Proteiner, pixlar och populationer: Arbetssätt och lärdomar från att stötta Svenska bidrag till globala biodata-resurser

NBIS - National Bioinformatics Infrastructure Sweden

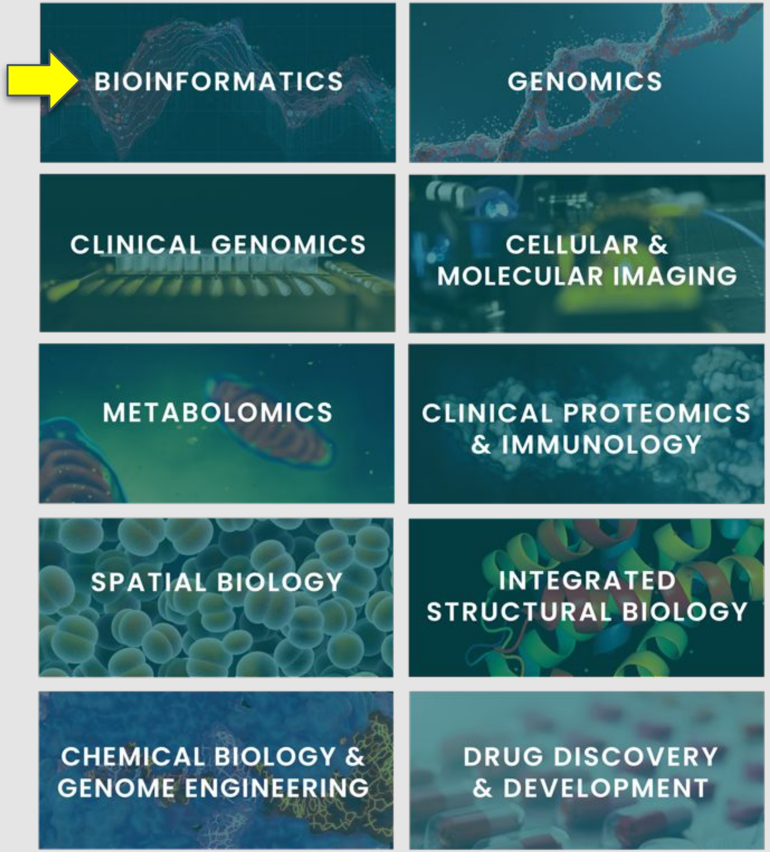
Wolmar Nyberg Åkerström, NBIS, SciLifeLab

2025-12-16

Omställningen till ett öppet vetenskapligt system – så arbetar vi, 16 December 2025, Online

https://doi.org/10.17044/scilifelab.30901943

SciLifeLab



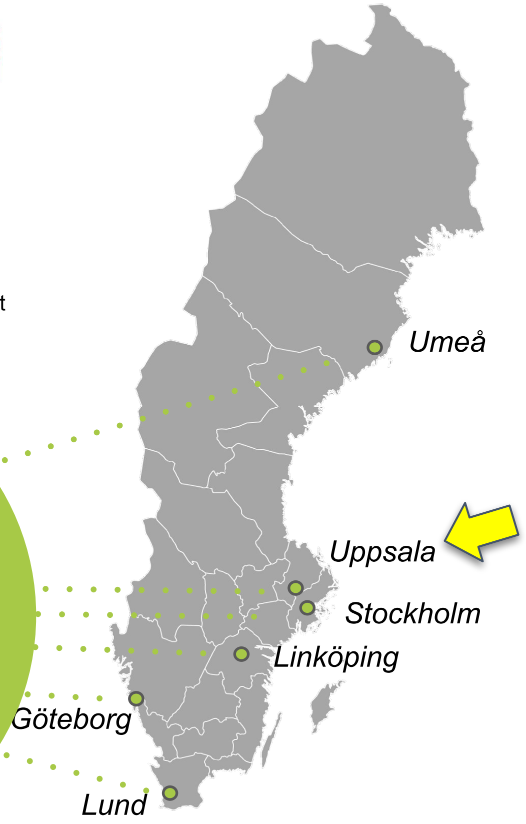
NBIS

NATIONAL BIOINFORMATICS INFRASTRUCTURE SWEDEN


Bengt Persson
Director

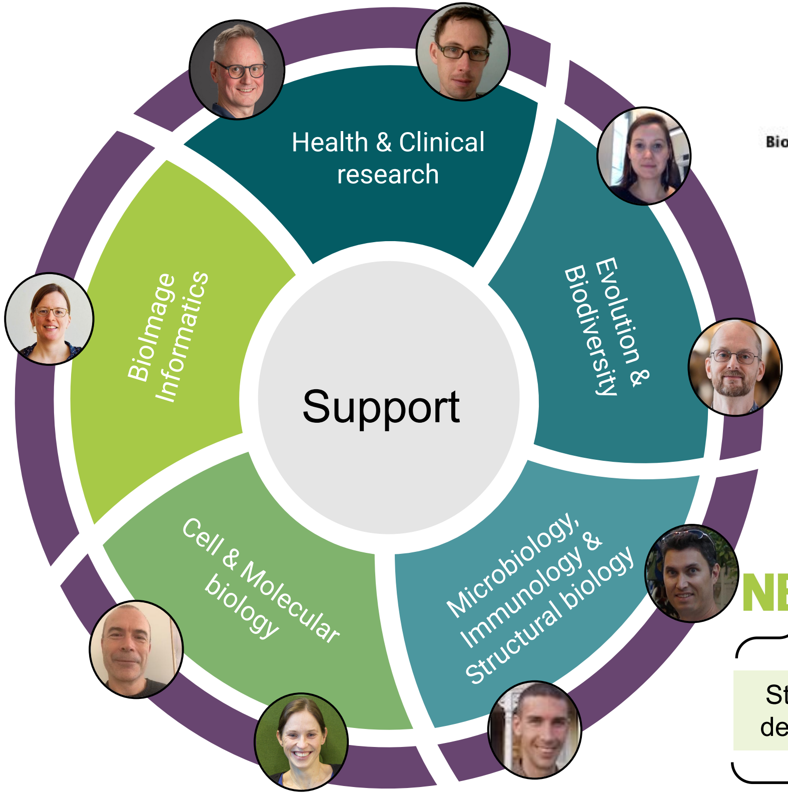

Björn Nystedt
Co-director

~130 staff at six different sites across Sweden with expertise in many different omics-related areas



NBIS research area teams & subjects

Support



Health & Clinical research

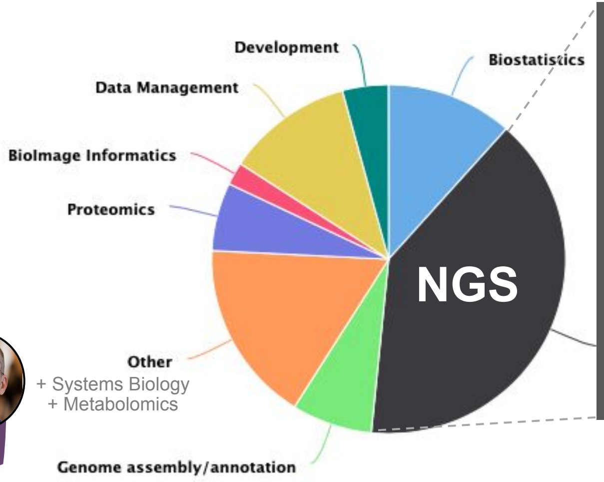
Evolution & Biodiversity

Microbiology, Immunology & Structural biology

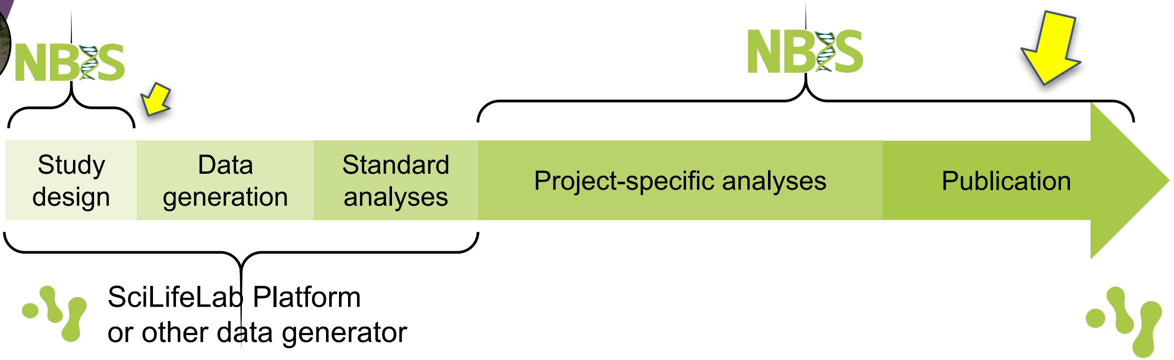
Cell & Molecular biology

BioImage Informatics

Support



Genomics
Transcriptomics
Single cell analysis
Epigenetics
Metagenomics
Integrative multi-omics
...



