

Fundamentals of ARCs

de.NBI RDM training – *Maximizing the Potential of Agricultural Research Data*

Dominik Brilhaus, [CEPLAS](#)

October 23rd, 2025



Introduce yourself

Please use zoom annotations

Used code / a programming language before? Experience with Git / GitLab / GitHub?

Operating system

- Windows
- Mac
- Linux

Experience with ARCs?

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

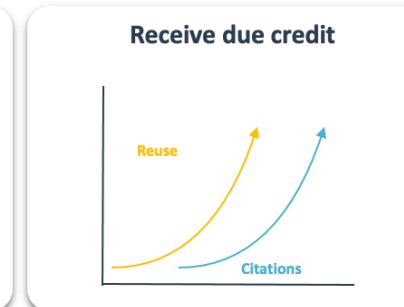
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[Scientific Data](#) 3, Article number: 160018 (2016) | [Cite this article](#)

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

The FAIR principles



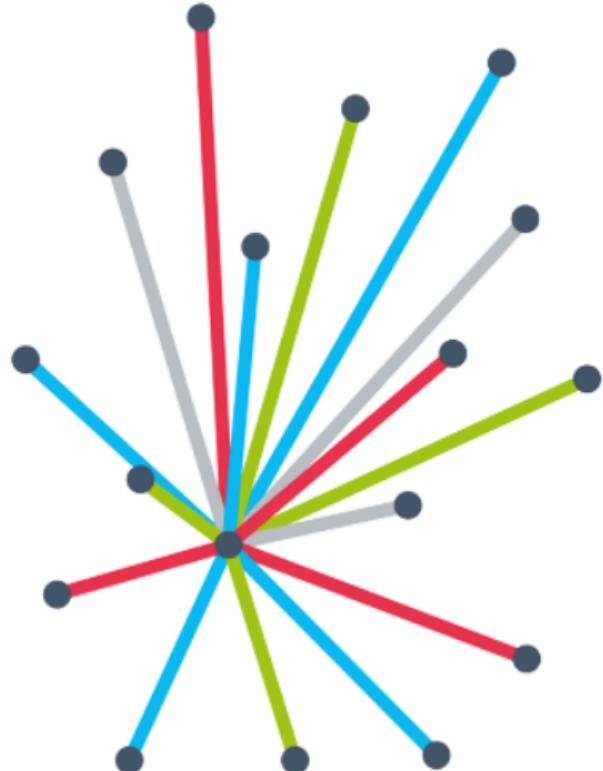
Is your data FAIR?

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?



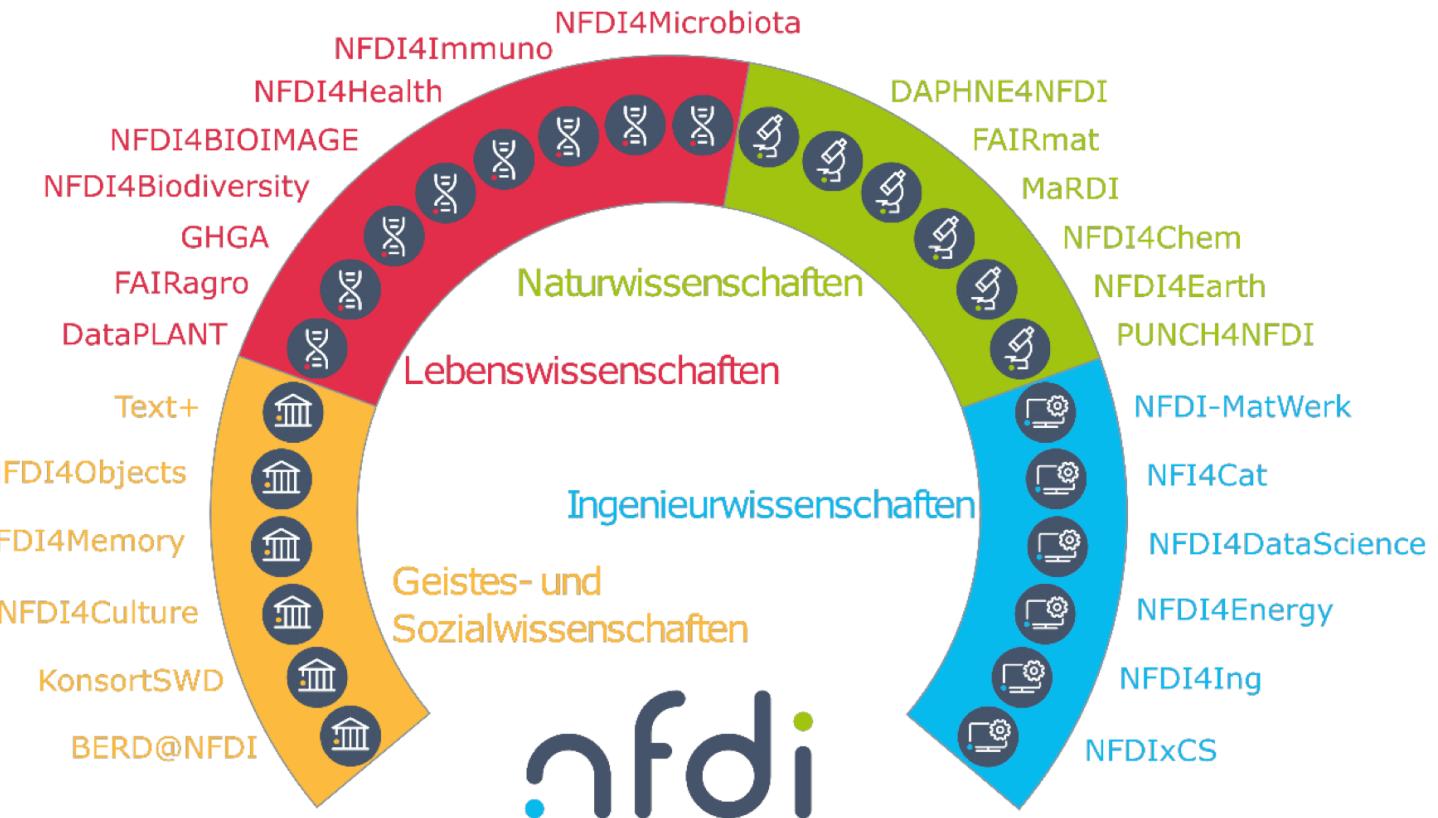
NFDI – Nationale Forschungsdaten Infrastruktur



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.

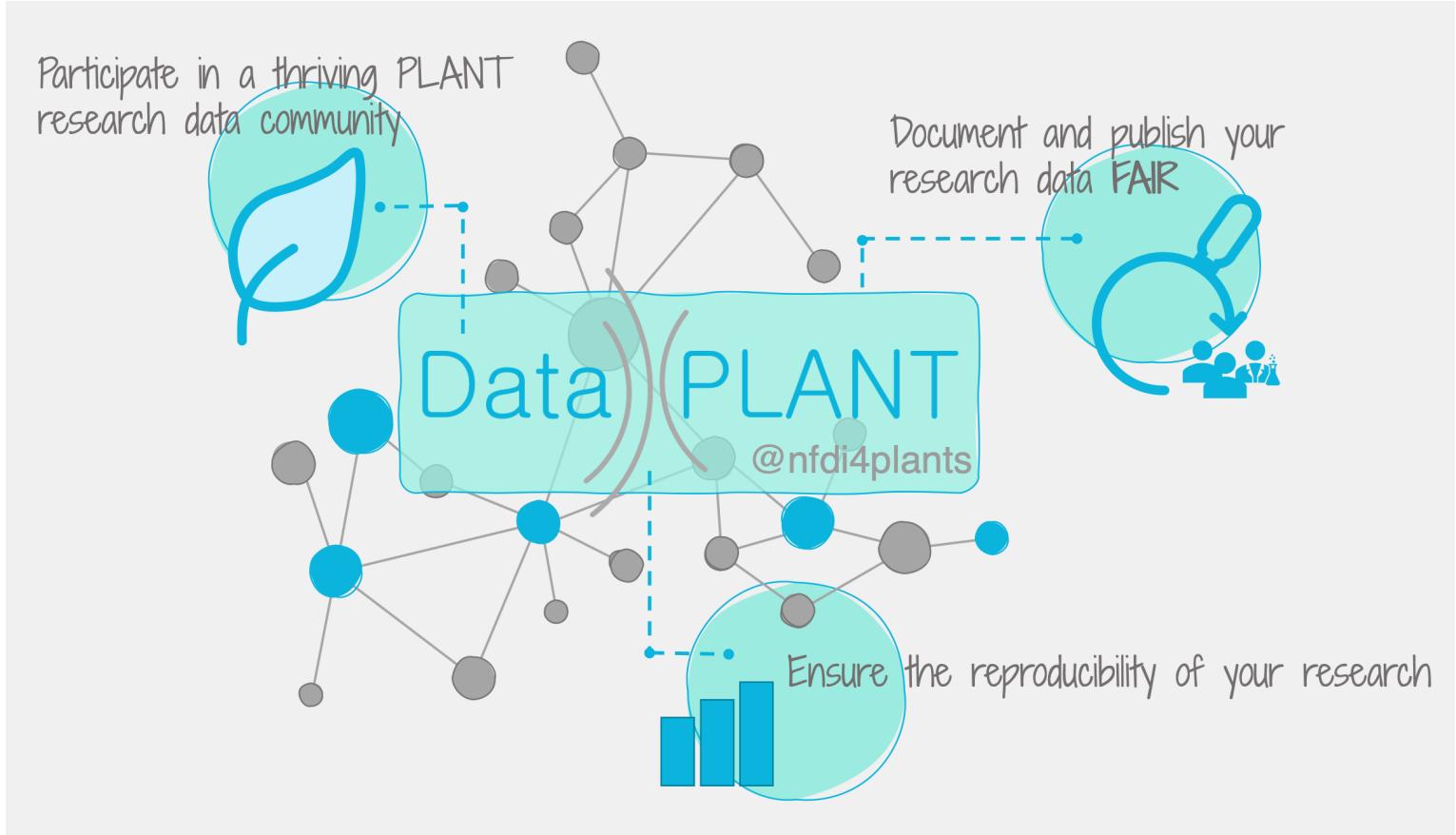
nfdi.de

NFDI – A community–targeted approach for RDM



nfdi.de

DataPLANT – NFDI4plants



<https://nfdi4plants.org>

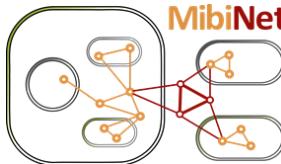
Data Stewardship between DataPLANT and the community

Community



CEPLAS

trr_341<sup>plant
ecological
genetics</sup>



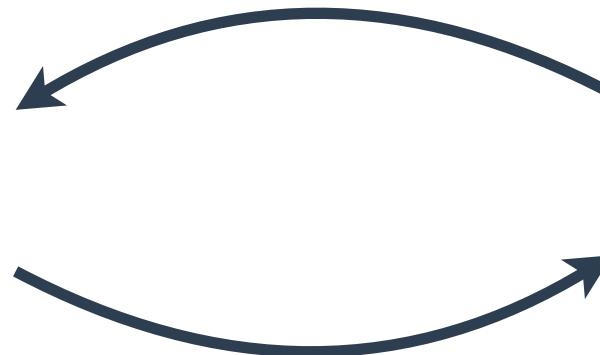
MibiNet

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>

Interaction during the course

Questions

- Please use the [google doc](#) to interact, raise questions and feedback
- I will provide all links for hands-on there

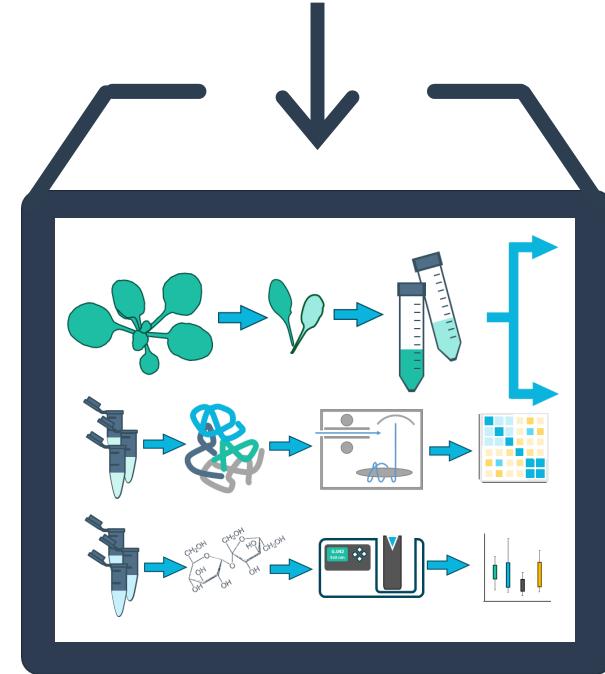
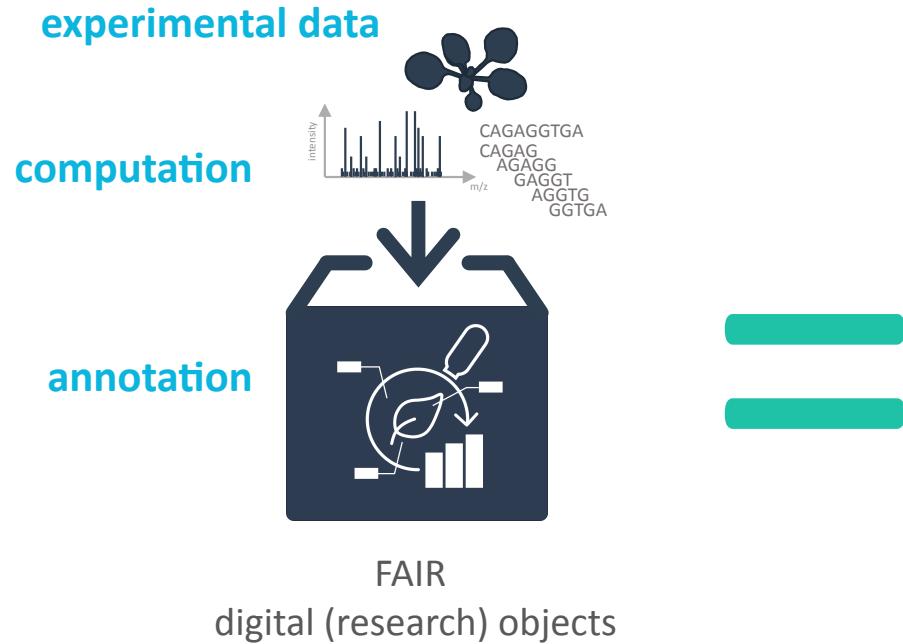
"I'm ready"

During the self-guided parts, please use Zoom reactions to tell me you're done with that part.

