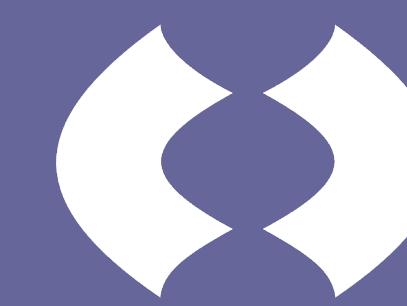


# BIMOLECULAR DATA SCIENCE IN PNEUMOLOGY

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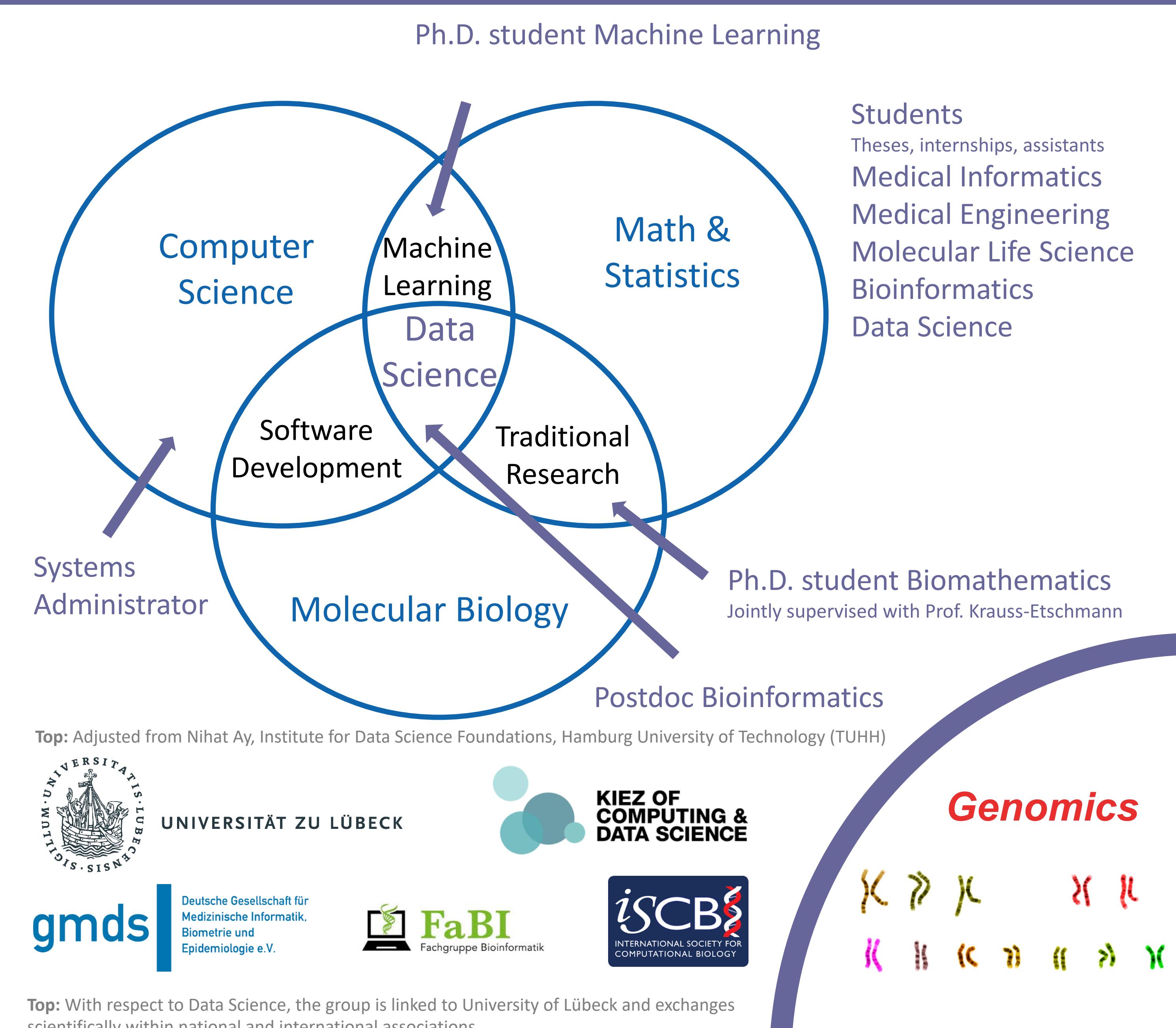
## OBJECTIVES