NBIS

NBIS

Study design

Data generation

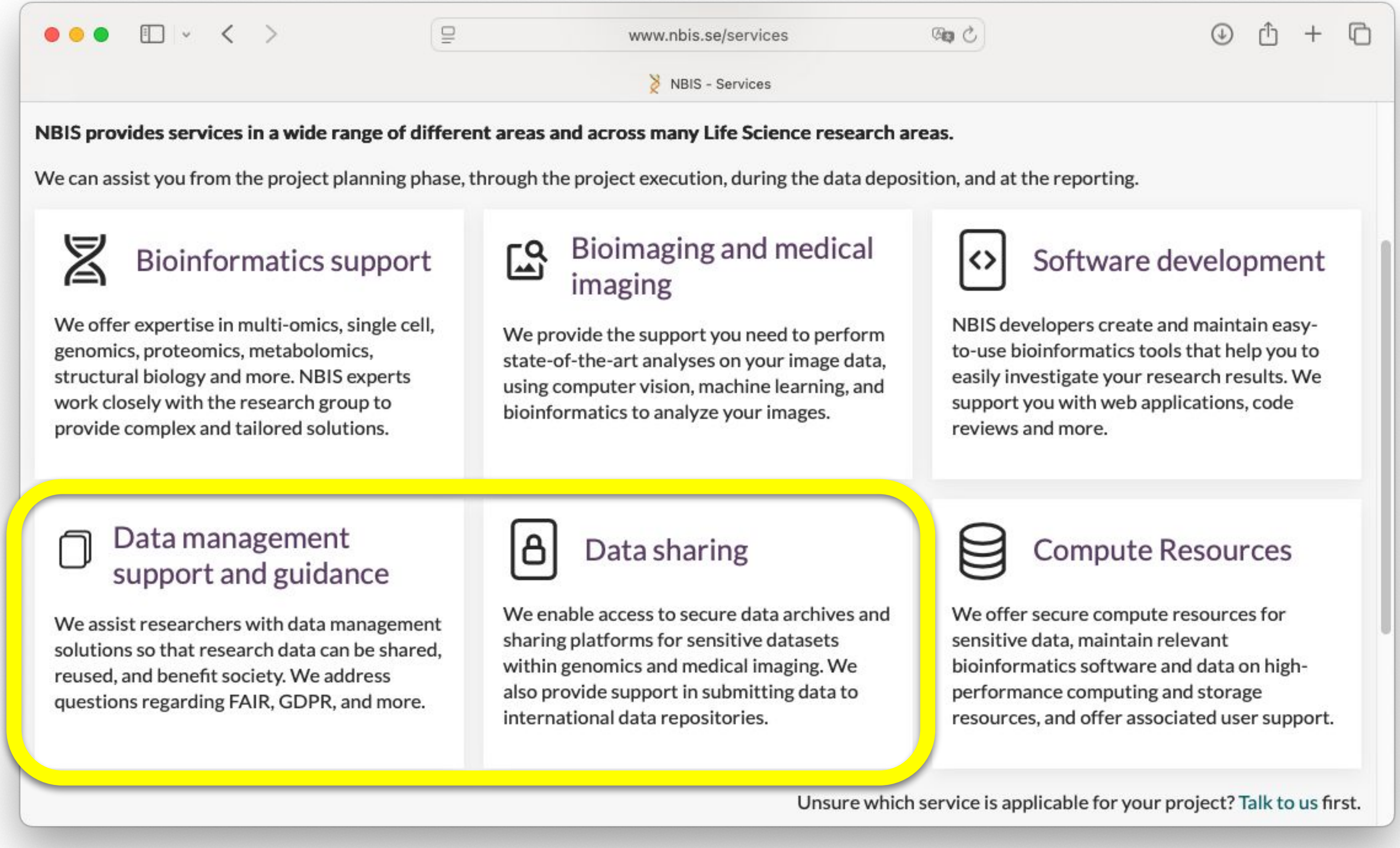
Standard analyses

Project-specific analyses

Publication

SciLifeLab Platform
or other data generator

Services for Swedish Life Science Research



NBIS provides services in a wide range of different areas and across many Life Science research areas.

We can assist you from the project planning phase, through the project execution, during the data deposition, and at the reporting.

Bioinformatics support

We offer expertise in multi-omics, single cell, genomics, proteomics, metabolomics, structural biology and more. NBIS experts work closely with the research group to provide complex and tailored solutions.

Bioimaging and medical imaging

We provide the support you need to perform state-of-the-art analyses on your image data, using computer vision, machine learning, and bioinformatics to analyze your images.

Software development

NBIS developers create and maintain easy-to-use bioinformatics tools that help you to easily investigate your research results. We support you with web applications, code reviews and more.

Data management support and guidance

We assist researchers with data management solutions so that research data can be shared, reused, and benefit society. We address questions regarding FAIR, GDPR, and more.

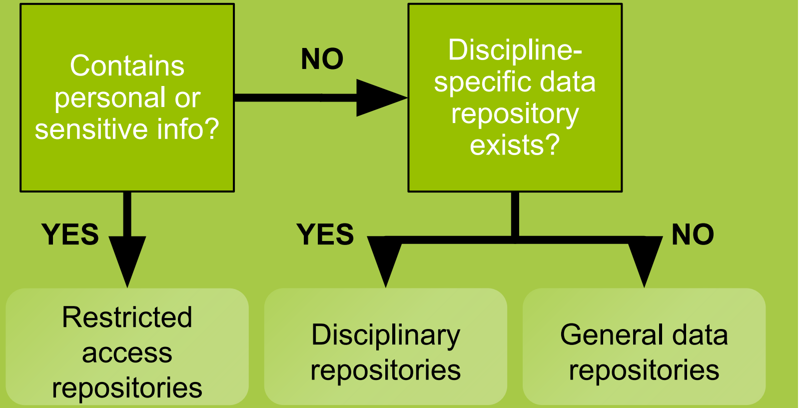
Data sharing

We enable access to secure data archives and sharing platforms for sensitive datasets within genomics and medical imaging. We also provide support in submitting data to international data repositories.

Compute Resources

We offer secure compute resources for sensitive data, maintain relevant bioinformatics software and data on high-performance computing and storage resources, and offer associated user support.

Unsure which service is applicable for your project? Talk to us first.


Contains personal or sensitive info?

NO

Discipline-specific data repository exists?

YES

YES

NO

Restricted access repositories

Disciplinary repositories

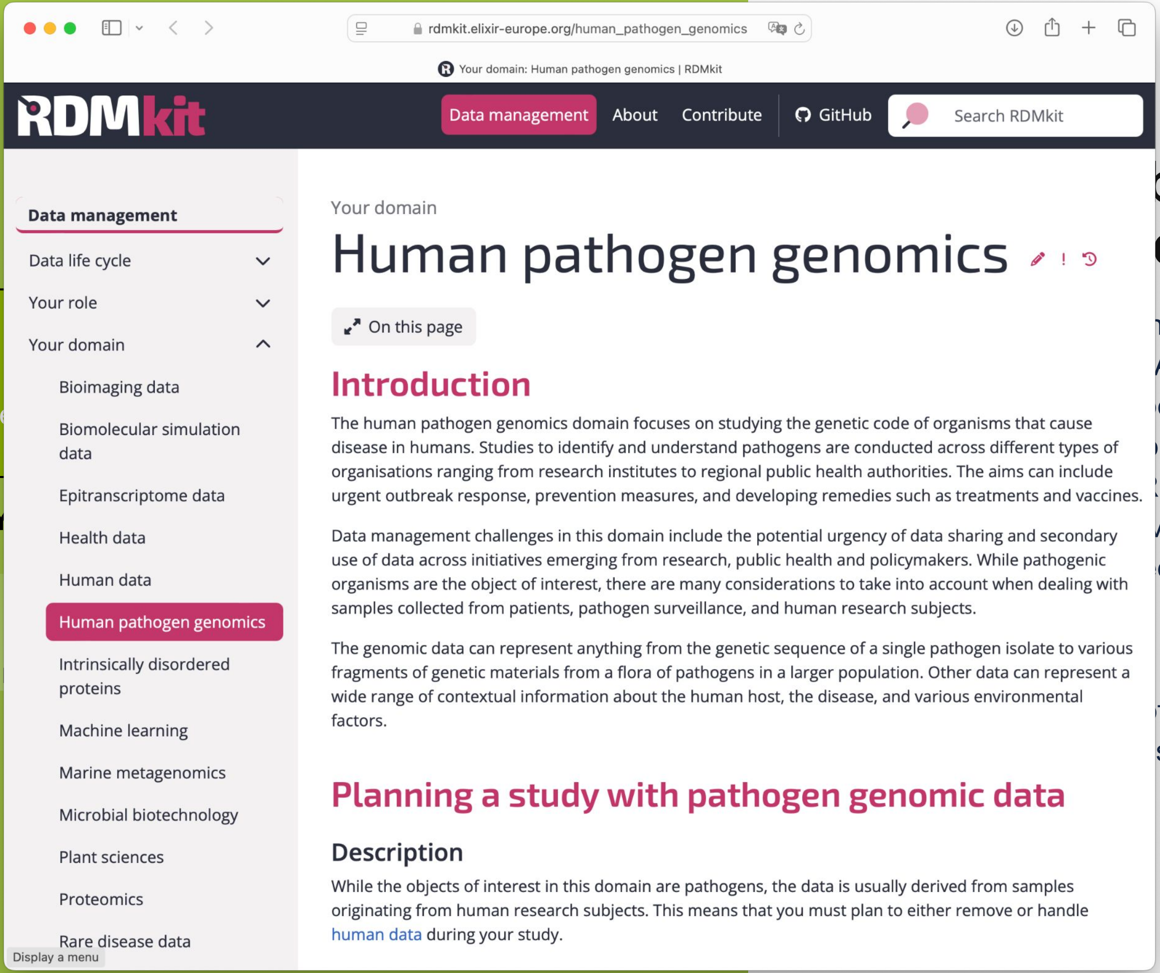
General data repositories

Data submission to public repositories

Making the data underlying your research publicly available to others is a fundamental part of a FAIR research process. When publicly available and appropriately described, data can be re-used by yourself as well as others. Domain-specific public repositories offer the most direct routes to making your data FAIR. This workshop will give you the why, where and how of data sharing via repository submission, including hands-on exercise. No prior knowledge is required in order to attend this workshop.

Learning outcomes:

- Know the benefits of data sharing
- Know how to find a suitable repository for different types of data
- Have experience of a repository submission



Your domain

Human pathogen genomics

Introduction

The human pathogen genomics domain focuses on studying the genetic code of organisms that cause disease in humans. Studies to identify and understand pathogens are conducted across different types of organisations ranging from research institutes to regional public health authorities. The aims can include urgent outbreak response, prevention measures, and developing remedies such as treatments and vaccines.

Data management challenges in this domain include the potential urgency of data sharing and secondary use of data across initiatives emerging from research, public health and policymakers. While pathogenic organisms are the object of interest, there are many considerations to take into account when dealing with samples collected from patients, pathogen surveillance, and human research subjects.

The genomic data can represent anything from the genetic sequence of a single pathogen isolate to various fragments of genetic materials from a flora of pathogens in a larger population. Other data can represent a wide range of contextual information about the human host, the disease, and various environmental factors.

Planning a study with pathogen genomic data

Description

While the objects of interest in this domain are pathogens, the data is usually derived from samples originating from human research subjects. This means that you must plan to either remove or handle human data during your study.

