



Data management tool in Life Sciences: the FAIRDOMhub

Flora D'Anna, PhD

Data Steward at ELIXIR Belgium



Advancing Data Stewardship:
insights from environmental and life science research

28th February 2020, Oostende

Research data are often not informative



RDA Plenary Cartoons by Auke Herrema.

Research Data Management (RDM) transforms Data into Information



RDA Plenary Cartoons by Auke Herrema.

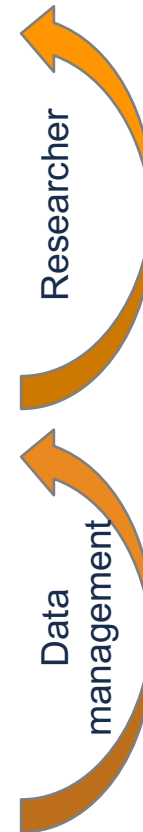
Knowledge

Information

- Findable
- Accessible
- Reusable

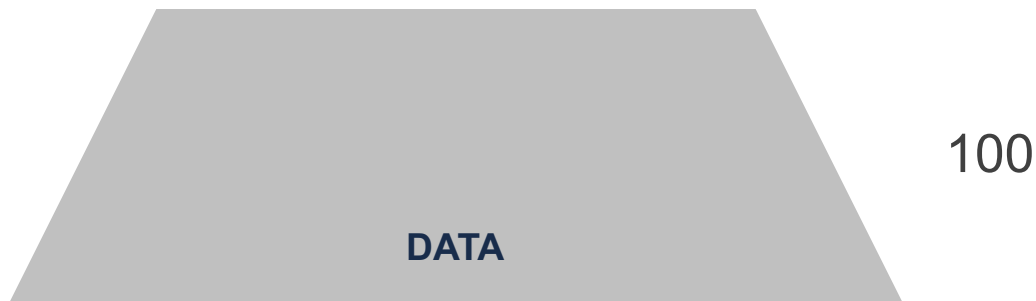
Data

- Unfindable
- Incomprehensible
- Not reusable



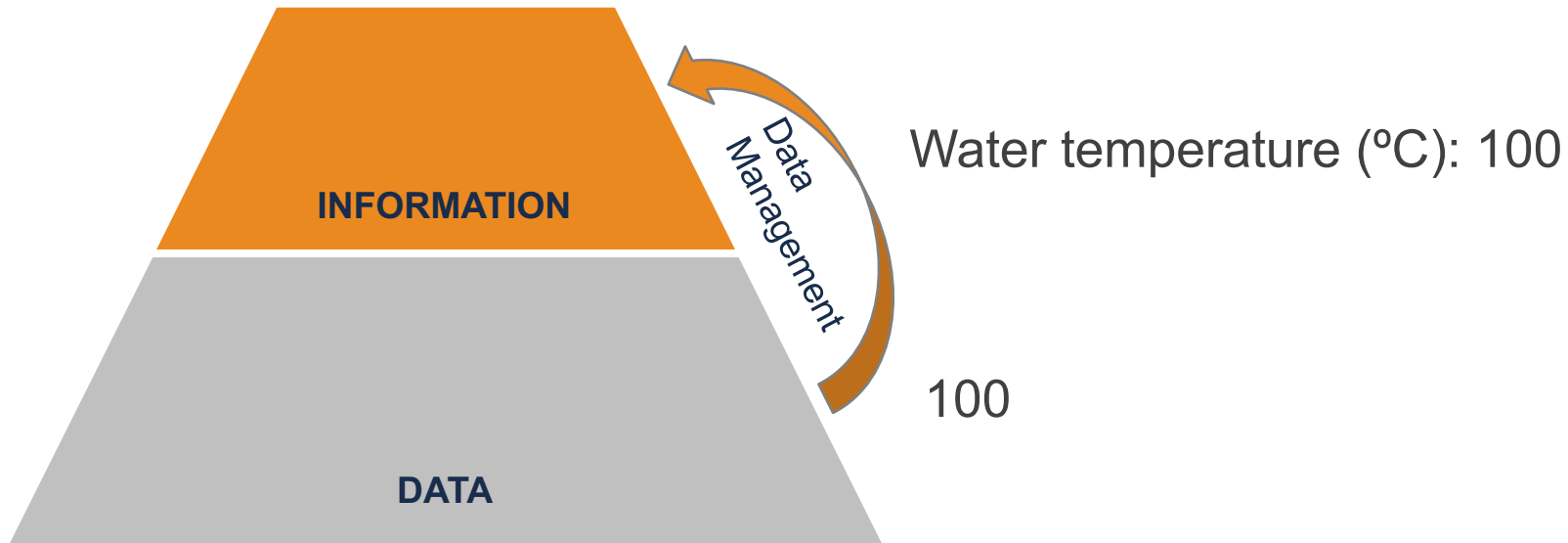
RDM transforms Data into Information, Information generates new Knowledge

