

# Metadata og dokumentasjon innen livsvitenskap

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## Data FAIRness i livsvitenskap

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Livsvitenskapen er er stort felt med mange typer data og enda flere typer metadata

Har jobbet siden 80-tallet med å standardisere

- Viktig å gjøre data tilgjengelig

- Viktig å kunne etterprøve andres forskning

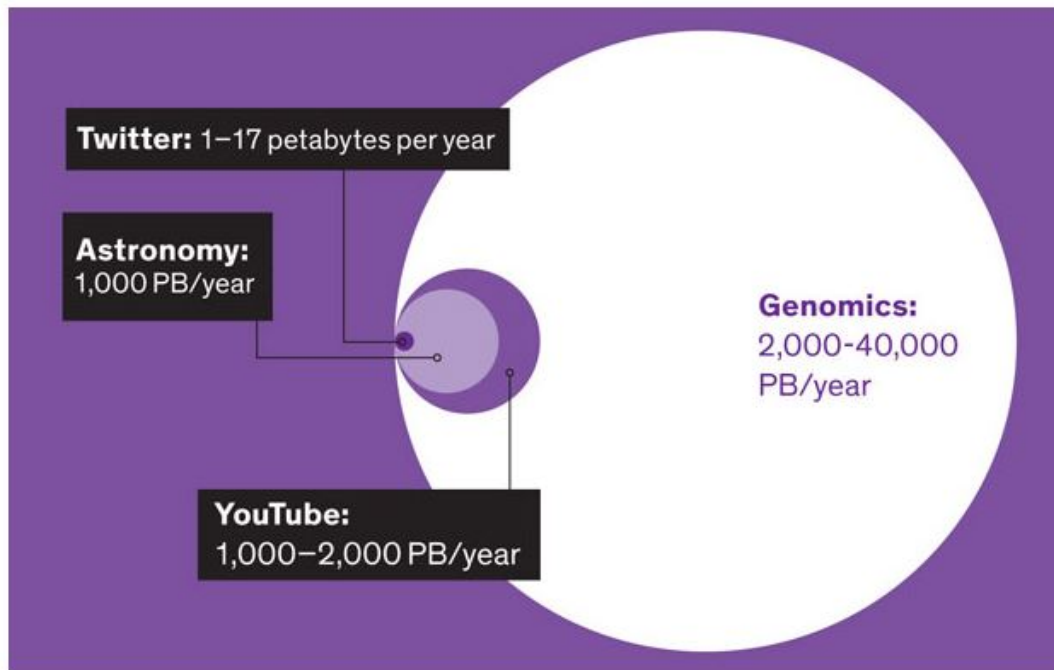
Felles er: Må arkivere data i offentlig tilgjengelige arkiv for å publisere

- Minstekrav til metadata informasjon ved deponering av data i offentlige arkiver

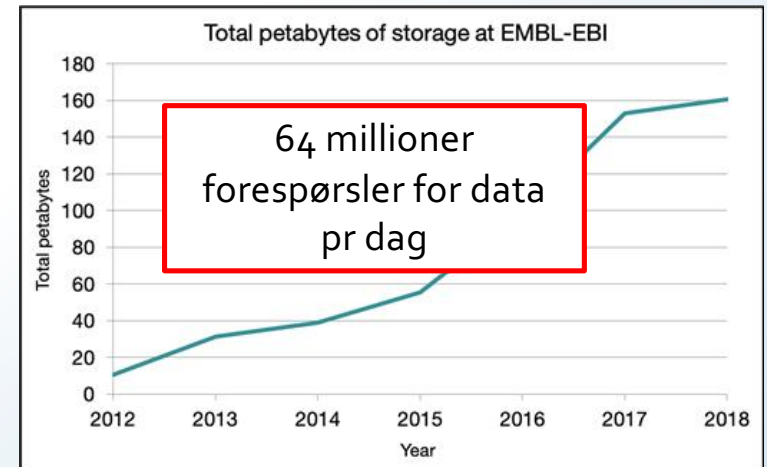
# Produksjon av livsvitenskapelig (Life Science) data er enorm