bmission to public
epositories

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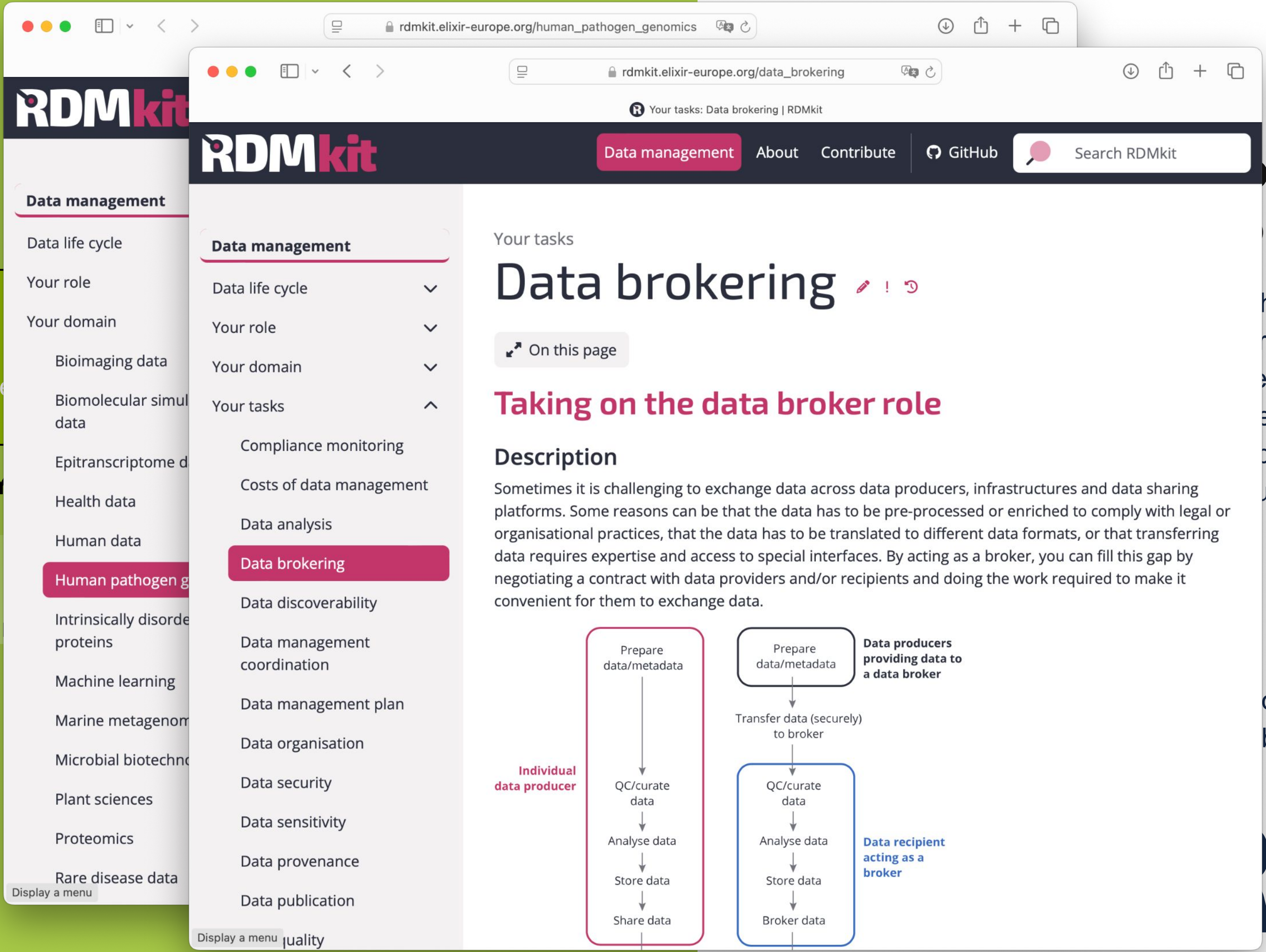

rdmkit.elixir-europe.org/human_pathogen_genomics

RDMkit

Data management

- Data life cycle
- Your role
- Your domain
  - Bioimaging data
  - Biomolecular simul data
  - Epitranscriptome d
  - Health data
  - Human data
  - Human pathogen g
  - Intrinsically disorde proteins
  - Machine learning
  - Marine metagenom
  - Microbial biotechn
  - Plant sciences
  - Proteomics
  - Rare disease data

Display a menu

rdmkit.elixir-europe.org/data_brokering

Your tasks: Data brokering | RDMkit

RDMkit — Data management · About · Contribute · GitHub · Search RDMkit

Data management

- Data life cycle
- Your role
- Your domain
- Your tasks
  - Compliance monitoring
  - Costs of data management
  - Data analysis
  - Data brokering
  - Data discoverability
  - Data management coordination
  - Data management plan
  - Data organisation
  - Data security
  - Data sensitivity
  - Data provenance
  - Data publication
  - uality

Display a menu

Your tasks

Data brokering

On this page

Taking on the data broker role

Description

Sometimes it is challenging to exchange data across data producers, infrastructures and data sharing platforms. Some reasons can be that the data has to be pre-processed or enriched to comply with legal or organisational practices, that the data has to be translated to different data formats, or that transferring data requires expertise and access to special interfaces. By acting as a broker, you can fill this gap by negotiating a contract with data providers and/or recipients and doing the work required to make it convenient for them to exchange data.

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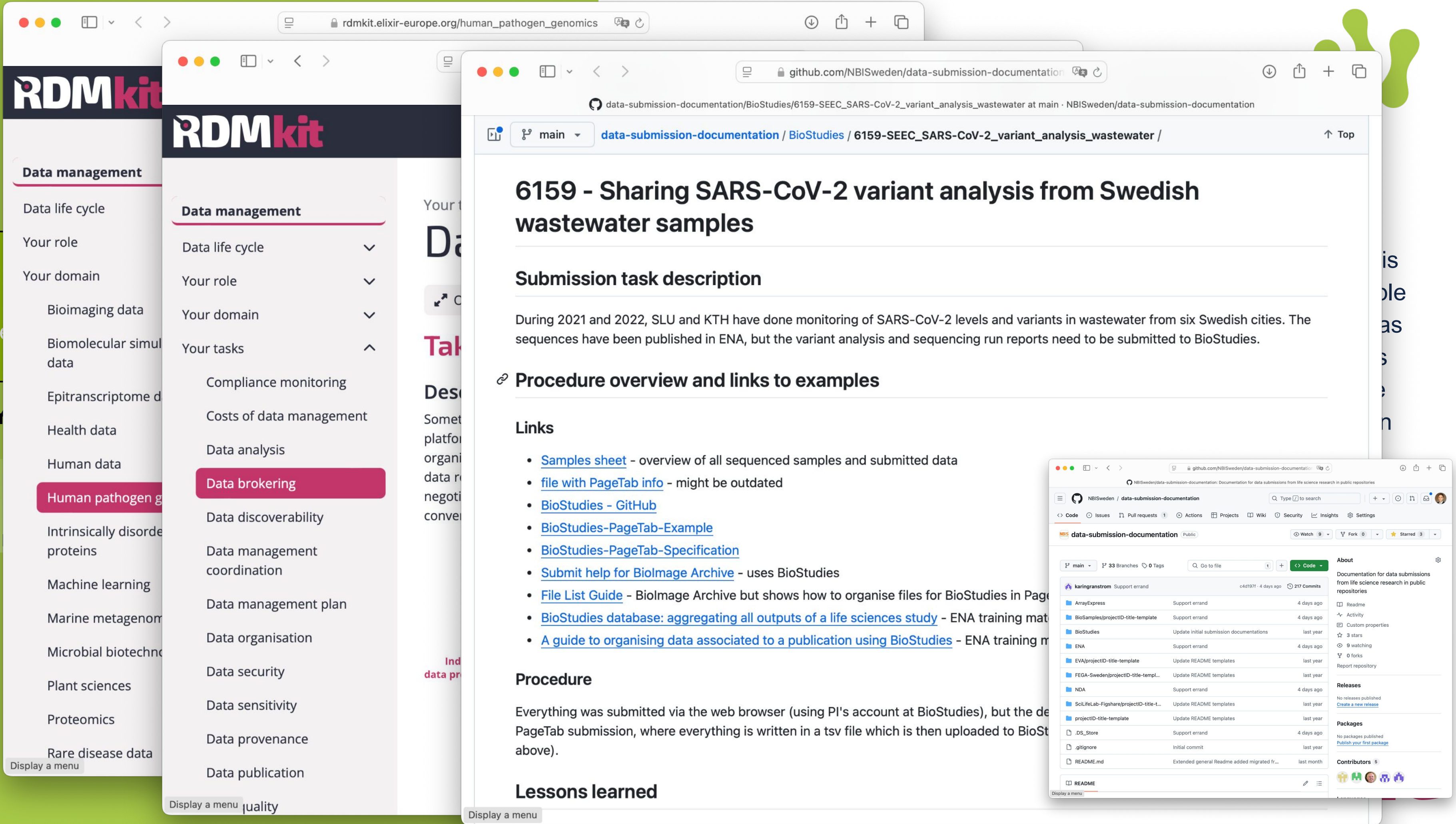


6159 - Sharing SARS-CoV-2 variant analysis from Swedish wastewater samples

Submission task description

During 2021 and 2022, SLU and KTH have done monitoring of SARS-CoV-2 levels and variants in wastewater from six Swedish cities. The sequences have been published in ENA, but the variant analysis and sequencing run reports need to be submitted to BioStudies.

Procedure overview and links to examples

Links

- Samples sheet - overview of all sequenced samples and submitted data
- file with PageTab info - might be outdated
- BioStudies - GitHub
- BioStudies-PageTab-Example
- BioStudies-PageTab-Specification
- Submit help for BioImage Archive - uses BioStudies
- File List Guide - BioImage Archive but shows how to organise files for BioStudies in Page
- BioStudies database: aggregating all outputs of a life sciences study - ENA training mat
- A guide to organising data associated to a publication using BioStudies - ENA training m

Procedure

Everything was submitted via the web browser (using PI's account at BioStudies), but the de PageTab submission, where everything is written in a tsv file which is then uploaded to BioSt above).

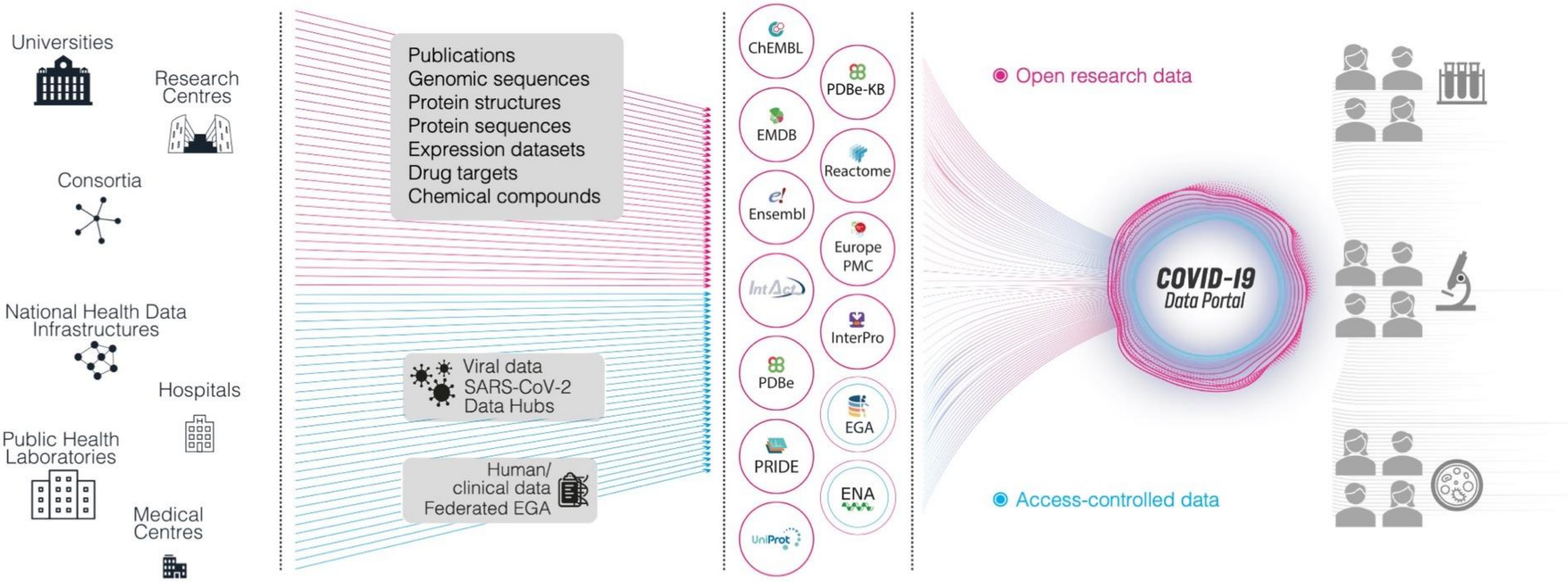
Lessons learned

ArrayExpress	Support errand	4 days ago
BioSamples/projectID-title-template	Support errand	4 days ago
BioStudies	Update initial submission documentations	last year
ENA	Support errand	4 days ago
EVA/projectID-title-template	Update README templates	last year
FEGA-Sweden/projectID-title-templ...	Update README templates	last year
NDA	Support errand	4 days ago
SciLifeLab-Figshare/projectID-title-t...	Update README templates	last year
projectID-title-template	Update README templates	last year
.DS_Store	Support errand	4 days ago
.gitignore	Initial commit	last year
README.md	Extended general Readme added migrated fr...	last month

