FAIR data and metadata

The X-omics FAIR Data Cube and its added value for multi-omics researchers

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Introduction

During the Research Data Life Cycle researchers take different roles. Sometimes we are study owners creating and describing new research data. On other occasions we search for existing data to plan new studies, reanalyze, or integrate data. This is facilitated by data that is Findable, Accessible, Interoperable and Reusable (FAIR). In Xomics we develop different tools that help researchers both create and reuse FAIR multi-omics data.

Creation of multi-omics data and metadata

In collaboration with the FAIR Genomes project and United for Metabolic Diseases (UMD), we develop metadata schemas for different omics data types. We use the Investigation-Study-Assay (ISA) metadata framework to capture experimental metadata and share example workflows for metadata creation. https://github.com/Xomics, https://github.com/fairgenomes





vantage6 server that allows to send computing requests to access-protected data. After being approved by local data owners, computations can be executed using Docker images. Results are sent back to the researcher.

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