

ARCify your research project

January, 2025

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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.

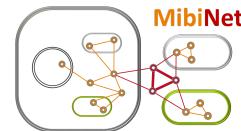
1. Slack Workspace for ad hoc support
2. Monthly user meeting (2nd Friday of the month)

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

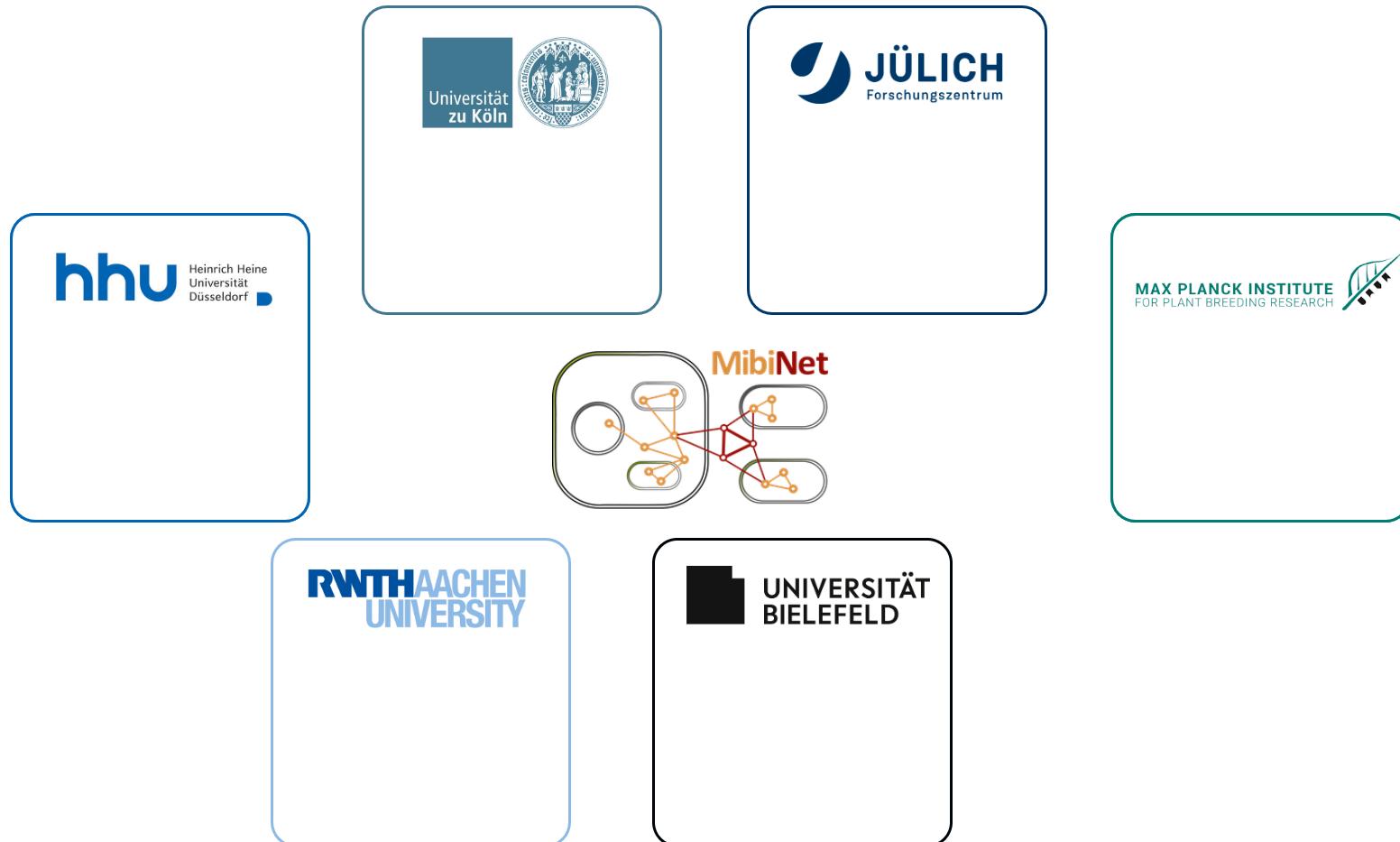
Is your data FAIR?

Findable | Accessible | Interoperable | Reusable

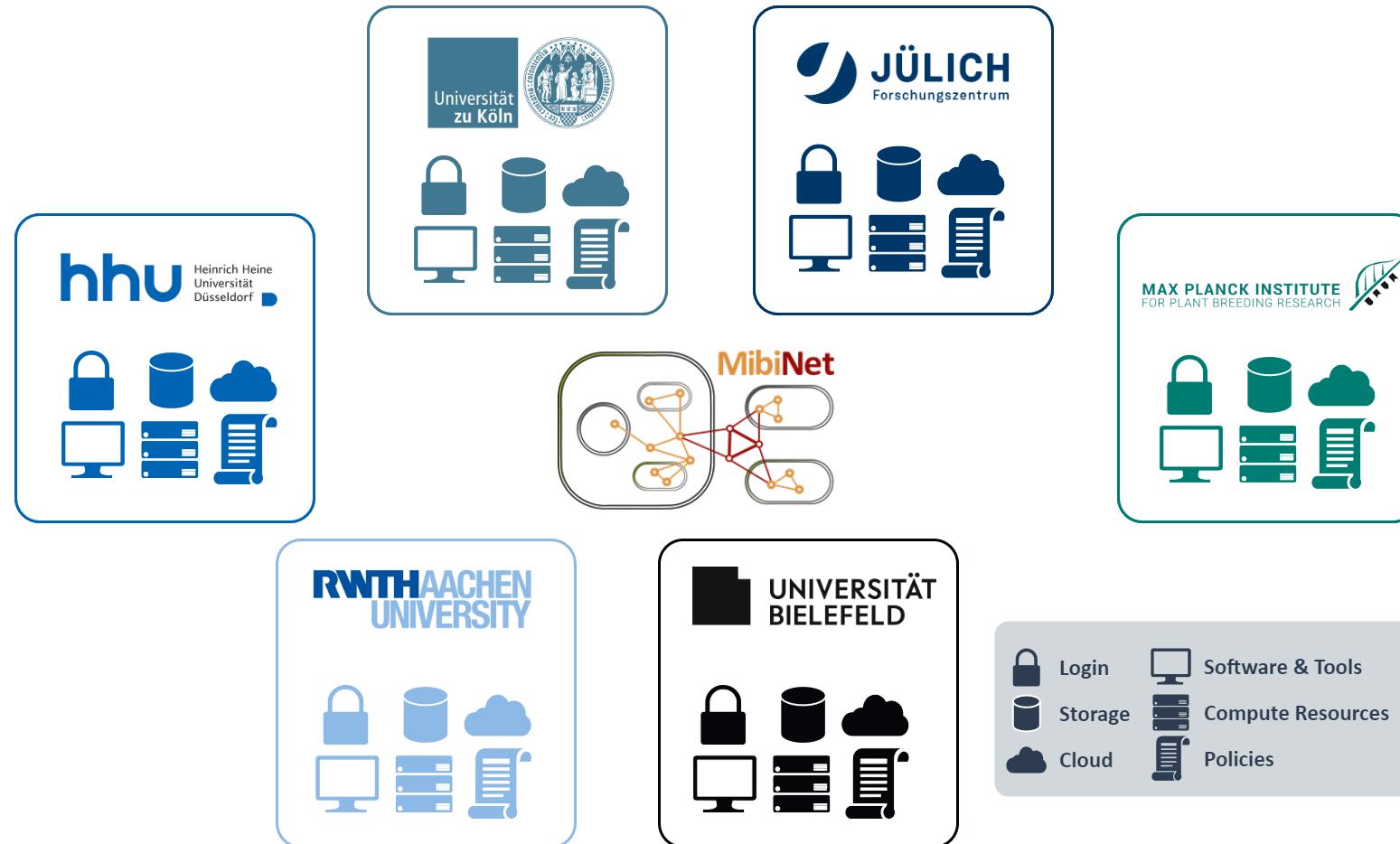
- Where do you store your data?
- How do you annotate your data?
- How do you share your data?
- What tools do you use to analyse your data?
- How do you reuse other people's data?