About

Documentation for data submissions from life science research in public repositories

Connected data resources



Data and metadata in context (I)

Study & data design → Sampling & specimen collection → Sample preparation → Sample analysis & data generation → Data processing to prepare inputs for analysis → Data analysis → Communicating results

Procedures
data protection,
ethics permit,
infrastructure,
standards,
protocols,
data dictionaries,
data access, …

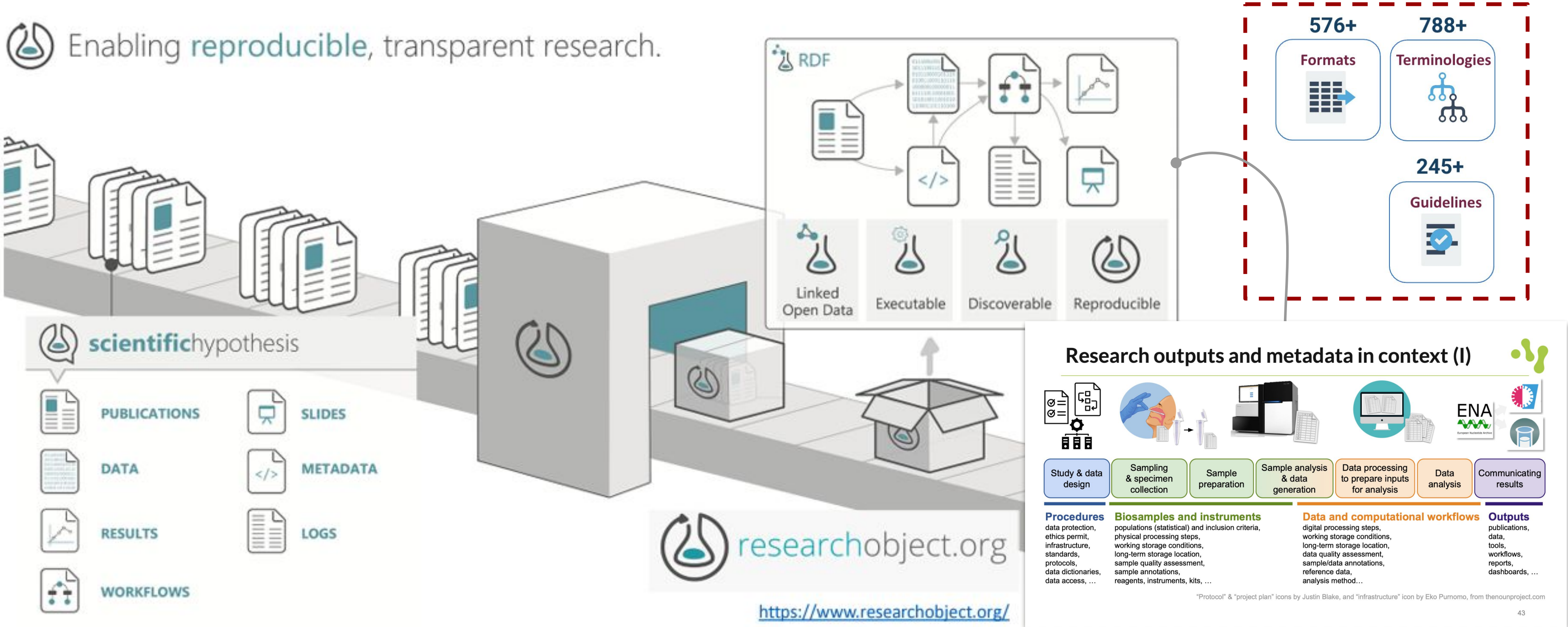
Biosamples and instruments
populations (statistical) and inclusion criteria,
physical processing steps,
working storage conditions,
long-term storage location,
sample quality assessment,
sample annotations,
reagents, instruments, kits, …

Data and computational workflows
digital processing steps,
working storage conditions,
long-term storage location,
data quality assessment,
sample/data annotations,
reference data,
analysis method…

Outputs
publications,
data,
tools,
workflows,
reports,
dashboards, …

“Protocol” & “project plan” icons by Justin Blake, and “infrastructure” icon by Eko Purnomo, from thenounproject.com

Data and metadata in context (II)



https://www.researchobject.org/

Research outputs and metadata in context (I)

Study & data design	Sampling & specimen collection	Sample preparation	Sample analysis & data generation	Data processing to prepare inputs for analysis	Data analysis	Communicating results

Procedures
data protection,
ethics permit,
infrastructure,
standards,
protocols,
data dictionaries,
data access, …

Biosamples and instruments
populations (statistical) and inclusion criteria,
physical processing steps,
working storage conditions,
long-term storage location,
sample quality assessment,
sample annotations,
reagents, instruments, kits, …

Data and computational workflows
digital processing steps,
working storage conditions,
long-term storage location,
data quality assessment,
sample/data annotations,
reference data,
analysis method…

Outputs
publications,
data,
tools,
workflows,
reports,
dashboards, …

"Protocol" & "project plan" icons by Justin Blake, and "infrastructure" icon by Eko Purnomo, from thenounproject.com

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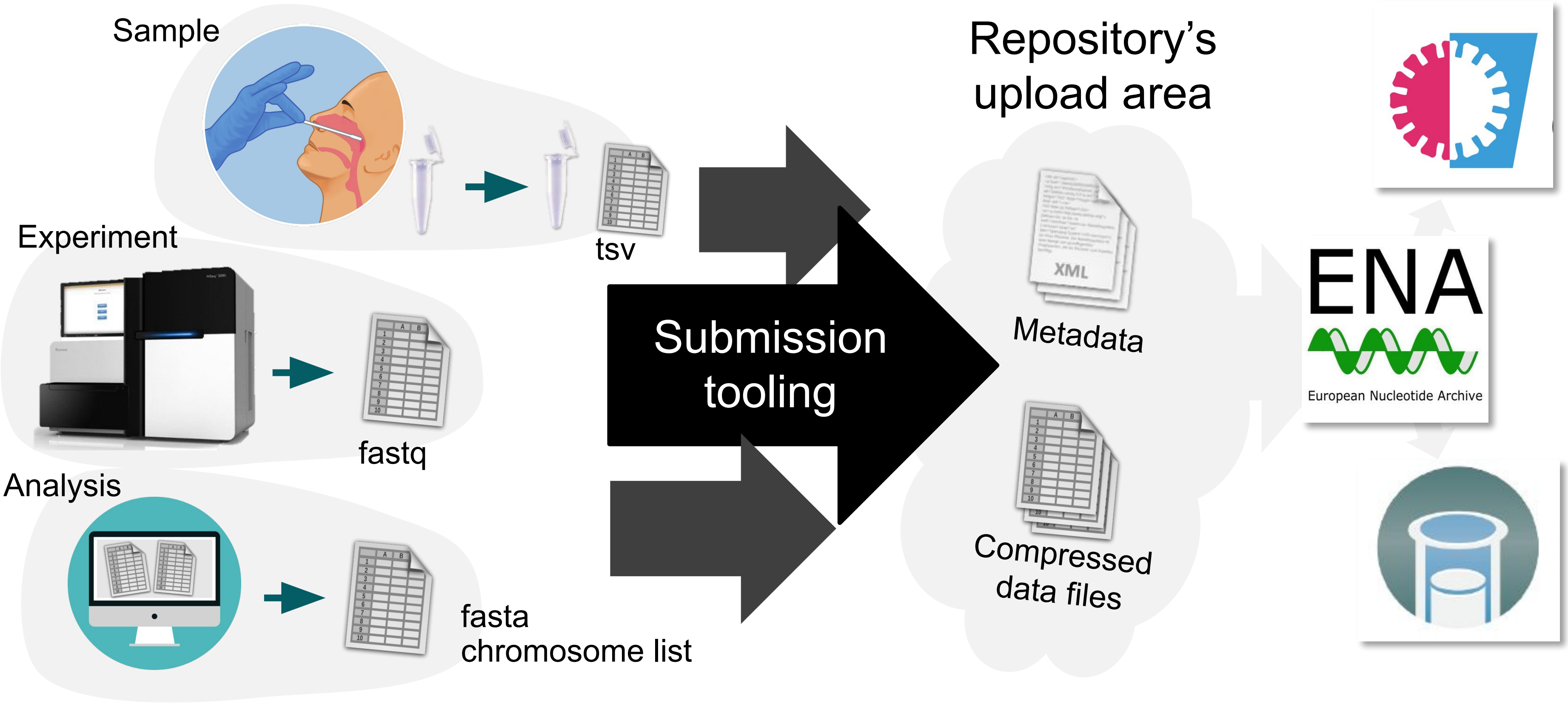
Depositing data to a repository



Sample

tsv

Experiment

fastq

Analysis

fasta
chromosome list

Submission tooling

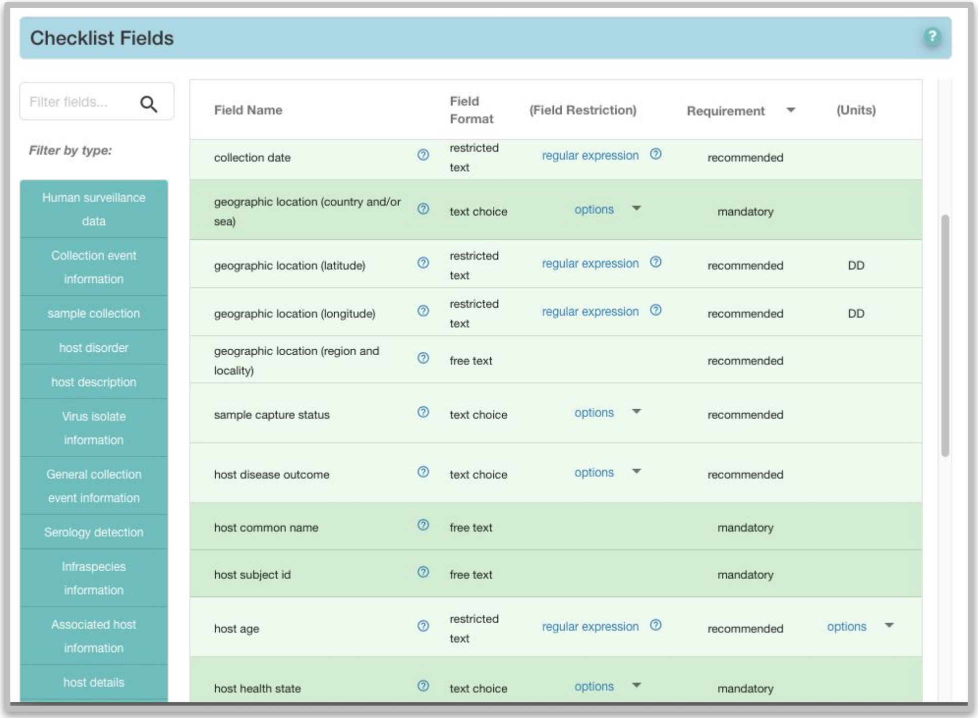
Repository’s upload area

Metadata

Compressed data files

Data repository conventions example

https://www.ebi.ac.uk/ena/browser/view/ERC000033



Checklist Fields

Filter fields...