Example



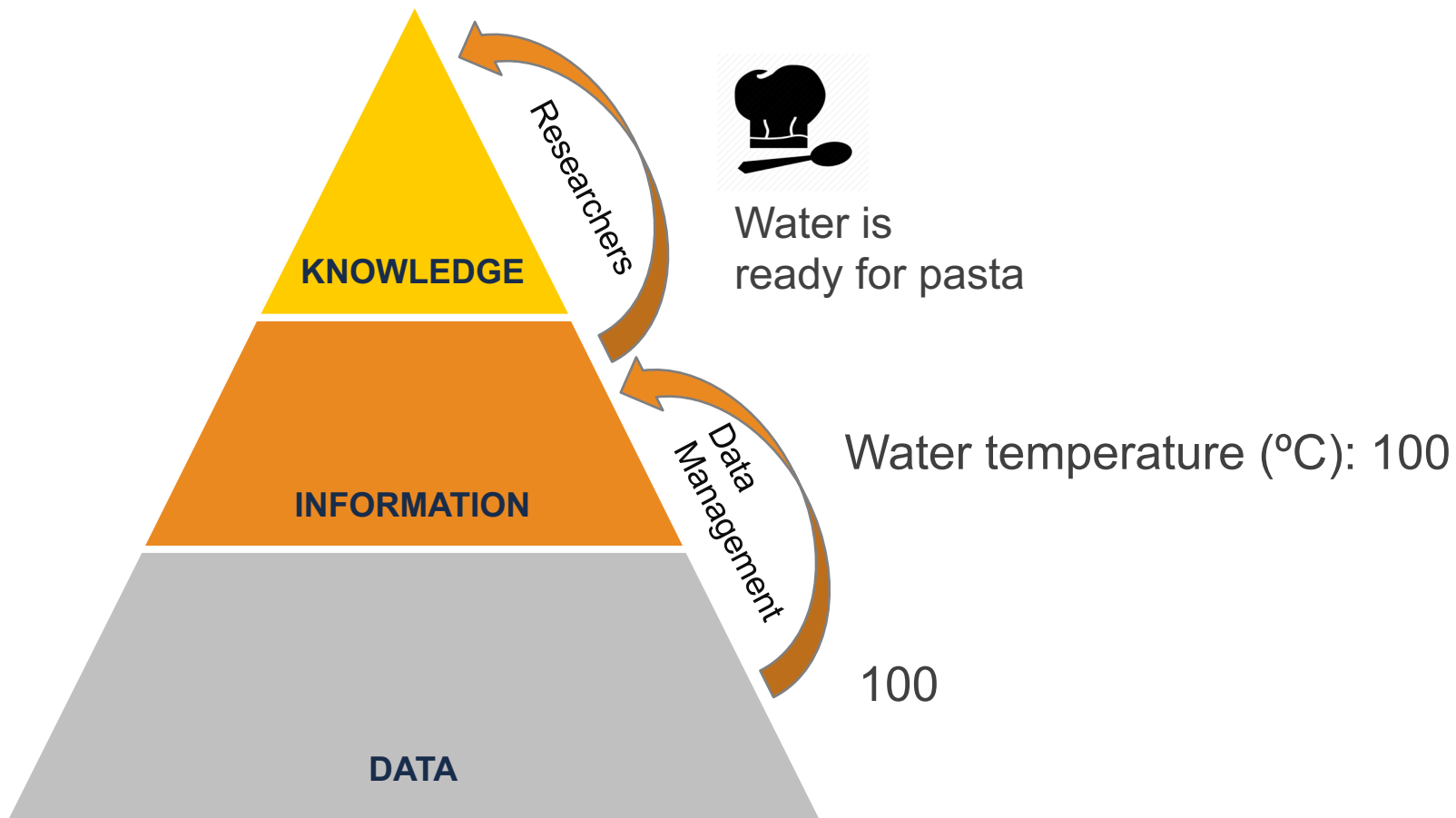
RDM transforms Data into Information, Information generates new Knowledge