MibiNet – One SFB, six locations

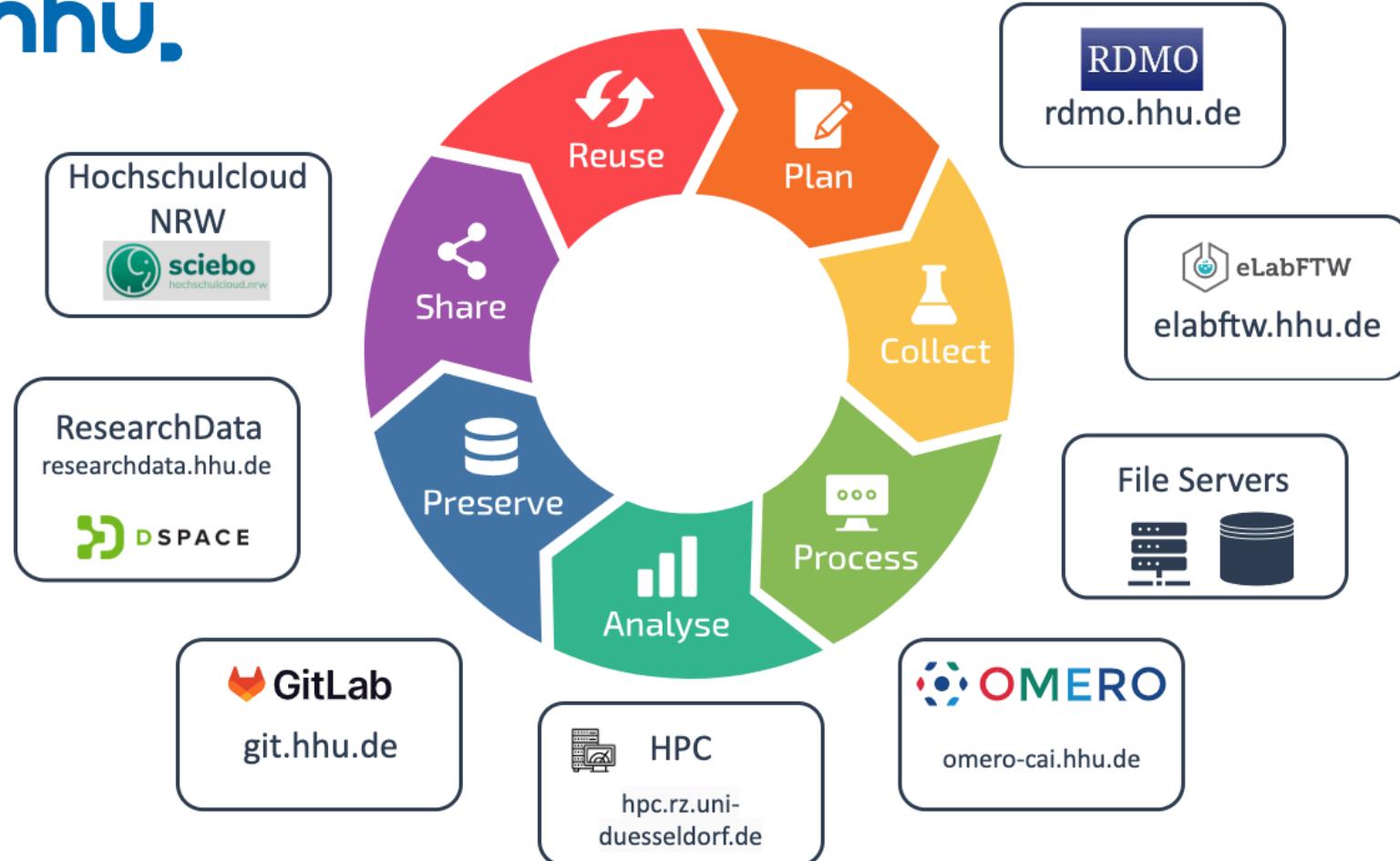


Data silos impede collaboration



Missing interfaces impede collaboration

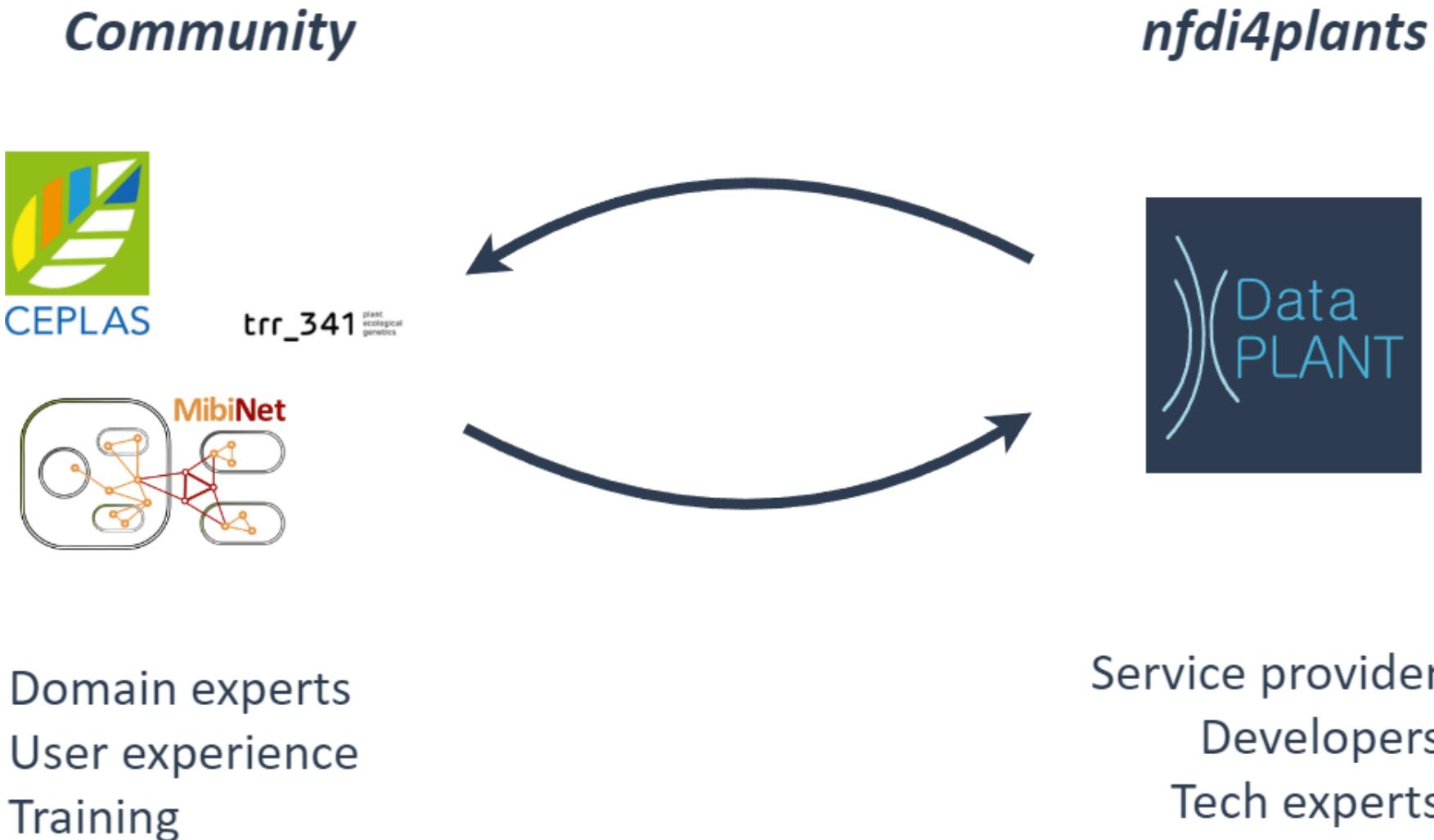
hhu.