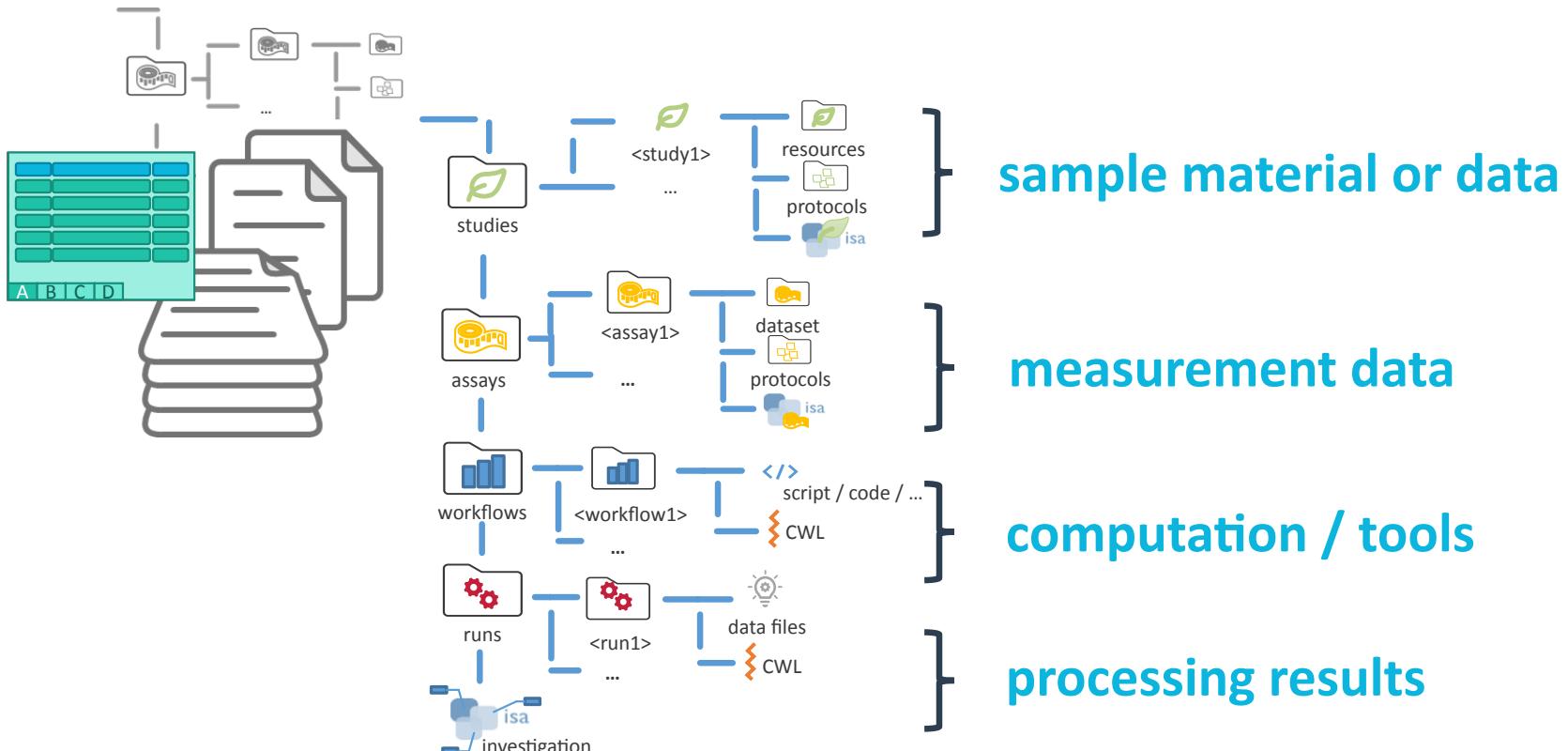


Yes

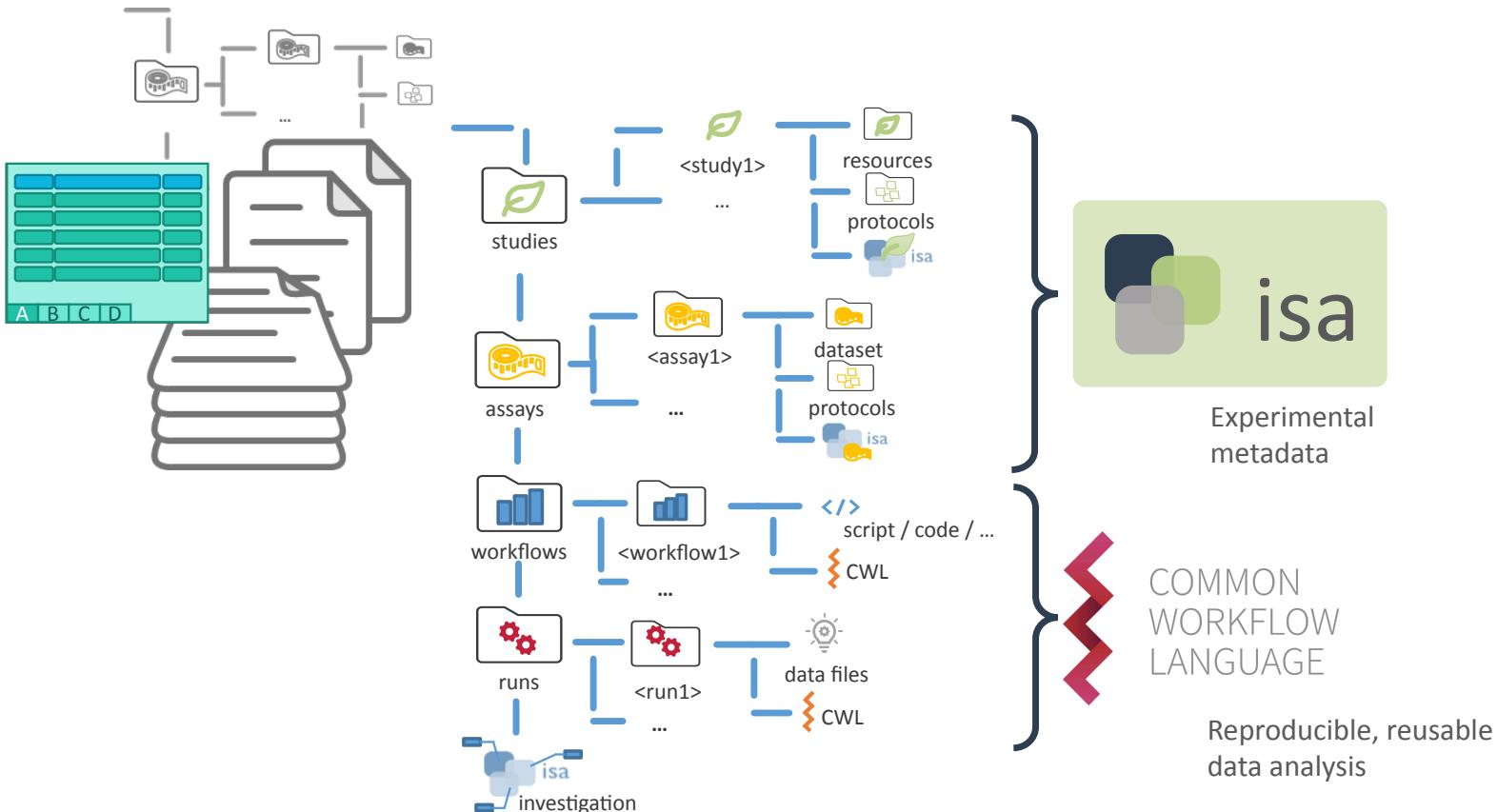
Annotated Research Context (ARC)



The ARC scaffold structure



ARC builds on standards



<https://isa-tools.org> | <https://www.commonwl.org> | <https://www.researchobject.org/ro-crate> | <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

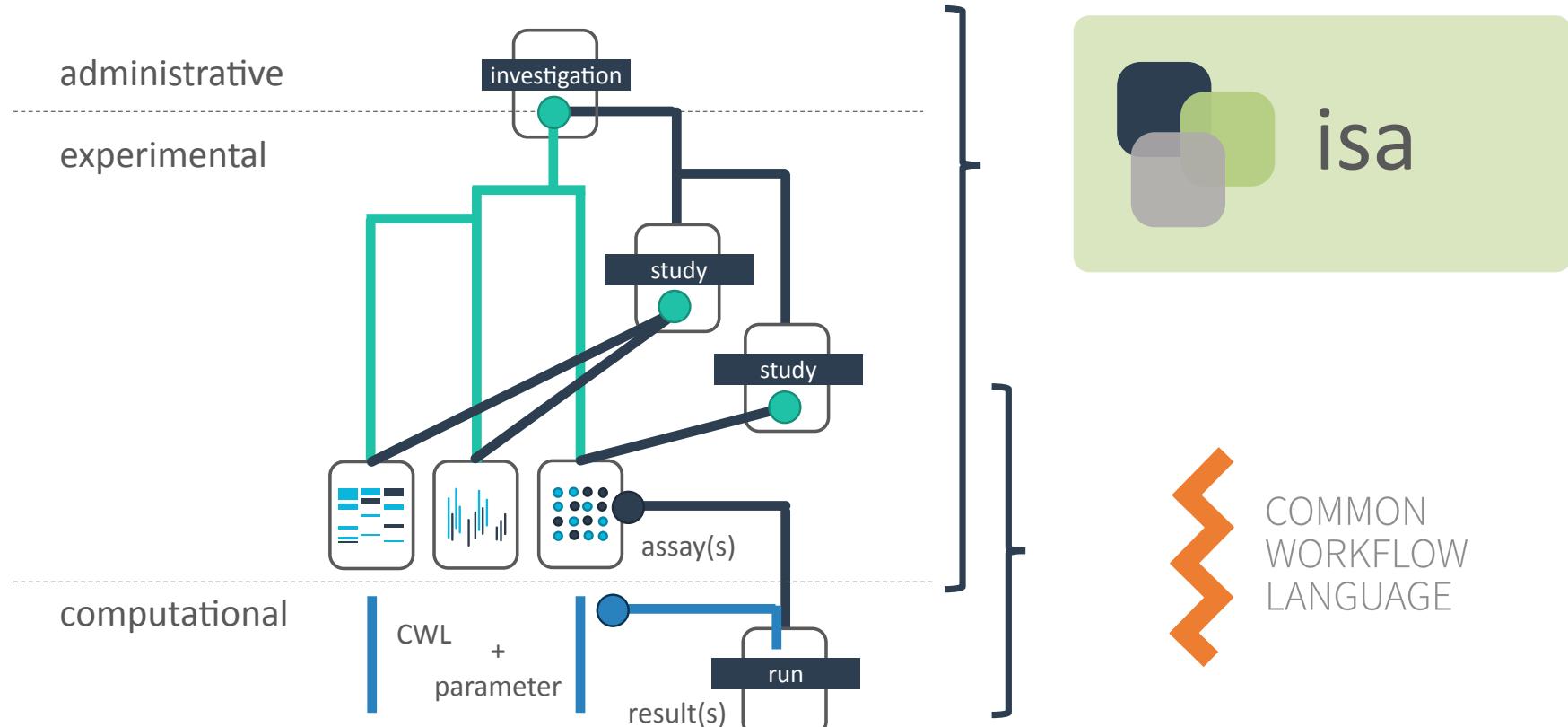
- Characteristics
- Parameters
- Components
- Factors

Assay

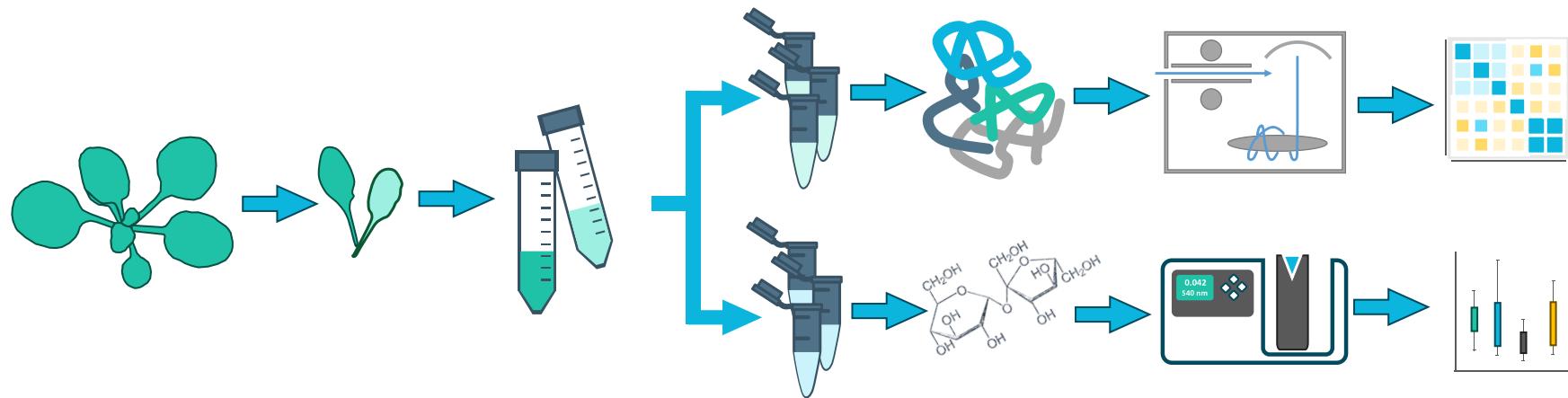
descriptive (meta)data
information on the measurement

- Characteristics
- Parameters
- Components
- Factors

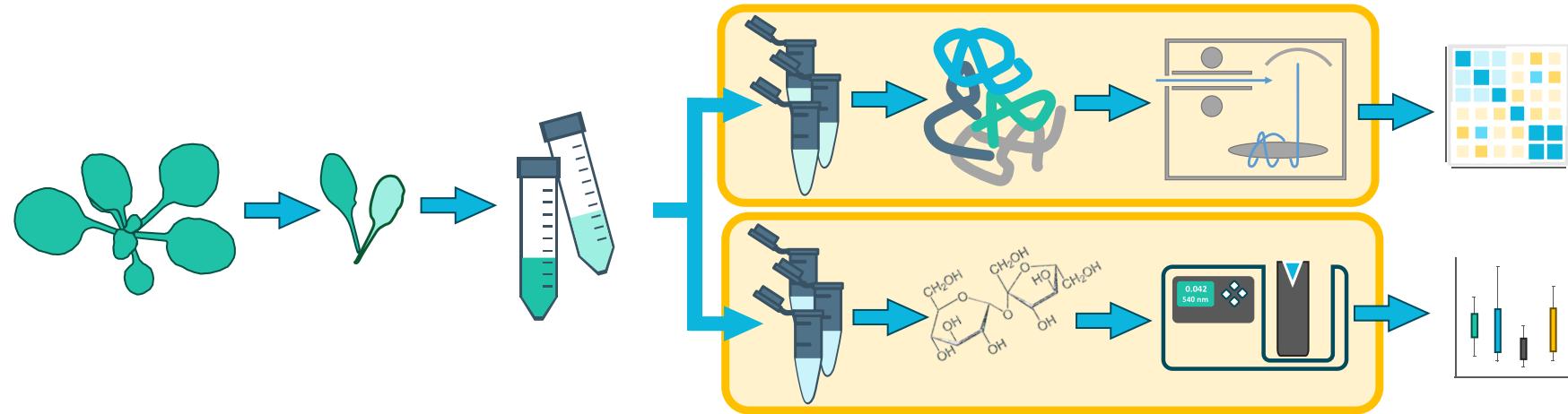
ISA and CWL – Connected by similarity



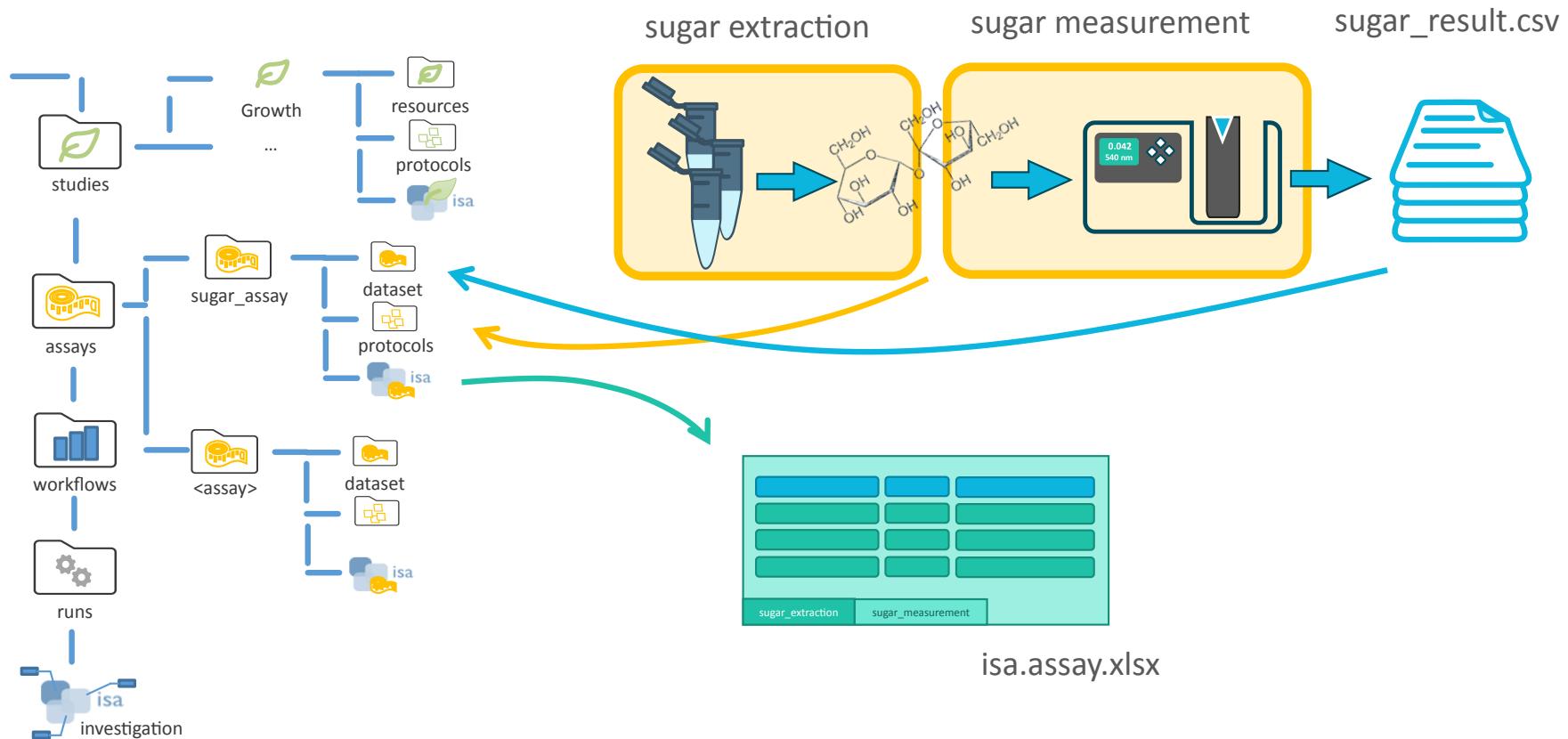
Metadata annotation – from sample to data



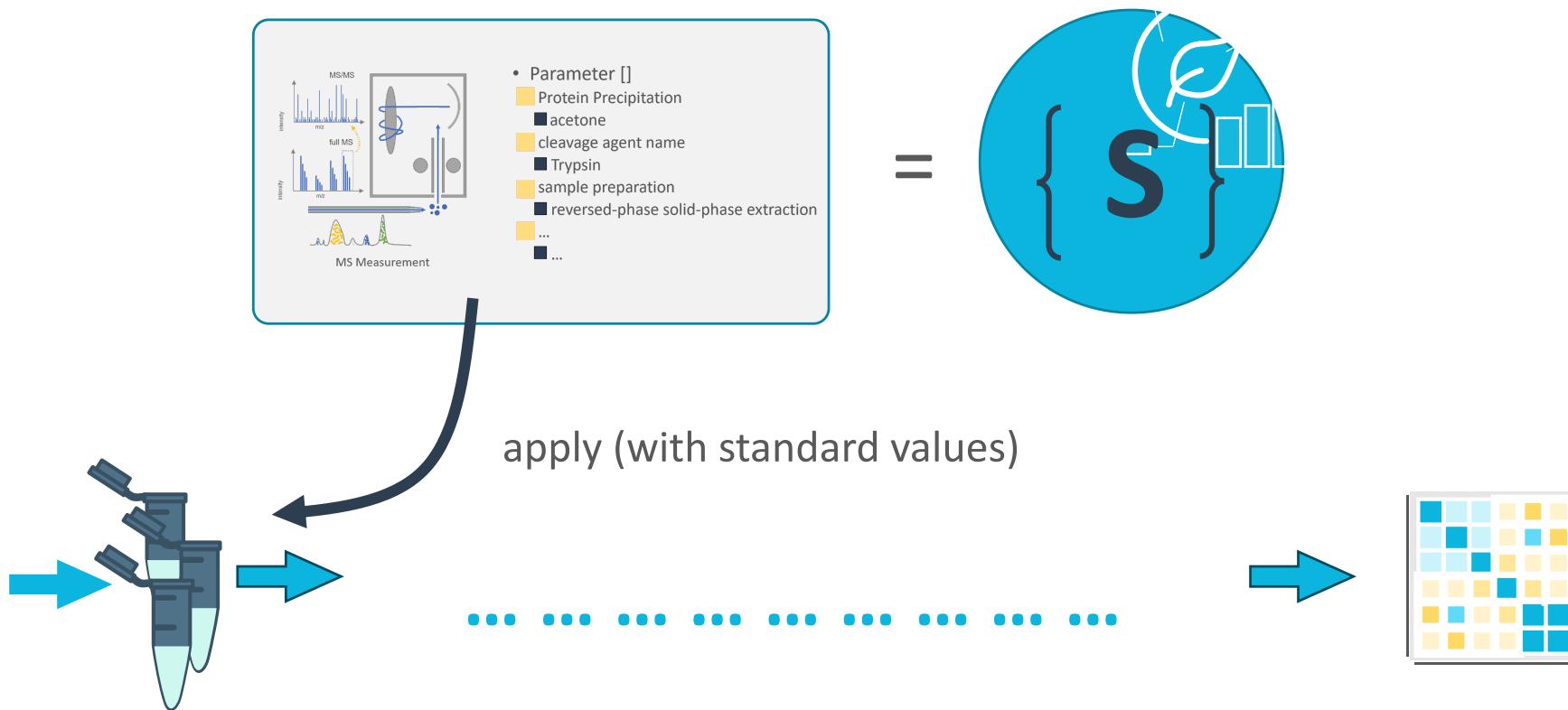
Modular separation of experimental processes



