



# Tentative agenda

## Morning

Time	Topics
09:00 - 09:15	Welcome, Intro RDM and NFDI
09:15 - 09:45	Overview DataPLANT, and DataPLANT Tool chain
09:45 - 10:30	Hands-on ARCitect
10:30 - 10:45	<i>Short break</i> ☕
10:45 - 11:45	Intro and Hands-on DataHUB
11:45 - 12:00	Q & A

## Afternoon

Time	Topics
12:00 - 13:00	<i>Lunch break</i> 🍕
13:00 - 14:00	Intro and Hands-on Metadata annotation with SWATE
14:00 - 15:00	Create your own ARC
15:00 - 15:15	<i>Short break</i> ☕
15:15 - 16:30	Create your own ARC
16:30 - 17:00	Q & A and wrap-up

# House-keeping

- Use the [pad](#) to raise questions and feedback
- Copy / paste links (hands-on)

# Training Materials

Slides are shared via [DataPLANT Training Material](#)

# Resources – join the open source movement

## DataPLANT (nfdi4plants)

DataPLANT Website: <https://nfdi4plants.org/>

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

DataHUB: <https://git.nfdi4plants.org>

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

HelpDesk: <https://helpdesk.nfdi4plants.org>

 You can help us by raising issues, bugs, ideas...

 NEW! ARC website: <https://arc-rdm.org>

# Continuous support

Data managers in Düsseldorf, Cologne, Jülich and close by (CEPLAS, MibiNet, TRR341) offer support.

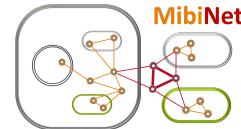
1. Slack Workspace for ad hoc support
2. Monthly user meeting (2nd Friday of the month)

→ [Details](#).



trr\_341

plant  
ecological  
genetics



# Introduce yourself

- Lab
- MibiNet / CEPLAS / TRR / ?
- Used code / programming language before
- Experience with Git / GitLab / GitHub?
- Have an ORCID
- My motivation / expectation
- My favorite lab assay

# Let's draw a typical lab workflow



# BYOD – Goals

- First few steps into ARC ecosystem
- Move existing datasets into ARCs
- Share them via the DataHUB
- Annotate with metadata
- Introduction into elabFTW
- elab2ARC tool

# FAIR data stewardship

- Findable
- Accessible
- Interoperable
- Reusable

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

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

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

## The FAIR Guiding Principles for scientific data management and stewardship

[Mark D. Wilkinson](#), [Michel Dumontier](#), [IJsbrand Jan Aalbersberg](#), [Gabrielle Appleton](#), [Myles Axton](#), [Arie Baak](#), [Niklas Blomberg](#), [Jan-Willem Boiten](#), [Luiz Bonino da Silva Santos](#), [Philip E. Bourne](#), [Jildau Bouwman](#), [Anthony J. Brookes](#), [Tim Clark](#), [Mercè Crosas](#), [Ingrid Dillo](#), [Olivier Dumon](#), [Scott Edmunds](#), [Chris T. Evelo](#), [Richard Finkers](#), [Alejandra Gonzalez-Beltran](#), [Alasdair J.G. Gray](#), [Paul Groth](#), [Carole Goble](#), [Jeffrey S. Grethe](#), [Jaap Heringa](#), [Peter A.C. 't Hoen](#), [Rob Hooft](#), [Tobias Kuhn](#), [Ruben Kok](#), [Joost Kok](#), [Scott J. Lusher](#), [Maryann E. Martone](#), [Albert Mons](#), [Abel L. Packer](#), [Bengt Persson](#), [Philippe Rocca-Serra](#), [Marco Roos](#), [Rene van Schaik](#), [Susanna-Assunta Sansone](#), [Erik Schultes](#), [Thierry Sengstag](#), [Ted Slater](#), [George Strawn](#), [Morris A. Swertz](#), [Mark Thompson](#), [Johan van der Lei](#), [Erik van Mulligen](#), [Jan Velterop](#), [Andra Waagmeester](#), [Peter Wittenburg](#), [Katherine Wolstencroft](#), [Jun Zhao](#) & [Barend Mons](#) 

— Show fewer authors

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

# The FAIR principles

<p><b>Findable</b> <b>Accessible</b> <b>Interoperable</b> <b>Reusable</b></p>	<p><b>Easier collaboration &amp; sharing</b></p> <pre>graph TD; A(( )) --&gt; B(( )); A(( )) --&gt; C(( )); A(( )) --&gt; D(( )); B(( )) --&gt; E(( )); C(( )) --&gt; E(( )); D(( )) --&gt; E(( ));</pre>	<p><b>Increased findability and visibility</b></p>	<p><b>Reproducibility</b></p>
<p><b>Added-value to the research community</b></p> <p>nfdi      NCBI EMBL-EBI</p>	<p><b>Compliance with funding policies</b></p> <pre>graph LR; A[Checkmark Icon] --- B[DFG Logo]; A --- C[EU Flag]</pre>	<p><b>Receive due credit</b></p> <p>FAIR</p> <p>Reuse</p> <p>Citations</p>	<p><b>Saves time &amp; workload</b></p> <p>FAIR</p> <p>Time wasted</p>

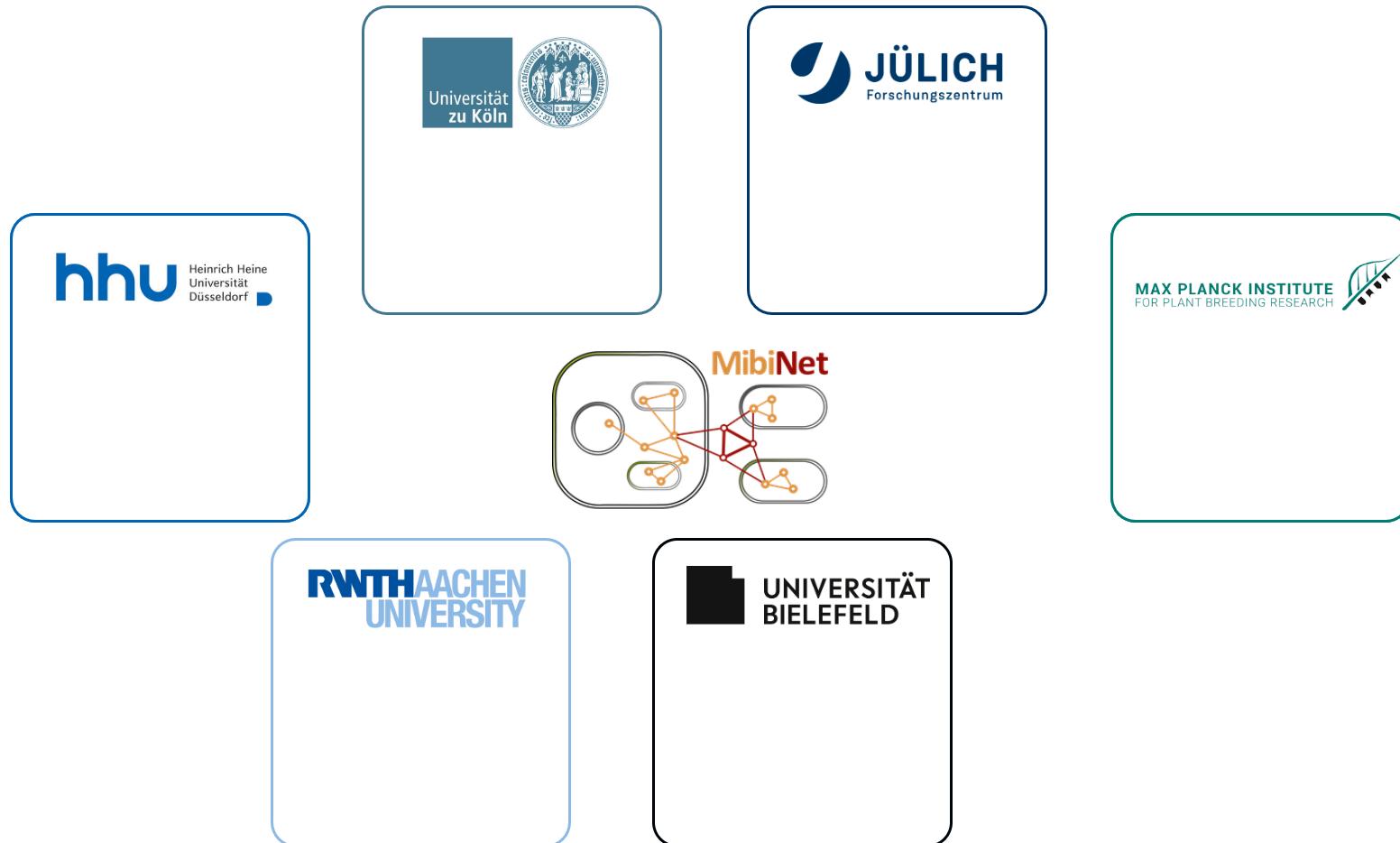
# Is your data FAIR?

Findable | Accessible | Interoperable | Reusable

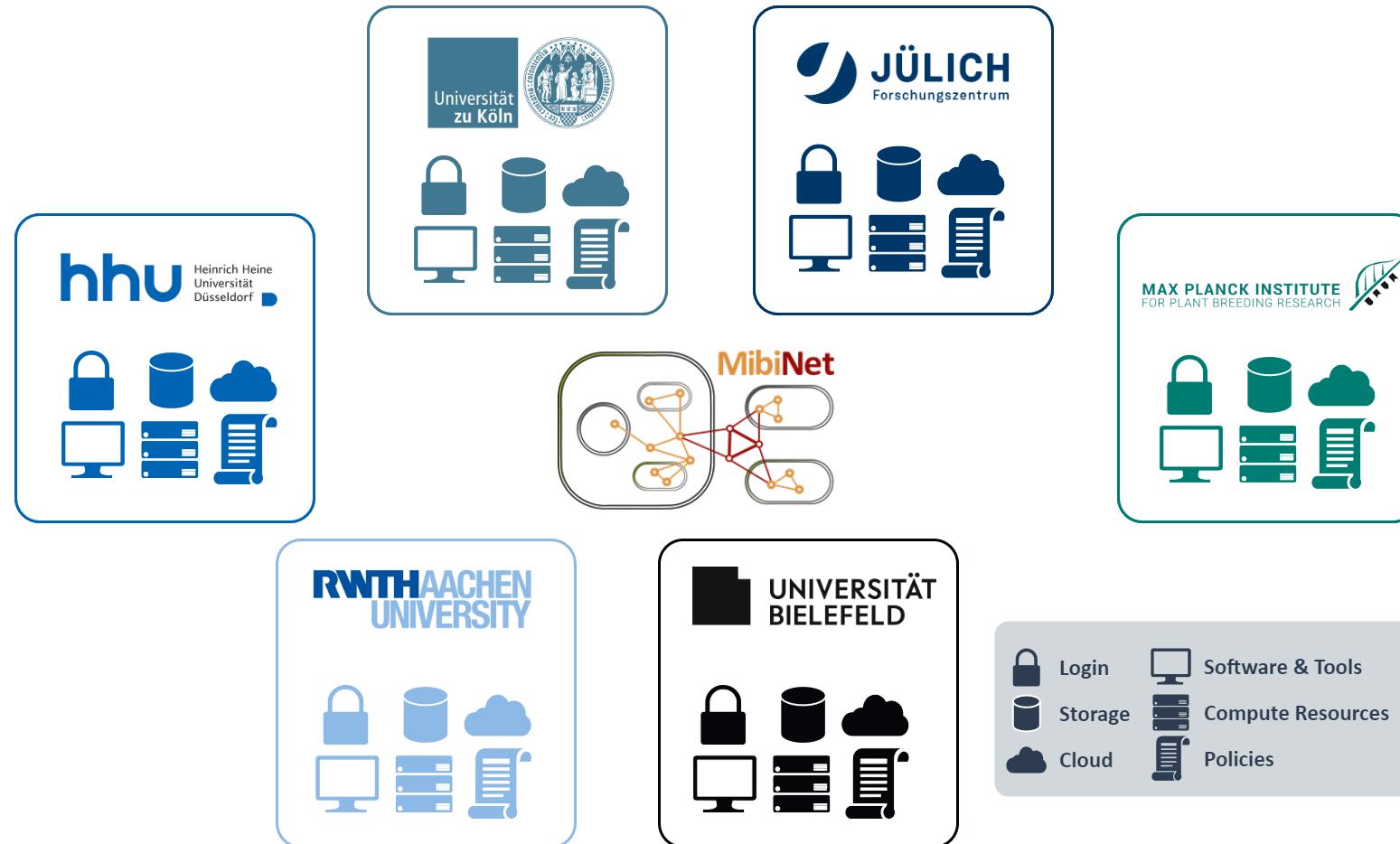
- Where do you store your data?
- How do you annotate your data?
- How do you share your data?
- What tools do you use to analyse your data?
- How do you reuse other people's data?



# MibiNet – One SFB, six locations

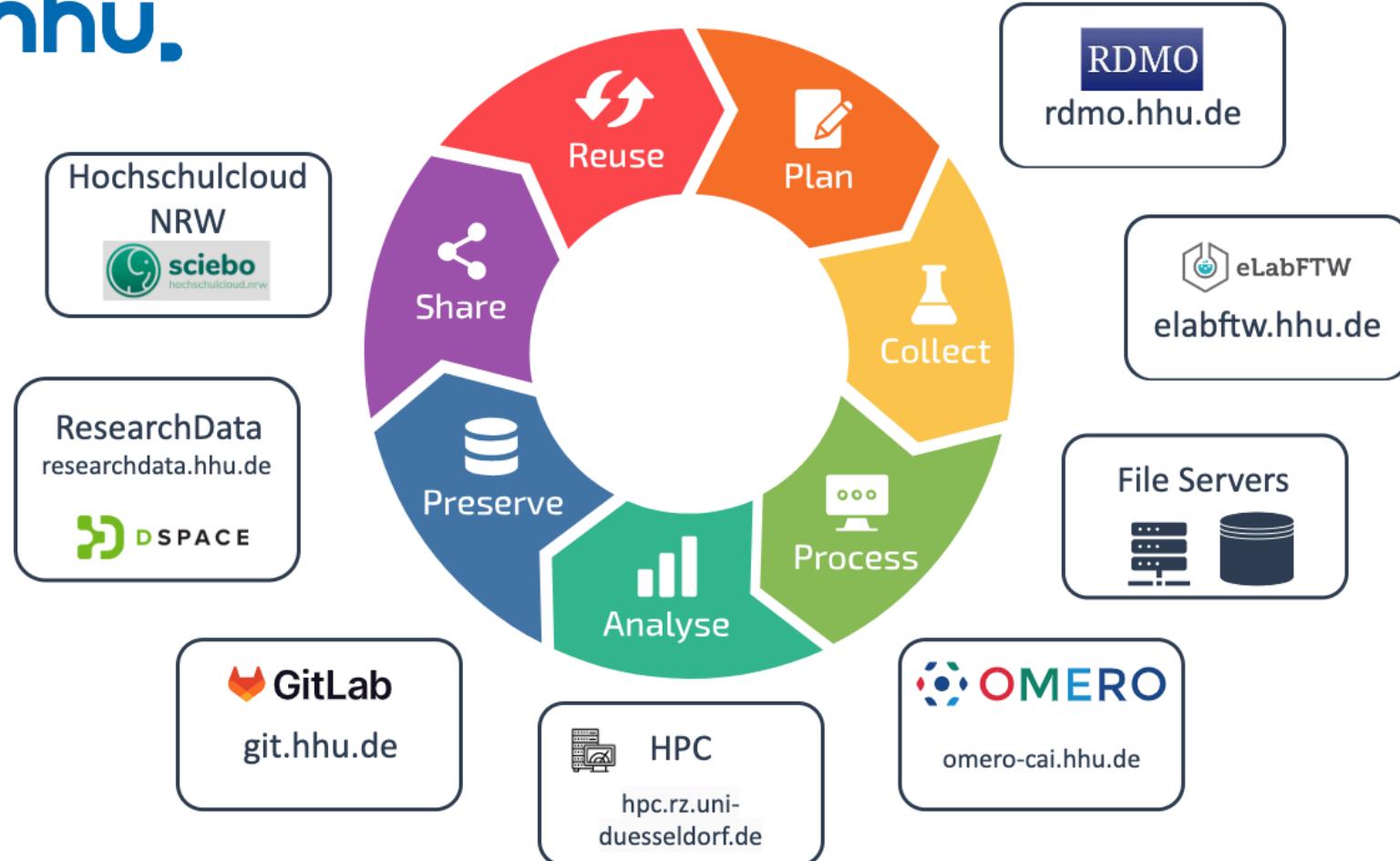


# Data silos impede collaboration



# Missing interfaces impede collaboration

hhu.



