



First lessons from the implementation of a biosample management system

Jakob Eckstein & Felix Mittermayer
Research Data Management Team
GEOMAR Helmholtz Centre for Ocean Research Kiel

Why do we need a central sample management system?



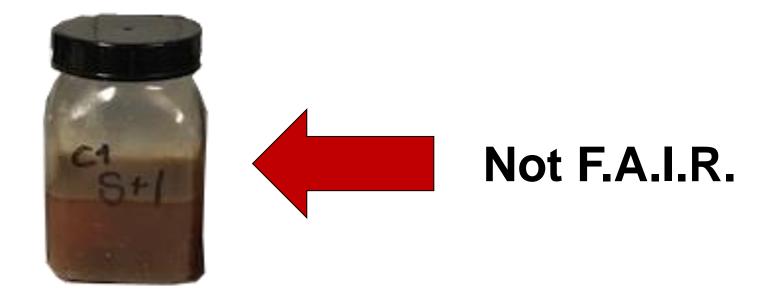
Why do we need a central sample management system?



Making research F.A.I.R. = Making sample collections F.A.I.R.



Making research F.A.I.R. = Making sample collections F.A.I.R.



Metadata is key



Sampling

- What?
- Where ?
- When?
- By whom?
- How ?

Metadata is key



Sampling

- What ?
- Where ?
- When?
- By whom ?
- How ?

Downstream

- How treated?
- How analysed?
- Data deposition ?
- Publication ?
- Are there other samples?
- Where stored?

Metadata is key



Sampling

- What ?
- Where ?
- When?
- By whom ?
- How ?

Downstream

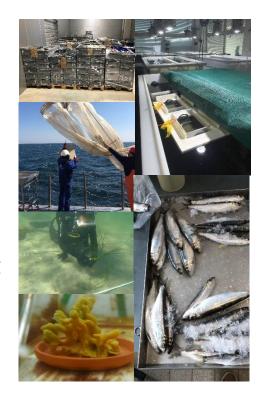
- How treated?
- How analysed?
- Data deposition ?
- Publication ?
- Are there other samples?
- Where stored?

Biosample Information System

Biosample ≠ Biosample ≠ Biosample

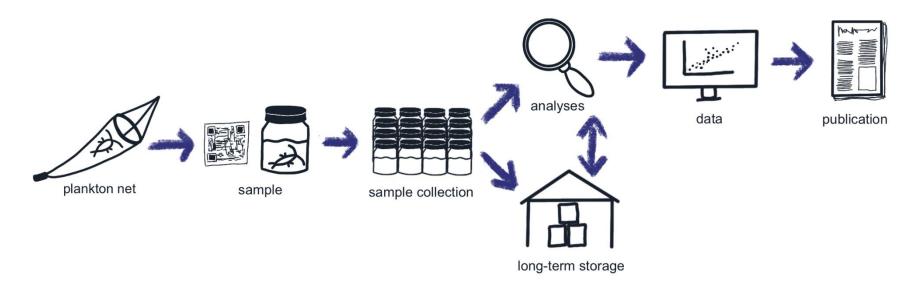


- Selected ten Lighthouse projects, covering different disciplines and working groups of the RDs Marine Ecology and Biogeochemistry
- Developend metadata and sample input files for various samples types
- Exchange with other members in AG samplemanagment
- Describe and publish SOPs for import into BIS



