

ARCify your research project

Hands-on ARC introduction @ AG Frommer, HHU

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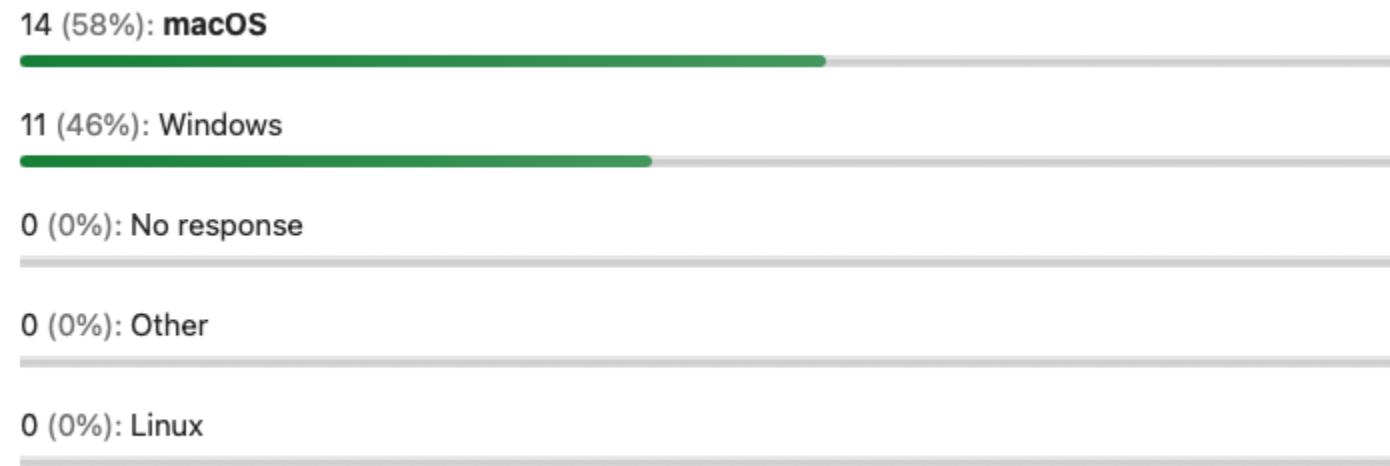
September 9th, 2025



Introduce yourself

- Used code / programming language before?
- Experience with Git / GitLab / GitHub?
- Operating system: Linux / Windows / Mac?
- Expectation

Your OS



Your experience with ARCs

14 (58%): **No response**

5 (21%): Participated in an ARC workshop before

4 (17%): Used ARCitect

3 (13%): Used DataHUB

3 (13%): Experience with code / programming language (Python, R, Bash, F#, etc.)

1 (4%): Used ARC Commander

1 (4%): Experience with Git / GitLab / GitHub

1 (4%): Experience with workflows (CWL, Snakemake, Nextflow) or workflow platforms (Galaxy, Workflowhub)

1 (4%): Explored the DataPLANT Knowledge Base

FAIR data stewardship

- Findable
- Accessible
- Interoperable
- Reusable

[nature](#) > [scientific data](#) > [comment](#) > [article](#)

[Open Access](#) | Published: 15 March 2016

The FAIR Guiding Principles for scientific data management and stewardship

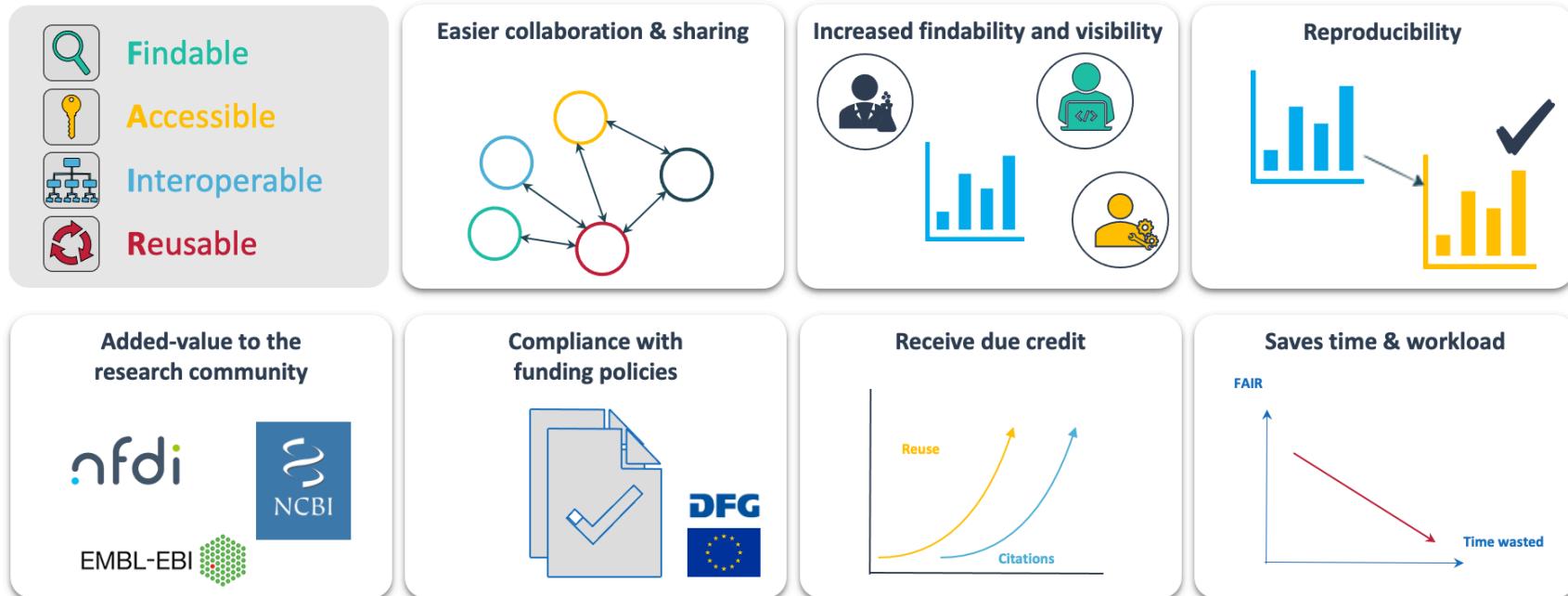
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<https://doi.org/10.1038/sdata.2016.18>

The FAIR principles



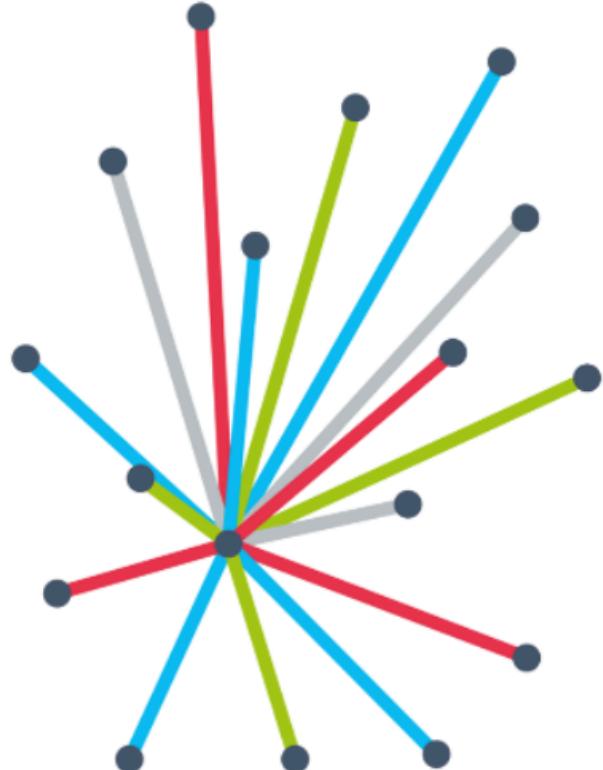
Is your data FAIR?

Findable | Accessible | Interoperable | Reusable

- Where do you store your data?
- How do you annotate your data?
- How do you share your data?
- What tools do you use to analyse your data?
- How do you reuse other people's data?



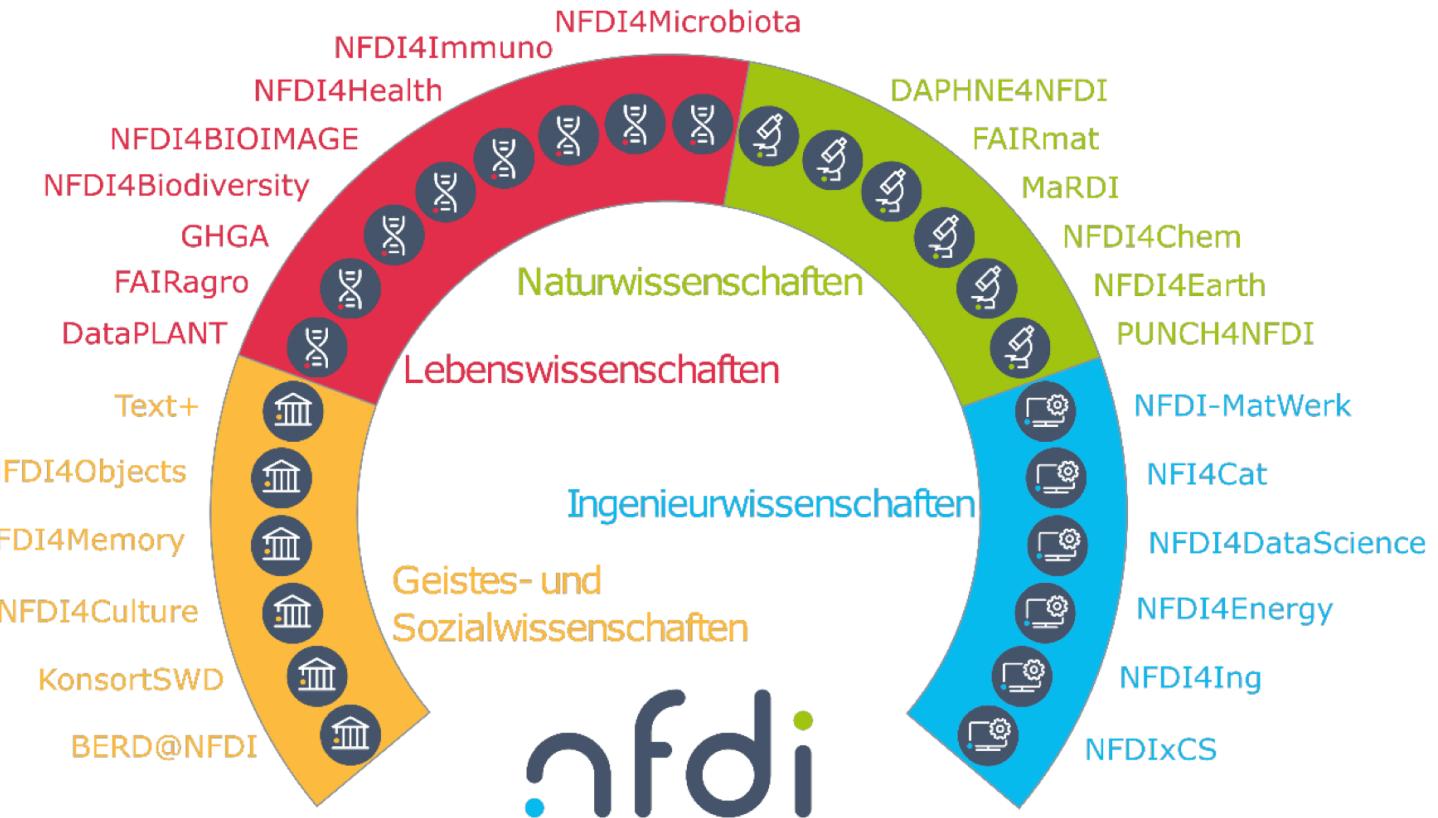
NFDI – Nationale Forschungsdaten Infrastruktur



The aim of the national research data infrastructure (NFDI) is to systematically manage scientific and research data, provide long-term data storage, backup and accessibility, and network the data both nationally and internationally.

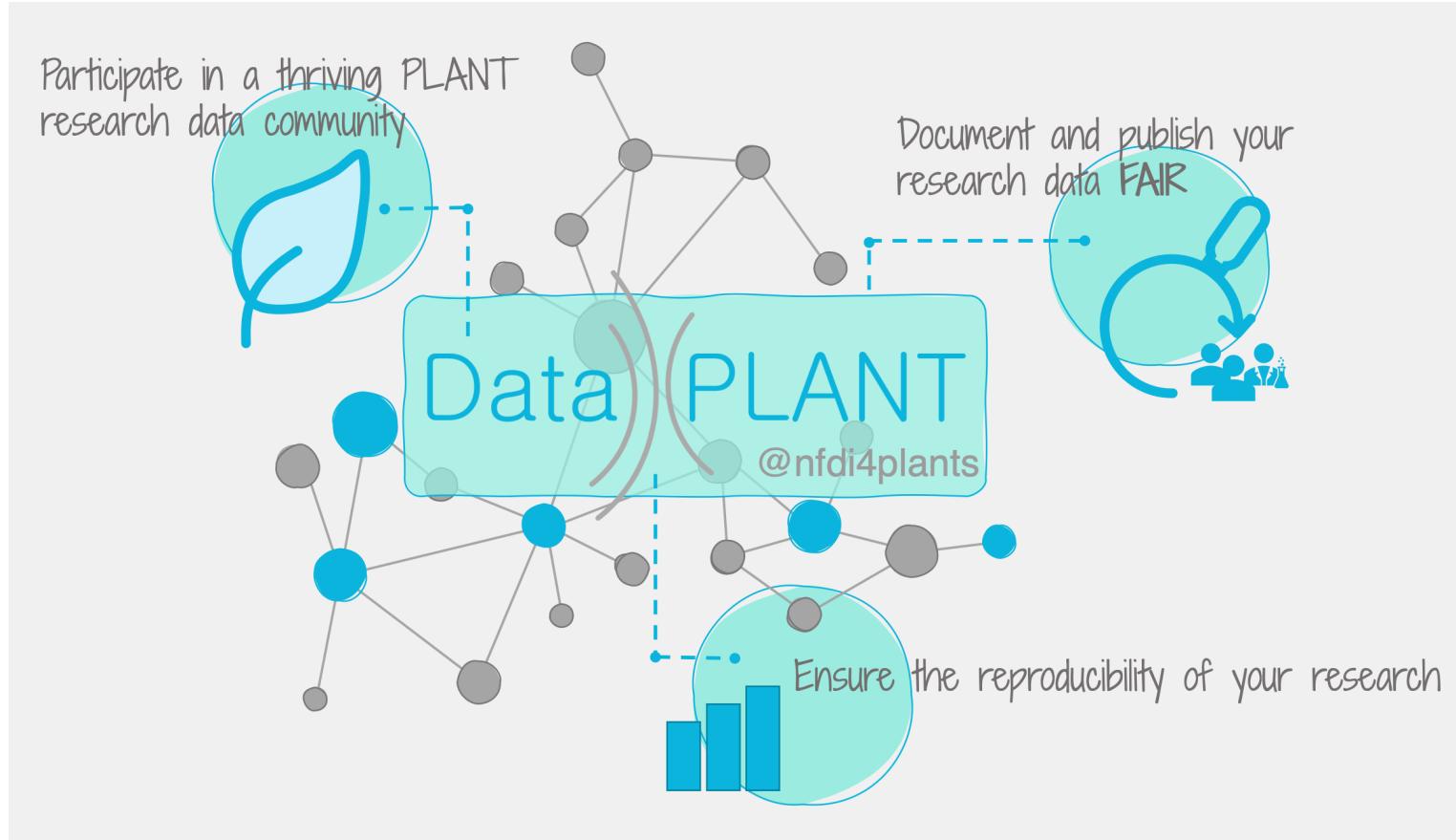
nfdi.de

NFDI – A community–targeted approach for RDM



nfdi.de

DataPLANT – NFDI4plants



- <https://nfdi4plants.org>
- <https://arc-rdm.org>

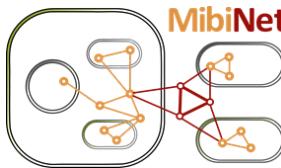
Data Stewardship between DataPLANT and the community

Community



CEPLAS

trr_341<sup>plant
ecological
genetics</sup>



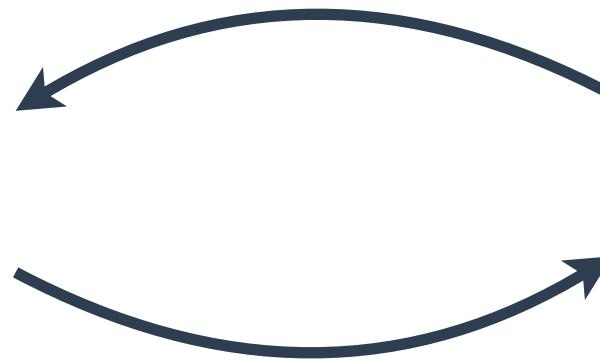
MibiNet

Domain experts
User experience
Training

nfdi4plants



Service provider
Developers
Tech experts



Resources



Info & materials

- DataPLANT Website: <https://nfdi4plants.org/>
- ARC website: <https://arc-rdm.org>
- Knowledge Base:
<https://nfdi4plants.org/nfdi4plants.knowledgebase/>

Tools and Services

- ARCitect: <https://github.com/nfdi4plants/arcitect>
- DataHUB: <https://git.nfdi4plants.org>

Continuous support

- HelpDesk: <https://helpdesk.nfdi4plants.org>
- Matrix for ad hoc support: <https://matrix.to/#/%23arc-user-support:matrix.org>
- User Support Meeting (2nd Friday of the month | 1 – 2pm):
<https://nfdi4plants.github.io/events/arc-user-support/>
- User Support Mailing List: [Click here to subscribe](#)

Open Source Development

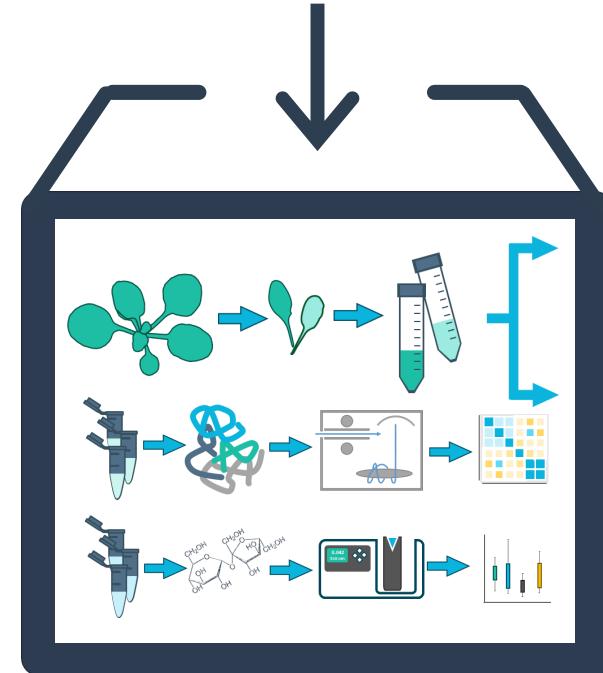
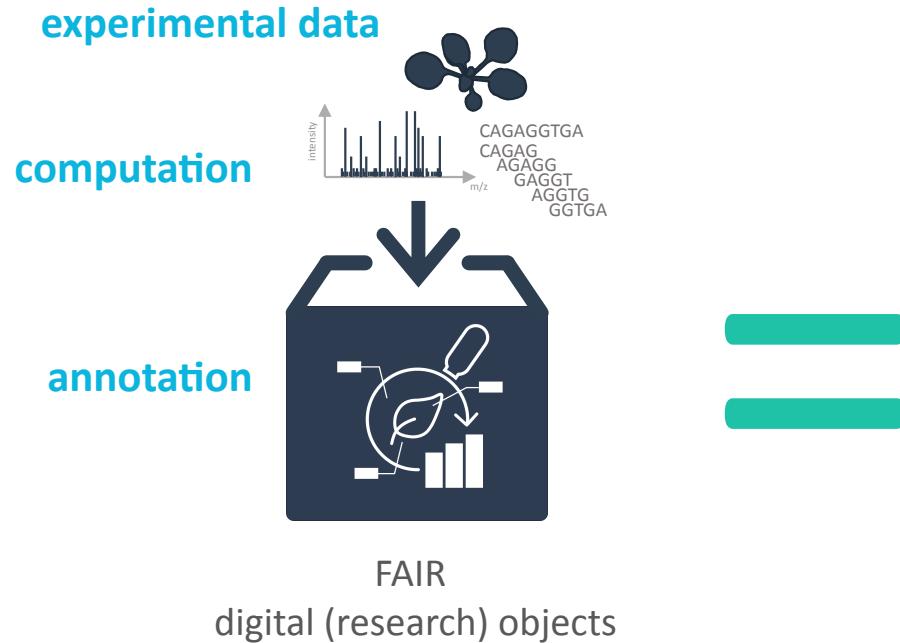
- GitHub: <https://github.com/nfdi4plants>