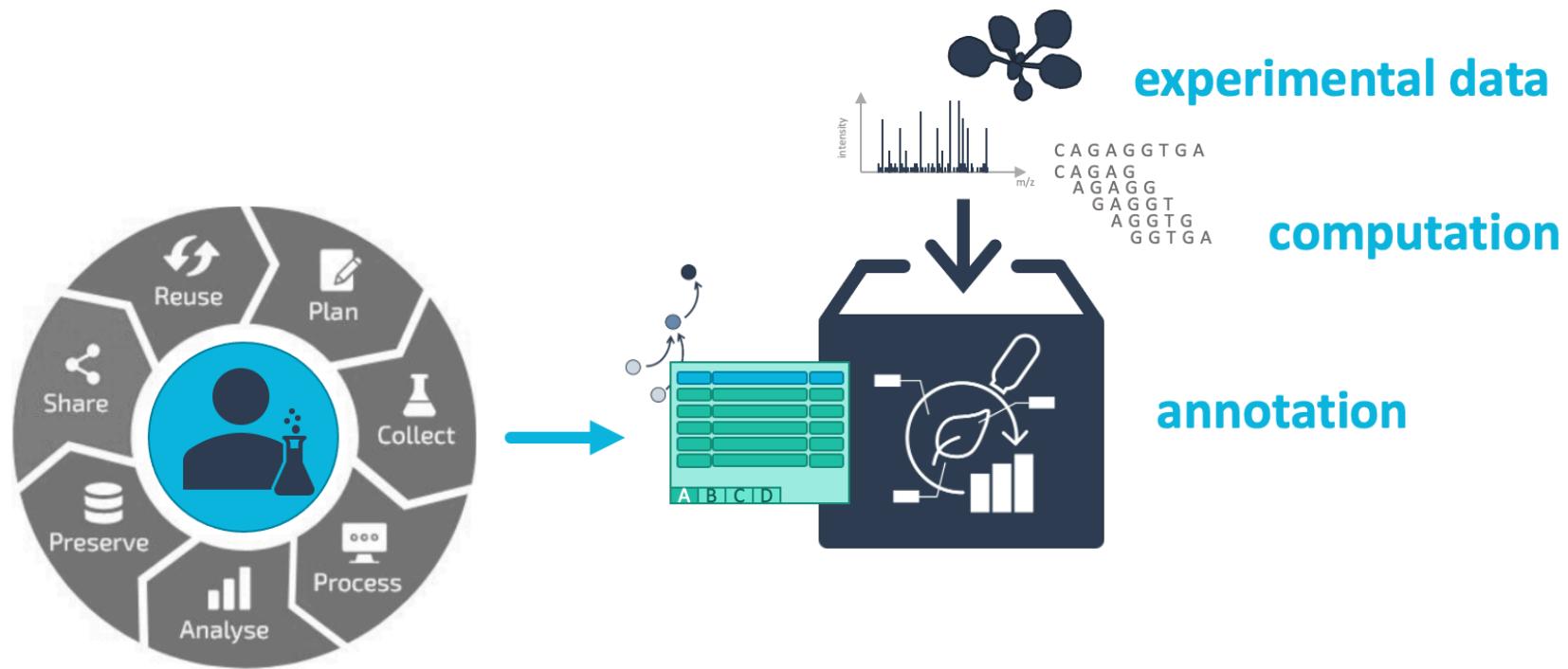
# MibiNet connection to NFDIs



# Data Stewardship between DataPLANT and the community

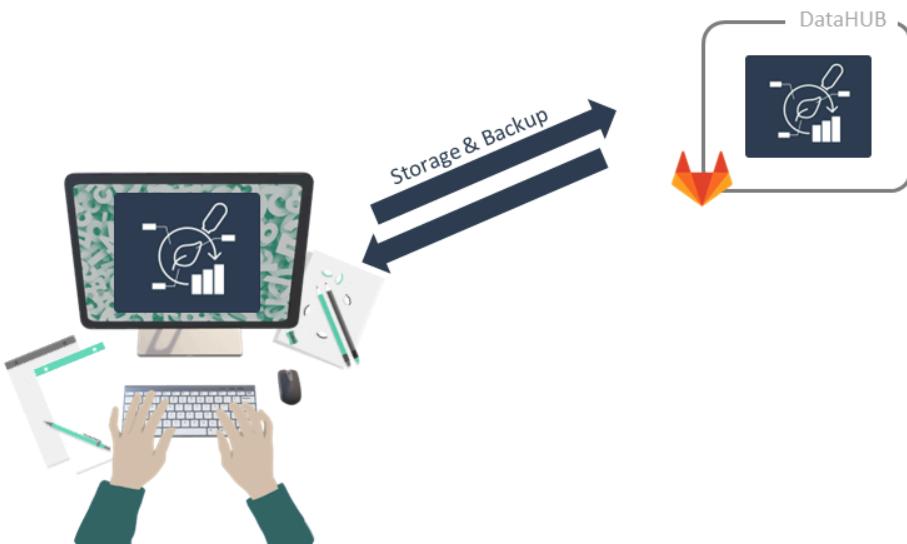


# Annotated Research Context (ARC)

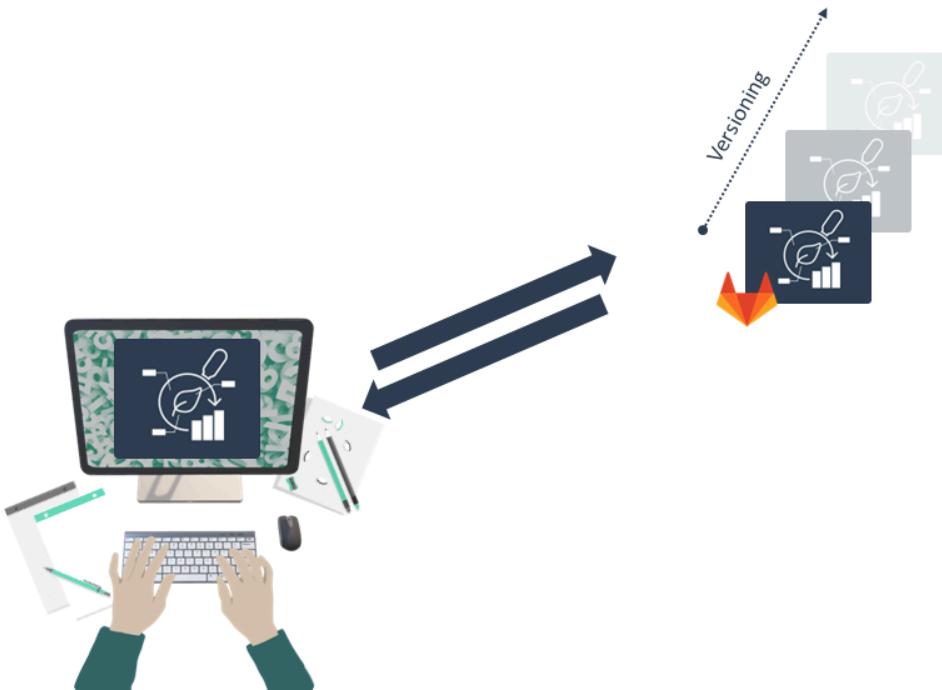


Your entire investigation in a single unified bag

# You can store your ARC in the DataHUB



# ARCs are versioned



# You can invite collaborators



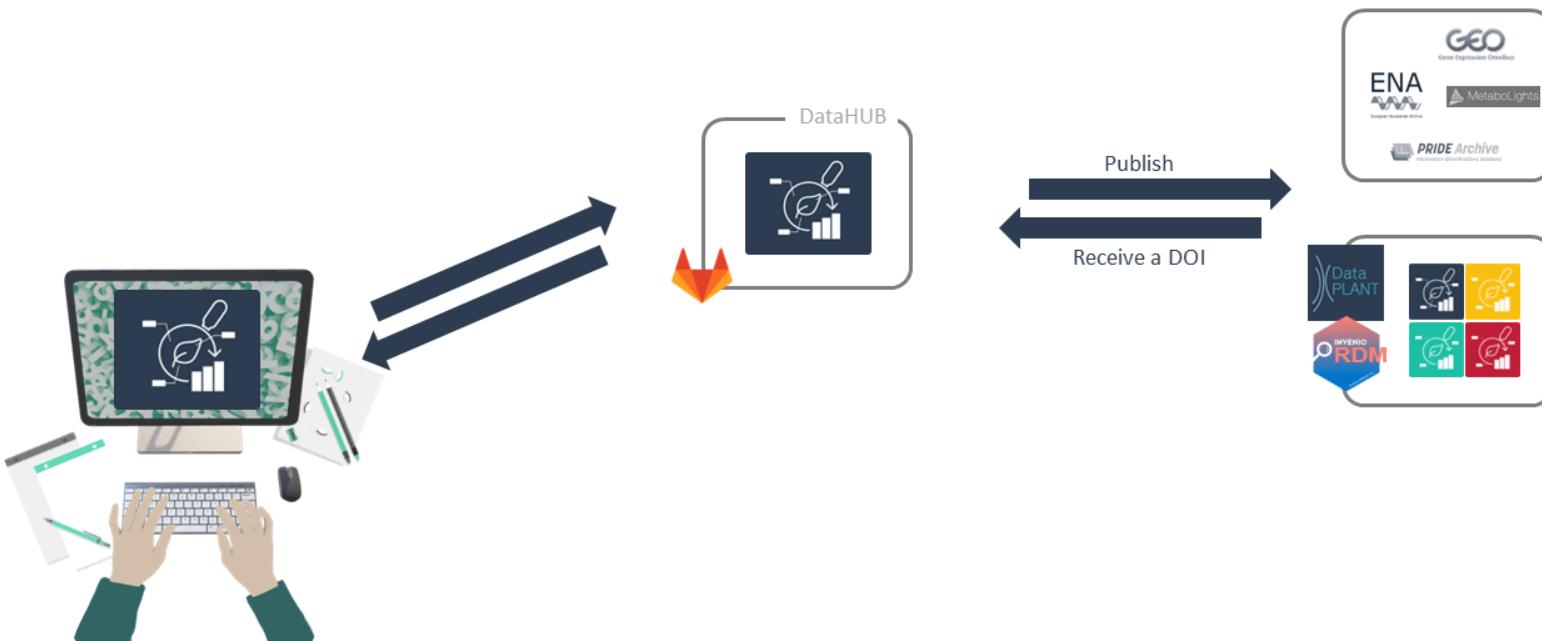
# Collaborate and contribute



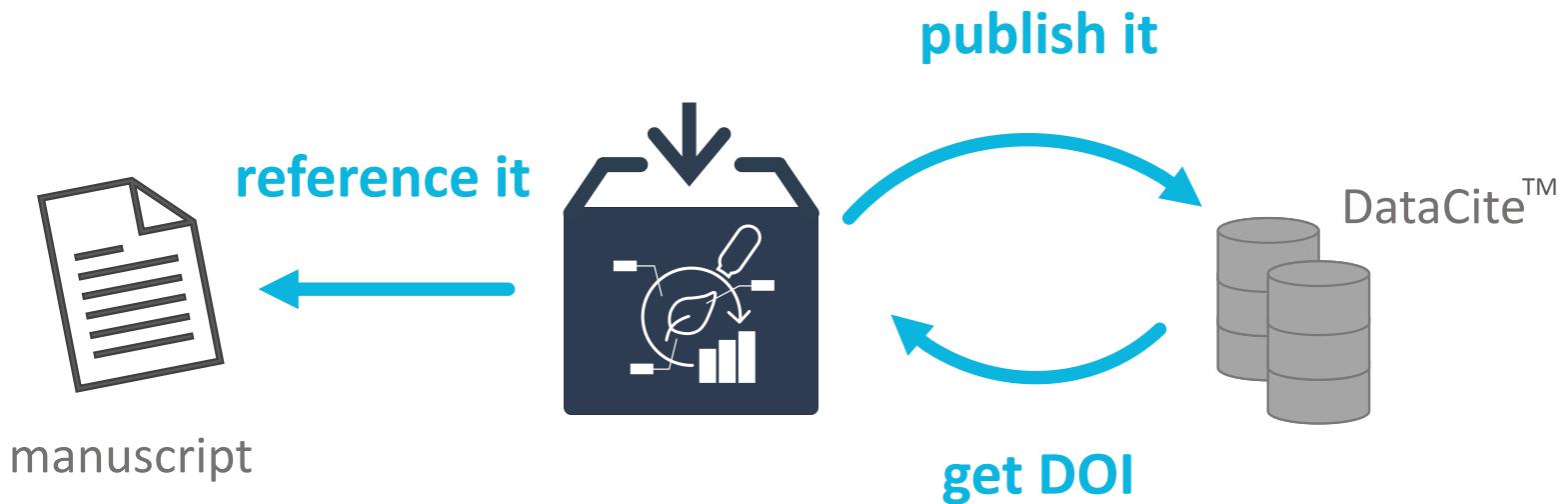
# Reuse data in ARCs



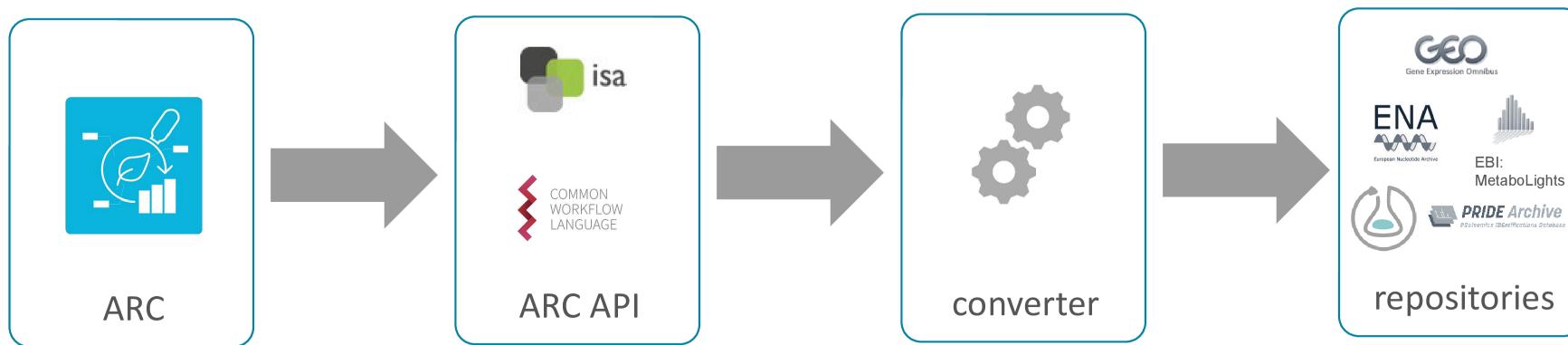
# Publish your ARC



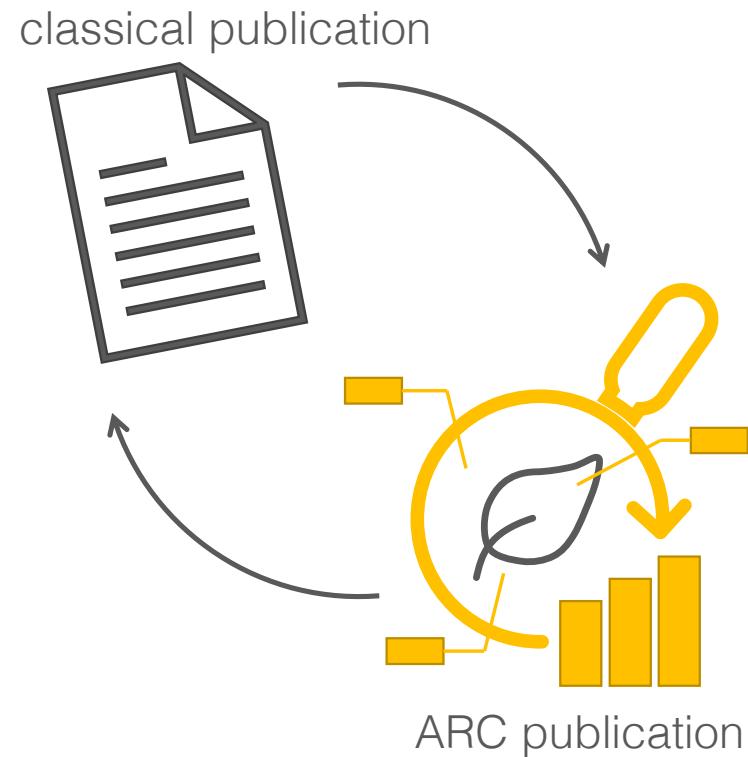
# Publish your ARC, get a DOI



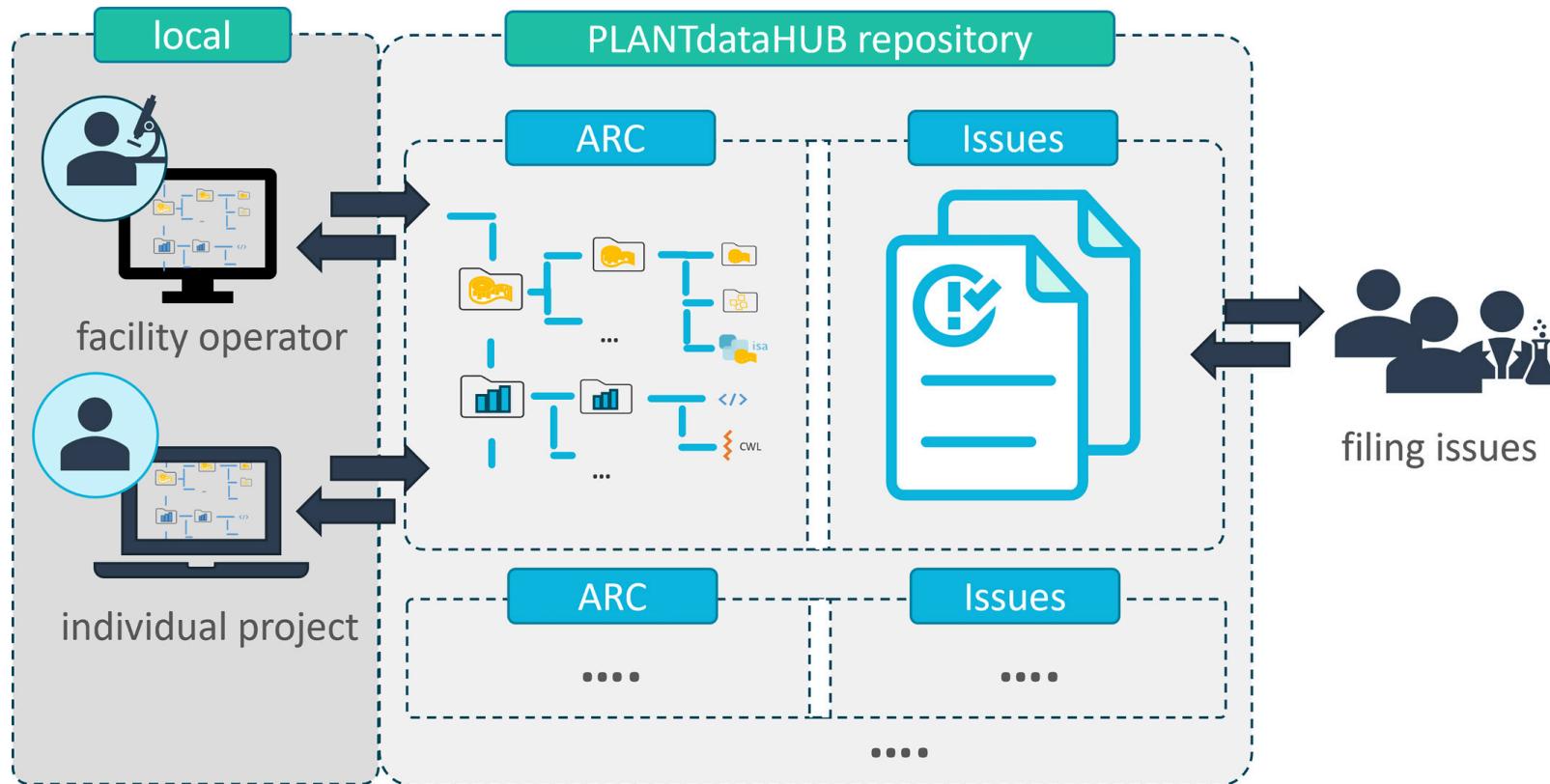
# From ARC to repositories



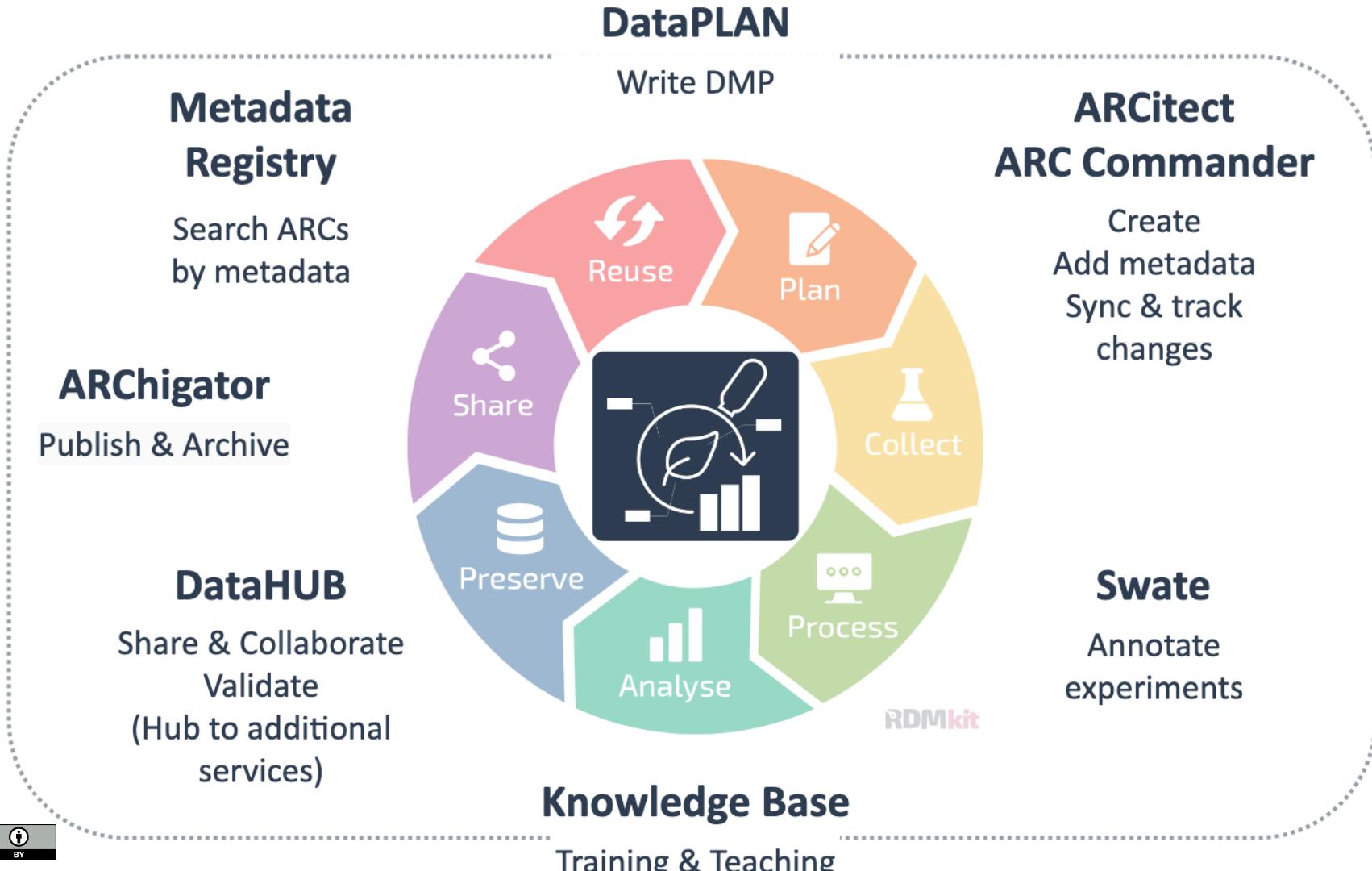
# Moving from paper to data publications



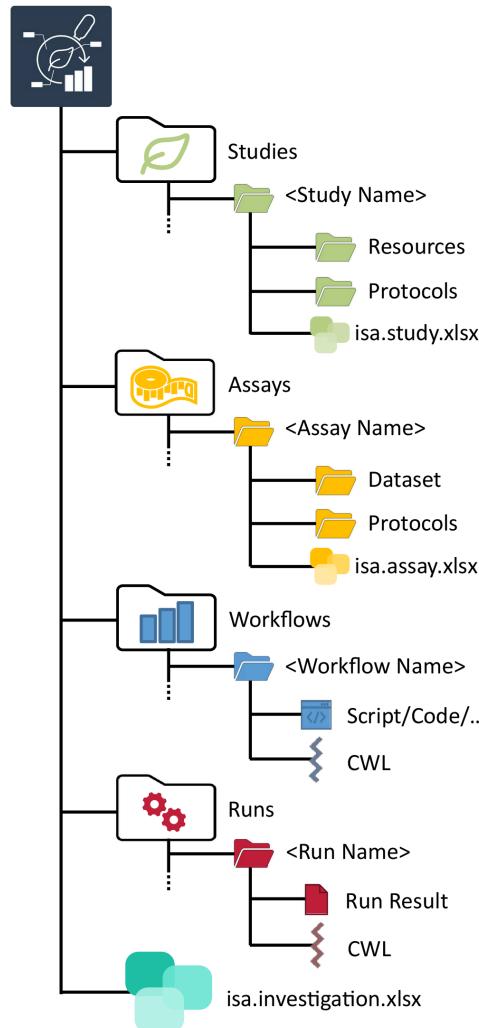
# Project management



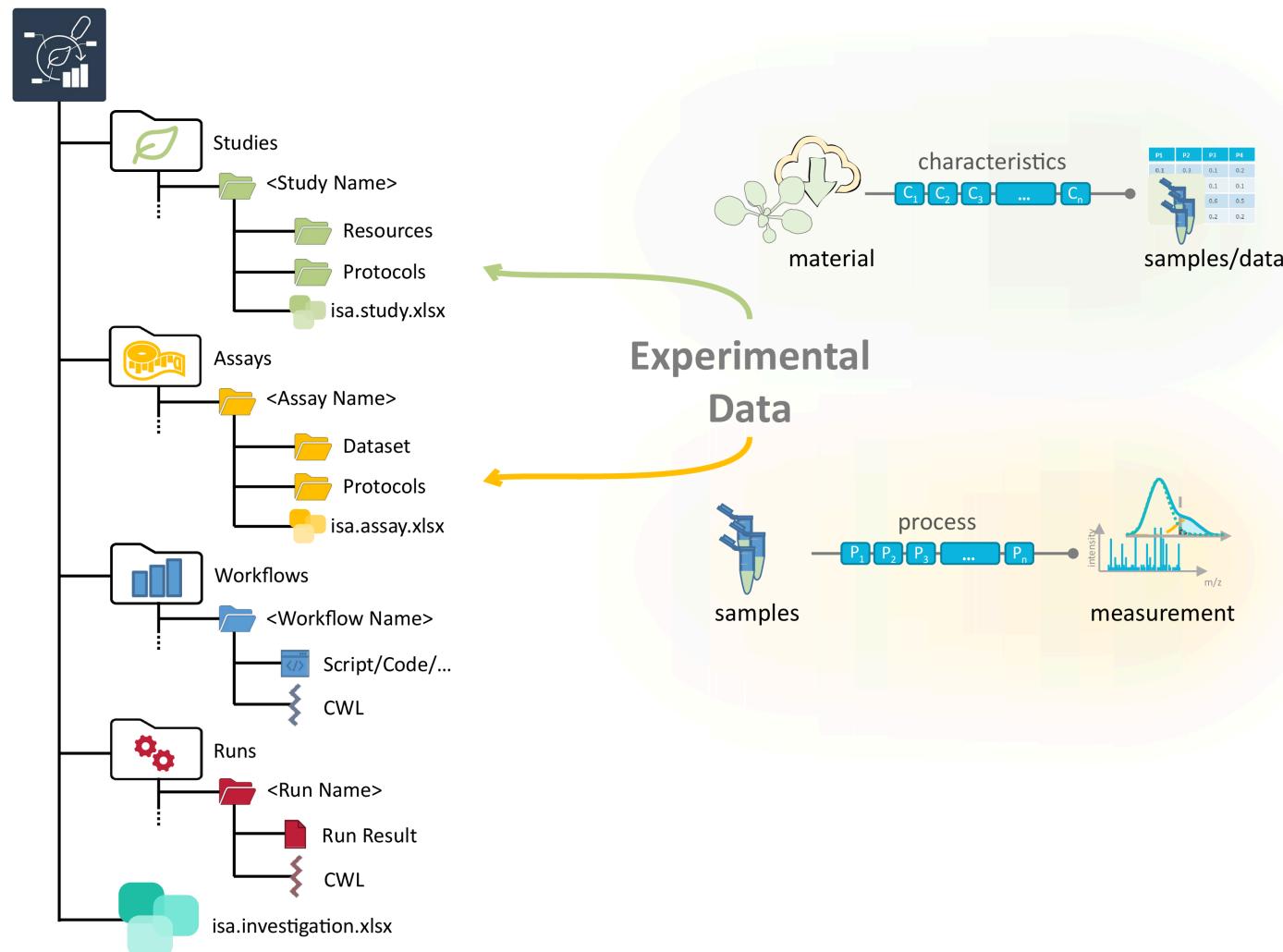
# The ARC ecosystem



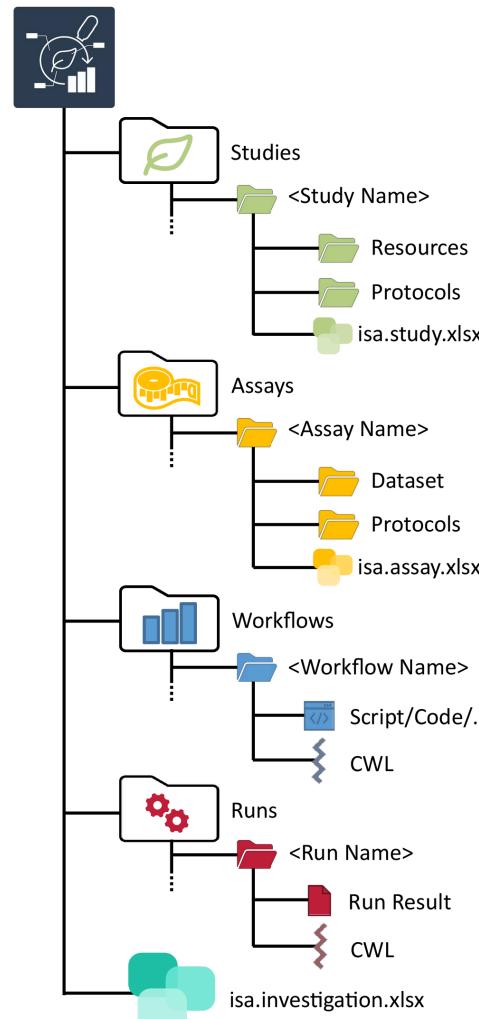
# What does an ARC look like?