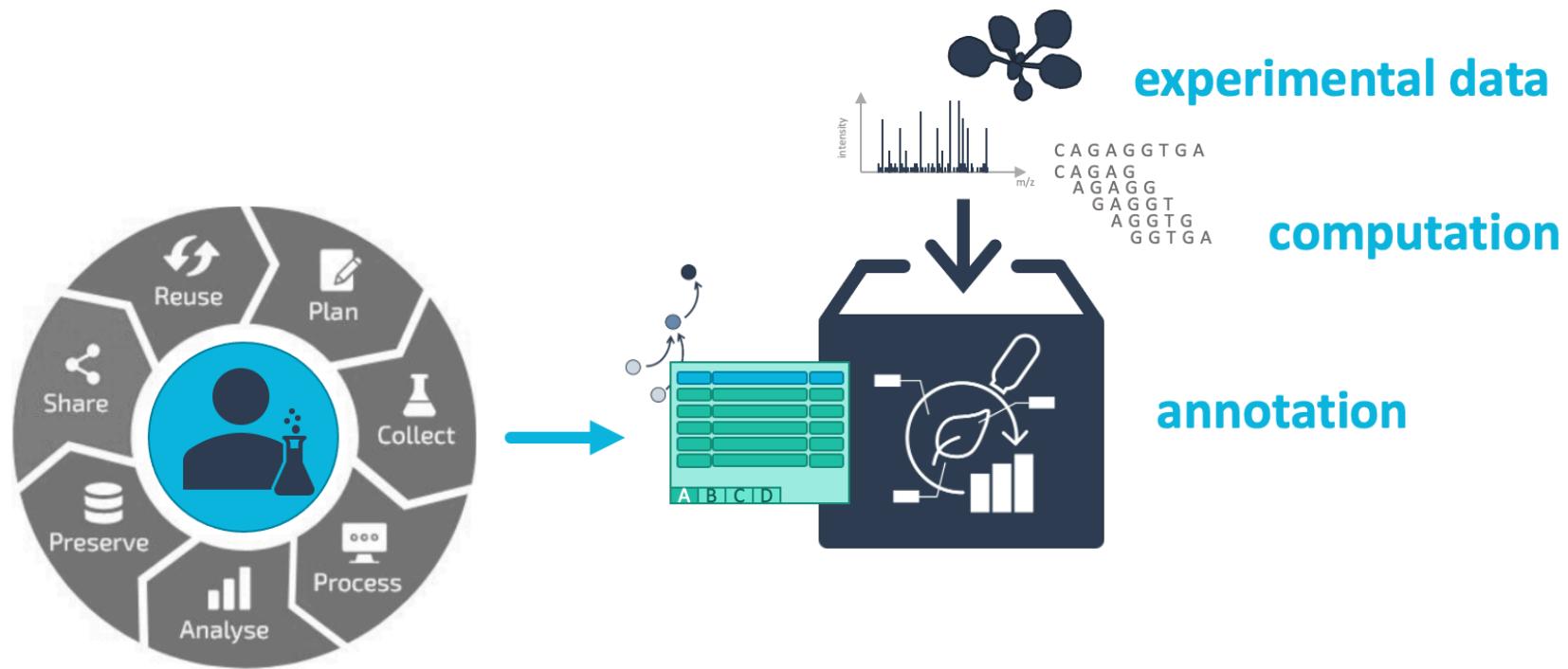
MibiNet connection to NFDIs



Data Stewardship between DataPLANT and the community

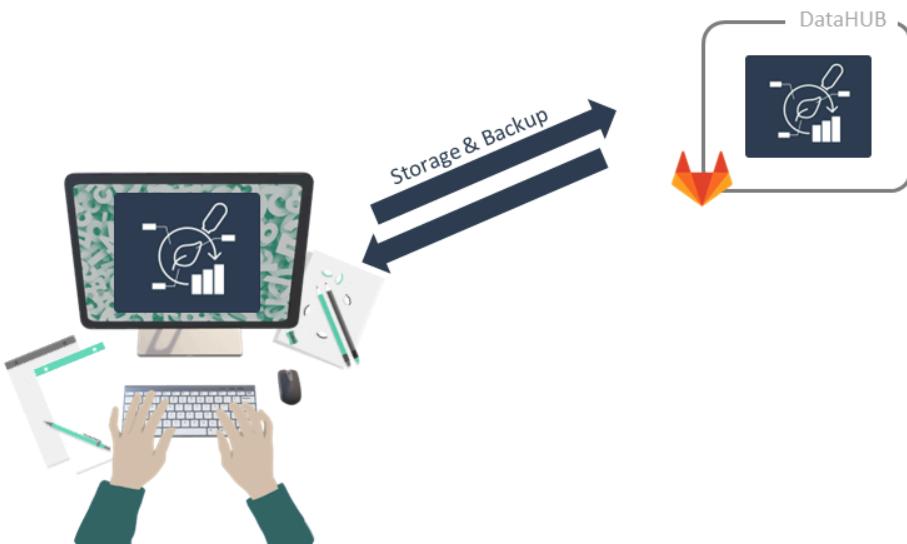


Annotated Research Context (ARC)

