

## Rebecca Alexis Senft

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

*Professional bioinformatics data scientist 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 2022 – present

- Lead contributor to designing, developing, and advocating for analysis workflows across image analysis data types – from optical screens to cell painting assays
- Delivered hit packages for CRISPR screens testing hundreds of genetic perturbations with image-based readouts using custom image analysis pipelines and python or R-based downstream hit-calling workflows
- Created quality control and downstream analysis workflows for optical pooled screening datasets with millions of cells and thousands of features. Hit calling using bootstrapping to calculate statistical significance, data visualization with UMAP and t-SNE; results presented at 2024 SBI2 conference
- Co-led a large-scale image analysis pipeline effort that was a collaboration across different departments and IT, my presentation about this collaboration was chosen as a long talk for our 2024 department of Data, AI, and Genome Sciences Retreat
- Developed a Nextflow pipeline to efficiently parallelize analysis of microscopy images with HPC or cloud computing resources using CellProfiler
- Used machine learning supervised classification methods (Random Forest, XGBoost) to differentiate gene and treatment perturbations using single cell data and 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 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 – present

- Created custom image analysis pipelines using CellProfiler for high-throughput analysis of 500,000+ images and millions of cells in a cloud environment (AWS).
- Contributed to open-source software development in Python of CellProfiler and CellProfiler Analyst by fixing bugs and contributing new functionalities, such as visualization of 3D datasets in CellProfiler Analyst.
- Developed custom image analysis pipelines using deep learning to segment cells in 2D and 3D
- Presented at 10 workshops teaching >300 biologists how to use CellProfiler to analyze their images. Also developed original workshops on how to use deep learning tools Cellpose and StarDist in CellProfiler.
- A leader on the image.sc forum, making 300+ posts answering user questions about image analysis.
- Designed custom documentation for DeepProfiler, a deep learning toolset for high-throughput microscopy image analysis (see Moshkov et al., 2022)

- 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).
- Organized a jamboree day to recreate and update our [webpage](#) for CellProfiler tutorials

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

Boston, MA  
 April 2016 – August 2021

- Identified a novel circuit from median raphe neurons to VGLUT3+ interneurons in cortex via specialized pericellular baskets using confocal microscopy in a transgenic mouse model (see Senft et al., 2021)
- Developed and validated an image analysis pipeline to quantify the neurochemical phenotype of highly collateralized axonal boutons across 13 forebrain target sites (see Senft et al., 2021)
- Coded a custom ImageJ image analysis macro to count mRNA puncta in fluorescent neurons, reducing the time necessary to complete analysis by over 80%. (see Okaty et al., 2020)
- Developed MicCheck, a web app built in R using Shiny to recommend microscopy metadata for biologists to report in publications (see Montero Llopis et al., 2021)

## SKILLS

**Programming languages:** R (tidyverse), Python (sci-kit learn, sci-kit image, numpy, pandas, polars, duckdb), Nextflow, ImageJ Macro Language, MATLAB, familiarity with SQL

**Software/Tools:** AWS, HPC, linux, conda, virtualenv, cellpose, CodeOcean, SlmA, CellProfiler, Git/GitHub, Jupyter Book, Jupyter Notebook, Quarto, RMarkdown, Shiny, Fiji/ImageJ, Morpheus, Imaris, Adobe Illustrator, PRISM

**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	
• <a href="#">Intro to CellProfiler Analyst</a>	2022
• <a href="#">Using Cellpose and StarDist in CellProfiler</a>	2022
Author, Broad Institute Imaging Platform blog, "Measure everything...ask questions later"	
• <a href="#">How to normalize cell painting data</a>	2022
• <a href="#">How to export tiles of large histology images in QuPath</a>	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. 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)