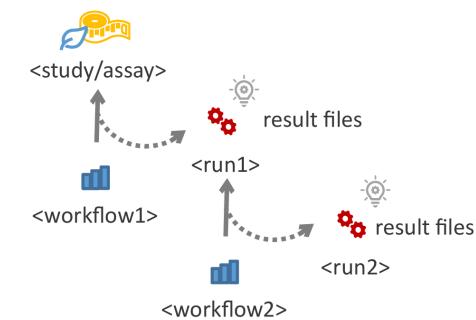
# ARCs store experimental data



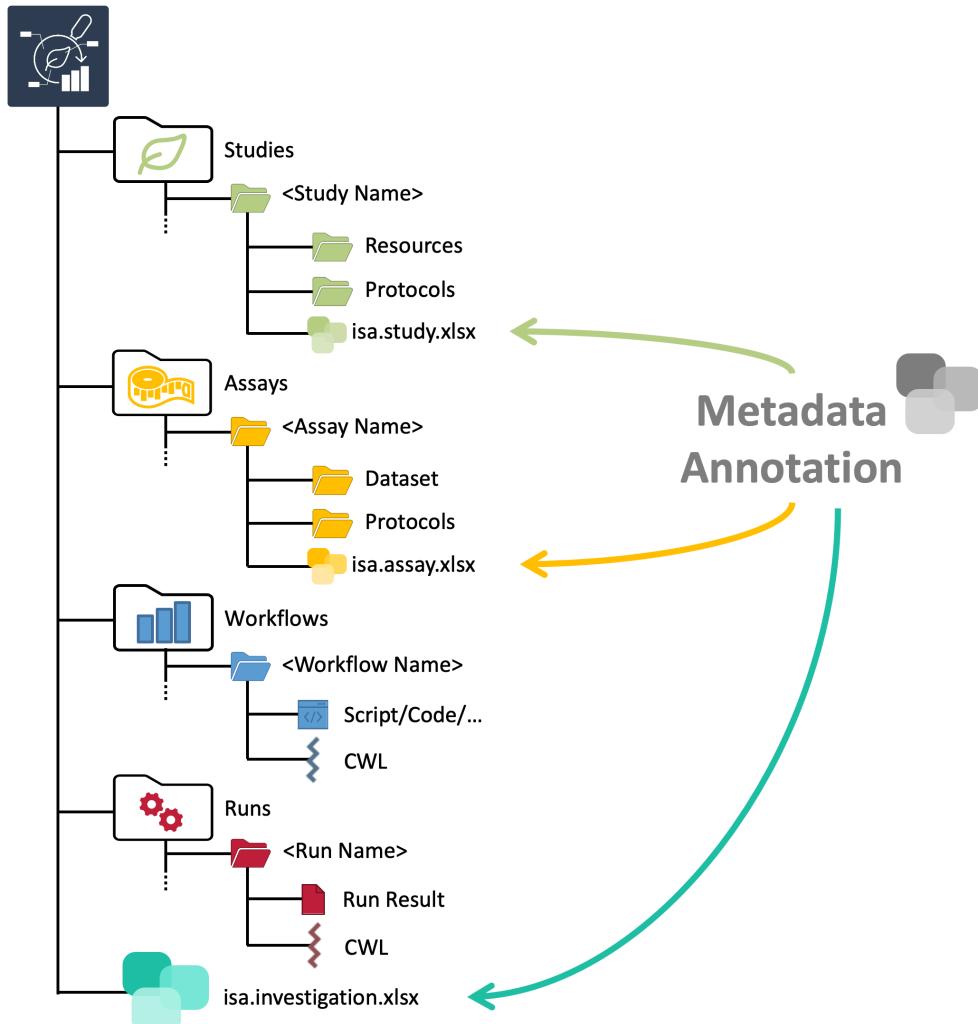
# Computations can be run inside ARCs



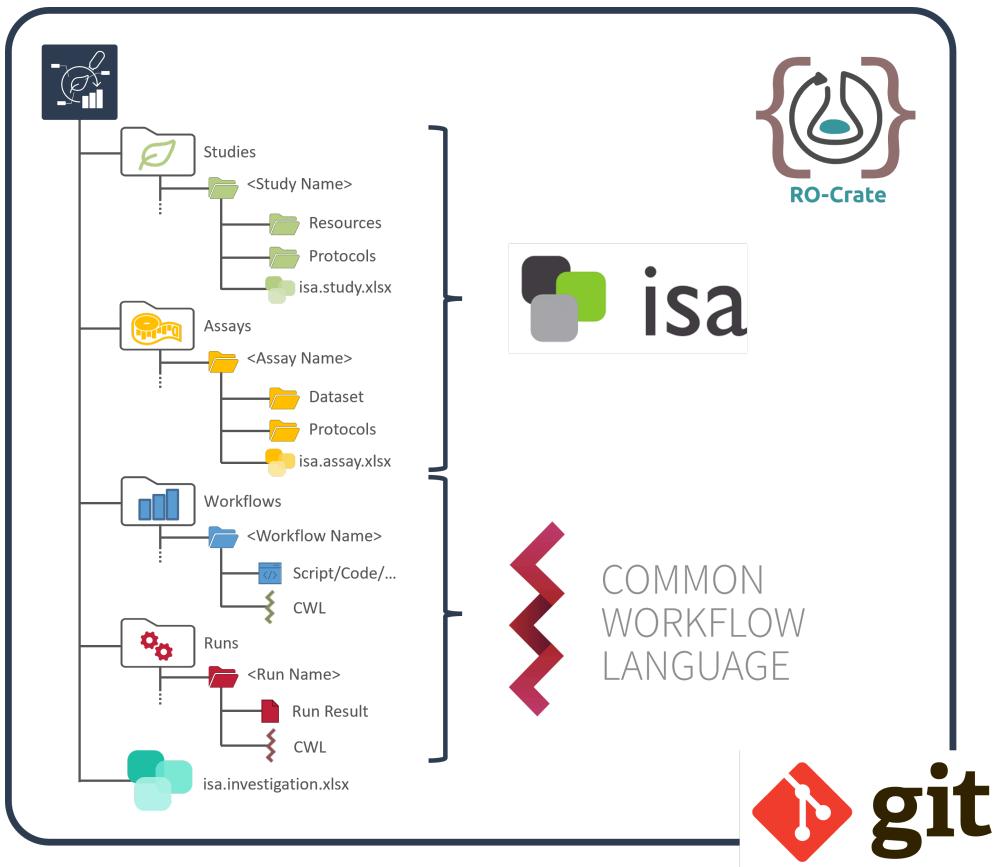
Data analysis  
Computation



# ARCs come with comprehensive metadata



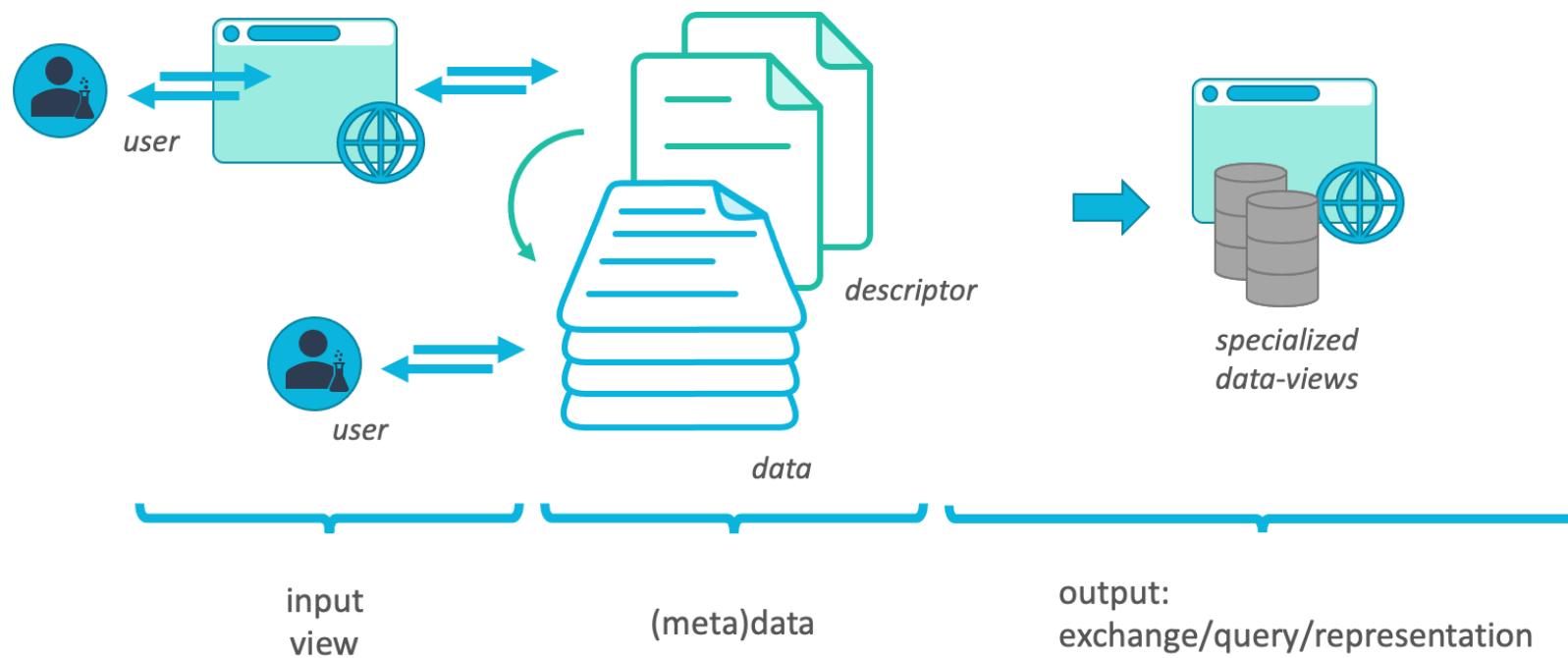
# ARC builds on standards



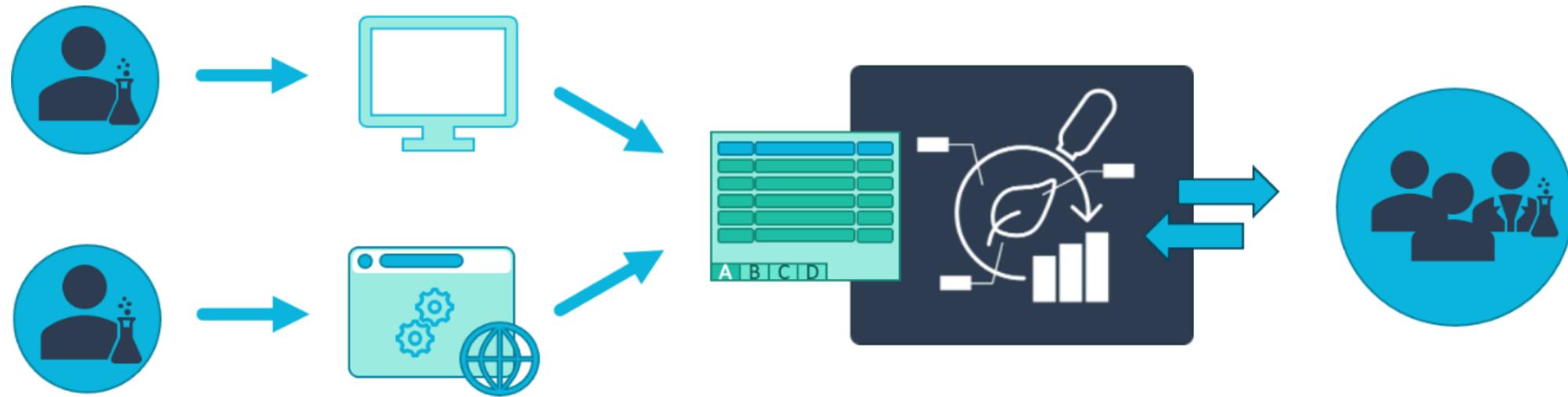
- RO-Crate: standardized exchange
- ISA: structured, machine-readable metadata
- CWL: reproducible, re-usable data analysis
- Git: version control

# Everything is a file

DataPLANT employs a **data-centric** approach to RDM



# No technical lock-in



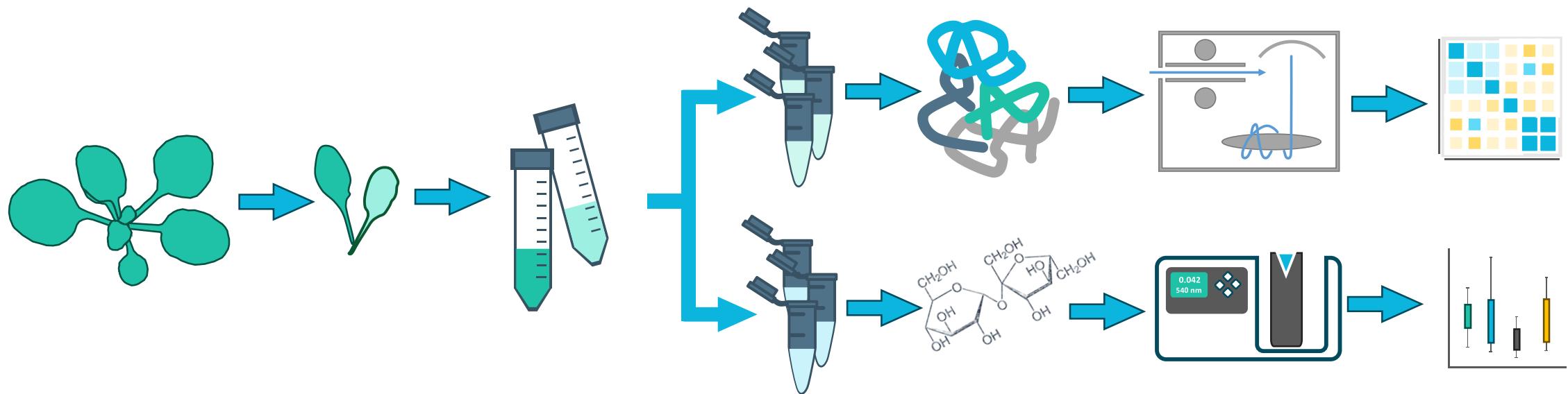
(Meta)data transparency with tool assistance but **no technical lock-in**

## Hands-on part 1: Start Here guide

[\*\*Start Here\*\*](#) guide in the DataPLANT knowledge base.

- follow the fictional researcher Viola on her journey to create her first ARC

# A small prototypic project



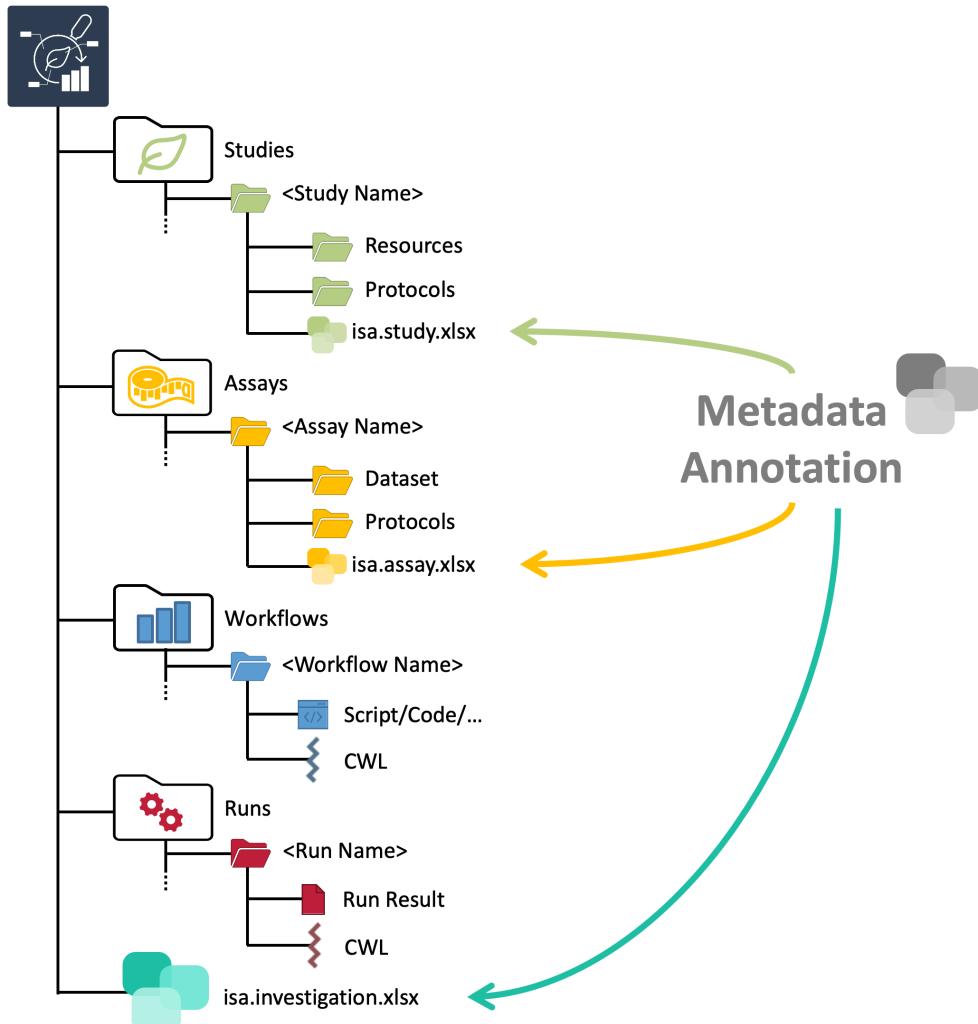
## Hands-on part 1: Setup and ARCitect

Follow the [Start Here guide](#) in the DataPLANT knowledge base.

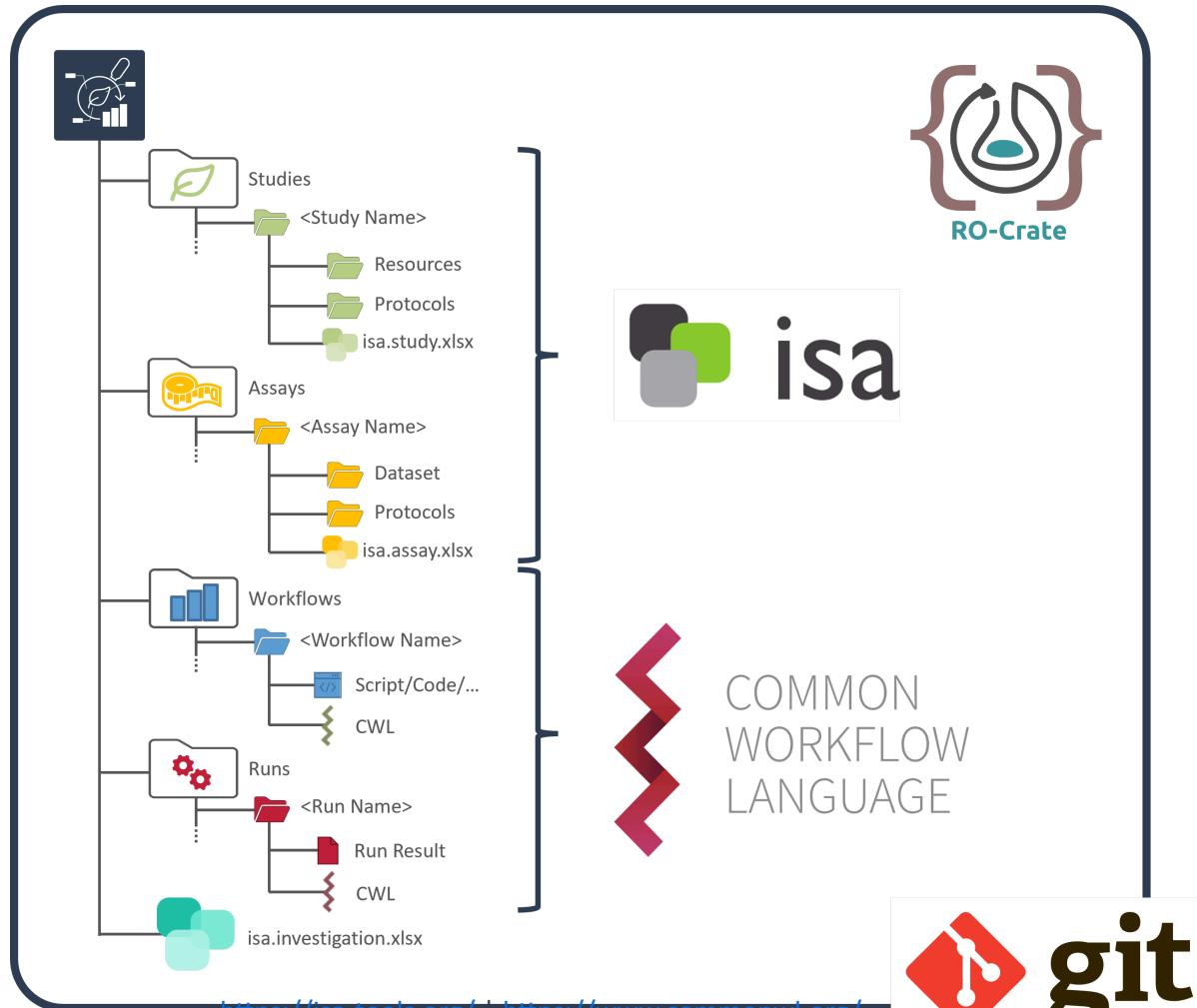
 Stop after step **Describing the Investigation**