Filter by type:

- Human surveillance data
- Collection event information
- sample collection
- host disorder
- host description
- Virus isolate information
- General collection event information
- Serology detection
- Infraspecies information
- Associated host information
- host details

Field Name	Field Format	(Field Restriction)	Requirement	(Units)
collection date	restricted text	regular expression	recommended	
geographic location (country and/or sea)	text choice	options	mandatory	
geographic location (latitude)	restricted text	regular expression	recommended	DD
geographic location (longitude)	restricted text	regular expression	recommended	DD
geographic location (region and locality)	free text		recommended	
sample capture status	text choice	options	recommended	
host disease outcome	text choice	options	recommended	
host common name	free text		mandatory	
host subject id	free text		mandatory	
host age	restricted text	regular expression	recommended	options
host health state	text choice	options	mandatory	

https://ena-docs.readthedocs.io/en/latest/submit/fileprep/reads.html

Fastq format

We recommend that read data is either submitted in BAM or CRAM format. However, single and paired reads are accepted as Fastq files that meet the following the requirements:

- Quality scores must be in Phred scale.
- Both ASCII and space delimitered decimal encoding of quality scores are supported. We will automatically detect the Phred quality offset of either 33 or 64.
- No technical reads (e.g. adapters, linkers, barcodes, primers) are allowed.
- Single reads must be submitted using a single Fastq file and can be submitted with or without read names.
- Paired reads must be submitted using two Fastq files.
- The first line for each read must start with '@'.
- The base calls and quality scores must be separated by a line starting with '+'.
- Paired read names must either use Casava 1.8 read names (regular expression: `^@(.+)( +|\\t+)([0-9]+):[YN]:[0-9]*[02468]($|:.*$)` or must end with `/1` or `/2` optionally followed by a space and a comment.
- Read names must not exceed a length of 256 characters.
- The Fastq files must be compressed using gzip or bzip2.
- The regular expression for bases is "^([ACGTNactgn.]*?)$"

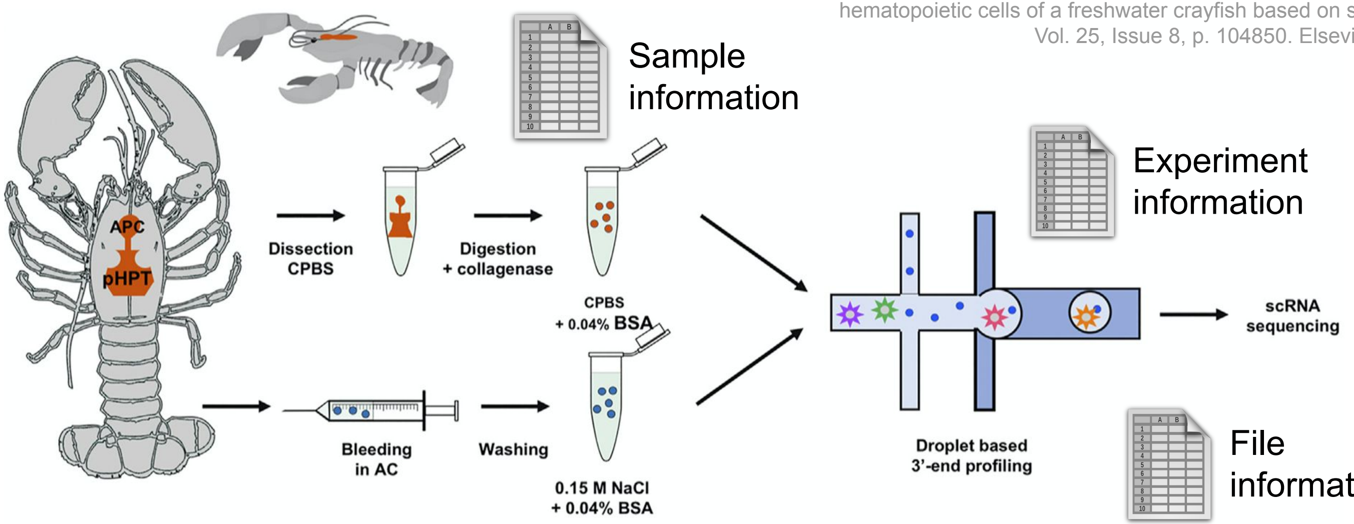
Example of Fastq file containing paired reads (prior to Casava 1.8):

```
@read_name/1
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
!''*((((***+))%%++)(%%).1***-+*''))**55CCF>>>>>>CCCCCCC65
@read_name/2
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
!''*((((***+))%%++)(%%).1***-+*''))**55CCF>>>>>>CCCCCCC65
...
```

Single-cell RNA sequencing example

“Protocol” icon by Justin Blake from thenounproject.com

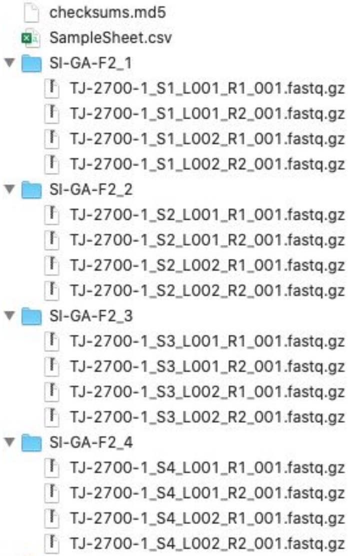
Söderhäll, I., Fasterius, E., Ekblom, C., & Söderhäll, K. (2022). Characterization of hemocytes and hematopoietic cells of a freshwater crayfish based on single-cell transcriptome analysis. In iScience Vol. 25, Issue 8, p. 104850. Elsevier. https://doi.org/10.1016/j.isci.2022.104850



Sample information

Experiment information

File information



```
checksums.md5
SampleSheet.csv
▼ SI-GA-F2_1
    TJ-2700-1_S1_L001_R1_001.fastq.gz
    TJ-2700-1_S1_L001_R2_001.fastq.gz
    TJ-2700-1_S1_L002_R1_001.fastq.gz
    TJ-2700-1_S1_L002_R2_001.fastq.gz
▼ SI-GA-F2_2
    TJ-2700-1_S2_L001_R1_001.fastq.gz
    TJ-2700-1_S2_L001_R2_001.fastq.gz
    TJ-2700-1_S2_L002_R1_001.fastq.gz
    TJ-2700-1_S2_L002_R2_001.fastq.gz
▼ SI-GA-F2_3
    TJ-2700-1_S3_L001_R1_001.fastq.gz
    TJ-2700-1_S3_L001_R2_001.fastq.gz
    TJ-2700-1_S3_L002_R1_001.fastq.gz
    TJ-2700-1_S3_L002_R2_001.fastq.gz
▼ SI-GA-F2_4
    TJ-2700-1_S4_L001_R1_001.fastq.gz
    TJ-2700-1_S4_L001_R2_001.fastq.gz
    TJ-2700-1_S4_L002_R1_001.fastq.gz
    TJ-2700-1_S4_L002_R2_001.fastq.gz
```

Sample collection protocol

Nucleic acid extraction protocol

Library construction protocol

Sequencing protocol

Sample information as (meta)data

ENA Checklist: ERC00001 – ENA default sample checklist

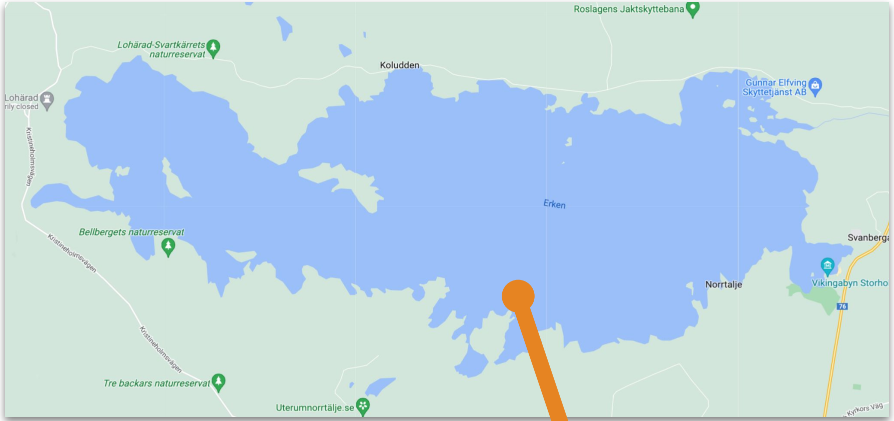
OLS / Experimental Factor Ontology EFO

Population	Organism	Pacifastacus leniusculus
	Genotype	wild type genotype
	Geographical location	Sweden, Lake Erken
Individual	Growth condition	laboratory aquarium since Sep 2020
	Sampling date	020-11-06
	Developmental stage	adult
	Body weight	35
	Sex	male
Specimen	Organism part	hematopoietic system
Sample	**Cell type**	**hemocyte**

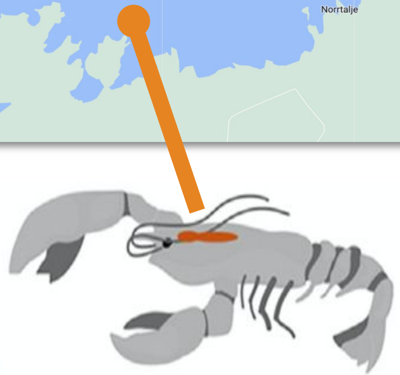
Sample collection protocols

Map data © Google. Crayfish derived from Illustration in Söderhäll et al. (2022).