1 PB tilsvarer 4000 høyoppløslige foto hver dag hele livet ditt

Projected annual storage in 2025

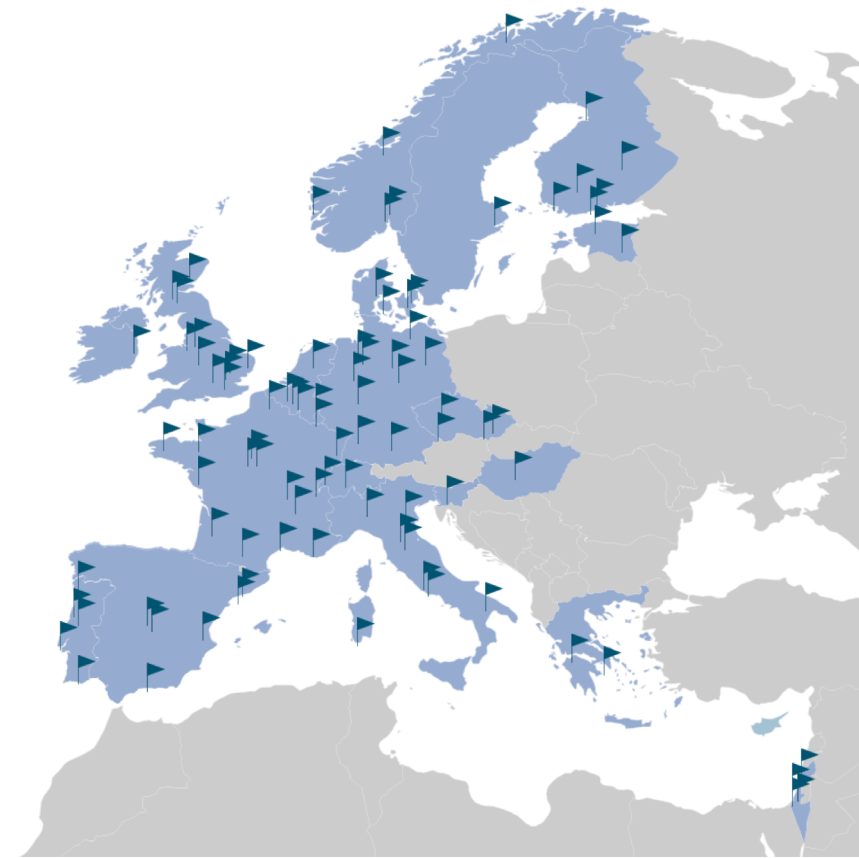
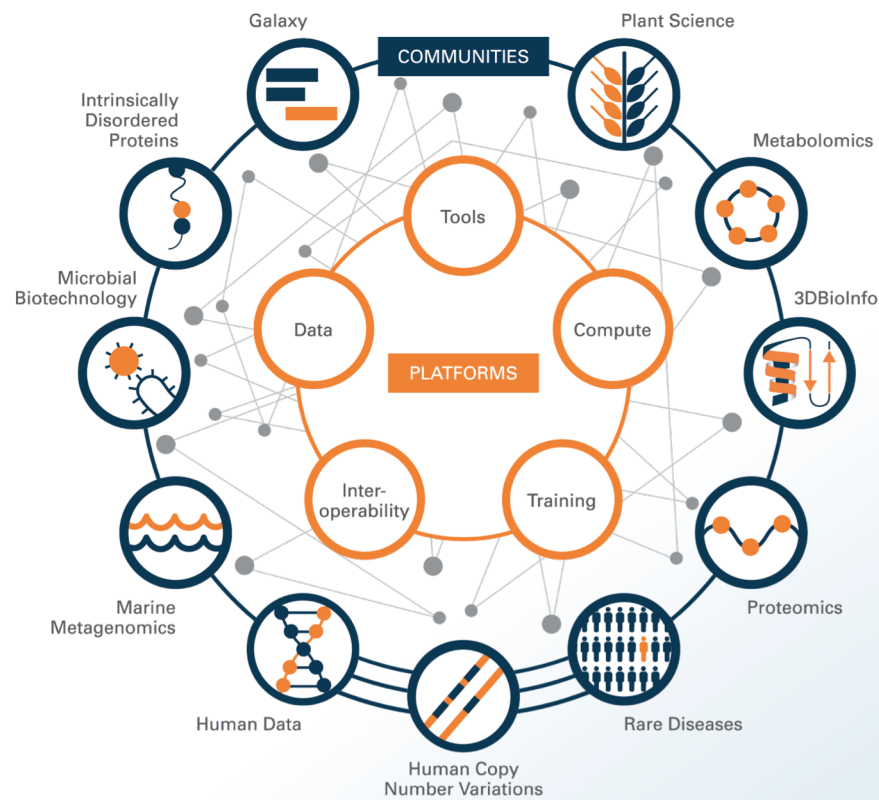


Source: "Big Data: Astronomical or Genomical?" PLoS Biology, 7 July 2015.



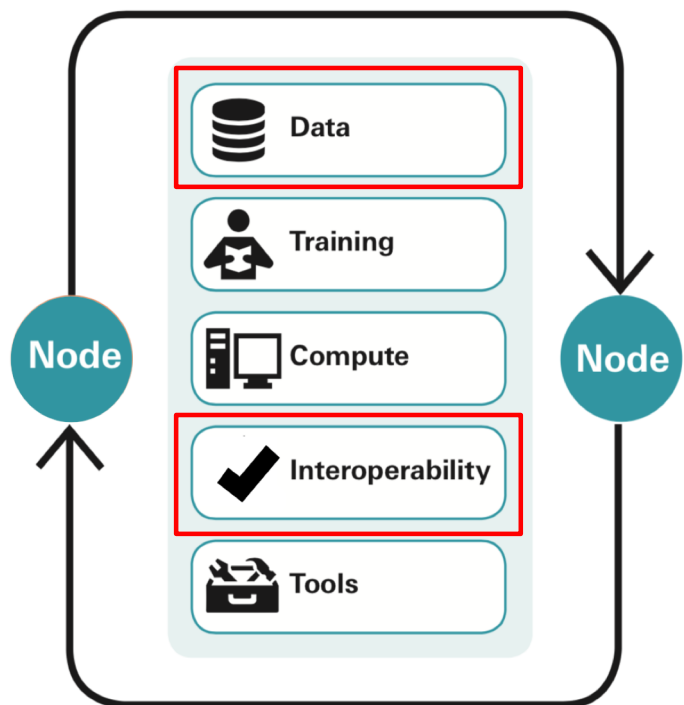
# ELIXIR – Europeisk distribuert infrastruktur for Life Science data

Samkjøring på europeisk nivå



# ELIXIR – Europeisk distribuert infrastruktur for Life Science data

Viktige plattformer for FAIR data



Bruk og gjenbruk av livsvitenskapelig data  
Tilbyr sikker og bærekraftig langtids arkivering

Pådriver for FAIRness – Søkbar og tilgjengelig  
Utvikler standarder for fil format, metadata, ontologier og kontrollert vokabular