**?** Please ask if you have any question/problems **?**

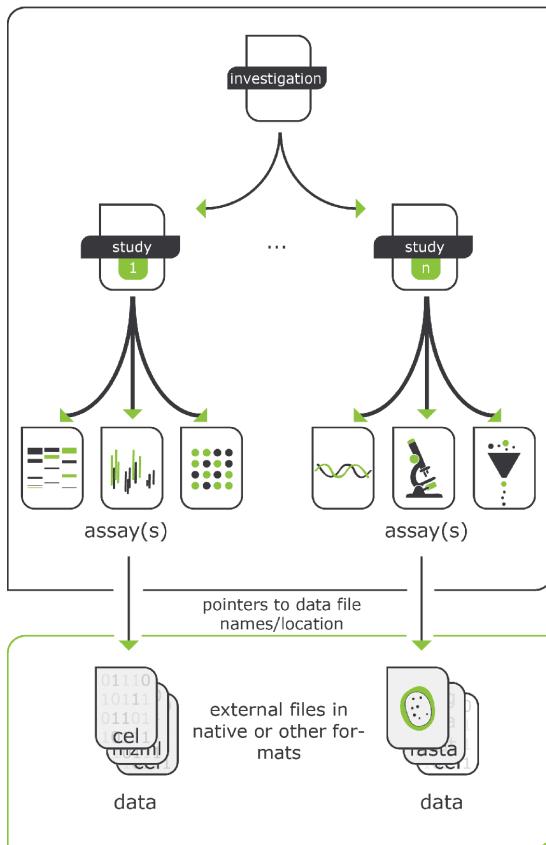
# ARCs come with comprehensive metadata



# ARC builds on standards



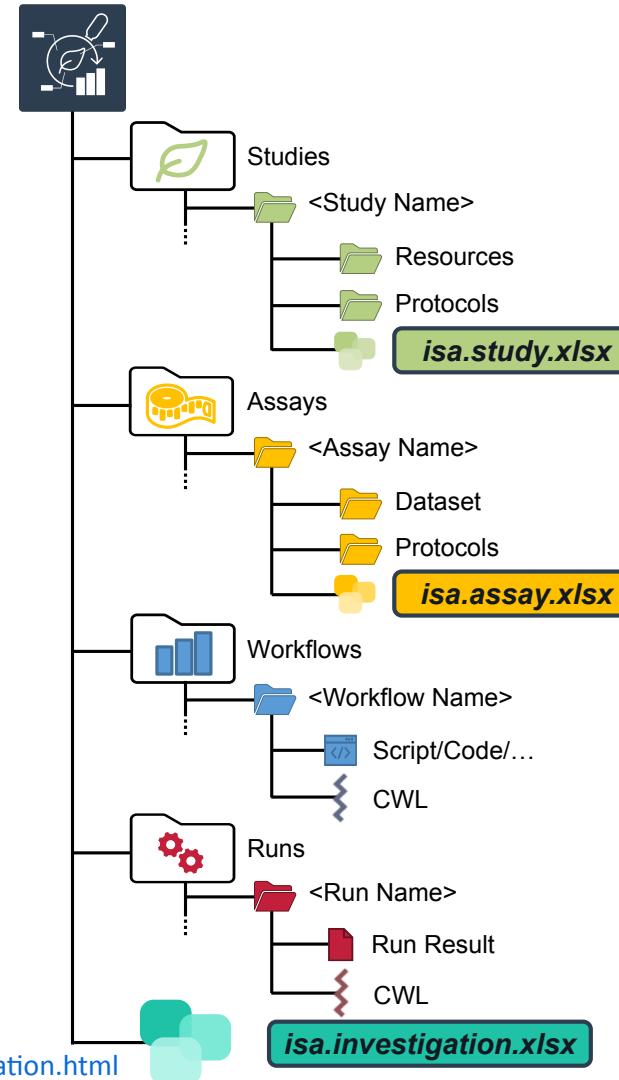
# ARC builds on ISA



**Investigation**  
Overall goals  
Scientific context

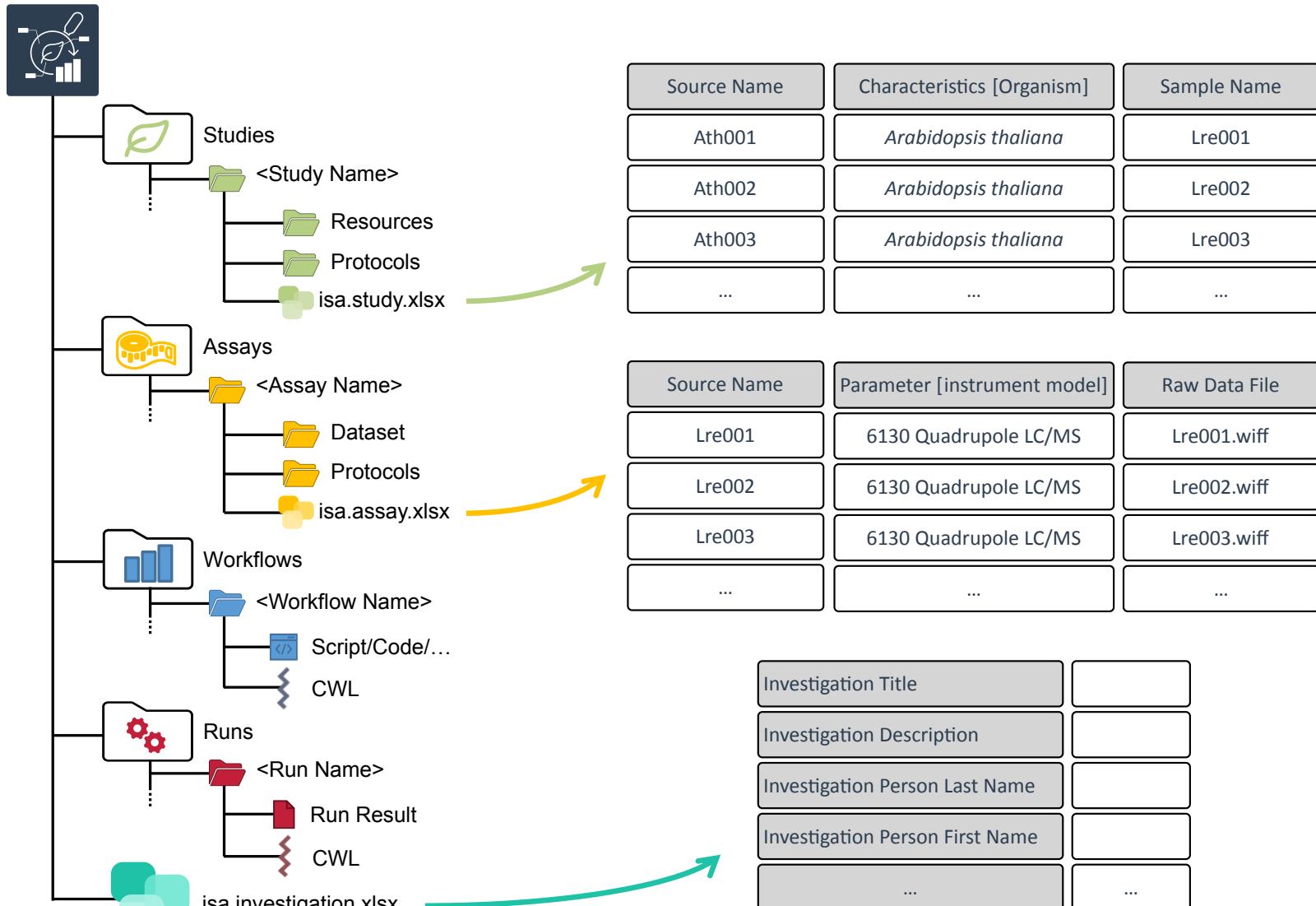
**Study**  
Experimental design

**Assay**  
Leading to  
(raw) data



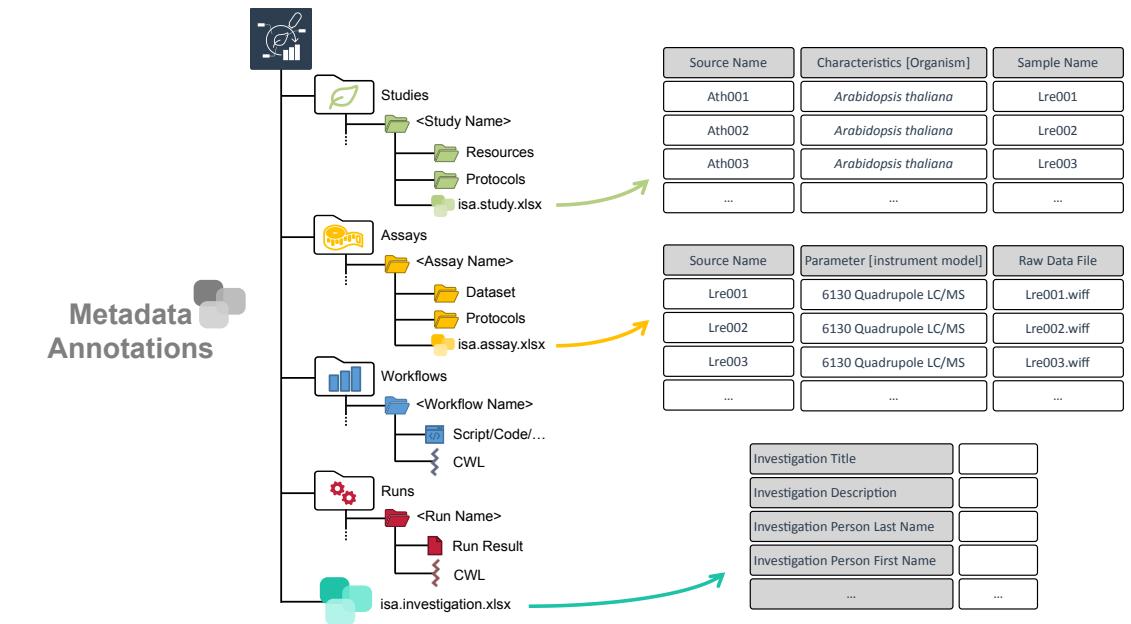
# ARC builds on ISA to connect data

Metadata Annotations

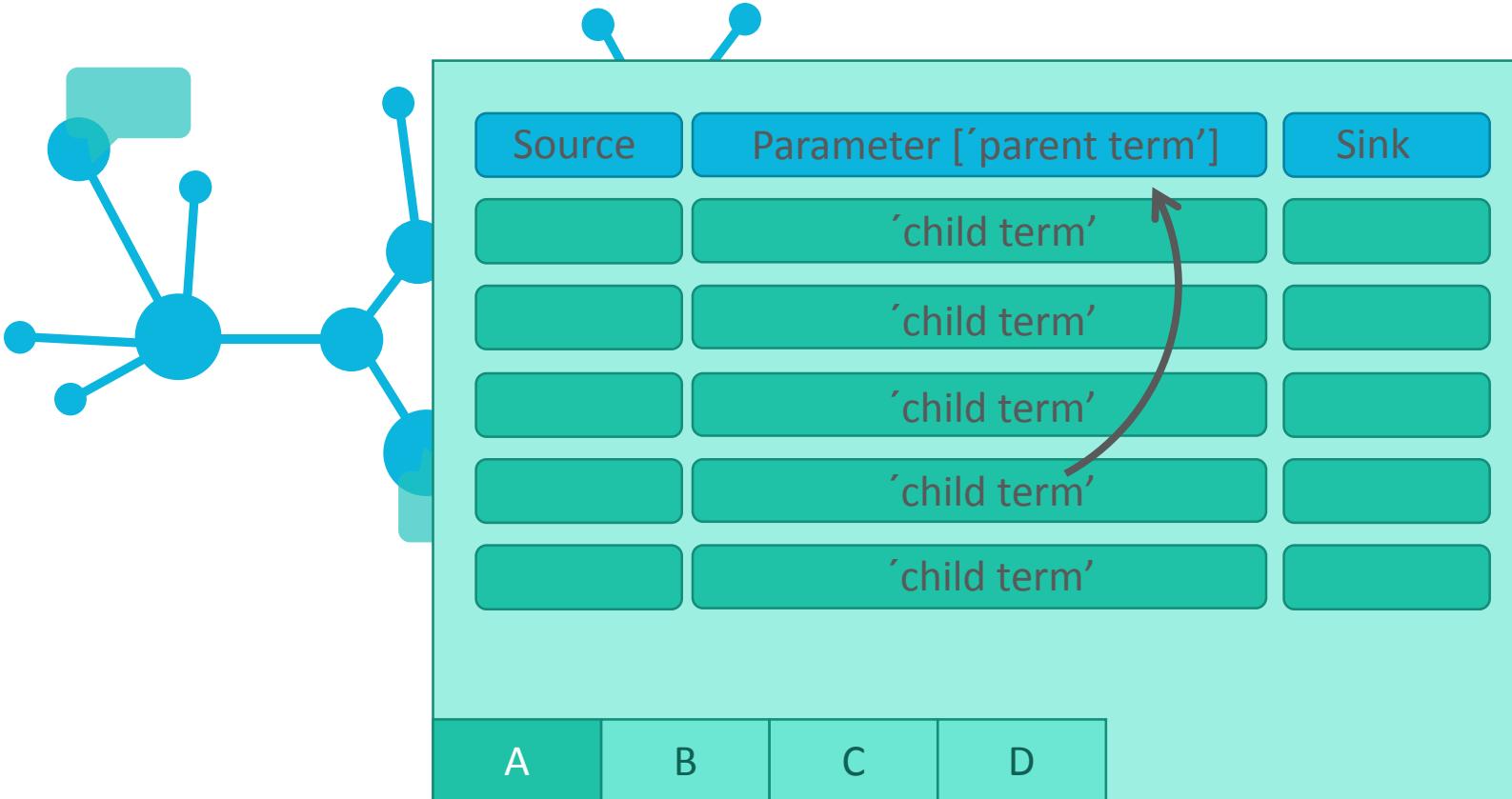


# ARC builds on ISA to link data

- Samples are linked study-to-assay, assay-to-assay
- Raw data is linked to assays
- Protocols can be referenced
- ...



# Annotation by flattening the knowledge graph



- Low-friction metadata annotation
- Familiar spreadsheet, row/column-based environment

# Annotation principle

Sample	Parameter [instrument model]	Data
	'TripleTOF4600'	
A	B	C
D		

- Low-friction metadata annotation
- Familiar spreadsheet, row/column-based environment

# Adding new building blocks

The screenshot shows the Swate software interface. On the left, there is a table with six rows of experimental data:

	Input [Source Name]	Characteristic [organism]	Factor [watering exposure]	Output [Sample Name]
1	DB_097	Talinum fruticosum	✓ 12 days drought	CAM_01
2	DB_099	Talinum fruticosum	✓ 12 days drought	CAM_02
3	DB_103	Talinum fruticosum	✓ 12 days drought	CAM_03
4	DB_161	Talinum fruticosum	✓ 12 days drought + 2 days rewatered	reC3_01
5	DB_163	Talinum fruticosum	✓ 12 days drought + 2 days rewatered	reC3_02
6	DB_165	Talinum fruticosum	✓ 12 days drought + 2 days rewatered	reC3_03

Below the table, there is a numeric input field with the value '1' and a '+' button. To the right of the table, a modal dialog box titled 'New building blocks' is open. This dialog has a search bar containing 'instrument model' and several categories listed on the left: Parameter, Factor, Characteristic, Component, More, and Output. A large green button labeled 'Add Column' is prominently displayed in the center of the dialog.

Swate can be used for the annotation of **isa.study.xlsx** and **isa.assay.xlsx** files

# Annotation Building Block types

- Input (e.g. Source Name, Sample Name)
- Protocol columns
- Characteristic // Parameter // Factor //
- Component
- Output (e.g. Sample Name, Raw Data File, Derived Data File)

The screenshot shows the MibitNet software interface. On the left is a table titled 'Widgets' with columns: Input [Source Name], Characteristic [organism], Factor [watering exposure], and Output [Sample Name]. The table contains six rows of data. A 'Factor' column is highlighted in blue. On the right is a 'New Parameter' dialog box with tabs for Parameter, Factor, Characteristic, Component, and More. The 'Factor' tab is selected. Arrows point from the labels 'Input', 'Characteristic', 'Factor', 'Output', and 'Sidebar' to their corresponding elements in the interface.

Input [Source Name]	Characteristic [organism]	Factor [watering exposure]	Output [Sample Name]
DB_097	Talinum fruticosum	✓ 12 days drought	CAM_01
DB_099	Talinum fruticosum	✓ 12 days drought	CAM_02
DB_103	Talinum fruticosum	✓ 12 days drought	CAM_03
DB_161	Talinum fruticosum	✓ 12 days drought + 2 days rewetared	reC3_01
DB_163	Talinum fruticosum	✓ 12 days drought + 2 days rewetared	reC3_02
DB_165	Talinum fruticosum	✓ 12 days drought + 2 days rewetared	reC3_03

New Parameter

Parameter    instrument model

Input →

Factor

Characteristic

Component

More →

Output →

Add Column

Help

Metadata plant\_material +

Sidebar

Let's take a detour on [Annotation Principles](#)

# Ontology term search

The screenshot shows the Swate interface with a table of experimental data and an ontology search sidebar.

**Table Data:**

	Input [Source Name]	Characteristic [Organism]	»	Factor [watering exposure]	»	Output [Sample Name]
1	DB_097		Q	12 days drought		CAM_01
2	DB_099			12 days drought		CAM_02
3	DB_103			12 days drought		CAM_03
4	DB_161			12 days drought + 2 days rewated		reC3_01
5	DB_163			12 days drought + 2 days rewated		reC3_02
6	DB_165			12 days drought + 2 days rewated		reC3_03

**Search Sidebar:**

Ontology term search  
Search for an ontology term to fill into the selected field(s)

Parent: Organism, MIAPPE:0041   [Use advanced search](#)

[Fill selected cells with this term](#)

Metadata   plant\_material   +

Swate Release Version v1.0.0-beta.03 Host Browser

Enable related term directed search to directly fill cells with child terms

# Fill your table with ontology terms

The screenshot shows the Swate interface. On the left, there is a table with four columns: Input [Source Name], Characteristic [Organism], Factor [watering exposure], and Output [Sample Name]. The table contains six rows of data. In the 'Characteristic [Organism]' column, the last row (DB\_165) has a green background. In the 'Factor [watering exposure]' column, the last three rows (DB\_161, DB\_163, DB\_165) have green backgrounds. The table has a dark header bar with icons for back, forward, and search.

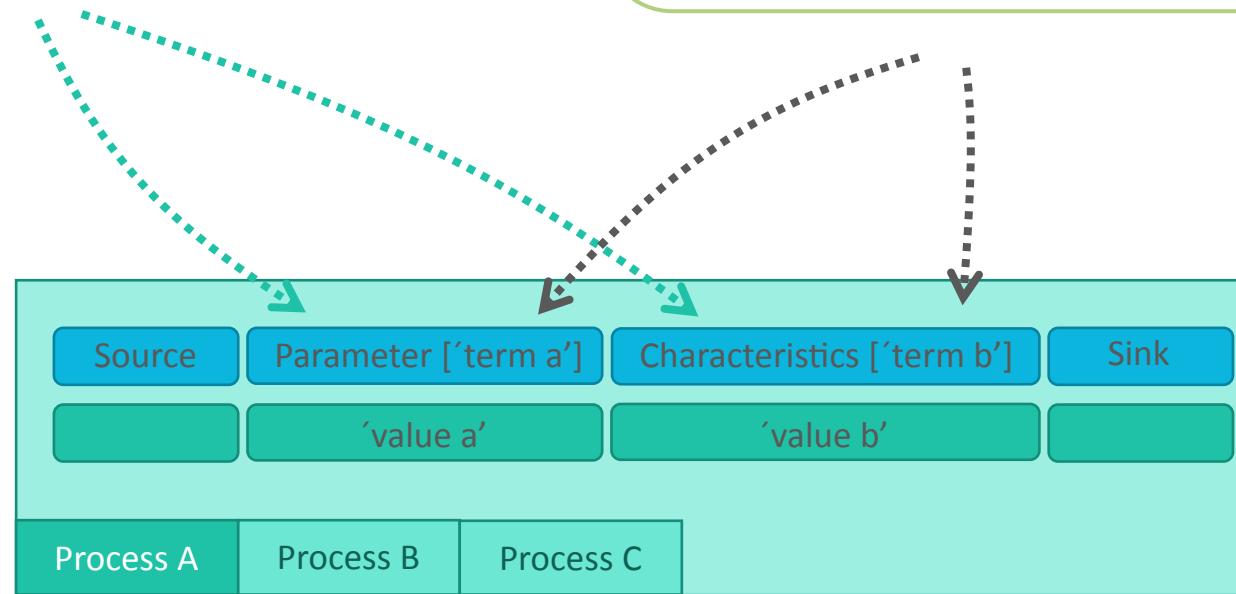
	Input [Source Name]	Characteristic [Organism]	Factor [watering exposure]	Output [Sample Name]
1	DB_097	Talinum fruticosum	✓ 12 days drought	CAM_01
2	DB_099	Talinum fruticosum	✓ 12 days drought	CAM_02
3	DB_103	Talinum fruticosum	✓ 12 days drought	CAM_03
4	DB_161	Talinum fruticosum	✓ 12 days drought + 2 days rewatered	reC3_01
5	DB_163	Talinum fruticosum	✓ 12 days drought + 2 days rewatered	reC3_02
6	DB_165	Talinum fruticosum	✓ 12 days drought + 2 days rewatered	reC3_03

Below the table are navigation buttons: a page number '1' and a '+' sign.

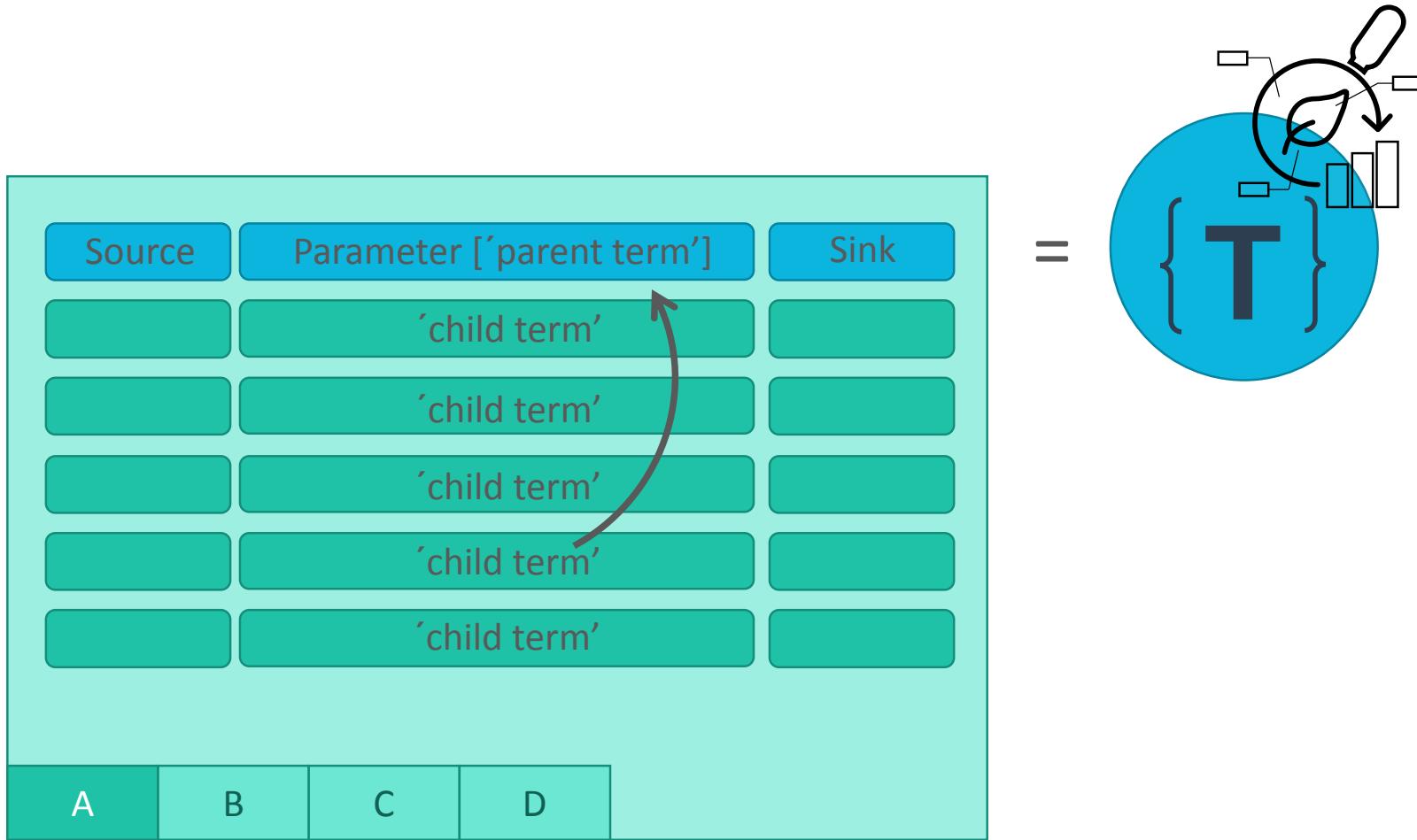
On the right, there is a sidebar titled 'SWATE' with a search bar. The search bar contains the text 'Talinum fruticosum'. Below the search bar, it says 'Parent: Organism, MIAPPE:0041' and 'Use advanced search'. A large green button at the bottom of the sidebar says 'Fill selected cells with this term'.

At the bottom left, there are tabs for 'Metadata' and 'plant\_material' (which is highlighted), with a '+' sign next to them. At the bottom right, it says 'Swate Release Version v1.0.0-beta.03 Host Browser'.

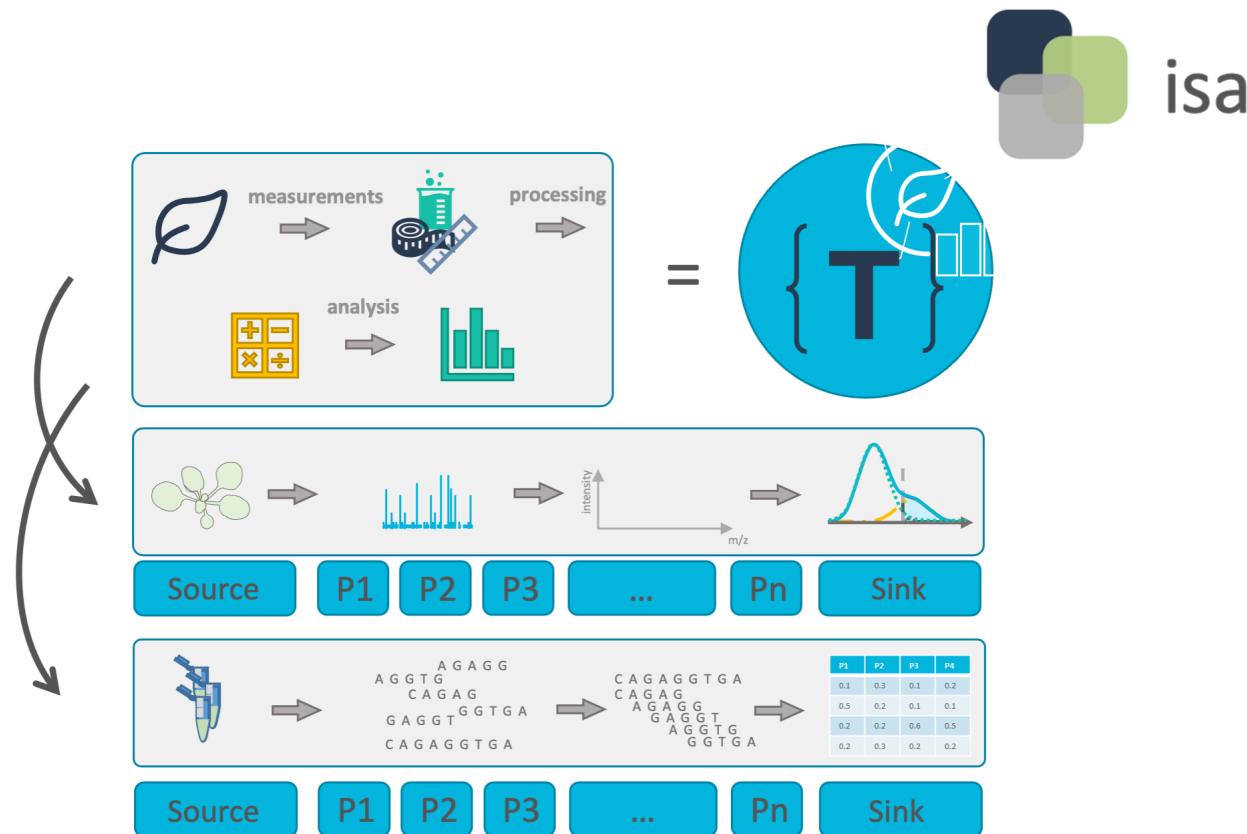
# Hierarchical combination of ontologies



