Bachelor’s / Master’s Thesis Project (Plants | Spatial Transcriptomics | Open-ST)

Decoding spatial gene expression patterns in plant development

We are offering a Bachelor’s or Master’s thesis project using **spatial transcriptomics (Open-ST)** to investigate how developmental programs are established and executed in plant tissues. You will work with cutting-edge spatial gene expression data and computational analysis workflows, gaining hands-on experience at the interface of **plant developmental biology** and **bioinformatics**.

We’re looking for a motivated student who has:

- **Some coding experience** (Python and/or R preferred) and willingness to learn more
- Comfort running scripts, **modifying code**, and **debugging simple errors**
- Familiarity with basic programming concepts: **data frames/matrices, loops, functions, plotting**
- Confidence using the **command line / terminal**
- A **basic understanding of molecular biology**
- Interest in omics data (prior exposure is a plus)

Scientific working style matters:

- Ability to follow documented pipelines and keep analyses reproducible
- Careful tracking of **parameters, software versions, and results**
- Curious mindset, asks questions, and enjoys collaborative problem-solving

Nice to have (not required):

- Single-cell/spatial analysis experience (e.g., **Seurat** or **Scanpy**)
- Differential gene expression, PCA/UMAP
- Git/version control
- Experience working on a server/HPC

If you’re excited about combining **plant development** with **spatial omics** and want to build your computational skills in a supportive environment, we’d love to hear from you.

How to apply: Please send a short email with your CV, a brief note on your coding experience (R/Python), and your study background to Sami Saarenpää (sami.saarenpaa@hu-berlin.de)