Rebecca Alexis Senft

Cambridge, MA • (518) 332-7332 • senftrebecca@gmail.com • Github ⬡: rsenft1 • website 🌐: rsenft1.github.io

Computational biologist with expertise in building scalable biological data infrastructure, metadata-rich pipelines, and cloud-enabled workflows for large imaging and functional genomics datasets.

EDUCATION

Harvard University   Cambridge, MA
PhD in Neuroscience   August 2015 – November 2020
- Funded by NIH Ruth L. Kirschstein Predoctoral Individual National Research Service Award

Swarthmore College   Swarthmore, PA
BA in Neuroscience with High Honors   August 2011 – June 2015

RESEARCH EXPERIENCE

Merck and Co., Inc.   Cambridge, MA.
Senior Scientist in Bioinformatics   March 2023 – present

- Designed **ETL pipelines** deployed on AWS for optical pooled screen datasets (TB-scale image data; millions of cells, thousands of features), covering QC through feature extraction and hit-calling, ensuring **reproducibility, traceability, and interoperability across assays**.
- Co-led development of a **Nextflow-based infrastructure initiative** to **standardize and scale** optical pooled screening image analysis workflows, enabling **metadata-aware, reproducible pipelines** in partnership with IT engineers and biologists.
- Developed a Python tool to **query and retrieve single-cell images from internal databases** (seconds per query), improving data provenance and interpretability.
- Delivered analysis packages from large CRISPR-based **functional genomics screens** (100s–1000s of perturbations) using Python and R workflows; applied ML methods for phenotype classification.
- Supported decision-making through analysis in ~7 projects across oncology, cardio-metabolic disease, and immunology and were presented to senior leadership and cross-functional teams.
- Maintained reproducible codebases with **Git/GitHub** and shared best practices across departments.

Broad Institute of MIT and Harvard   Cambridge, MA
Postdoctoral Associate in Beth Cimini's lab   August 2021 – March 2023

- Built **scalable image analysis pipelines** using CellProfiler for high-throughput analysis of 500,000+ microscopy images and millions of cells on AWS.
- Contributed to **open-source development** in Python for CellProfiler and CellProfiler Analyst, including containerized plugins and new features such as 3D visualization.
- Taught 300+ biologists across 10+ workshops on reproducible image analysis
- Authored documentation for DeepProfiler, a deep learning toolkit for image-based profiling
- Performed large-scale data wrangling and clustering for ~13,000 different gene overexpression ORFs.
- Designed pipelines and statistical simulations to validate assay stability, ensuring robust and reproducible workflows for virus detection assays (Siddiqui et al., 2025).

Harvard University Medical School   Boston, MA
Graduate Student in Susan Dymecki's lab   April 2016 – August 2021

- Designed automated image analysis pipelines to quantify complex neurobiology across 13 brain regions, creating scalable, reproducible data workflows.
- Developed MicCheck, an R/Shiny application that **standardizes microscopy metadata collection** and reporting, enabling consistent, interoperable, and reproducible imaging datasets.

SKILLS

Programming & Software Engineering: Python (NumPy, pandas, scikit-learn, scikit-image, Polars), R (tidyverse, Shiny), SQL, MATLAB; Linux, Git, conda, Docker, CI/CD; CodeOcean.

Data Infrastructure & Engineering: Nextflow, ETL pipelines, reproducible pipeline development, data ingestion/standardization pipelines, DuckDB; experience with metadata systems, data provenance

Cloud & HPC: Cloud (AWS S3, EC2, lambda), HPC (PBS Pro), Docker, CI/CD

Data Science & ML: Dimensionality reduction (UMAP, t-SNE), supervised ML (Random Forest, XGBoost), clustering, feature extraction, image-based profiling

Visualization & Decision Support: R/Shiny, Jupyter, Quarto, analytical dashboards, reproducible reporting

Image analysis: CellProfiler, cellpose, StarDist, SImA, FIJI/ImageJ, Imaris, ImageJ Macro Language

Experimental skills: fluorescence microscopy (confocal and widefield), immunohistochemistry, RNAscope/*in situ* hybridization, AAVs, microdissection, DNA extraction

OPEN SCIENCE & LEADERSHIP

MISSIONS Day Merck internal microscopy conference organizer	2024
Images to Knowledge (I2K) Organizing Committee member and Scientific Committee member	2022
Broad Institute presenter and TA for workshops on image analysis with CellProfiler for 300+ total participants	2022
A leader on the image.sc forum, making 300+ posts answering questions about image analysis.	2022-present

Creator of official video tutorials for CellProfiler
- *Intro to CellProfiler Analyst* — 2022
- *Using Cellpose and StarDist in CellProfiler* — 2022

Author, Broad Institute Imaging Platform blog, "Measure everything…ask questions later"
- *How to normalize cell painting data* — 2022
- *How to export tiles of large histology images in QuPath* — 2022

Olympus Neuroscience Week Junior Scientist Presenter	2020
Advanced Imaging Methods (AIM) Workshop Presenter	2022
MATLAB Bootcamp in Quantitative Methods Teaching Fellow (Harvard)	2020
Thinking About Data (intermediate MATLAB statistics course) Teaching Fellow (Harvard)	2017, 2020
Quantitative Microscopy and Experimental Design Nanocourse Co-instructor of Record (Harvard)	2019

SELECTED HONORS AND AWARDS

Harvard Center for Biological Imaging Simmons Award	2020
Society for Neuroscience Trainee Professional Development Award	2019
NIH Ruth L. Kirschstein Predoctoral Individual National Research Service Award F31NS108406	2018 – 2021
Harvard University Distinction in Teaching Award	2018
National Science Foundation GRFP Honorable Mention	2015, 2016

SELECTED PUBLICATIONS
Full list of publications available on my google scholar profile

1. Serrano, Erik, Srinivas Niranj Chandrasekaran, Dave Bunten, Kenneth I. Brewer, Jenna Tomkinson, Roshan Kern, Michael Bornholdt et al. "Reproducible image-based profiling with Pycytominer." *Nature Methods* (2025): 1-4.

2. Weisbart, Erin, Callum Tromans-Coia, Barbara Diaz-Rohrer, David R. Stirling, Fernanda Garcia-Fossa, **Rebecca A. Senft**, Mark C. Hiner, Marcelo B. de Jesus, Kevin W. Eliceiri, and Beth A. Cimini. "Cellprofiler Plugins–an easy image analysis platform integration for containers and python tools." *Journal of microscopy* 296, no. 3 (2024): 227-234.

3. Moshkov, Nikita, Michael Bornholdt, Santiago Benoit, Matthew Smith, Claire McQuin, Allen Goodman, **Rebecca A. Senft** et al. "Learning representations for image-based profiling of perturbations." *Nature communications* 15, no. 1 (2024): 1594.

4. **Senft, Rebecca A**., Barbara Diaz-Rohrer, Pina Colarusso, Lucy Swift, Nasim Jamali, Helena Jambor, Thomas Pengo et al. "A biologist's guide to planning and performing quantitative bioimaging experiments." *PLoS Biology* 21, no. 6 (2023): e3002167.

5. Montero Llopis, Paula, **Rebecca A. Senft**, Tim J. Ross-Elliott, Ryan Stephansky, Daniel P. Keeley, Preman Koshar, Guillermo Marqués, Ya-Sheng Gao, Benjamin R. Carlson, Thomas Pengo, Mark A. Sanders, Lisa A. Cameron, Michelle S. Itano. Best practices and tools for reporting reproducible fluorescence microscopy methods. (2021). *Nature Methods.*