# Checklists and Templates



# Realization of lab-specific metadata templates



Facilities can define their most common workflows as templates

# Directly import templates via Swate

- DataPLANT curated
- Community templates

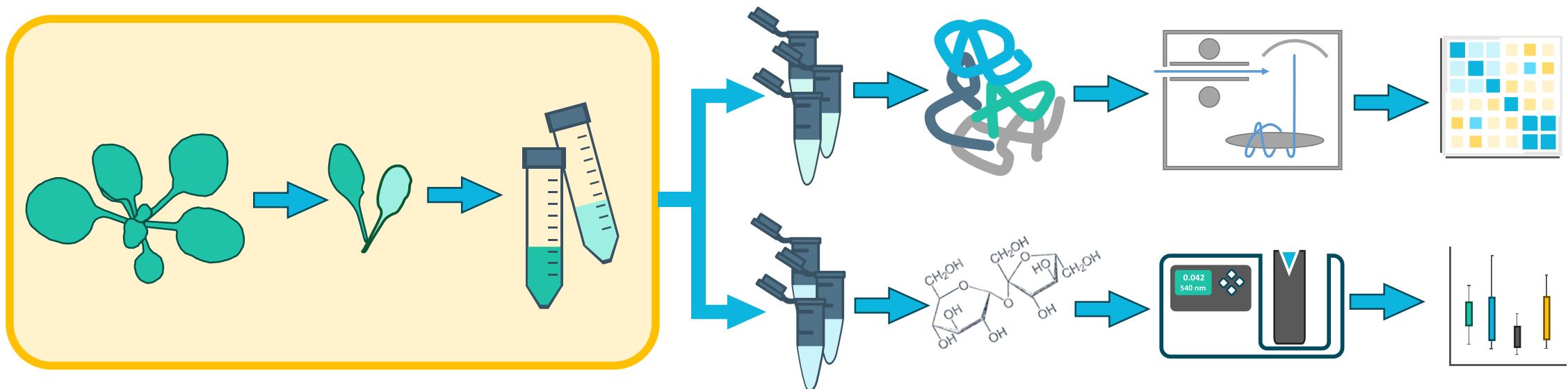
The screenshot shows the Swate web application interface. At the top, there is a dark header bar with several small icons. Below the header is a search bar with two input fields: "Search by template name" and "Search for tags". Underneath the search bar is a dropdown menu labeled "Select community" with "DataPLANT official" selected. The main content area is a table listing various templates. The columns are "Template Name", "Community", and "Template Version". Each row contains a link icon at the end. The table lists the following templates:

Template Name	Community	Template Version
DNA extraction	curated	1.1.7
Data Processing (PRIDE minimal)	curated	1.0.0
GEO - Minimal information RNA assays	curated	1.0.1
GEO - Minimal information RNA extraction	curated	1.0.0
GEO - Minimal information computational analysis	curated	1.0.0
GEO - Minimal information plant growth	curated	1.0.0
Genome assembly	curated	1.1.7

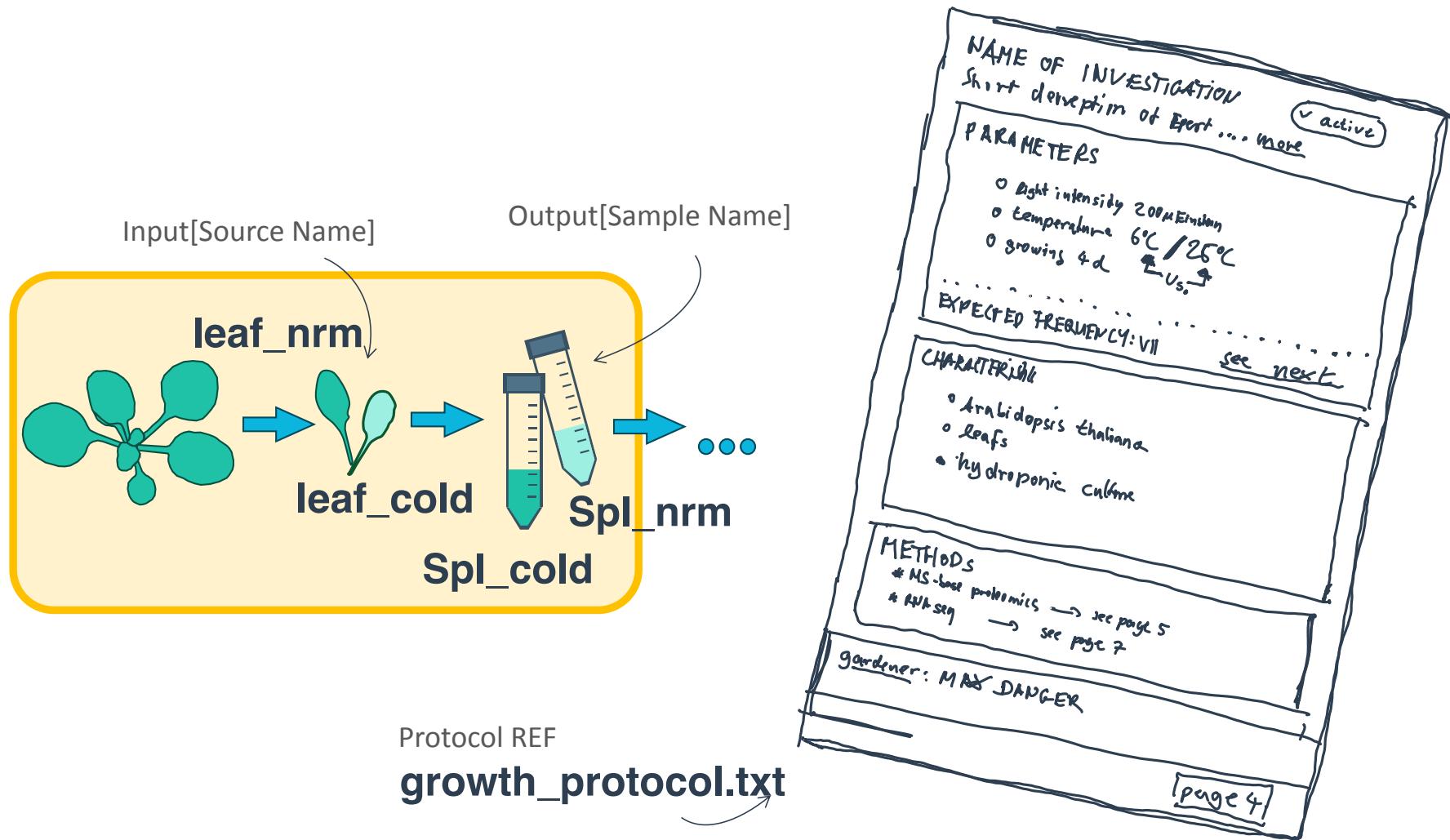
## Hands-on part 2: Start Here guide, study & assay part

[\*\*Start Here\*\*](#) guide in the DataPLANT knowledge base.

# 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		

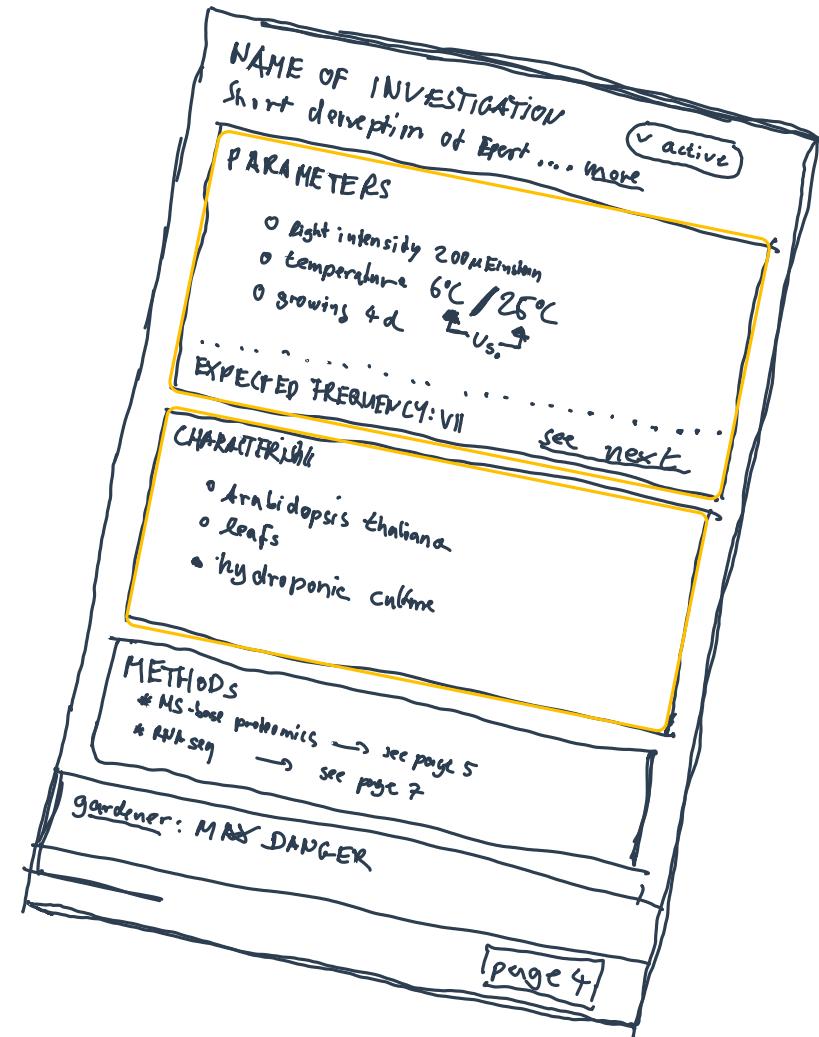
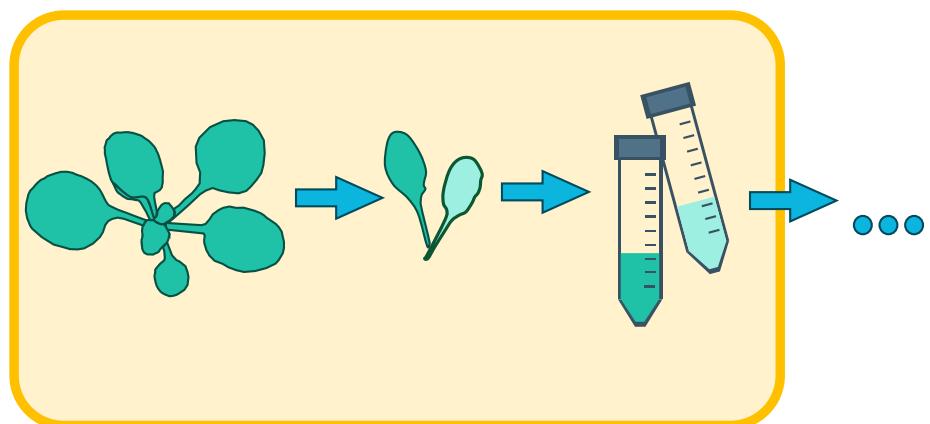
# Referencing a protocol

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

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

- 💡 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

# 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](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](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](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](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?

**About OLS**  
The Ontology Lookup Service (OLS) is a repository for biomedical ontologies that aims to provide a single point of access to the latest ontology versions. You can browse the ontologies through the website as well as programmatically via the OLS API. OLS is developed and maintained by the Samples, Phenotypes and Ontologies Team (SPOT) at EMBL-EBI.

**Related Tools**  
In addition to OLS the SPOT team also provides the Oxo and ZOOMA services. Oxo provides cross-ontology mappings between terms from different ontologies. ZOOMA is a service to assist in mapping data to ontologies in OLS.

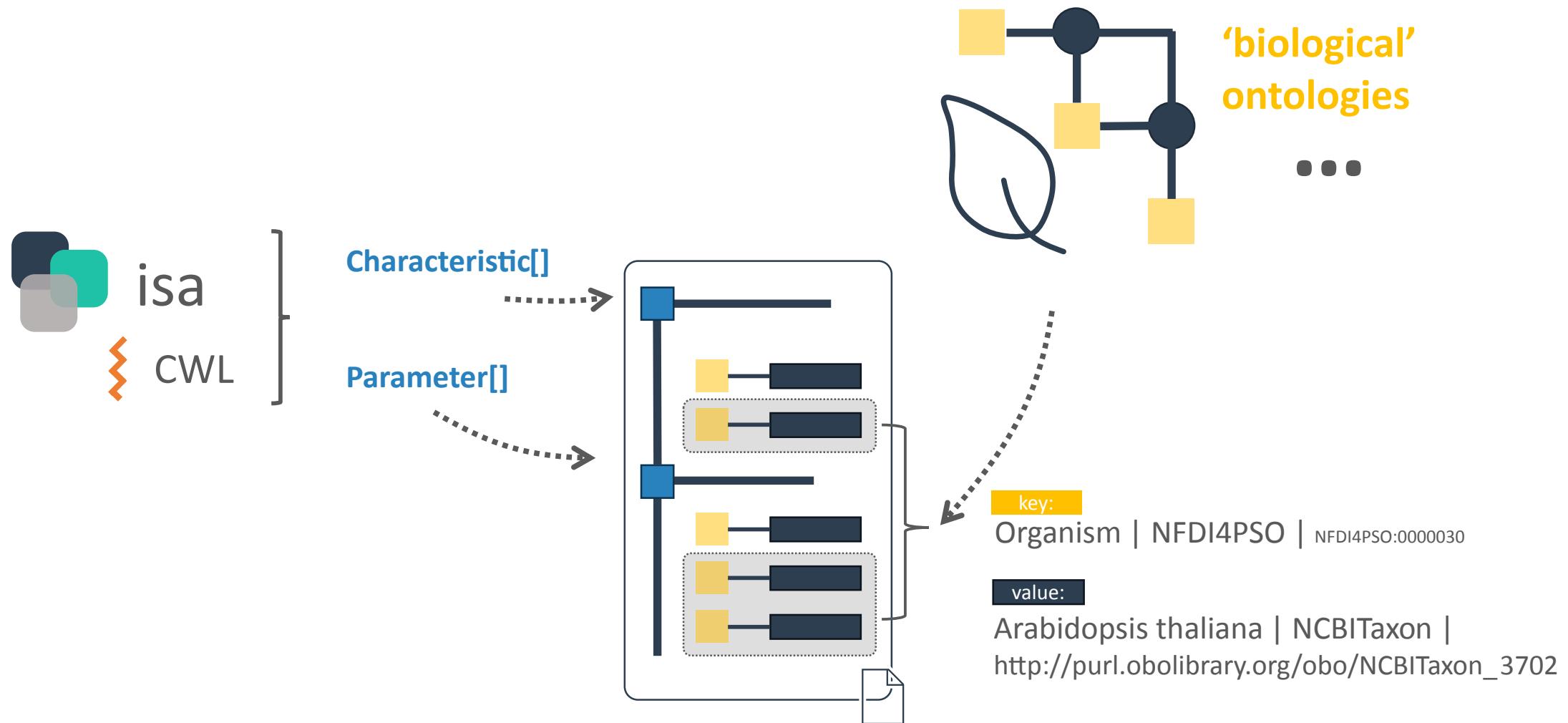
**Report an Issue**  
For feedback, enquiries or suggestion about OLS or to request a new ontology please use our GitHub issue tracker. For announcements relating to OLS, such as new releases and new features sign up to the OLS announce mailing list.

FOLLOW US  
 X

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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  $\mu$ Einstein
-  Temperature 6°C / 25°C
-  Growing 4d

## Characteristics []

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

# Finding the metadata vocabulary and descriptors

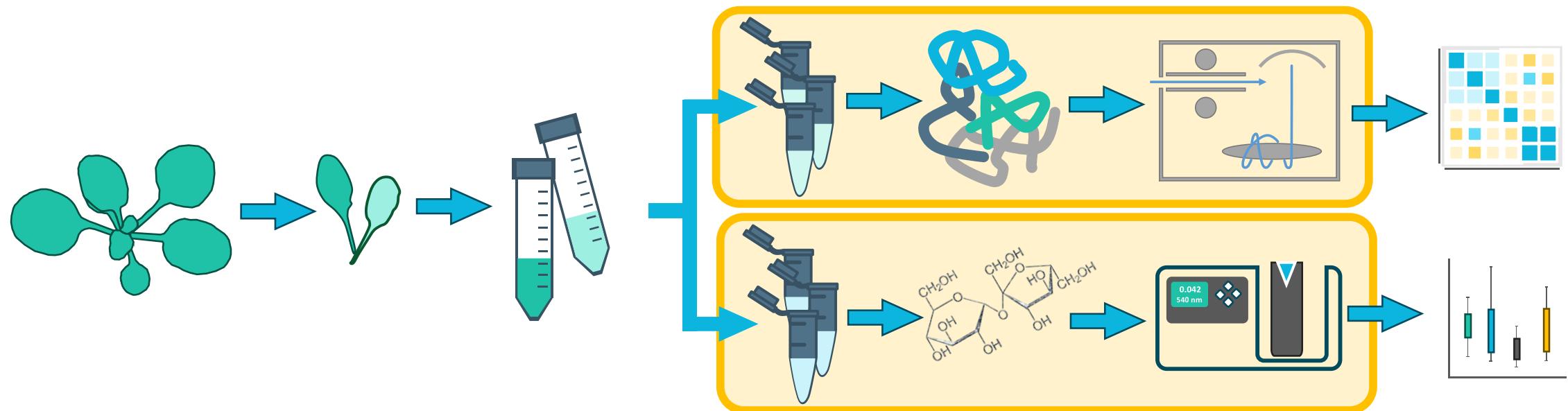
## Parameters []

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

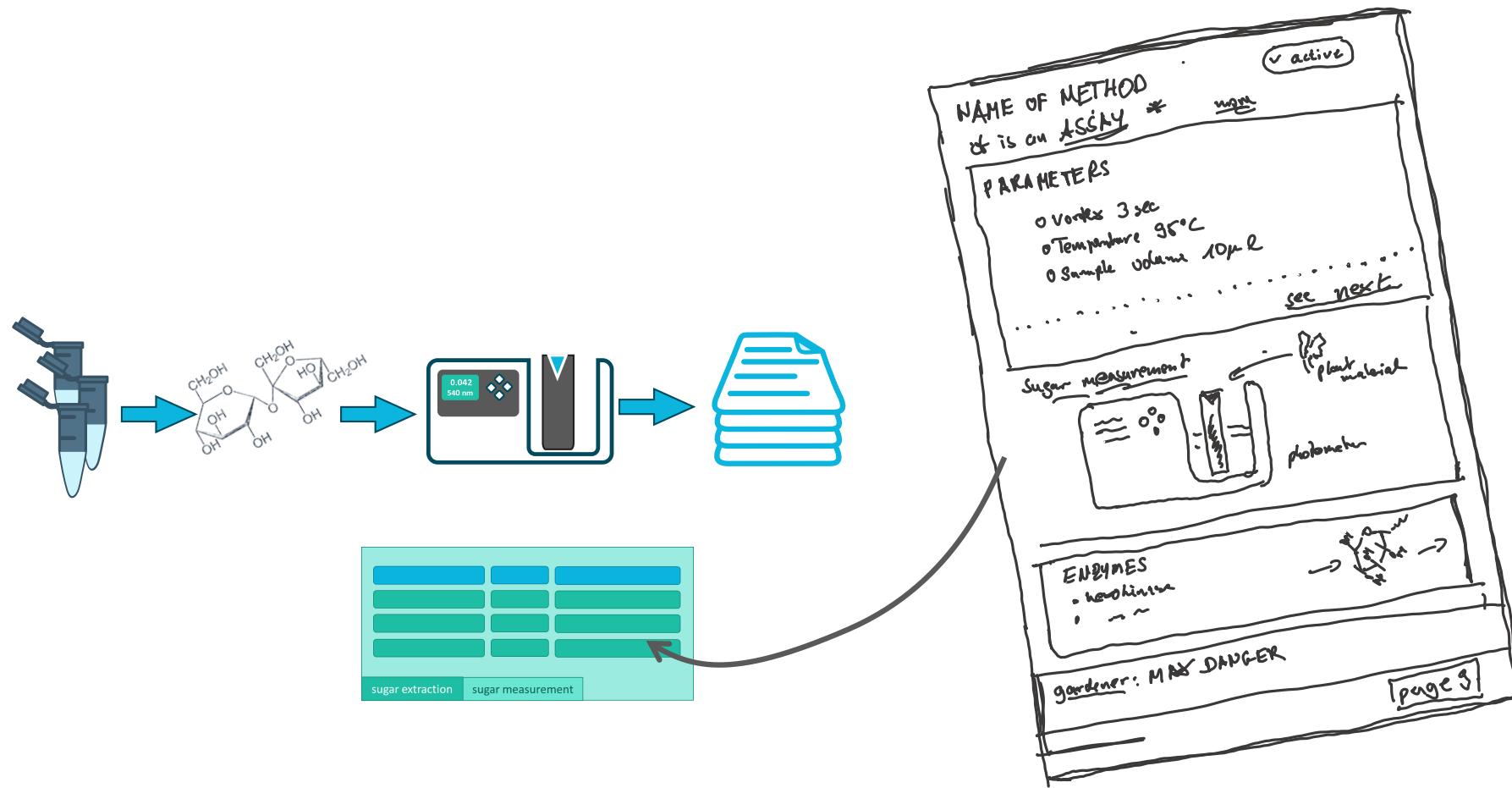
## Characteristics []