- Obtain freshwater crayfish (adult males) from lake Erken, Sweden (59.8 N 18.6 E)
- Maintain in the crayfish facility in running tap water,10-12°C, 12:12 light:dark cycle…
- Feed once a week

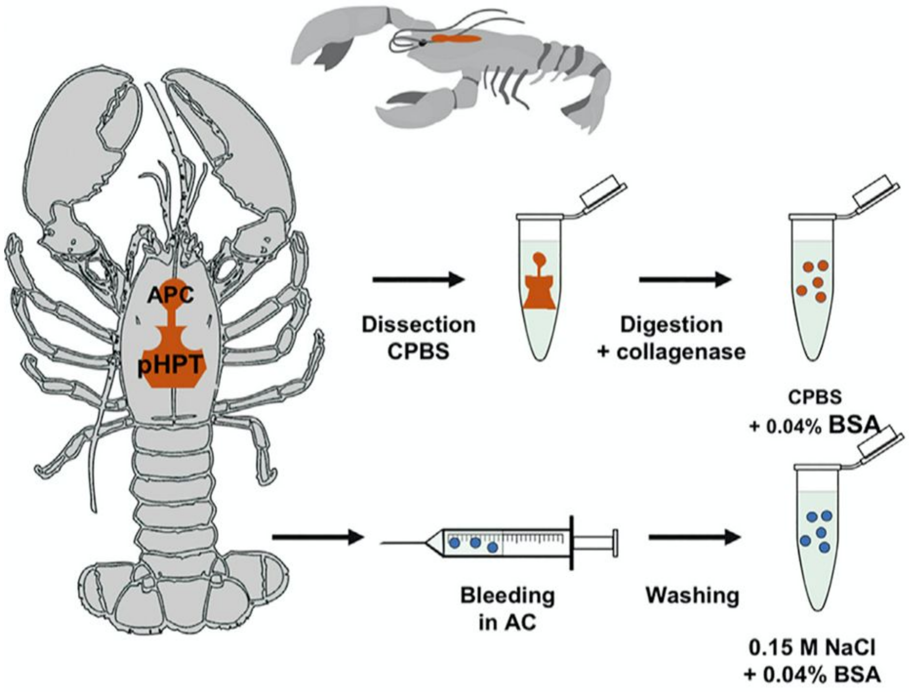


Map data © Google



Nucleic acid extraction protocol

Protocol illustration derived from Illustration in Söderhäll et al. (2022).

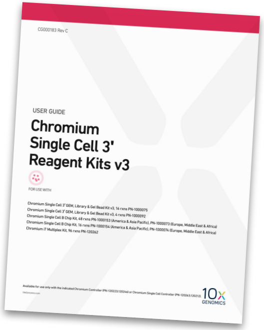


- Dissect and digest into single cells by incubation in 300 µl of 0.1% collagenase … at room temperature for 20 min on a rotating plate … then filtered through a 40 mm cell strainer
- Pool isolated cells from four animals for scRNA-seq

Library construction protocol

- Prepare sequencing libraries using Chromium Single Cell 3’ reagent kit v3 (cat# 1000075/1000073/120262, 10xGenomics)
- According to the manufacturer’s protocol

  CG000183
  Single Cell 3’ Reagent Kit User Guide, v3 chemistry, 10xGenomics



CG000183 Rev C

USER GUIDE

Chromium Single Cell 3' Reagent Kits v3

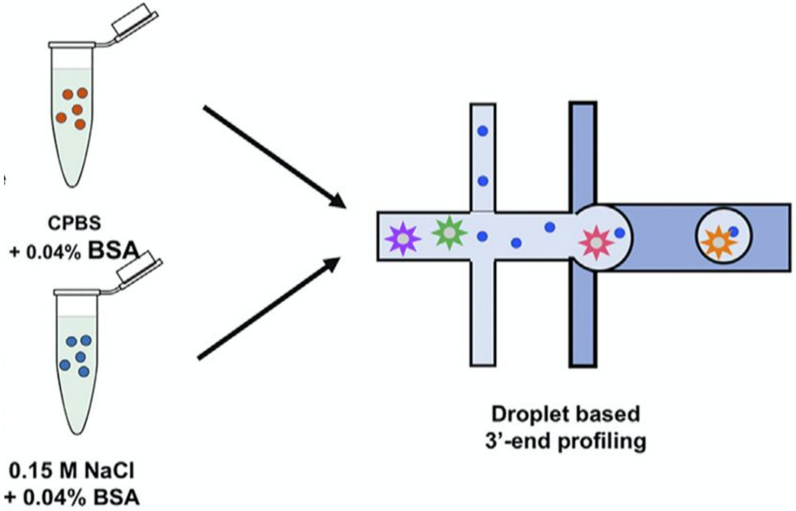
FOR USE WITH

Chromium Single Cell 3' GEM, Library & Gel Bead Kit v3, 16 rxns PN-1000075
Chromium Single Cell 3' GEM, Library & Gel Bead Kit v3, 4 rxns PN-1000092
Chromium Single Cell B Chip Kit, 48 rxns PN-1000153 (America & Asia Pacific), PN-1000073 (Europe, Middle East & Africa)
Chromium Single Cell B Chip Kit, 16 rxns PN-1000154 (America & Asia Pacific), PN-1000074 (Europe, Middle East & Africa)
Chromium i7 Multiplex Kit, 96 rxns PN-120262

Available for use only with the indicated Chromium Controller (PN-120223;120246) or Chromium Single Cell Controller (PN-120263;120212).

10x GENOMICS

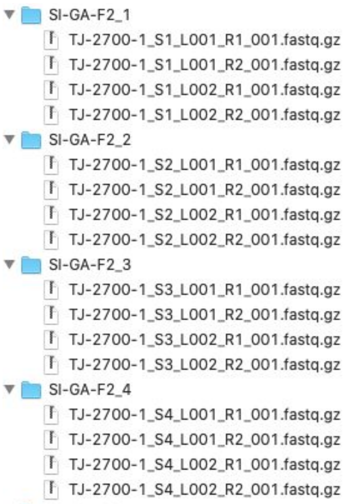
Protocol illustration derived from Illustration in Söderhäll et al. (2022).



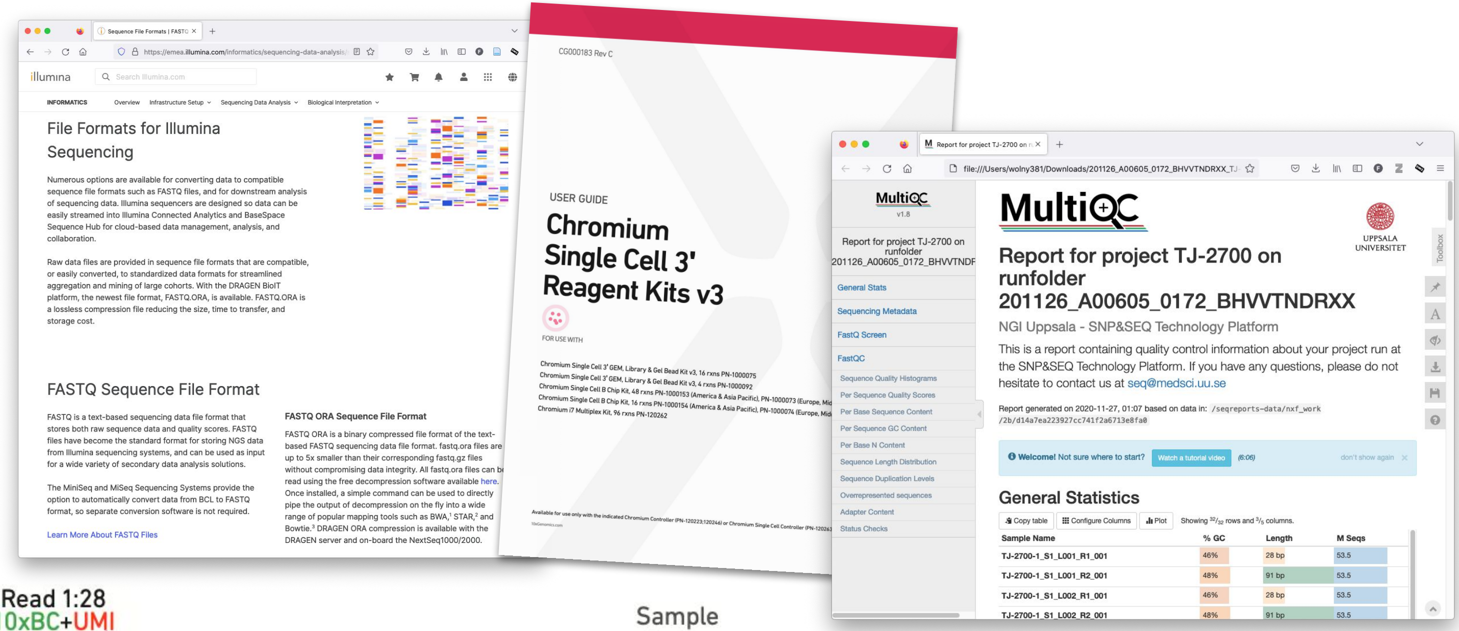
Sequencing protocol

- 28+8+0+91 bp read length
- NovaSeq 6000 system
- SP flowcell
- v1 sequencing chemistry
- Include a sequencing library for the phage PhiX as 1% spike-in in the sequencing run

Files Delivered from Sequencing



- SI-GA-F2_1
  - TJ-2700-1_S1_L001_R1_001.fastq.gz
  - TJ-2700-1_S1_L001_R2_001.fastq.gz
  - TJ-2700-1_S1_L002_R1_001.fastq.gz
  - TJ-2700-1_S1_L002_R2_001.fastq.gz
- SI-GA-F2_2
  - TJ-2700-1_S2_L001_R1_001.fastq.gz
  - TJ-2700-1_S2_L001_R2_001.fastq.gz
  - TJ-2700-1_S2_L002_R1_001.fastq.gz
  - TJ-2700-1_S2_L002_R2_001.fastq.gz
- SI-GA-F2_3
  - TJ-2700-1_S3_L001_R1_001.fastq.gz
  - TJ-2700-1_S3_L001_R2_001.fastq.gz
  - TJ-2700-1_S3_L002_R1_001.fastq.gz
  - TJ-2700-1_S3_L002_R2_001.fastq.gz
- SI-GA-F2_4
  - TJ-2700-1_S4_L001_R1_001.fastq.gz
  - TJ-2700-1_S4_L001_R2_001.fastq.gz
  - TJ-2700-1_S4_L002_R1_001.fastq.gz
  - TJ-2700-1_S4_L002_R2_001.fastq.gz



File Formats for Illumina Sequencing

Numerous options are available for converting data to compatible sequence file formats such as FASTQ files, and for downstream analysis of sequencing data. Illumina sequencers are designed so data can be easily streamed into Illumina Connected Analytics and BaseSpace Sequence Hub for cloud-based data management, analysis, and collaboration.

Raw data files are provided in sequence file formats that are compatible, or easily converted, to standardized data formats for streamlined aggregation and mining of large cohorts. With the DRAGEN BioIT platform, the newest file format, FASTQ.ORA, is available. FASTQ.ORA is a lossless compression file reducing the size, time to transfer, and storage cost.

FASTQ Sequence File Format

FASTQ is a text-based sequencing data file format that stores both raw sequence data and quality scores. FASTQ files have become the standard format for storing NGS data from Illumina sequencing systems, and can be used as input for a wide variety of secondary data analysis solutions.

The MiniSeq and MiSeq Sequencing Systems provide the option to automatically convert data from BCL to FASTQ format, so separate conversion software is not required.