- Bioinformatics consulting
- Computing & OMICS data storage infrastructure
- Standardized OMICS data analyses
- Computational and collaborative research projects

## EXPERTISE

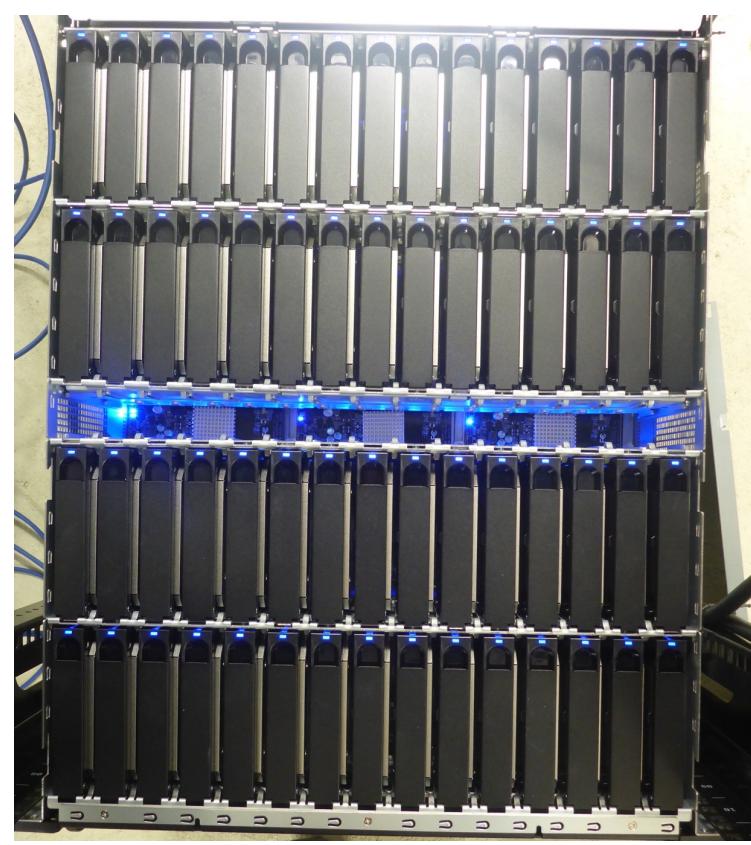
- Sequencing data analyses
- Genomics & Transcriptomics
- Systems Genetics
- Long read sequencing-based Epigenomics & Epitranscriptomics

## DATA SCIENCE GROUP SETUP

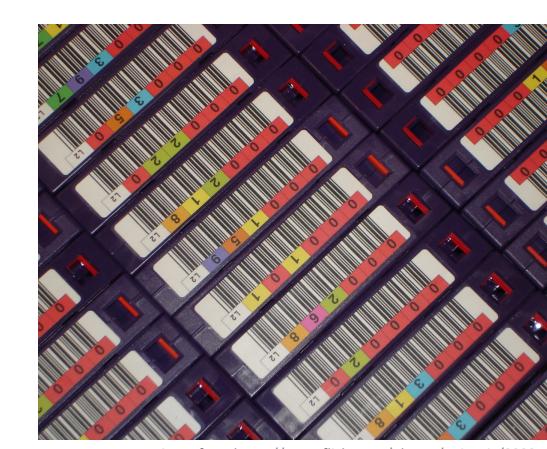


## COMPUTING & STORAGE

- Harmonizing and extending high performance computing infrastructure at Research Center Borstel
- Setup of OMICS data storage