Example



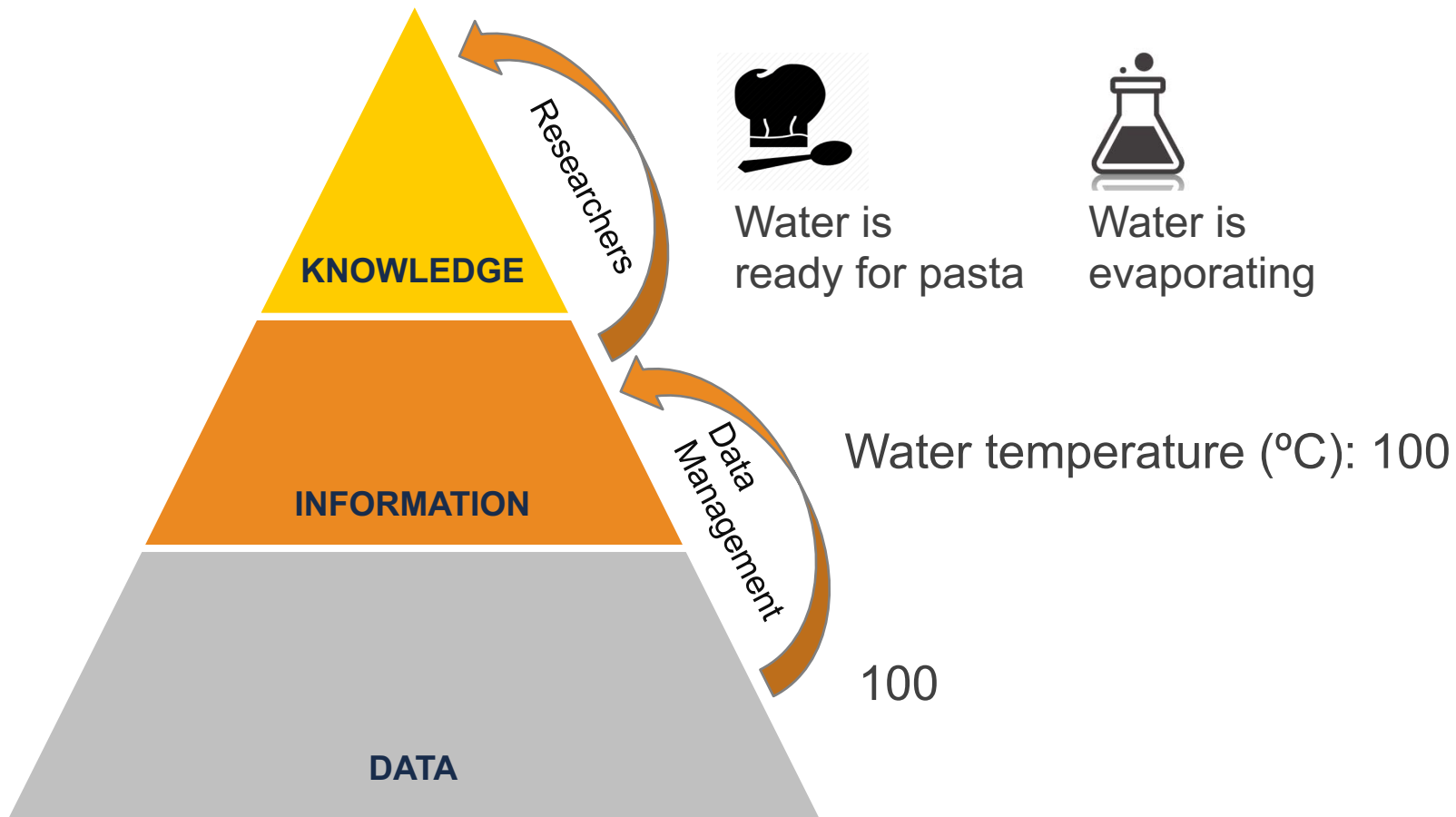
RDM transforms Data into Information, Information generates new Knowledge

