



TRAINING: SPATIAL OMICS DATA ANALYSIS WITH MAWA

Want to learn how to process and analyze your spatial proteomics/transcriptomics data? Join us for four virtual hour-long sessions at NIH, where you'll get hands-on, step-by-step training using sample datasets (.csv, .tsv, .txt) with MAWA (Multiplex Analysis Web Apps). This user-friendly, graphical software platform offers an end-to-end solution for your analysis workflow following cell segmentation of your tissue.

What You'll Learn:

- **File Handling:** Efficiently manage your datasets.
- **Phenotyping:** Identify and categorize cell types.
- **Spatial Analysis:** Analyze spatial relationships within your data.

Why Attend?

- **Easy-To-Use Platform:** MAWA offers an intuitive interface suitable for both novices and experts.
- **High Performance:** Efficiently handles large datasets with millions of cells or objects.
- **Free Access:** MAWA is available for free use.

Don't miss this opportunity to enhance your data analysis skills with MAWA!

Tue 10/15, 1-2 PM
Introduction to NIDAP.
MAWA fundamentals.
Supervised
phenotyping.
Andrew Weisman, Ph.D.

Tue 10/22, 1-2 PM
Unsupervised
phenotyping.
Andrei Bombin, Ph.D.

Tue 10/29, 1-2 PM
Pairwise spatial analysis
using hypothesis
testing.
Andrew Weisman, Ph.D.

Wed 11/6, 11-12 PM
Neighborhood analysis
using spatial UMAP.
Dante Smith, Ph.D.

Hosted by:
NCI CCR BTEP

All at NIH are welcome!

Register for each session
individually at links above.

Questions:
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