# Eksempel på et livsvitenskapelig prosjekt

Kartlegging av mikroorganismer i Barentshavet



# Data produksjon i et typisk livsvitenskapelig prosjekt

Metadata produseres i flere deler av prosjektet – Alt må dokumenteres

Ulike fagdomener opererer med ulike standarder

Prøve innsamling



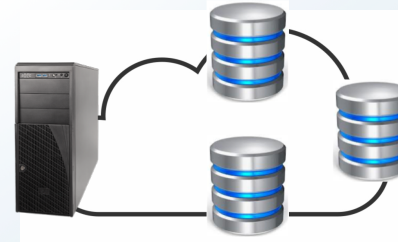
Data produksjon



Data lagring/deling



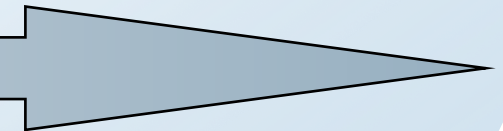
Data prosessering



Data arkivering



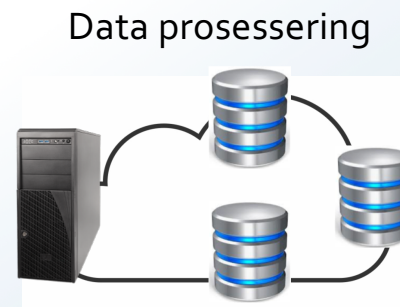
Data management



# Data produksjon i et typisk livsvitenskapelig prosjekt

Metadata produseres i flere deler av prosjektet – Alt må dokumenteres

Ulike fagdomener opererer med ulike standarder





# Registrering av metadata for innsamling av prøver

## Metadata standarder - kontrollert vokabular for å kunne sammenligne

Structured comment name	Item	Description	Examples	Expected value	Value syntax	Preferred units / suffix
alt_elev	Geographic location (altitude/elevation)	Sample taken at given elevation above sea level, defined in meters(m) as a positive floating number with two decimals.	Ex 1: 3.06 Ex 2: 1.80-2.15	-	{float} or {range}	meters (m)
collection_date	Collection date	The time of sampling, either as an instance (single point in time) or interval. In case no exact time is available, the date/time can be right truncated.	Ex 1: 2008-01-23T19:23:10+00:00 Ex 2: 2011-11-10 Ex 3: 2001-12 Ex 7: 2015 Ex 4: 2003--2006 Ex 5: 2010-01--2011-03 Ex 6: 2011-05-28--2011-08-10	date and time, range	{timestamp}	-
depth	Depth	Please refer to the definitions of depth in the environmental packages. Water: Sample taken at given depth below sea level, defined in meters(m) as a positive floating number or as a range, both with two decimals.	Ex 1: 355.20 Ex 2: 2.00-5.00	-		meters (m)
env_biome	Environment (biome)	In environmental biome level are the major classes of ecologically similar communities of plants, animals, and other organisms. Biomes are defined based on factors such as plant structures, leaf types, plant spacing, and other factors like climate. Examples include: desert, taiga, deciduous woodland, or coral reef. EnvO (v1.53) terms listed under environmental biome can be found from the link:( <a href="http://www.environmentontology.org/Browse-EnvO">http://www.environmentontology.org/Browse-EnvO</a> )	Ex 1: coral reef Ex 2: tropical	EnvO	{free text}	-
env_biome_ENVO	Environment	Corresponding ENVO identifier related to the	Ex 1: ENVO:00000150	EnvO	{accession}	-

- Not collected → missing
- 250 M → 250
- Not applicable → NA
- Superficial → missing
- 1 m → 1
- 2 m → 2
- 2901.0 → 2901
- 0 m. → 0
- 1912 ft → 582.80
- 40 mm from surface → 0.04
- 0.75 m above seafloor → missing
- 700meters → 700
- Intracellular → missing
- Surface water of 0 meter → 0
- Zero → 0
- Below surface → Missing