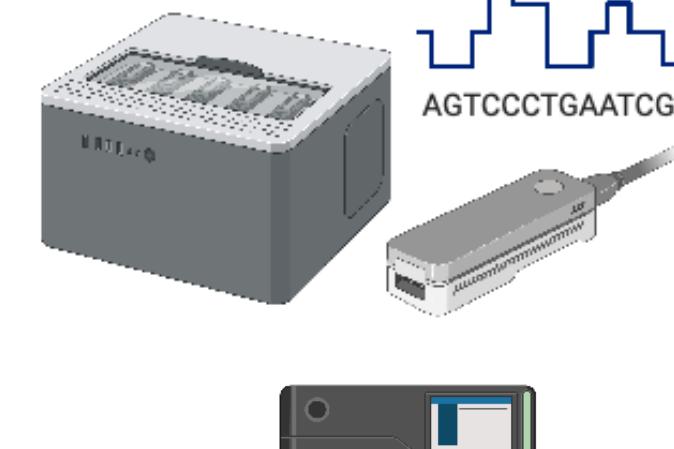
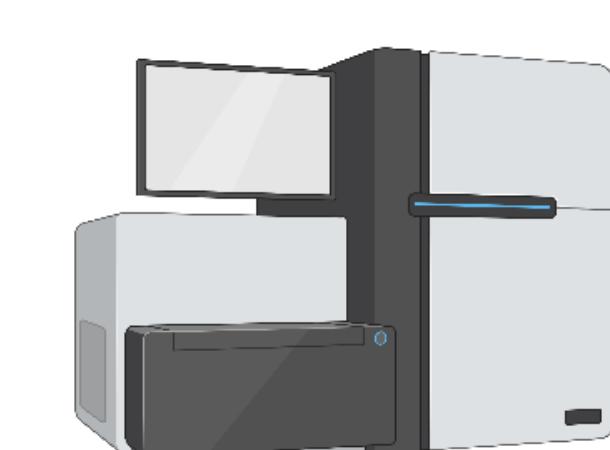
Top: Research center Borstel has a server room solely dedicated to OMICS data storage and analyses, with a new, extendable 1 PB Synology NAS (HD6500) for data storage



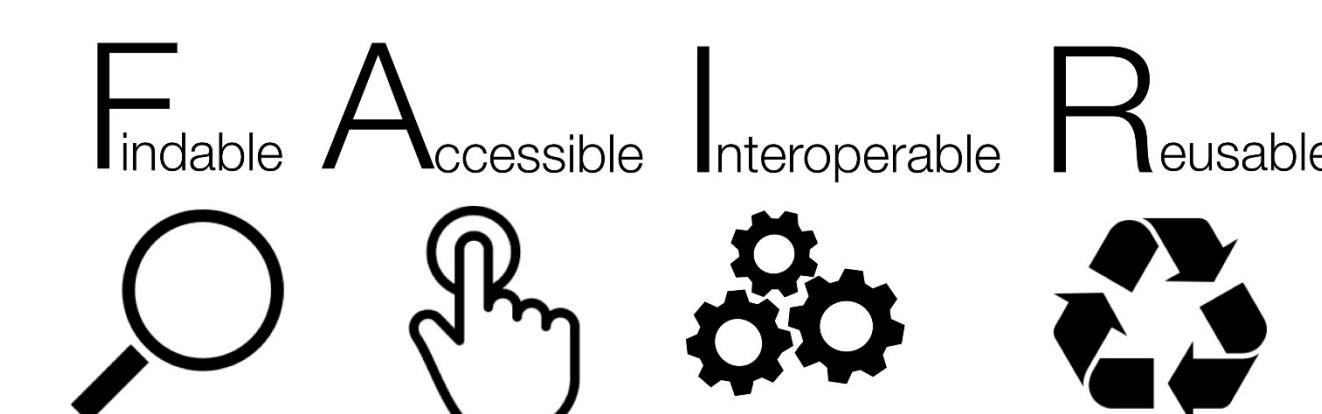
Left: Raw OMICS data backup on tape for long-term data retention