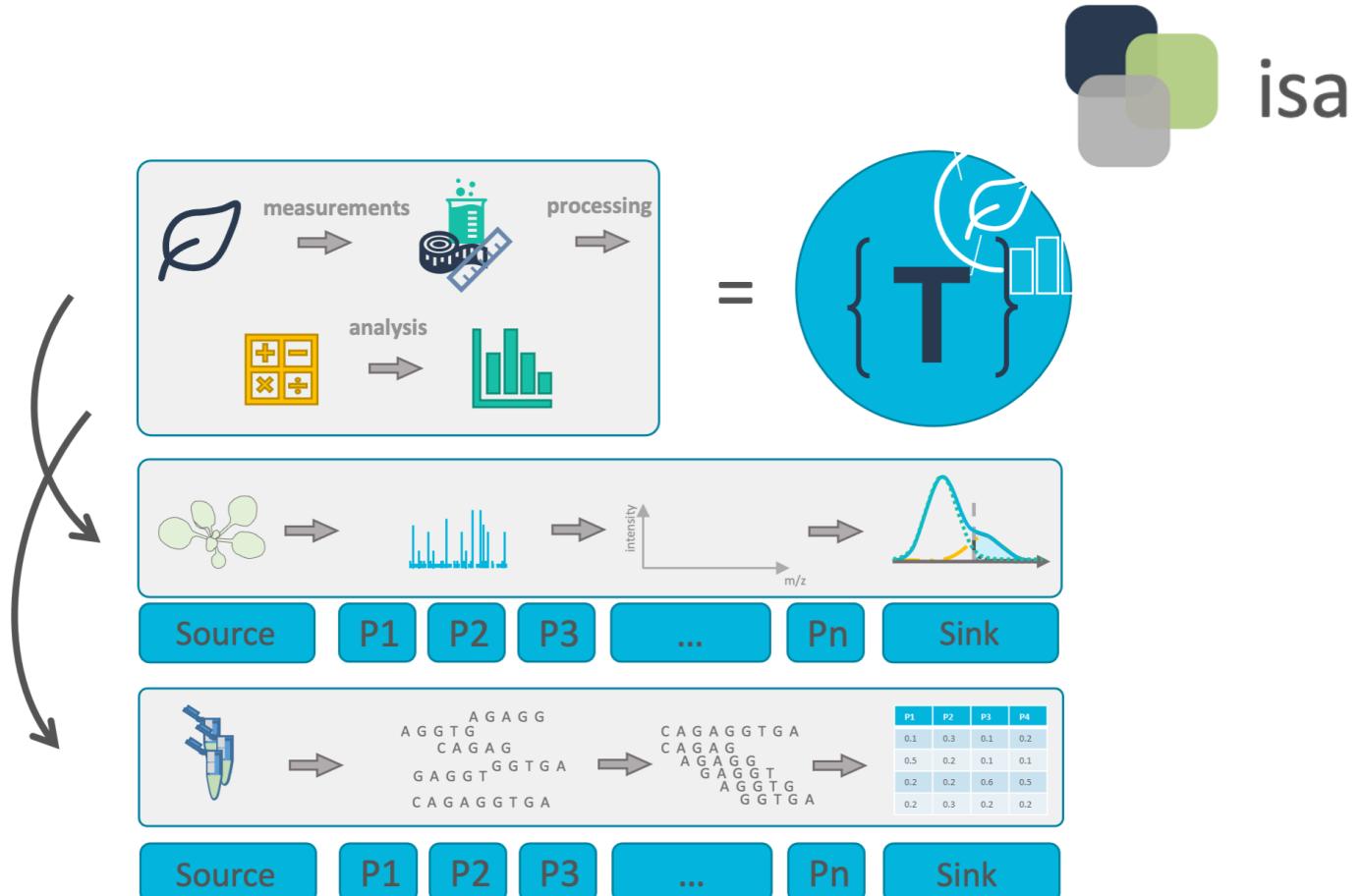
Modular separation of experimental processes



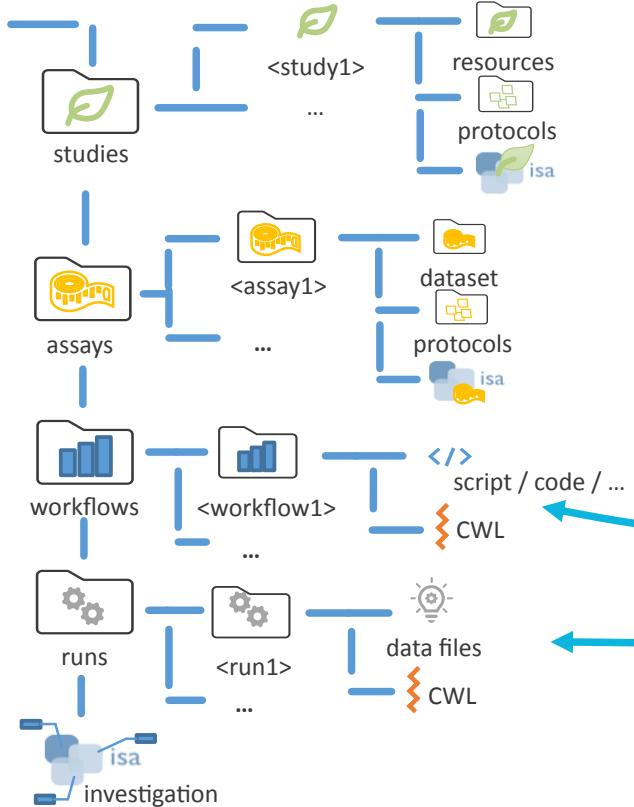
Applying standard procedures to sample record



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

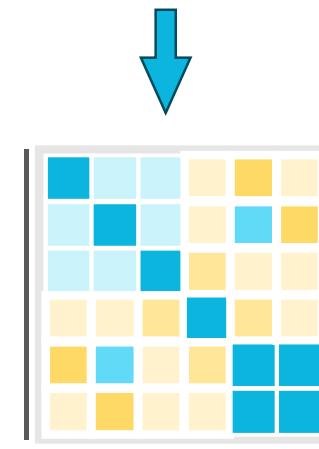
# Read the CSV file
data = pd.read_csv('result.csv')

# 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)

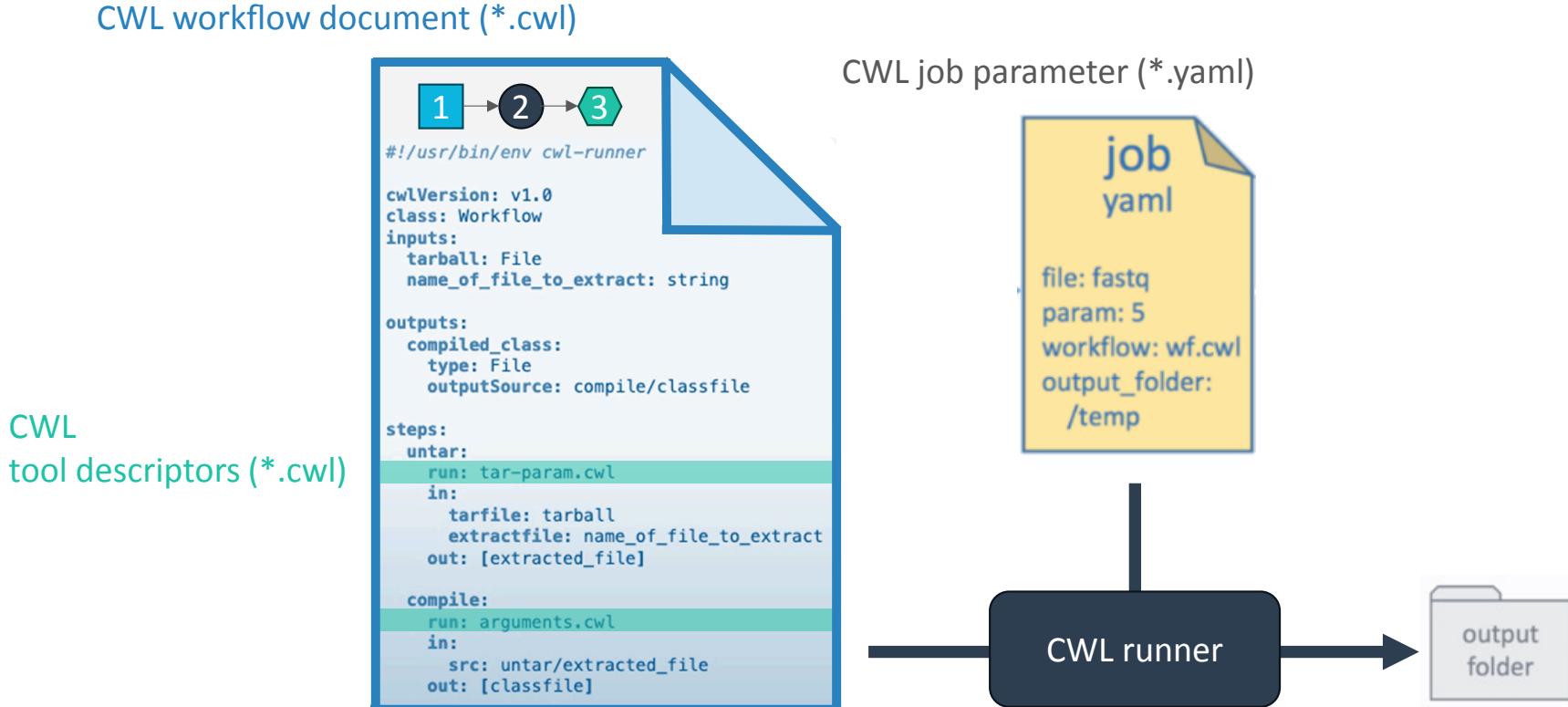
# Create a heatmap using Plotly
fig = px.imshow(data,
                 labels=dict(x="Columns", y="Rows", color="Value"),
                 x=data.columns,
                 y=data.index)