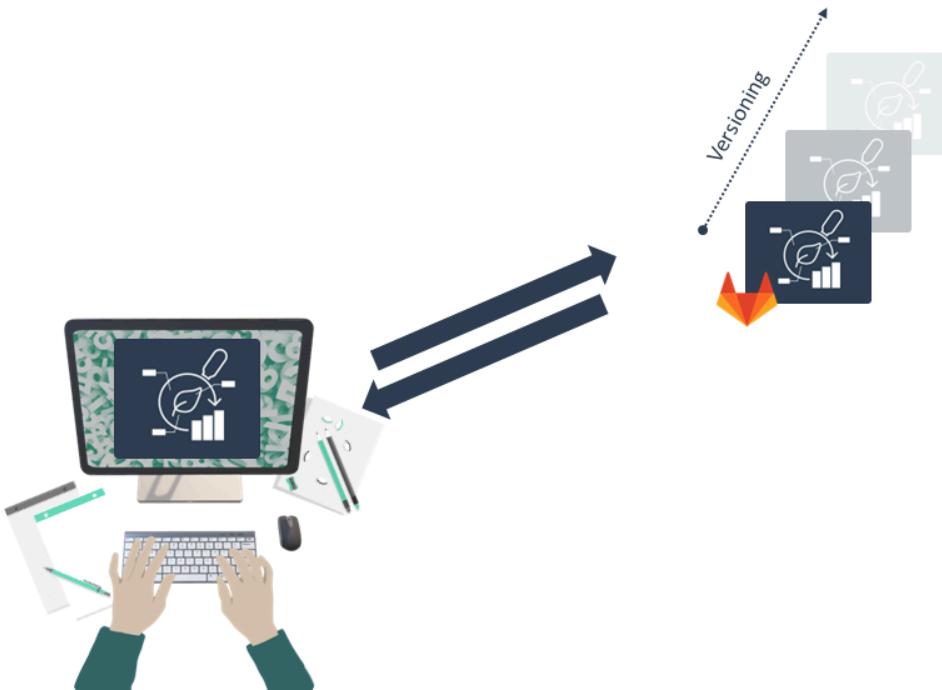


Your entire investigation in a single unified bag

You can store your ARC in the DataHUB



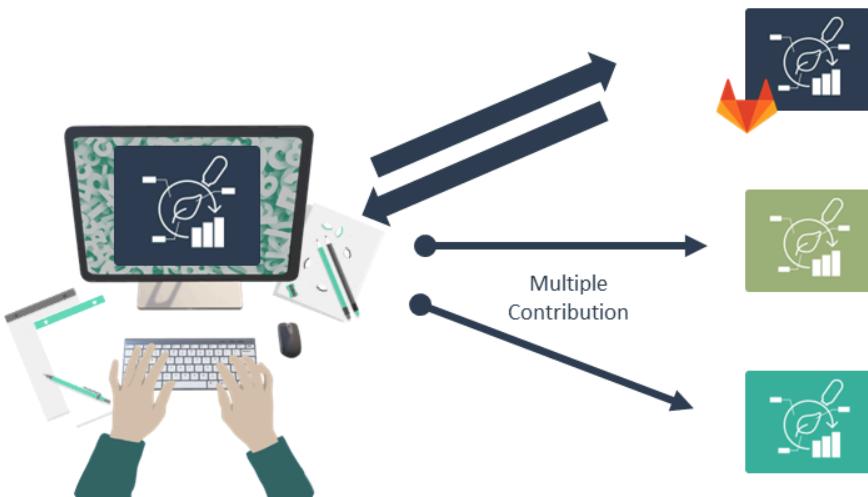
ARCs are versioned



You can invite collaborators



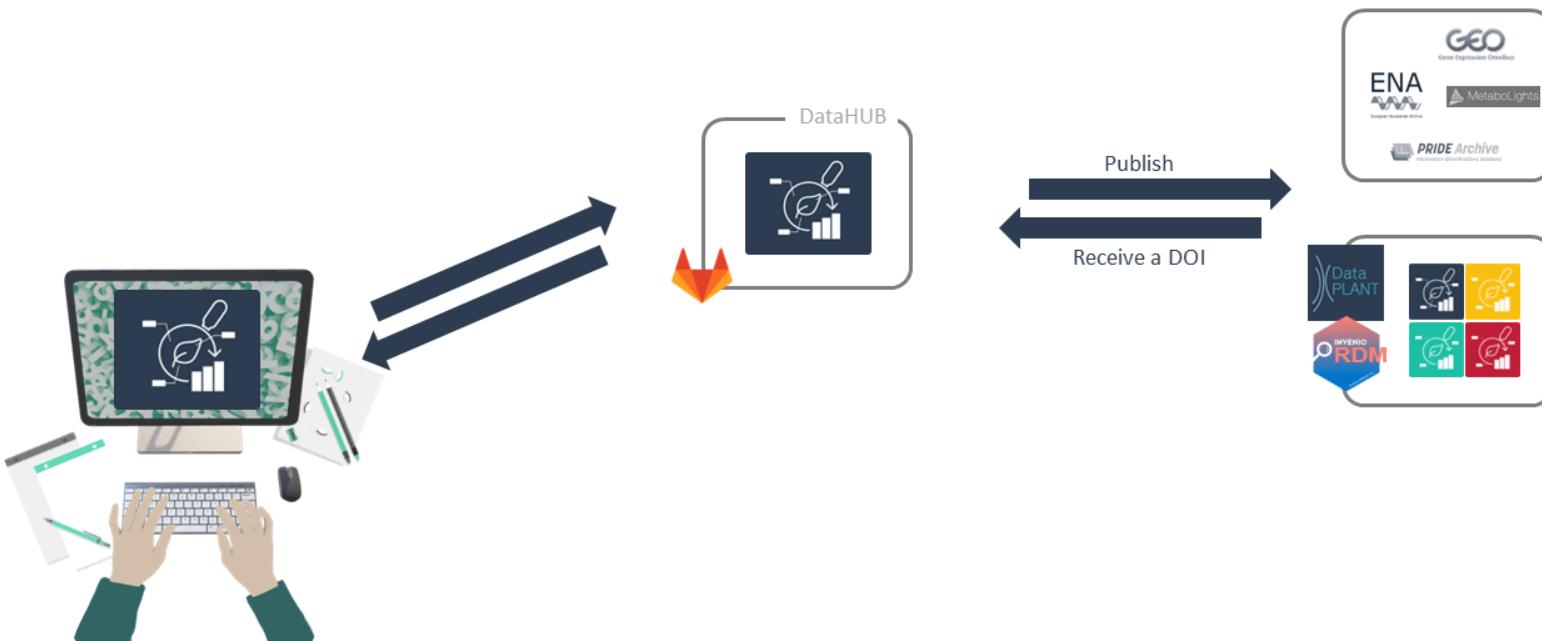