# Registrering av metadata for innsamling av prøver

Metadata standarder – ontologi kan brukes til å linke prøver sammen

Preferred Name	Definitions	ENVO ID	Link
Marine biome	An aquatic biome that comprises systems of open-ocean and unprotected coastal habitats, characterized by exposure to wave action, tidal fluctuation, and ocean currents as well as systems that largely resemble these. Water in the marine biome is generally within the salinity range of seawater: 30 to 38 ppt.	ENVO:00000447	<a href="http://purl.obolibrary.org/obo/ENVO_00000447">http://purl.obolibrary.org/obo/ENVO_00000447</a>
Epeiric sea biome	The epeiric sea (also known as an epicontinental sea) biome comprises of a shallow seas that extend over part of a continent. Epeiric seas are usually associated with the marine transgressions of the geologic past, which have variously been due to either global eustatic sea level changes, local tectonic deformation, or both, and are occasionally semi-cyclic.	ENVO:01000045	<a href="http://purl.obolibrary.org/obo/ENVO_01000045">http://purl.obolibrary.org/obo/ENVO_01000045</a>
Estuarine biome	Expressions of the estuarine biome occur at wide lower courses of rivers where they flow into a sea. Estuaries experience tidal flows and their water is a changing mixture of fresh and salt.	ENVO:01000020	<a href="http://purl.obolibrary.org/obo/ENVO_01000020">http://purl.obolibrary.org/obo/ENVO_01000020</a>
Marginal sea biome	The marginal sea biome comprises parts of an ocean partially enclosed by land such as islands, archipelagos, or peninsulas. Unlike Mediterranean seas, marginal seas have ocean currents caused by ocean winds. Many marginal seas are enclosed by island arcs that were formed from the subduction of one oceanic plate beneath another.	ENVO:01000046	<a href="http://purl.obolibrary.org/obo/ENVO_01000046">http://purl.obolibrary.org/obo/ENVO_01000046</a>
Marine benthic biome	The marine benthic biome (benthic meaning 'bottom') encompasses the seafloor and includes such areas as shores, littoral or intertidal areas, marine coral reefs, and the deep seabed.	ENVO:01000024	<a href="http://purl.obolibrary.org/obo/ENVO_01000024">http://purl.obolibrary.org/obo/ENVO_01000024</a>
Marine mud	A liquid or semi-liquid mixture of water and some combination of soil, silt, and clay.	ENVO:00005795	<a href="http://purl.obolibrary.org/obo/ENVO_00005795">http://purl.obolibrary.org/obo/ENVO_00005795</a>
Marine pelagic biome	The marine pelagic biome (pelagic meaning open sea) is that of the marine water column, from the surface to the greatest depths.	ENVO:01000023	<a href="http://purl.obolibrary.org/obo/ENVO_01000023">http://purl.obolibrary.org/obo/ENVO_01000023</a>
Marine salt marsh biome	The marine salt marsh biome comprises marshes that are transitional intertidal between land and salty or brackish marine water (e.g.: sloughs, bays, estuaries). It is dominated by halophytic (salt tolerant) herbaceous plants. The daily tidal surges bring in nutrients, which tend to settle in roots of the plants within the salt marsh. The natural chemical activity of salty (or brackish) water and the tendency of algae to bloom in the shallow unshaded water also allow for great biodiversity.	ENVO:01000022	<a href="http://purl.obolibrary.org/obo/ENVO_01000022">http://purl.obolibrary.org/obo/ENVO_01000022</a>
Marine upwelling biome	A marine biome which contains communities adapted to living in an environment determined by an upwelling process.	ENVO:01000858	<a href="http://purl.obolibrary.org/obo/ENVO_01000858">http://purl.obolibrary.org/obo/ENVO_01000858</a>
Marine water	A significant accumulation of water which is part of a marine biome. Ideal like	ENVO:00000000	<a href="http://purl.obolibrary.org/obo/ENVO_00000000">http://purl.obolibrary.org/obo/ENVO_00000000</a>

Ontology Lookup Service (OLS) er en ressurs for biomedisinsk ontologier.



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Epeiric sea biome	The epeiric sea (also known as an epicontinental sea) biome comprises of a shallow seas that extend over part of a continent. Epeiric seas are usually	ENVO:01000045	<a href="http://purl.obolibrary.org/obo/ENVO_01000045">http://purl.obolibrary.org/obo/ENVO_01000045</a>

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**Ontology Lookup Service**

Home | **Ontologies** | Documentation | About

OLS > eNanoMapper Ontology | ENM > **ENVO:00000447**

## marine biome

[http://purl.obolibrary.org/obo/ENVO\\_00000447](http://purl.obolibrary.org/obo/ENVO_00000447)

An aquatic biome that comprises systems of open-ocean and unprotected coastal habitats, characterized by exposure to wave action, tidal fluctuation, and ocean currents as well as systems that largely resemble these. Water in the marine biome is generally within the salinity range of seawater: 30 to 38 ppt. [ MA:ma ISBN-10:0618455043 ORCID:0000-0002-4366-3088 <https://en.wikipedia.org/wiki/Ocean> ]

Tree view | Term history

- entity
  - material entity
    - biome
      - aquatic biome
        - marine biome**

Graph view | Reset tree | Show all siblings

**Term info**

- database cross reference
  - SPIRE:Marine
- has obo namespace
  - ENVO
- has related synonym
  - marine realm
- id

Ontologien ENVO beskriver i dette tilfellet miljøet innsamlingen ble foretatt



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Epeiric sea biome	The epeiric sea (also known as an epicontinental sea) biome comprises of a shallow seas that extend over part of a continent. Epeiric seas are usually	ENVO:01000045	<a href="http://purl.obolibrary.org/obo/ENVO_01000045">http://purl.obolibrary.org/obo/ENVO_01000045</a>

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**Ontology Lookup Service**

Home **Ontologies** Documentation About

OLS > Gazetteer **GAZ** > **GAZ:00002699**

## Kingdom of Norway

[http://purl.obolibrary.org/obo/GAZ\\_00002699](http://purl.obolibrary.org/obo/GAZ_00002699)

A country and constitutional monarchy in Northern Europe that occupies the western portion of the Scandinavian Peninsula. It is bordered by Sweden, Finland, and Russia. The Kingdom of Norway also includes the Arctic island territories of Svalbard and Jan Mayen. Norwegian sovereignty over Svalbard is based upon the Svalbard Treaty, but that treaty does not apply to Jan Mayen. Bouvet Island in the South Atlantic Ocean and Peter I Island and Queen Maud Land in Antarctica are external dependencies, but those three entities do not form part of the kingdom. [ url:http://en.wikipedia.org/wiki/Norway ]

**Synonyms:** Kongeriket Norge {language: Norwegian}, Norway, Kongeriket Noreg {language: Norwegian}

Tree view | Term history

- geographic location
  - Kingdom of Norway**
    - Bouvet Islands
    - Dronning Maud Land
    - Jan Mayen
    - Metropolitan Norway

Graph view | Reset tree | Show all siblings

**Term info**

database cross reference

- ISO3166-1:NO
- ISO3166-2:NO
- ISO3166-1:578
- ISO3166-1:NOR

ABBREVIATION

Ontologien GAZ beskriver i dette tilfellet den geografiske lokasjonen innsamlingen ble foretatt