Training Material

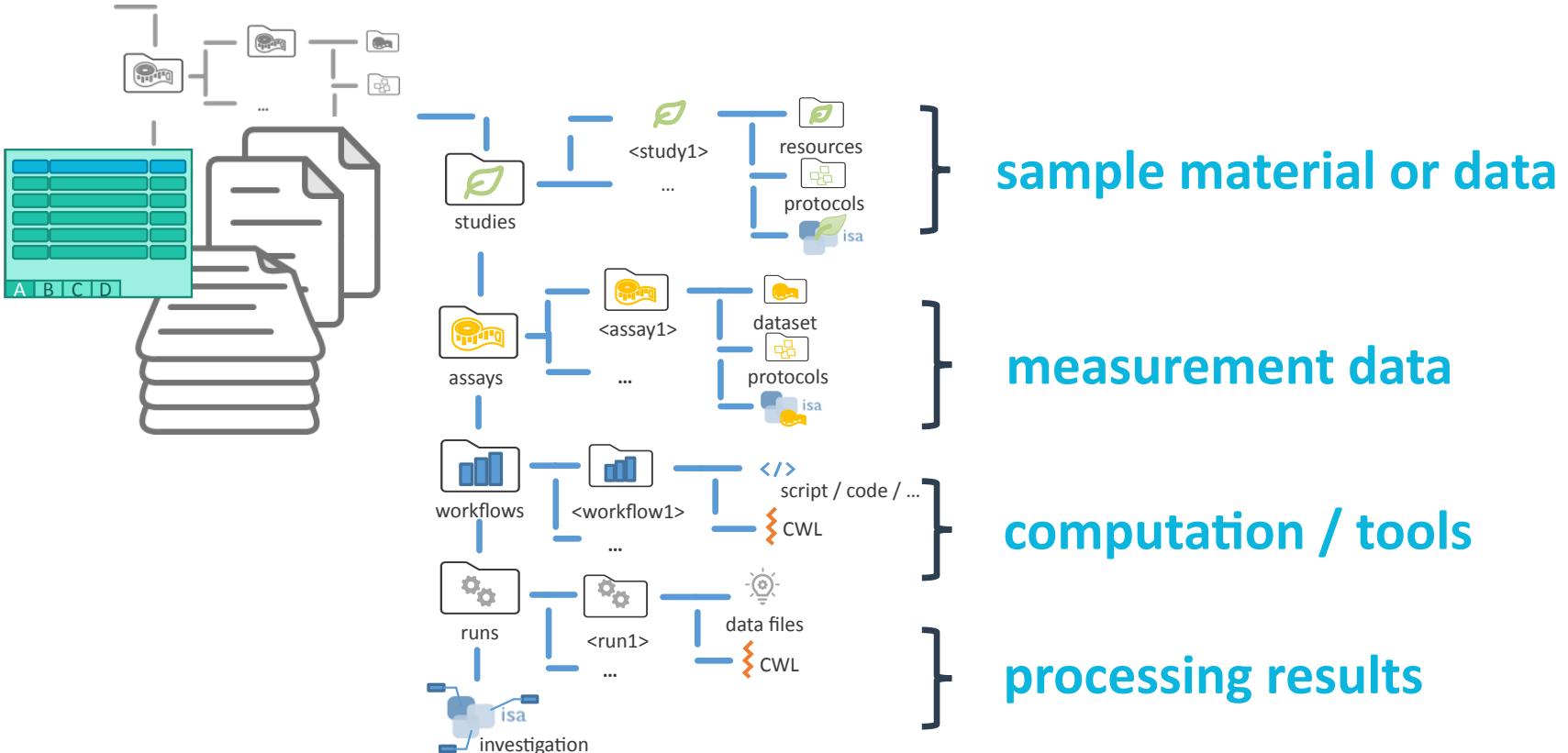
- Use the pad to raise questions and feedback
- Provide links for hands-on



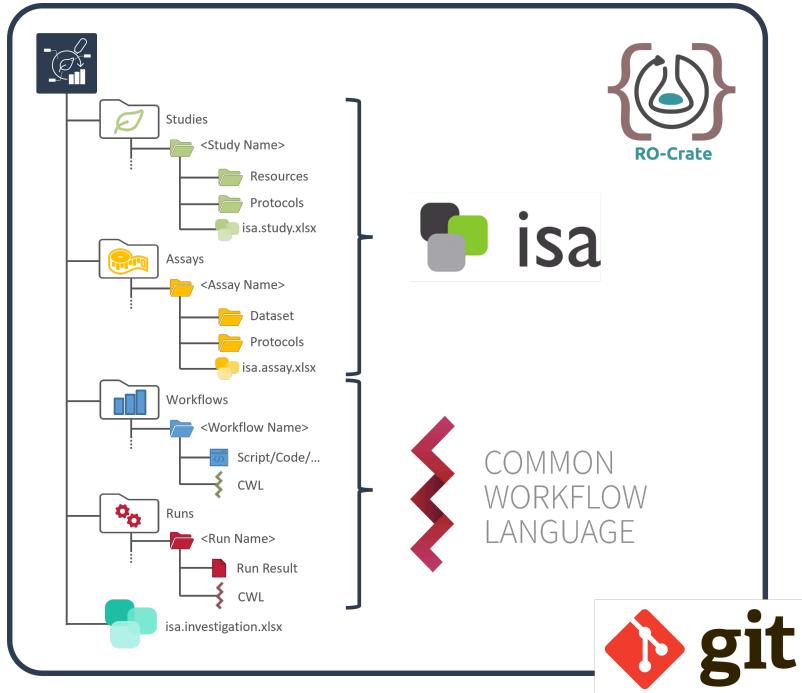
Annotated Research Context (ARC)



The ARC scaffold structure



ARC builds on standards



RO-Crate

- Standardized exchange
- <https://www.researchobject.org/ro-crate/>

ISA

- Structured, machine-readable metadata
- <https://isa-tools.org/>

CWL

- Reproducible, re-usable data analysis
- <https://www.commonwl.org/>

Git

- Version control
- <https://git-scm.com>

ISA abstract model in a nutshell



isa

Investigation
administrative (meta)data

- Summary
 - Titel
 - Description
- Person
- Organisation
- Publication reference

Study
descriptive (meta)data
information on the subject

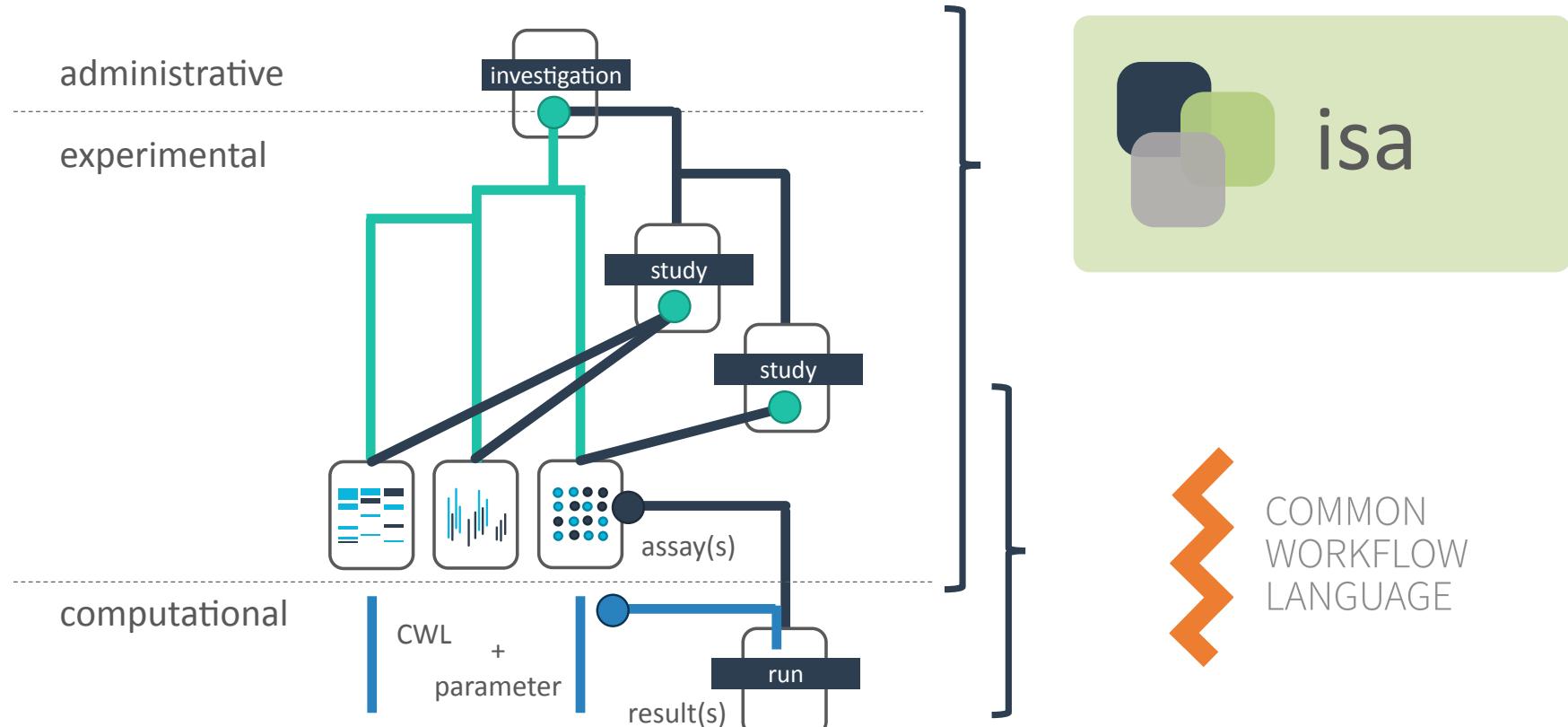
- Characteristics
- Parameters
- Components
- Factors

Assay

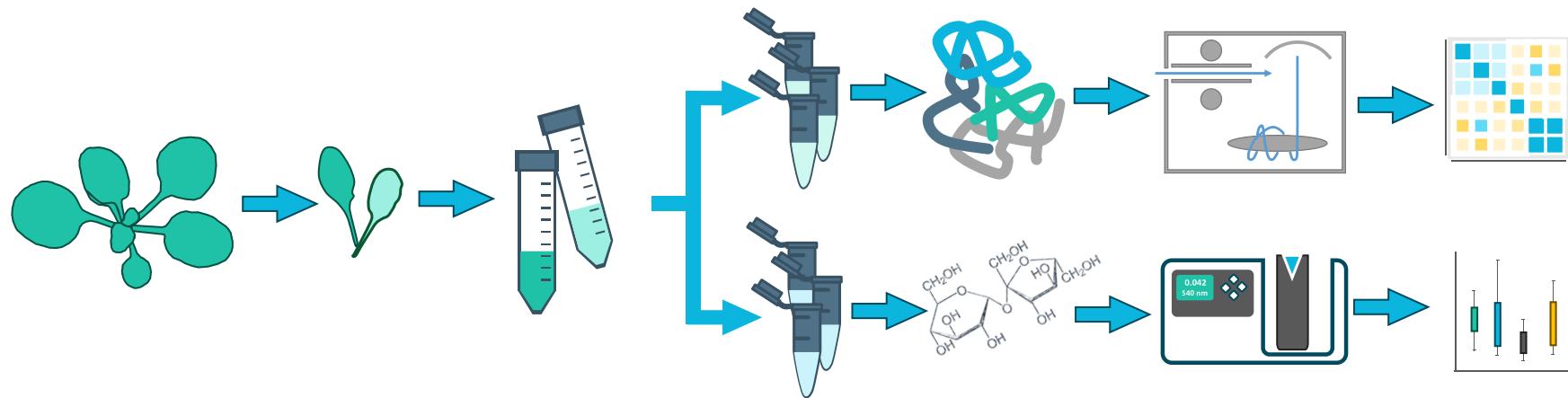
descriptive (meta)data
information on the measurement

- Characteristics
- Parameters
- Components
- Factors

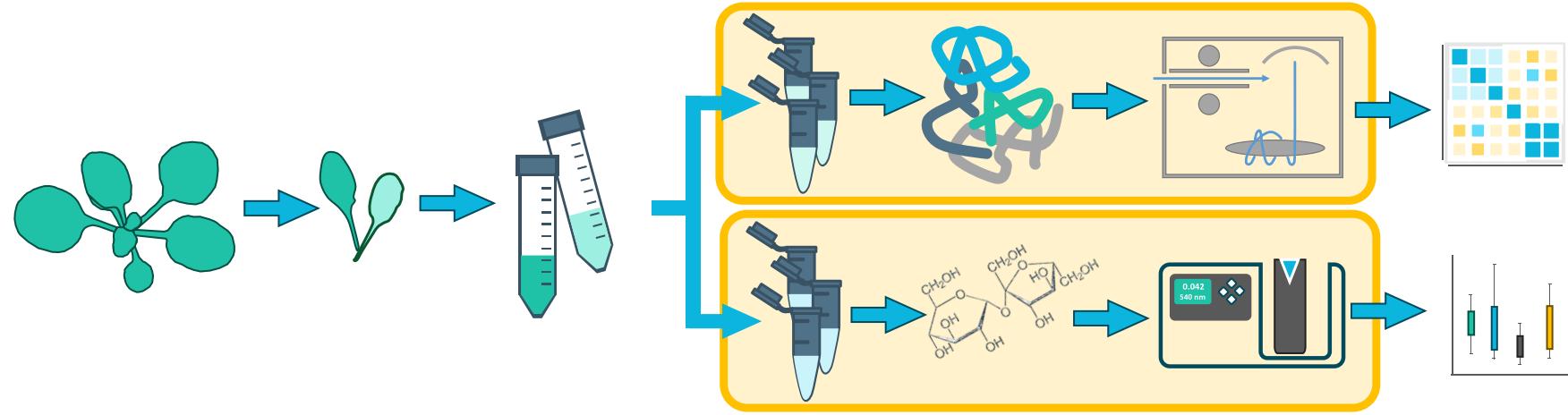
ISA and CWL – Connected by similarity



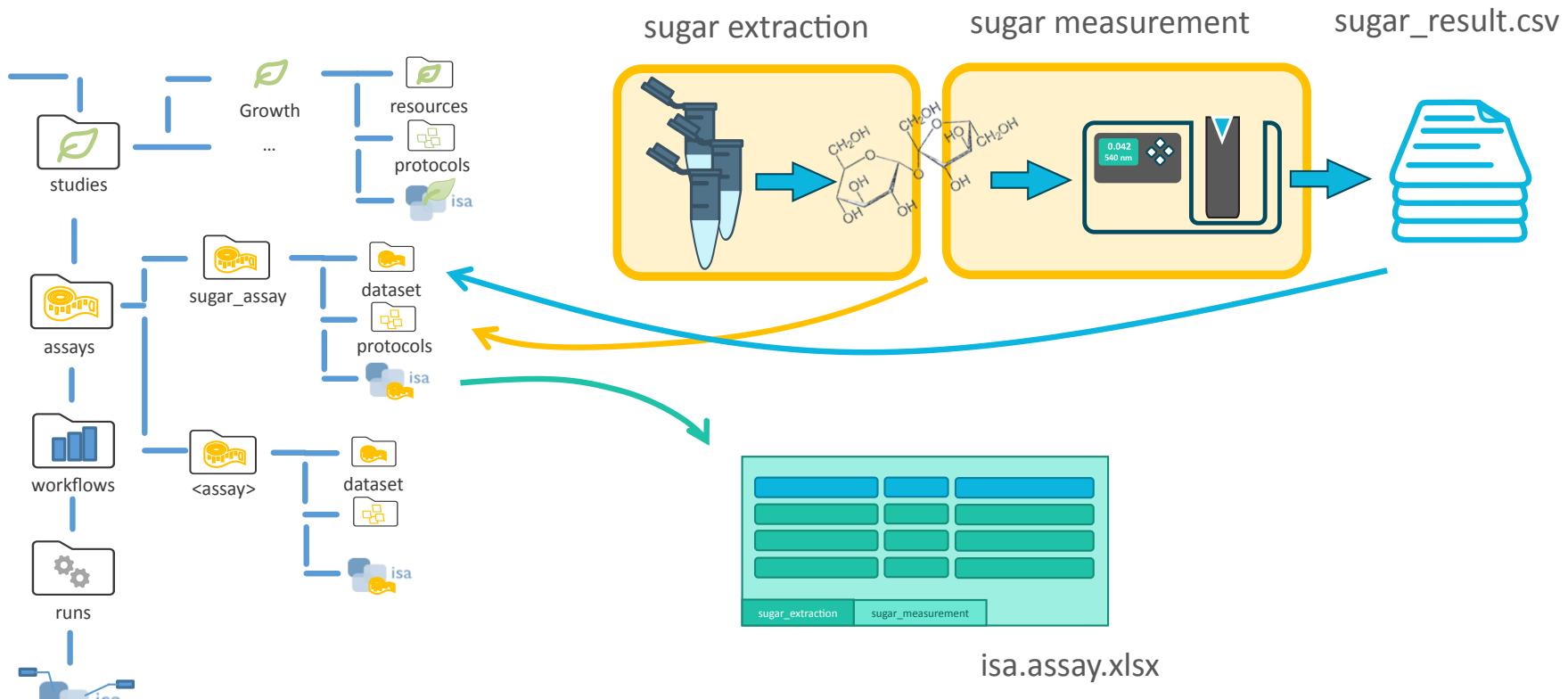
Metadata annotation – from sample to data



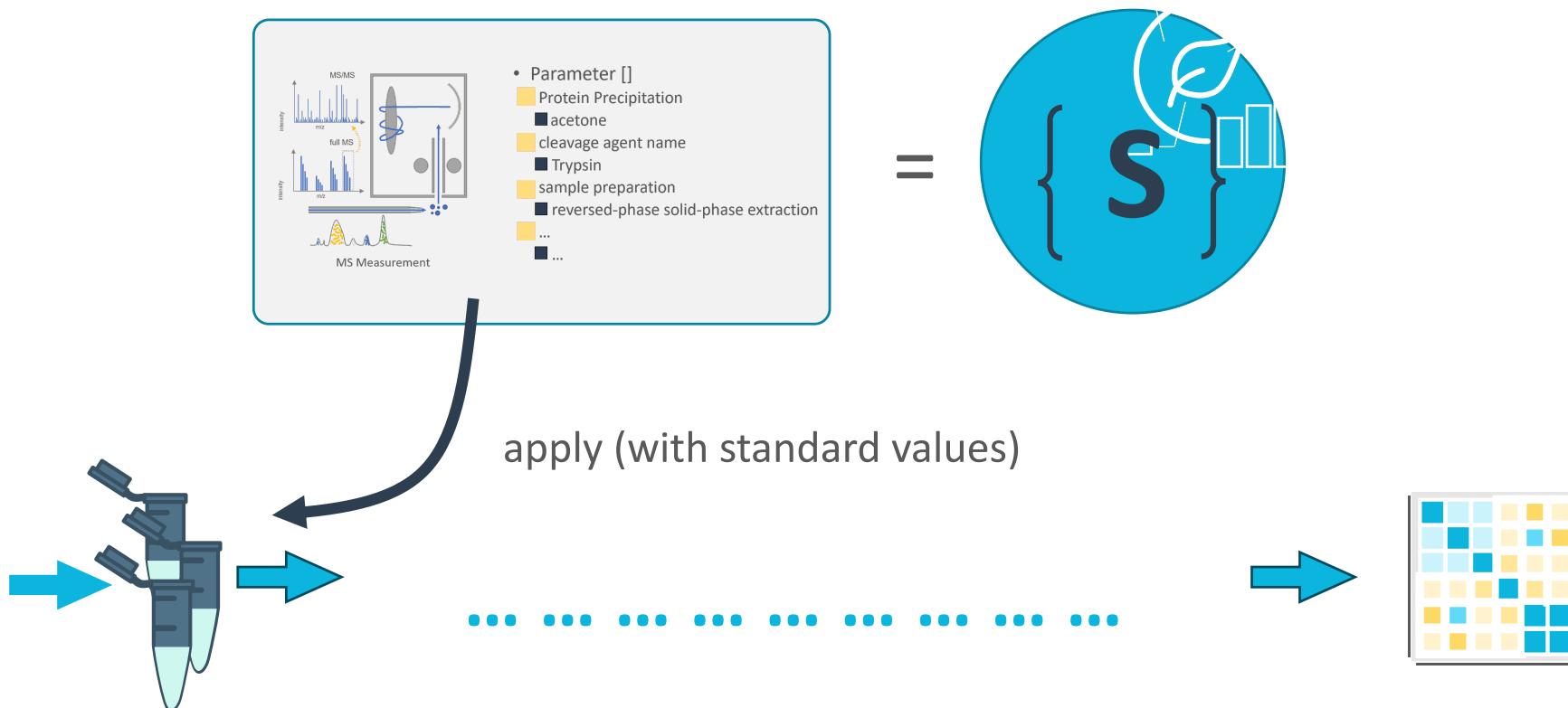
Modular separation of experimental processes



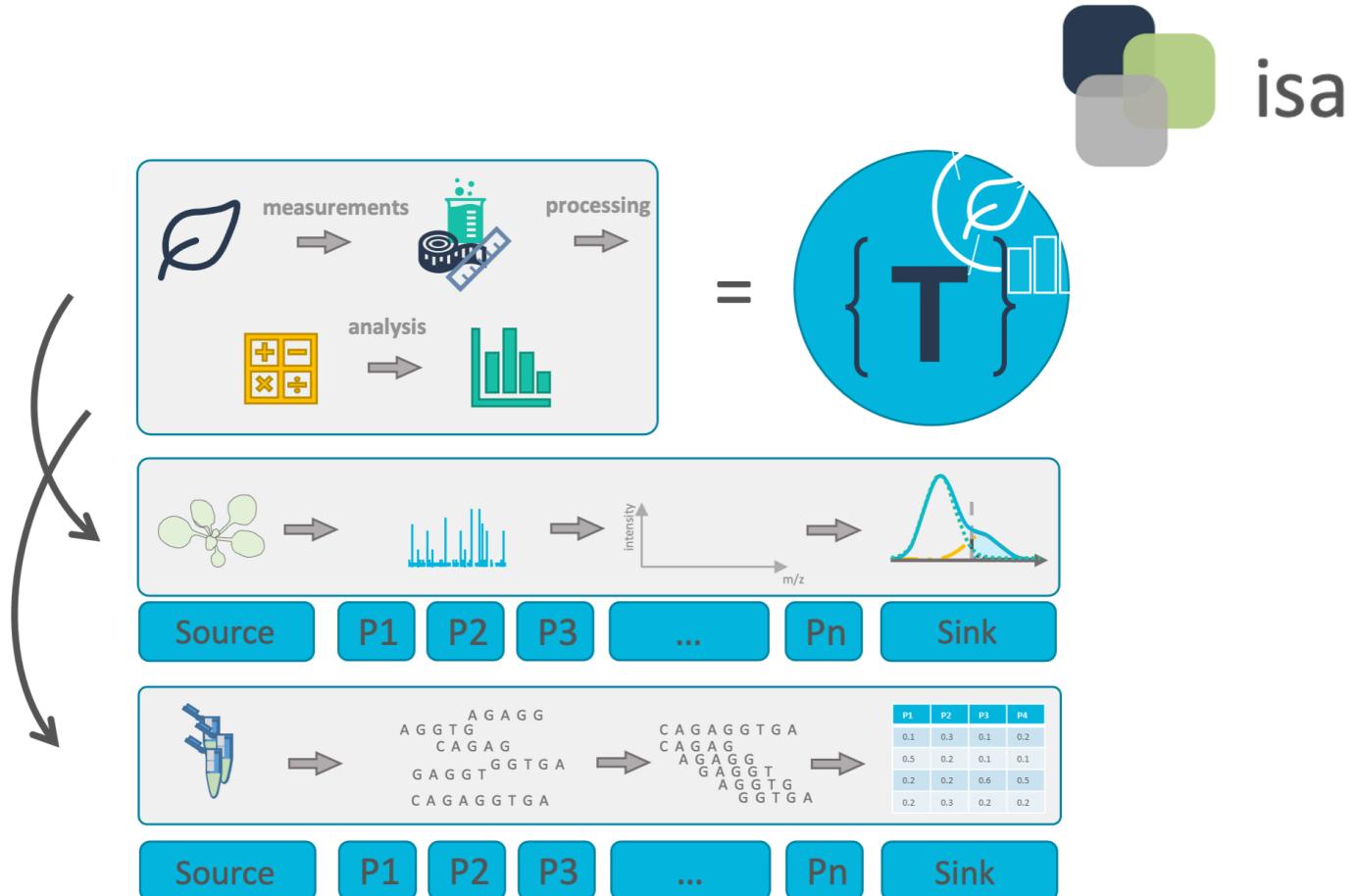
Modular separation of experimental processes