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

heatmap.py

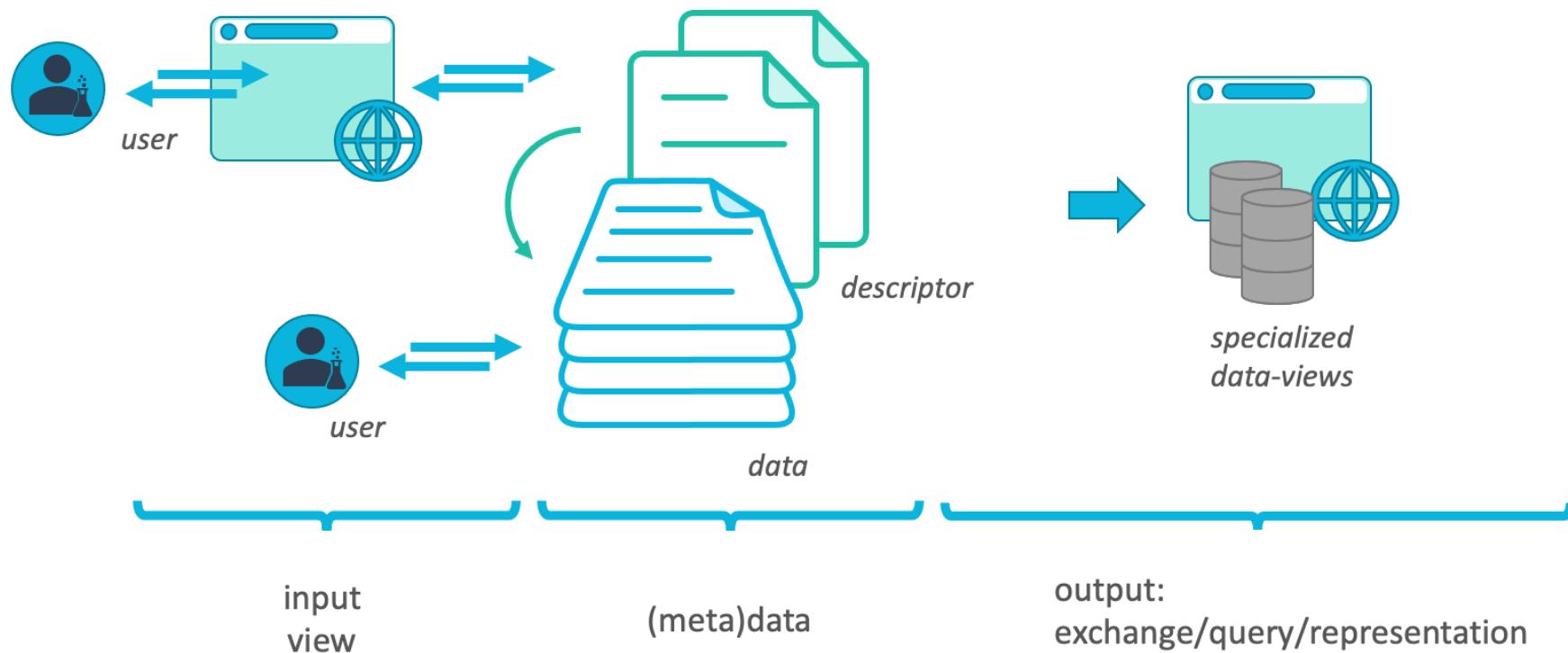


Metadata annotation – from data to result

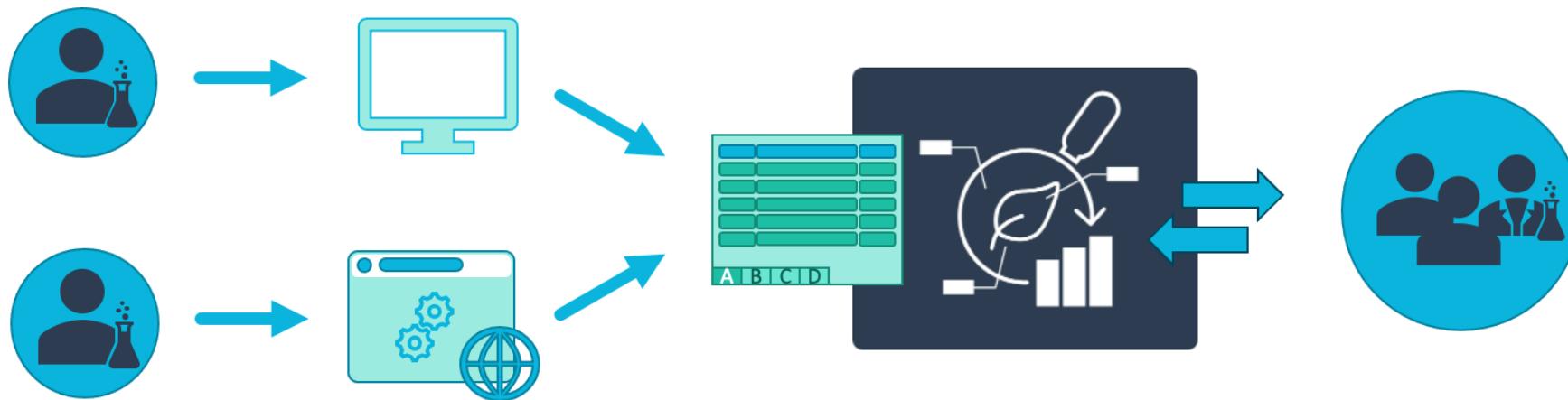


Everything is a file

The ARC is a data-centric approach to RDM

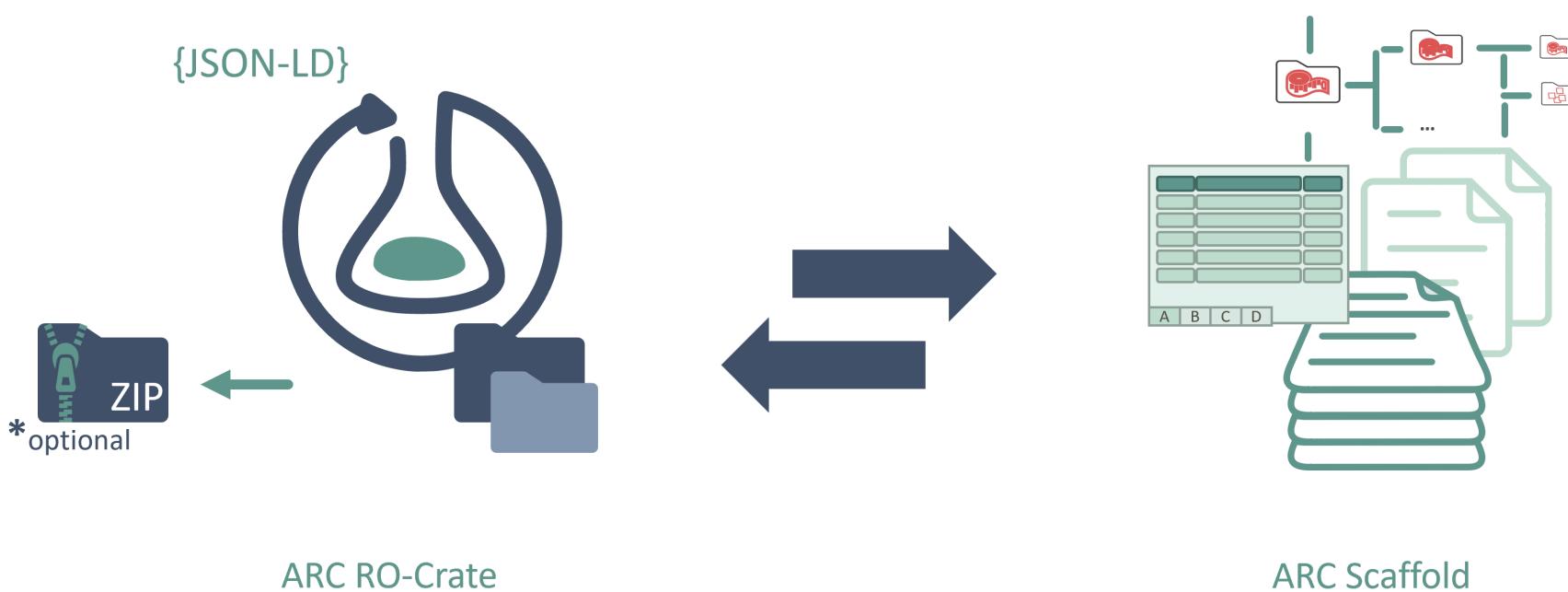


No technical lock-in



(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

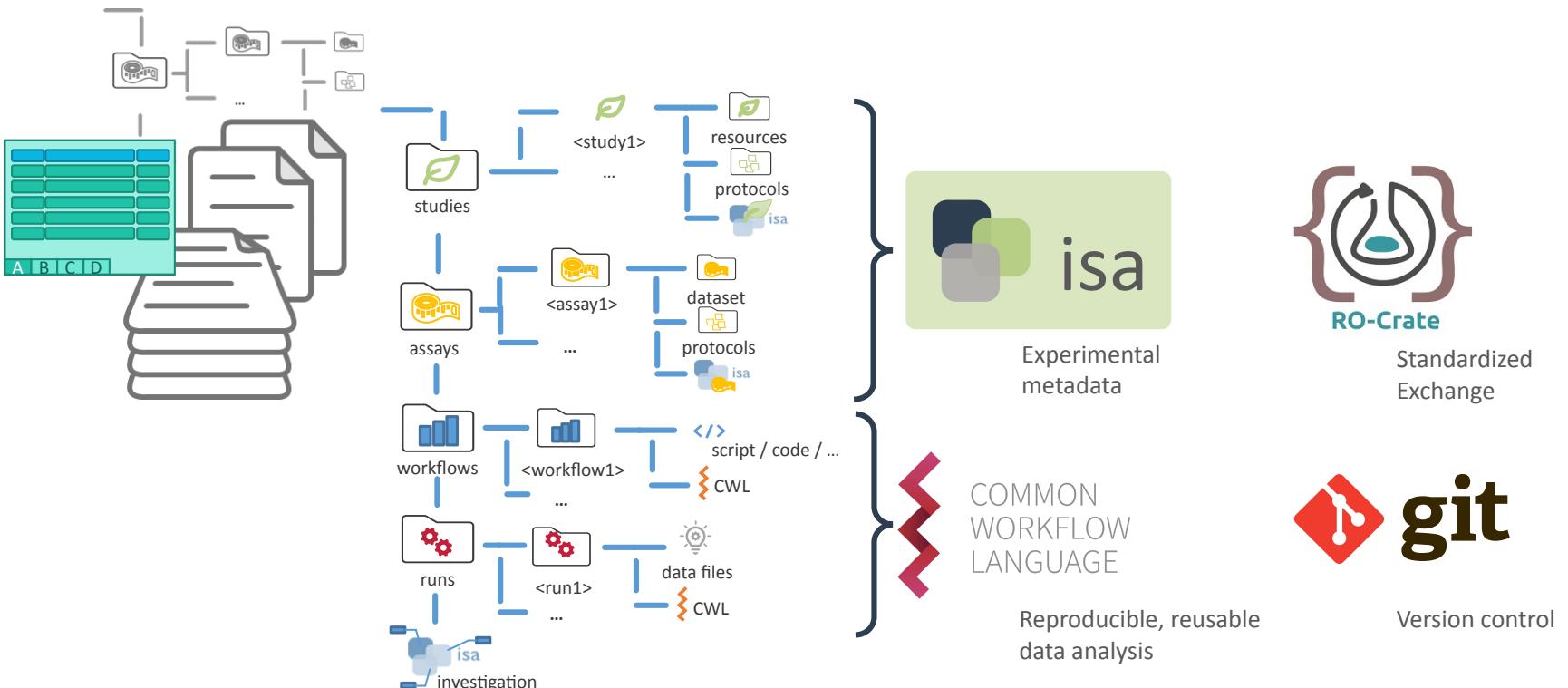
```
{  
  "Identifier": "Proteomics_MS",  
  "MeasurementType": {  
    "annotationValue": "Proteomics_MS",  
    "termSource": "MS",  
    "termAccession": "https://purl.obolibrary.org/obo/FMS_1003348"  
  },  
  "TechnologyType": ...  
  ...  
  "Tables": [  
    {  
      "name": "ProtDigest",  
      "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] (TCEP). A green checkmark is present next to the 'acetone' entry.

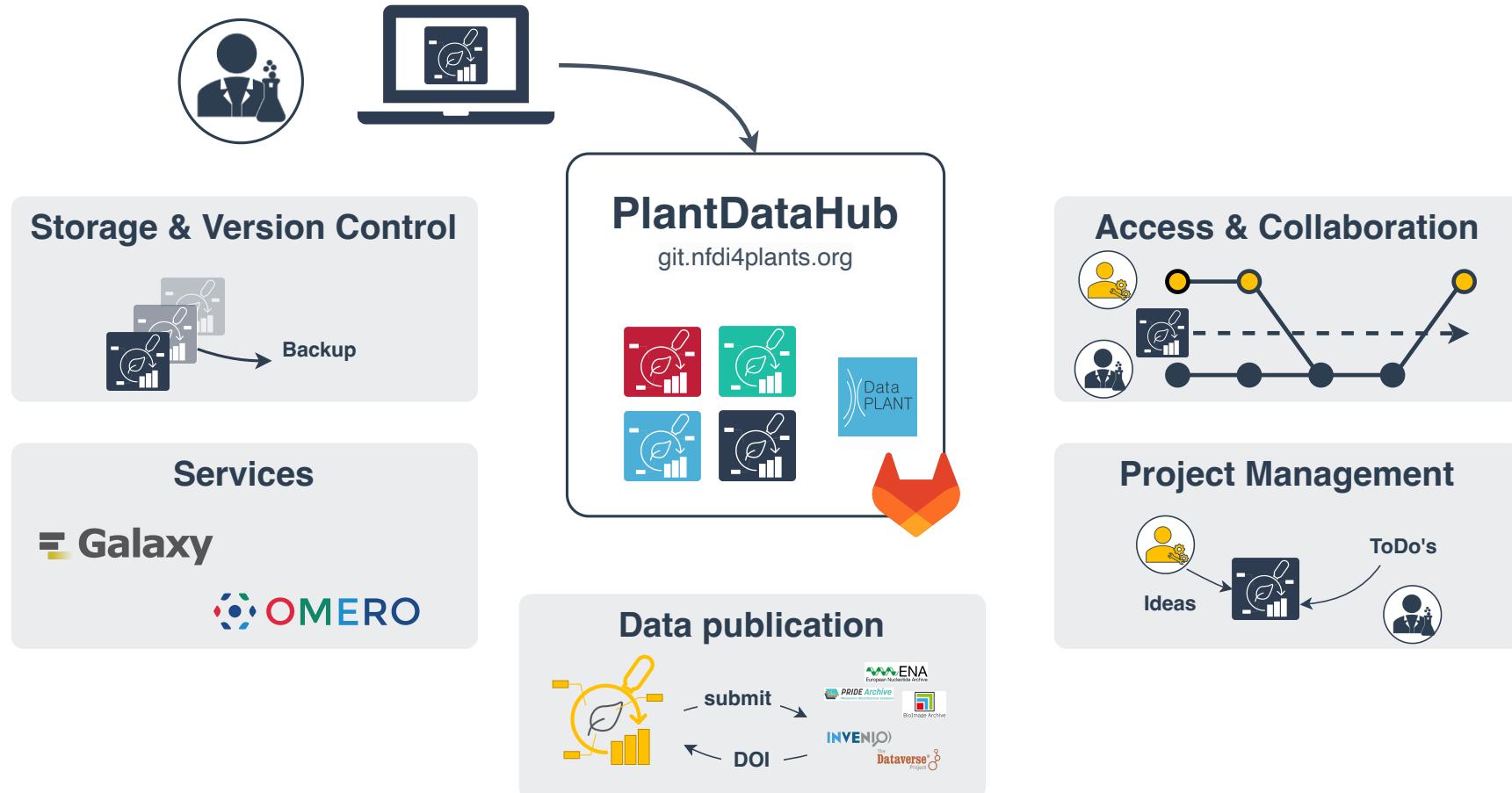
Parameter [sample mass] >>	Parameter [Protein Precipitation] >>	Parameter [alkylating agent] >>	Parameter [red]
10 microgram	acetone	Chloroacetamide	TCEP

ARC builds on standards

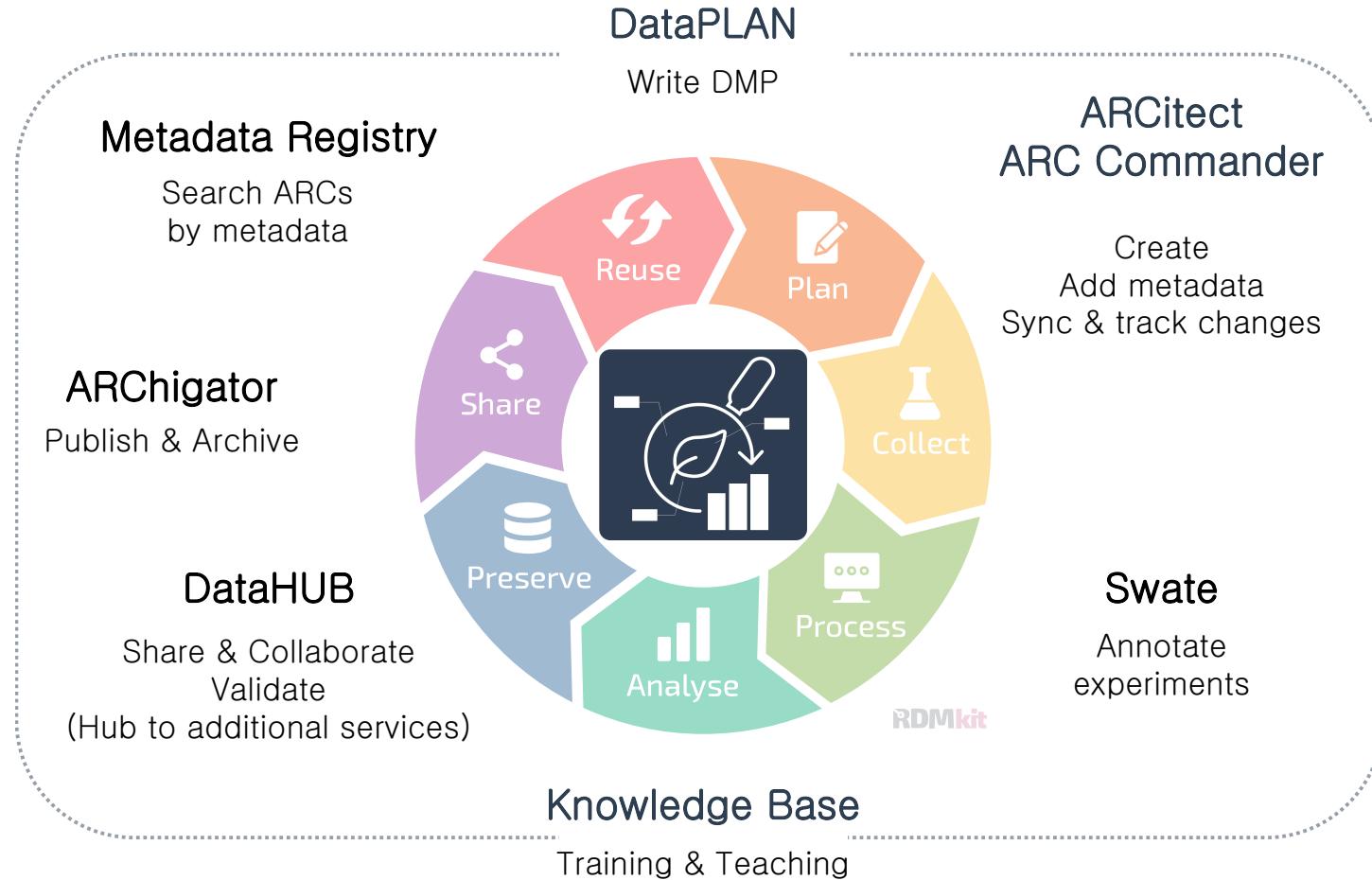


<https://isa-tools.org> | <https://www.commonwl.org> | <https://www.researchobject.org/ro-crate> | <https://git-scm.com>

ARC and DataHUB as entry point



The ARC ecosystem



Acknowledgements



Team Kaiserslautern

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

Team Freiburg

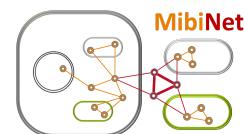
- Dirk von Suchodeletz
- Jonathan Bauer
- Marcel Tschöpe
- Julian Weidhase

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 and discuss ARC features
- ...

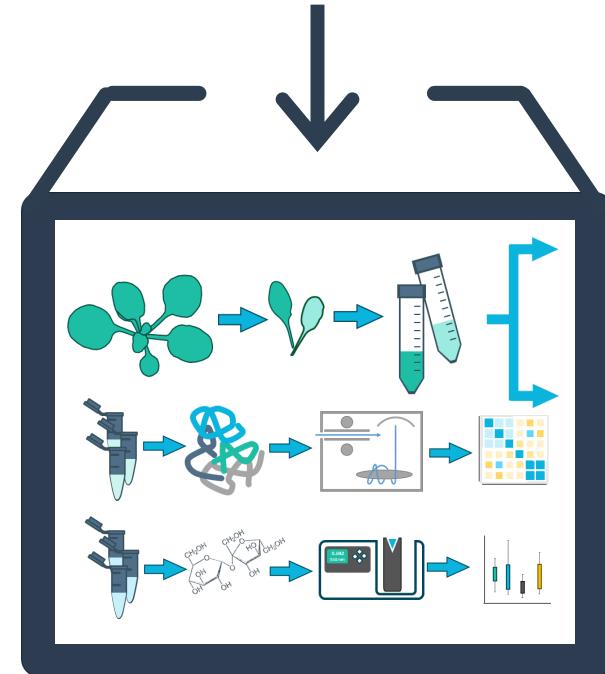
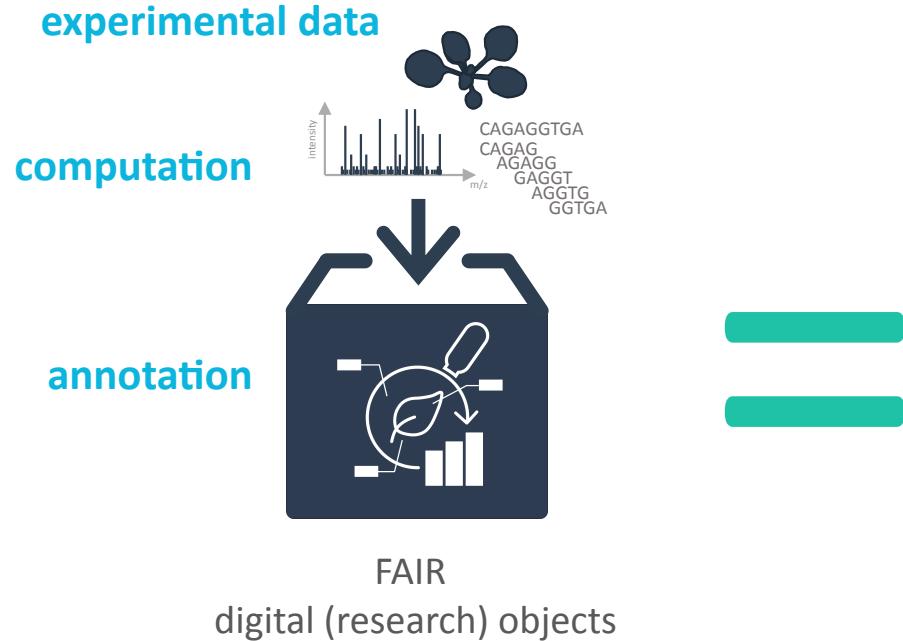
Start an ARC for your investigation



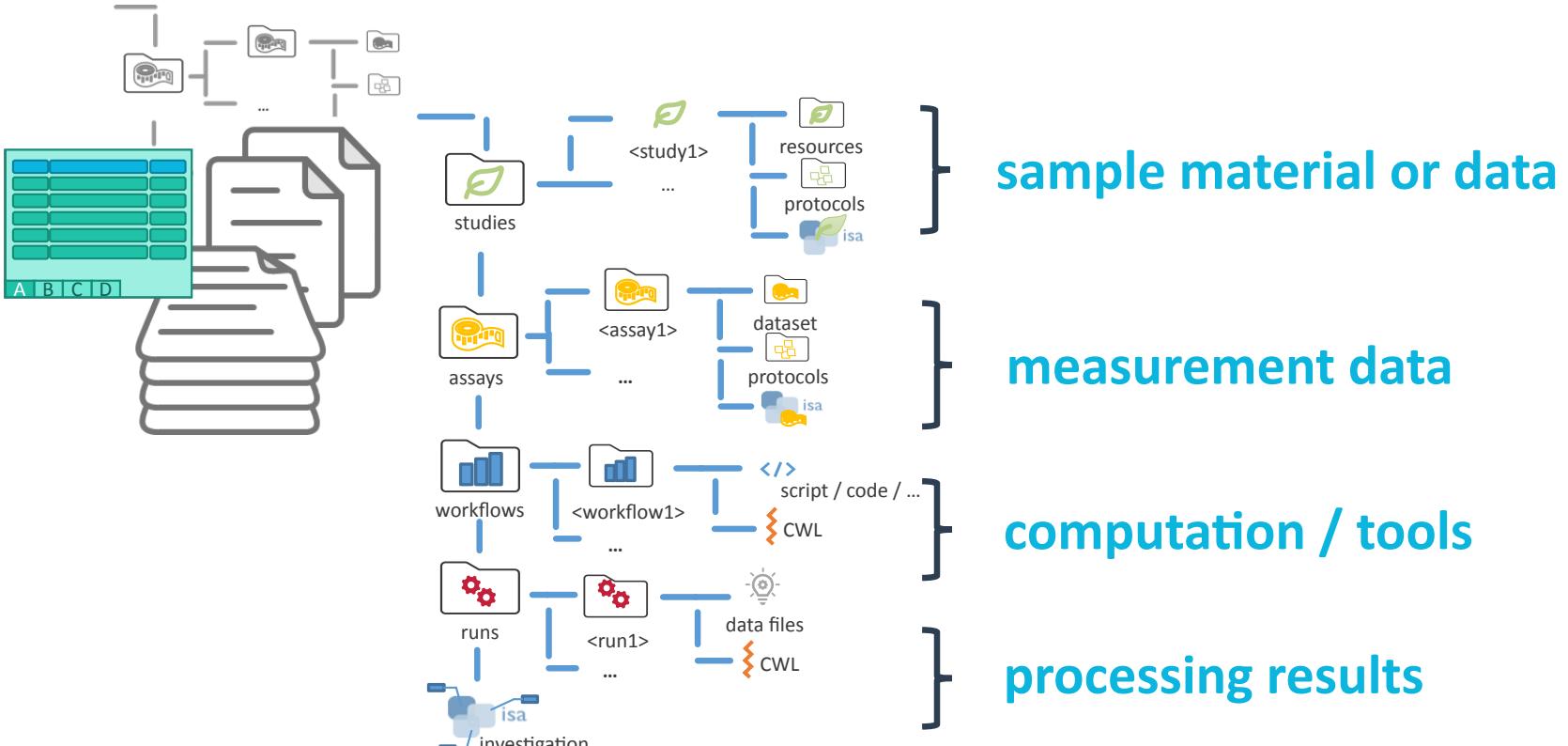
Hands-on

Follow the [Start Here guide](#) until Describe the investigation

ARC: Annotated research context



The ARC scaffold structure



