
A practical introduction to Spatial Transcriptomics

Join us for an in-depth Spatial Transcriptomics tutorial
at TMF tutorials in Freiburg (Tutorial sponsored by PM4Onco)

Date: April 01, 2025 | Duration: 1 – 5 PM
Location: Universität Freiburg, Kollegiengebäude 1 (KG1),
Platz der Universität 3, 79098 Freiburg
Language: English

This tutorial is organized by the **EkoEstMed junior research group** at the University of Freiburg as part of the **PM4Onco project** (<https://pm4onco.de>). PM4Onco is a collaborative initiative within Germany's National Decade Against Cancer, dedicated to establishing a sustainable infrastructure for integrating and exchanging clinical and biomedical research data to advance personalized cancer treatment. By harmonizing diverse datasets and leveraging artificial intelligence, PM4Onco aims to identify targeted therapies for rare and aggressive cancers. Thanks to the support of PM4Onco, we are pleased to offer this tutorial **free of charge**.

About the Tutorial

This hands-on session is designed to provide researchers with the theoretical foundation, analytical skills, and practical experience needed to explore spatially resolved gene expression.

Why Spatial Transcriptomics?

Spatial transcriptomics is transforming genomics, histology, and systems biology by allowing researchers to analyze gene expression within its native tissue architecture. This technology has revolutionized cancer research, neuroscience, developmental biology, and personalized medicine by revealing spatial patterns of gene activity that drive cellular function and disease progression.

Who Should Attend?

- Bioinformaticians and computational biologists integrating spatial data into their analyses.
- Researchers in cancer biology, neuroscience, immunology, and developmental biology seeking spatial insights.
- Data scientists working with high-dimensional transcriptomic data.

Important: The hands-on exercises will be conducted in R, ensuring accessibility for researchers with a background in bioinformatics, genomics, and molecular biology. Basic R programming skills are required.

What You Will Learn?

- Understand the fundamental principles of spatial transcriptomics and its applications.
- Gain hands-on experience with state-of-the-art analytical tools (Seurat in R).
- Learn best practices for quality control and normalization to ensure robust data.
- Explore spatial gene expression patterns in tissue structure and function.
- Perform gene set enrichment analysis in a spatial context.

Agenda

1. Introduction to Spatial Biology – Overview of spatial transcriptomics and its impact.
2. Setting Up Your Analysis Environment – Hands-on exploration of leading software tools.
3. Data Processing & Quality Control – Tackling data sparsity and normalization.
4. Interpreting Spatial Expression Patterns – Connecting gene expression to tissue structure.
5. Advanced Functional analysis: Uncovering tissue composition with Gene-Set Enrichment and Cell type deconvolution.
6. Q&A and Discussion – Interactive session to address specific research questions.

Registration

Limited Spots Available! To ensure an interactive and high-quality learning experience, participation is limited to a **maximum of 15 attendees**.

Hybrid Option (Under Discussion): While we are exploring the possibility of a hybrid format, in-person attendance is strongly recommended due to the hands-on nature of the session.

Important: Technical support for troubleshooting and bug-fixing will not be available for online participants.

Register now and secure your spot!

<https://www.tmf-ev.de/veranstaltungen/tmf-tutorials-2025>

Contact

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#ScientificConference #R