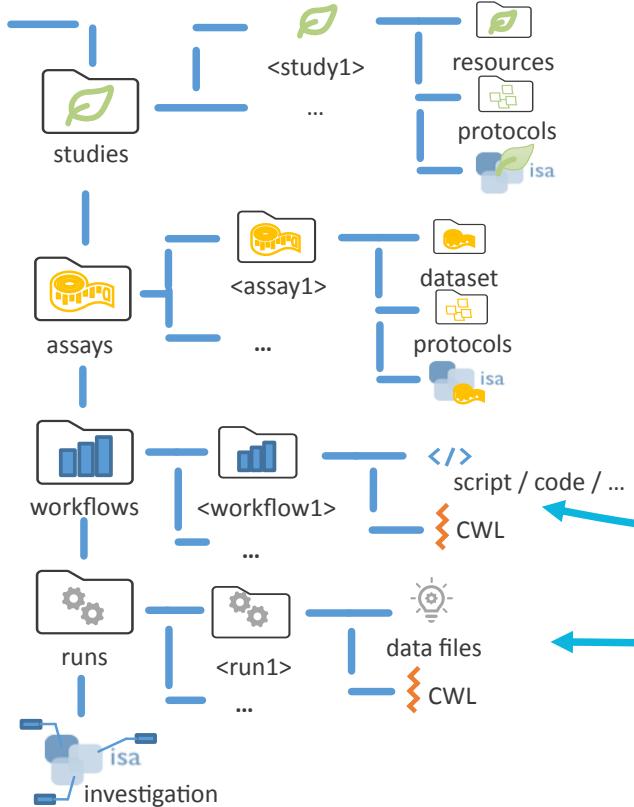
Applying standard procedures to sample record



Realization of lab-specific metadata with templates



Data analysis: CWL workflows and runs



```
python
Copy code

import pandas as pd
import plotly.express as px

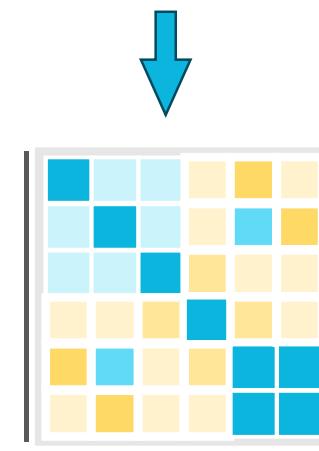
# Read the CSV file
data = pd.read_csv('result.csv')

# If the CSV doesn't have a clear index or row/column names, you may need to manually set
# For example, if the first column should be the index, you can use:
# data = pd.read_csv('result.csv', index_col=0)

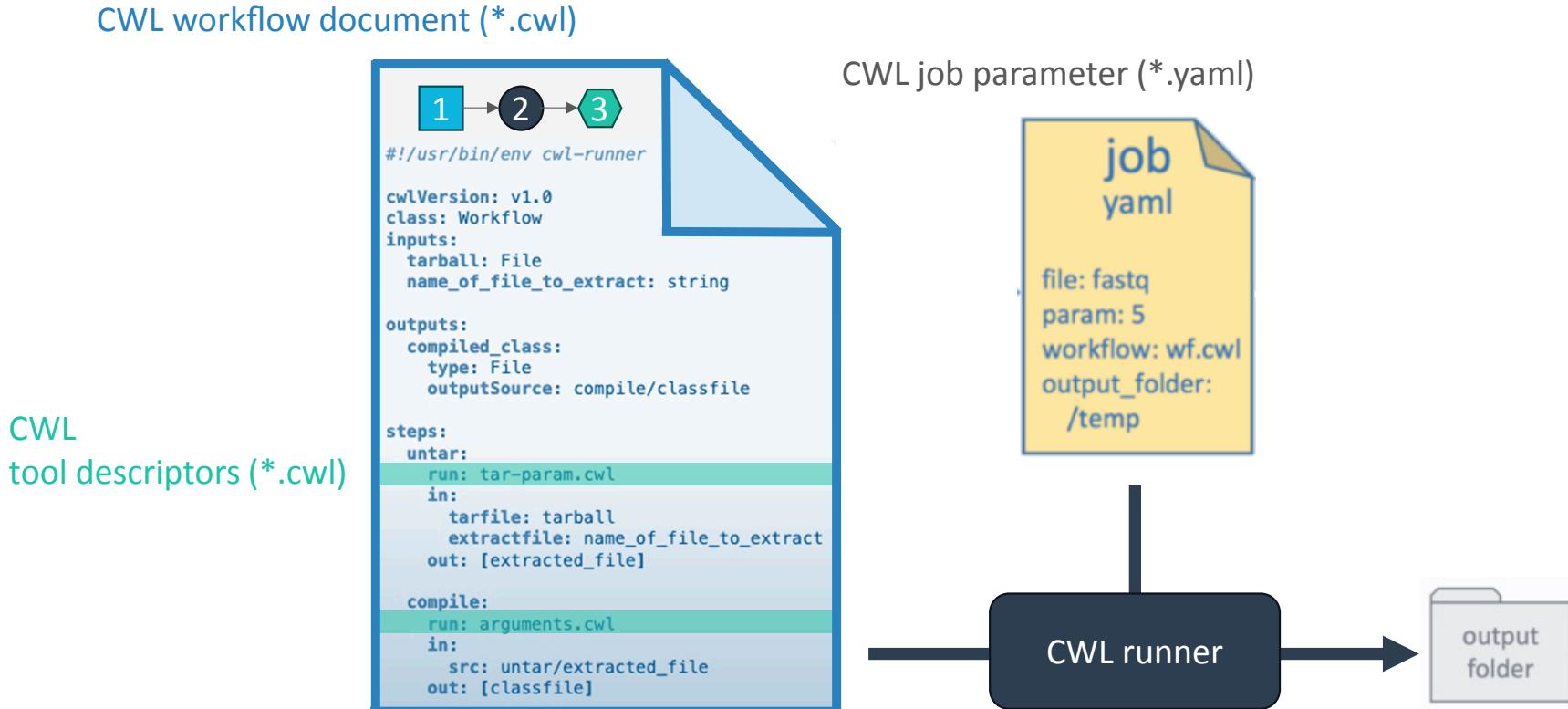
# Create a heatmap using Plotly
fig = px.imshow(data,
                 labels=dict(x="Columns", y="Rows", color="Value"),
                 x=data.columns,
                 y=data.index)

# Show the heatmap
fig.show()
```

heatmap.py

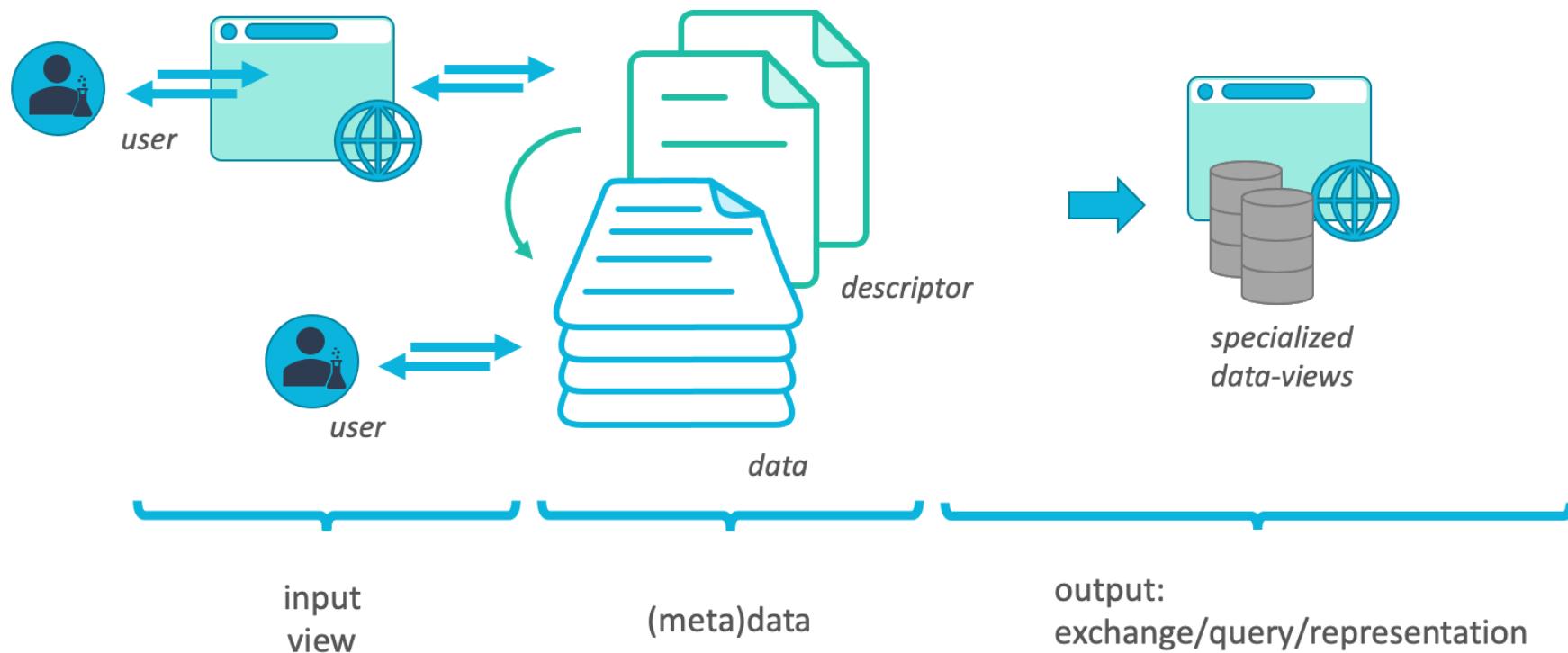


Metadata annotation – from data to result

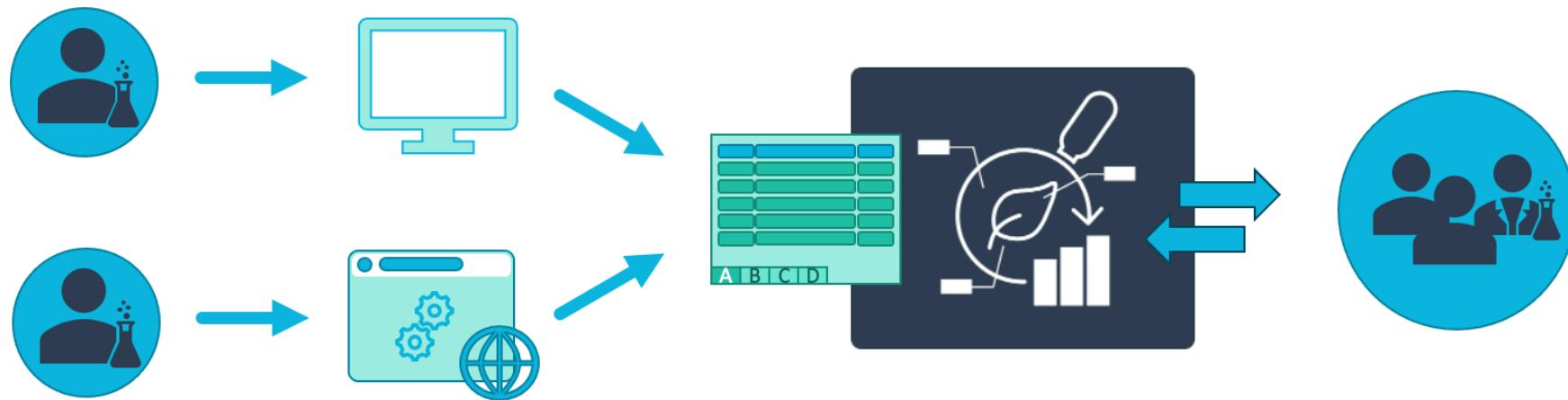


Everything is a file

The ARC is a data-centric approach to RDM

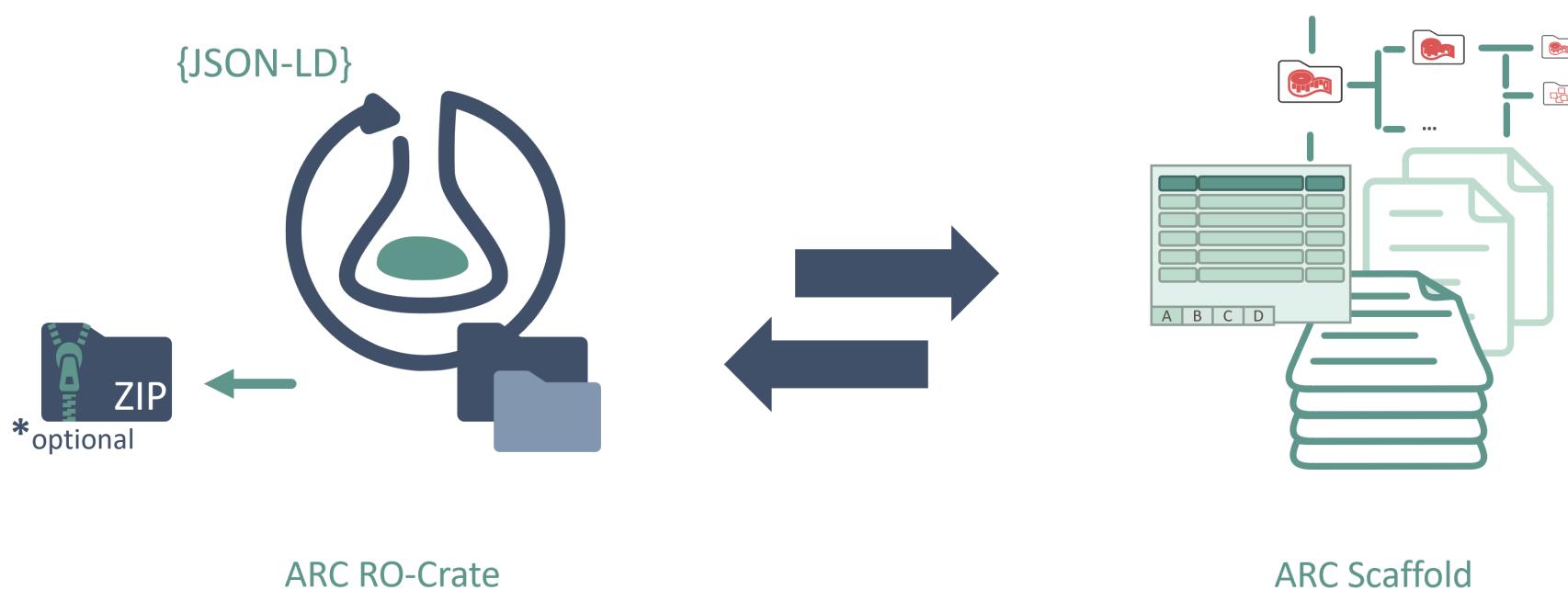


No technical lock-in



(Meta)data transparency with tool assistance but **no technical lock-in**

Two representations of the ARC



Two sides of the same coin

"Developer View": RO-Crate

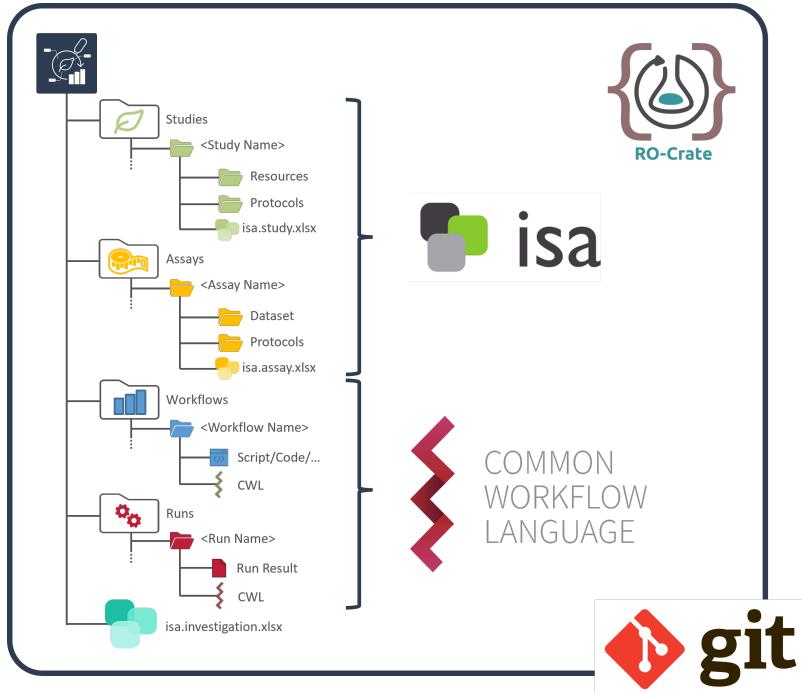
```
{  
  "Identifier": "Proteomics_MS",  
  "MeasurementType": {  
    "annotationValue": "Proteomics_MS",  
    "termSource": "MS",  
    "termAccession": "https://purl.obolibrary.org/obo/FMS_1003348"  
  },  
  "TechnologyType": ...  
  ...  
  "Tables": [  
    {  
      "name": "ProtDigest",  
      "header": [  
        {  
          "headertype": "Parameter",  
          "values": [  
            {  
              "annotationValue": "sample mass",  
              "termSource": "MS",  
              "termAccession": "https://purl.obolibrary.org/obo/FMS_1003348"  
            }  
          ]  
        }  
      ]  
    }  
  ]  
}
```

"User View": ARC Scaffold and metadata tables

The screenshot shows the ARCIct application interface. On the left, the ARCIct sidebar displays a file structure for a project named 'AthalianaColdStressSugar'. The 'assays' folder contains sub-folders like 'Proteomics_DataAnalysis' and 'SugarMeasurement', each with its own README.md file. On the right, a detailed view of the 'Assay Metadata' for the 'Proteomics_MS' assay is shown. This view includes fields for Identifier (Proteomics_MS), Measurement Type (Proteomics_MS), Technology Type (Mass Spectrometry), Technology Platform (timsTOF Pro 2), and Performers (PeptideMS_Bruker, ProtDigest). Below this, a table lists experimental parameters: Parameter [sample mass] (10 microgram), Parameter [Protein Precipitation] (acetone), Parameter [alkylating agent] (Chloroacetamide), and Parameter [red...]

| Parameter [sample mass] >> | Parameter [Protein Precipitation] >> | Parameter [alkylating agent] >> | Parameter [red...] |
|----------------------------|--------------------------------------|---------------------------------|--------------------|
| 10 microgram | acetone | Chloroacetamide | TCEP |