Workflows and import to BIS

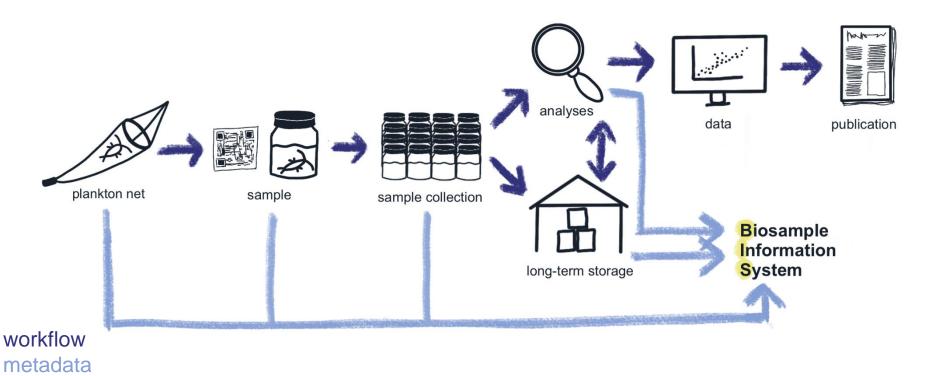




workflow

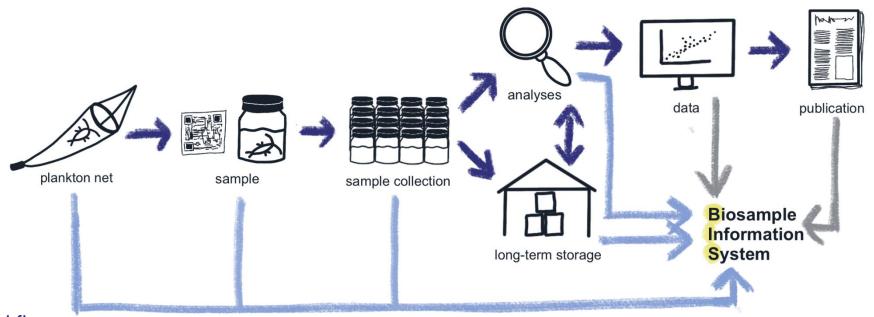
Workflows and import to BIS





Workflows and import to BIS

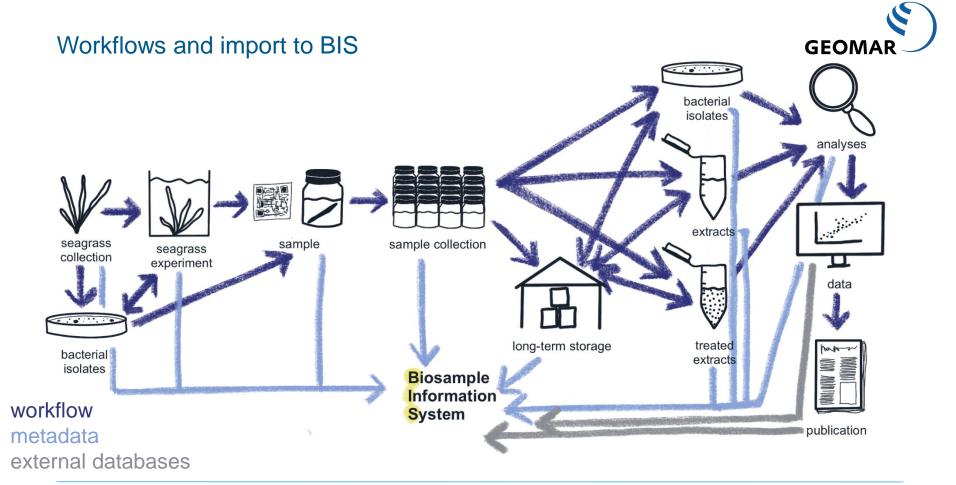




workflow

metadata

external databases



Challenges









Labellinlyroej

Metadata availability

Scientist's availability

Nagoya-Protocol on access to genetic resources



For every sample collected in a non-german EEZ after
 12.10.2014 a waiver from the national focal point of the country in question is needed

 Nagoya case number and information on possible restrictions (yes/no) is depositet in BIS

 Nagoya coordinator can produce waiver upon request and inform about possible restrictions



Dr.Jan Dierking nagoyaprotokoll@geomar.de

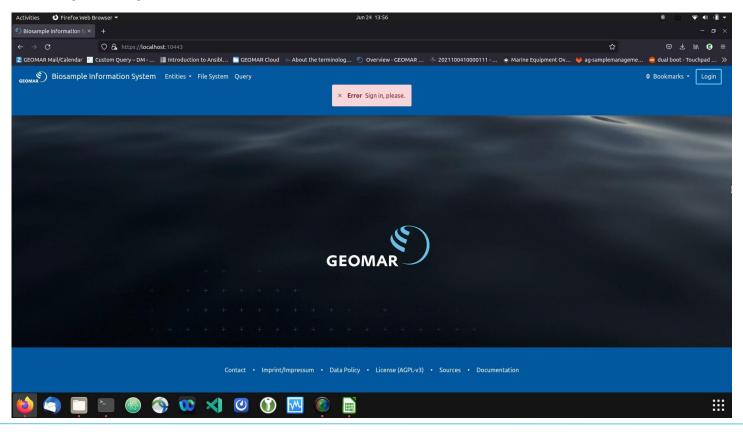
BIS Prototype



- Based on CaosDB An Open and Scientific Database:
 - Flexible Database Backend
 - WebUI (Web User Interface)
 - Different APIs (python, C++, julia, Mathlab, ...)
 - Open Source (AGPL v3)

