

RHAPSODY

- Federating clinical data for biomedical
research in type 2 diabetes -

Thomas Sparsø

22 & 23 October 2018 • IMI Scientific Symposium • Brussels, Belgium

Rhapsody

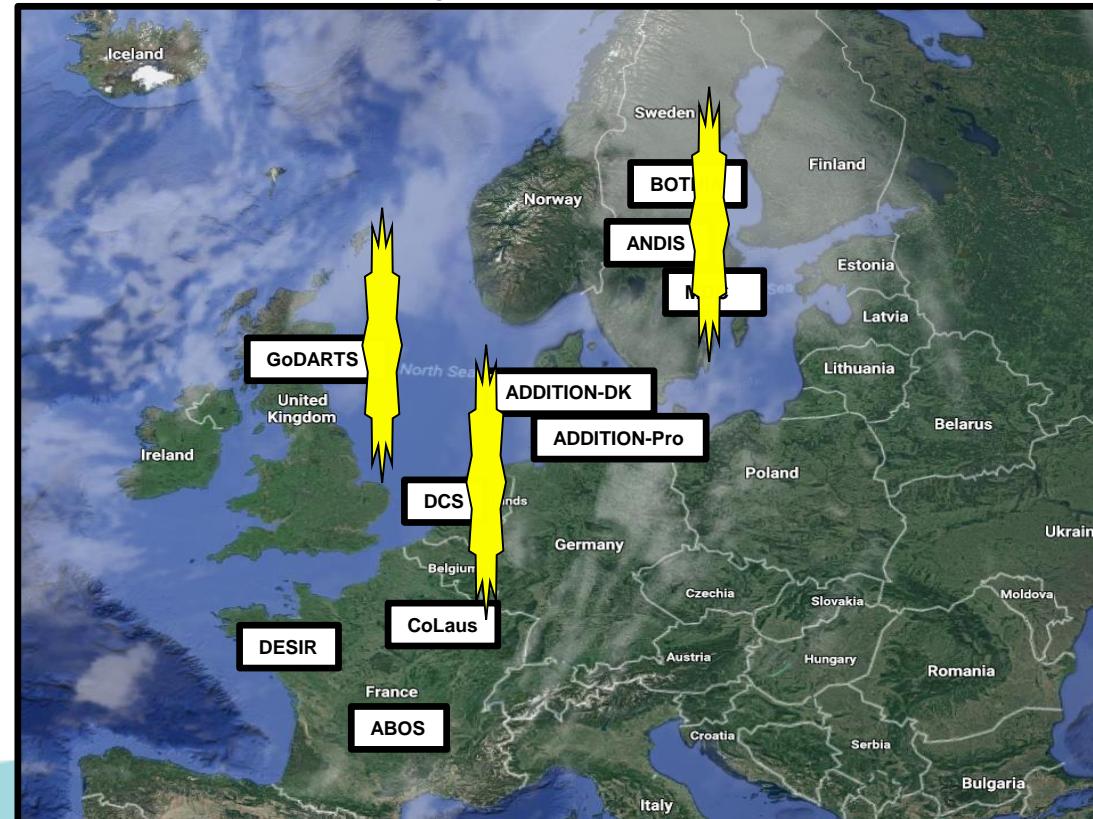
- *Gain insight into the biology of diabetes progression*

- Improve prediction of type 2 diabetes and its progression
 - Multi-omics platforms
- Support patient segmentation
 - Define subsets of type 2 diabetes
 - Define fast and slow progressors