# Data produksjon i et typisk livsvitenskapelig prosjekt

Metadata produseres i flere deler av prosjektet – Alt må dokumenteres

Ulike fagdomener opererer med ulike standarder

Prøve innsamling



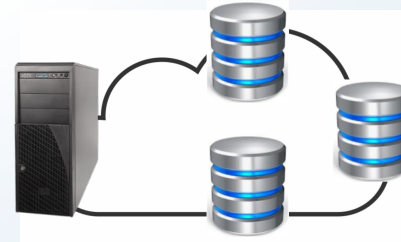
Data produksjon



Data lagring/deling



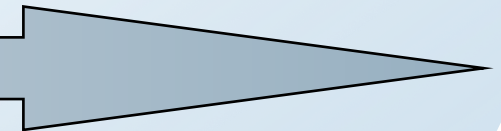
Data prosessering



Data arkivering



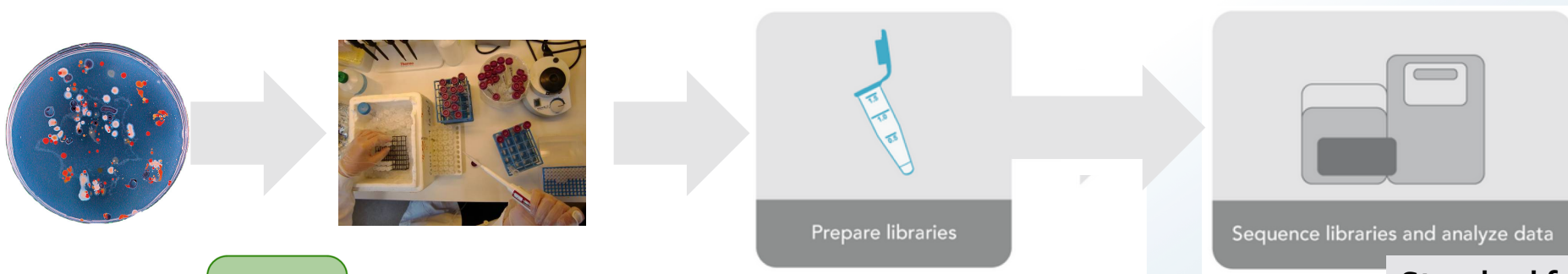
Data management



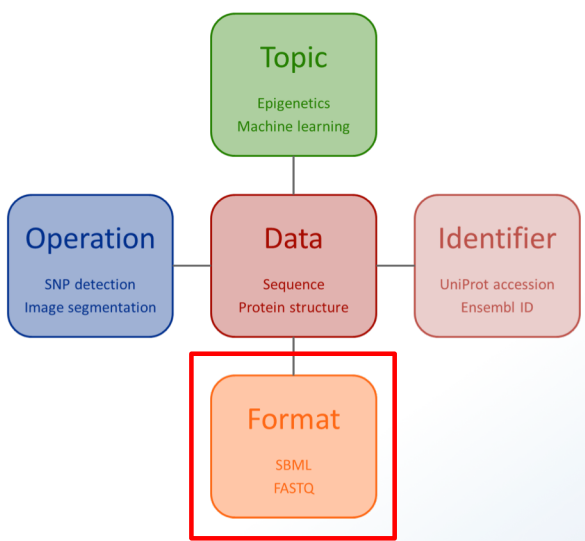


# Registrering av metadata for bearbeiding av prøver og produksjon av DNA sekvensdata

Beskrivelse av protokoller for bearbeiding av materiale og hvordan data er generert



Standard formater for produsert data



Ontology Lookup Service

Home Ontologies Documentation About

EDAM > format:1931

Search EDAM

### FASTQ-illumina

http://edamontology.org/format\_1931

FASTQ Illumina 1.3 short read format.

- Format
  - Format (by type of data)
    - Sequence record format
      - Sequence trace format
        - FASTQ-like format
          - FASTQ-like format (text)
            - FASTQ-illumina**

EDAM ontologien beskriver i dette tilfellet data formatet

# Data produksjon i et typisk livsvitenskapelig prosjekt

Metadata produseres i flere deler av prosjektet – Alt må dokumenteres

Ulike fagdomener opererer med ulike standarder

Prøve innsamling



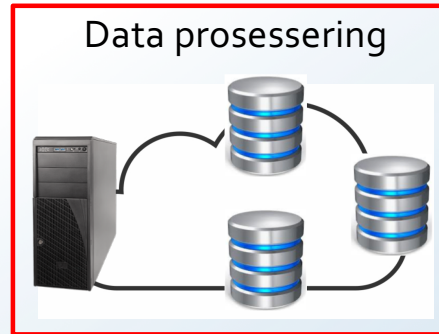
Data produksjon



Data lagring/deling



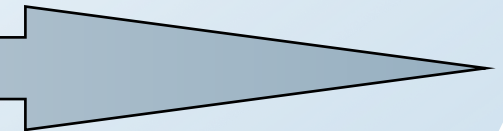
Data prosessering

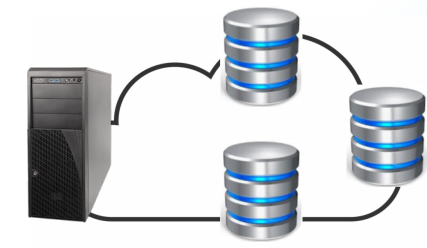


Data arkivering



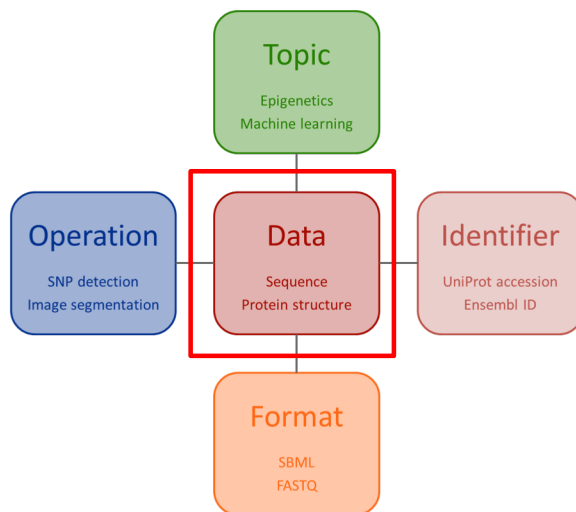
Data management





# Registrering av metadata for data analyser

Beskrivelse av data analysemetoder: verktøy, databaser, dataformater



**Ontology Lookup Service**

Home | **Ontologies** | Documentation | About

OLS > Bioinformatics operations, data types, formats, identifiers and topics > EDAM > data:3494