ARC builds on standards



RO-Crate

- Standardized exchange

• <https://www.researchobject.org/ro-crate/>

ISA

- Structured, machine-readable metadata

• <https://isa-tools.org/>

CWL

- Reproducible, re-usable data analysis

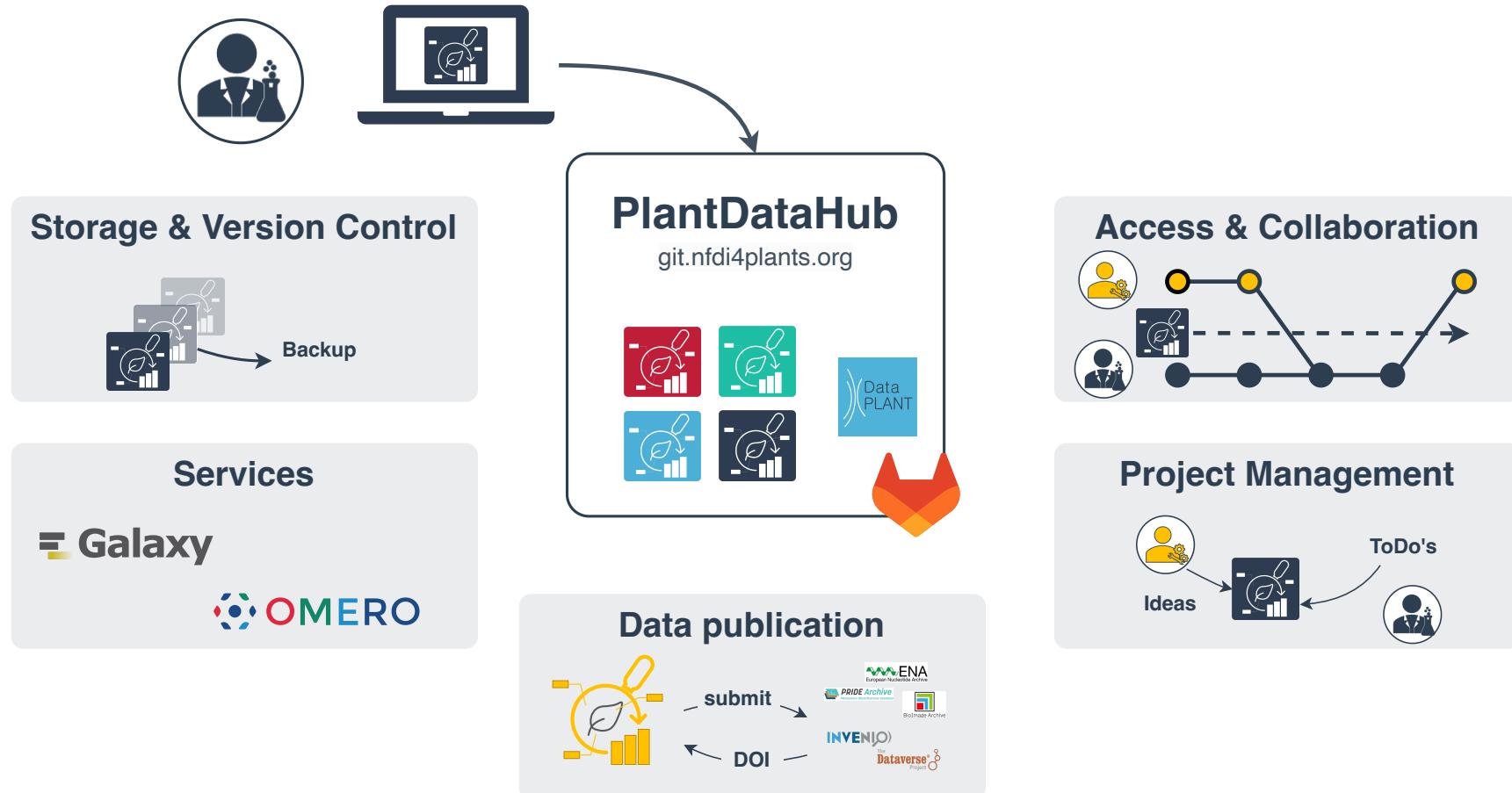
• <https://www.commonwl.org/>

Git

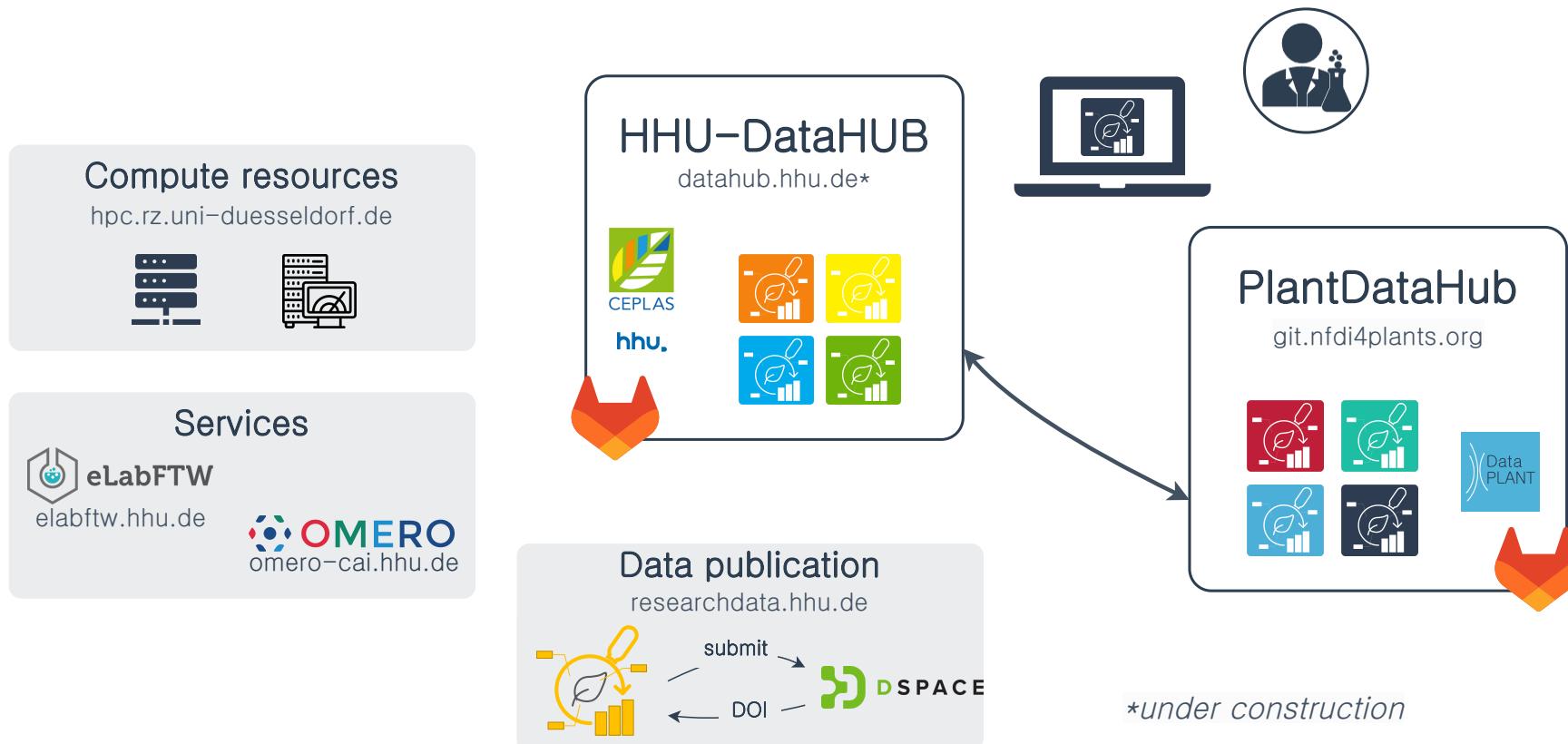
- Version control

• <https://git-scm.com>

ARC and DataHUB as entry point

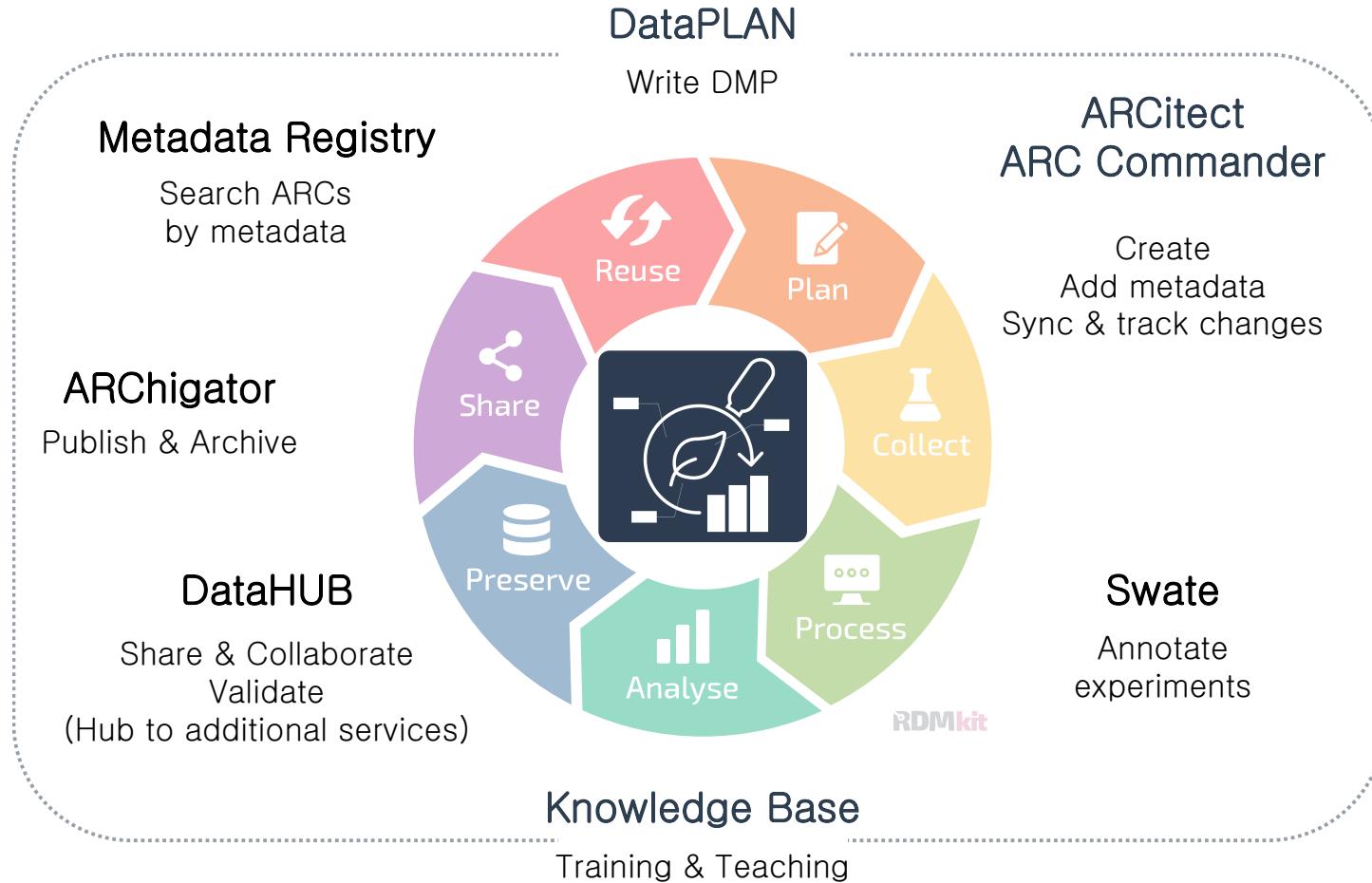


HHU-DataHUB – On-premise DataHUB node



i Under Development

The ARC ecosystem



Acknowledgements



Team Kaiserslautern

- Timo Mühlhaus
- Lukas Weil
- Kevin Frey
- Kevin Schneider
- Jonas Lukasczyk

Team Freiburg

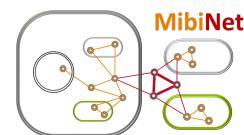
- Dirk von Suchodeletz
- Jonathan Bauer
- Marcel Tschöpe
- Julian Weidhase

Team Jülich

- Stella Eggels
- Angela Kranz



- Björn Usadel
- Vittorio Tracanna
- Yaser Alashloo



- Sabrina Zander

Goals for today

- Get an idea of the ARC concept
- Create and upload a simple ARC
- Explore
- ...

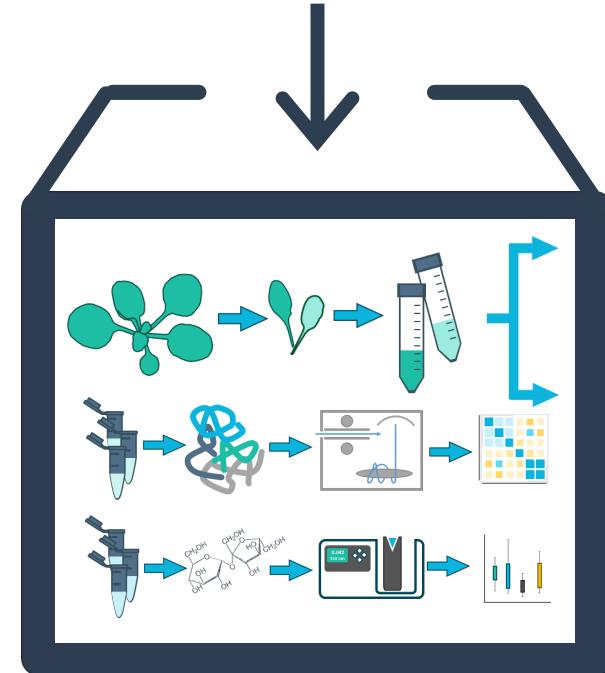
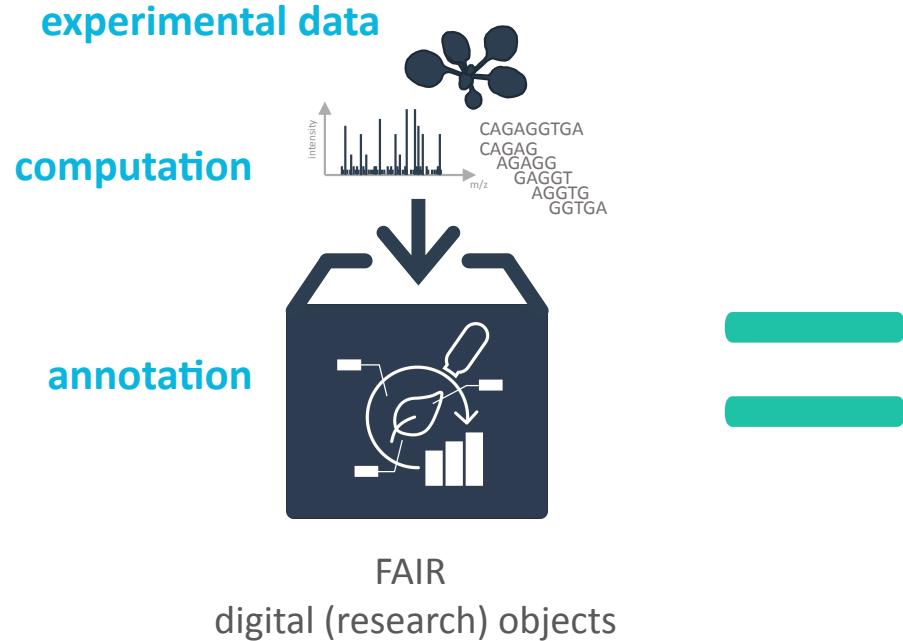
Start an ARC for your investigation with one study



