

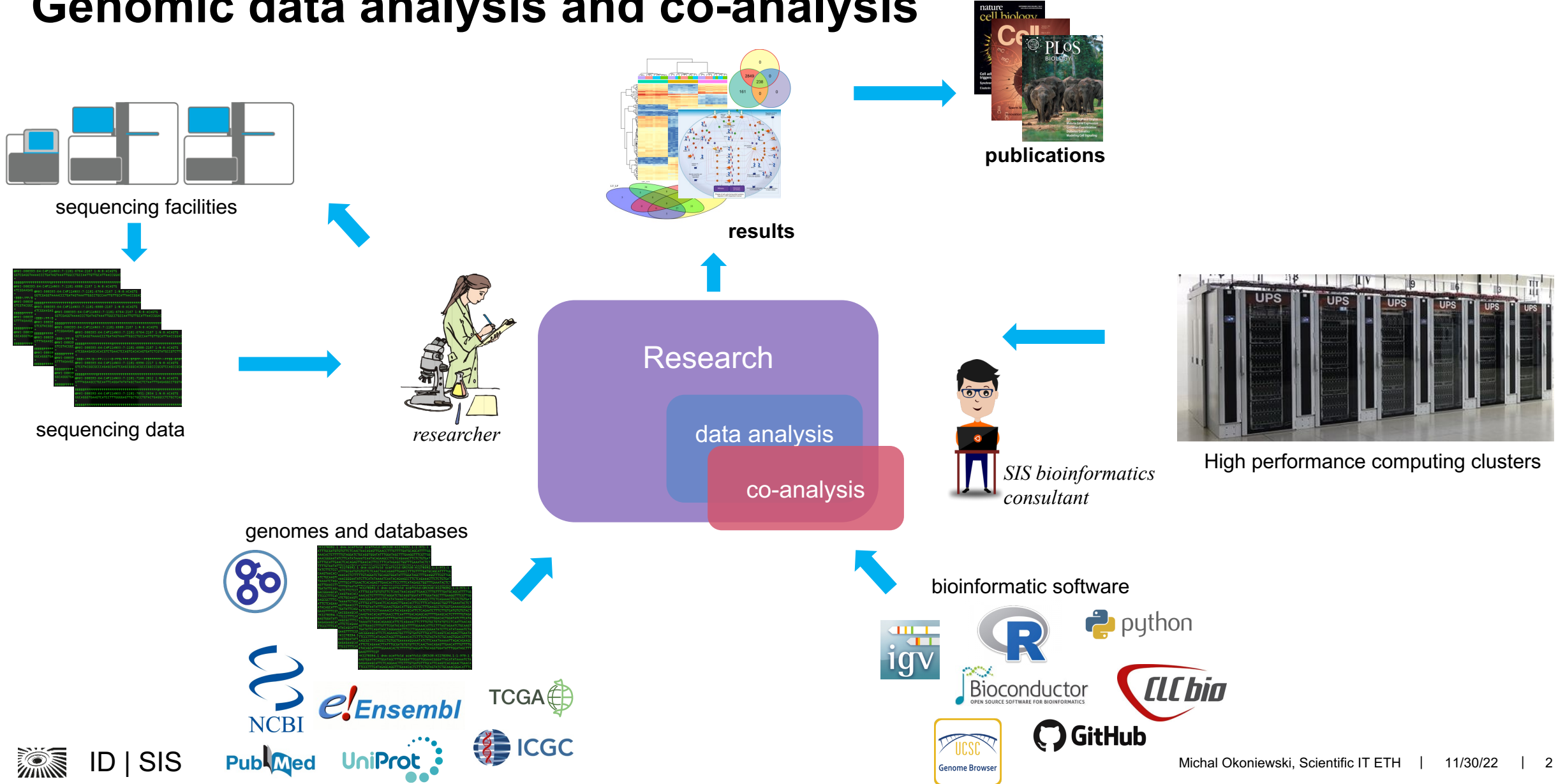


Bioinformatics co-analysis service at the ETH Zurich

Scientific IT Services

Michał Okoniewski

Genomic data analysis and co-analysis



Co-analysis



- A term invented for the new type of service, in discussions with B.Rinn and T. Wüst
- It is a combination of data analytics and individualized bioinformatics and IT training
- Mostly done with departments that have subscription: DBIOL, DBSSE, some cases in DHEST and DERDW
- Around 100 projects done:
 - Ca 15 projects/year since 2015
 - 10 co-authorships and acknowledgements
 - Training: 5 users trained to be bioinformaticians, 50 running data analysis independently