Collaborate and contribute



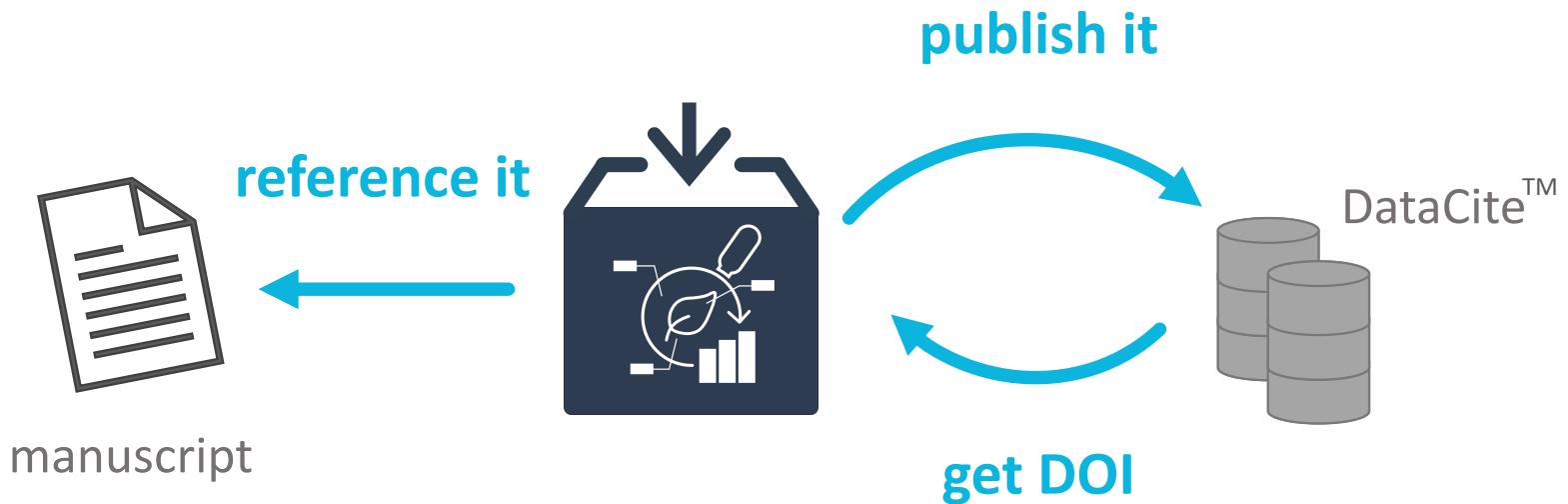
Reuse data in ARCs



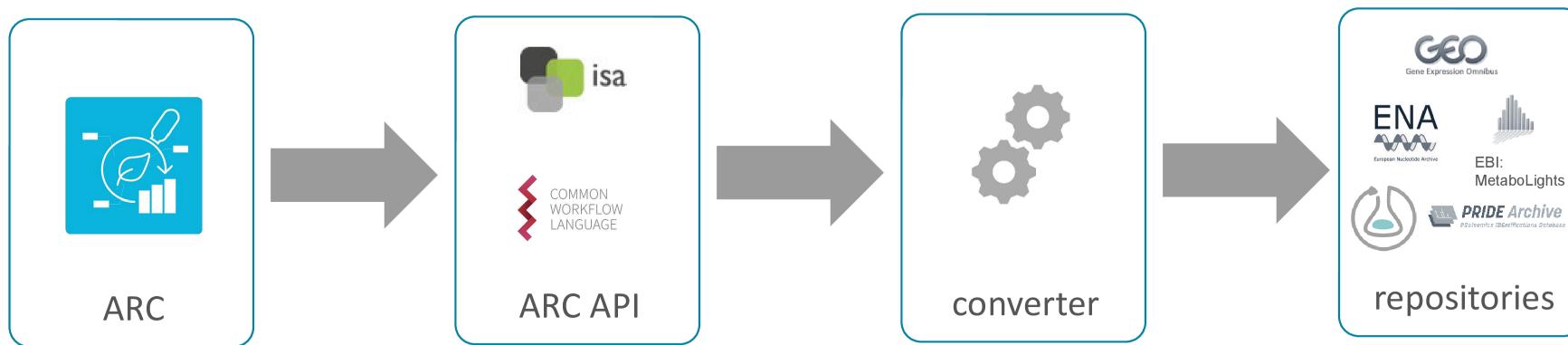
Publish your ARC



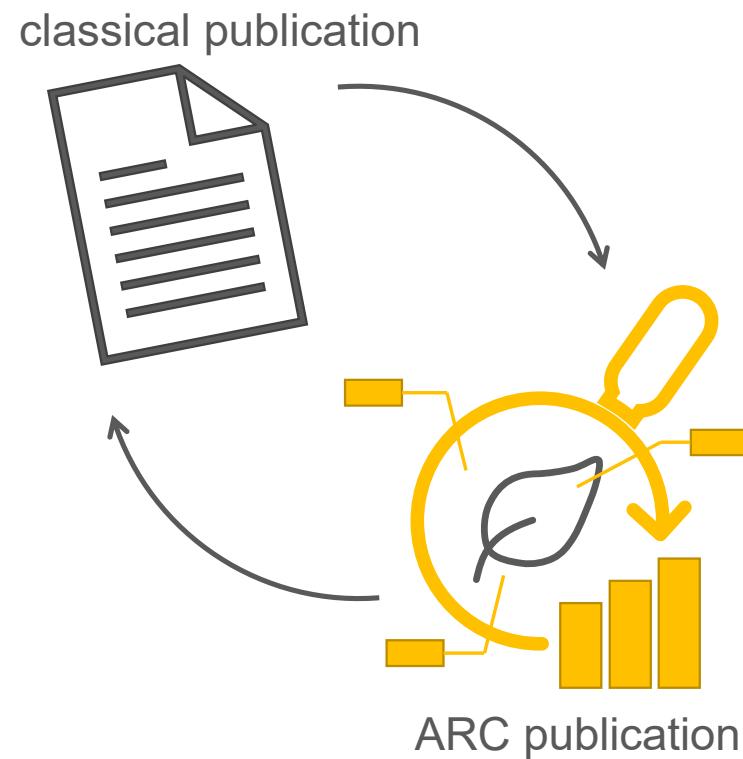
Publish your ARC, get a DOI



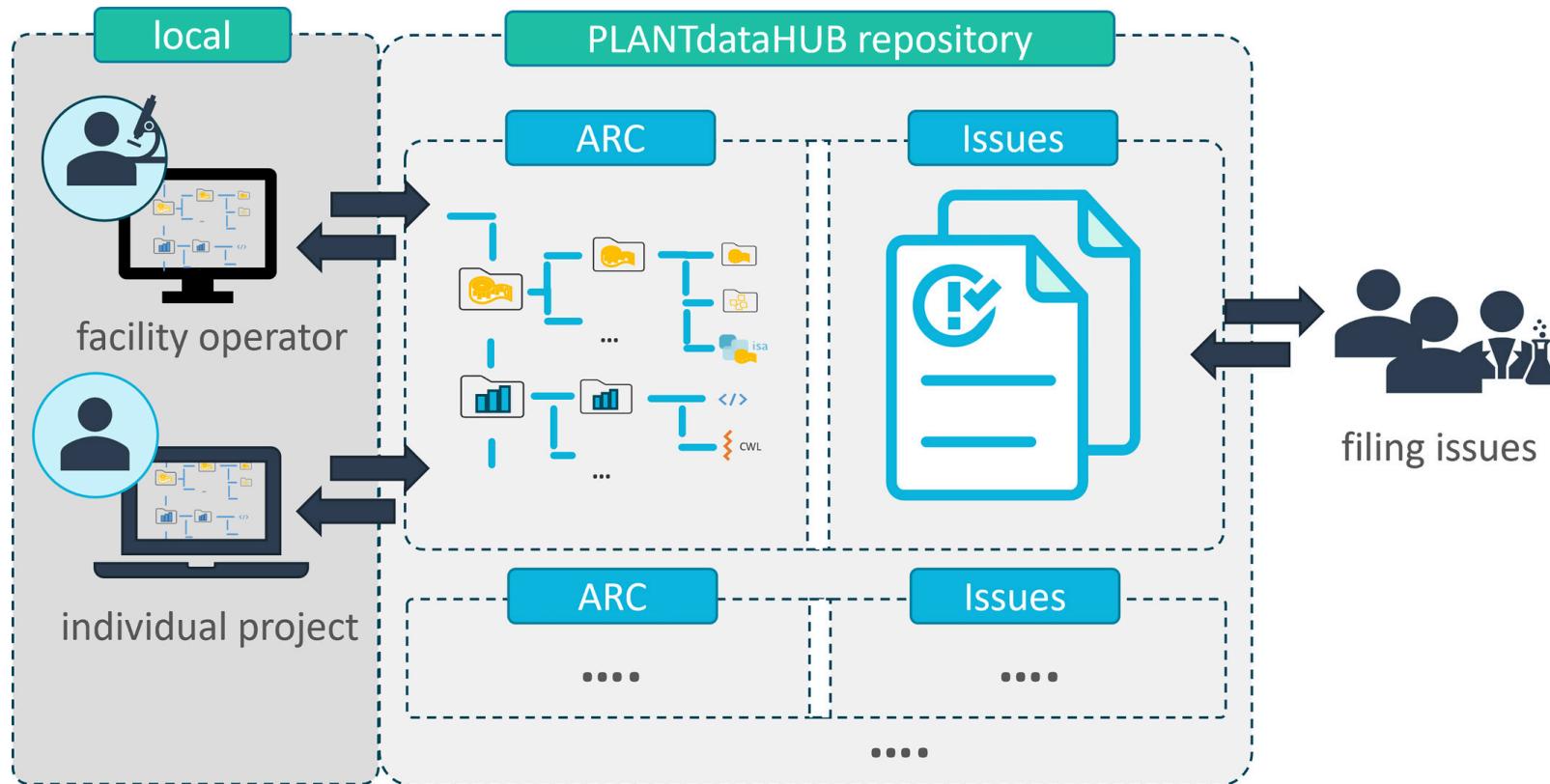
From ARC to repositories