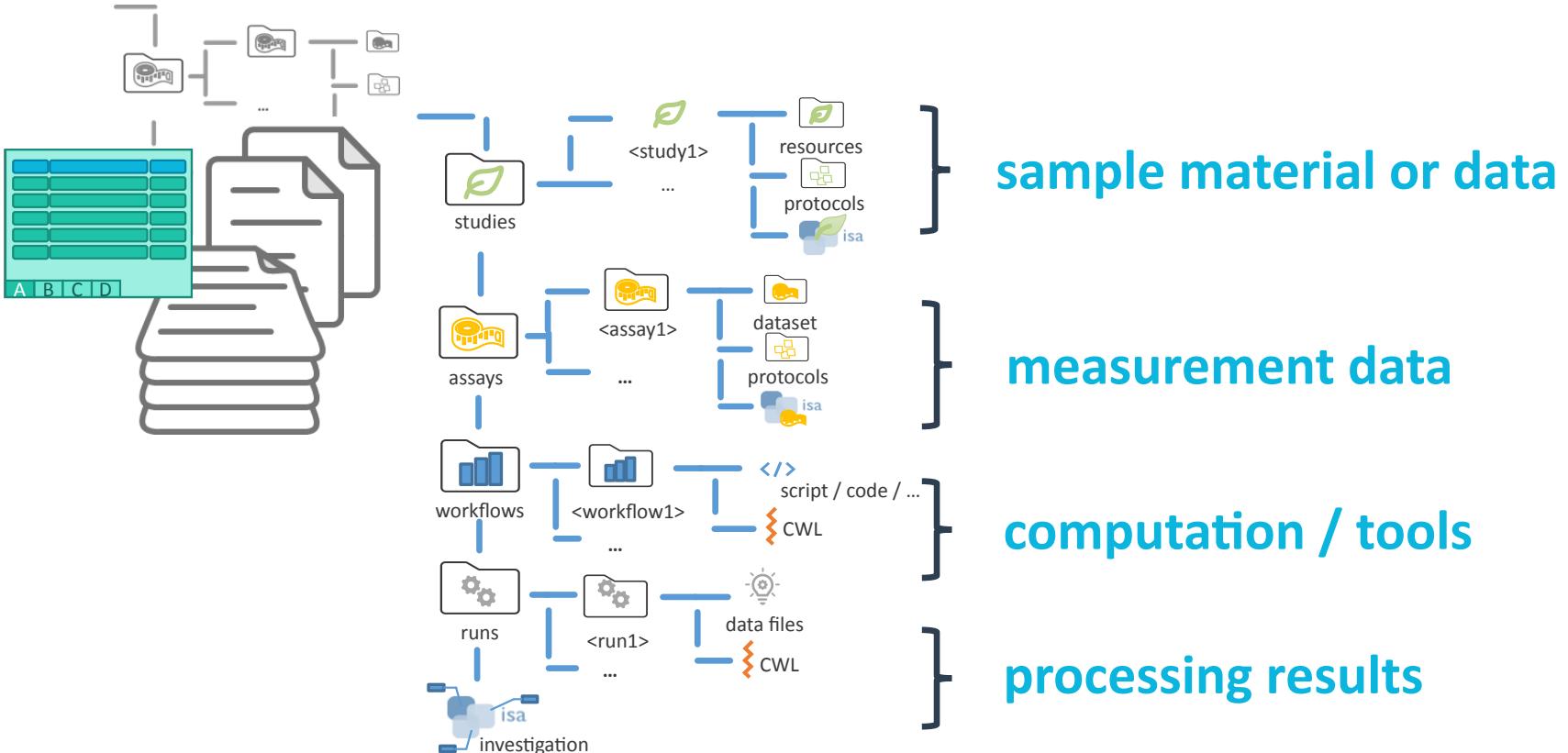
Hands-on

Follow the [Start Here guide](#) until Check point 1

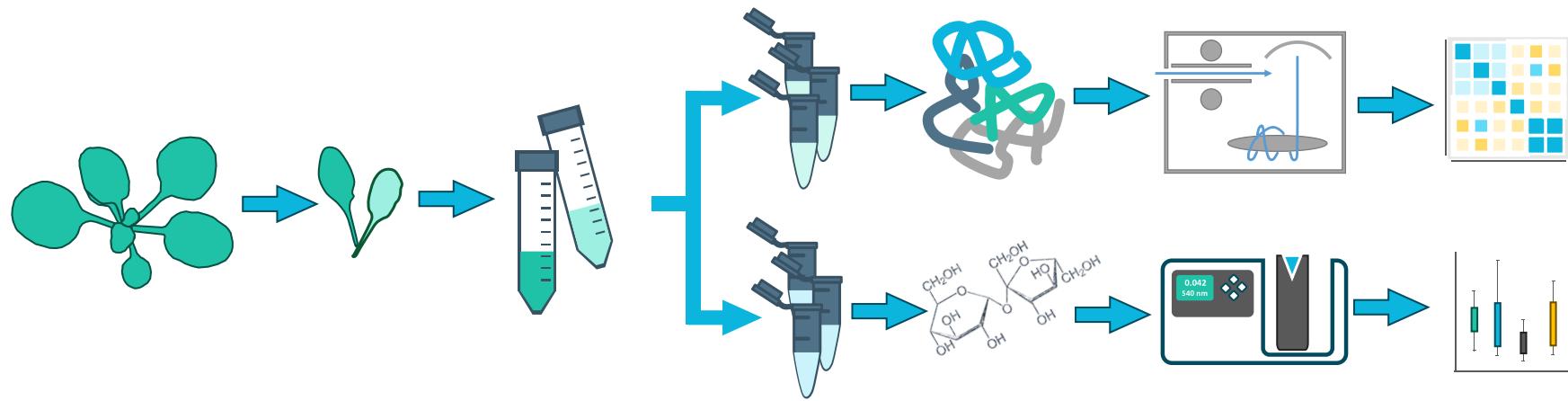
ARC: Annotated research context



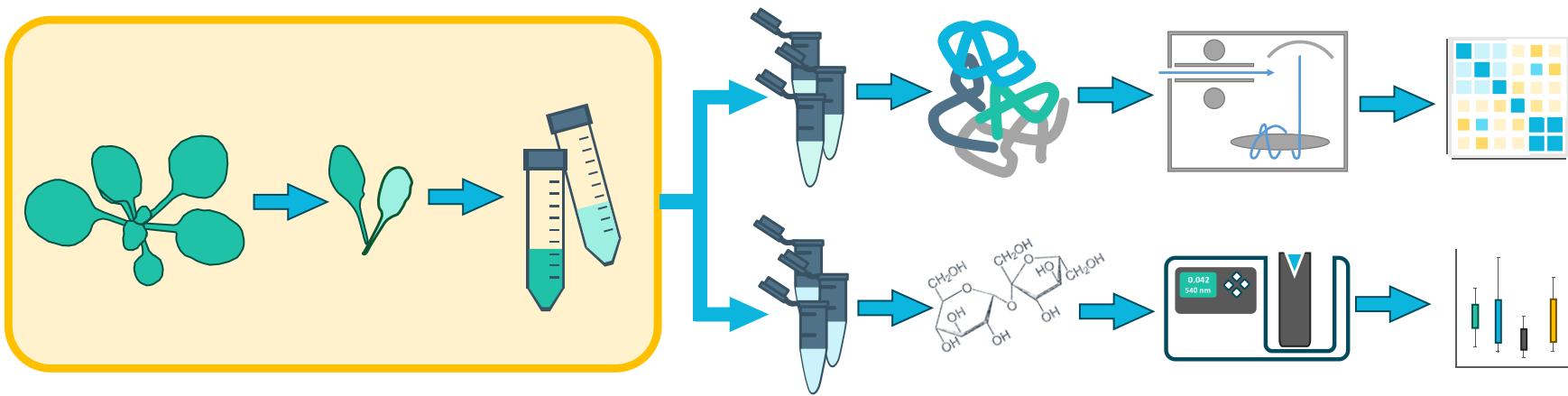
The ARC scaffold structure



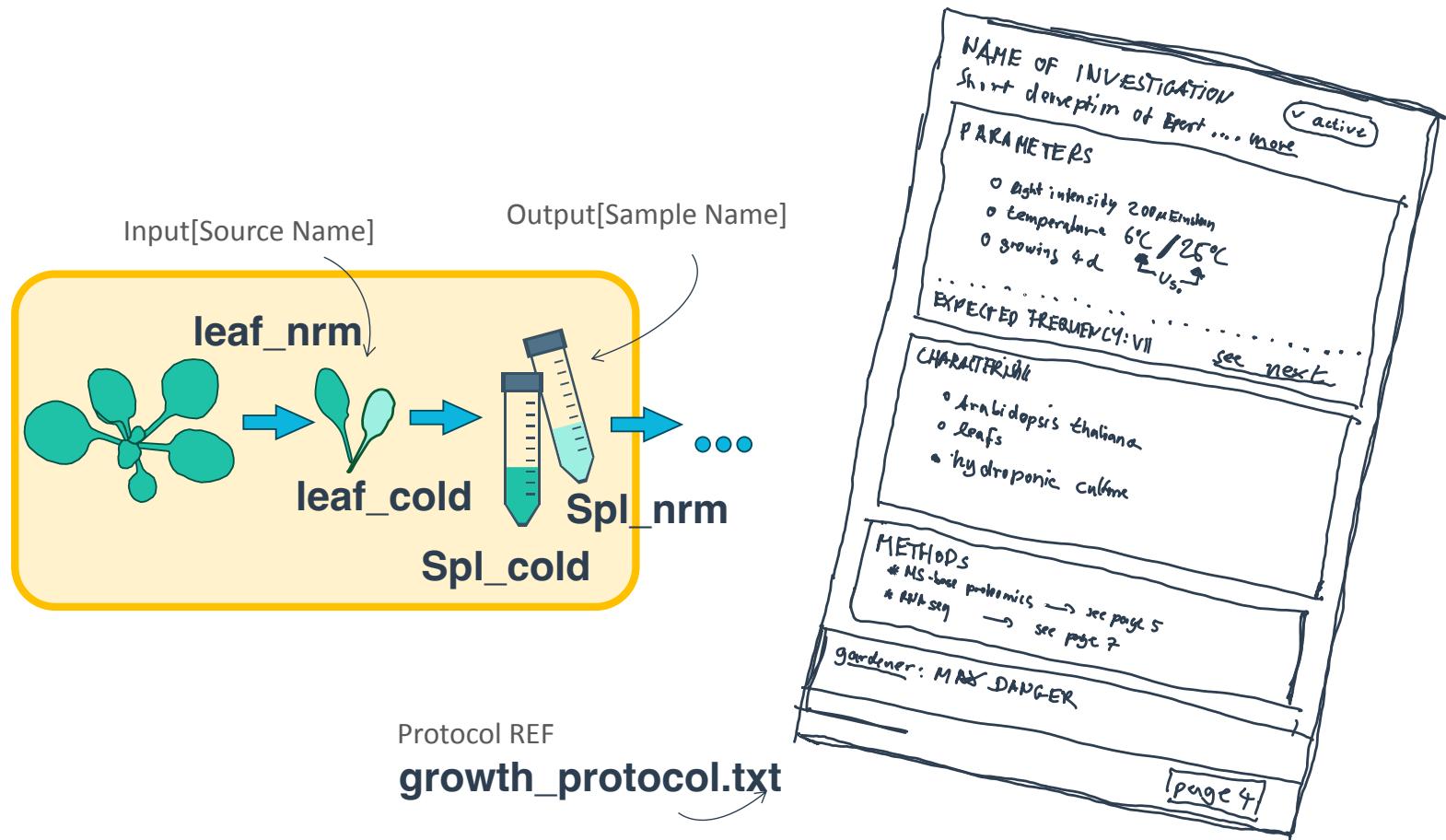
A small prototypic project



Divide and conquer for reproducibility



Identifying the ‘study’ part



A table-based organization schema

| Input[Source Name] | | Output[Sample Name] |
|--------------------|---|---------------------|
| leaf_nrm | | spl_nrm |
| leaf_cold | | spl_cold |
| | | |
| | | |
| | | |
| | | |
| A | B | C |
| D | | |

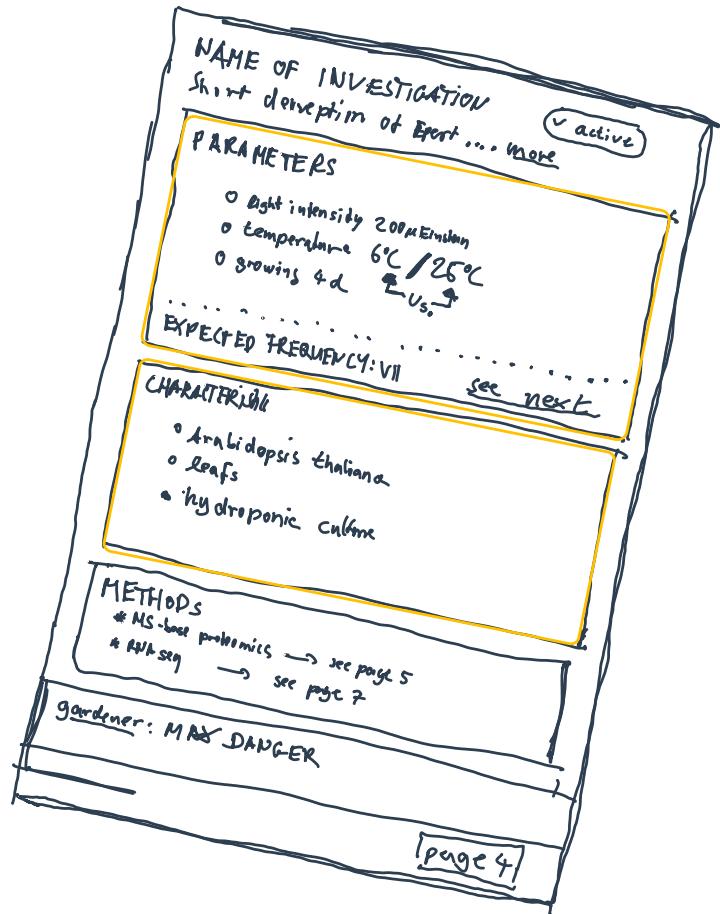
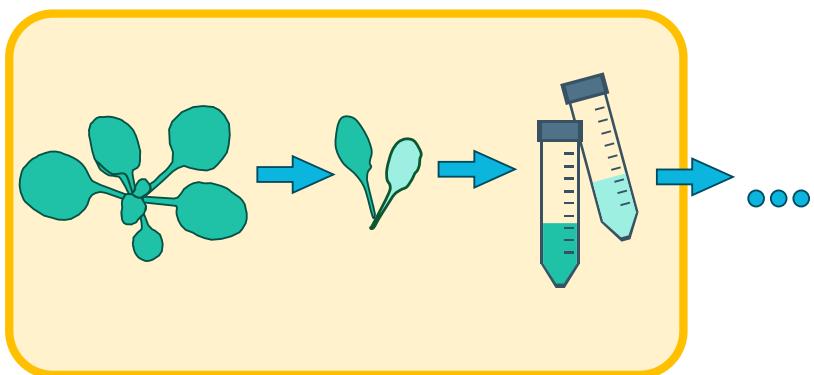
Referencing a protocol

This allows you to reference the free-text, human-readable protocol.

- 💡 It is recommended that the protocol is in an open format (.md|.txt|.docx|…)
- 💡 But everything is possible also an URI to an electronic lab notebook

| Input[Source Name] | Protocol REF | Output[Sample Name] |
|--------------------|---------------------|---------------------|
| leaf_nrm | growth_protocol.txt | spl_nrm |
| leaf_cold | growth_protocol.txt | spl_cold |
| | | |
| | | |
| | | |
| A | B | C |
| D | | |

Parameterizing the ‘study’



Finding the right metadata vocabulary

Parameters []

- Light intensity 200 µEinstein
- Temperature 6°C / 25°C
- Growing 4d

Characteristics []

- *Arabidopsis thaliana*
- Leaf
- Hydroponic culture
- Columbia

OLS: Finding the right metadata vocabulary

Temperature Dependence

Temperature:Dependence_Annotation



http://purl.uniprot.org/core/Temperature_Dependence_Annotation

Indicates the optimum temperature for enzyme activity and/or the variation of enzyme activity with temperature variation; the thermostability/thermolability of the enzyme is also mentioned when it is known.

Ontology: UNIPROT RDFS

temperature

AFO:/result#AFR_0001584



http://purl.allotrope.org/ontologies/result#AFR_0001584

A temperature (datum) is a quantity facet that quantifies some temperature. [Allotrope]

Ontology: AFO

temperature

FBcv:0000466



http://purl.obolibrary.org/obo/FBcv_0000466

Mutation caused by exposure to a temperature that is higher or lower than 25 degrees Celsius.

Ontology: FBCV

temperature

PATO:0000146



http://purl.obolibrary.org/obo/PATO_0000146

A physical quality of the thermal energy of a system.

Ontology: PATO

Also appears in:

NGBO

HTN

CAO

ZP

AGRO

OMIABIS

OBIB

MONDO

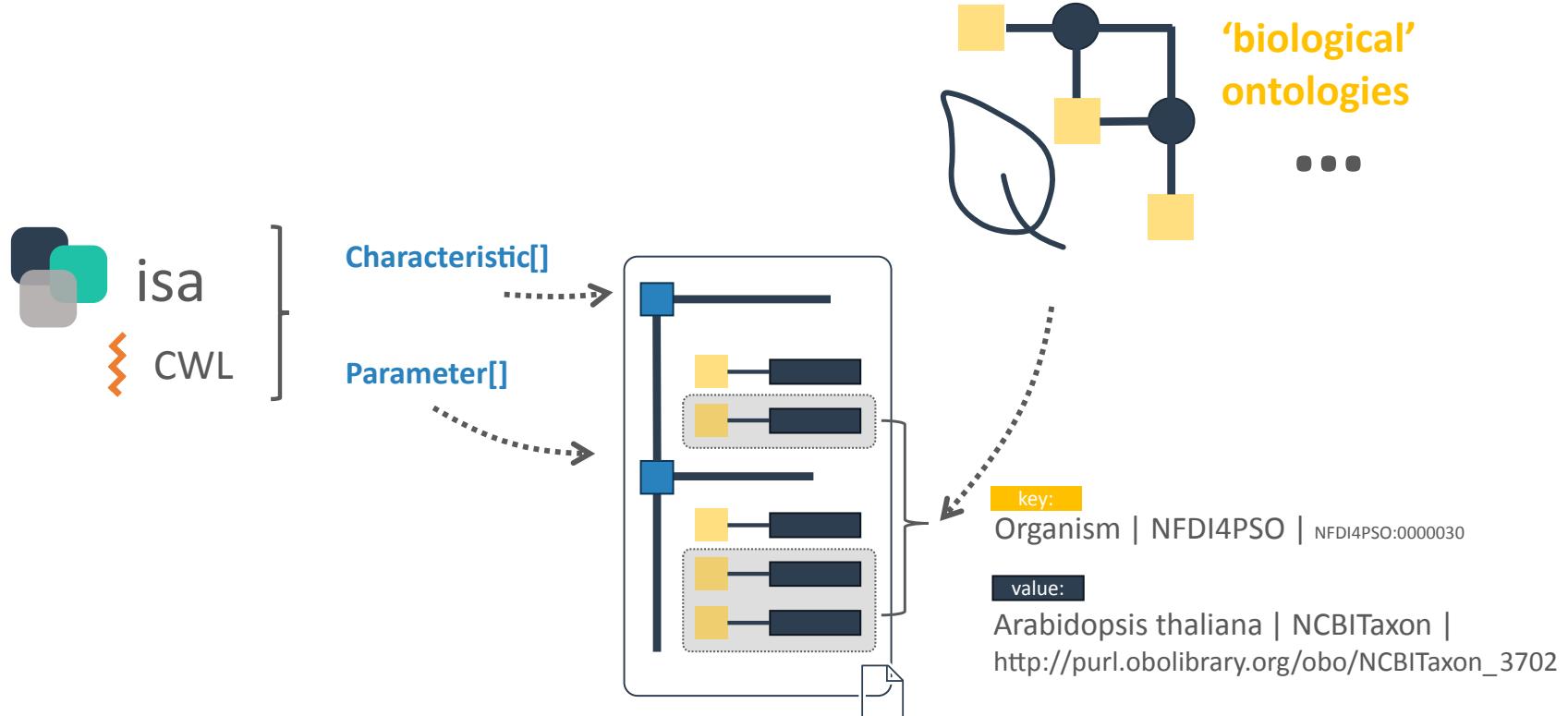
TXPO

MCO

+

Ontology Lookup Service (OLS): <https://www.ebi.ac.uk/ols4/>

Finding the metadata vocabulary and descriptors



Finding the metadata vocabulary and descriptors

Parameters []

-   Light intensity 200 µEinstein
-   Temperature 6°C / 25°C
-   Growing 4d

Characteristics []

-   Arabidopsis thaliana
-   Leaf
-   Hydroponic culture
-   Columbia

Finding the metadata vocabulary and descriptors

Parameters []

-  Light intensity
 -  200 µEinstein
-  Temperature
 -  6°C / 25°C
-  Growth time
 -  4d

Characteristics []

-  Organism
 -  Arabidopsis thaliana
-  Tissue
 -  Leaf
-  Growth medium
 -  Hydroponic culture
-  Ecotype
 -  Columbia

Check point 1

Task

- ✓ I've created an ARC for my project!
- ✓ I've added metadata about the overall investigation
- ✓ I've added a study for my samples

