de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

elixir GERMANY

BIH — Berlin Institute of Health @Charité

HD-HUB

Provision of Software and Services with a Focus on Human Bioinformatics

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Contract Nr. W-de.NBI-001

Short description of the project

Aim: Support translational research by providing best practices, environments, guidelines, training and services.

- Develop and provide best practice guidelines for single-cell & spatial transcriptomics, addressing interoperability, tools, and training for single-cell & spatial transcriptomics.
- Provide collaborative research environments for working with sensitive human data.
- Develop tools for management, automation and FAIRification of bioinformatics workflows.

de.NBI services

Management and automation of data analysis workflows (https://gitlab.com/one-touch-pipeline)
- WESKIT: management of Snakemake and Nextflow workflows
- OTP: automation of cancer genomics workflows

Deep Envirotyping GeoSpatial Database (DEGDB): Enrichment of cohorts with geo-spatial data.

JupyterHub at BIH (https://jhub.bihealth.org): Working environment for research projects.

Cell-segmentation-free spatial transcriptomics analysis suite (https://github.com/HiDiHlabs)
- SSAM
- SSAM-lite
- Sainsc
- SpatialLeiden
- Ovrl.py
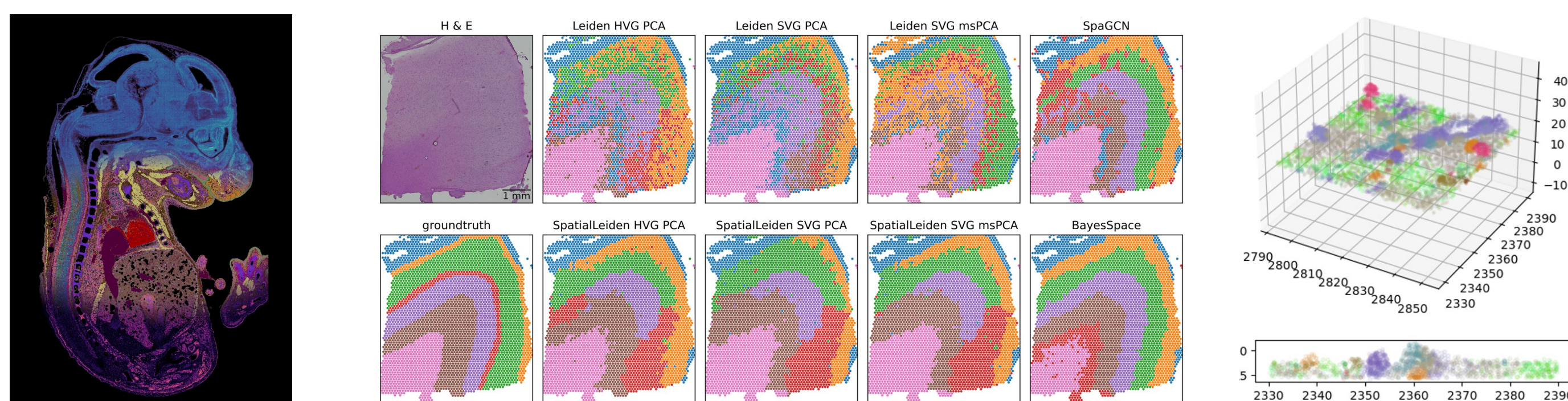
Images: Sainsc cell-type map of mouse embryo (left); SpatialLeiden clustering of brain (middle); overl.py finds cell overlaps (right).

General information on the project

Staff paid from de.NBI: 2 FTEs
Other staff involved:
- Roland Eils (PI)
- Naveed Ishaque (PI)
- Sven Twardziok (PI)
- 3 FTEs contributing to the project (technician, software developer, project manager)

Progress report

Services
- Improving stability and deployment of WESKIT
- OTP2EOSC: deploying OTP in the cloud
- Spatial transcriptomics tools (Sainsc, SpatialLeiden)

Cloud activities
- Support of research projects using the de.NBI cloud
- Contribution to ELIXIR on Cloud framework
- Support BioHackathon projects with cloud resources

ELIXIR engagement
- Co-lead compute platform work package 3
- Representing ELIXIR activities in GA4GH
- Co-lead of the ELIXIR Single-Cell Omics Community
- SCONE Implementation Study
- Spatial2Galaxy CMR Open Science Tier call

de.NBI training and education

Training courses and workshops
- EMBO Spatial Omics Data Analysis course, Virtual
- ELIXIR Spatial Omics Data Analysis course, Switzerland
- ELIXIR Cloud workshop at ELIXIR AHM 2024

ELIXIR BioHackathon Europe
- Standards and ontologies for single cell experiments
- Cell type-specific and druggable pathway models and maps
- Perturb-Bench
- The BioHackathon Cloud

de.NBI BioHackathon Germany
- SpaceHack 1.0 (2022)
- SpaceHack 2.0 (2023)
- SpaceHack 3.0 (2024)

Images: attendees of the „SpaceHack 2.0"

- Secure Processing Environments as a Service in the de.NBI Cloud (2024)

Publications

[1] A mini-review on perturbation modelling across single-cell omic modalities (10.1016/j.csbj.2024.04.058)
[2] Optimizing Xenium In Situ data utility by quality assessment and best practice analysis workflows (Accepted, *Nature Methods*)
[3] SpaceTx: a roadmap for benchmarking spatial transcriptomics exploration of the brain (10.48550/arXiv.2301.08436)
[4] Ontologies for single-cell experiments (10.37044/osf.io/wr93q)
[5] Roadmap for a European cancer data management and precision medicine infrastructure (10.1038/s43018-023-00717)
[6] Establishing the ELIXIR Microbiome Community (10.12688/f1000research.144515.1)
[7] Creating cloud platforms for supporting FAIR data management in biomedical research projects (10.12688/f1000research.140624.3)
[8] Sainsc: a computational tool for segmentation-free analysis of in-situ capture (10.1101/2024.08.02.603879)
[9] SpatialLeiden - Spatially-aware Leiden clustering (10.1101/2024.08.23.609349)

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