 - Mostly “3 days of work” ad-hoc projects but also several long-term collaborations

Co-analysis principles



data analysis

co-analysis



*SIS bioinformatician
consultant*

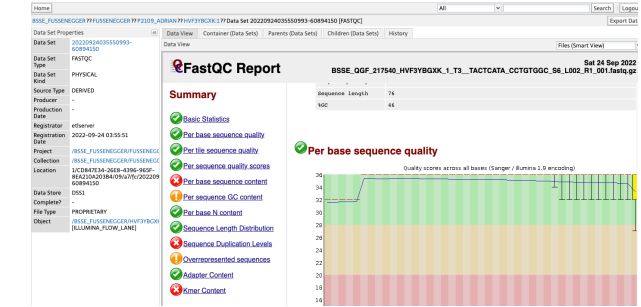
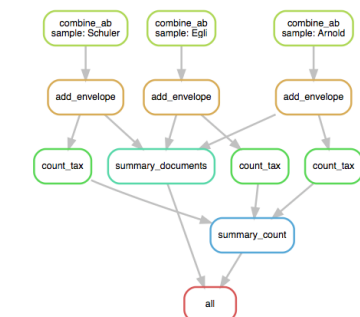
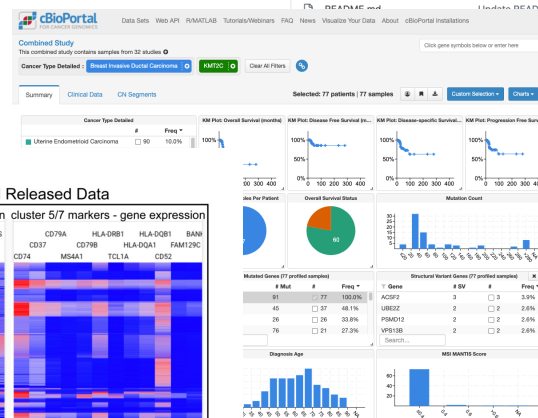
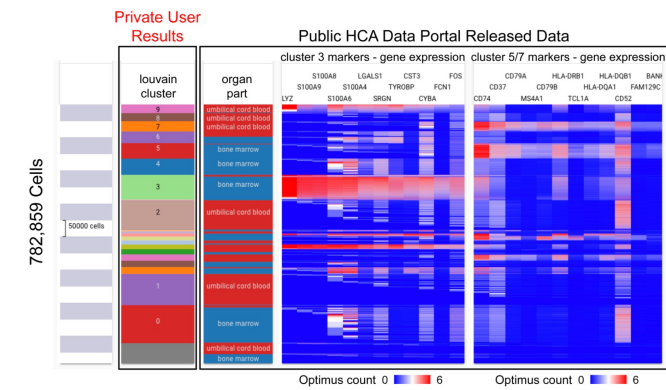
- SIS team is here to help you!
- The purpose is decided by the researcher
- The researcher can learn as much as wants/needs
- IT tasks can be outsourced to SIS or done together if possible
- An upper SIS workload limit is set at the start