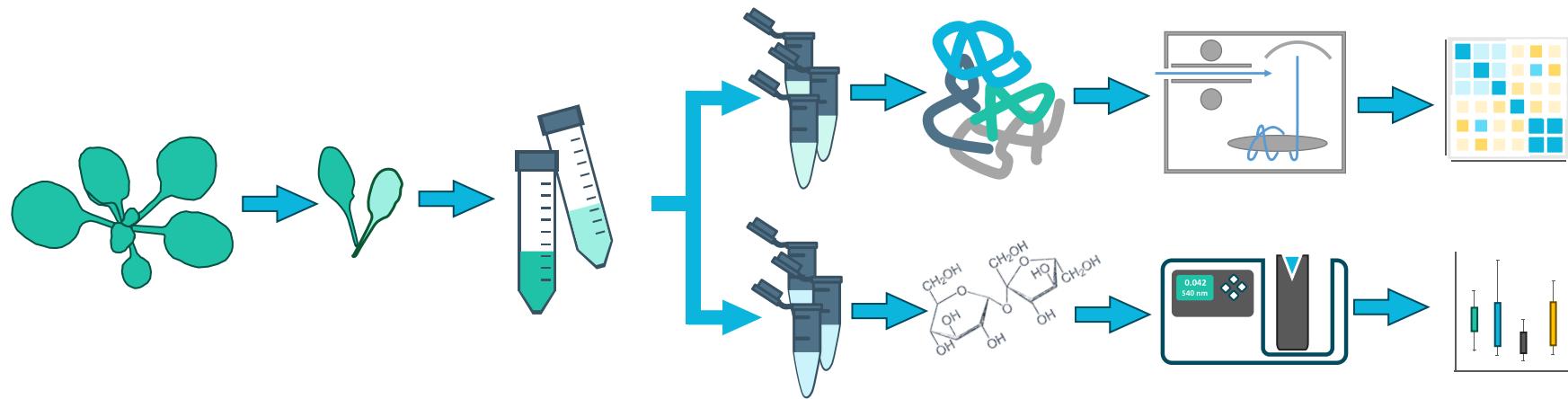
Add and describe a study



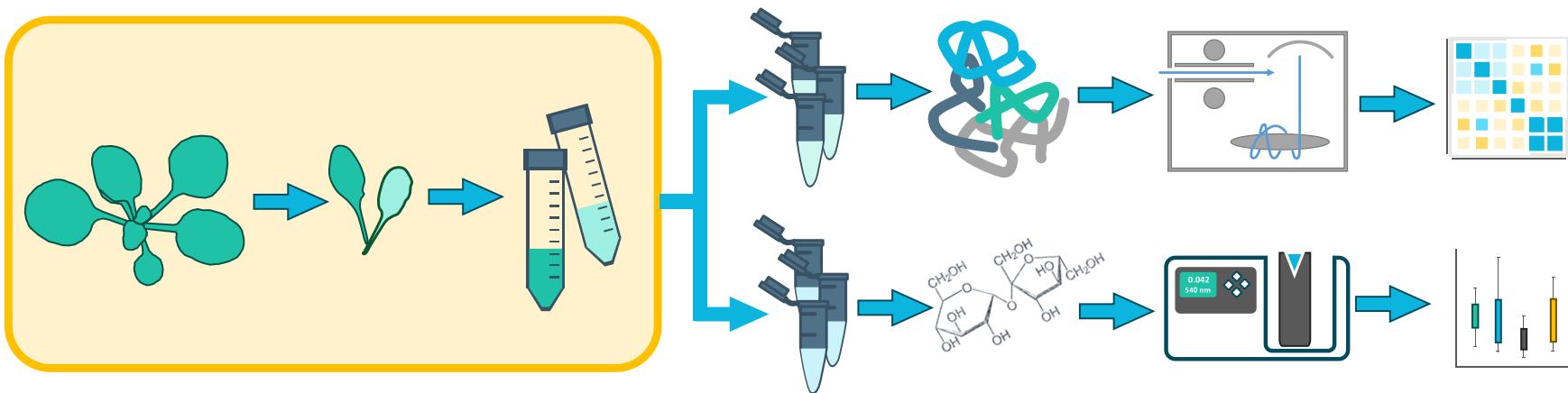
Hands-on

Follow the [Start Here guide](#) until Add a study

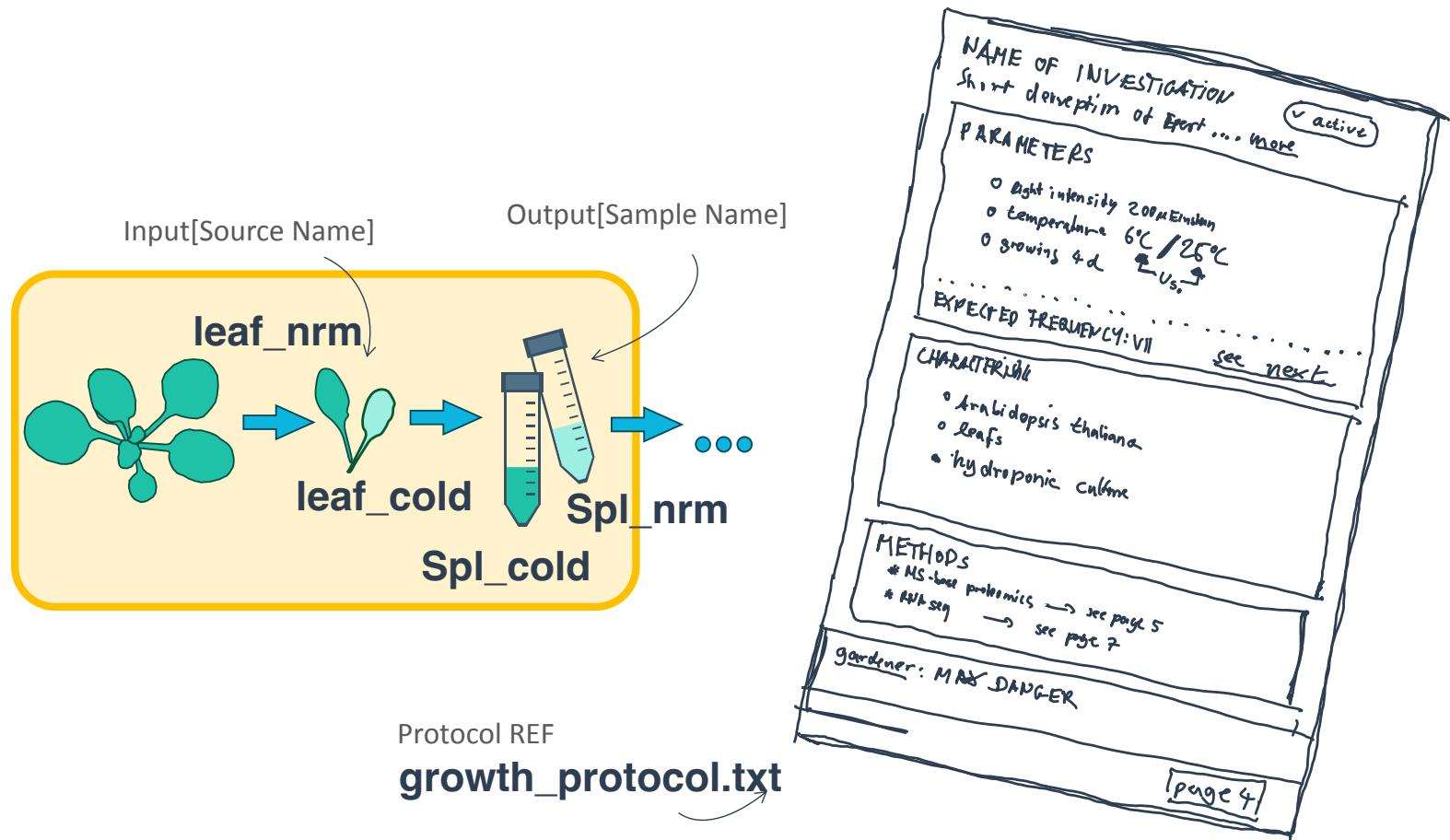
A small prototypic project



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		

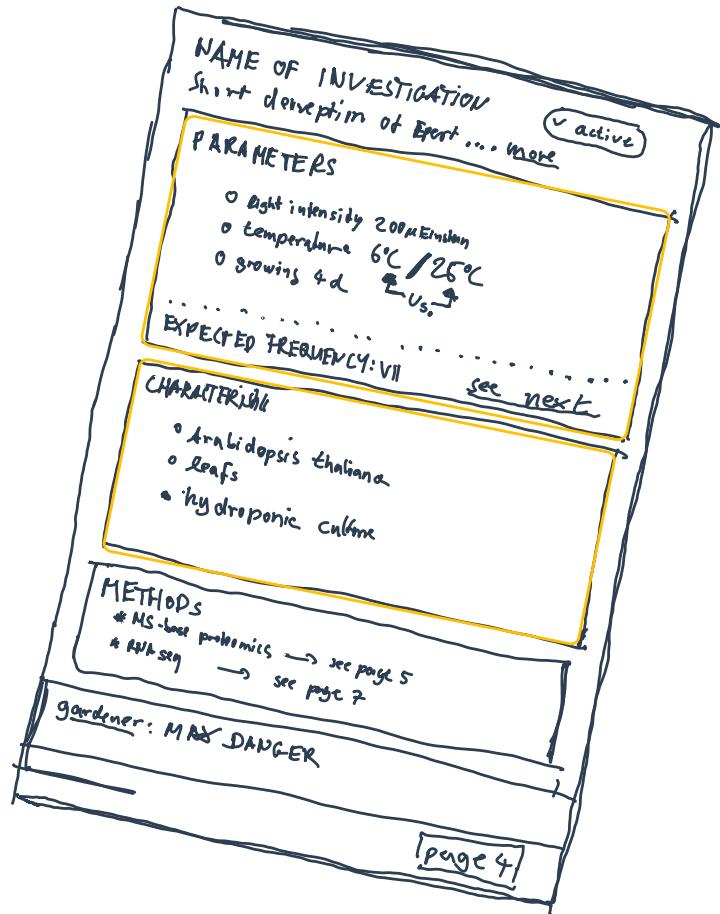
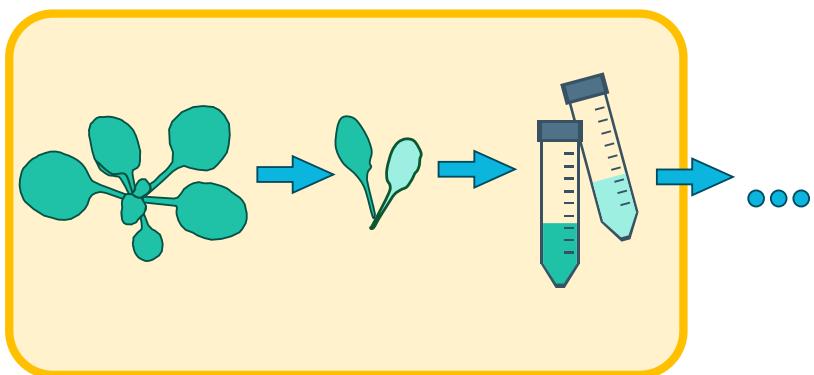
Referencing a protocol

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

+

Welcome to the EMBL-EBI Ontology Lookup Service

temperature

Exact match Include obsolete terms Include imported terms

Examples: diabetes, GO:0098743

Looking for a particular ontology?

Data Content

Updated 4 Oct 2024 Fri 17:50 +02:00

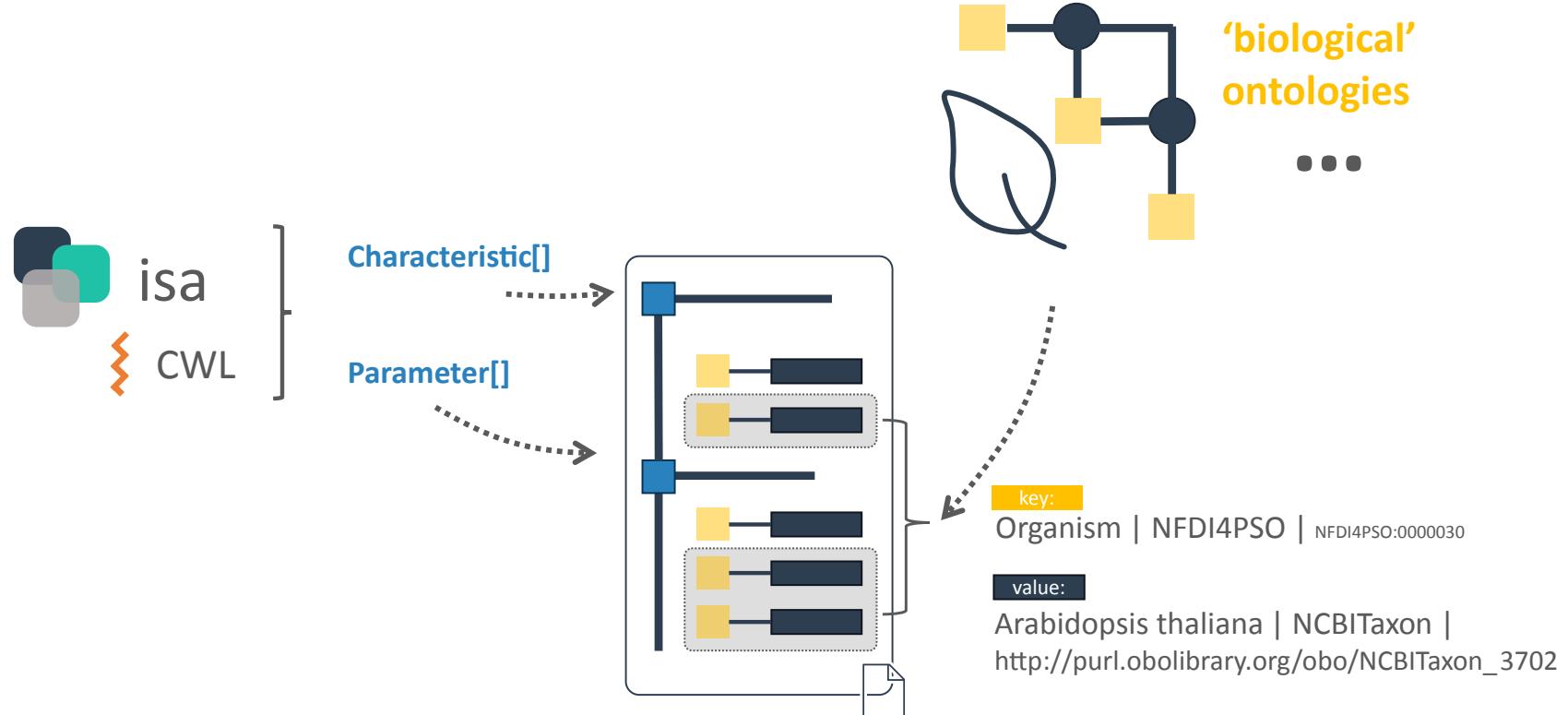
- 265 ontologies
- 8,595,500 classes
- 45,471 properties
- 697,188 individuals

FOLLOW US

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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 μ Einstein
- Temperature
 - 6°C / 25°C
- Growth time
 - 4d

Characteristics []

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

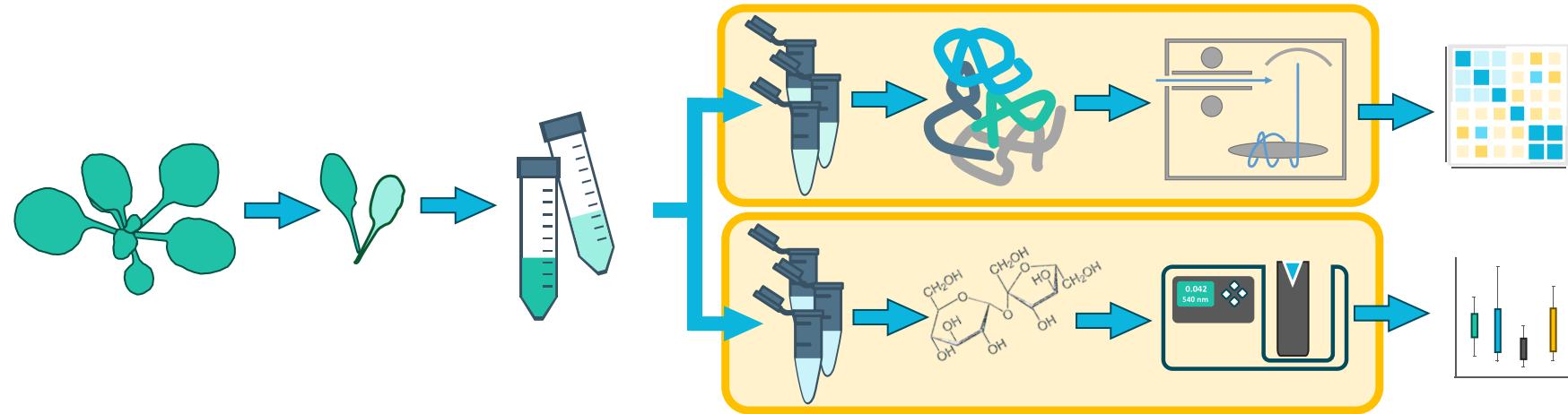
Add and describe an assay



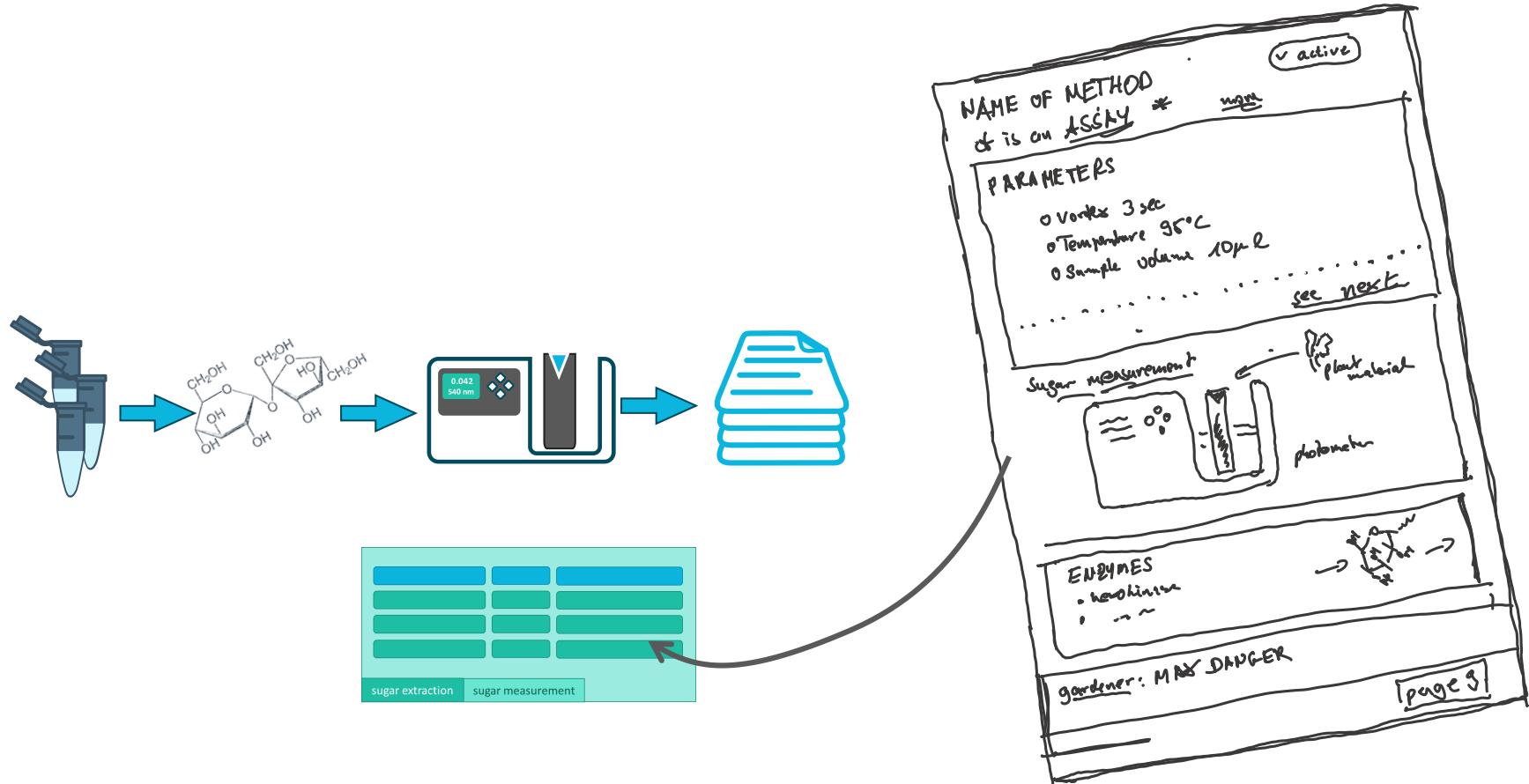
Hands-on

Follow the [Start Here guide](#) until Add assay data

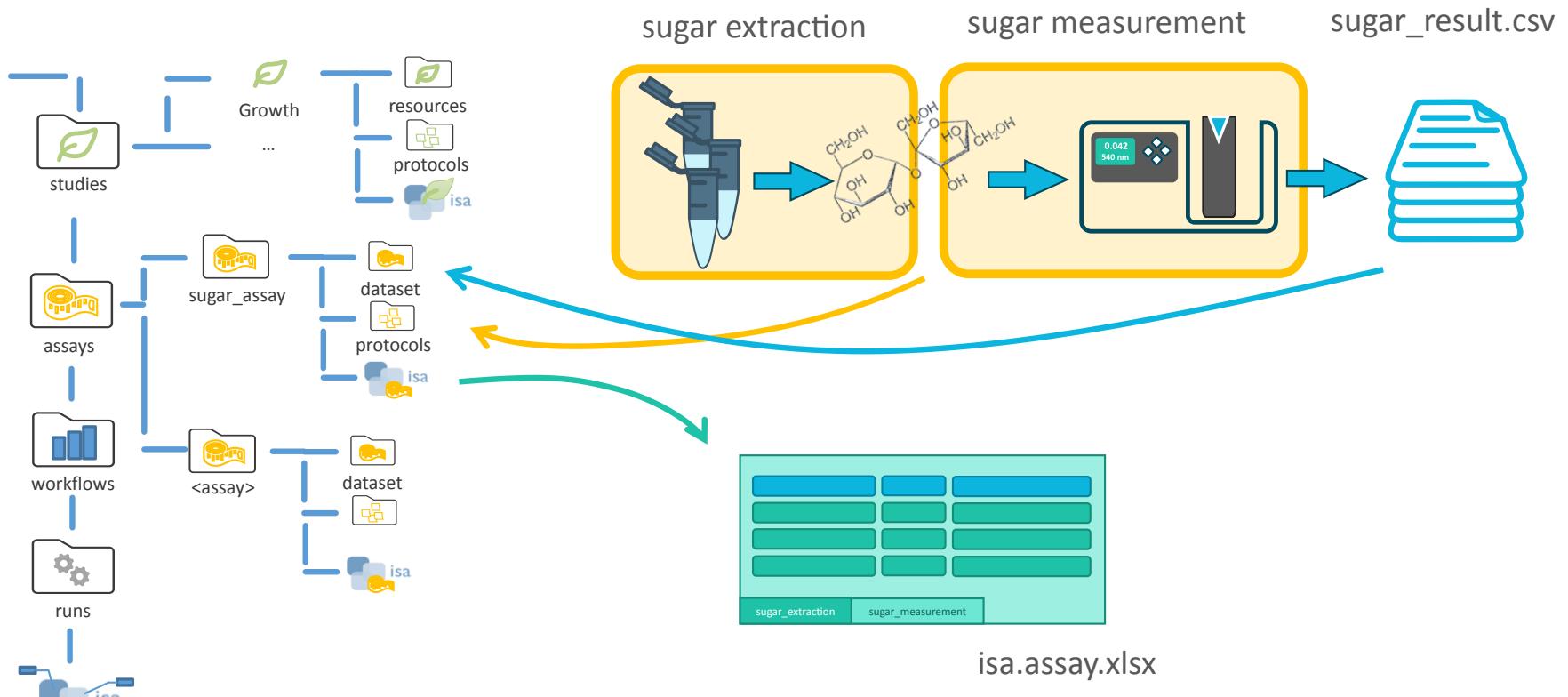
Identifying assays



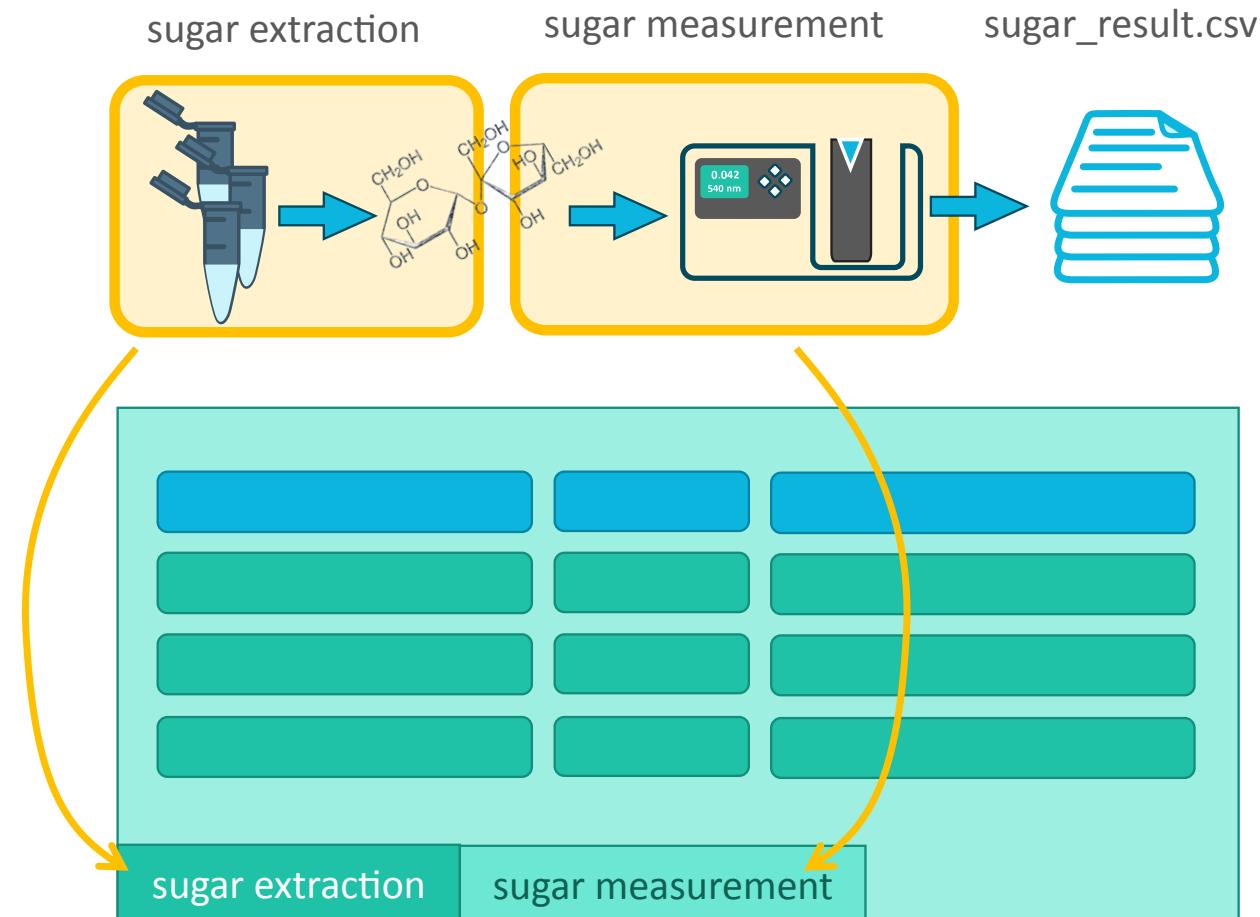
Assay for sugar measurement



Separating different assay elements



Isolating the lab processes in an assay



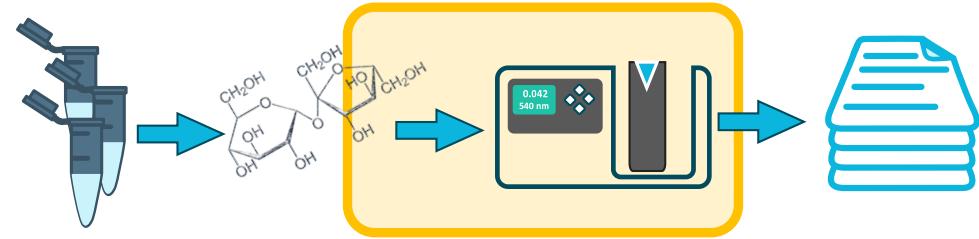
Parameteterization: sugar extraction

- 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



Share your ARC



Hands-on

Follow the [Start Here guide](#) until Share your ARC via the DataHUB

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

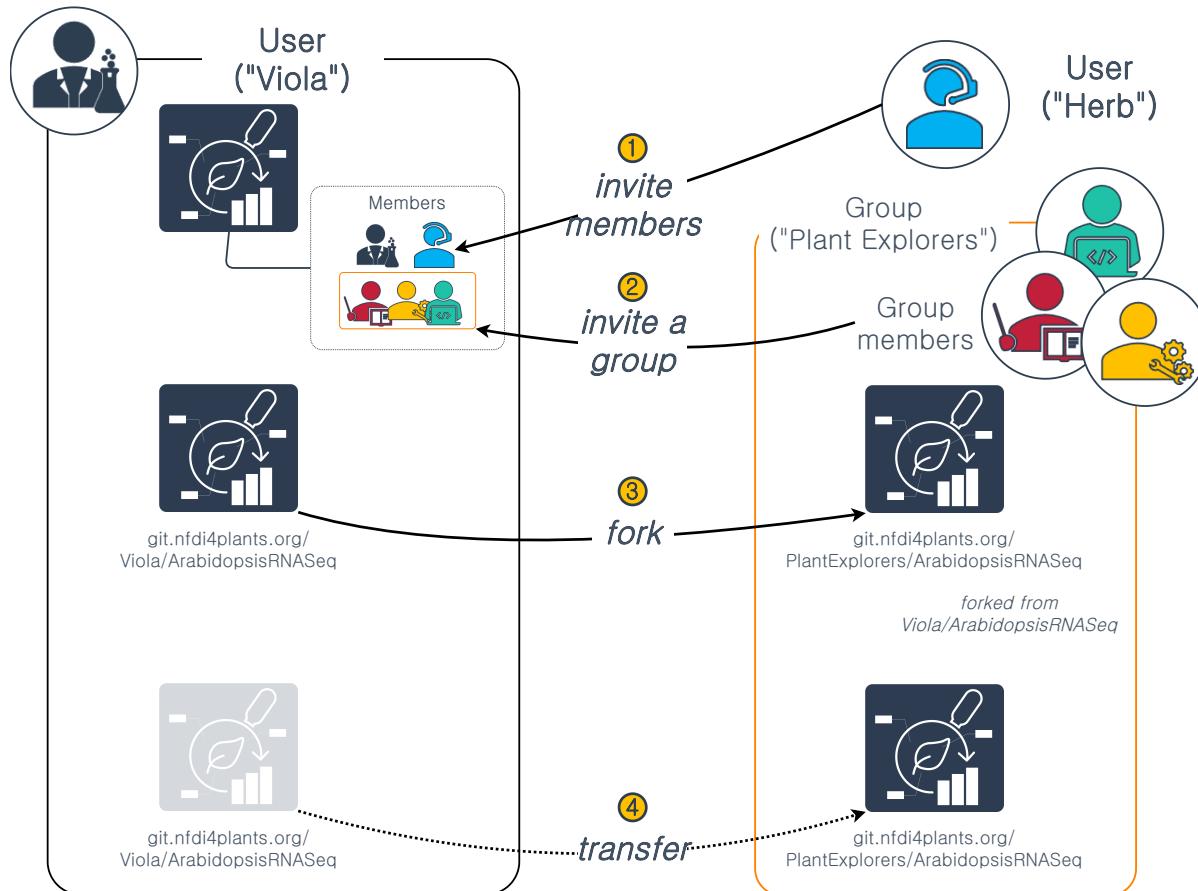
Project = ARC

- 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 elements highlighted:

- Project sidebar (left):** Includes sections for Project, Manage (1), Plan (2), Code (3), Build, Secure, Deploy, Operate, Monitor, Analyze, Settings (4), and Help.
- Header:** Shows the current user (Demo User) and repository (Demo_ARC). A search bar is also present.
- Project title:** "Demo_ARC" with a lock icon (5).
- Code dropdown menu:** Contains options like History, Find file, Edit, and Code (selected) (8).
- Commit list:** Shows a single commit named "arc init" authored by Demo User 4 minutes ago. The commit ID is 7a8c9714. The list also includes .gitignore and isa.investigation.xlsx files.
- Project information sidebar (right):** Displays statistics such as 1 Commit, 2 Branches, 0 Tags, 7 KIB Project Storage, and Auto DevOps status. It also lists optional additions like README, LICENSE, CHANGELOG, CONTRIBUTING, Kubernetes cluster, Wiki, and Integrations.
- Created on:** July 13, 2024.

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

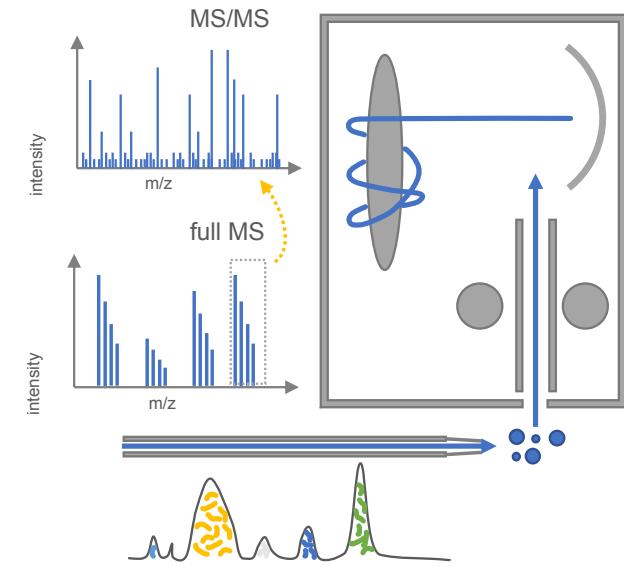
Save time using standard methods and SOPs

Parameter []

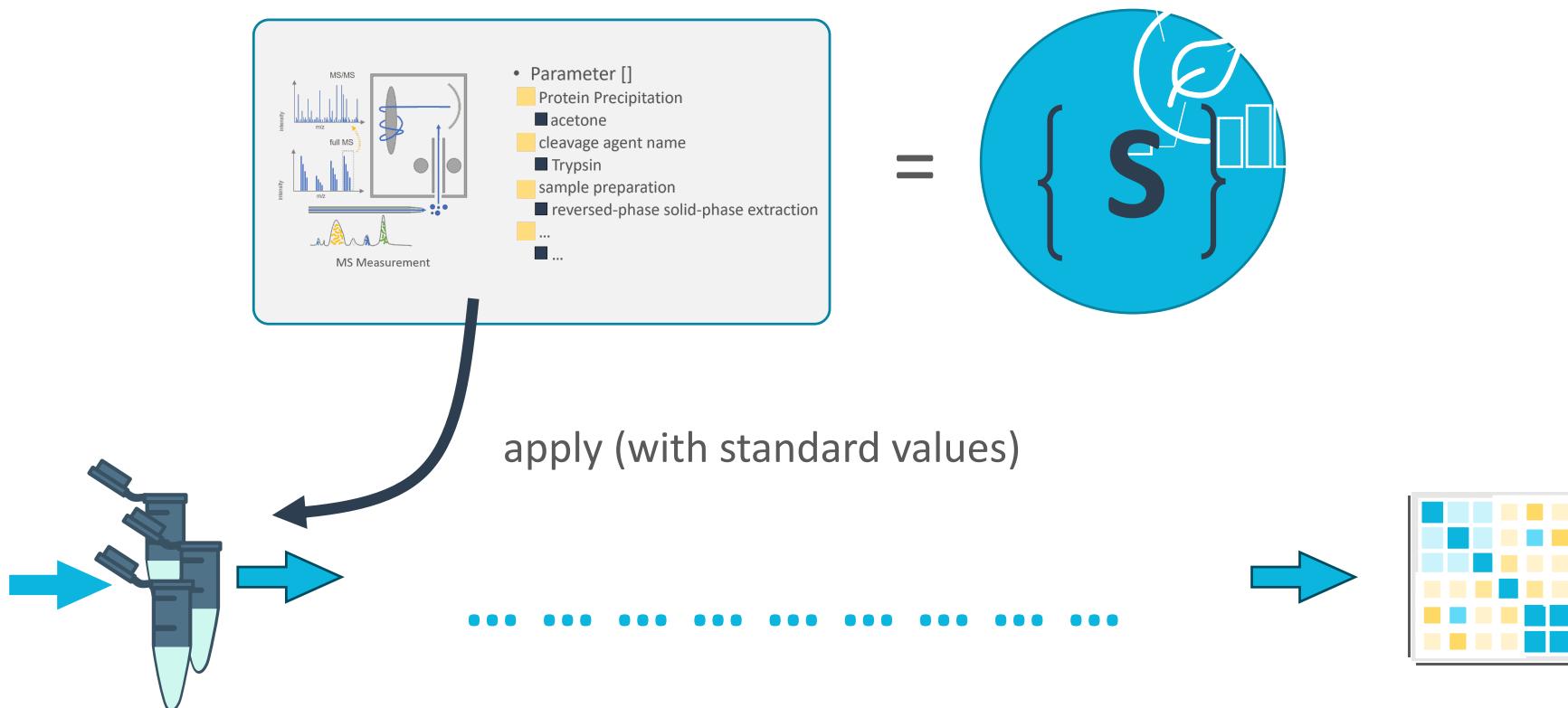
- Protein Precipitation
 - acetone
- cleavage agent name
 - Trypsin
- sample preparation
 - reversed-phase solid-phase extraction
- ...

Component []

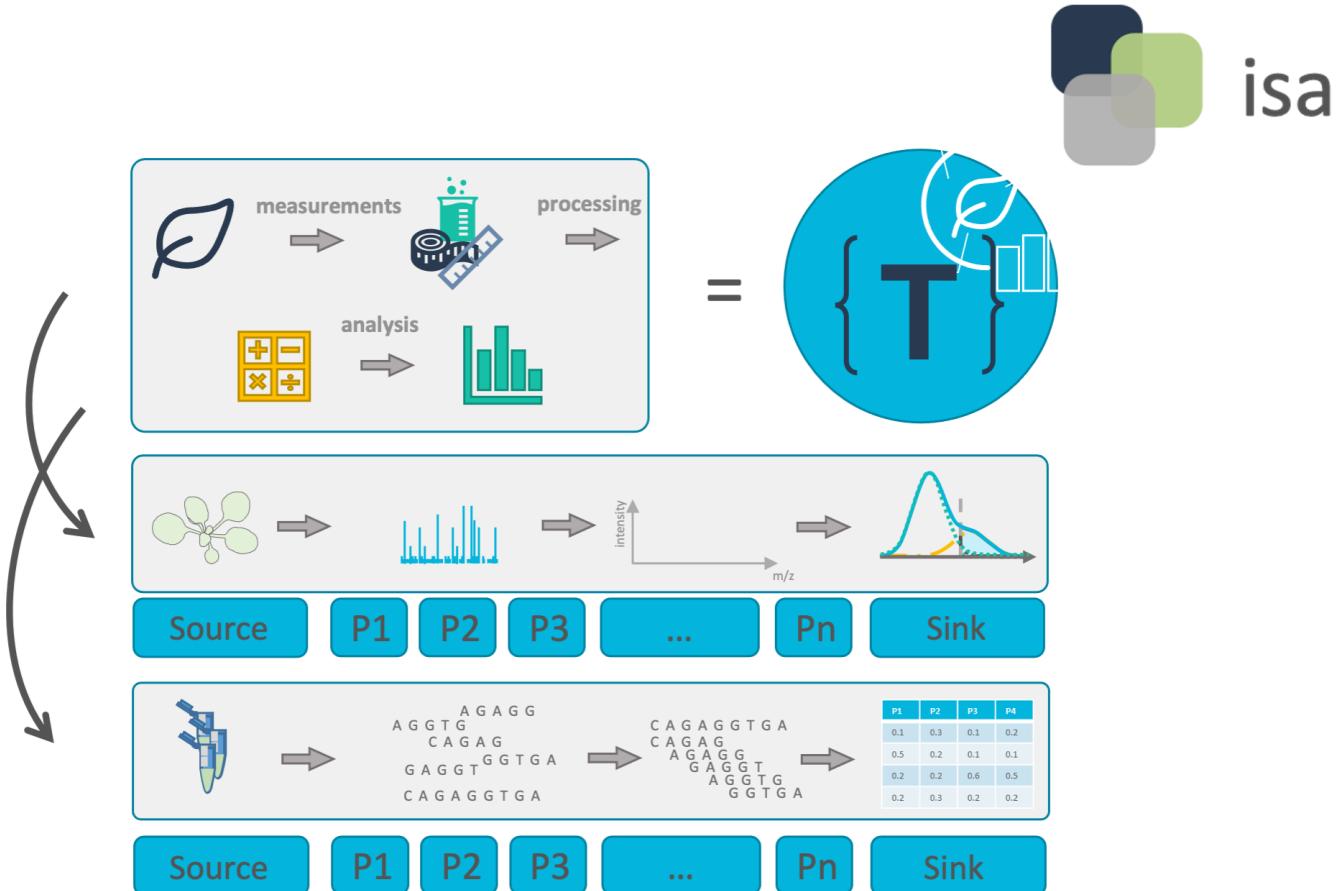
- chromatography instrument model
 - nanoElute2
- chromatography column model
 - PepSep C18 1.9u, 25cm x 75um ...



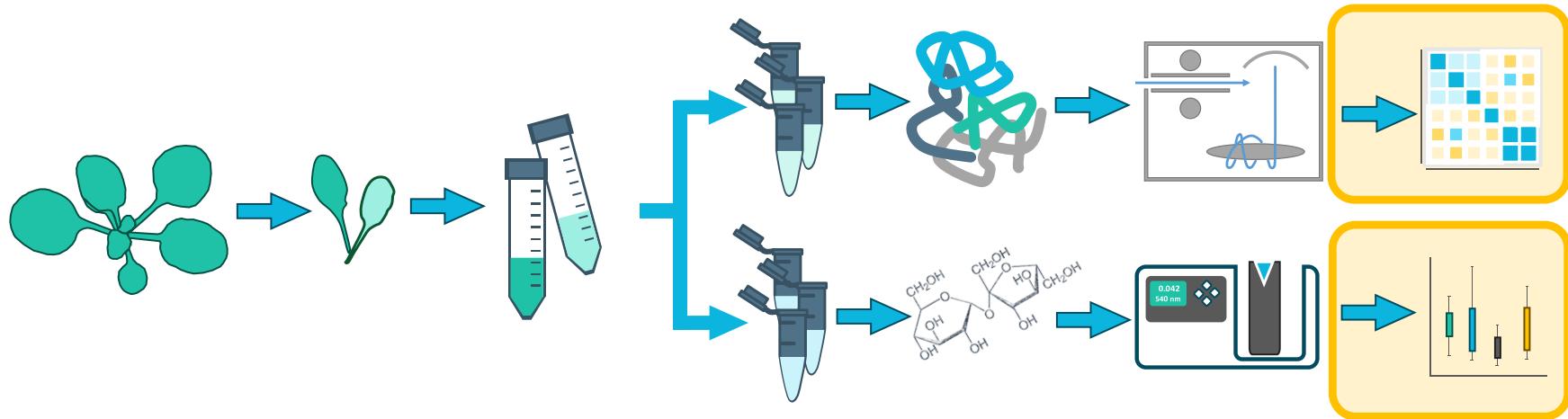
Applying standard procedures to sample record



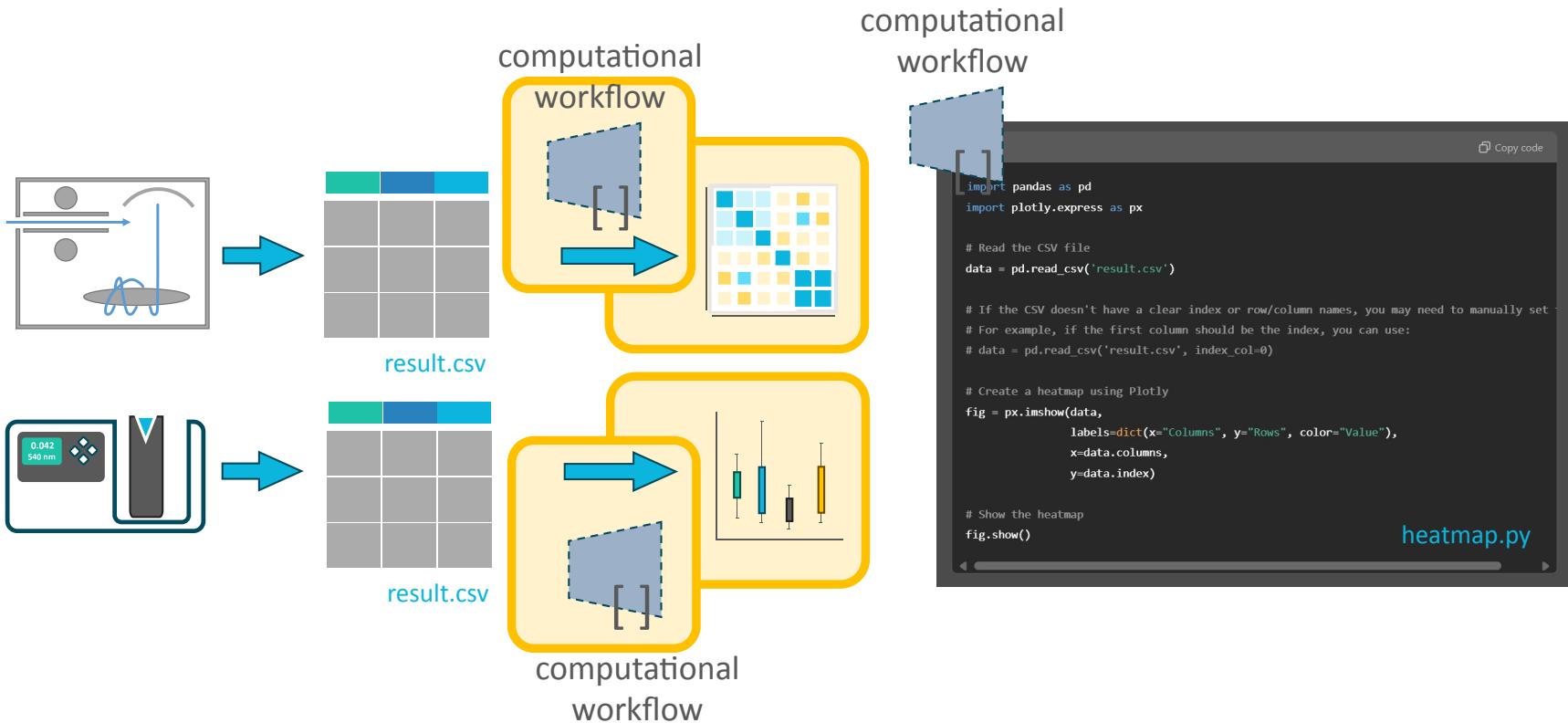
Realization of lab-specific metadata with templates



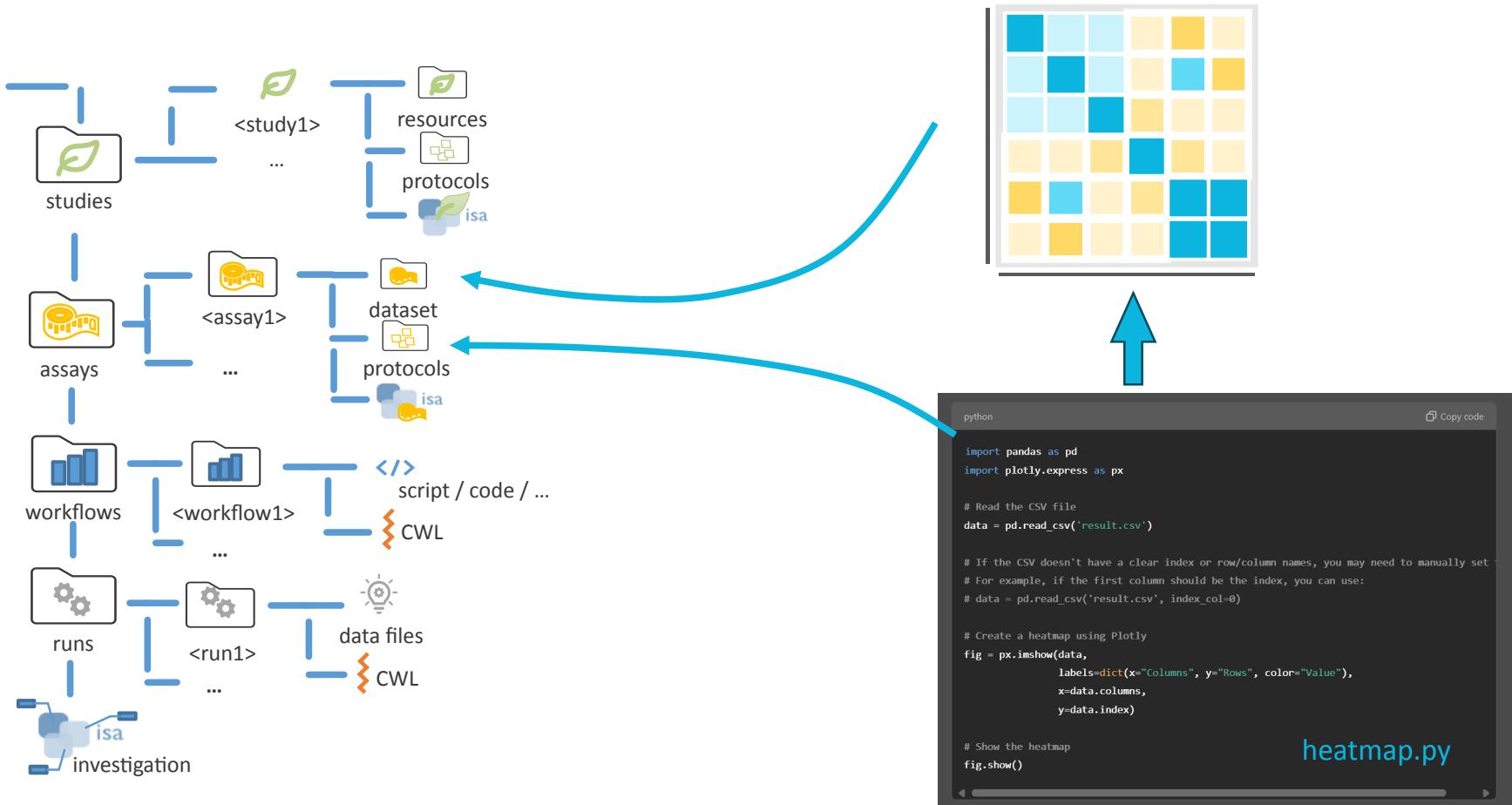
Options to annotate the data analysis



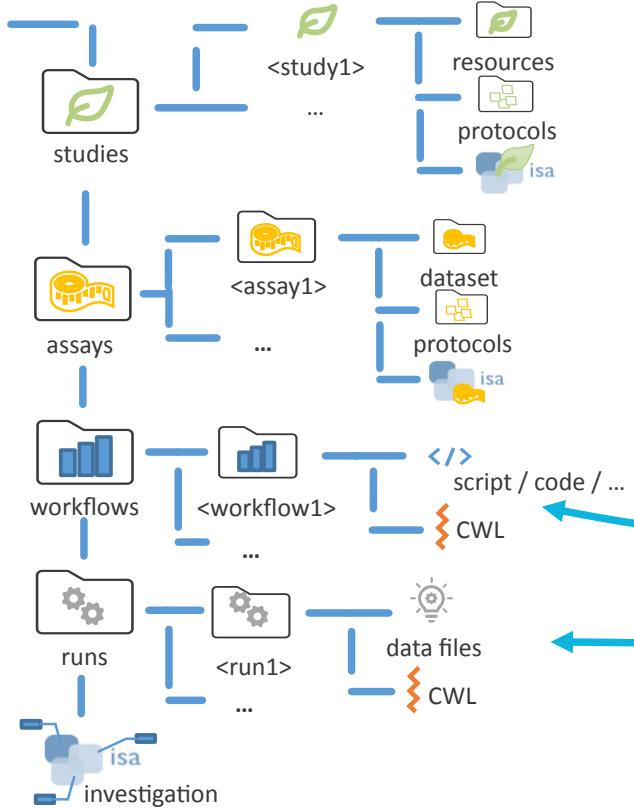
A computational workflow is like a protocol



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:

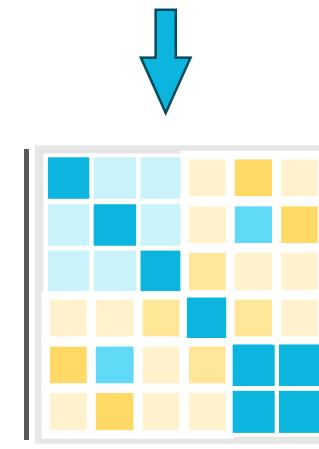
```
python
import pandas as pd
import plotly.express as px