Left: The compute cluster uses slurm for job scheduling



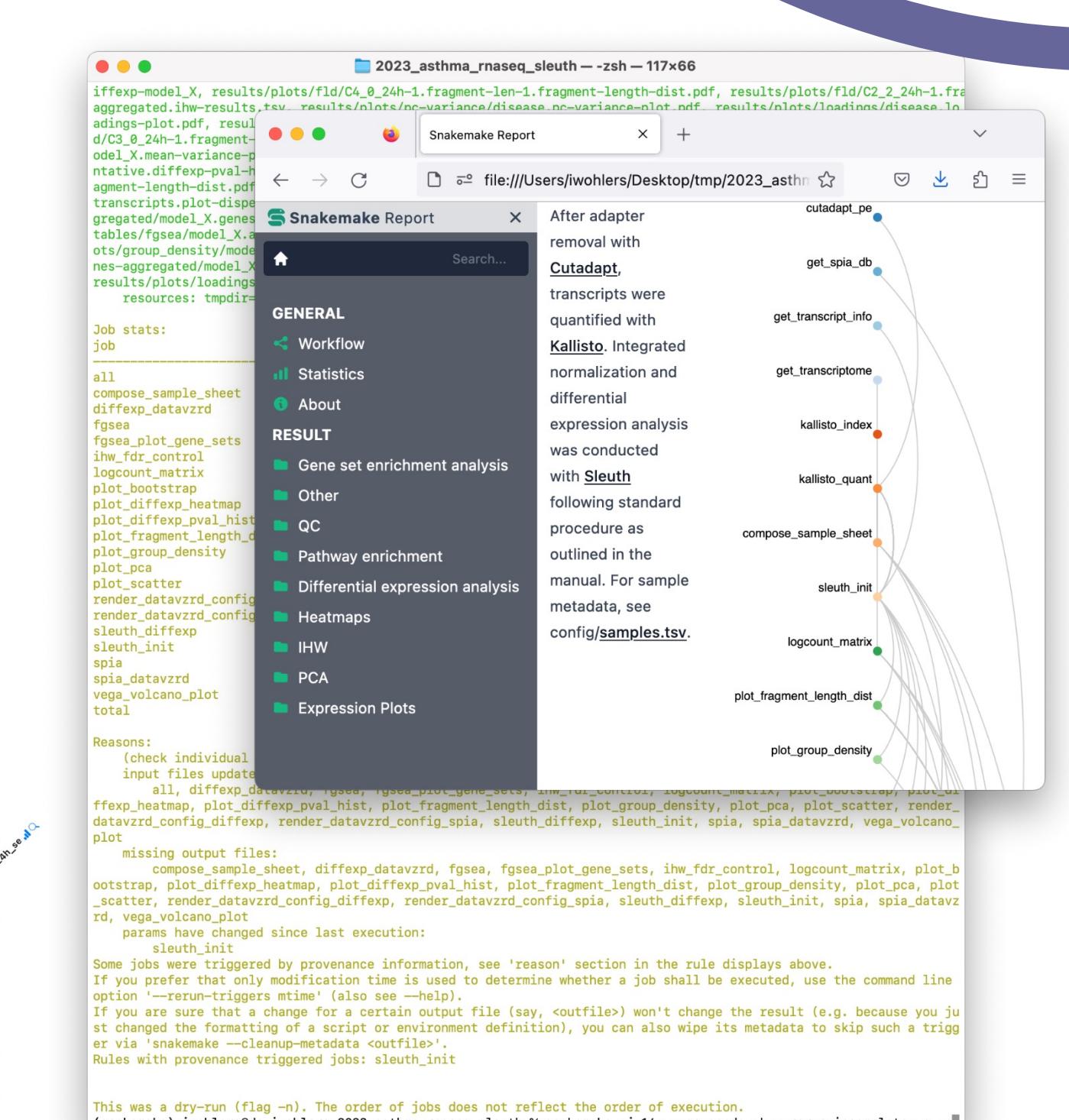
Left/bottom: The group is in the process of setting up a FAIR, center-wide data management for OMICS data.