Example



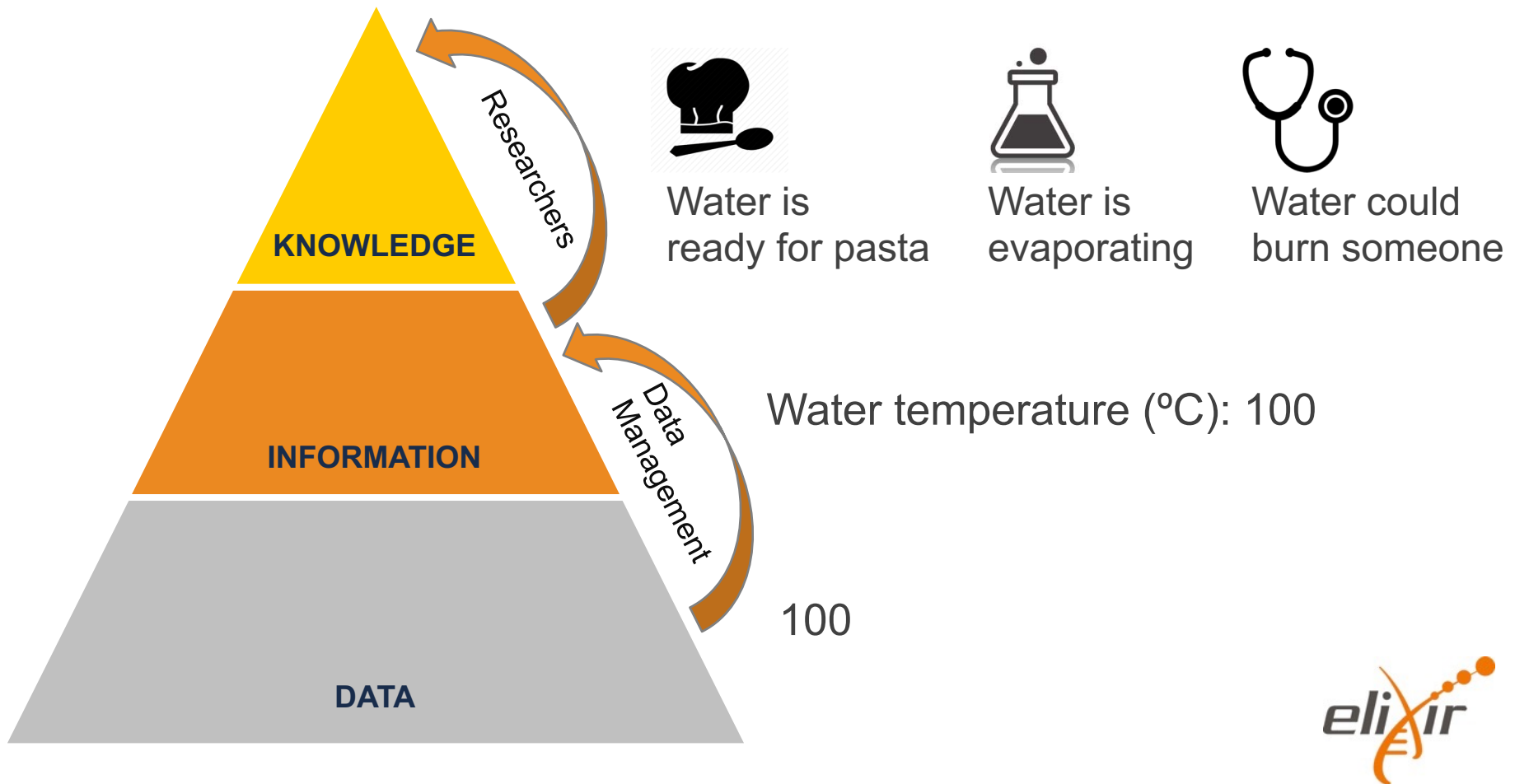
RDM transforms Data into Information, Information generates new Knowledge

Example



RDM transforms Data into Information, Information generates new Knowledge

Example



Develop a RDM Platform for Researchers

FAIRDOMhub.be



FAIRDOM

Powered by



SEEK



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FAIRDOMhub.be will enable
researchers to make their
data **FAIR by design**



Develop a RDM Platform for Researchers

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FAIRDOMhub.be will enable researchers to make their data **FAIR by design**

F_{indable} A_{ccessible} I_{nteroperable} R_{eusable}



Important: FAIR data both for your future-self and society



Outline



FAIRDOMhub.be as RDM tool

1. What is it?
2. What is it for?
3. How does it work?
4. What are the advantages for researchers?



FAIRDOMhub.be

What is it?



- Free web-based registry/platform for RDM (<https://fairdomhub.be/test/>)
- Based on the open source web platform SEEK, developed by the FAIRDOM initiative



FAIRDOMhub.be

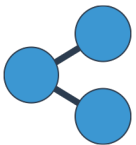
What is it for?



Organise your project in a standard simple structure



Describe your experimental design and samples with metadata schemas and ontology



Share your (meta)data with colleagues by using fine grained sharing permissions



FAIRDOMhub.be

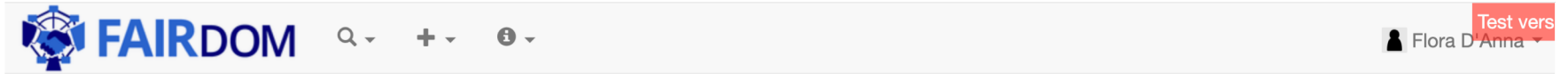
How does it work?