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

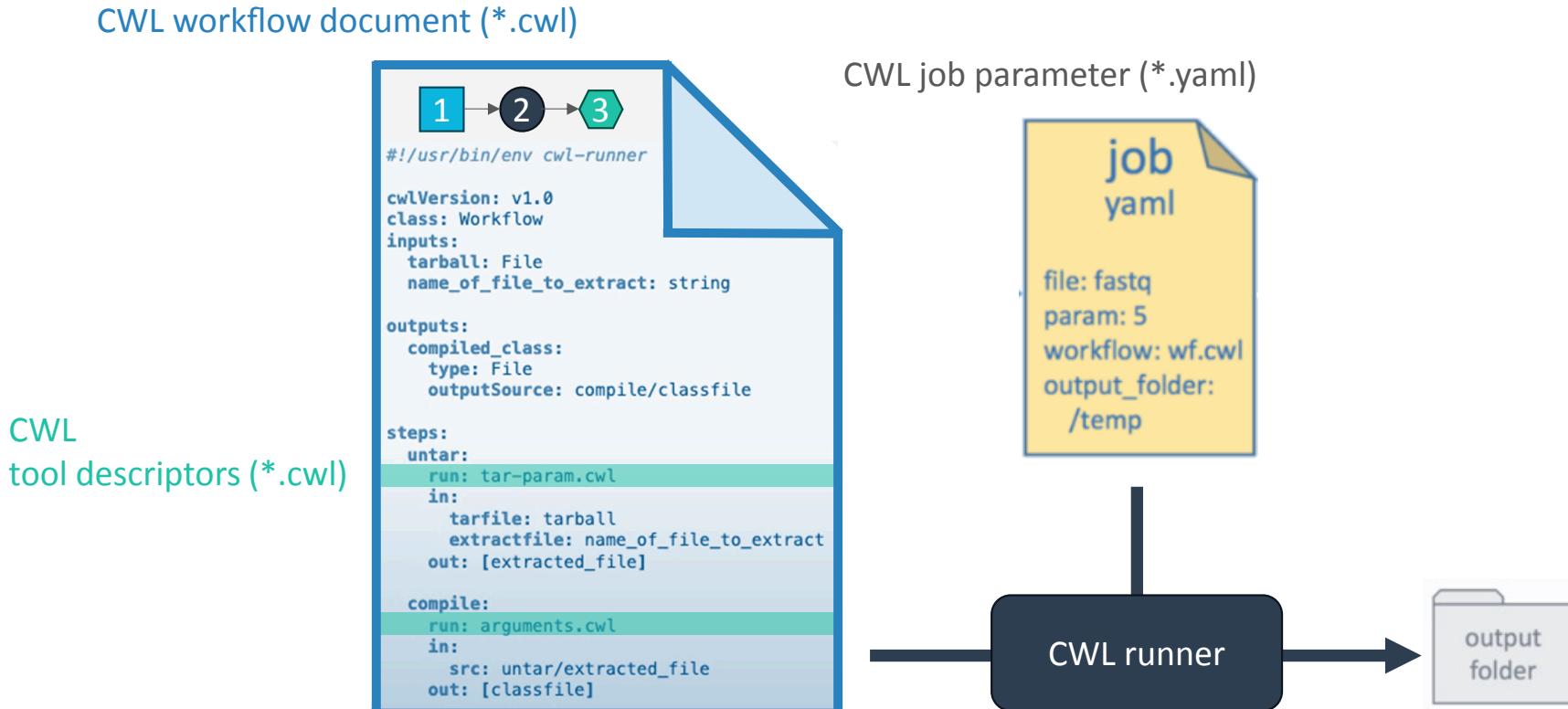
# If the CSV doesn't have a clear index or row/column names, you may need to manually set
# For example, if the first column should be the index, you can use:
# data = pd.read_csv('result.csv', index_col=0)

