

Swiss federated European Genome-Phenome Archive (fEGA)

SPHN/PHRT Data for health symposium

Mark Ibberson, Director Vital-IT Group, SIB

What is the Federated European Genome Phenome Archive (FEGA)?

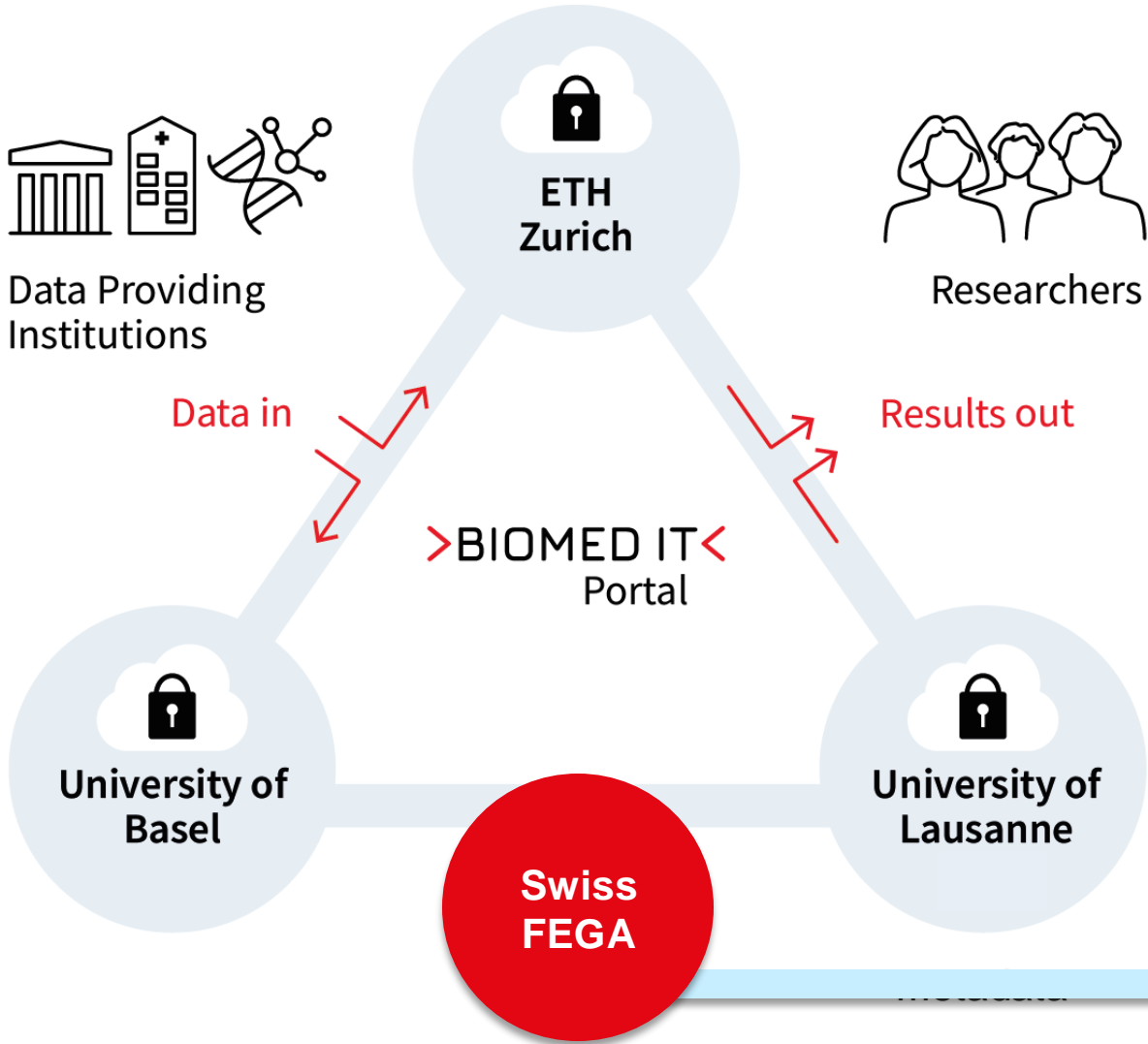


- Repository for archiving human genomic, phenotypic and clinical data
- Important for publishing (e.g. accession codes) and for making data reusable
- Complies with national genomics initiatives and data governance
- One national node per country
- Available datasets are searchable via the central EGA catalogue