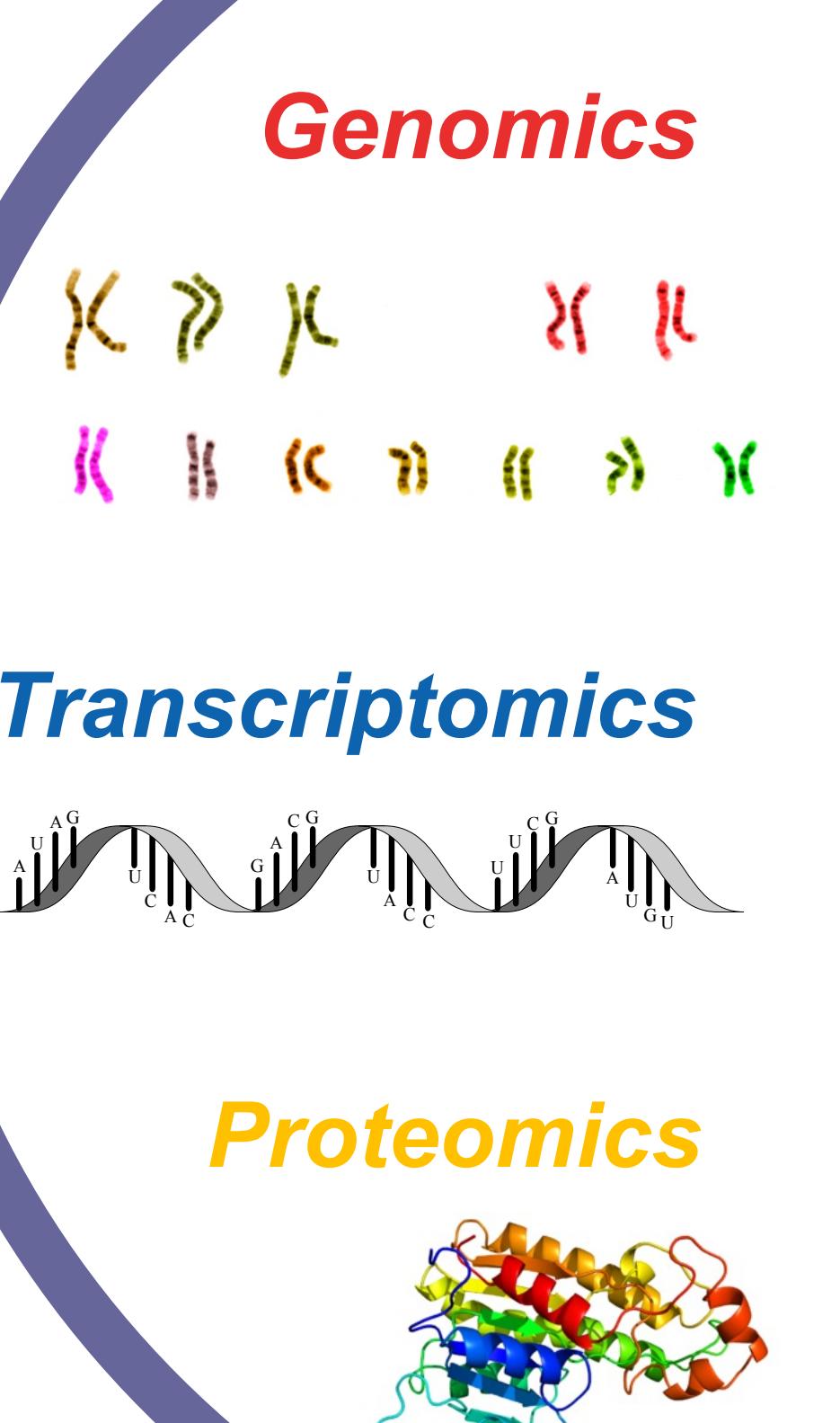
Top: Illumina, ONT and PacBio sequencers on campus generate big data