Example projects in co-analysis mode

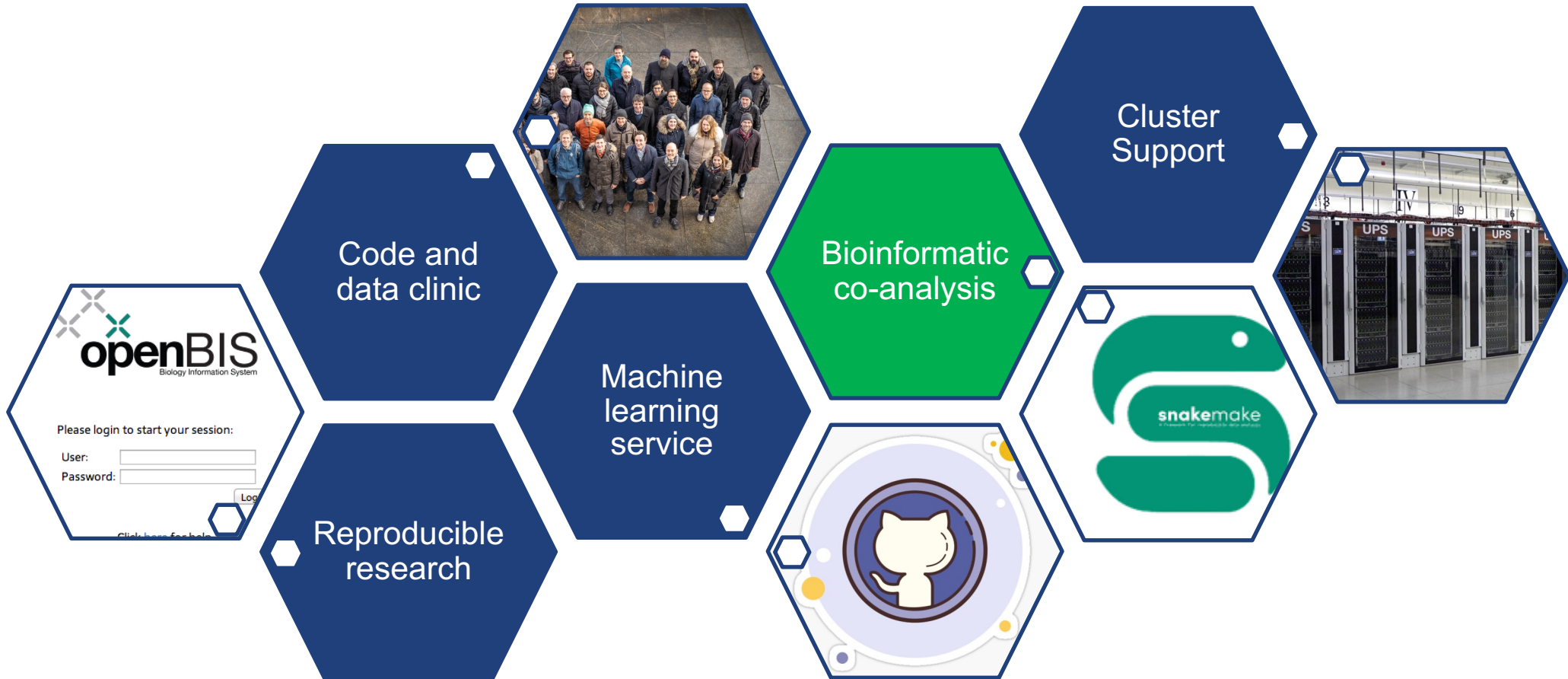
- Making long-term computing tasks parallel on the computing cluster
- Code profiling and optimization: R, python, bash.
- RNA-seq analysis, or any other -omics data
- Reproducible analysis workflows, eg. snakemake
- Non-typical analysis, eg. alternative splicing, UTRs, promoters etc
- Making 3-rd party software or code run
- Database and data management consultancy
- Help with genomic repositories: upload to GEO, SRA and analysis of public data
- Multi-omics
- Linking to the Machine Learning service and to Cluster Support