**DNA sequence**

[http://edamontology.org/data\\_3494](http://edamontology.org/data_3494)

A DNA sequence.

**Synonyms:** DNA sequences

Tree view | Term history

- Data
  - Sequence
    - Nucleic acid sequence
      - DNA sequence**

Graph view | Reset tree | Show all siblings

**Term info**

**Subsets:** data, edam

**Created in:** 1.8

**Term relations**

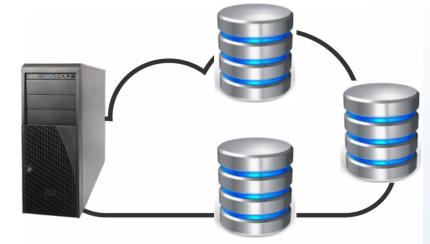
**Subclass of:**

- Nucleic acid sequence

EDAM ontologien beskriver i dette tilfellet data type

# Registrering av metadata for data analyser

## Kontrollert vokabular for verktøy og databaser



 Search bio.tools 17121 tools [About](#) [Login](#) [Sign-up](#)

### European Nucleotide Archive (ENA) (biotools:ena)

<http://www.ebi.ac.uk/ena> 

[Data submission, annotation and curation >](#) [Transcription factors and regulatory sites >](#) [Gene transcripts >](#) [Nucleic acid sites, features and motifs >](#)

[Database portal](#) [Web service](#) 

A globally comprehensive data resource for nucleotide sequence, spanning raw data, alignments and assemblies, functional and taxonomic annotation and rich contextual data relating to sequenced samples and experimental design. Serving both as the database of record for the output of the world's sequencing activity and as a platform for the management, sharing and publication of sequence data.

- Sequence similarity search >
- Deposition >
- Sequence assembly >
- Data retrieval >

**BioTools vokabularet beskriver i dette unik ID for dette dataarkivet**

# Data produksjon i et typisk livsvitenskapelig prosjekt

Metadata produseres i flere deler av prosjektet – Alt må dokumenteres

Ulike fagdomener opererer med ulike standarder

Prøve innsamling



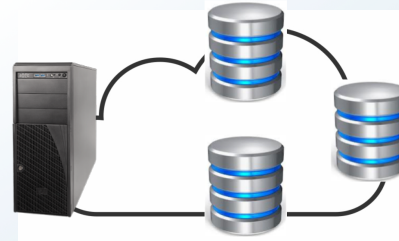
Data produksjon



Data lagring/deling



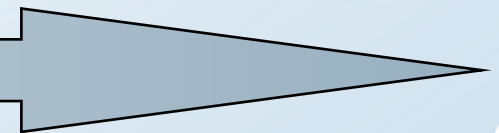
Data prosessering



Data arkivering



Data management





# Rapportering av metadata ved arkivering

Domene spesifikke arkiver – ulike krav til metadata, ulike standarder (f.eks MIxS)

ELIXIR Core Data Resource list

Core Data Resource	Data type
<a href="#">ArrayExpress</a>	Functional Genomics Data from high-throughput functional genomics experiments.
<a href="#">CATH</a>	A hierarchical domain classification of protein structures in the Protein Data Bank.
<a href="#">ChEBI</a>	Dictionary of molecular entities focused on 'small' chemical compounds.
<a href="#">ChEMBL</a>	Database of bioactive drug-like small molecules, it contains 2-D structures, calculated properties and abstracted bioactivities.
<a href="#">EGA</a>	Personally identifiable genetic and phenotypic data resulting from biomedical research projects.
<a href="#">ENA</a>	Nucleotide sequencing information, covering raw sequencing data, sequence assembly information and functional annotation.
<a href="#">Ensembl</a>	Genome browser for vertebrate genomes that supports research in comparative genomics, evolution, sequence variation and transcriptional regulation.
<a href="#">Ensembl Genomes</a>	Comparative analysis, data mining and visualisation for the genomes of non-vertebrate species.
<a href="#">Europe PMC</a>	Europe PMC is a repository, providing access to worldwide life sciences articles, books, patents and clinical guidelines.
<a href="#">Human Protein Atlas</a>	The Human Protein Atlas contains information for a large majority of all human protein-coding genes regarding the expression and localization of the corresponding proteins based on both RNA and protein data.
The IMEx Consortium: represented by <a href="#">IntAct</a> and <a href="#">MINT</a>	IntAct provides a freely available, open source database system and application programming interface for molecular interaction data. MINT focuses on experimental interactions mined from the scientific literature.
<a href="#">InterPro</a>	Functional analysis of protein sequences and domains, predicting the presence of protein families, domains and functional sites.