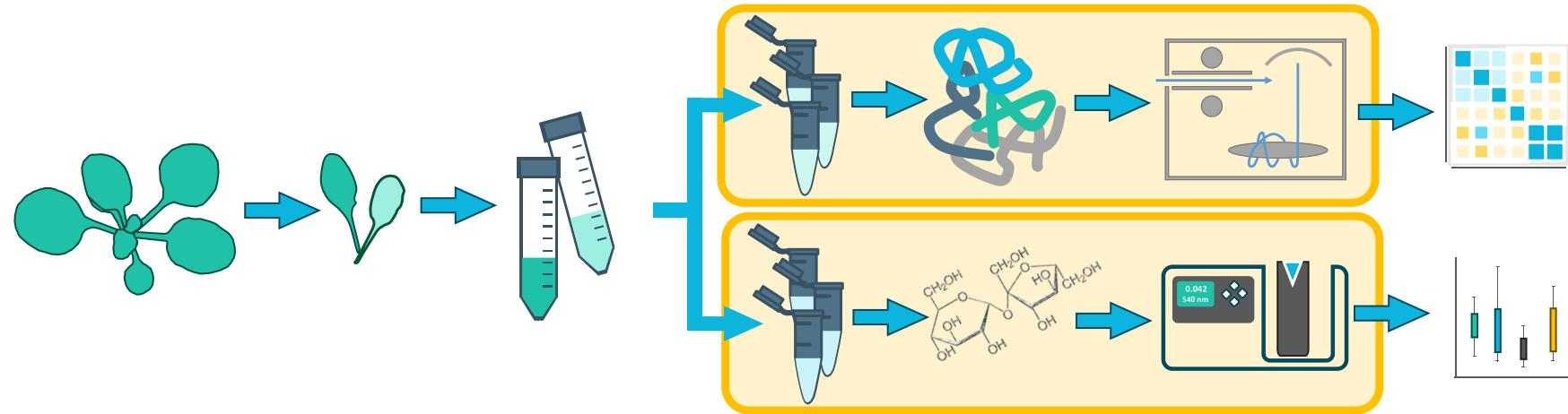
Add an assay and share your ARC



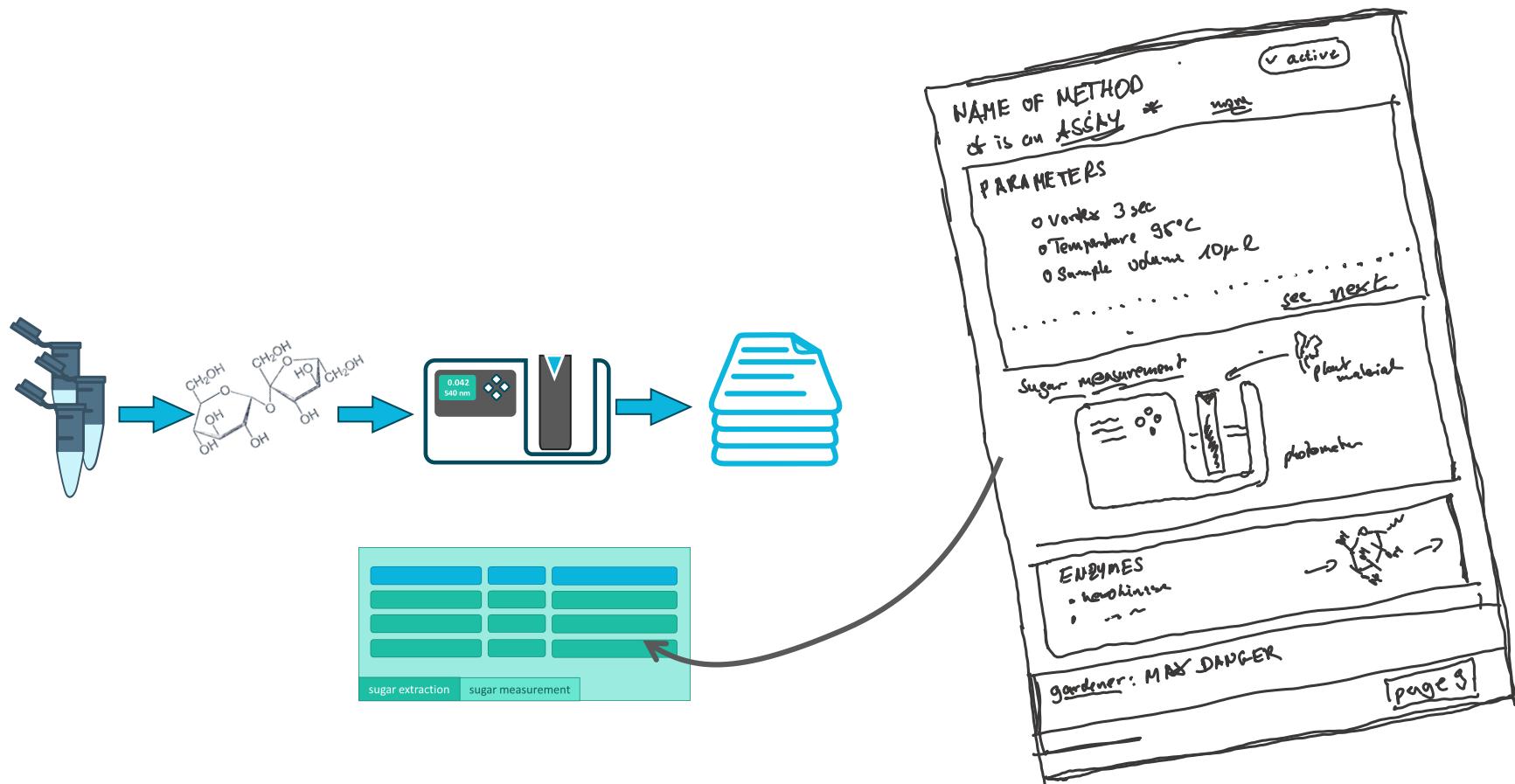
Hands-on

Follow the [Start Here guide](#) until Check point 2

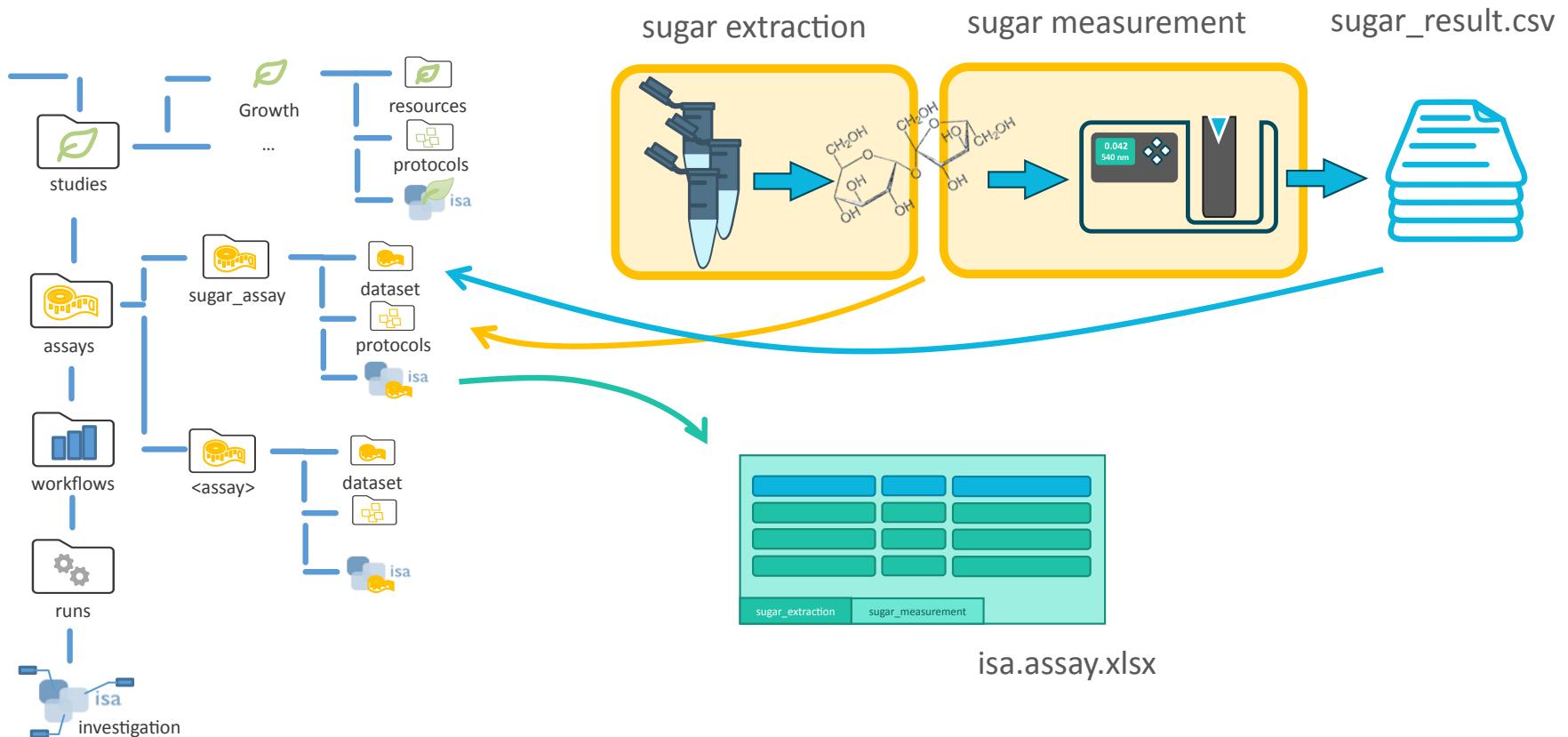
Identifying assays



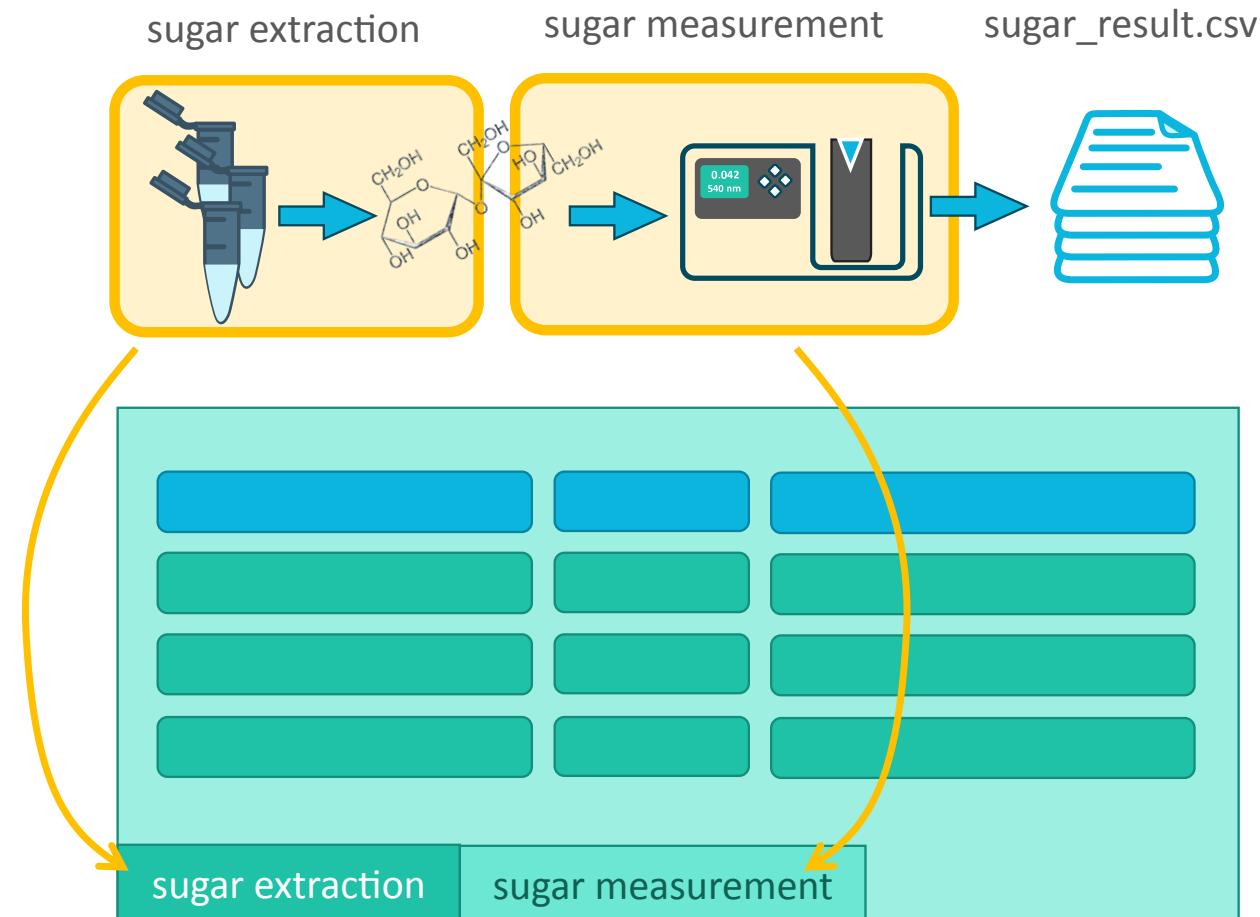
Assay for sugar measurement



Separating different assay elements



Isolating the lab processes in an assay



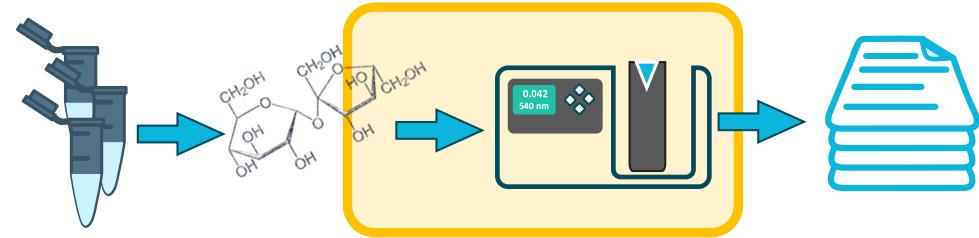
Parameteterization: sugar extraction

- Vortex Mixer
 - 3 seconds
- Temperature
 - 95 degree celsius



Parameteterization: sugar measurement

- ■ technical replicate
 - ■ 1,2,3,...
- ■ sample volume
 - ■ 10 microliter
- ■ buffer volume
 - ■ 190 microliter
- ■ cycle count
 - ■ 5



DataHUB terminology and data sharing

Choosing the proper role

When inviting new members to an ARC or group, you can choose between different levels.

Permissions & Roles

Roles are assigned when adding a user to an ARC or to a group. This is a very simplified summary.

Guest – Can only see the ARC's wiki

Reporter – Can read, but not add or edit data

Developer – Reporter permissions + can read, add, and edit data

Maintainer – Developer permissions + can add new members

Owner – Maintainer + can delete ARC, manage memberships and permissions

💡 By default you are **Owner** of an ARC you create or upload to the DataHUB.

Projects and Groups are not the same

- "Project" = ARC
- "Groups" = Group of users

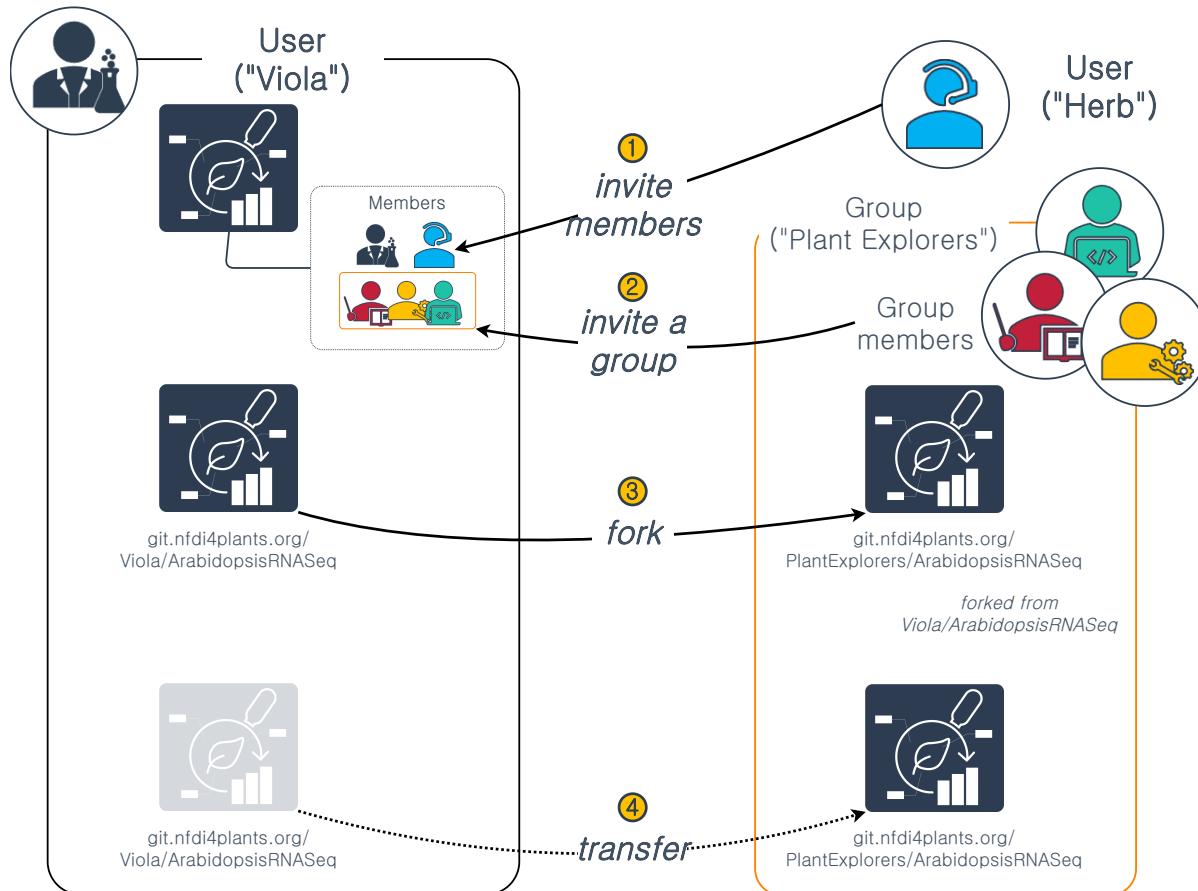
Project = ARC

- In the DataHUB, ARCs are called "projects"; they are the same.
- An ARC can be shared with individual users (invited as "members") or a group.

DataHUB Groups = Group of members (e.g. lab)

- A "Group" is a group of users with specific [permissions](#)
- A group can share ARCs
- A group can be invited to an ARC
- Groups can have subgroups

Options to share an ARC via the DataHUB



Namespaces

- Every user has a personal namespace, where they can upload or create new ARCs
- Every group and subgroup has its own namespace

| Type | URL | Namespace | Name |
|----------------------------|---|------------------------|------------------------|
| A personal ARC | https://git.nfdi4plants.org/brilator/Facultative-CAM-in-Talinum | brilator | Dominik Brilhaus |
| An group-shared ARC | https://git.nfdi4plants.org/hhu-plant-biochemistry/Samuilov-2018-BOU-PSP | hhu-plant-biochemistry | HHU Plant Biochemistry |

Visibility

The visibility of ARCs and groups can be managed individually for each ARC or group

Visibility

The visibility of each ARC can be managed in the settings of the ARC

Private – ARC access must be granted explicitly to each user or group.

Internal – ARC can be accessed by any logged in user.

Public – ARC can be accessed without authentication.

💡 By default every ARC and every group is set to **private**.

ARC DataHUB members // ARC Investigation contacts

The screenshot shows the 'Project members' section of the DataHUB interface. It includes a search bar, navigation icons, and a table of members. The table columns are Account, Source, Max role, Expiration, and Activity. The members listed are:

| Account | Source | Max role | Expiration | Activity |
|---|---|------------|-----------------|---|
| Adriano Nunes-Nesi @nunesnesi | HHU Plant Biochemistry by Sebastian Triesch | Maintainer | Expiration date | User created: Jul 05, 2023 Access granted: Jul 10, 2023 Last activity: Aug 09, 2023 |
| Andreas Weber @andreas.weber | HHU Plant Biochemistry by Sebastian Triesch | Maintainer | Expiration date | User created: Mar 10, 2023 Access granted: Jul 31, 2023 Last activity: Sep 11, 2023 |
| Dominik Brilhaus It's you @brilator | Direct member by Dominik Brilhaus | Owner | Expiration date | User created: Feb 21, 2022 Access granted: Dec 06, 2023 Last activity: Mar 26, 2024 |
| Franziska Fichtner @franziska.fichtner | HHU Plant Biochemistry by Sebastian Triesch | Maintainer | Expiration date | User created: Aug 11, 2023 Access granted: Aug 11, 2023 Last activity: Aug 11, 2023 |

DataHUB: ARC members

https://git.nfdi4plants.org/hhu-plant-biochemistry/Samuilov-2018-BOU-PSP/-/project_members

The screenshot shows the ARCIct interface for the 'Samuilov-2018-BOU-PSP' project. It includes a sidebar with options like Login, New ARC, Open ARC, etc., and a main panel with sections for Identifier, Description, and Contacts.

Identifier: Samuilov-2018-BOU-PSP

Description: (empty)

Contacts:

| Contact | Score |
|----------------------------------|-------|
| Sladjana Samuilov <orcid> | 4/10 |
| Nadine Rademacher <orcid> | 3/10 |
| Samantha Flachbart <orcid> | 3/10 |
| Leila Arab <orcid> | 3/10 |
| Saleh Alfarraj <orcid> | 3/10 |
| Franziska Kuhnert <orcid> | 3/10 |
| Stanislav Kopriwa <orcid> | 3/10 |
| Andreas P. M. Weber <orcid> | 4/10 |
| Tabea Mettler-Altmann <orcid> | 3/10 |

ARCIct: Investigation Contacts

Investigation contacts are not automatically invited as members to the ARC.

Version control

Check out the **commit history** of your ARC via Repository (2) or directly via commits (7)

The screenshot shows the Data PLANT CEPLAS interface with the following numbered callouts:

- Manage
- Plan
- Code
- Build
- Secure
- Deploy
- Operate
- Monitor
- Analyze
- Settings
- Help

Key UI elements include:

- D Demo_ARC**: Project name in the header.
- Code**: Selected tab in the top navigation bar.
- History**: Tab in the top navigation bar.
- Find file**: Tab in the top navigation bar.
- Edit**: Tab in the top navigation bar.
- Project information**: Pipeline status (passed), Star count (0), Fork count (0), and a three-dot menu.
- 1 Commit**: Summary of project activity.
- 2 Branches**: Summary of branches.
- 0 Tags**: Summary of tags.
- 7 KIB Project Storage**: Summary of storage usage.
- Auto DevOps enabled**: Project status.
- Add README**, **Add LICENSE**, **Add CHANGELOG**, **Add CONTRIBUTING**, **Add Kubernetes cluster**, **Add Wiki**, **Configure Integrations**: Action buttons.
- Created on**: Date of project creation (July 13, 2024).

The main content area displays a table of files and their last commit details:

| Name | Last commit | Last update |
|------------------------|-------------|---------------|
| assays | arc init | 4 minutes ago |
| runs | arc init | 4 minutes ago |
| studies | arc init | 4 minutes ago |
| workflows | arc init | 4 minutes ago |
| .gitignore | arc init | 4 minutes ago |
| isa.investigation.xlsx | arc init | 4 minutes ago |

Check point 2

Task

- ✓ I've added measurement data as an assay
- ✓ I've uploaded my ARC to the DataHUB to have a version-controlled save copy
- ✓ I've shared the ARC with colleagues, so they can explore my findings and contribute

Resources



Info & materials

- DataPLANT Website: <https://nfdi4plants.org/>
- ARC website: <https://arc-rdm.org>
- Knowledge Base:
<https://nfdi4plants.org/nfdi4plants.knowledgebase/>

Tools and Services

- ARCitect: <https://github.com/nfdi4plants/arcitect>
- DataHUB: <https://git.nfdi4plants.org>

Continuous support

- HelpDesk: <https://helpdesk.nfdi4plants.org>
- Matrix for ad hoc support: <https://matrix.to/#/%23arc-user-support:matrix.org>
- User Support Meeting (2nd Friday of the month | 1 – 2pm):
<https://nfdi4plants.github.io/events/arc-user-support/>
- User Support Mailing List: [Click here to subscribe](#)

Open Source Development

- GitHub: <https://github.com/nfdi4plants>

Acknowledgements



Team Kaiserslautern

- Timo Mühlhaus
- Lukas Weil
- Kevin Frey
- Kevin Schneider
- Jonas Lukasczyk

Team Freiburg

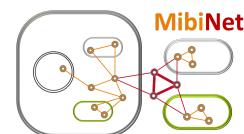
- Dirk von Suchodeletz
- Jonathan Bauer
- Marcel Tschöpe
- Julian Weidhase

Team Jülich

- Stella Eggels
- Angela Kranz



- Björn Usadel
- Vittorio Tracanna
- Yaser Alashloo



- Sabrina Zander

Use SOPs and annotate your data analysis



Hands-on

Follow the [Start Here guide](#) until Check point 3

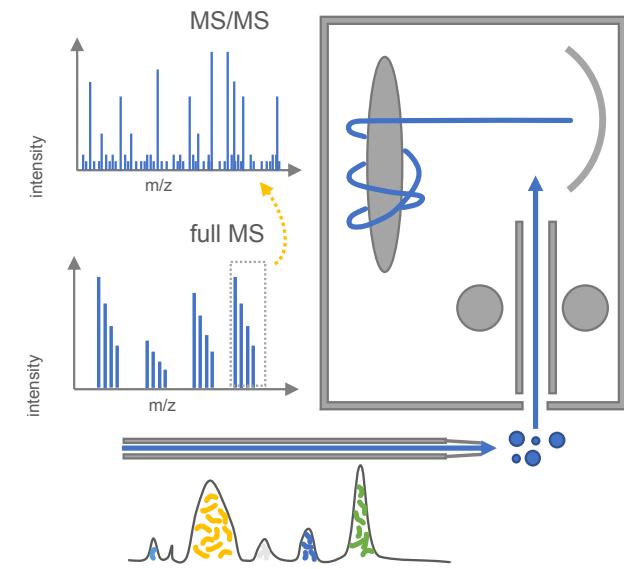
Save time using standard methods and SOPs

Parameter []

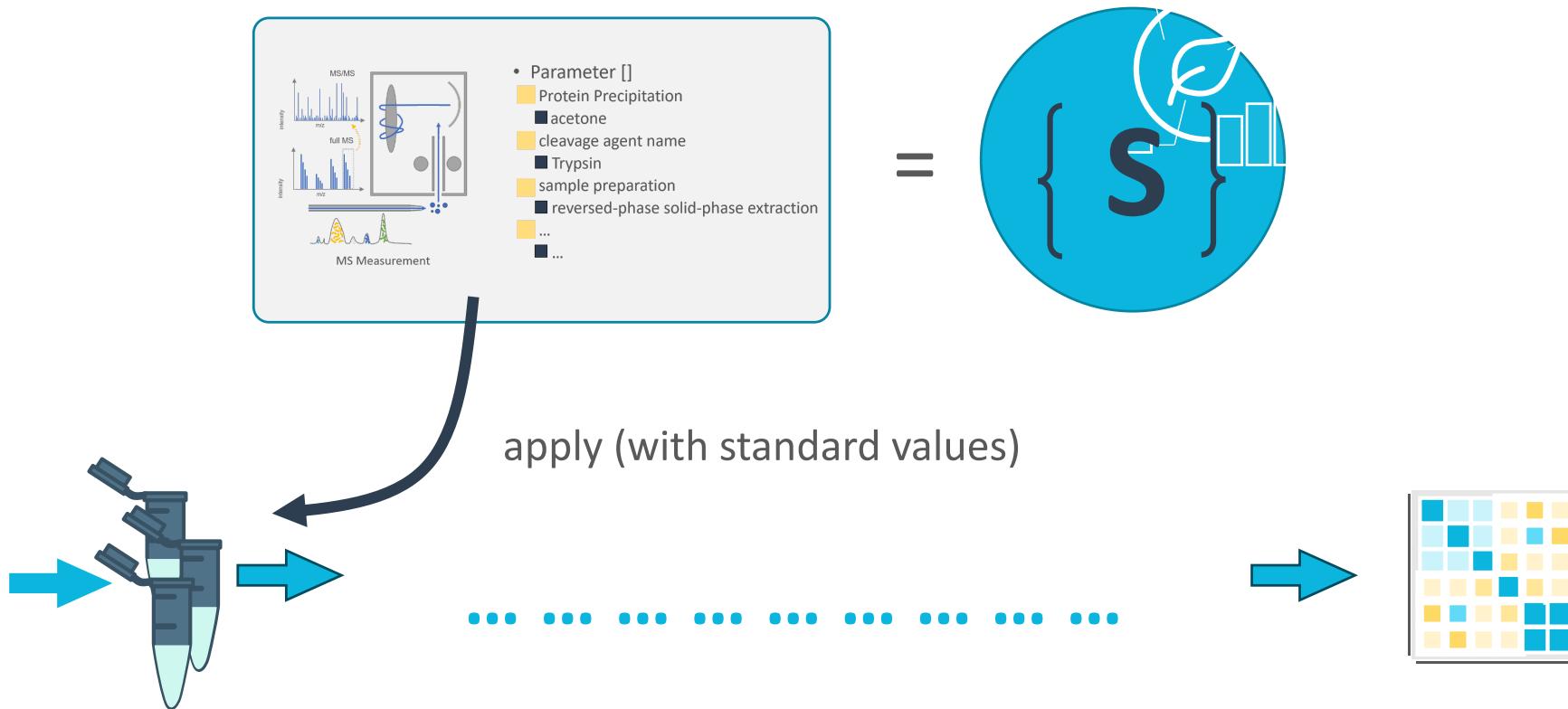
- Protein Precipitation
 - acetone
- cleavage agent name
 - Trypsin
- sample preparation
 - reversed-phase solid-phase extraction
- ...