Reproducible research use

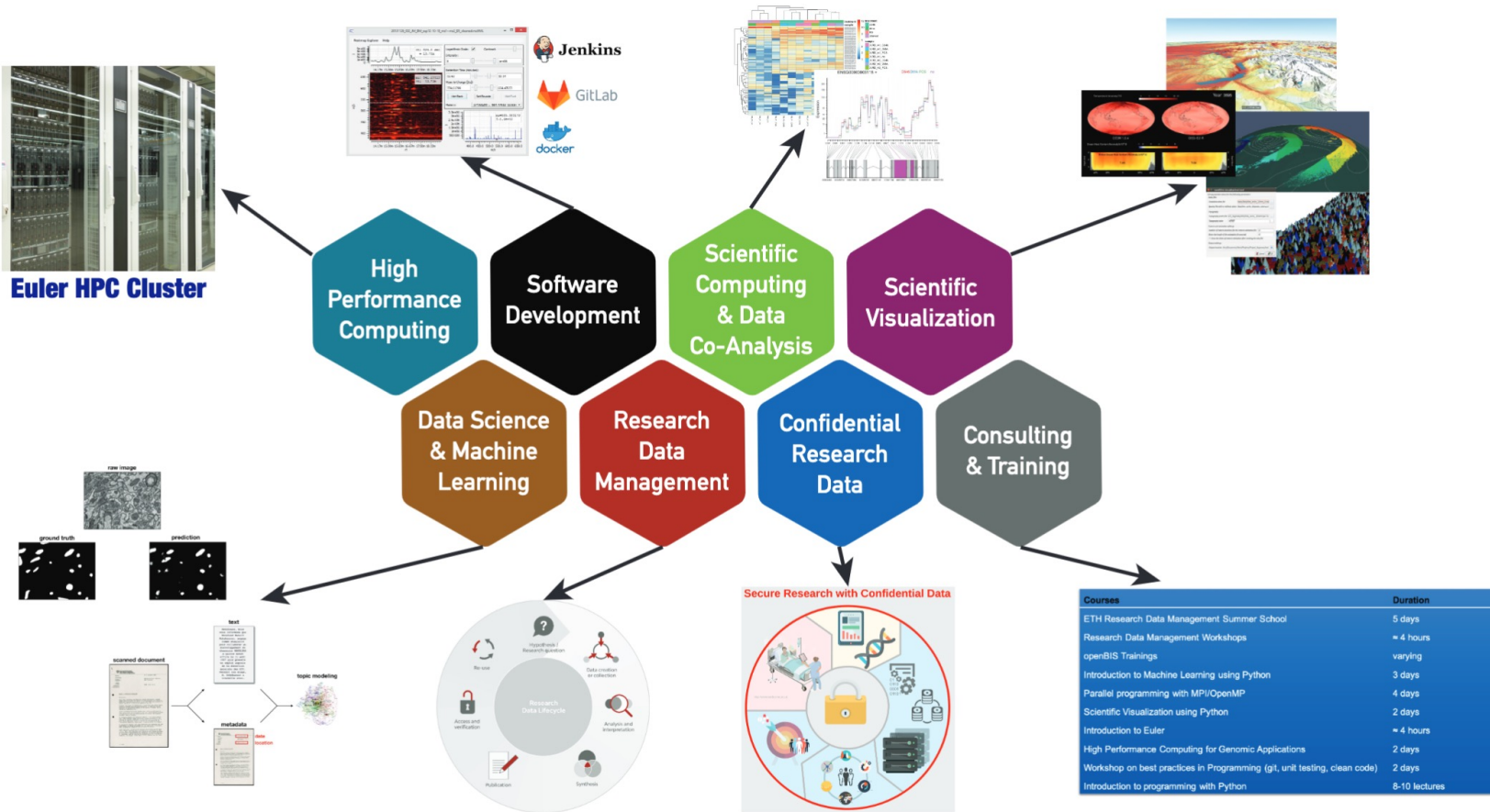
- Data management tools: openBIS, core lab systems
- Workflow managers: snakemake
- Github templates of workflows
- Public databases and repositories