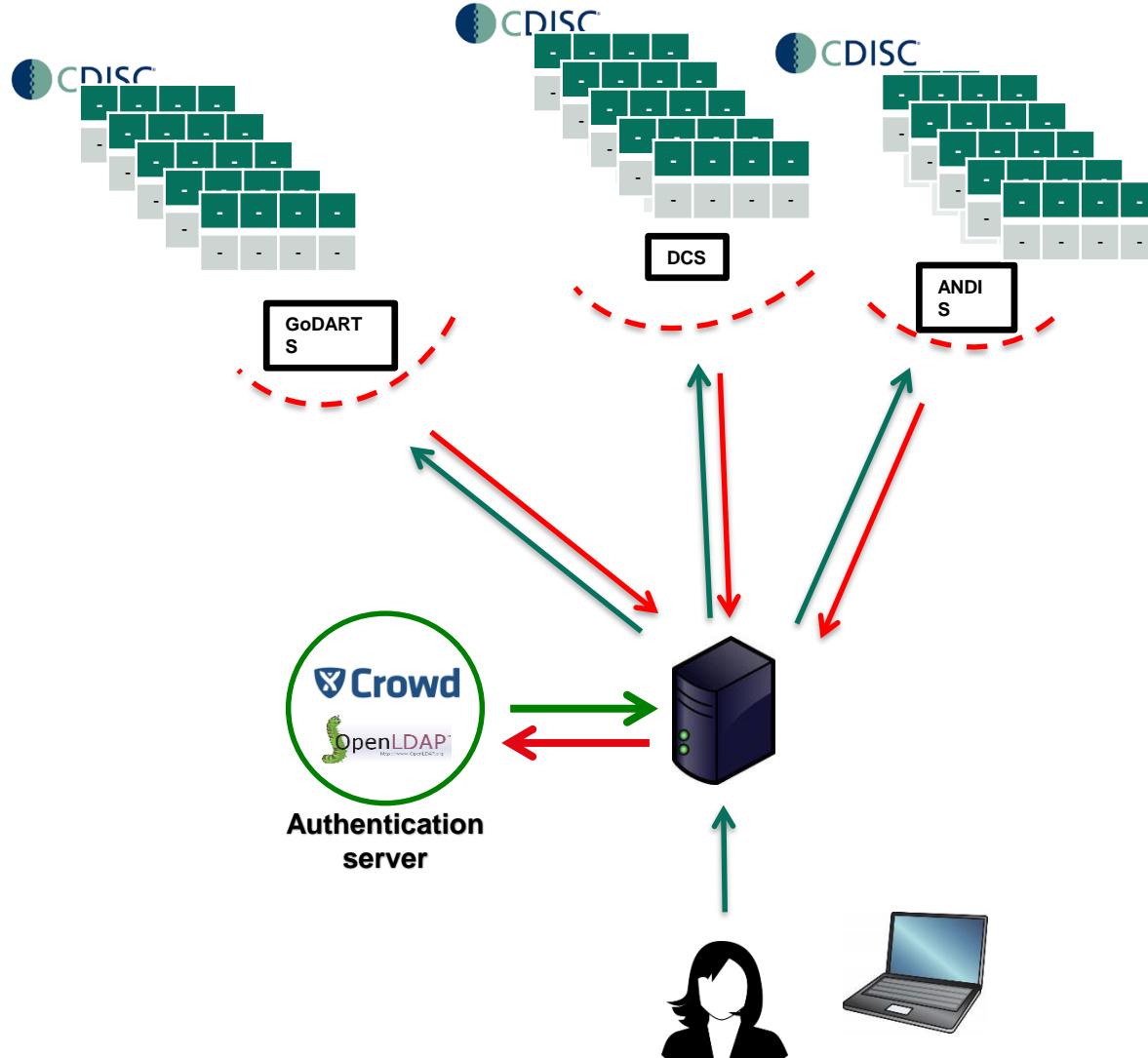


- 1) Deploy a server
- 2) Harmonize the clinical data (CDISC)
- 3) Upload clinical data to the server
- 4) Upload multi omics data to the server
 - a) SomaLogic
 - b) Metabolomics
 - c) Lipidomics
 - d) MicroRNA

Study populations



The federated database system



- Login: username + password
- Load tables
- Filtering and subsetting of tables
- Powerful federated analysis
 - Meta data is returned