- 1) Group leader requests an account (or Programme) for the lab and create Project(s)
- 2) Researchers register in *fairdomhub.be* and join one or more Projects of the lab and/or create new project(s)
- 3) Researchers organise projects, describe experiments and share (meta)data

FAIRDOMhub.be

How does it work?



You can configure the text that goes here within the Admin pages: Site Configuration->Home page settings.

Announcements

No announcements

Tags [\[show all\]](#)

My Projects

Explore Projects

Create Project



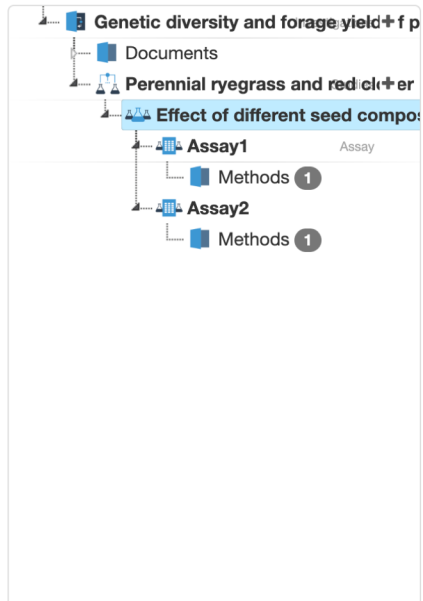


Genetic diversity and forage yield of perennial ryegrass

- Dashboard
- Overview
- Asset report
- Actions

Project Investigation Study

Delete



Details Design Sample Source Design Workflow

Title: Effect of different seed compositions and time on genetic diversity of perennial ryegrass

Description:

Hypothesis:

Experimentalists:

The following people...

Start typing a person's name and select from the list that appears. You can select multiple people.

can...

Update

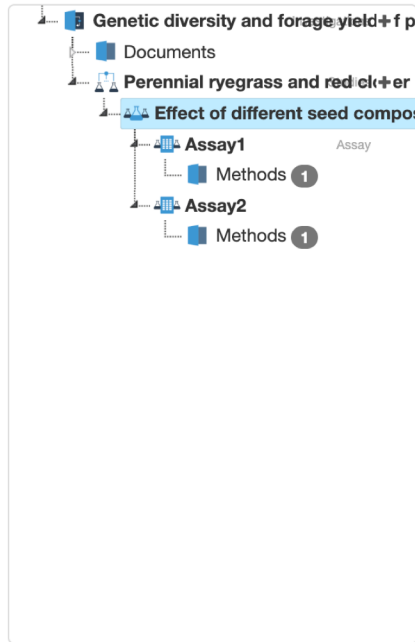




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Project Investigation Study Delete



Details Design Sample Source Design Workflow

Experimental factors

+ Add Variable

Experimental factors		Factors levels	
Plot	+ Add Level	01	🗑️
		02	
Time	+ Add Level	4M	🗑️
		12M	

Response variables

+ Add Variable + Add sub-sample

Response variables	Material	Sub-sample of	
allele frequency	pool of 40 leaves (observational unit)		🗑️





test vers

Response variables ⓘ	Material ⓘ	Sub-sample of
allele frequency	pool of 40 leaves (observational unit)	

Blocking variables

Covariates

Confounding variables

Replicates

[+ Add Variable](#)

Replicates	Number	Description	
Sample	1	one leaf of perennial regrass from a random plant	
Observational Unit (pool)	4	1 pool of 40 leaves (sample), from each plot at each time point	
Biological Replicate	2	Each plot is in 2 blocks	
Sub-Unit	2	2 replicate tissue pools created from each sample by weighing 5mg from each leaf sample of the respective plots	
Technical Replicate	3	3 libraries from each sub-unit	
Sequencing replicate	2	2 parallel lane, in the same flow cell, per technical replicate	

Design of experiment

RCBD Randomized complete block design with two biological repl

[Save Design](#) or [Generate Sample](#)





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Genetic diversity and forage yield + f p

- Documents
- Perennial ryegrass and red clover
 - Effect of different seed composition
 - Assay1 Assay
 - Methods 1
 - Assay2
 - Methods 1

Details Design Sample Source Design Workflow

Control variables

+ Add Variable + Add Column

Organism	Organism part	Developmental stage
Lolium perenne	leaf	
	leaf tip	
	leaf component	
	leaf vascular tissue	