Component []

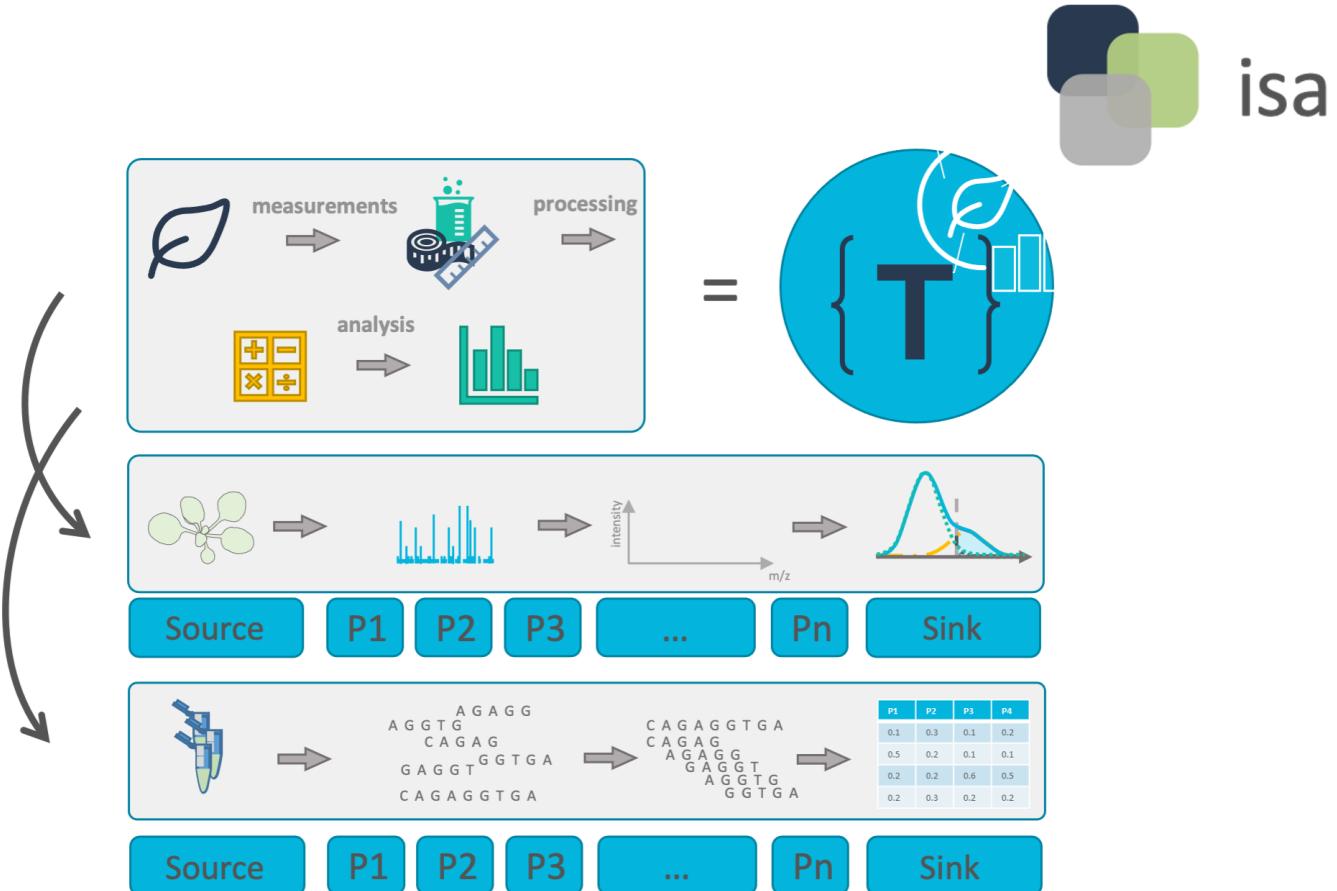
- chromatography instrument model
 - nanoElute2
- chromatography column model
 - PepSep C18 1.9u, 25cm x 75um ...



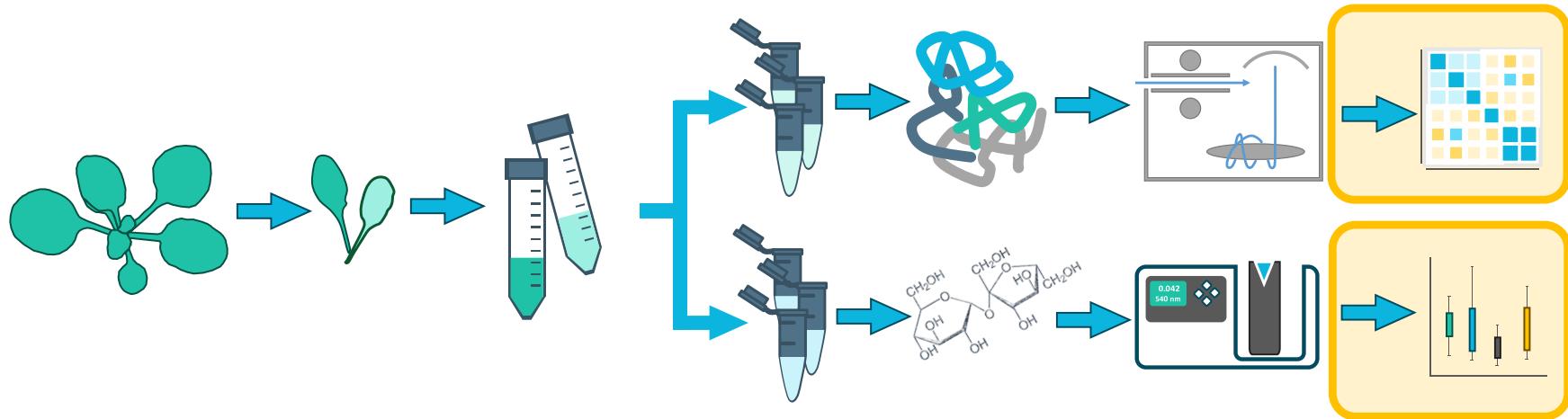
Applying standard procedures to sample record



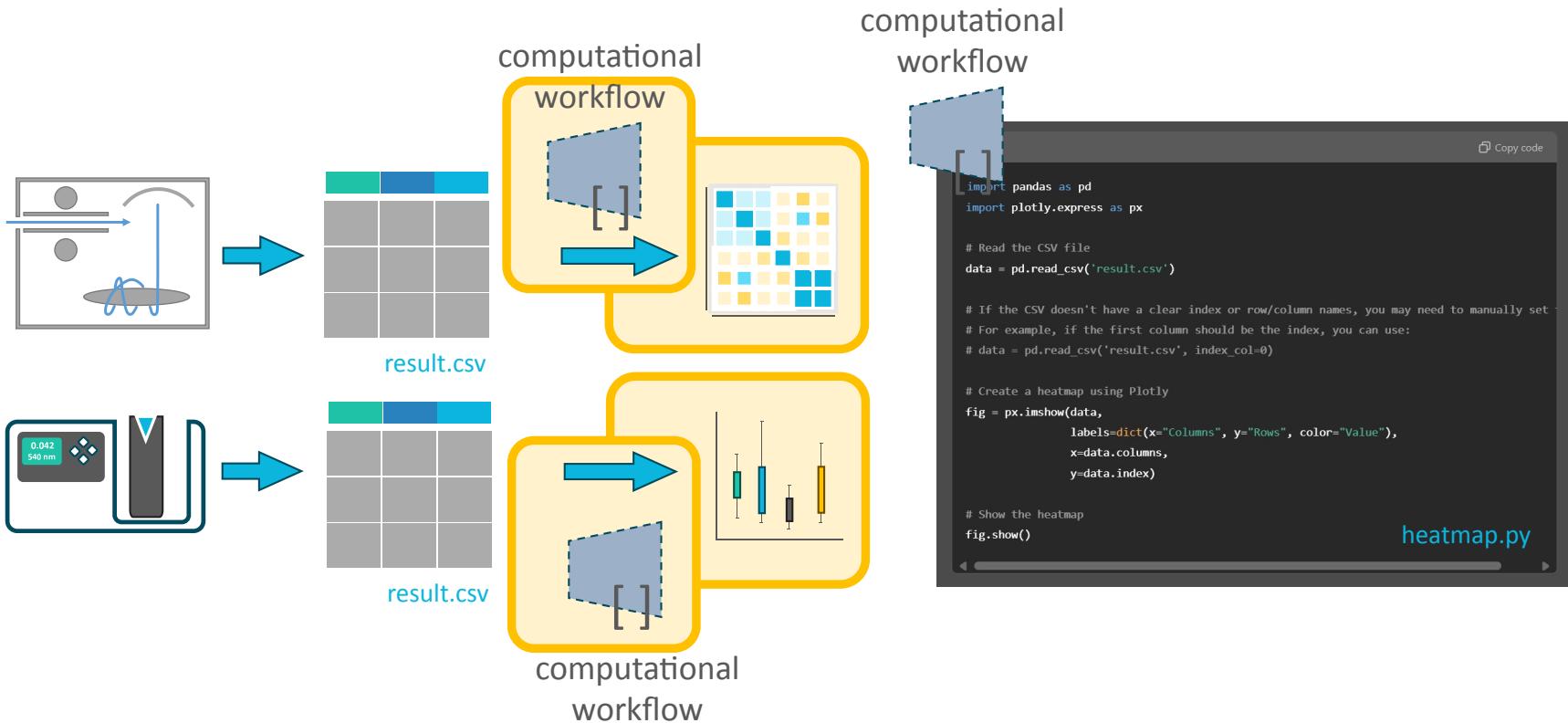
Realization of lab-specific metadata with templates



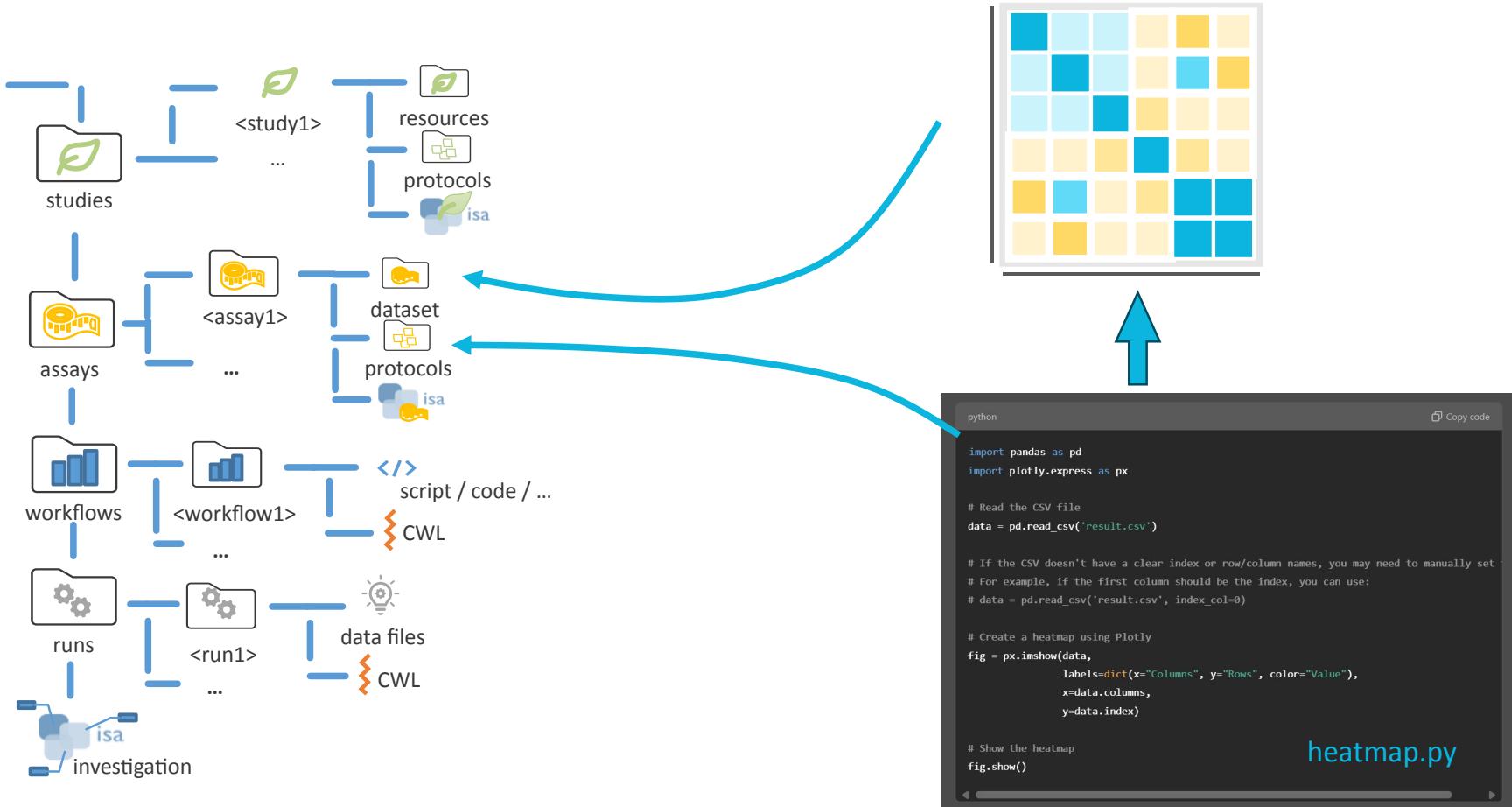
Options to annotate the data analysis



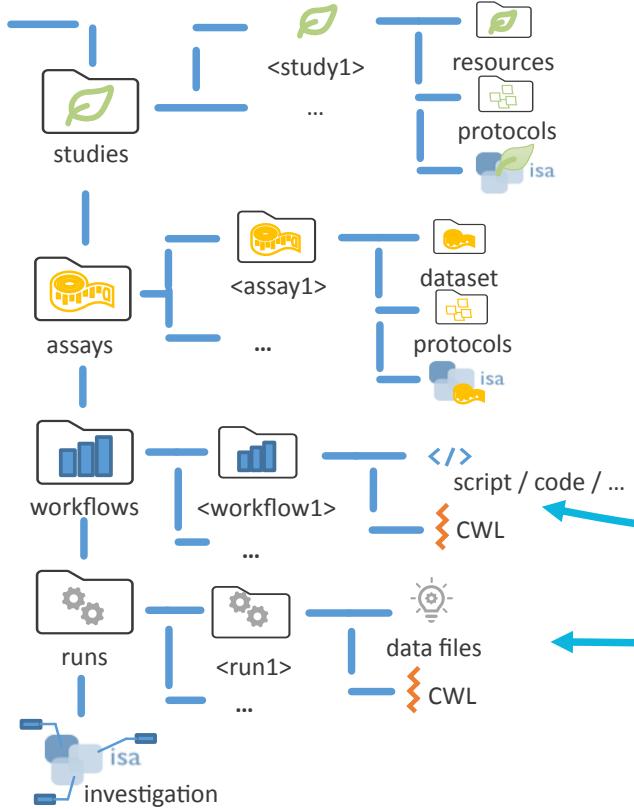
A computational workflow is like a protocol



Option I: Create a virtual assay



Option II: Create a workflow and run



A screenshot of a code editor window titled "heatmap.py" containing the following Python code:

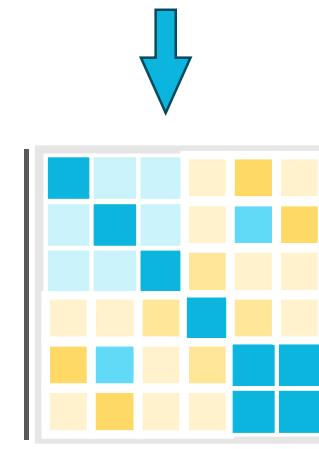
```
python
import pandas as pd
import plotly.express as px

# Read the CSV file
data = pd.read_csv('result.csv')

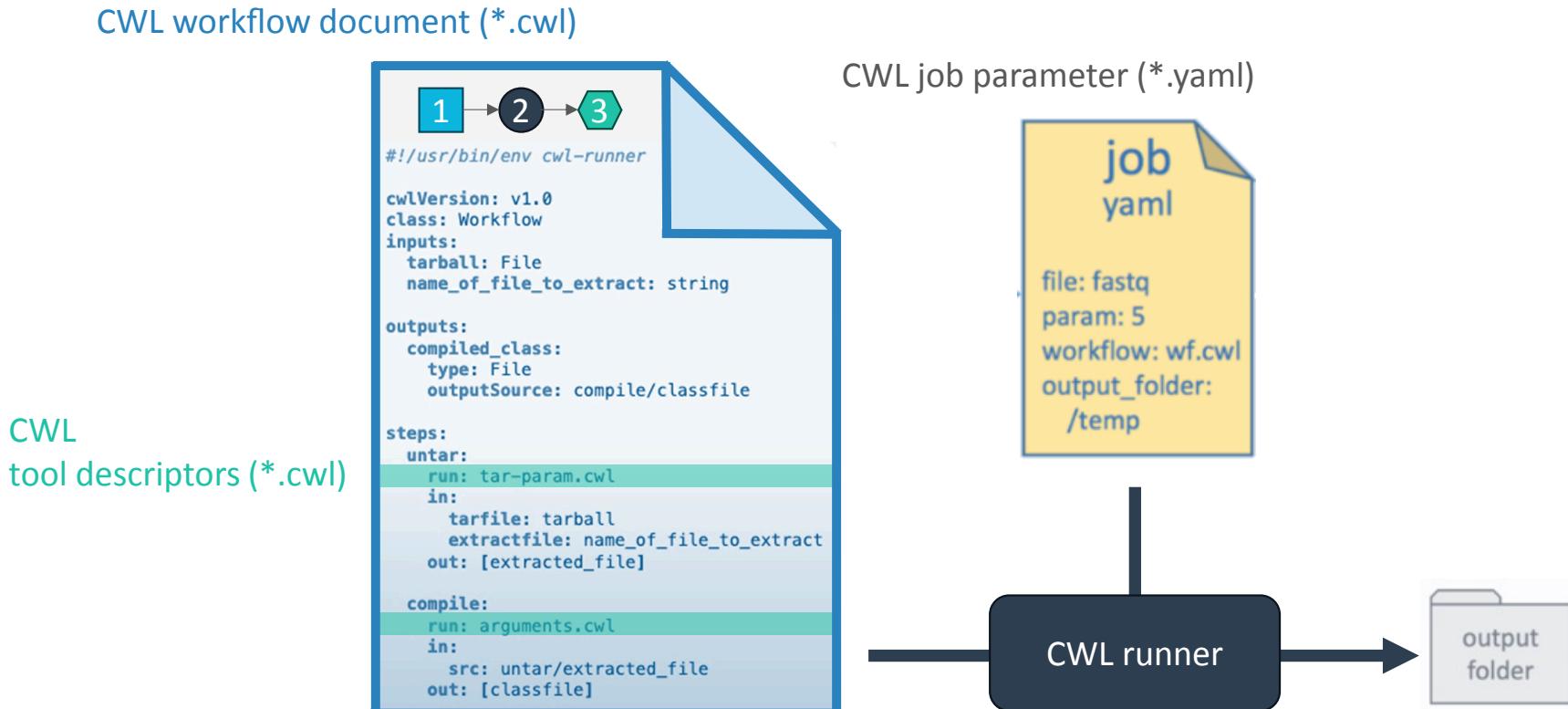
# If the CSV doesn't have a clear index or row/column names, you may need to manually set
# For example, if the first column should be the index, you can use:
# data = pd.read_csv('result.csv', index_col=0)

# Create a heatmap using Plotly
fig = px.imshow(data,
                 labels=dict(x="Columns", y="Rows", color="Value"),
                 x=data.columns,
                 y=data.index)

# Show the heatmap
fig.show()
```