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

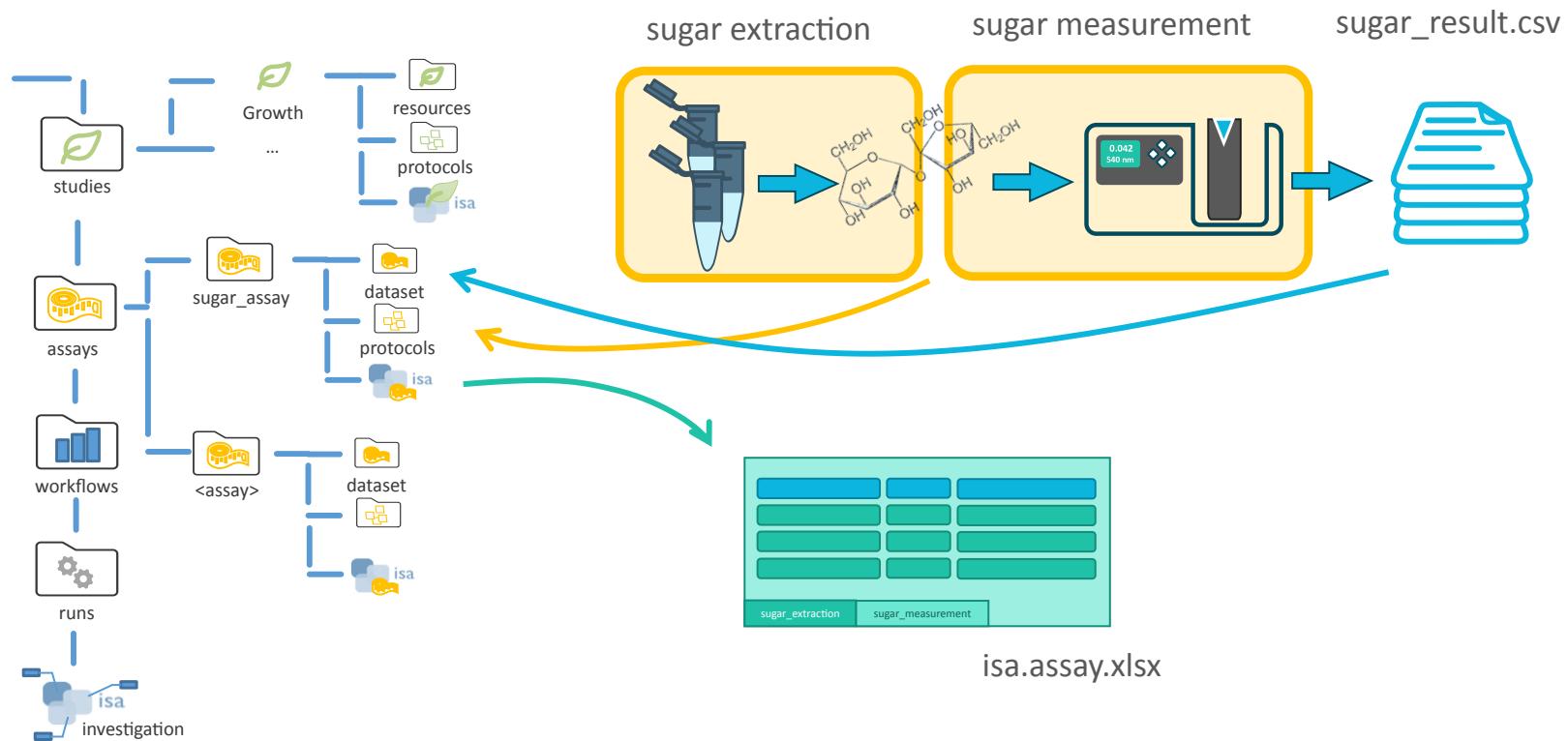
# Identifying assays



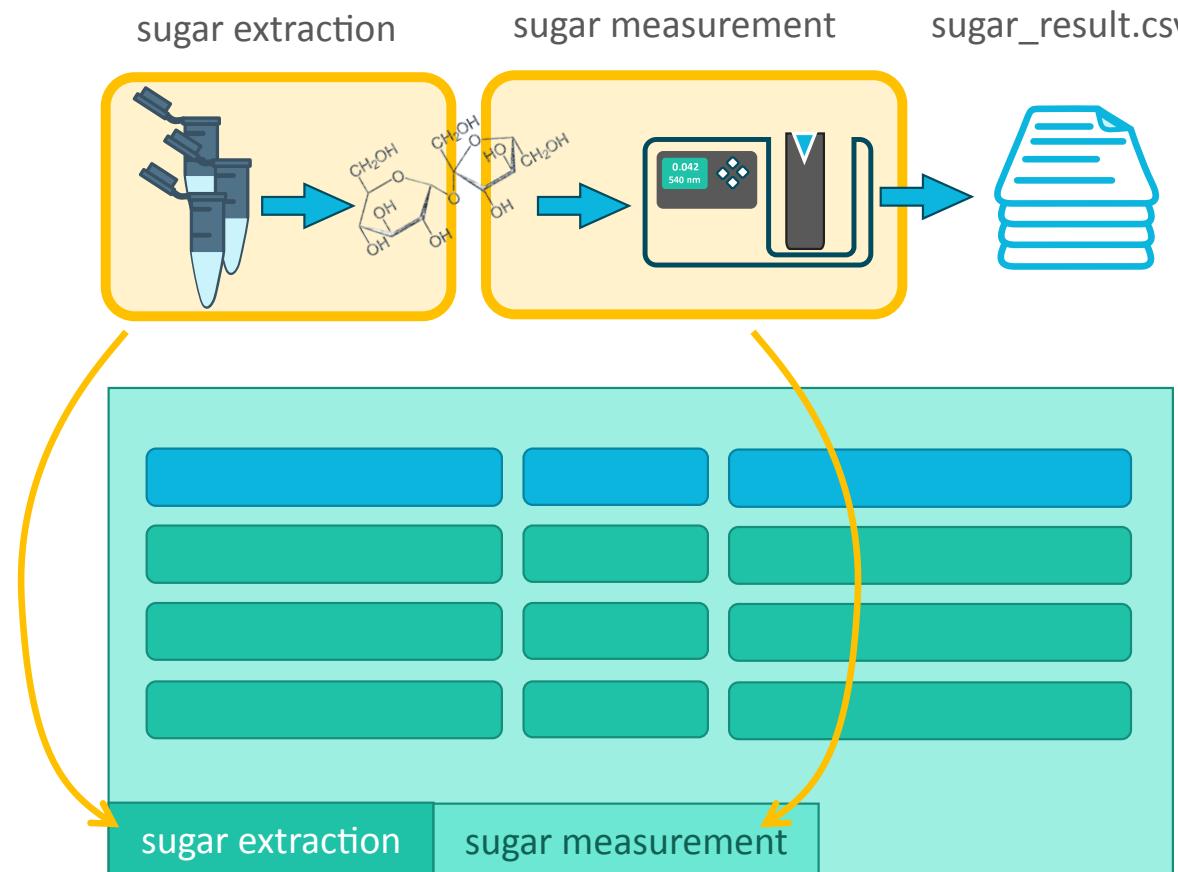
# Assay for sugar measurement



# Separating different assay elements

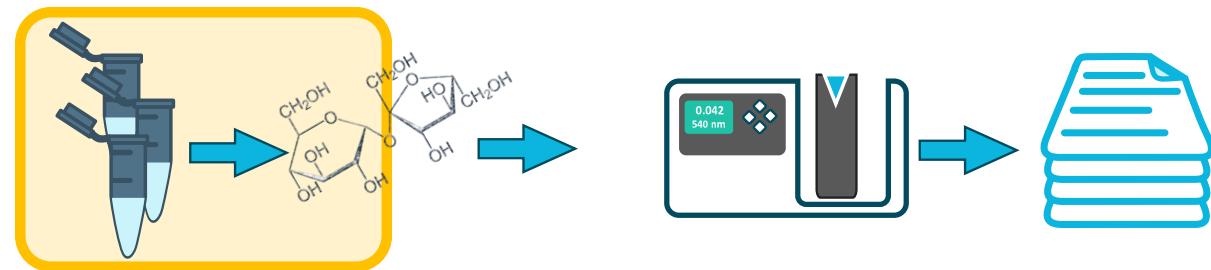


# Isolating the lab processes in an assay



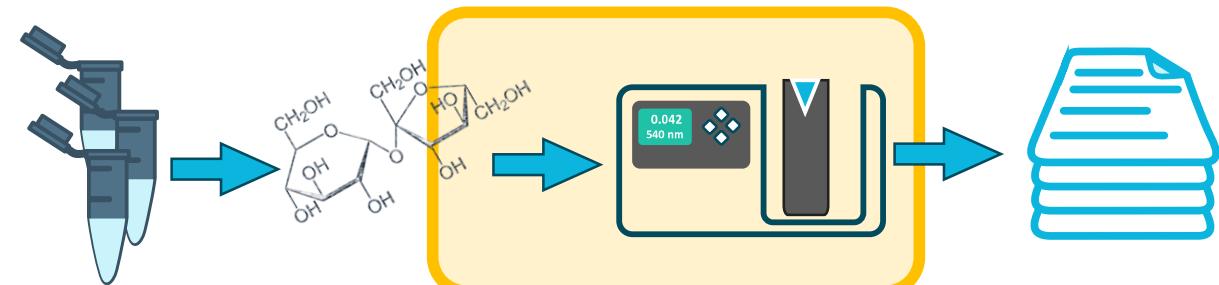
# Parameteterization: sugar extraction

- 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



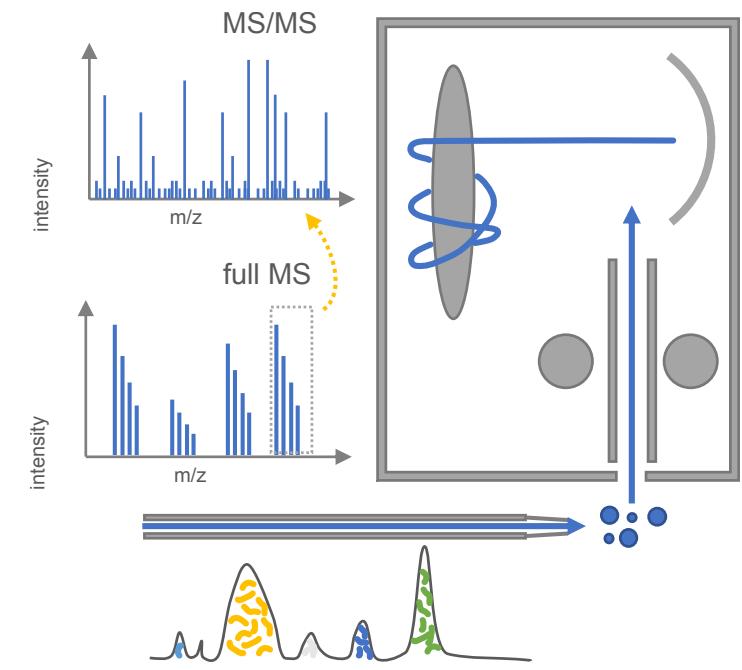
# Save time using standard methods and SOPs

## Parameter []

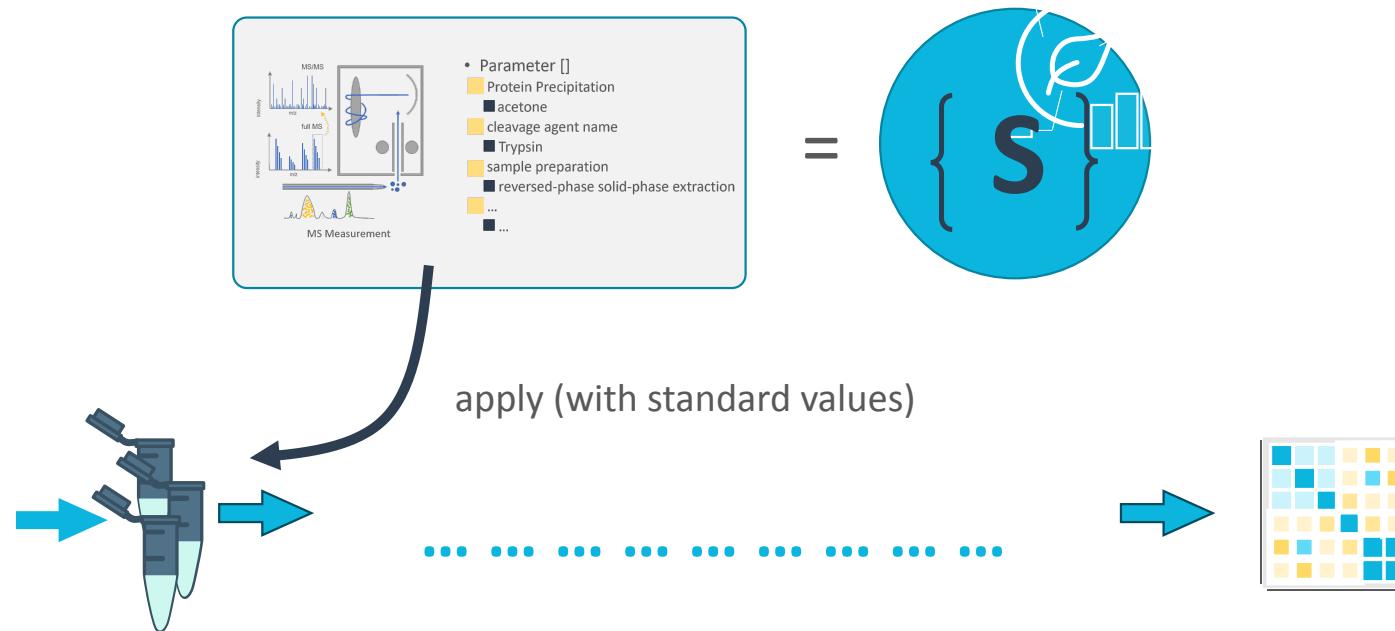
- █ Protein Precipitation
  - █ acetone
- █ cleavage agent name
  - █ Trypsin
- █ sample preparation
  - █ reversed-phase solid-phase extraction
- ...

## Component []

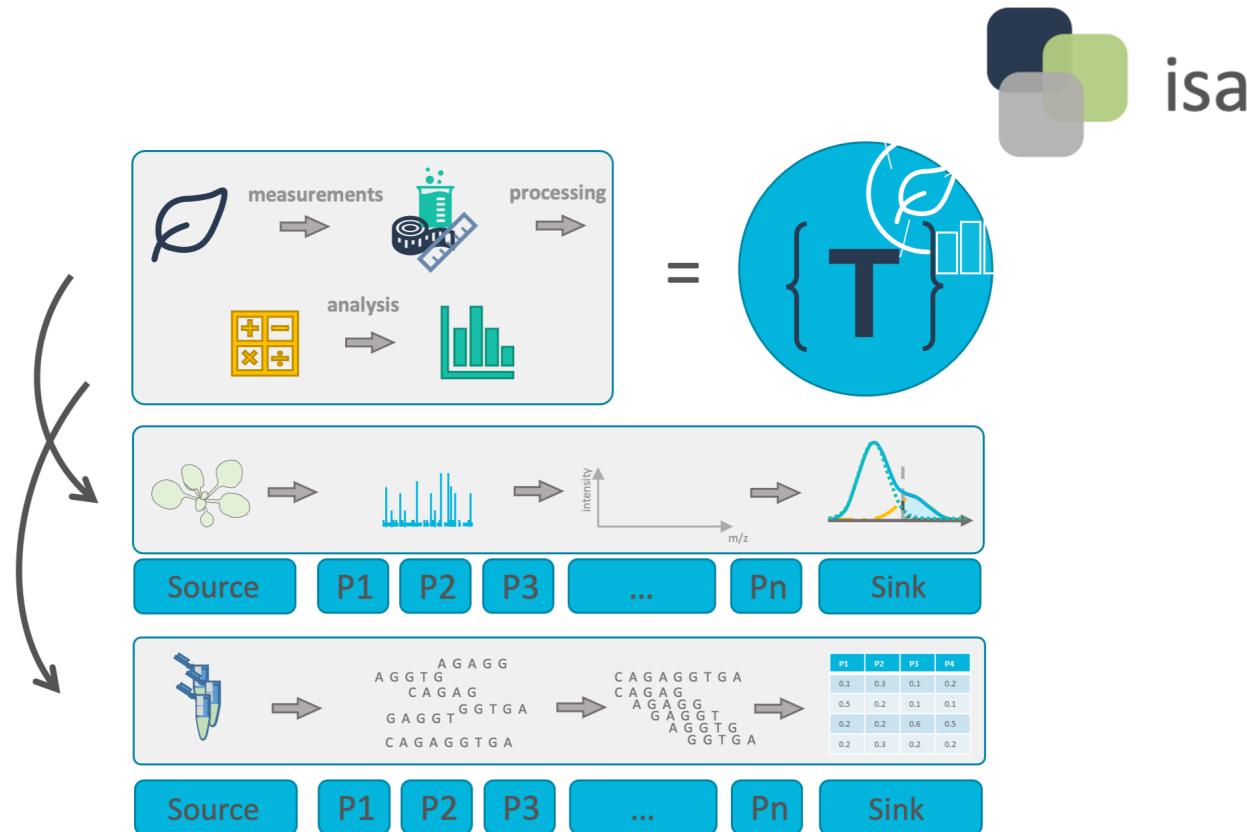
- █ chromatography instrument model
  - █ nanoElute2
- █ chromatography column model
  - █ PepSep C18 1.9 $\mu$ , 25cm x 75 $\mu$ m
- ...  
...



## Applying standard procedures to sample record



# Realization of lab-specific metadata with templates



Facilities can define their most common workflows as templates

## Hands-on part 2: ARCitect (and Swate)

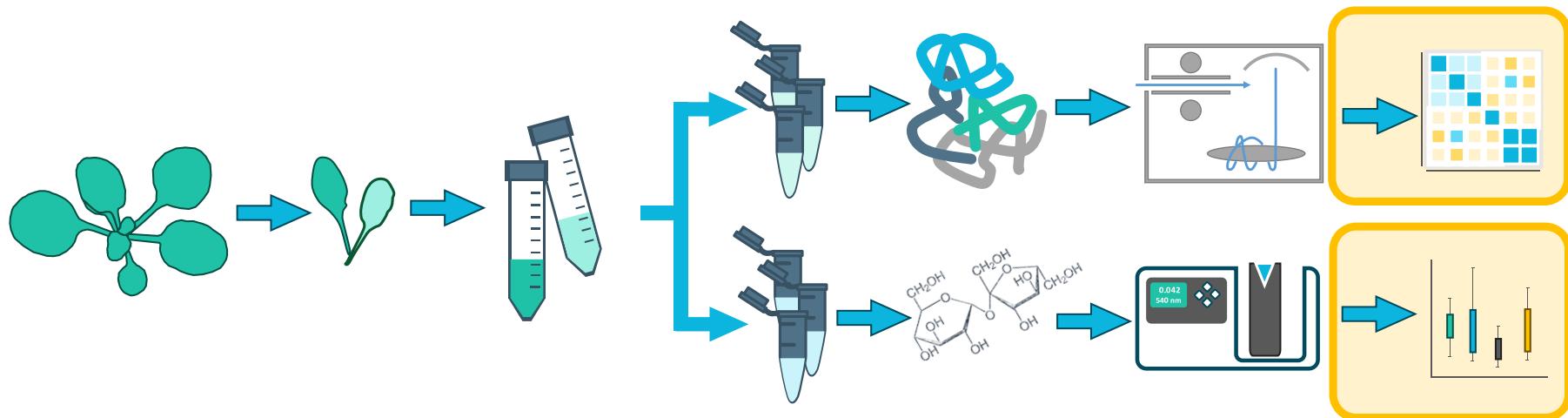
Continue the [Start Here](#) guide in the DataPLANT knowledge base.



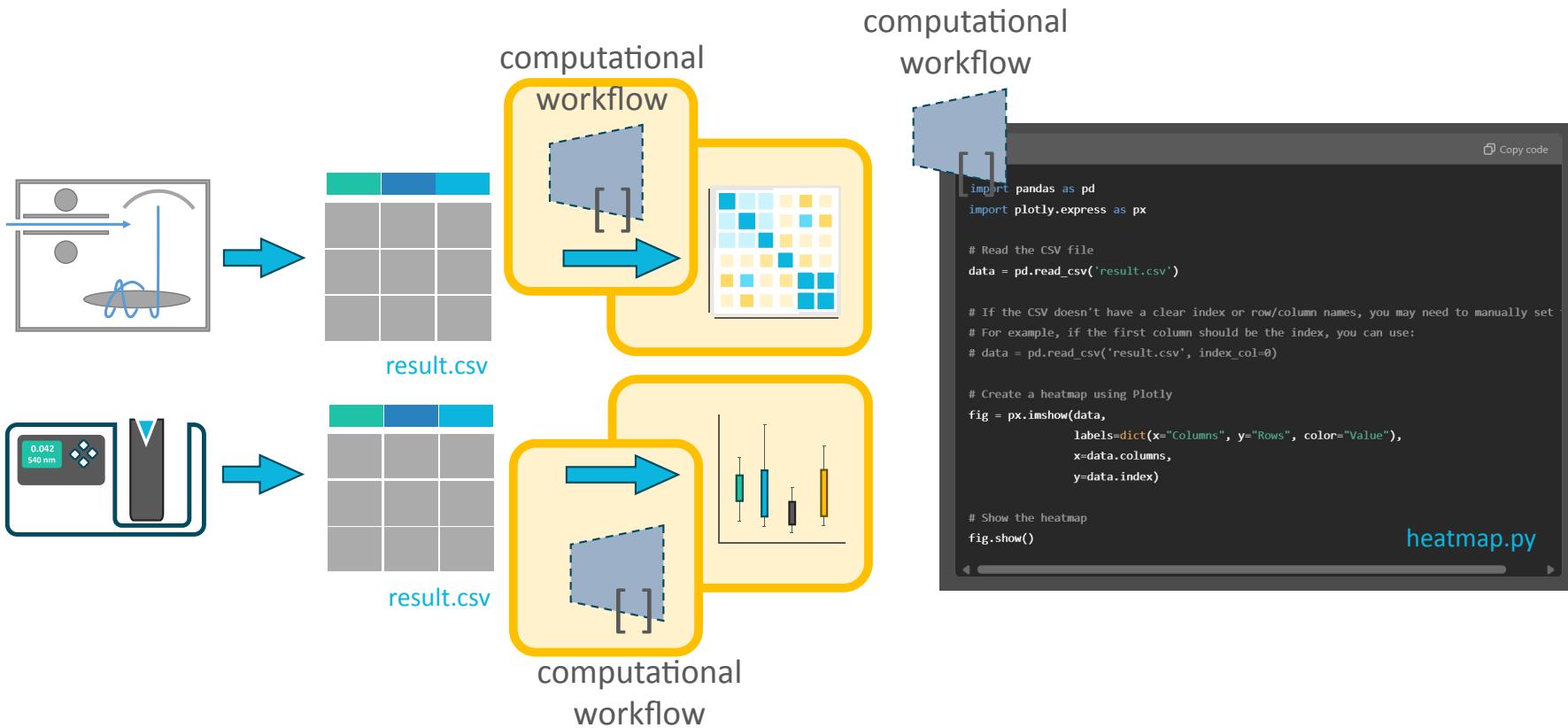
Stop after step [Add assay data](#)

## Hands-on part 3: Data

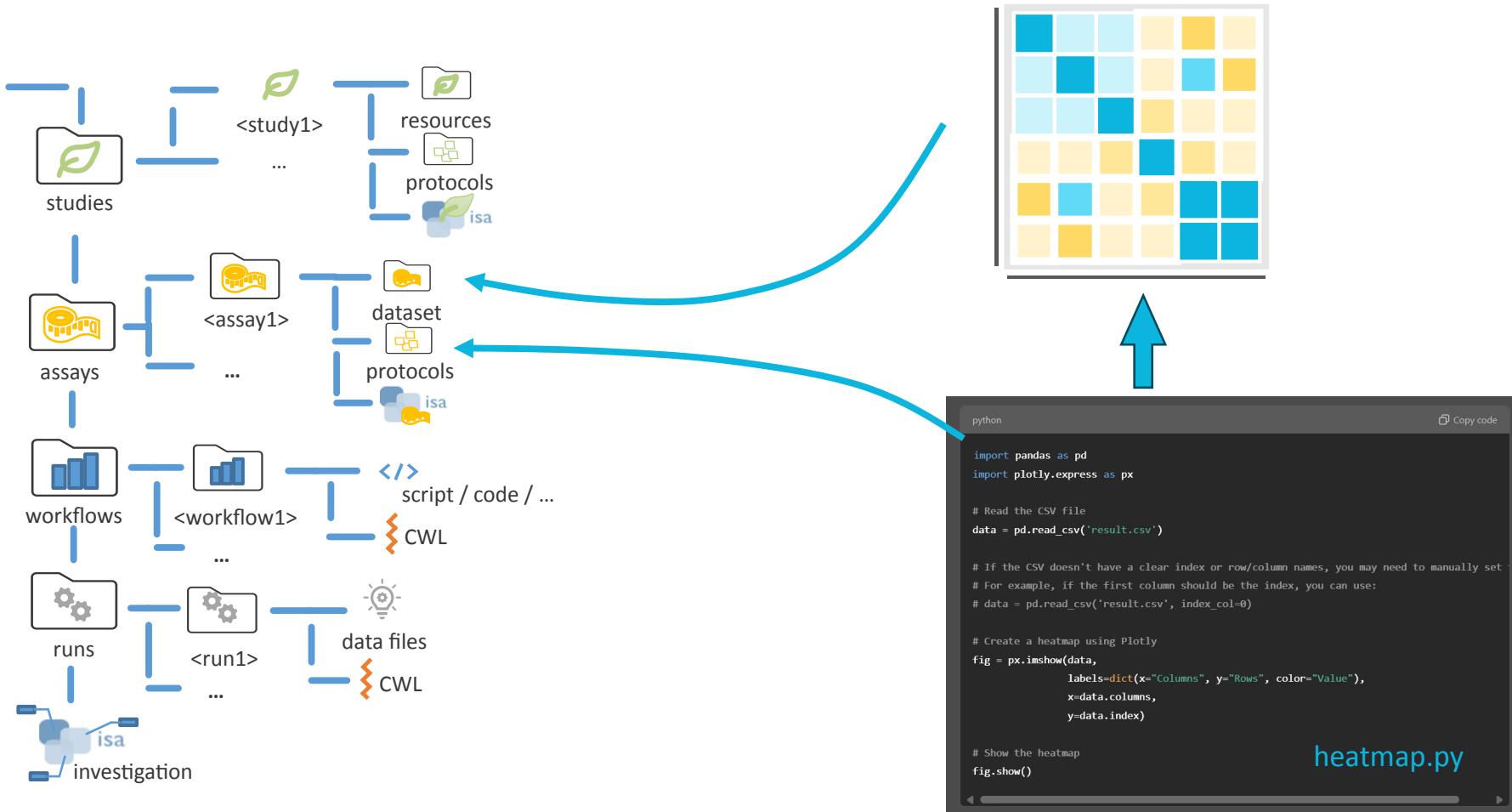
## Options to annotate the data analysis



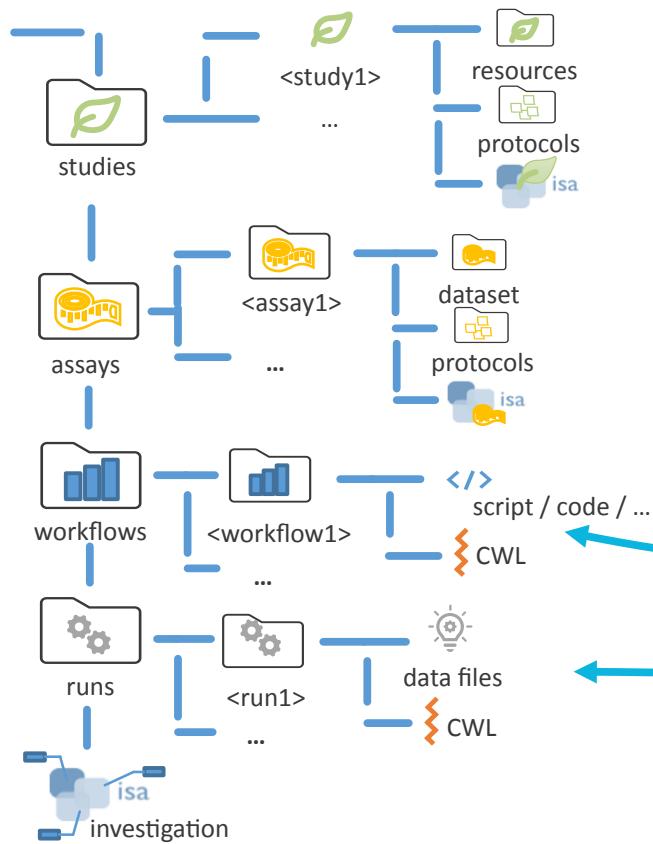
# A computational workflow is like a protocol