Genetic diversity and forage yield of perennial ryegrass

[Dashboard](#) [Overview](#) [Asset report](#) [Actions](#)

Project Investigation Study Delete

- Genetic diversity and forage yield+ f p
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 - Assay2
 - Methods 1

Details Design Workflow

```
graph LR; SampleSource --> Pooling[Pooling and Splitting]; Pooling --> SubUnit; SubUnit --> LibraryPrep; LibraryPrep --> Libraries; Libraries --> Sequencing; Sequencing --> FAsqFiles;
```

into SubUnit

Set input and output count of items: Inputs: 1 Outputs: 1

Drag & drop these items to the canvas: Method Input/Output

Save

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How does it work?



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Project Investigation Study Assay Delete

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 - Assay2
 - Methods 1
 - Assay3
 - Methods 1

FAsqFiles Libraries SubUnit SampleSource

+Add Row +Add Column Save



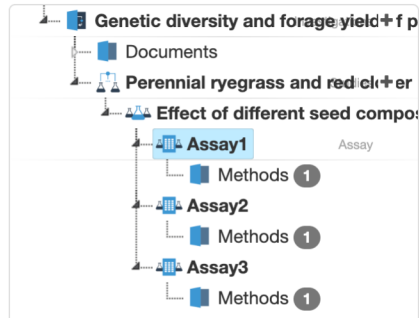


Genetic diversity and forage yield of perennial ryegrass

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Project Investigation Study Assay

Delete



FASTqFiles Libraries SubUnit SampleSource

+Add Row +Add Column Save

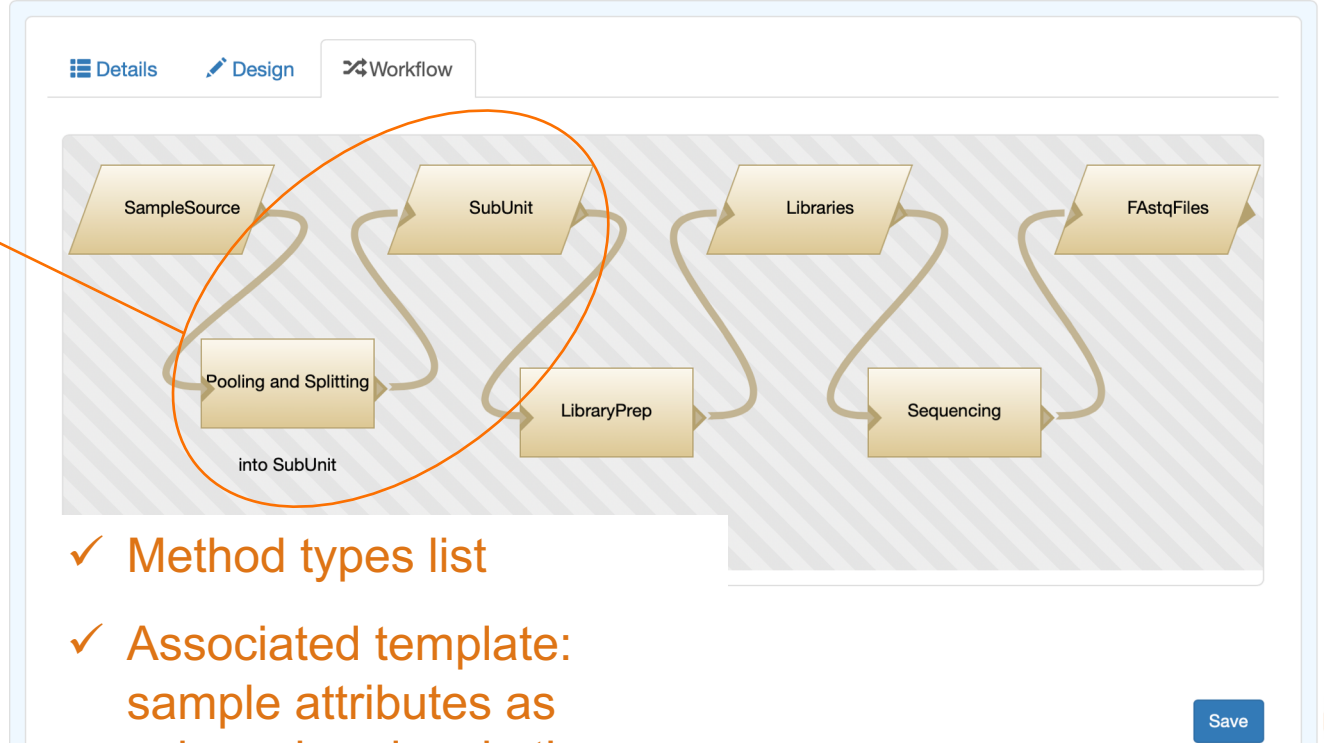
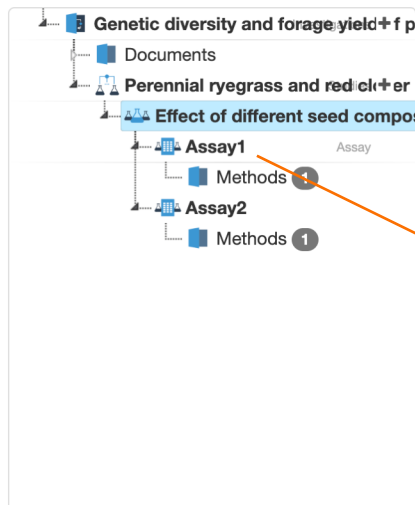
Block	Plot	Time	ObservationalUnit_Name
MA	01	4	01MA-4M
MB	01	4	01MB-4M
MA	02	4	02MA-4M
MB	02	4	02MB-4M
MA	01	12	01MA-12M
MB	01	12	01MB-12M
MA	02	12	02MA-12M
MB	02	12	02MB-12M