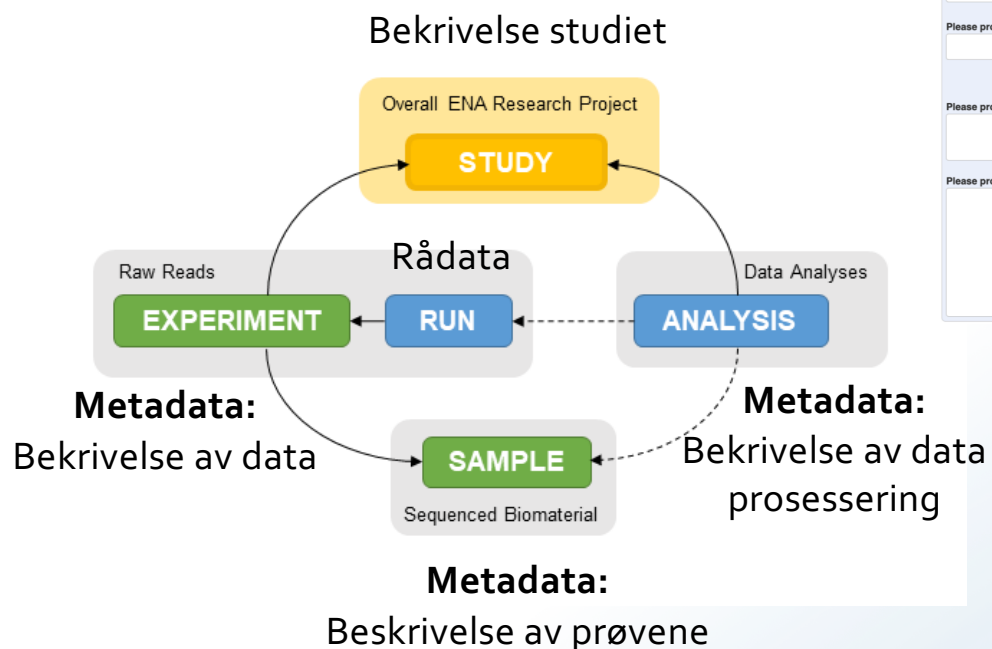
**Note:** This list is not exhaustive and is subject to change.

Specification projects	MIGS	MIMS	MIMARKS	New checklists
Checklists	EU, BA, PL, VI, DRG	metagenomes	survey, specimen	e.g., pan-genomes
Shared descriptors	collection date, environmental package, environment (biome), environment (feature), environment (material), geographic location (country and/or sea, region), geographic location (latitude and longitude), investigation type, project name, sequencing method, submitted to INSDC			
Checklist-specific descriptors	assembly, estimated size, finishing strategy, isolation and growth condition, number of replicons, ploidy, propagation, reference for biomaterial		target gene	
Applicable environmental packages (measurements and observations)	Air Host-associated Human-associated Human-oral Human-gut Human-skin Human-vaginal		Microbial mat/biofilm Miscellaneous natural or artificial environment Plant-associated Sediment Soil Wastewater/sludge Water	



# ENA – European Nucleotide Archive

Portal for arkivering av data. Metadata er påkrevd



Please specify the release date of your study:  
*This is when your study will be made public.*  
20-Dec-2019

Please provide a short name for the study:

Please provide a short descriptive title for the study: (\*)

Please provide attributes to add a deeper description of the study:

Tag	FieldType

Add

Please provide PubMed IDs of publications you want to associate with the study:  
*(numeric value)*

PubMed IDs

Add

For genome assembly projects only: In this study, will you provide functional genome annotation? (\*)  
**PLEASE ANSWER WITH YES IF YOU HAVE ANNOTATION. Locus tag prefixes are only associated to studies providing functional genome annotation.**

Yes  
 No

Please provide an abstract

Please select the most appropriate checklist from the list below then click the **Next >>** button.

- Environmental Checklists  
This group currently includes Genomic Standards Consortium (GSC) MixS sample checklists
- Marine Checklists  
This group currently includes Micro B3 and Tara Oceans sample checklists
- Pathogens Checklists  
This group currently includes several prokaryote and virus pathogen sample checklists
- Other Checklists  
This group currently includes the ENA default sample checklist and a few project specific checklists

- ENA Global Microbial Identifier Proficiency Test (GMI PT) checklist  
Minimum information to standardize metadata related to samples used in GMI PT (Global Microbial Identifier Proficiency Test). A checklist for reporting metadata of GMI PT samples associated with molecular data. This minimum metadata standard was developed by the COMPARE platform and can be used for submission of sample metadata derived from Campylobacter coli, Campylobacter jejuni, Listeria monocytogenes, Klebsiella pneumoniae, Salmonella enterica, Escherichia coli and Staphylococcus aureus.
- ENA mutagenesis by carcinogen treatment checklist  
Minimum information required for reporting samples associated with genomic data, derived from carcinogen induced animal tumours. This minimum metadata standard was developed in collaboration with Duncan Odum lab for the Mouse Liver Cancer Evolution Project.
- ENA Plant Sample Checklist  
ENA implementation of plant specimen contextual information associated with molecular data. This checklist has been developed in collaboration with the NCBI-GenBank and iPlant data resources under the umbrella of the Genomic Standards Consortium.
- ENA default sample checklist  
Minimum information required for the sample
- PDX Checklist  
Minimum information required for reporting samples associated with patient-derived xenograft (PDX) models or patient samples
- ENA Crop Plant sample enhanced annotation checklist  
The ENA Crop sample enhanced checklist has been developed in collaboration with a number of EMBL-EBI teams to capture enriched annotation of published crop plant samples that lack sufficient reported metadata and are typically associated with systematic travel

Når arkiveringen av data er komplett mottar man en bekreftelse og et unikt referansenummer

Your study accession number is: **PRJEA30703**

## Publisering av studiet

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Livsvitenskapelig tidsskrift krever at data er tilgjengelig i offentlige dataarkiv

### BMC Genomics



Research article

Open Access

**The genome sequence of the fish pathogen *Aliivibrio salmonicida* strain LF11238 shows extensive evidence of gene decay**

### Data availability

The metagenomic sequence data generated during the current study have been deposited in the European Nucleotide Archive (ENA) under the study accession number **PRJEA30703**

## Hvordan finne publisert data

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God metadata beskrivelse er essensielt for å effektivt finne relevant informasjon

DEMO: Hvordan finne informasjon og da fra dette studiet?