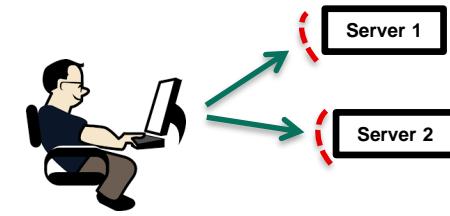
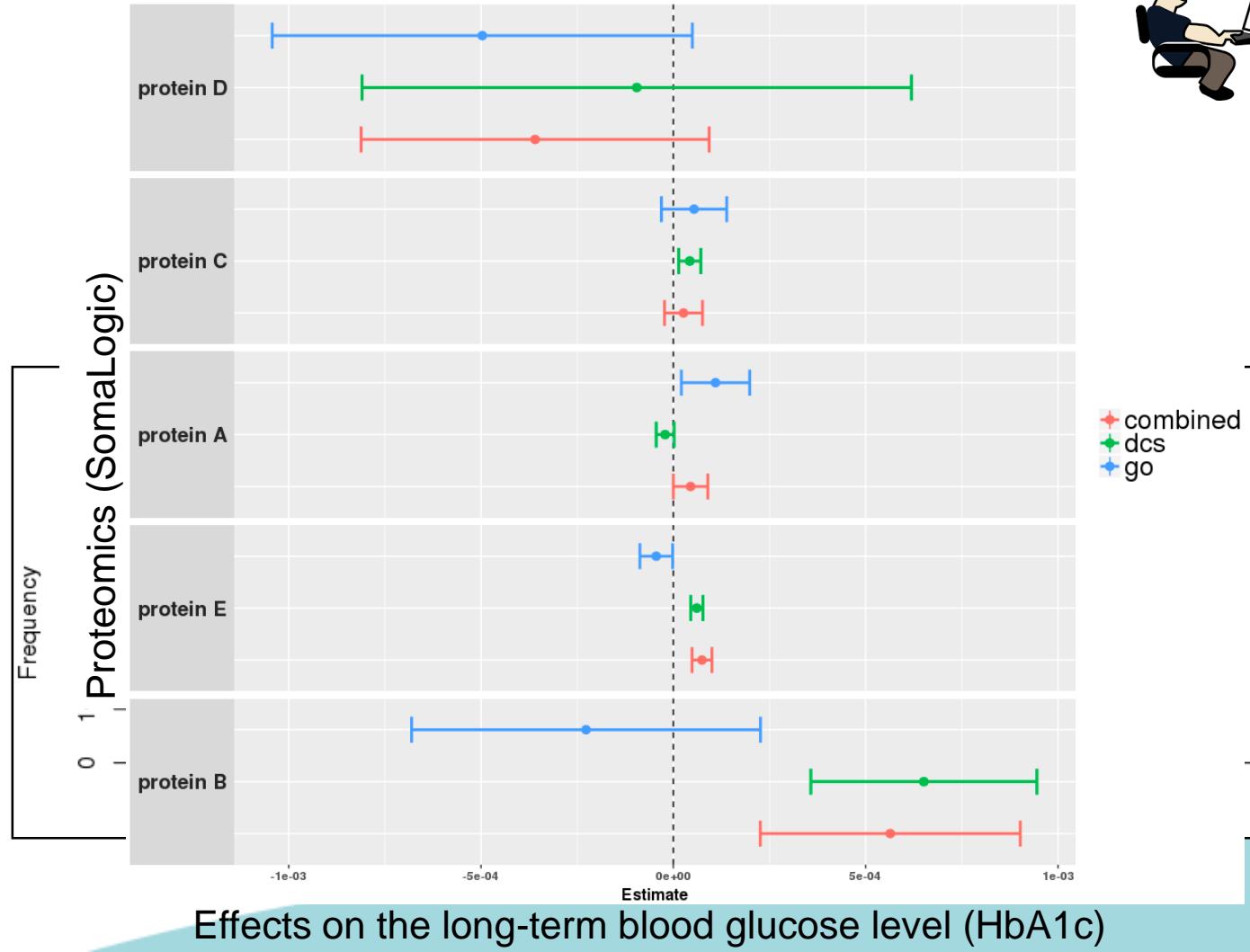


Swiss Institute of
Bioinformatics

Real data analyses in Rhapsody



- *Through the federated data system*



Concluding remarks

- The federated data system is “live” and working in Rhapsody
 - Enables standardised analysis across multiple observational cohorts in Rhapsody
 - Reproducible results
 - High flexibility
- Identify robust biomarkers for assessing disease risk and progression in type 2 diabetes
 - Correlation of multi-omics data with clinical relevant traits
 - Patient segmentation: Cluster diabetes study population in subsets of diabetes