## STANDARDIZED ANALYSES

- Reproducible, community supported workflows e.g. from nf-core or from the snakemake workflow catalog
- Available: bulk RNA-Seq data analyses using workflows rna-seq-kallisto-sleuth and rna-seq-star-deseq2

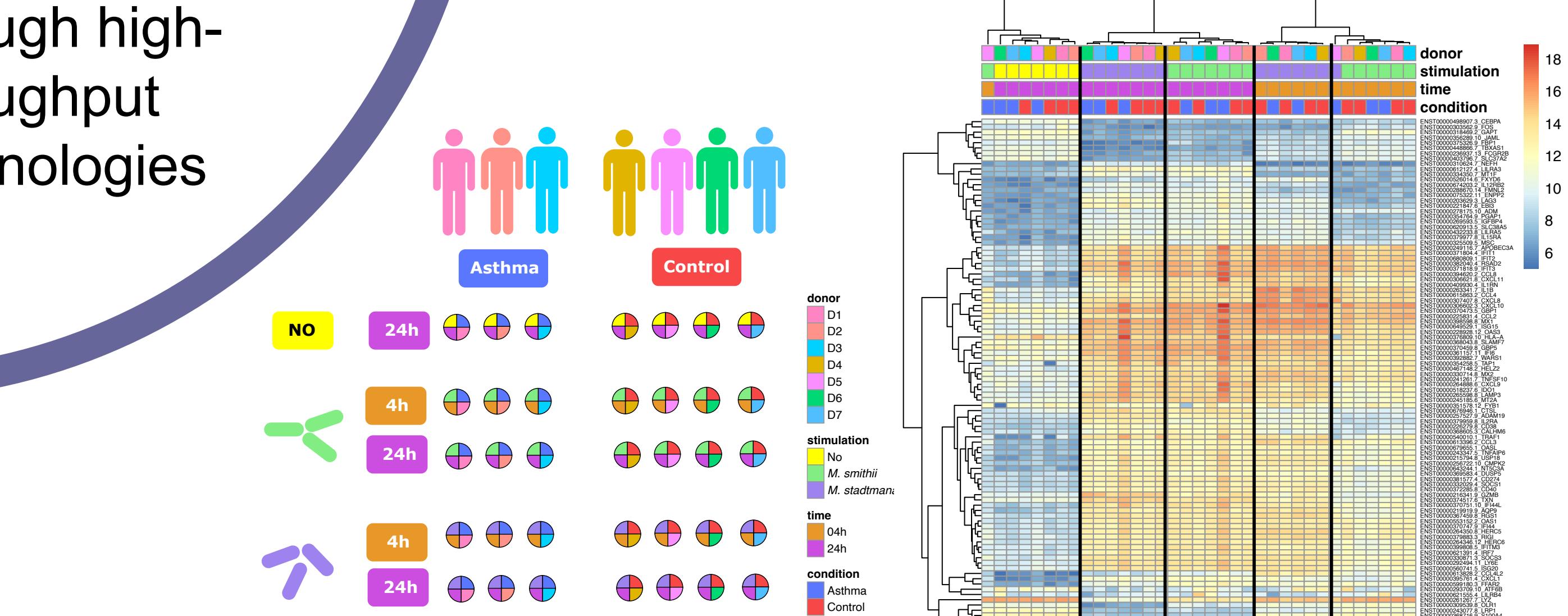


Left / Bottom: HTML result tables generated by the RNA-Seq workflow



**OMICS**  
The collective characterization and quantification of many biological entities as well as their function, structure and dynamics through high-throughput technologies