Learn More About FASTQ Files

FASTQ ORA Sequence File Format

FASTQ ORA is a binary compressed file format of the text-based FASTQ sequencing data file format. fastq.ora files are up to 5x smaller than their corresponding fastq.gz files without compromising data integrity. All fastq.ora files can be read using the free decompression software available here. Once installed, a simple command can be used to directly pipe the output of decompression on the fly into a wide range of popular mapping tools such as BWA,[1] STAR,[2] and Bowtie.[3] DRAGEN ORA compression is available with the DRAGEN server and on-board the NextSeq1000/2000.

CG000183 Rev C

USER GUIDE

Chromium Single Cell 3' Reagent Kits v3

FOR USE WITH

Chromium Single Cell 3' GEM, Library & Gel Bead Kit v3, 16 rxns PN-1000075
Chromium Single Cell 3' GEM, Library & Gel Bead Kit v3, 4 rxns PN-1000092
Chromium Single Cell B Chip Kit, 48 rxns PN-1000153 (America & Asia Pacific), PN-1000073 (Europe, Mid
Chromium Single Cell B Chip Kit, 16 rxns PN-1000154 (America & Asia Pacific), PN-1000074 (Europe, Mid
Chromium i7 Multiplex Kit, 96 rxns PN-120262

Available for use only with the indicated Chromium Controller (PN-120223;120246) or Chromium Single Cell Controller (PN-120263

10xGenomics.com

Report for project TJ-2700 on runfolder 201126_A00605_0172_BHVVTNDRXX

NGI Uppsala - SNP&SEQ Technology Platform

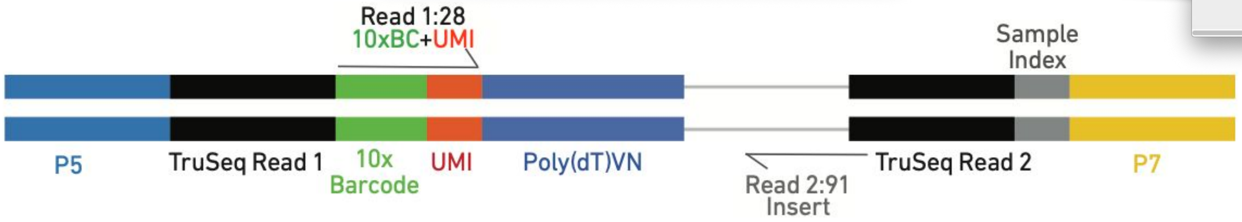
This is a report containing quality control information about your project run at the SNP&SEQ Technology Platform. If you have any questions, please do not hesitate to contact us at seq@medsci.uu.se

Report generated on 2020-11-27, 01:07 based on data in: `/seqreports-data/nxf_work/2b/d14a7ea223927cc741f2a6713e8fa0`

General Statistics

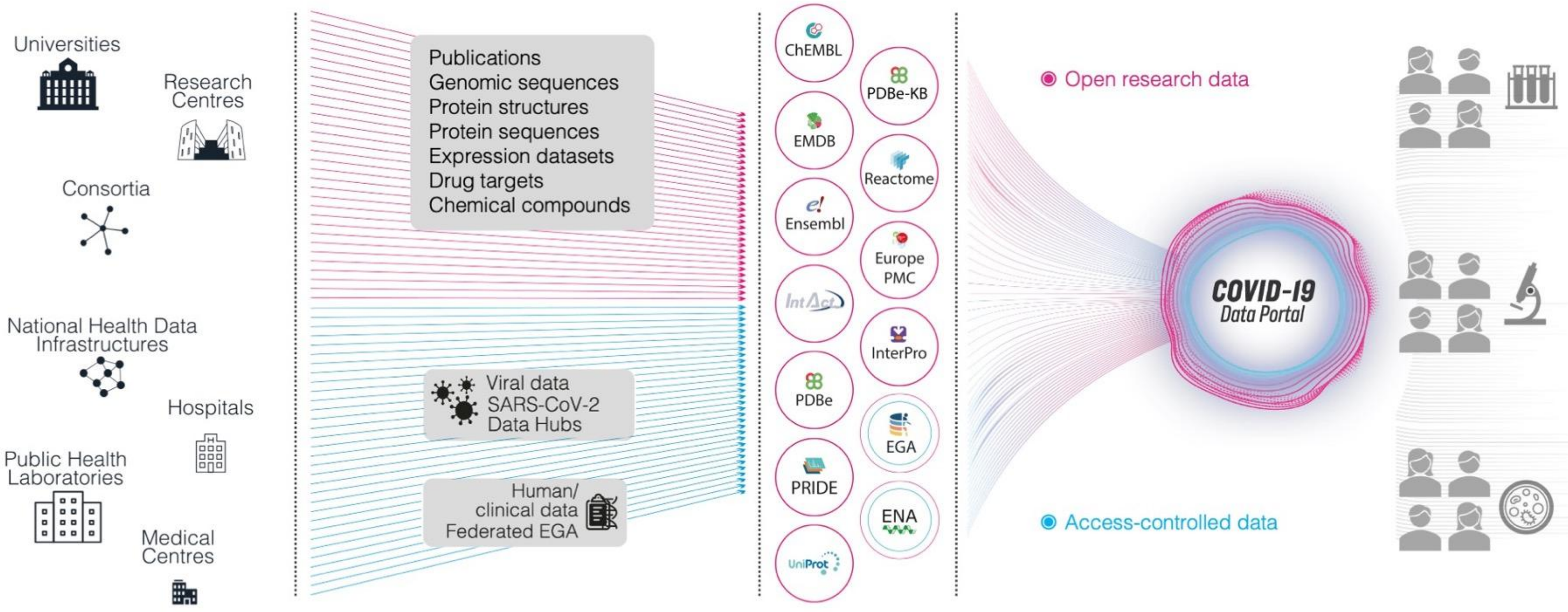
Showing 32/32 rows and 3/5 columns.

Sample Name	% GC	Length	M Seqs
TJ-2700-1_S1_L001_R1_001	46%	28 bp	53.5
TJ-2700-1_S1_L001_R2_001	48%	91 bp	53.5
TJ-2700-1_S1_L002_R1_001	46%	28 bp	53.5
TJ-2700-1_S1_L002_R2_001	48%	91 bp	53.5



- 201126_A00605_0172_BHVVTNDRXX_TJ-2700_multiqc_report.html
- checksums.md5
- SampleSheet.csv

Connected data resources



Universities

Research Centres

Consortia

National Health Data Infrastructures

Hospitals

Public Health Laboratories

Medical Centres

Publications
Genomic sequences
Protein structures
Protein sequences
Expression datasets
Drug targets
Chemical compounds

Viral data
SARS-CoV-2
Data Hubs

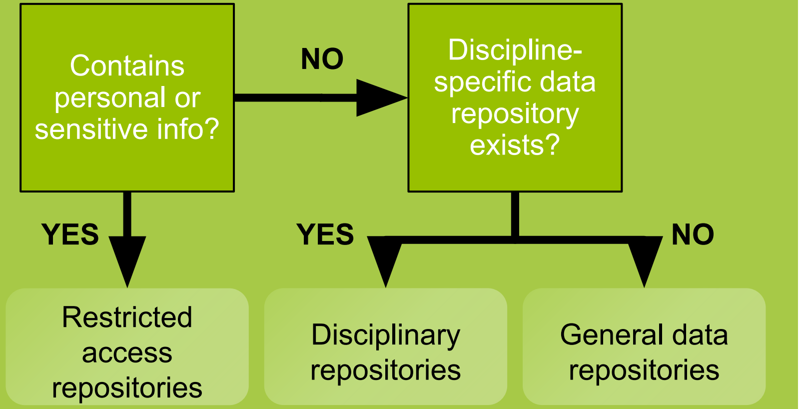
Human/
clinical data
Federated EGA

ChEMBL
PDBe-KB
EMDB
Reactome
Ensembl
Europe PMC
IntAct
InterPro
PDBe
EGA
PRIDE
ENA
UniProt

Open research data

COVID-19
Data Portal

Access-controlled data



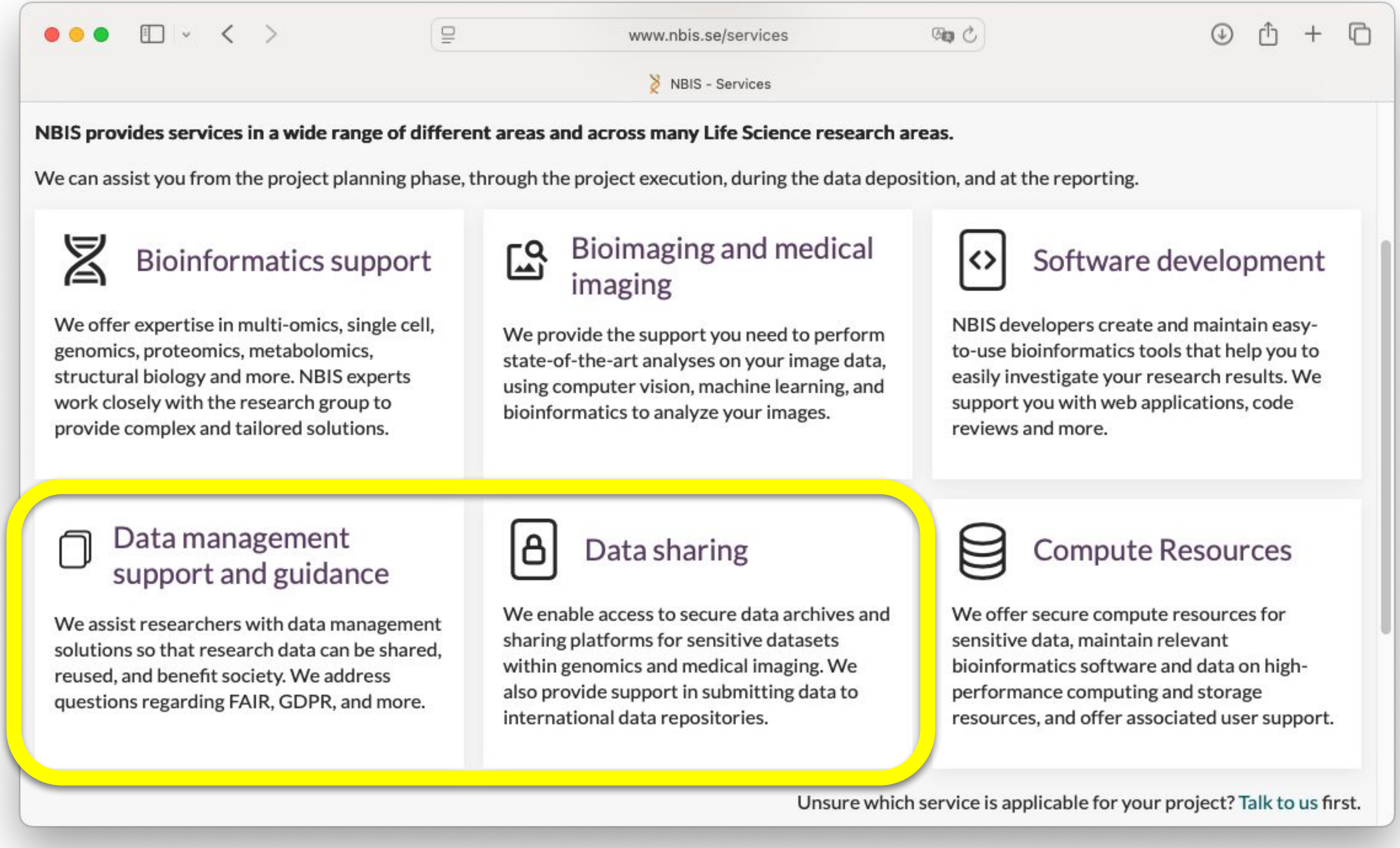
Data submission to public repositories

Making the data underlying your research publicly available to others is a fundamental part of a FAIR research process. When publicly available and appropriately described, data can be re-used by yourself as well as others. Domain-specific public repositories offer the most direct routes to making your data FAIR. This workshop will give you the why, where and how of data sharing via repository submission, including hands-on exercise. No prior knowledge is required in order to attend this workshop.