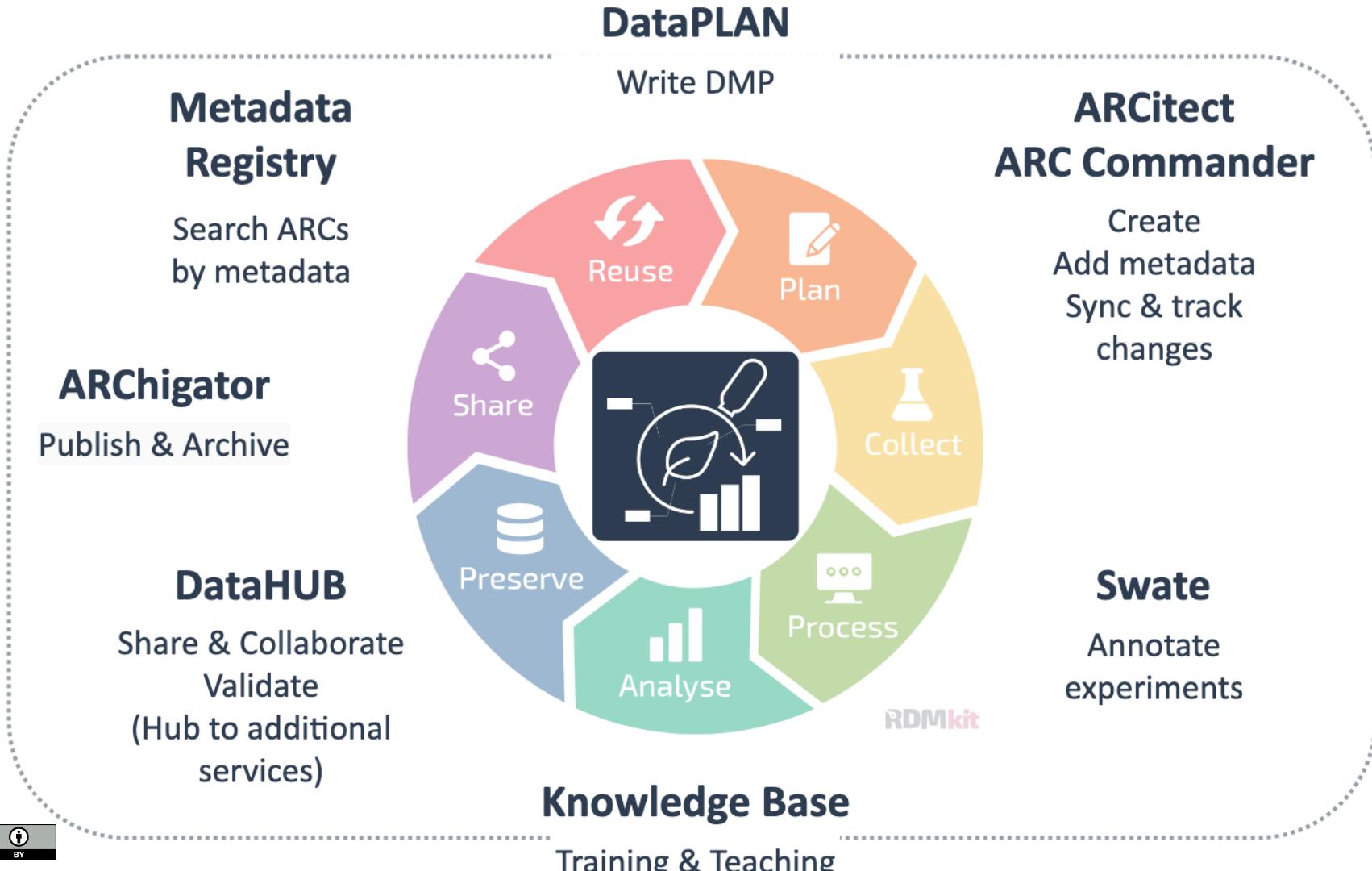
Moving from paper to data publications



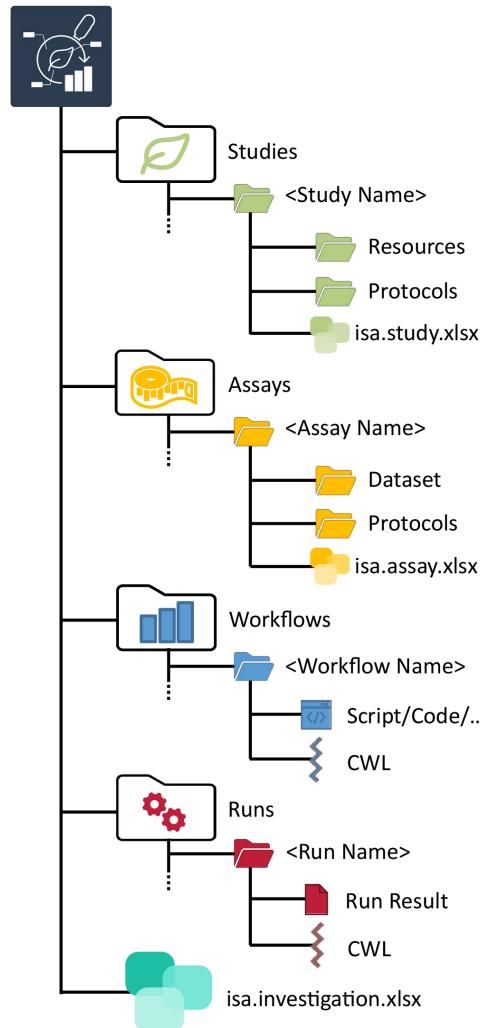
Project management



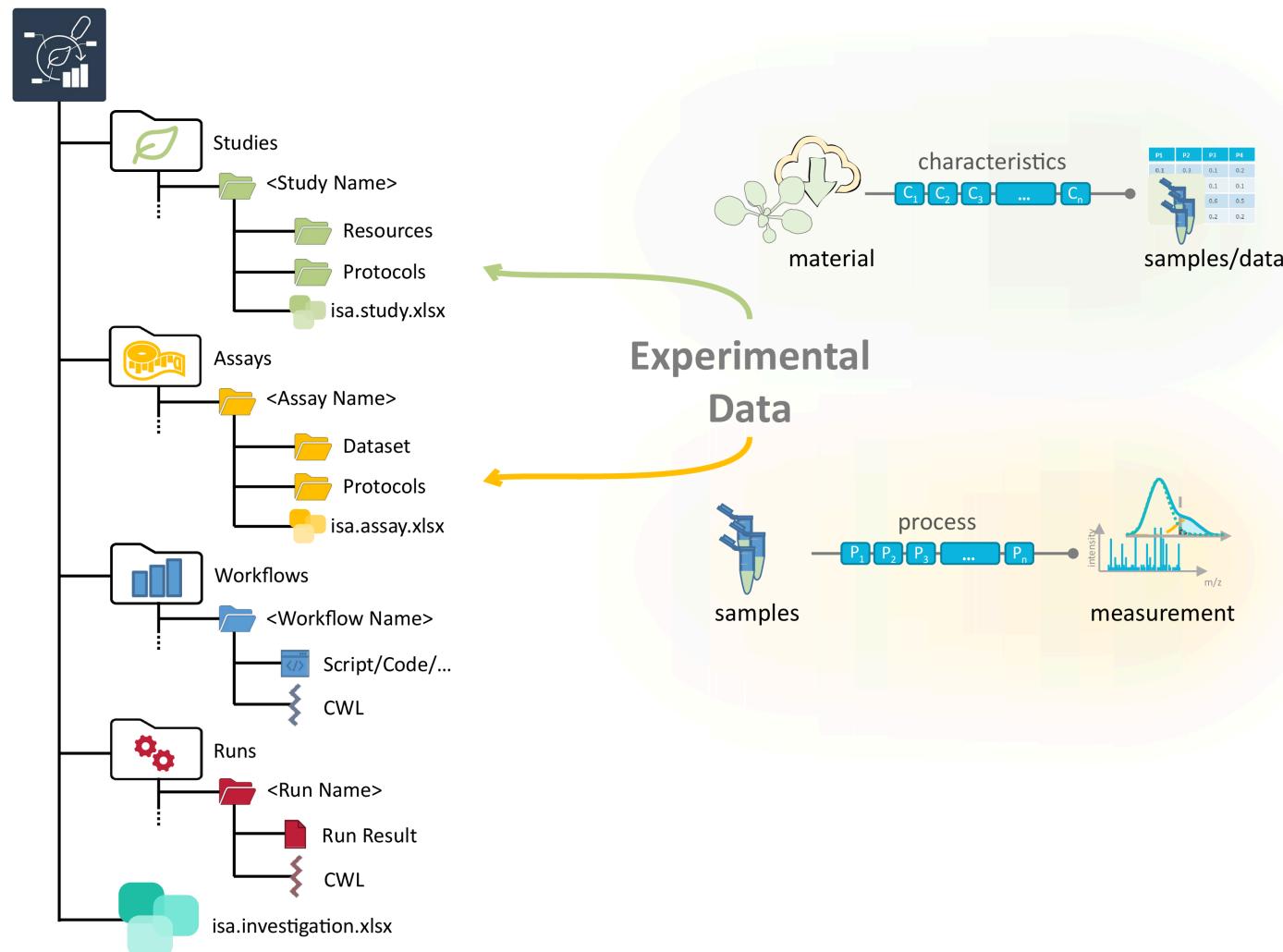
The ARC ecosystem



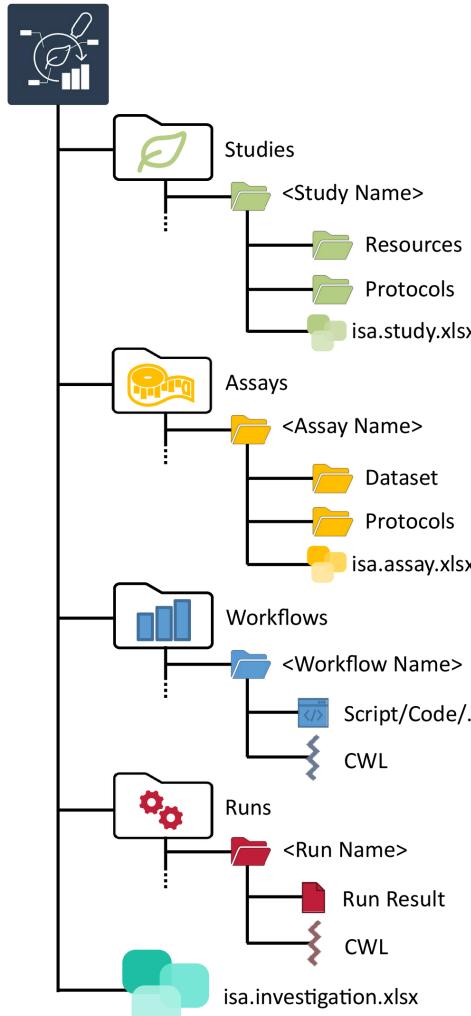
What does an ARC look like?