Genetic diversity and forage yield of perennial ryegrass

Dashboard Overview Asset report Actions

Project Investigation Study Delete

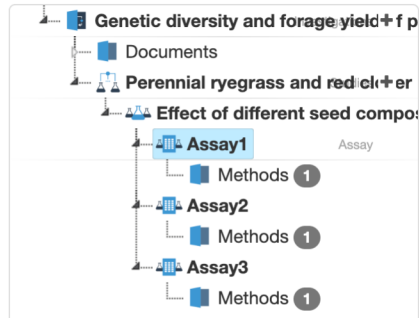


- ✓ Method types list
- ✓ Associated template: sample attributes as column headers in the output table

Genetic diversity and forage yield of perennial ryegrass

Project Investigation Study Assay

Delete



FASTqFiles Libraries **SubUnit** SampleSource

+Add Row +Add Column Save

Block	Plot	Time	ObservationalUnit_Name	SubUnit	SubUnit_Name
MA	01	4	01MA-4M	1	01MA-4M-pool1
MB	01	4	01MB-4M	1	01MB-4M-pool1
MA	02	4	02MA-4M	1	02MA-4M-pool1
MB	02	4	02MB-4M	1	02MB-4M-pool1
MA	01	12	01MA-12M	1	01MA-12M-pool1
MB	01	12	01MB-12M	1	01MB-12M-pool1
MA	02	12	02MA-12M	1	02MA-12M-pool1
MB	02	12	02MB-12M	1	02MB-12M-pool1
MA	01	4	01MA-4M	2	01MA-4M-pool2
MB	01	4	01MB-4M	2	01MB-4M-pool2
MA	02	4	02MA-4M	2	02MA-4M-pool2
MB	02	4	02MB-4M	2	02MB-4M-pool2



Genetic diversity and forage yield of perennial ryegrass

Project Investigation Study Assay

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 - Assay1
 - Methods 1
 - Assay2
 - Methods 1
 - Assay3
 - Methods 1

FastqFiles Libraries SubUnit SampleSource

+Add Row +Add Column Save

Block	Plot	Time	ObservationalUnit_Name	SubUnit	SubUnit_Name	Lib_Concentration	Unit	260/280
MA	01	4	01MA-4M	1	01MA-4M-pool1	35	ng/ul	1.8
MB	01	4	01MB-4M	1	01MB-4M-pool1	42	ng/ul	1.9
MA	02	4	02MA-4M	1	02MA-4M-pool1	30	ng/ul	1.8
MB	02	4	02MB-4M	1	02MB-4M-pool1	44	ng/ul	1.9
MA	01	12	01MA-12M	1	01MA-12M-pool1	40	ng/ul	2
MB	01	12	01MB-12M	1	01MB-12M-pool1	35	ng/ul	1.7
MA	02	12	02MA-12M	1	02MA-12M-pool1	30	ng/ul	1.9
MB	02	12	02MB-12M	1	02MB-12M-pool1	28	ng/ul	2
MA	01	4	01MA-4M	2	01MA-4M-pool2	25	ng/ul	2
MB	01	4	01MB-4M	2	01MB-4M-pool2	30	ng/ul	1.8
MA	02	4	02MA-4M	2	02MA-4M-pool2	32	ng/ul	1.8
MB	02	4	02MB-4M	2	02MB-4M-pool2	43	ng/ul	1.8



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What are the advantages for researchers?