# Option I: Create a virtual assay



# Option II: Create a workflow and run



```
python
Copy code

import pandas as pd
import plotly.express as px

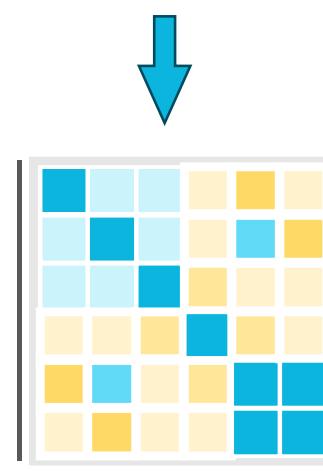
# Read the CSV file
data = pd.read_csv('result.csv')

# 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)

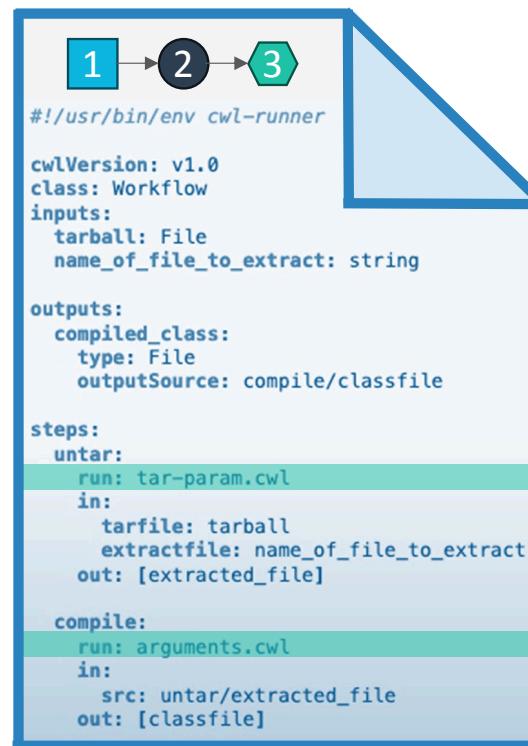
# Show the heatmap
fig.show()
```

heatmap.py



# Use CWL to wrap your workflow

CWL workflow document (\*.cwl)



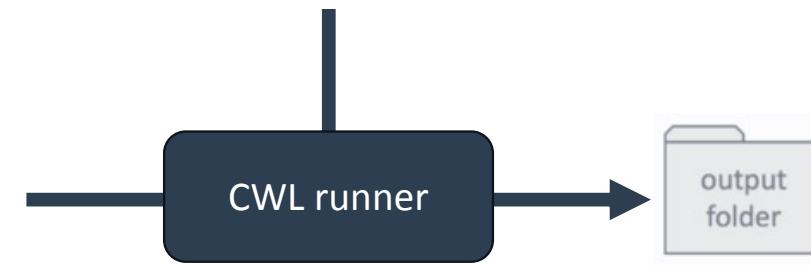
```
graph LR; 1[1] --> 2((2)); 2 --> 3[3];  
#!/usr/bin/env cwl-runner  
cwlVersion: v1.0  
class: Workflow  
inputs:  
  tarball: File  
  name_of_file_to_extract: string  
  
outputs:  
  compiled_class:  
    type: File  
    outputSource: compile/classfile  
  
steps:  
  untar:  
    run: tar-param.cwl  
    in:  
      tarfile: tarball  
      extractfile: name_of_file_to_extract  
      out: [extracted_file]  
  
  compile:  
    run: arguments.cwl  
    in:  
      src: untar/extracted_file  
      out: [classfile]
```

CWL  
tool descriptors (\*.cwl)

CWL job parameter (\*.yaml)



```
file: fastq  
param: 5  
workflow: wf.cwl  
output_folder:  
  /temp
```



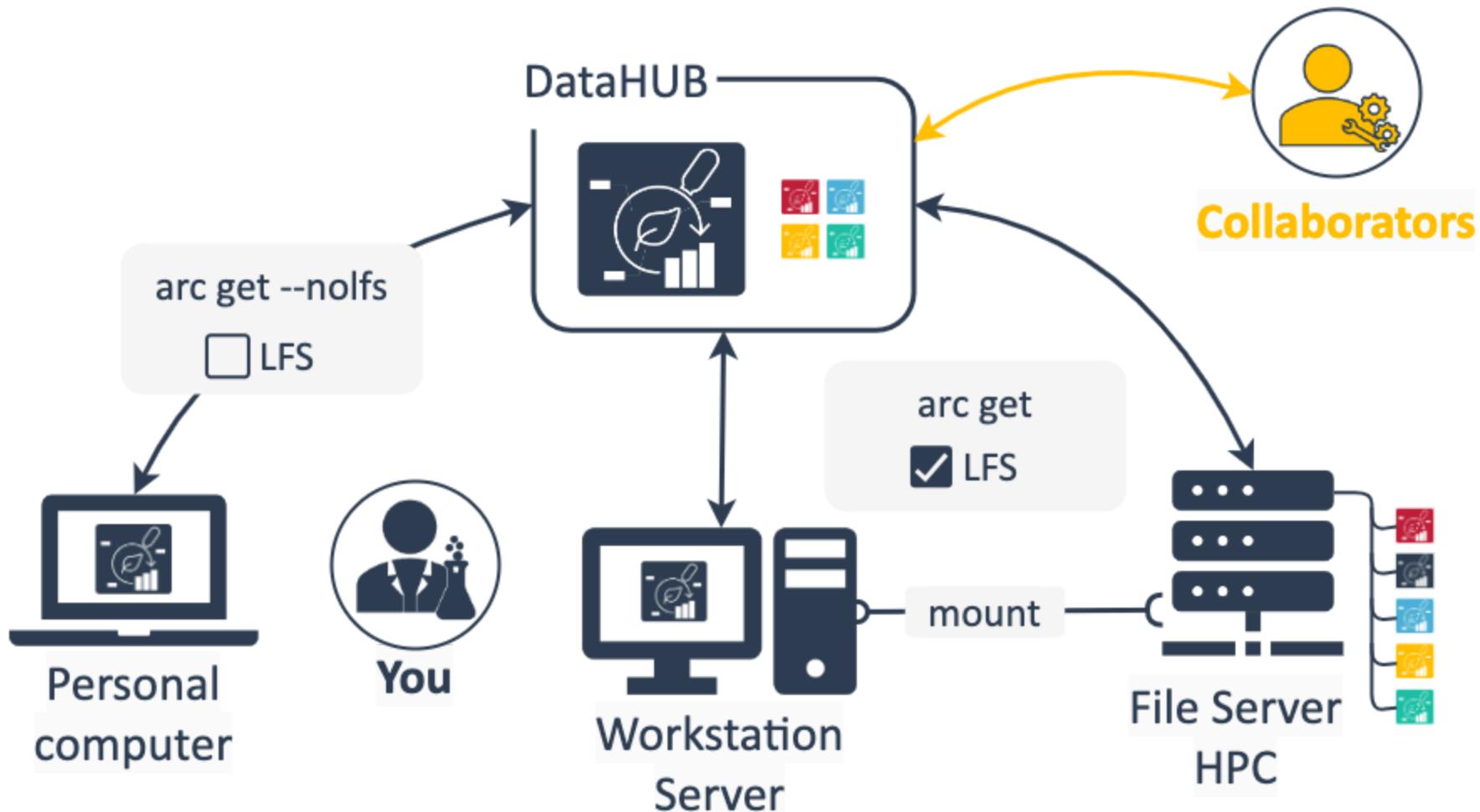
## Hands-on part 3: Data

Continue the [Start Here](#) guide in the DataPLANT knowledge base.

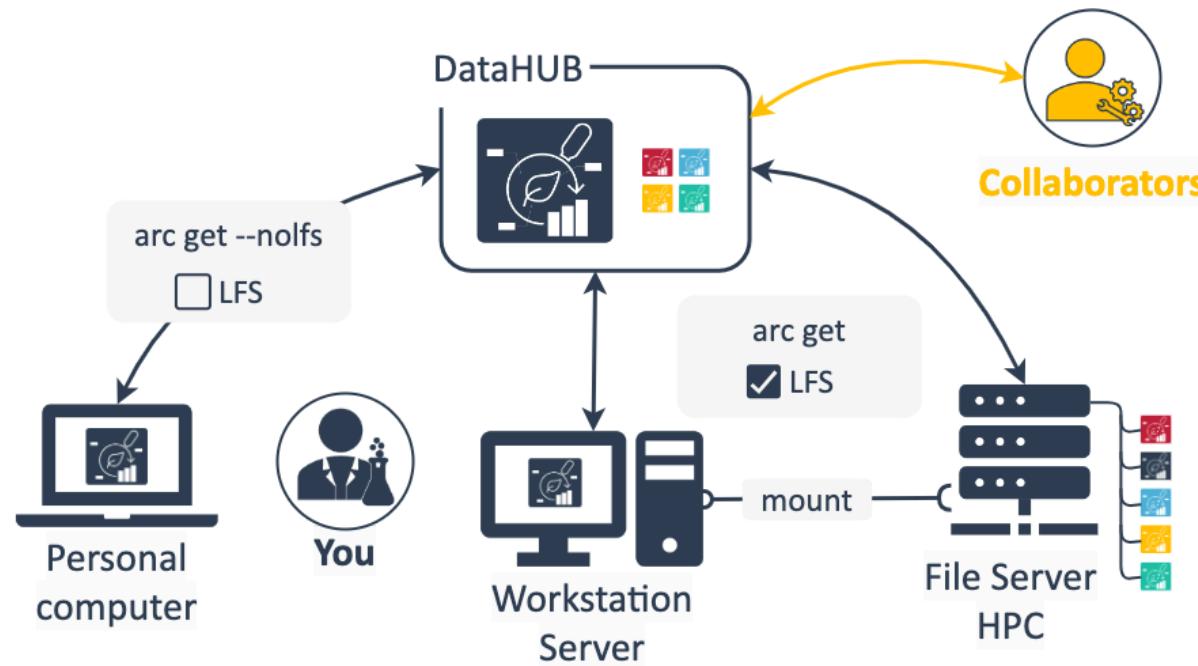
-  We will skip the **Add a datemap** step
-  Do the **Data analysis** step and stop

# DataHUB concepts and terminology

# Where do I store my ARC?



# ARC storage and sharing



- DataHUB as "ground truth" / original clone
- You can sync and communicate all changes to your ARC via the DataHUB

💡 ARCitect and ARC commander provide options to avoid syncing large files (LFS = Large file storage)

# Example setup to store and use ARCs

## Personal computer

- work on small files
- annotate metadata
- add scripts, protocols

## Workstation / Server

- work on large files
- run computations

## FileShare

- mount to local machine, sync ARC from there

## HPC

- direct connection HPC to DataHUB (depends on security settings)
- or mount to local machine and sync, ARC from there

# Projects and Groups are not the same

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

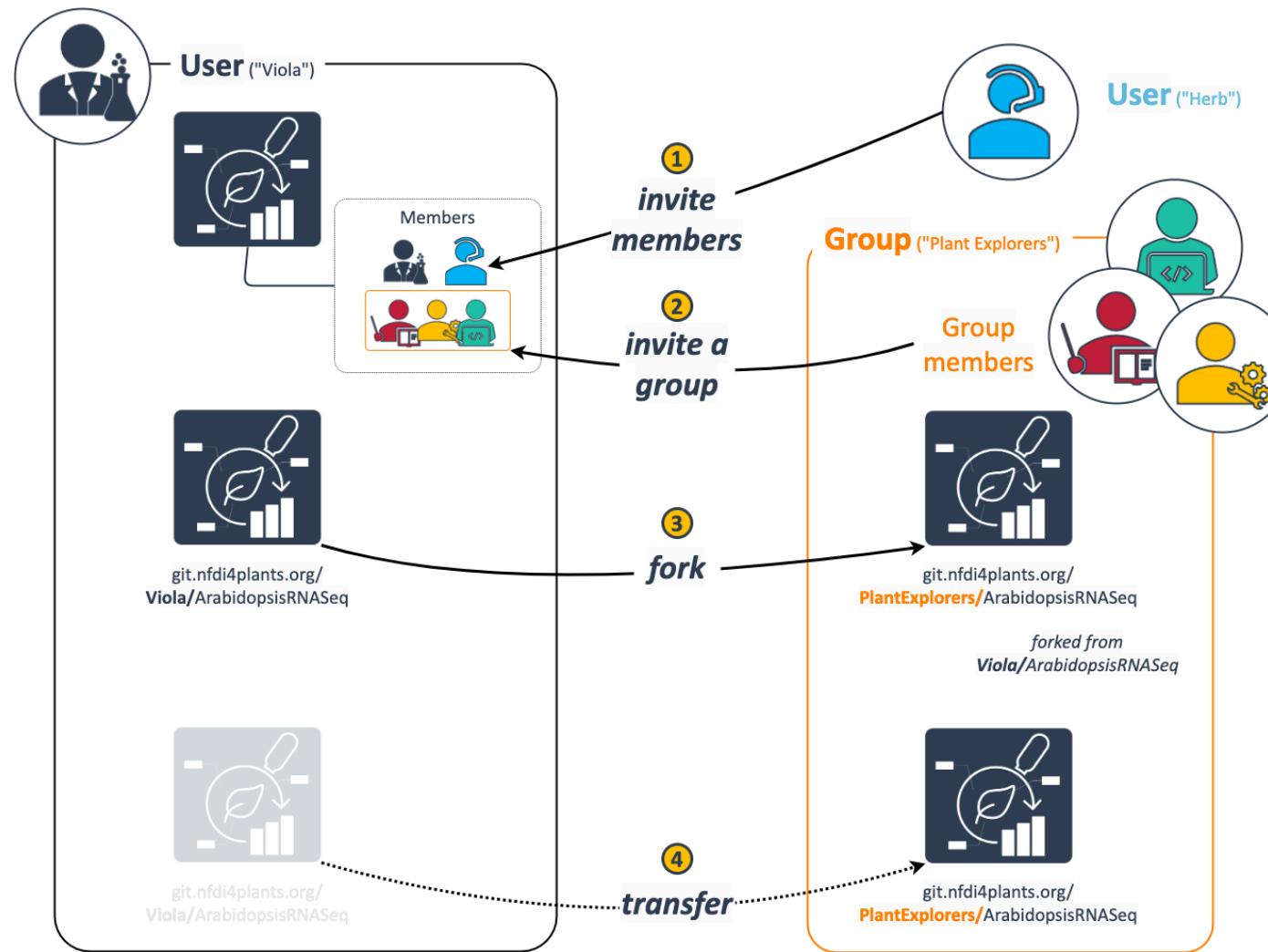
# Project = ARC

- 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

- 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	<a href="https://git.nfdi4plants.org/brilator/Facultative-CAM-in-Talinum">https://git.nfdi4plants.org/brilator/Facultative-CAM-in-Talinum</a>	brilator	Dominik Brilhaus
An group-shared ARC	<a href="https://git.nfdi4plants.org/hhu-plant-biochemistry/Samuilov-2018-BOU-PSP">https://git.nfdi4plants.org/hhu-plant-biochemistry/Samuilov-2018-BOU-PSP</a>	hhu-plant-biochemistry	HHU Plant Biochemistry

 **Personal** is not the same as **private**

# 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**.

# Permissions & Roles

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.

# ARC DataHUB members // ARC Investigation contacts

The screenshot shows the 'Members' section of a project named 'Samuilov-2018-BOU-PSP'. It includes a search bar, buttons for 'Import from a project', 'Invite a group', and 'Invite members', and a table with columns for Account, Source, Max role, Expiration, and Activity. The table lists four members:

Account	Source	Max role	Expiration	Activity
Adriano Nunes-Nesi @unesnesi	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 @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](https://git.nfdi4plants.org/hhu-plant-biochemistry/Samuilov-2018-BOU-PSP/-/project_members)

The screenshot shows the 'Samuilov-2018-BOU-PSP' page in ARCIct. It includes sections for Identifier, Title, Description, and Contacts. The 'Contacts' section lists ten individuals with their scores and links to their profiles.

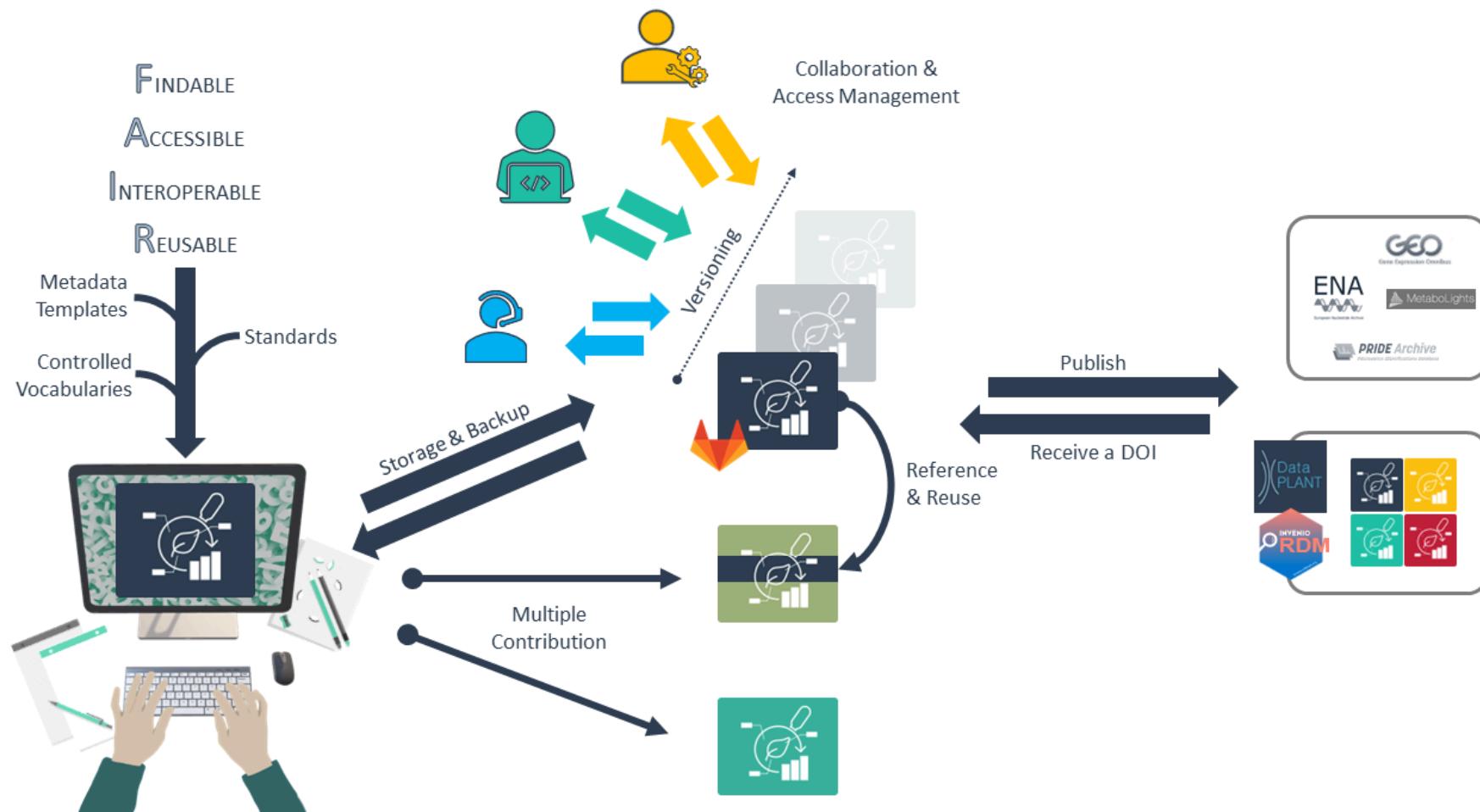
Contact	Score
Sladjana Samuilov <orcid>	4/10
Nadine Rademacher <orcid>	3/10
Samantha Flachbart <orcid>	3/10
Leila Arab <orcid>	3/10
Saleh Alfarraj <orcid>	3/10
Franziska Kuhnert <orcid>	3/10
Stanislav Kopriva <orcid>	3/10
Andreas P. M. Weber <orcid>	4/10
Tabea Mettler-Altmann <orcid>	3/10

**ARCIct: Investigation Contacts**

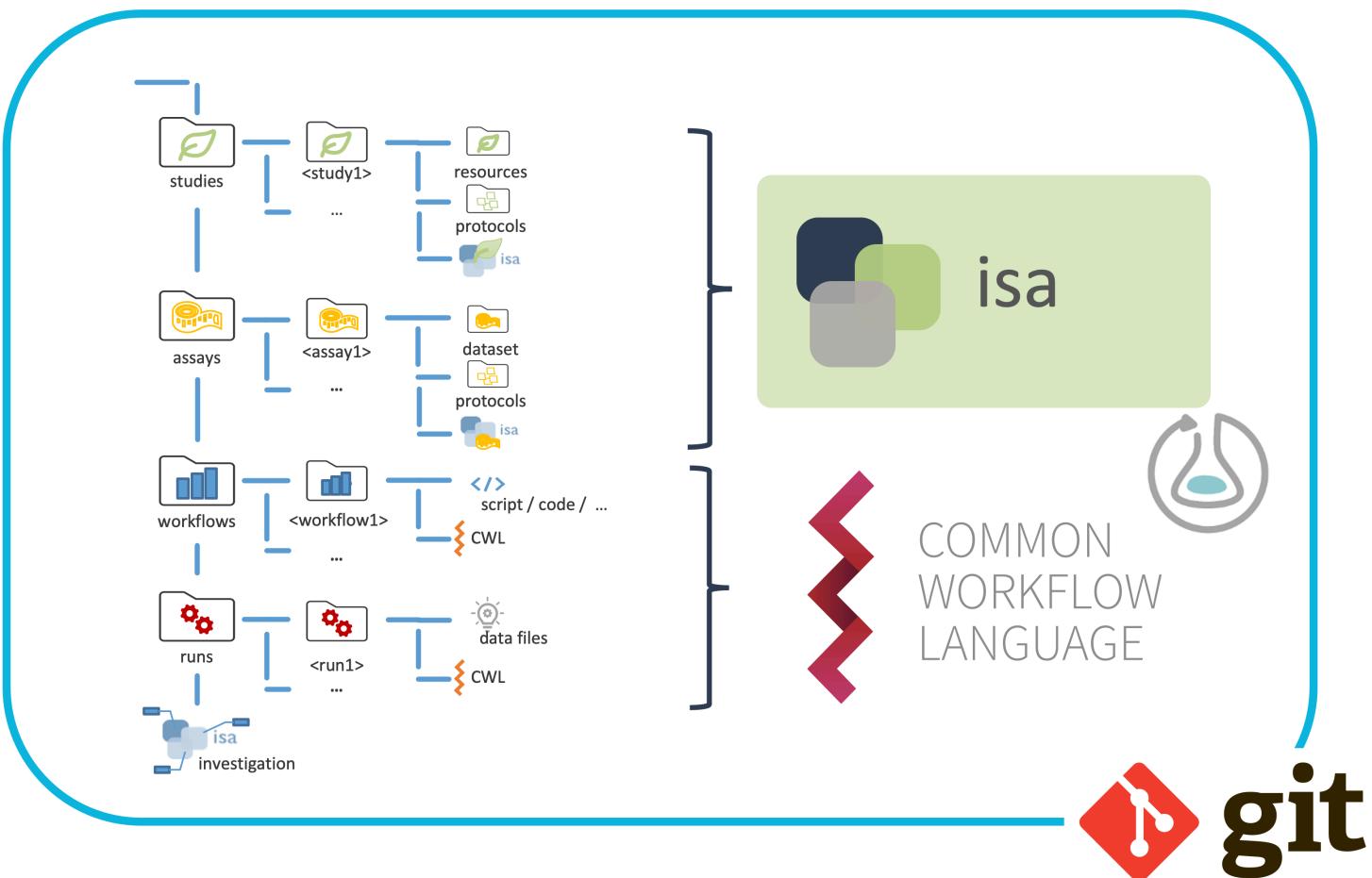
Investigation contacts are not automatically invited as members to the ARC.

