, Taiyao Wang, Qi Zhao, Joshua Goldford, Ioannis Ch. Paschalidis, Daniel Segrè. Microbes distributing metabolism: How cross-feeding interactions support metabolic division of labor. 2018 Boston University Microbiome Day. Boston, MA. February 14, 2018. (Won Best Poster Presentation)

Meghan Thommes*, Taiyao Wang, Qi Zhao, Joshua Goldford, Ioannis Ch. Paschalidis, Daniel Segrè. Computational design of metabolic division of labor for synthetic microbial communities. 2017 Metabolic Pathway Analysis Conference. Boseman, MT. July 24-28, 2017. Abstract Book, page 83. (Won Best Poster Presentation)