### **BMC Genomics**



Research article

**Open Access**

**The genome sequence of the fish pathogen *Aliivibrio salmonicida* strain LF11238 shows extensive evidence of gene decay**

### **Data availability**

The metagenomic sequence data generated during the current study have been deposited in the European Nucleotide Archive (ENA) under the study accession number **PRJEA30703**

# Mange standarder innen livsvitenskapen

ELIXIR Norge tilbyr sluttbrukere hjelp

Data innsamling



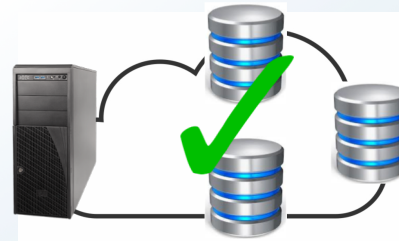
Data produksjon



Data lagring/deling



Data prosessering



Data arkivering

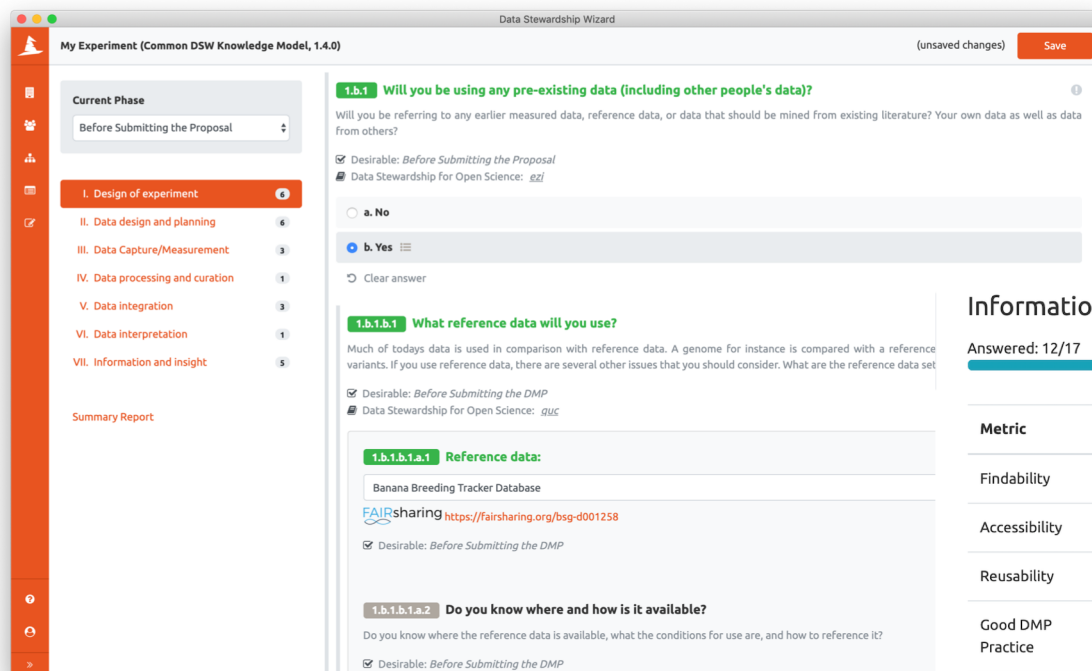


Data management



# ELIXIR tilbyr domene-spesifikke DMPs til sluttbrukere

Alle forskningsprosjekter må ha en data management plan (DMP) for å få finansiering  
 Utformet som spørreskjema med få fritekst felt – FAIR vurdering



**My Experiment (Common DSW Knowledge Model, 1.4.0)** (unsaved changes) **Save**

**Current Phase:** Before Submitting the Proposal

**I. Design of experiment** (1)

II. Data design and planning (6)

III. Data Capture/Measurement (3)

IV. Data processing and curation (1)

V. Data integration (3)

VI. Data interpretation (1)

VII. Information and insight (5)

Summary Report

**1.b.1 Will you be using any pre-existing data (including other people's data)?**

Will you be referring to any earlier measured data, reference data, or data that should be mined from existing literature? Your own data as well as data from others?

Desirable: Before Submitting the Proposal  
 Data Stewardship for Open Science: *gzl*

a. No

b. Yes

**1.b.1.b.1 What reference data will you use?**

Much of today's data is used in comparison with reference data. A genome for instance is compared with a reference variants. If you use reference data, there are several other issues that you should consider. What are the reference data set?

Desirable: Before Submitting the DMP  
 Data Stewardship for Open Science: *guc*

**1.b.1.b.1.a.1 Reference data:**

Banana Breeding Tracker Database

**FAIRsharing** <https://fairsharing.org/bsg-d001258>

Desirable: Before Submitting the DMP

**1.b.1.b.1.a.2 Do you know where and how it is available?**

Do you know where the reference data is available, what the conditions for use are, and how to reference it?

Desirable: Before Submitting the DMP

## Information and insight

Answered: 12/17

Metric	Measure
Findability	0.70
Accessibility	0.22
Reusability	1.00
Good DMP Practice	0.67
Openness	0.69