Learning outcomes:

- Know the benefits of data sharing
- Know how to find a suitable repository for different types of data
- Have experience of a repository submission

Services for Swedish Life Science Research



NBIS provides services in a wide range of different areas and across many Life Science research areas.

We can assist you from the project planning phase, through the project execution, during the data deposition, and at the reporting.

Bioinformatics support

We offer expertise in multi-omics, single cell, genomics, proteomics, metabolomics, structural biology and more. NBIS experts work closely with the research group to provide complex and tailored solutions.

Bioimaging and medical imaging

We provide the support you need to perform state-of-the-art analyses on your image data, using computer vision, machine learning, and bioinformatics to analyze your images.

Software development

NBIS developers create and maintain easy-to-use bioinformatics tools that help you to easily investigate your research results. We support you with web applications, code reviews and more.

Data management support and guidance

We assist researchers with data management solutions so that research data can be shared, reused, and benefit society. We address questions regarding FAIR, GDPR, and more.

Data sharing

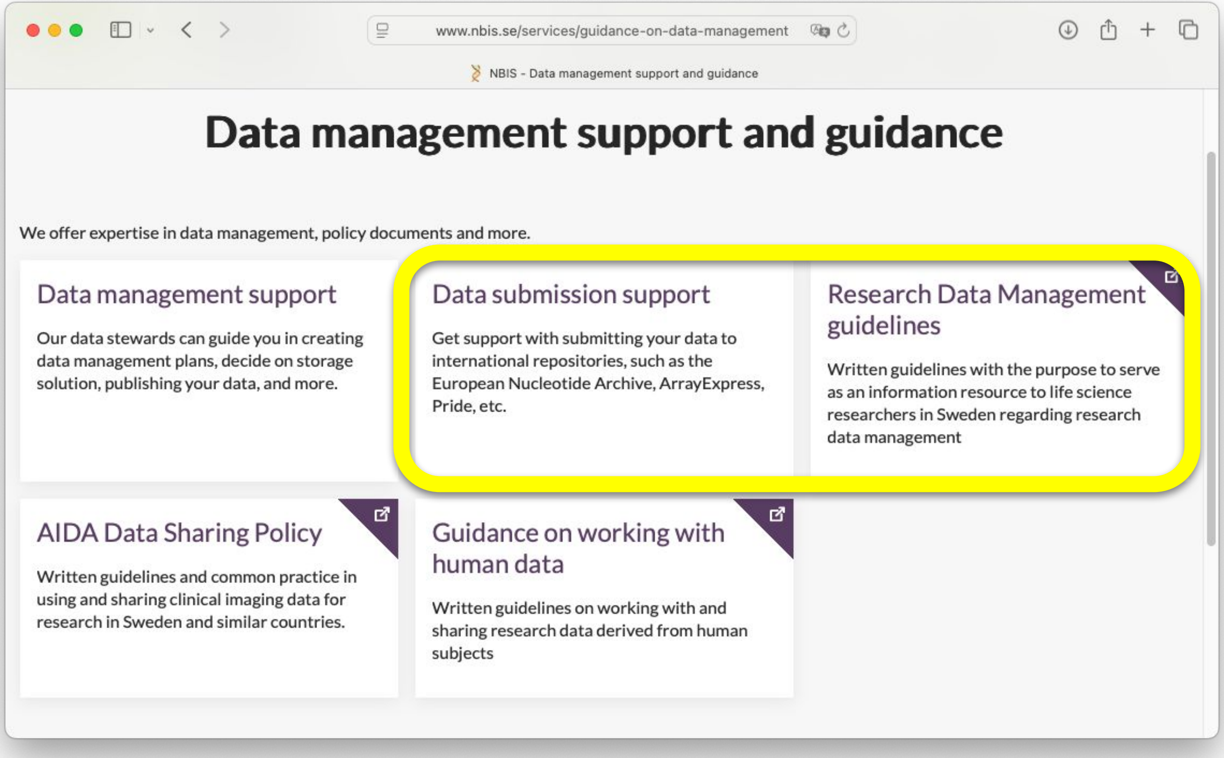
We enable access to secure data archives and sharing platforms for sensitive datasets within genomics and medical imaging. We also provide support in submitting data to international data repositories.

Compute Resources

We offer secure compute resources for sensitive data, maintain relevant bioinformatics software and data on high-performance computing and storage resources, and offer associated user support.

Unsure which service is applicable for your project? Talk to us first.

Services for Swedish Life Science Research



www.nbis.se/services/guidance-on-data-management

NBIS - Data management support and guidance

Data management support and guidance

We offer expertise in data management, policy documents and more.

Data management support

Our data stewards can guide you in creating data management plans, decide on storage solution, publishing your data, and more.

Data submission support

Get support with submitting your data to international repositories, such as the European Nucleotide Archive, ArrayExpress, Pride, etc.

Research Data Management guidelines

Written guidelines with the purpose to serve as an information resource to life science researchers in Sweden regarding research data management

AIDA Data Sharing Policy

Written guidelines and common practice in using and sharing clinical imaging data for research in Sweden and similar countries.

Guidance on working with human data

Written guidelines on working with and sharing research data derived from human subjects

Data management support and guidance

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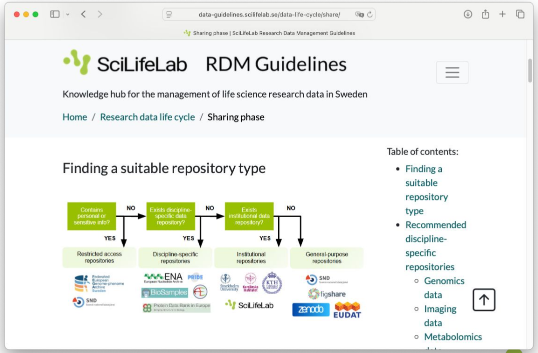


data-guidelines.scilifelab.se/data-life-cycle/share/

Sharing phase | SciLifeLab Research Data Management Guidelines

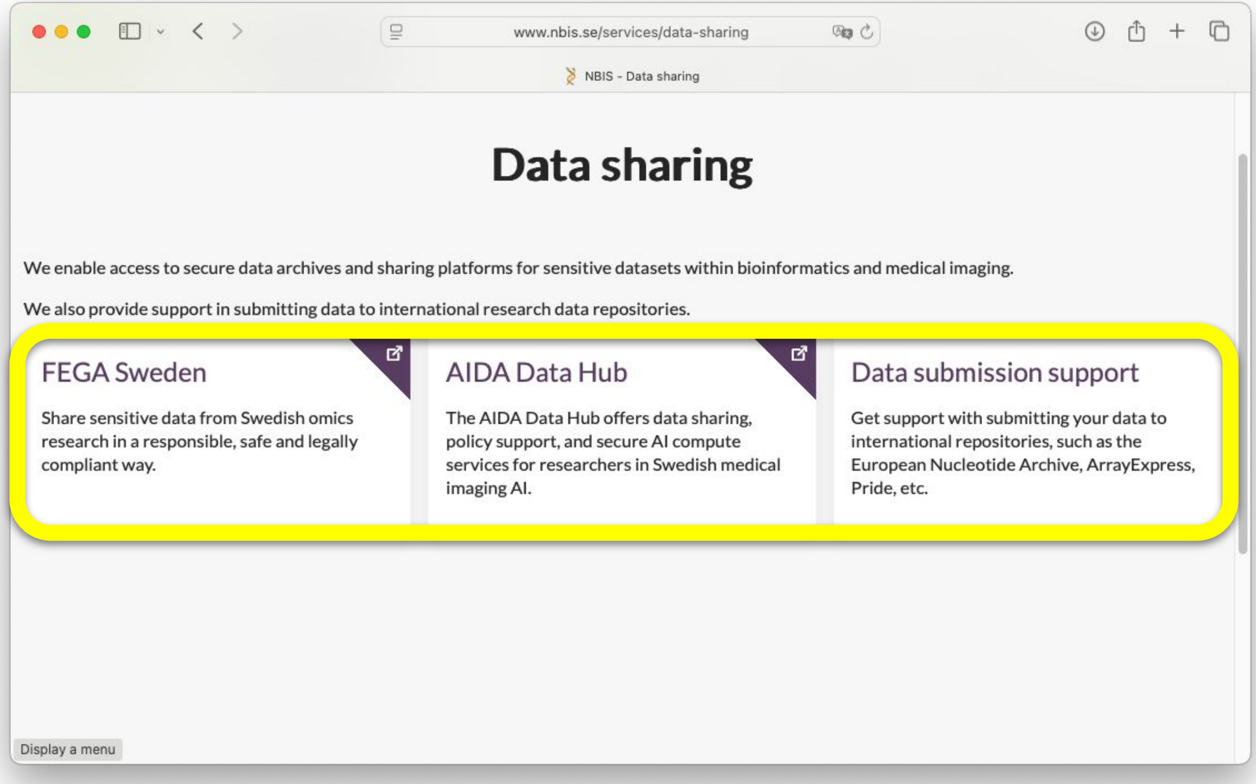
SciLifeLab RDM Guidelines

Knowledge hub for the management of life science research data in Sweden

Home / Research data life cycle / Sharing phase

Finding a suitable repository type

Services for Swedish Life Science Research



Data sharing

We enable access to secure data archives and sharing platforms for sensitive datasets within bioinformatics and medical imaging.

We also provide support in submitting data to international research data repositories.

FEGA Sweden

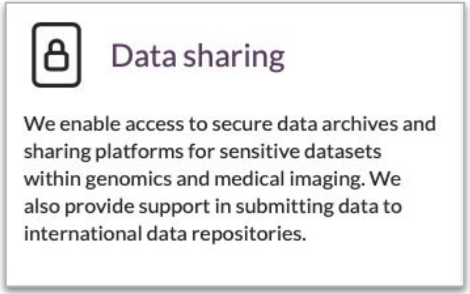
Share sensitive data from Swedish omics research in a responsible, safe and legally compliant way.

AIDA Data Hub

The AIDA Data Hub offers data sharing, policy support, and secure AI compute services for researchers in Swedish medical imaging AI.

Data submission support

Get support with submitting your data to international repositories, such as the European Nucleotide Archive, ArrayExpress, Pride, etc.



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