# Hands-on part 4: DataHUB

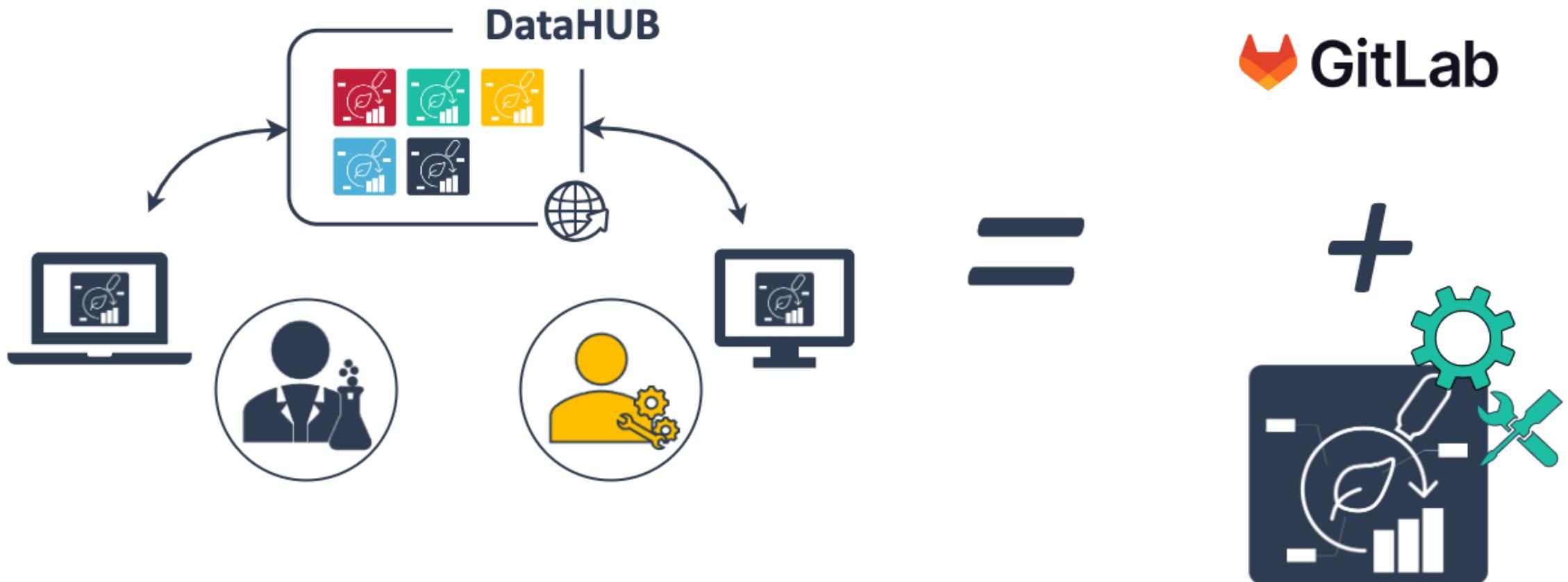
# DataHUB overview



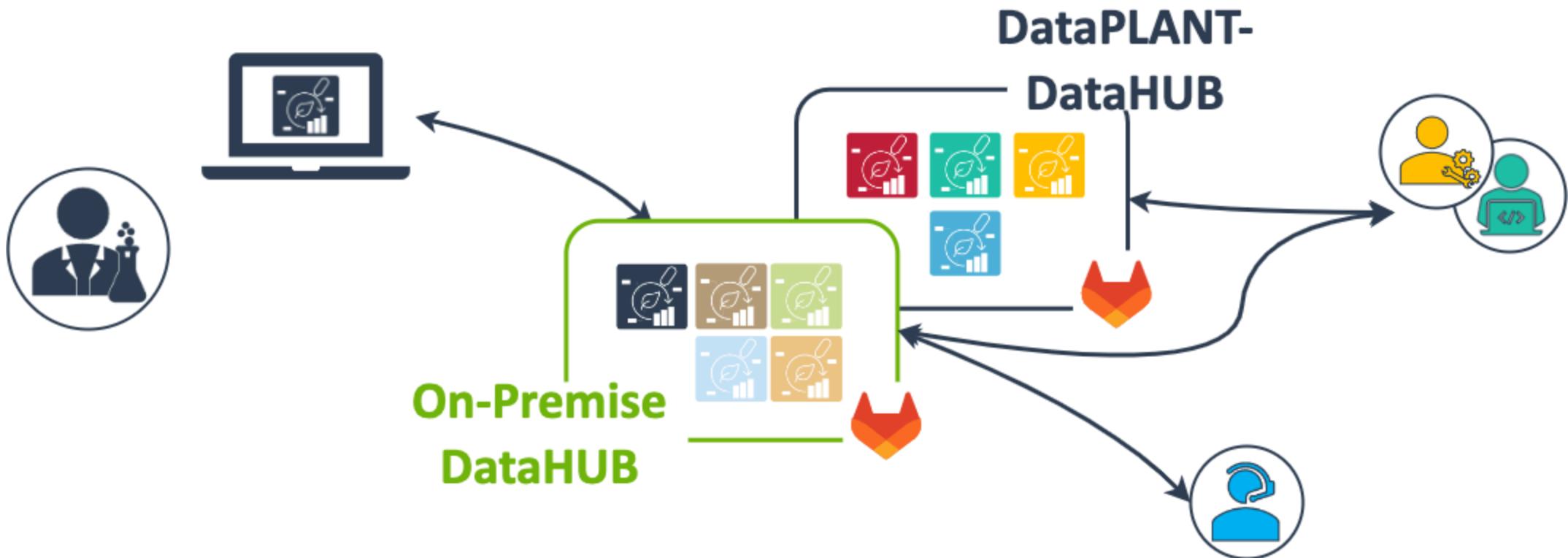
# ARC builds on standards + Git



# The DataPLANT DataHUB – a GitLab *Plus*

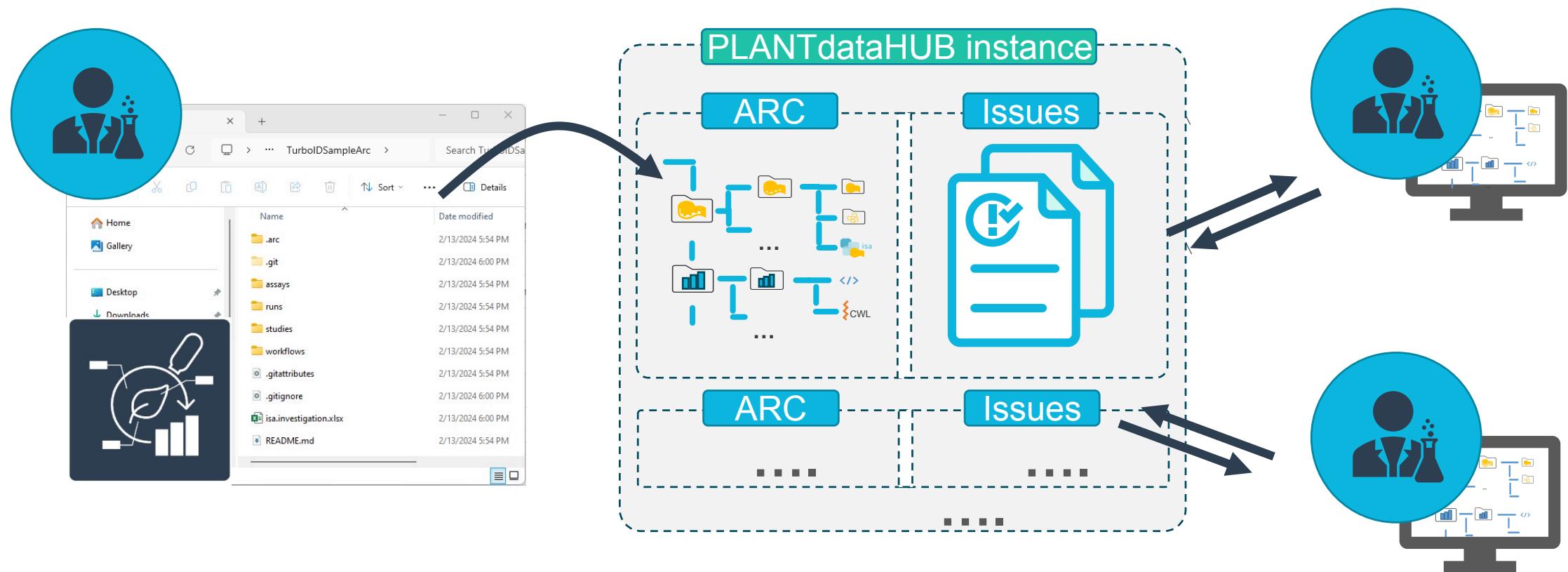


# On-premise DataHUBs

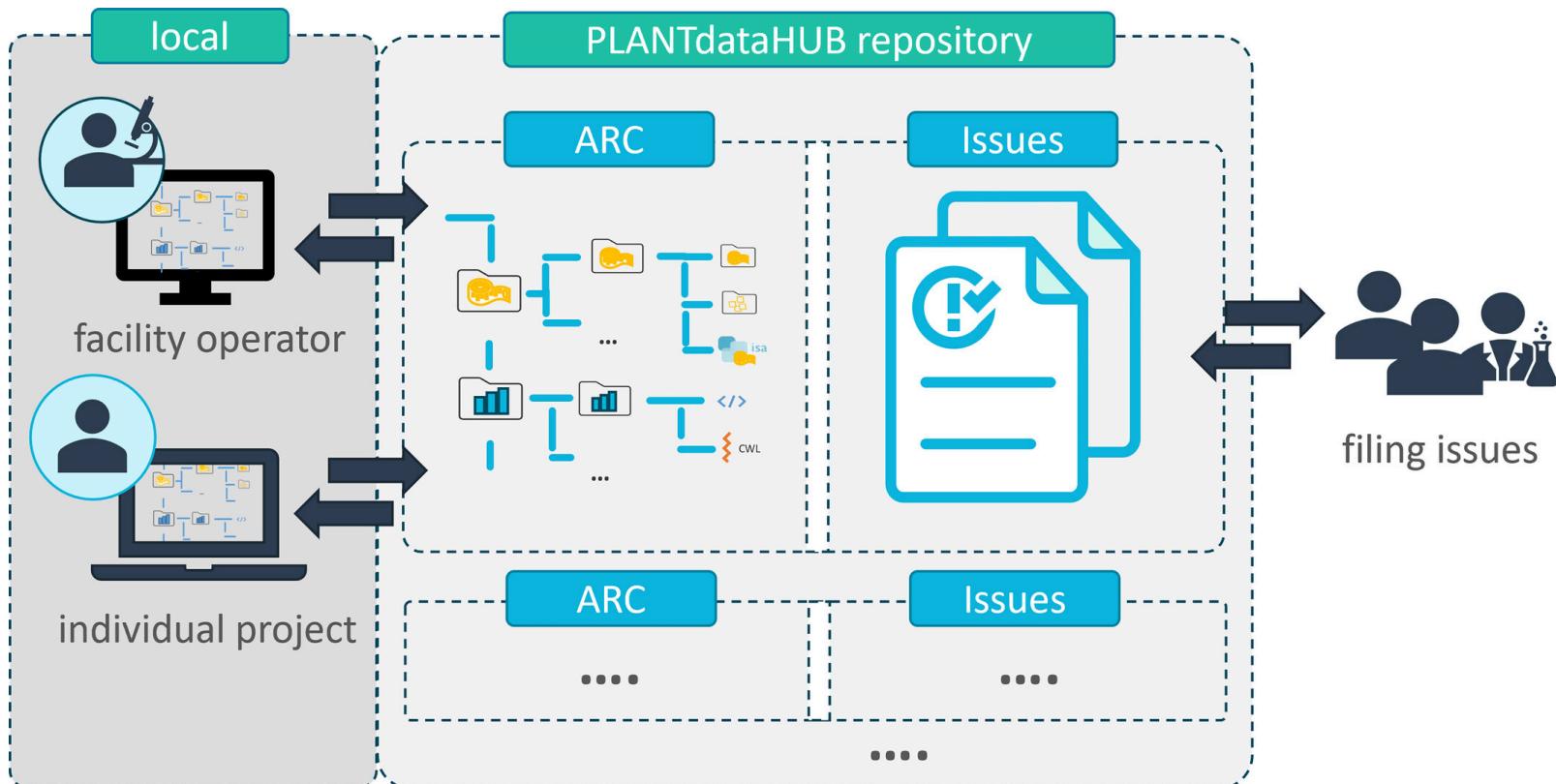


ARC services are available as on-premise option

# Using the DataHUB to collaborate



# Project management



# ARCs come with their own wiki space

- directly associated to your ARC
- same access rights as your ARC
- share meeting minutes or ideas with collaboration partners
- keep ARC clean of files that are not considered "research data"

The screenshot shows a DataHub interface for an ARC named 'Demo\_ARC'. The sidebar on the left contains links for Project (Demo\_ARC), Pinned, Manage, Plan, Issues (0), Issue boards, Milestones, Wiki (which is currently selected), Code, Build, Secure, and Help. The main content area has a header 'Home' and a message about CQC pipelines. It includes sections for 'Home' (last edited by Demo User just now), 'Meeting Schedule' (with a list of dates: 2024-06-12 Kick-off, 2024-06-27 Proposal discussion, 2024-07-04 Discuss RNA-seq pipeline), and 'Ideas and drafts' (Golden Gate protocol).

## Hands-on part 4: DataHUB

Continue the [Start Here](#) guide in the DataPLANT knowledge base.



Until the final **complete** step

# elabFTW Introduction

# Login into eLabFTW HHU

The screenshot shows the login interface for eLabFTW HHU. At the top center is the eLabFTW logo, which consists of a stylized flask icon containing blue liquid and the text "eLabFTW". Below the logo is a horizontal line. Underneath the line, the text "Über Ihre Institution anmelden" is displayed. Below this text is a sub-instruction "Wählen Sie einen Identitätsanbieter aus". A dropdown menu is open, showing the option "HHU-IDM". To the right of the dropdown is a checked checkbox labeled "Anmeldung merken". Below these elements is a teal-colored button labeled "Anmelden". At the bottom left of the page, there is a footer bar with icons for social media (Twitter, Facebook, etc.) and a link to "DATENSCHUTZ-BESTIMMUNGEN". At the bottom right, there is text indicating the page is "Bereitgestellt von eLabFTW" and was "Seite generiert in 0.00437 Sekunden".

# eLab-FTW - Dashboard

Dashboard  
Welcome Sabrina

---

Experiments [Create](#)

Browse by category [IMAGING](#) [BEHAVIOUR](#) [METABOLISM](#) [DISEASE](#) [NEURO](#) [ASSAY](#) [STUDY](#)

Browse by status [RUNNING](#) [SUCCESS](#) [REPEAT](#) [FAIL](#) [DRAFT](#)

Last modified experiments

- [INV0001\\_A1\\_Sugar measurement](#) 23 seconds ago
- [INV0001\\_A1\\_Sugar Extraction](#) 1 minute ago
- [Growth Protocol for Arabidopsis thaliana](#) 9 minutes ago

Resources [Create](#)

Browse by category [STANDARD](#) [INVESTIGATION](#) [STUDY](#)

Last modified resources

- [STUDY INV0001\\_S1\\_AthalianaColdStress](#) 15 minutes ago
- [INVESTIGATION INV0001\\_A.thaliana\\_ColdStress\\_Sugar](#) 17 minutes ago

Scheduled bookings [Scheduler](#)

# eLabFTW - Experiment panel

The screenshot shows the eLabFTW Experiment panel. At the top, there is a navigation bar with links for EXPERIMENTS (which is highlighted in blue), RESOURCES, TEAM, SEARCH, and DOCUMENTATION. To the right of the navigation bar are icons for search, notifications, help, and user profile.

The main area is titled "Experiments" and features a "Create" button in the top right corner. Below the title, there is a "Expand all - Select all" link and a set of filter and sorting options: Scope, Filters, and Sort.

The experiment list table has columns for Date, Title, Next step, Category, Status, Tags, Rating, and Owner. The first experiment listed is "INV0001\_A1\_Sugar measurement" (Status: SUCCESS, Owner: Sabrina Zander). The second experiment listed is "INV0001\_A1\_Sugar Extraction" (Status: RUNNING, Owner: Sabrina Zander).

At the bottom of the experiment list, there is a "Load more" button. The footer of the page includes links for X, GitHub, and other social media, along with links for PRIVACY POLICY and TERMS OF SERVICE. On the right side of the footer, it says "Powered by eLabFTW 5.1.12" and "Made with ❤ by Deltablot".

Date	Title	Next step	Category	Status	Tags	Rating	Owner
2025-01-09	INV0001_A1_Sugar measurement		SUCCESS	A.thaliana INV001 sugar	Sabrina Zander		
2025-01-09	INV0001_A1_Sugar Extraction		RUNNING	A.thaliana INV001 sugar	Sabrina Zander		

Default "working area" for protocols of daily lab work

# eLabFTW - Resource panel

Screenshot of the eLabFTW Resource panel interface.

The top navigation bar includes links for EXPERIMENTS, **RESOURCES**, TEAM, SEARCH, and DOCUMENTATION, along with a search bar, notification bell, help icon, and user profile icon.

## Resources

Expand all - Select all

Date	Title	Next step	Category	Status	Tags	Rating	Owner
2025-01-09	INV0001_S1_AthalianaColdStress		STUDY	A.thaliana INV001			Sabrina Zander
2025-01-09	Growth Protocol for Arabidopsis thaliana		METHODE	A.thaliana			Sabrina Zander
2025-01-09	INV0001_A.thaliana_ColdStress_Sugar		INVESTIGATION	A.thaliana INV001			Sabrina Zander

**Create**

Load more

X | Q | M | S | PRIVACY POLICY | TERMS OF SERVICE | Powered by eLabFTW 5.1.12  
Made with ❤ by Deltabet

Place to categorize content

# eLabFTW - Experiment information

The screenshot shows the eLabFTW experiment information page for 'INV0001\_A1\_Sugar Extraction'. The page includes fields for Started on (09.01.2025), ID (185), Category (Assay), Status (Running), Tags (A.thaliana, INV001, sugar), and MAIN TEXT (Last saved: 6 minutes ago). Annotations highlight several features:

- signature**: Points to the signature icon in the top right.
- timestamp**: Points to the timestamp icon in the top right.
- different export functions**: Points to the download icons in the top right.
- status**: Points to the status dropdown menu.
- tags**: Points to the tags input field.
- sharing**: Points to the sharing settings below the tags.
- pin**: Points to the pin icon in the top right.
- lock**: Points to the lock icon in the top right.
- request action**: Points to the request action icon in the top right.
- More options**: Points to the 'More options' button in the top right.
- Transfer ownership**: Points to the Transfer ownership option in the dropdown menu.
- See revisions**: Points to the See revisions option in the dropdown menu.
- See changelog**: Points to the See changelog option in the dropdown menu.
- Archive/Unarchive**: Points to the Archive/Unarchive option in the dropdown menu.
- Delete**: Points to the Delete option in the dropdown menu.

# eLabFTW - Tag usage

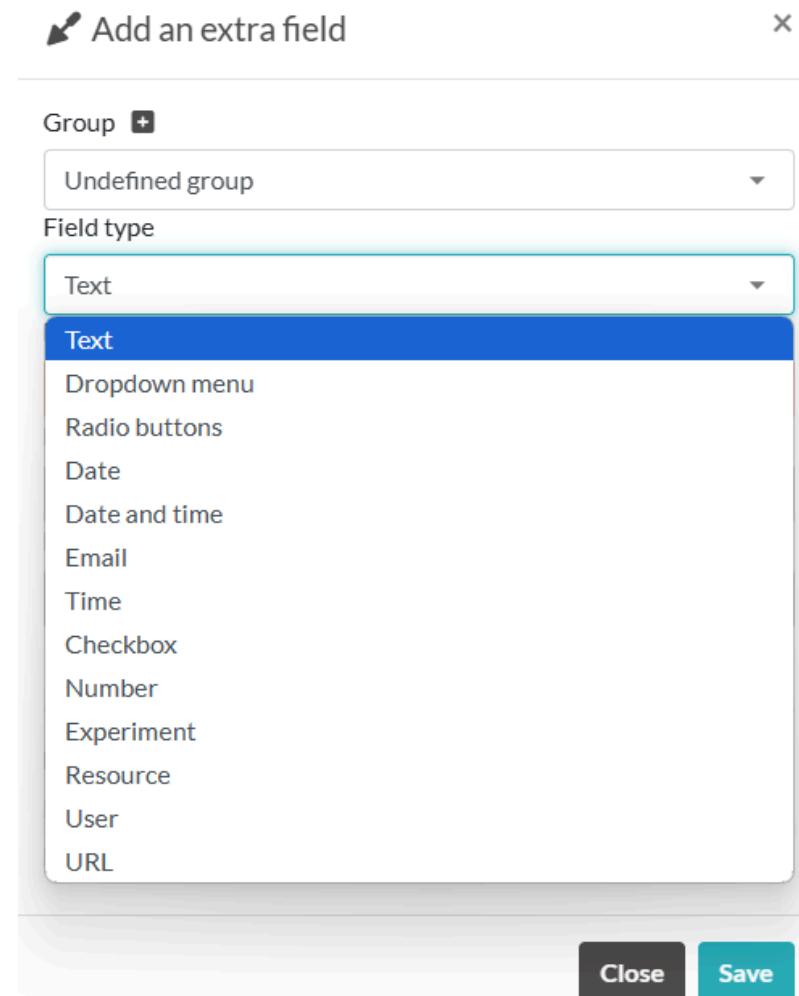
Very individual, some examples:

- Investigation ID
- Subgroup
- Organism /part (e.g. A.taliana, leaf, root, mitochondria)
- Goal (strain generation, plasmid genertion)
- Methode (e.g. transformation, western blot, extraction, biolector)
- Genes/ Proteins (e.g. mKate2, eGfp, Rrm4)

Use keywords you would search/filter for

 Make rules for tag usage

# eLabFTW - Extra fields



# eLabFTW - Extra fields examples

Dropdown	URL	Number	Date
<p>Field type Dropdown menu</p> <p>Name (required) *</p> <p>Antibiotic used</p> <p>Description</p> <p>Select the antibiotic used</p> <p>Choices</p> <p>Kanamycin</p> <p>Streptomycin</p> <p>Ampicillin</p> <p>Add another choice</p> <p><input type="checkbox"/> Allow selection of multiple values?</p>	<p>EXTRA FIELDS</p> <p>UNDEFINED GROUP</p> <p>OMERO dataset <a href="https://omero-cai.hhu.de/webclient/?show=dataset-12881">https://omero-cai.hhu.de/webclient/?show=dataset-12881</a></p>	<p>Extra fields</p> <p>End date 06 / 09 / 2021</p> <p>Magnification 20X</p> <p>Pressure (Pa) 12</p> <p>Wavelength (nm) 488 405 647</p>	<p>Field type Number</p> <p>Name (required) *</p> <p>Drug concentration</p> <p>Description</p> <p>Indicate the drug concentration</p> <p>Available units</p> <p>ng/mL</p> <p>µg/mL</p> <p>mg/mL</p> <p>Add another choice</p>

# eLabFTW - Experiment categories examples

- Study
- Assay
- Discussion
- Teaching
- Demo
- R&D
- Production

# eLabFTW - Categories in Resources

Use Resources to categorize content & manage lab

Use unique identifier & naming conventions ( e.g. Methode MTH0001, Media MED0001, Plasmid PL0001)

- Investigation
- Plant sheet
- Plasmid sheet
- Collections
- Methode
- Manual
- Media & Solution

# eLabFTW - Scheduler

SCHEDULER   MEMBERS   EMAIL   PROCUREMENT REQUESTS BETA

Filter by category   Equipment - Zeiss AXIO Observer Z1 Inverted Fluorescence Microscope   Scope

< > today   6 - 12 Jan 2025   week list month

	Mon 06/01	Tue 07/01	Wed 08/01	Thu 09/01	Fri 10/01	Sat 11/01	Sun 12/01
00							
01							
02							
03							
04							
05							
06					6:00 - 12:30 (Sabrina Zander)		
07							
08							
09							
10							
11							
12							

# eLabFTW - Booking parameter

You can modify booking parameter for reach Resource

Zeiss AXIO Observer Z1 Inverted Fluorescence Microscope Create

[←](#)

Started on	09.01.2025 <a href="#"></a>	Custom ID <a href="#" style="background-color: #2e3436; color: white; padding: 2px 5px; border-radius: 3px;">Get next</a>
ID	115	Transfer ownership
Category	Equipment	See revisions
Status	Not set	See changelog
Tags	Add a tag	Archive/Unarchive

[▶ Suggested tags](#)

[Modify booking parameters](#)  
 [Modify procurement parameters](#)  
 [Transfer ownership](#)  
 [See revisions](#)  
 [See changelog](#)  
 [Archive/Unarchive](#)  
 [Delete](#)

# eLabFTW - Templates

# eLabFTW - Tipps and tricks

# eLabFTW - Support

# elab2ARC Documentation

<https://nfdi4plants.github.io/nfdi4plants.knowledgebase/resources/elab2arc/>

# Conversion



The elab2ARC tool will automatically convert your eLabFTW experiments into ARC format

- create a new assay folder with eLabFTW experiment name as assay name (green)
- create the assay folder structure (dataset/protocols/isa.assay)
- convert experiment main text into a .md file and store it in the protocol folder (purple)
- add all attachments of the eLabFTW experiment into the dataset folder (yellow)
- enter name/email/affiliation of the eLabFTW experiment metadata into the isa.assay sheet