<https://blog.ega-archive.org/safe-access-to-sensitive-human-data-federated-ega>

Swiss FEAGA is being built on BioMed-IT

>BIO
MED
IT<



Swiss FEAGA is a partnership of 6 institutions



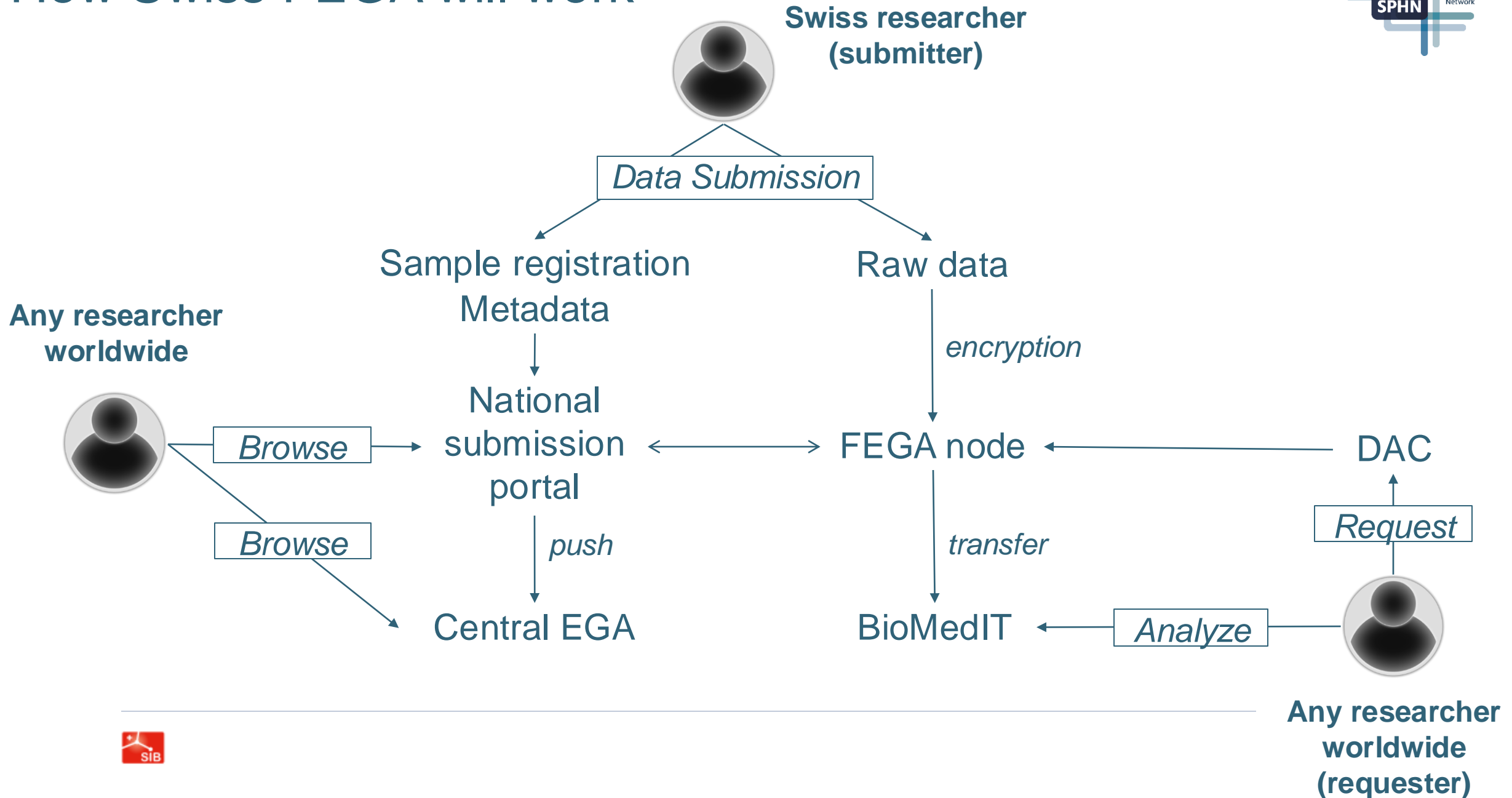
Swiss Institute of
Bioinformatics



Federated
European
Genome-phenome
Archive
Switzerland



How Swiss FEGA will work

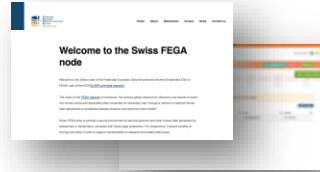


Main partner roles



Swiss Institute of Bioinformatics

- Leading house
- Submission portal



- Expert knowledge, user interfaces
- Submitter and requestor engagement



- Submitter and requestor engagement



- Multi-omics digital objects
- DAC portal



- Development and deployment of FEGA services



- Backend cloud storage

Outlook until end 2025

- Work is underway to implement a Swiss FEGA node
- An initial version (minimum viable product) will be available by end 2024
- Signatures to officially join the FEGA network planned end 2024/early 2025
- First datasets are expected in Q1 2025 (pilot datasets) and Q2 2025 (first production datasets)
- Interface testing and process optimization will be done during 2025 in collaboration with data submitters and requestors
- Metadata expansion to different –omics data types (e.g. metabolomics, proteomics) (including multi-omics digital objects) during 2025
- Final production version delivered by end 2025

If you are a potential data submitter/requestor
Please contact us!



fega.coordination@sib.swiss
www.fega.swiss

Questions