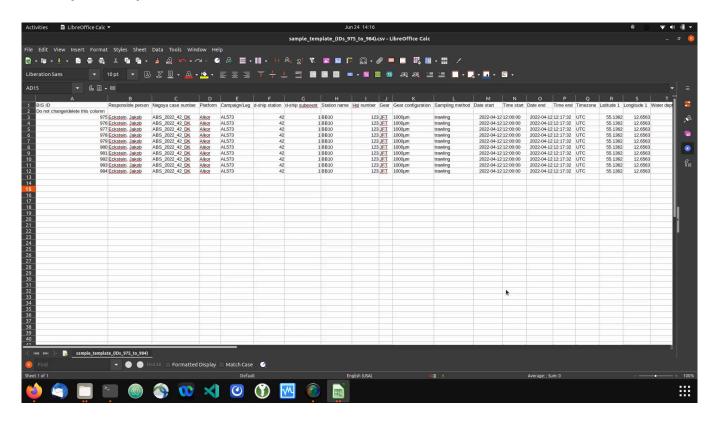
Demo: Sample Import 1





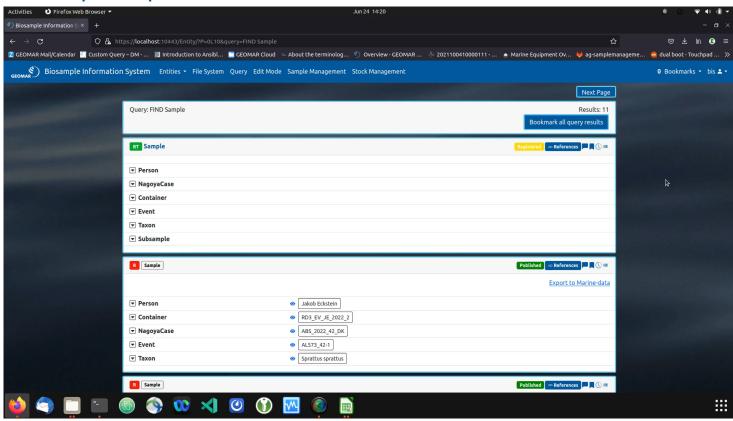
Demo: Sample Import 2





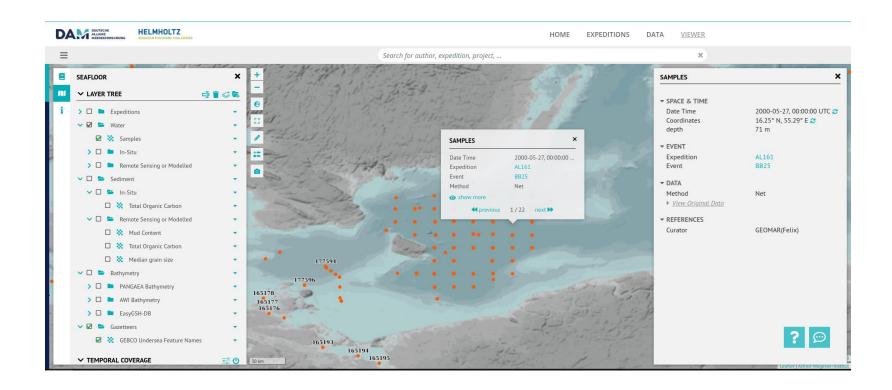
Demo: Sample Export





Demo: Sample on MarineData





Lessons learned



• ,Biosamples' are very diverse

Managing them centrally can be pretty demanding

To become FAIR, we still have to centralize biosample management

Developing the Biosample Information System is possible

Resources and funding

GEOMAR

 SOPs for data collection and labelling for BIS will be available soon

 Guest log-in to BIS available upon request (biosamples@geomar.de)

Contact us <u>biosamples@geomar.de</u>

CaosDB: https://caosdb.org/

• BIS: https://git.geomar.de/dm/bis