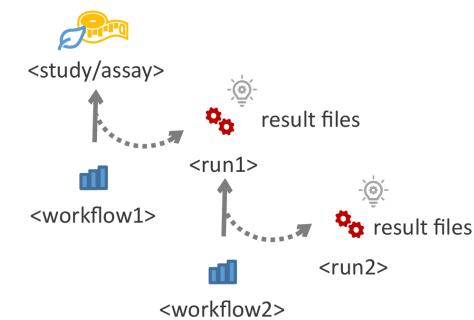
ARCs store experimental data



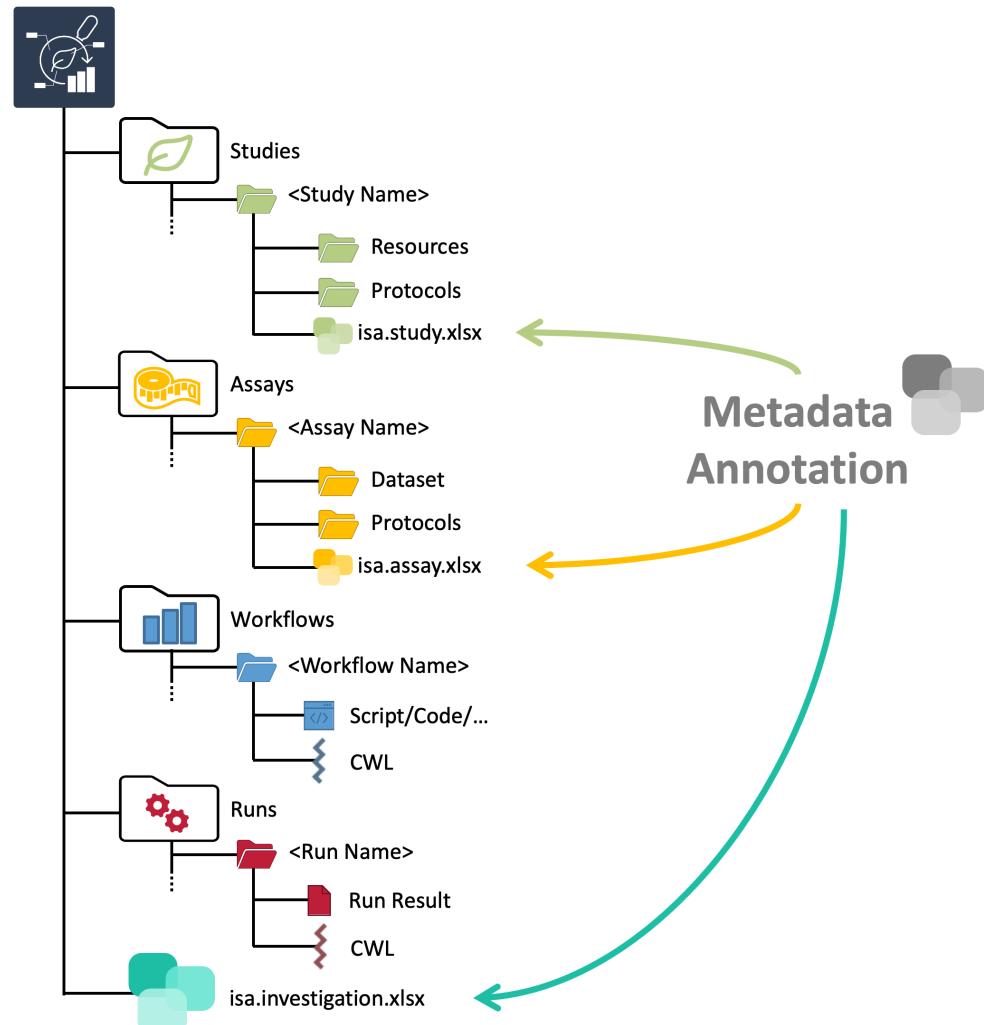
Computations can be run inside ARCs



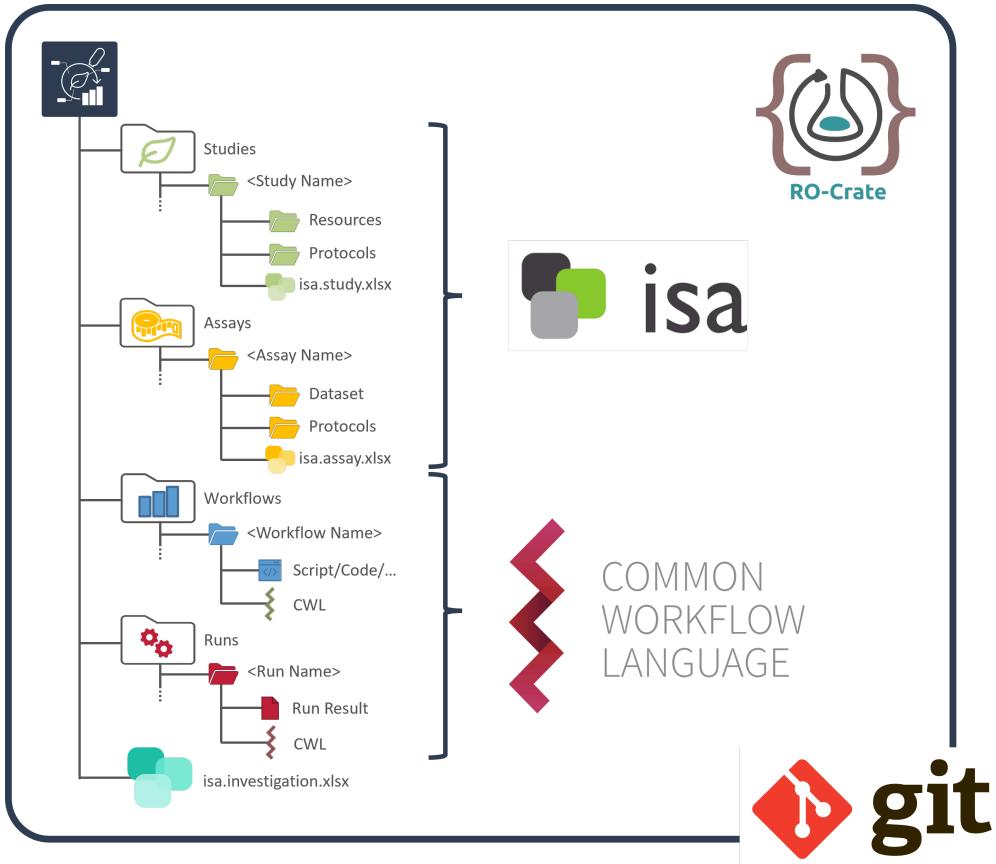
Data analysis
Computation



ARCs come with comprehensive metadata



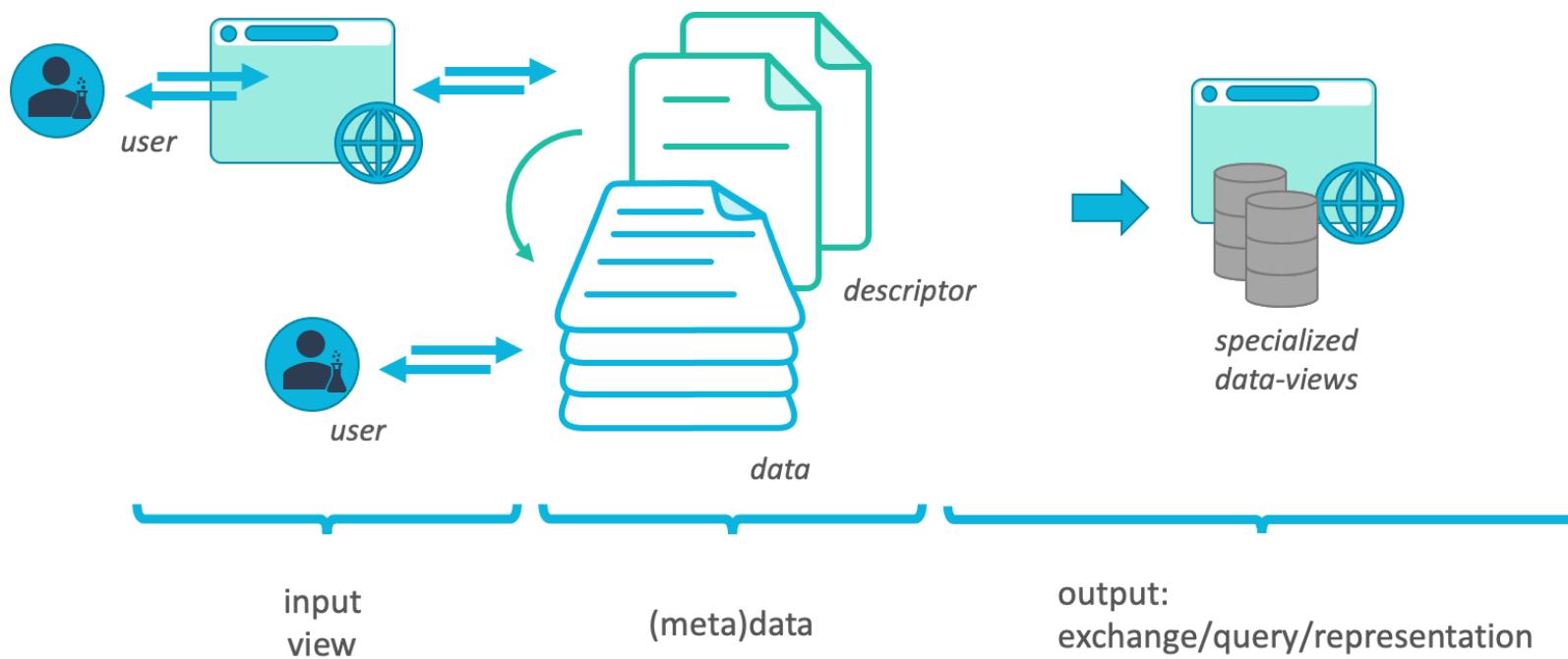
ARC builds on standards



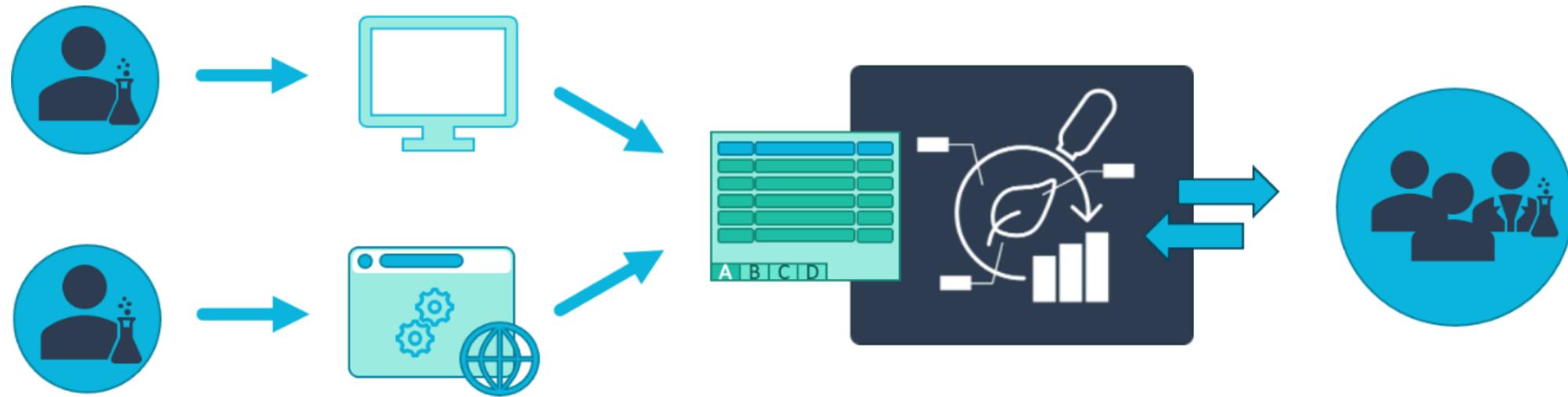
- RO-Crate: standardized exchange
- ISA: structured, machine-readable metadata