Use CWL to wrap your workflow

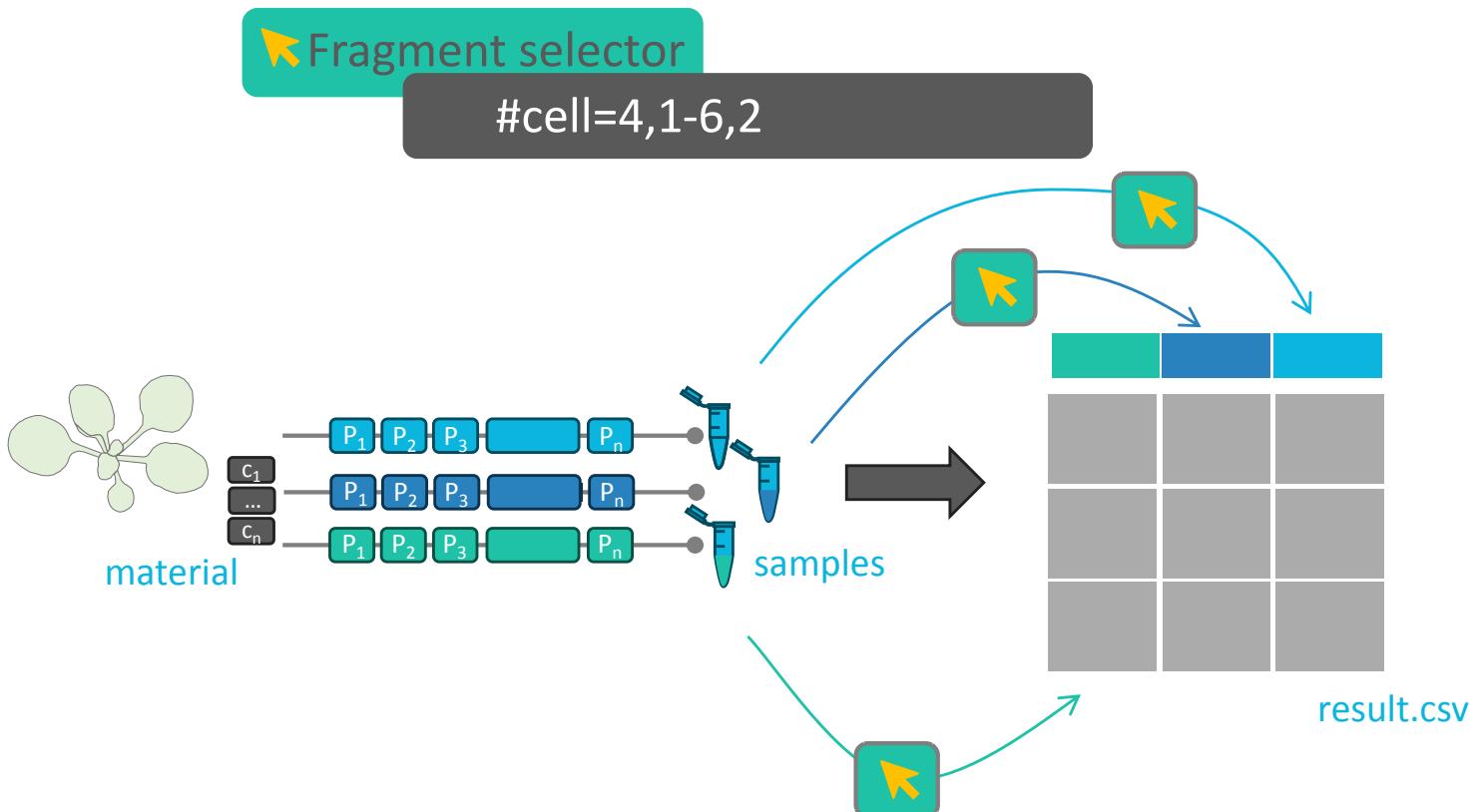


DataMAPs

Mechanisms to annotate the result data

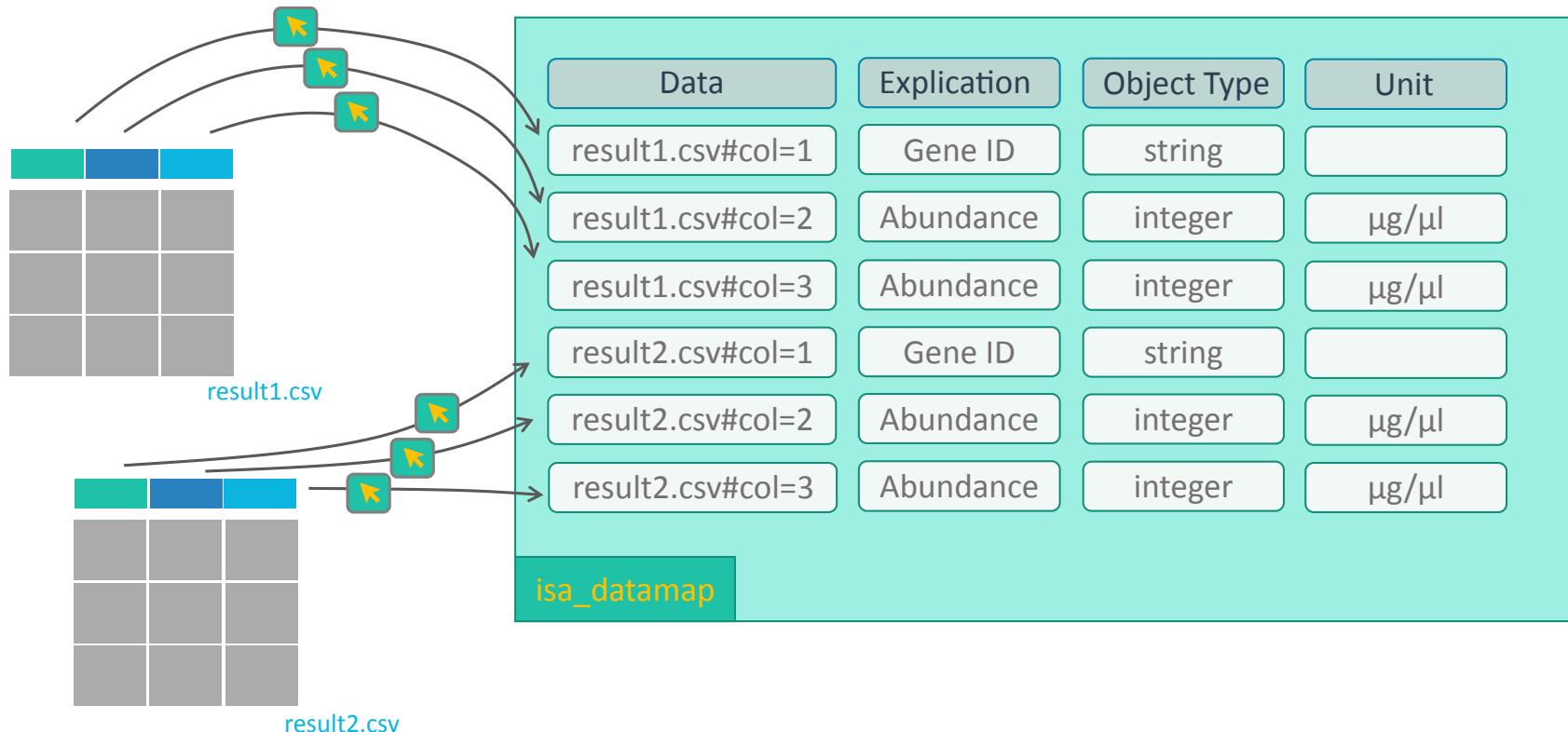
Point into results – Fragment selectors

Connecting samples to data points



DataMAP: Annotation for the fragment selectors

Annotating contents of result files



Check point 3

☒ Task

- ✓ I've added experimental details from SOPs
- ✓ In addition to the raw data, my ARC now contains the annotated data analysis
- ✓ Using a datemap I can point to the content of my result files

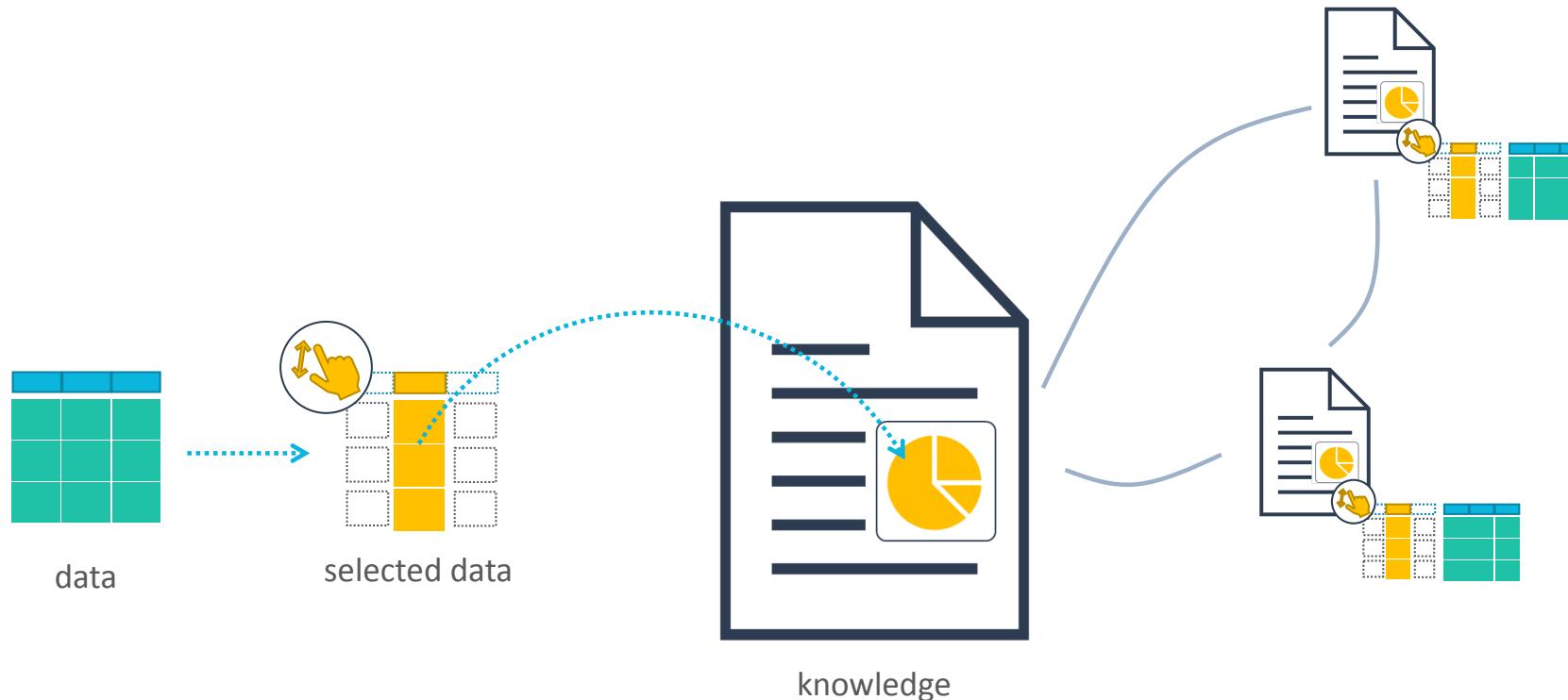
Validate and publish your ARC



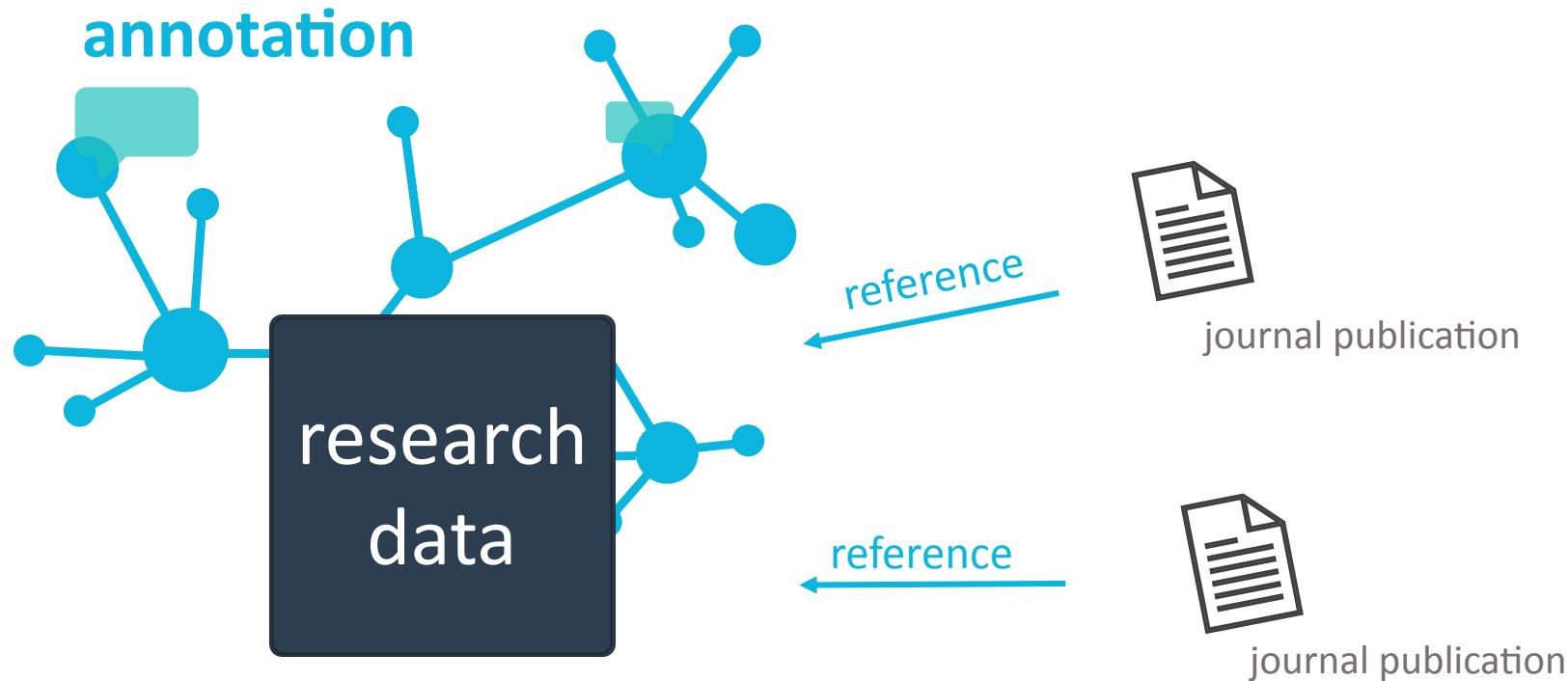
Hands-on

Follow the [Start Here](#) guide until Check point 4

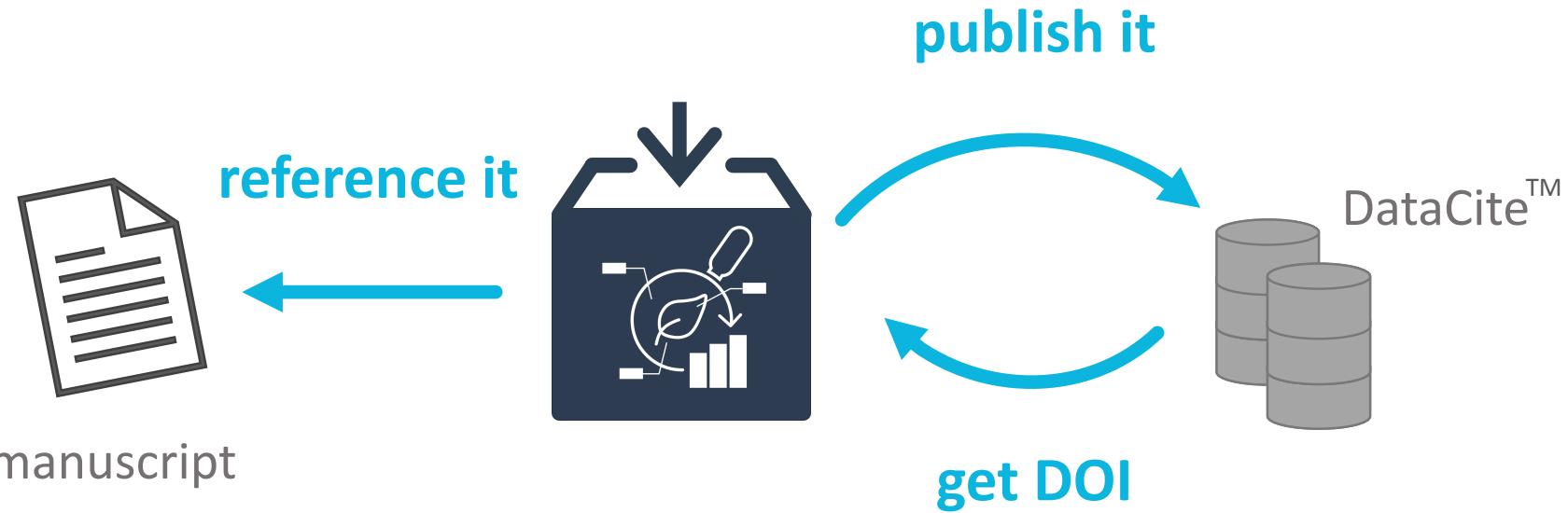
ARC data publication



Moving from paper to data publications



Publish your ARC, get a DOI



Publish your ARC with a few clicks



Ru_ChlamyHeatstress

Project ID: 122

24 h
48 h

Star 1

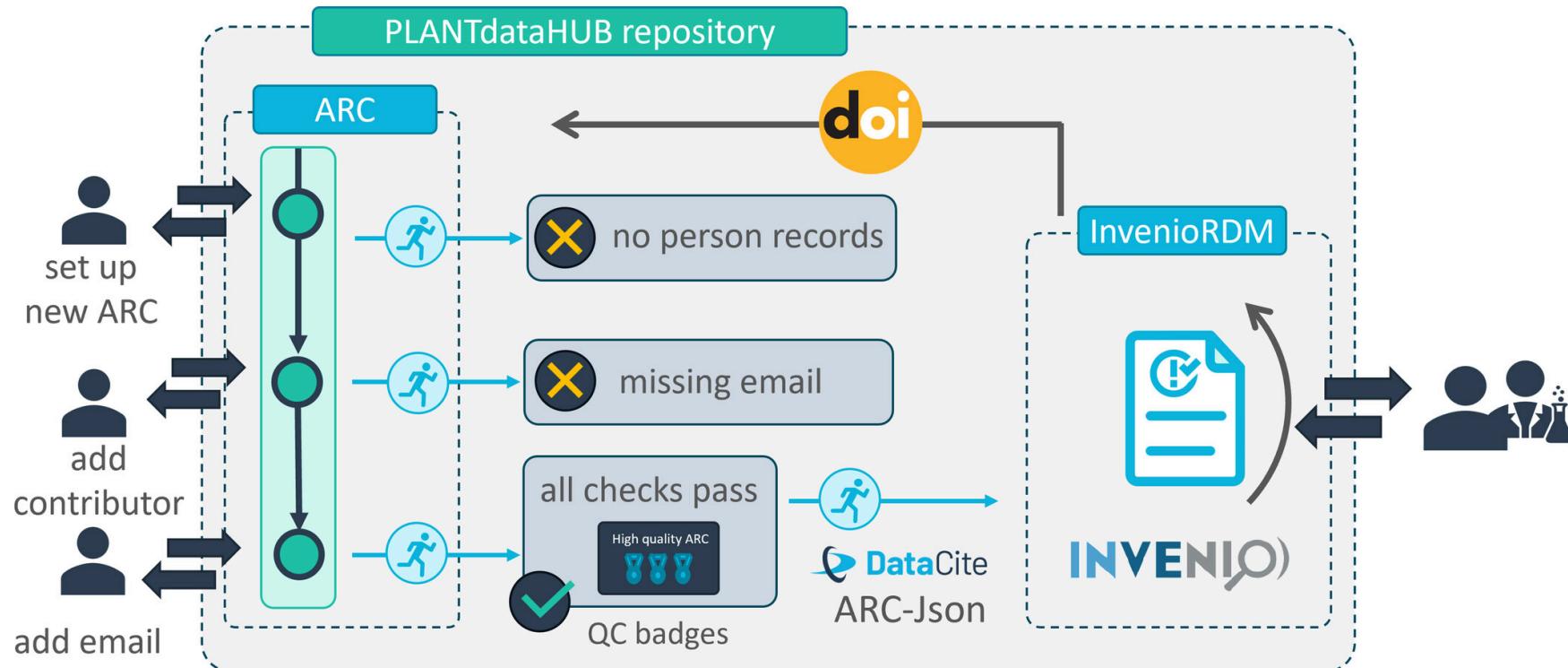
-o 53 Commits 1 Branch 0 Tags 293.9 GB Project Storage

Topics: Chlamydomonas, abiotic stress, proteomics + 1 more

Algae cultures were grown mixotrophically (TAP). After 24h of 35°C/40°C the cells were shifted back to room temperature for 48h. 'omics samples were taken.

1 pipeline passed 2 Publish ARC 3 arc quality 301/301

Validate & publish



Weil, H.L., Schneider, K., et al. (2023), PLANTdataHUB: a collaborative platform for continuous FAIR data sharing in plant research.
Plant J. <https://doi.org/10.1111/tpj.16474>

Validation towards publication

 **Ru_ChlamyHeatstress** 

[main](#) [Ru_ChlamyHeatstress](#) [History](#) [Find file](#) [Code](#) [⋮](#)

 **add validation_packages.yml**
Kevin Schneider authored 2 months ago  da71d3c9 

| Name | Last commit | Last update |
|------------------------|-----------------------------------|--------------|
| .arc | add validation_packages.yml | 2 months ago |
| assays | Add missing data files | 1 year ago |
| publication | add publication, add zScores | 2 years ago |
| runs | add tpm data | 1 year ago |
| studies | add publication information | 1 year ago |
| workflows | Update | 2 years ago |
| .gitattributes | rename missing samples; #2 | 1 year ago |
| .gitignore | add gitignore | 1 year ago |
| README.md | Add doi badge | 1 year ago |
| isa.investigation.xlsx | add author emails and adapt title | 1 year ago |

 **README.md**

Chlamydomonas reinhardtii heat stress time course experiment

DOI [10.60534/9e5jx-75d83](https://doi.org/10.60534/9e5jx-75d83)

 Star 2 [⋮](#)

Project information
Algae cultures were grown mixotrophically (TAP). After 24h of 35°C/40°C the cells were shifted back to room temperature for 48h. 'omics samples were taken.

Chlamydomonas abiotic stress
proteomics + 1 more

 pipeline  invenio 

-o- 55 Commits
2 Branches
0 Tags

 README
Auto DevOps enabled

Created on
July 11, 2022

Receive a DOI

Published September 7, 2023 | Version v1

Dataset 

Systems-wide investigation of responses to moderate and acute high temperatures in the green alga *Chlamydomonas reinhardtii*.

Zhang, Ningning¹; Mattoon, Erin¹; McHargue, Will¹ ; Venn, Benedikt² ; Zimmer, David² ; Pecani, Kresti³; Jeong, Jooyeon¹; Anderson, Cheyenne⁴; Chen, Chen⁴; Berry, Jeffrey¹; Xia, Ming¹; Tzeng, Shin-Cheng¹ ; Becker, Eric¹; Pazouki, Leila¹; Evans, Bradley¹; Cross, Fred³; Cheng, Jianlin⁴; Czymbek, Kirk¹ ; Schröder, Michael⁵ ; Mühlhaus, Timo² ; Zhang, Ru¹ 

Show affiliations

Style APA 

1

Citation

Zhang, N., Mattoon, E., McHargue, W., Venn, B., Zimmer, D., Pecani, K., Jeong, J., Anderson, C., Chen, C., Berry, J., Xia, M., Tzeng, S.-C., Becker, E., Pazouki, L., Evans, B., Cross, F., Cheng, J., Czymbek, K., Schröder, M., ... Zhang, R. (2023). Systems-wide investigation of responses to moderate and acute high temperatures in the green alga *Chlamydomonas reinhardtii*. [Data set]. DataPLANT. <https://doi.org/10.60534/9e5jx-75d83>

2

Details

DOI

DOI [10.60534/9e5jx-75d83](https://doi.org/10.60534/9e5jx-75d83)

Resource type

Dataset

Publisher

DataPLANT

Export

JSON

Export

Check point 4

Task

- ✓ My ARC is now validated and submitted for publication!

Resources



Info & materials

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- Knowledge Base:
<https://nfdi4plants.org/nfdi4plants.knowledgebase/>

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- User Support Mailing List: [Click here to subscribe](#)

Open Source Development

- GitHub: <https://github.com/nfdi4plants>

Acknowledgements



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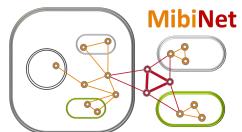
- Stella Eggels
- Angela Kranz



CEPLAS

Cluster of Excellence on Plant Sciences

- Björn Usadel
- Vittorio Tracanna
- Yaser Alashloo



- Sabrina Zander