- Organizing your experiments will be straightforward. You will always know “what file is what” and “where it is” (even after many years)
- You will not have to worry about backup and README file anymore: everything is safely stored and well described
- Collaboration with colleagues and data sharing with technical core facilities will be easier
- Submitting your data from *fairdomhub.be* to repository will be fast and easy



FAIRDOMhub.be

What are the advantages for researchers?



ELIXIR Deposition
Databases list



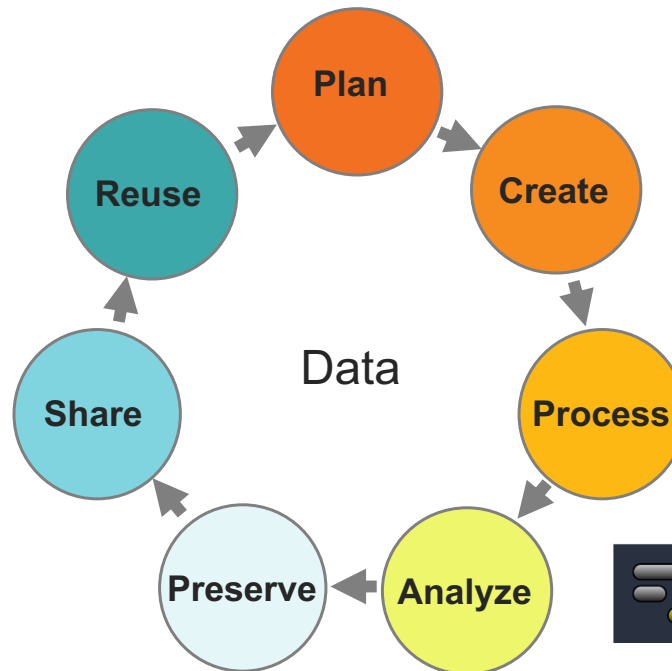
European Nucleotide Archive



IntAct



Other...



FAIRDOMhub.be



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SEEK



Summary



FAIRDOMhub.be as RDM tool

1. What is it?

- Free, intuitive and “researcher” friendly web based platform for RDM

2. What is it for?

- Organize, describe and share (meta)data according to standards

3. How does it work?

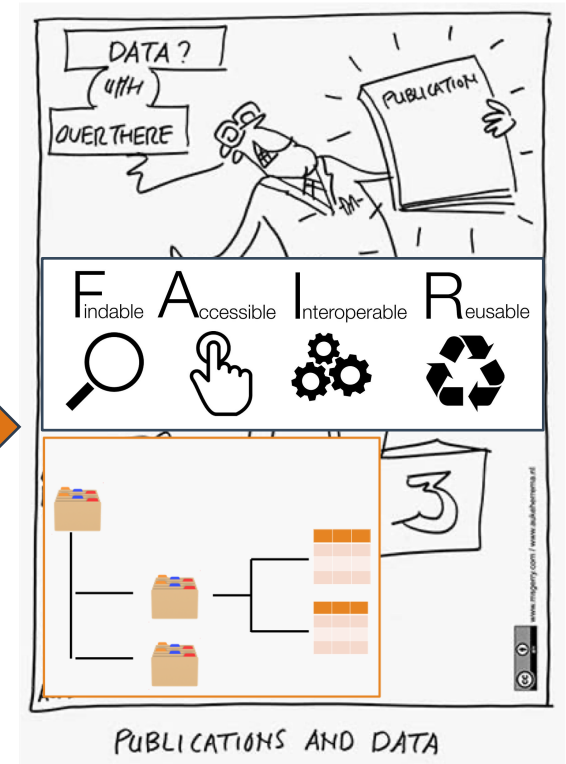
- Based on the general workflow “Input samples” → Method → “Output samples”

4. What are the advantages for researchers?

- Efficient data management and data sharing



Conclusion



RDA Plenary Cartoons by Auke Herrema.

RDA Plenary Cartoons by Auke Herrema.

Acknowledgements



Vahid Kiani, Software Developer at ELIXIR Belgium



DEPARTEMENT
ECONOMIE
WETENSCHAP &
INNOVATIE





Links

**ELIXIR Deposition
Databases list**

<https://elixir-europe.org/platforms/data/elixir-deposition-databases>



<https://fair-dom.org/platform/seek/>



<https://dmponline.be/projects>



<https://usegalaxy.be>