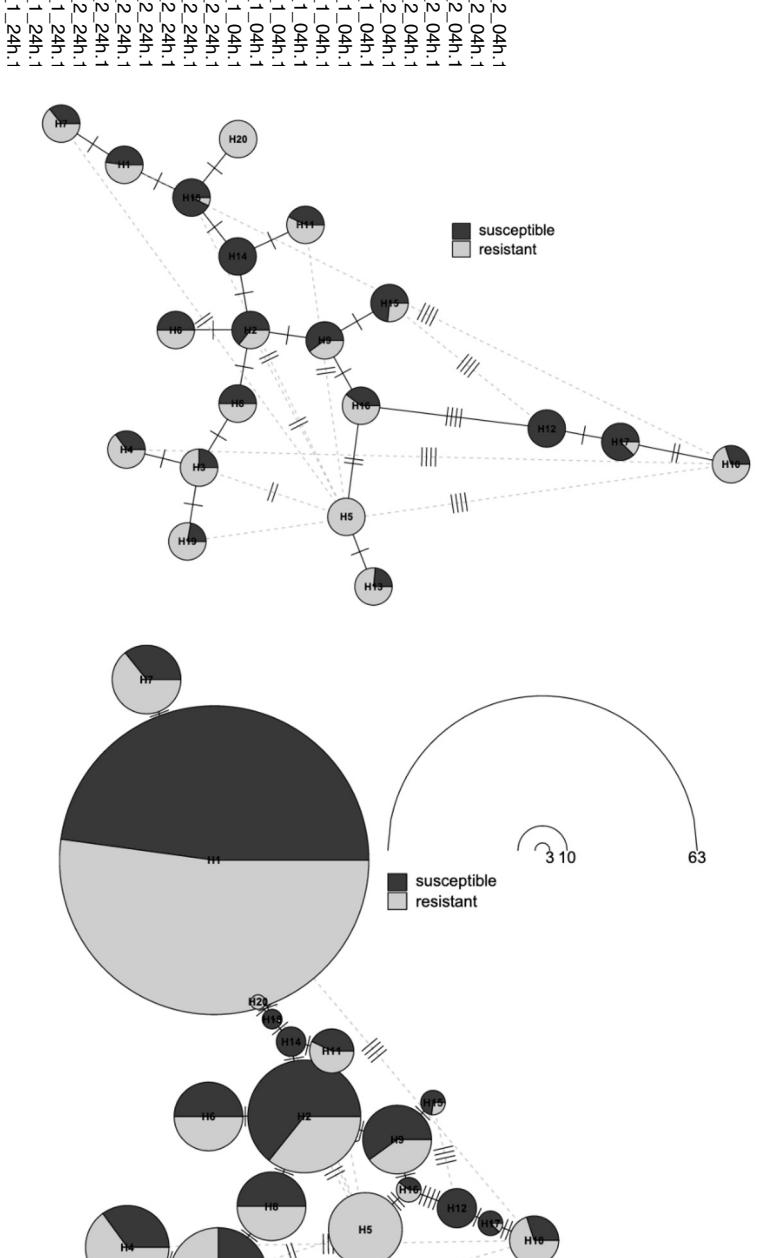
## RESEARCH PROJECTS



Top: Collaboration with Research Center Borstel priority area **Chronic Lung Diseases** – Archaea as possible immune system trainers in the context of asthma, investigated via transcriptome analysis of *methanospira* stimulated PBMCs

Right: Collaboration with Research Center Borstel priority area **Infections** – Network of *Haemophilus influenzae ftsI* gene-related haplotypes together with antibiotic resistance and susceptibility of corresponding isolates, investigated within an interactive, web-based application developed in the Data Science group

- RNA-Seq data analysis
- Nanopore-based methylation analyses
- Nanopore-based Epitranscriptomics
- Association and polygenic scores
- Deep learning-based phenotype prediction
- De novo assembly
- Genomic haplotype-based characterization



Collaborations: Research Center Borstel  
Leibniz Lung Center



UCCSH

Universitäres Cancer Center  
Schleswig-Holstein



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