Complementary services to co-analysis in SIS ETH



Scientific IT Services - Empowering Your Research

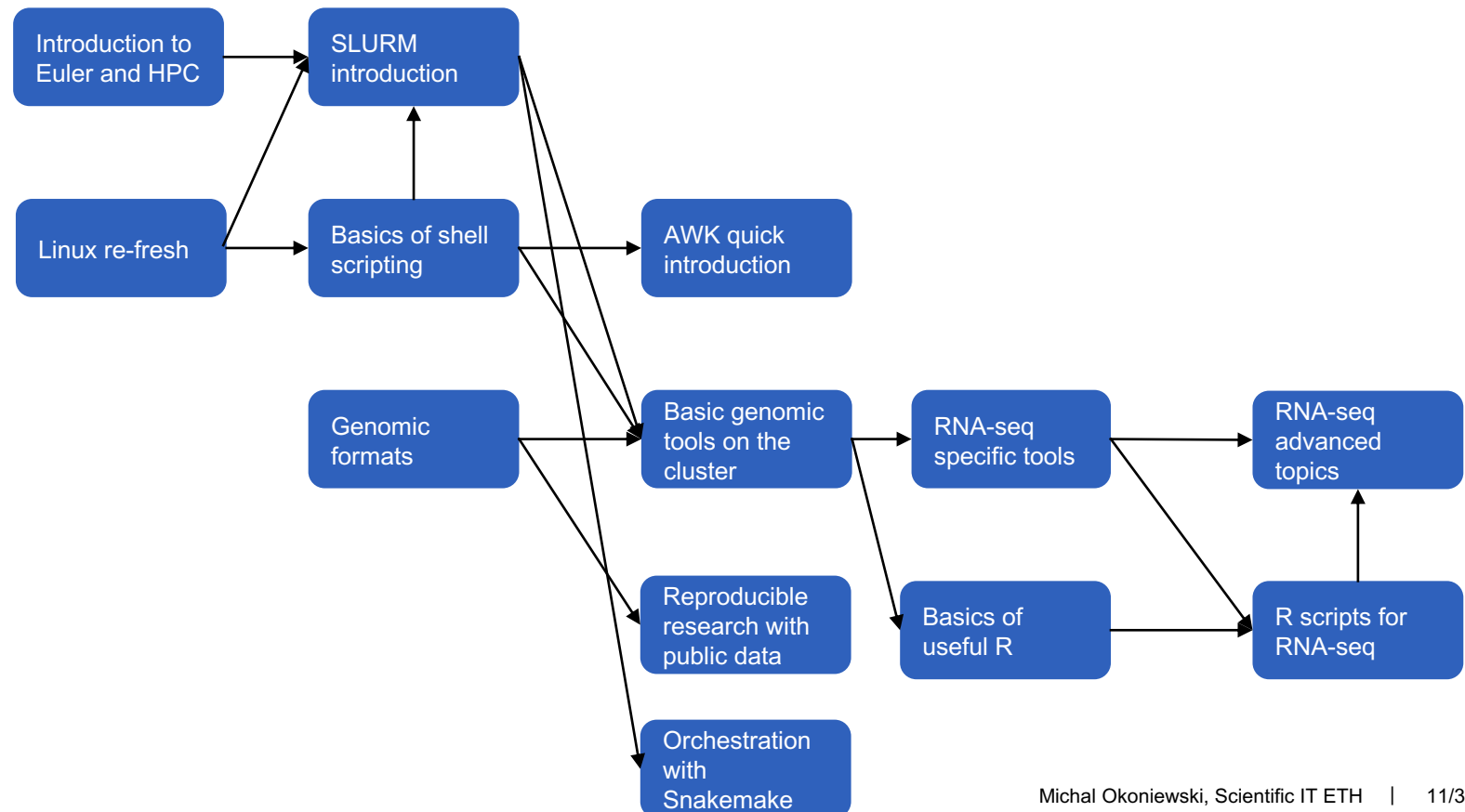


<https://sis.id.ethz.ch>
sis.helpdesk@ethz.ch



The course “HPC for genomic applications”

- Preparing the users, mostly new PhD students and postdocs for co-analysis
- 10 editions done
- 200 people trained



Thank you!

Bioinformatics co-analysis service at the ETH Zurich