# 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

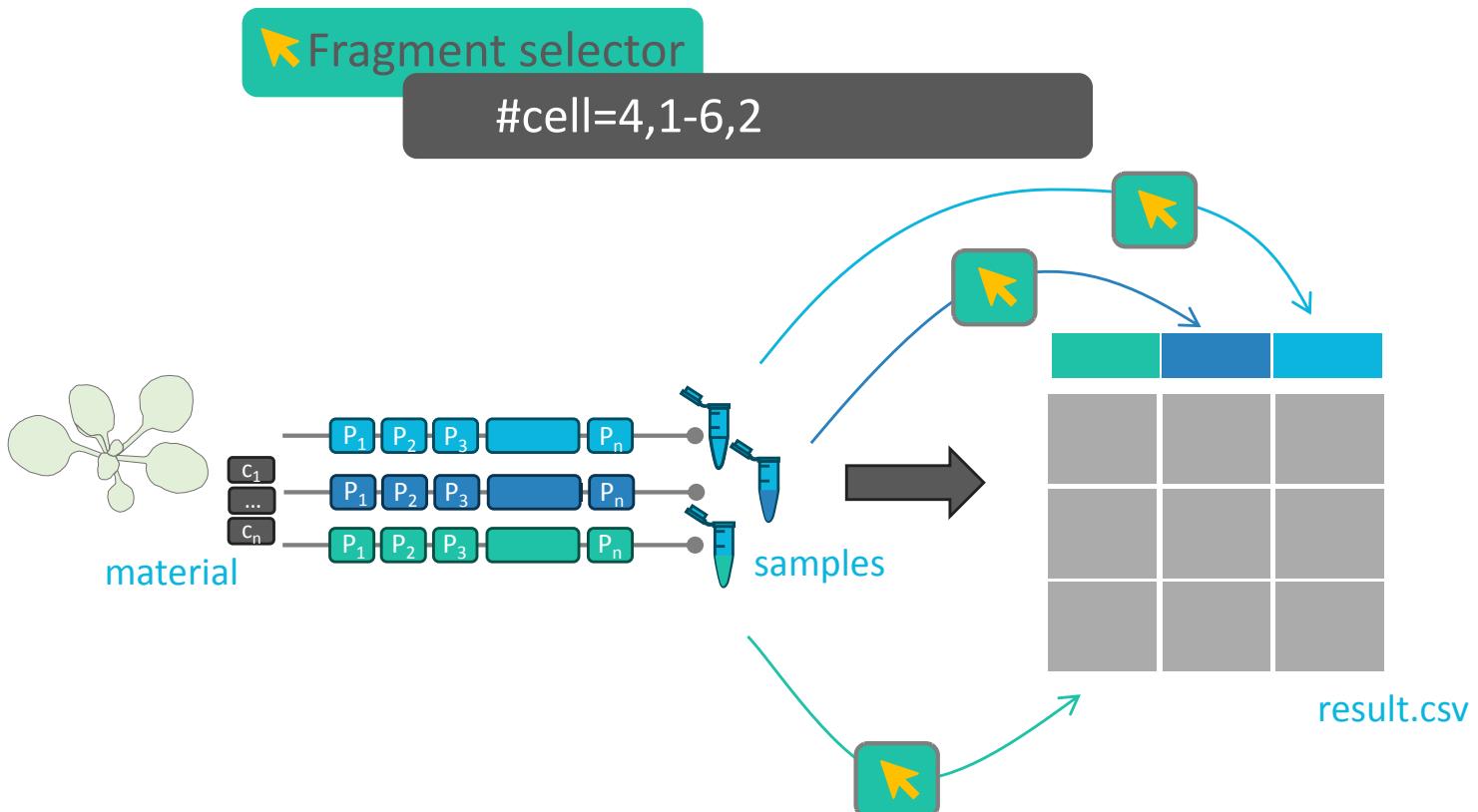


DataMAPs

Mechanisms to annotate the result data

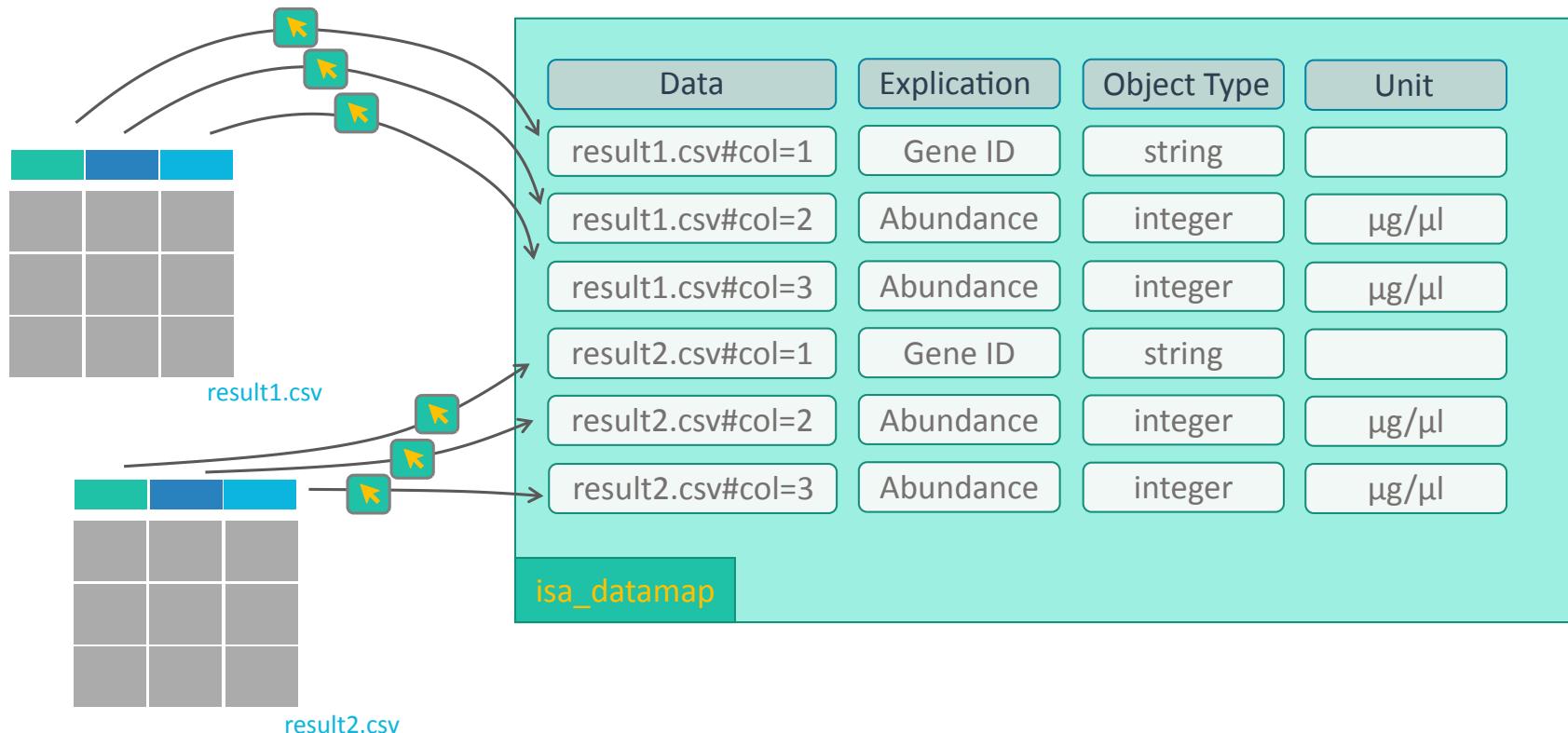
Point into results – Fragment selectors

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

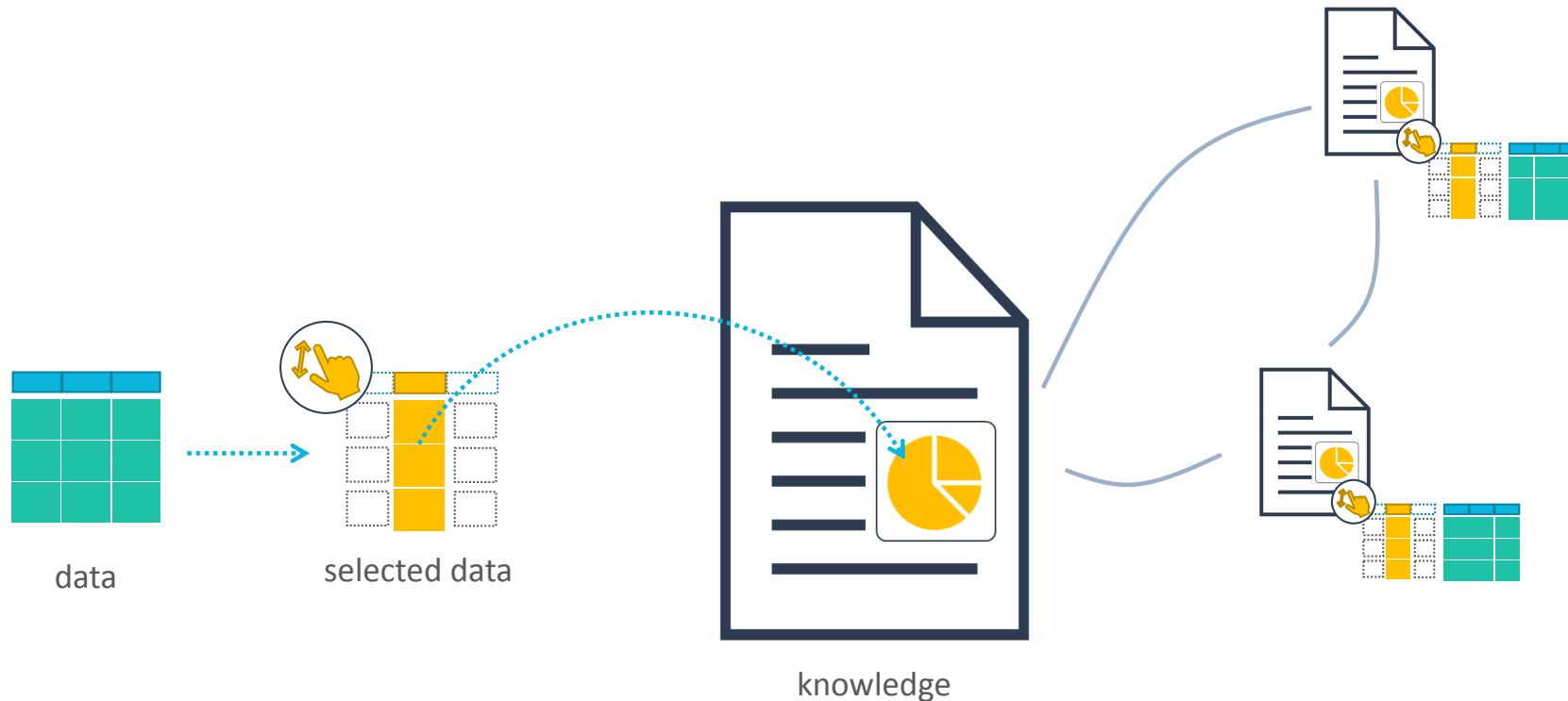
Validate and publish your ARC



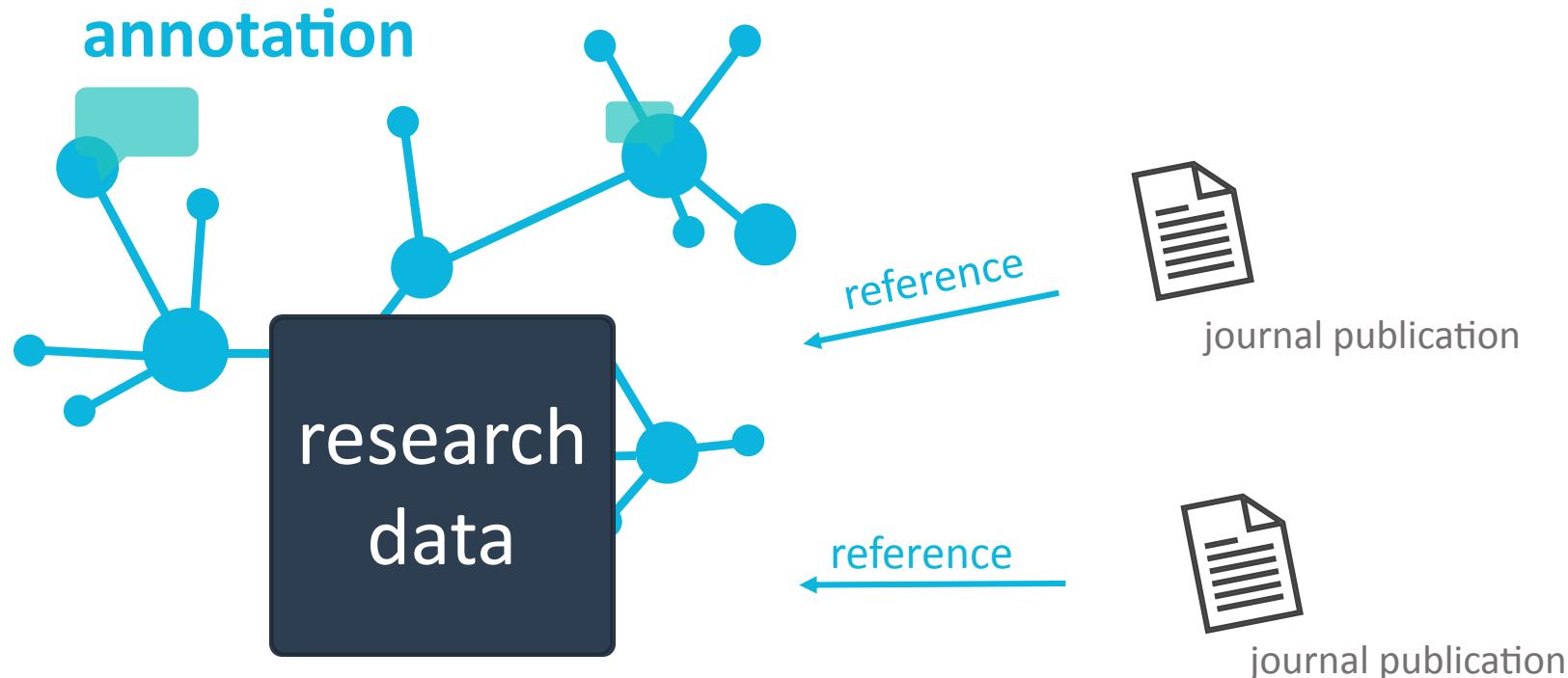
Hands-on

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

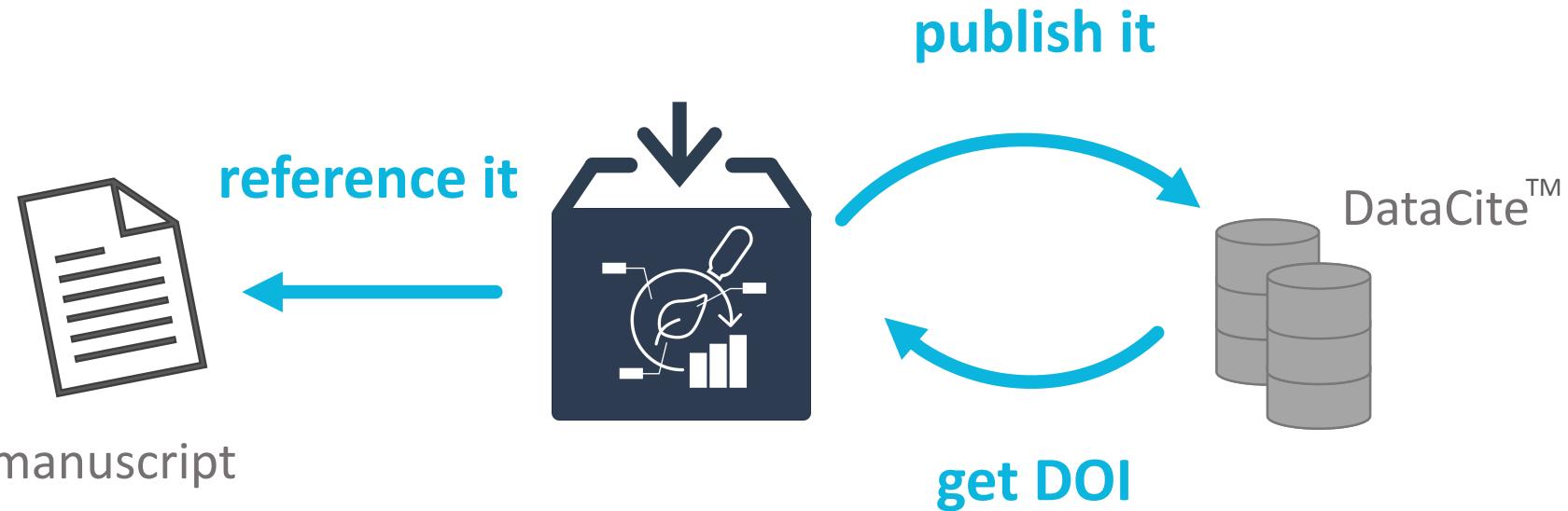
ARC data publication



Moving from paper to data publications



Publish your ARC, get a DOI



Publish your ARC with a few clicks

 **Ru_ChlamyHeatstress** 

Project ID: 122 

 Star 1

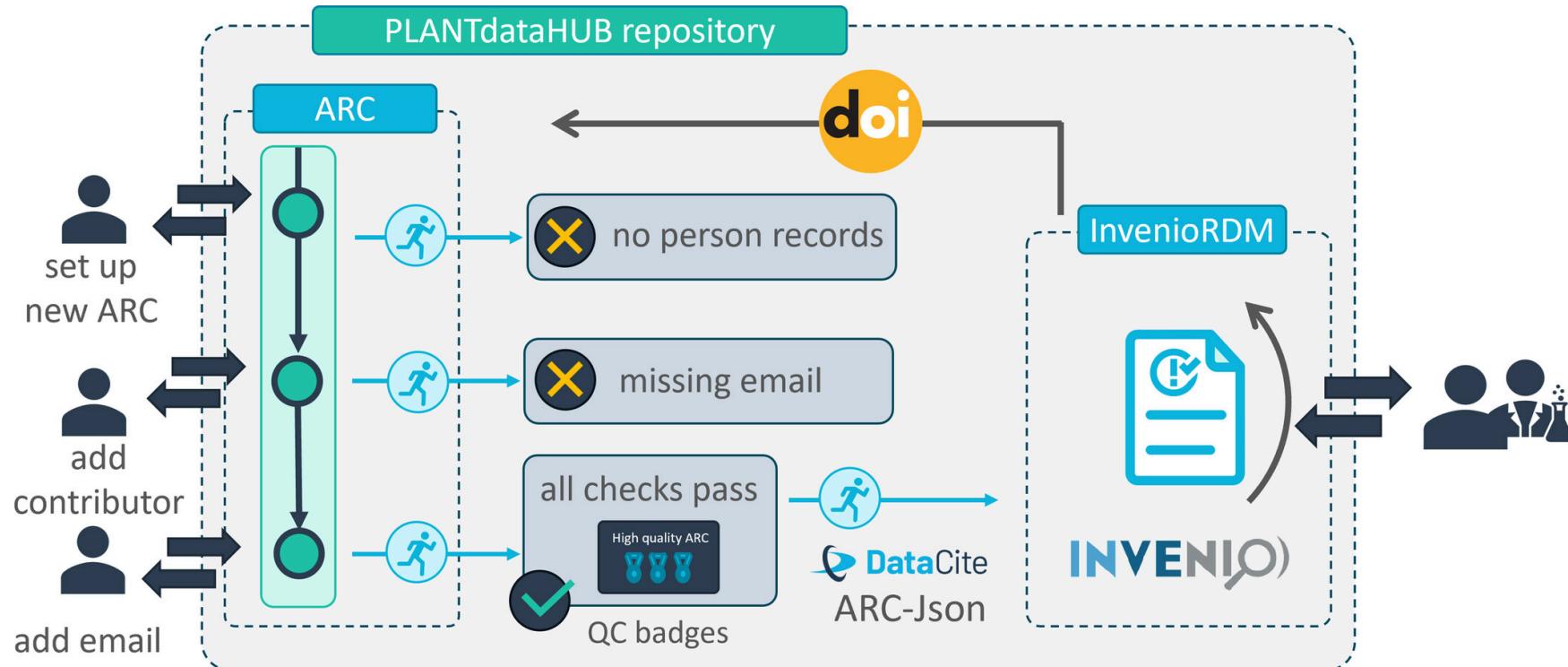
-o 53 Commits  1 Branch  0 Tags  293.9 GB Project Storage

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  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 10/10

-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; Czymmek, 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., Czymmek, 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

Description

hosted on: <https://git.nfd4plants.org/projects/122>

Files

arc-summary.md

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

File contents:

- root
 - isa.investigation.xlsx
 - README.md
 - runs

Check point 4

Task

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

Resources



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<https://nfdi4plants.github.io/events/arc-user-support/>
- User Support Mailing List: [Click here to subscribe](#)

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

Acknowledgements



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- Jonas Lukasczyk

Team Freiburg

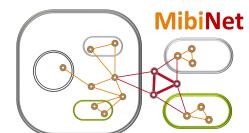
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- Jonathan Bauer
- Marcel Tschöpe
- Julian Weidhase

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