

Rebecca Alexis Senft

Cambridge, MA • (518) 332-7332 • senftrebecca@gmail.com • Github : [rsenft1](https://github.com/rsenft1) • website : rsenft1.github.io

Professional computational biologist and image analyst with a background in biology and neuroscience

EDUCATION

Harvard University

PhD in Neuroscience

Cambridge, MA

August 2015 – November 2020

- Funded by NIH Ruth L. Kirschstein Predoctoral Individual National Research Service Award

Swarthmore College

BA in Neuroscience with High Honors

Swarthmore, PA

August 2011 – June 2015

RESEARCH EXPERIENCE

Merck and Co., Inc.

Senior Scientist in Bioinformatics

Cambridge, MA

March 2023 – present

- Led development of analysis workflows across diverse image data types, including optical screens and Cell Painting assays, with a focus on single-cell data
- Delivered hit packages from large CRISPR-based functional genomics screens using Python and R workflows
- Built scalable QC and analysis pipelines for pooled optical screening datasets (millions of cells, thousands of features); implemented hit-calling using bootstrapping and visualized results via UMAP and t-SNE; presented at 2024 SBI2 Conference
- Co-led large-scale image analysis pipeline initiative across departments and IT; presented as a long talk at 2024 Data, AI, and Genome Sciences Retreat
- Developed a Nextflow pipeline to efficiently parallelize analysis of microscopy images on HPC/cloud using CellProfiler
- Queried and integrated single cell datasets using SQL and duckdb for downstream bioinformatics workflows
- Applied supervised ML (Random Forest, XGBoost) to classify gene/treatment effects from image-derived features
- Presented analysis results and statistical methods at meetings for senior leadership as well as wet lab scientists and IT engineers
- Version controlled code using Git/GitHub; my how-tos on GitHub, HPC and AWS have been shared across departments
- Mentored two co-op students on projects analyzing optical pooled screening image phenotype data using machine learning and developing a shiny app to display results to biologists
- Managed a contractor to support image analysis assay development for optical pooled screens

Broad Institute of MIT and Harvard

Postdoctoral Associate in Beth Cimini's lab

Cambridge, MA

August 2021 – March 2023

- Built custom image analysis pipelines in 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 bug fixes and new features (e.g., 3D data visualization)
- Developed custom image analysis pipelines using deep learning to segment cells in 2D and 3D
- Taught >300 biologists across 10+ workshops on image analysis; developed training on integrating deep learning tools into CellProfiler workflows
- Authored user documentation for DeepProfiler, a deep learning toolkit for image-based profiling (see Moshkov et al., 2022)
- A leader on the image.sc forum, making 300+ posts answering user questions about image analysis.

- Performed data wrangling and hierarchical clustering for custom analyses of a dataset with ~13,000 different gene overexpression ORFs.
- Designed CellProfiler pipelines and python code to track fluorescent beads over time in an assay to detect a panel of viruses. Coded bootstrapping simulations to validate assay stability (in prep).

Harvard University Medical School
Graduate Student in Susan Dymecki's lab

Boston, MA
 April 2016 – August 2021

- Identified a novel serotonergic circuit using confocal microscopy in a transgenic mouse model (see Senft et al., 2021)
- Designed and validated image analysis pipelines to quantify axonal bouton neurochemical phenotypes across 13 brain regions
- Automated mRNA puncta quantification with a custom ImageJ macro, reducing analysis time by >80% (see Okaty et al., 2020)
- Developed MicCheck, an R/Shiny web app guiding microscopy metadata reporting for publications (see Montero Llopis et al., 2021)

SKILLS

Programming languages and tools: Python (NumPy, pandas, scikit-learn, scikit-image, polars), R (tidyverse, Shiny), SQL, duckdb, Nextflow, MATLAB, Git/GitHub, AWS, HPC, Linux, conda, virtualenv, CodeOcean, Jupyter (Notebook, Book), Quarto, RMarkdown, Adobe Illustrator, GraphPad Prism

Data & ML: ETL pipelines, data wrangling, data integration, bootstrapping, dimensionality reduction (UMAP, t-SNE), supervised ML (Random Forest, XGBoost), image-based profiling, feature extraction, unsupervised clustering, custom pipelines for 2D/3D image segmentation, DRUGseq RNAseq quality control

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

Experimental skills: fluorescence microscopy (confocal and widefield), immunohistochemistry, RNAscope/*in situ* hybridization, stereotaxic mouse surgery, working with AAVs, mouse behavior, mouse epilepsy models, microdissection, mouse colony management, DNA extraction, PCR, writing IACUC amendments.

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
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

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. Chandrasekaran, Srinivas Niranj, Eric Alix, John Arevalo, Adriana Borowa, Patrick J. Byrne, William G. Charles, Zitong S. Chen et al. "Morphological map of under-and over-expression of genes in human cells." *bioRxiv* (2024): 2024-12.
3. 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.
4. Lacoste, Jessica, Marzieh Haghighi, Shahan Haider, Chloe Reno, Zhen-Yuan Lin, Dmitri Segal, Wesley Wei Qian et al. "Pervasive mislocalization of pathogenic coding variants underlying human disorders." *Cell* 187, no. 23 (2024): 6725-6741.
5. Cimini, Beth A., Callum Tromans-Coia, David R. Stirling, Suganya Sivagurunathan, **Rebecca A. Senft**, Pearl V. Ryder, Esteban Miglietta et al. "A postdoctoral training program in bioimage analysis." *Molecular Biology of the Cell* 35, no. 9 (2024): pe2.
6. 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.
7. Maddaloni, Giacomo., YoonJeung Chang., **Rebecca A. Senft** et al. Adaptation to photoperiod via dynamic neurotransmitter segregation. *Nature* 632, 147–156 (2024). <https://doi.org/10.1038/s41586-024-07692-7>
8. Siddiqui, Sameed M., Nicole L. Welch, Tien G. Nguyen, Amaya Razmi, Tianyi Chang, **Rebecca Senft**, Jon Arizti-Sanz et al. "Bead-based approaches to CRISPR diagnostics." *medRxiv* (2023): 2023-09.
9. **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.
10. Tromans-Coia, Callum, Barbara Diaz-Rohrer, Erin Weisbart, 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." *arXiv e-prints* (2023): arXiv-2306.
11. **Senft, Rebecca A.** and Susan M. Dymecki. Neuronal pericellular baskets: neurotransmitter convergence and regulation of network excitability. (2021). *Trends in Neurosciences*.
12. 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*.
13. **Senft Rebecca A.** , Morgan E. Freret, Nikita Sturrock, Susan M. Dymecki. Neurochemically and hodologically distinct ascending VGLUT3 versus serotonin subsystems comprise the r2-Pet1 median raphe (2021). *Journal of Neuroscience*.
14. Okaty*, Benjamin W., Nikita Sturrock*, Yasmin Escobedo Lozoya, YoonJeung Chang, **Rebecca A. Senft**, Krissy A. Lyon, Olga V. Alekseyenko and Susan M. Dymecki. A single-cell transcriptomic and anatomic atlas of mouse dorsal raphePet1 neurons. (2020) *Elife*. (* These authors contributed equally)