- CWL: reproducible, re-usable data analysis
- Git: version control

Everything is a file

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



No technical lock-in



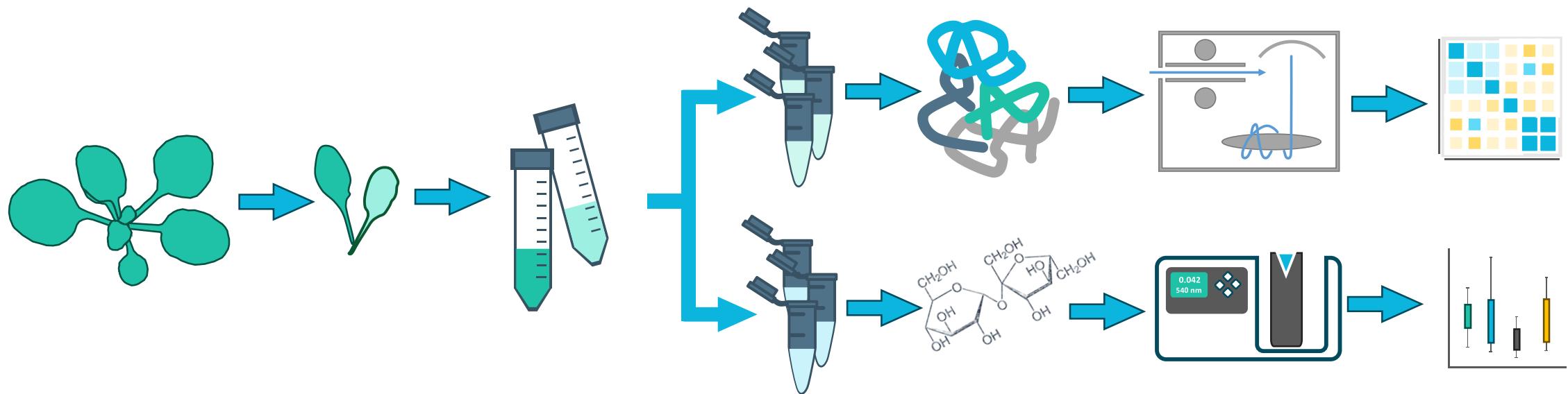
(Meta)data transparency with tool assistance but **no technical lock-in**

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



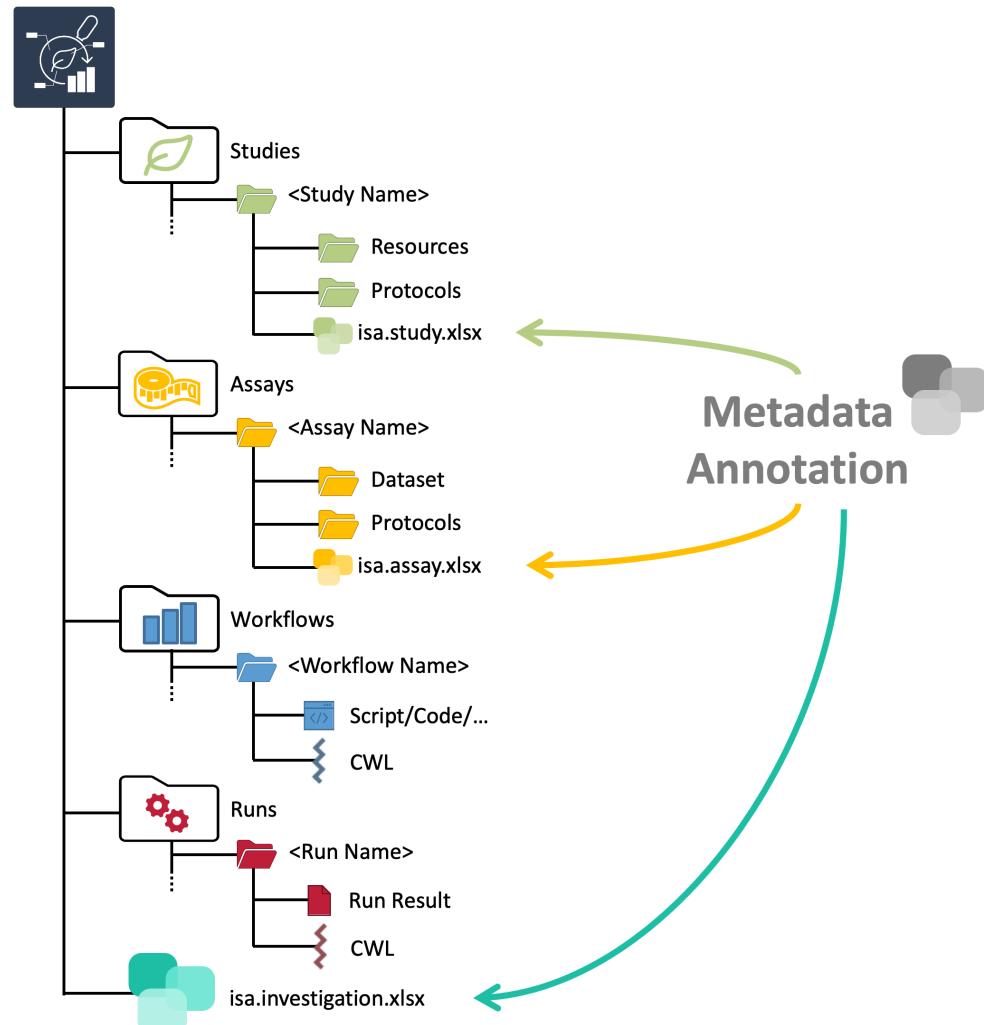
Hands-on part 1: Setup and ARCitect

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

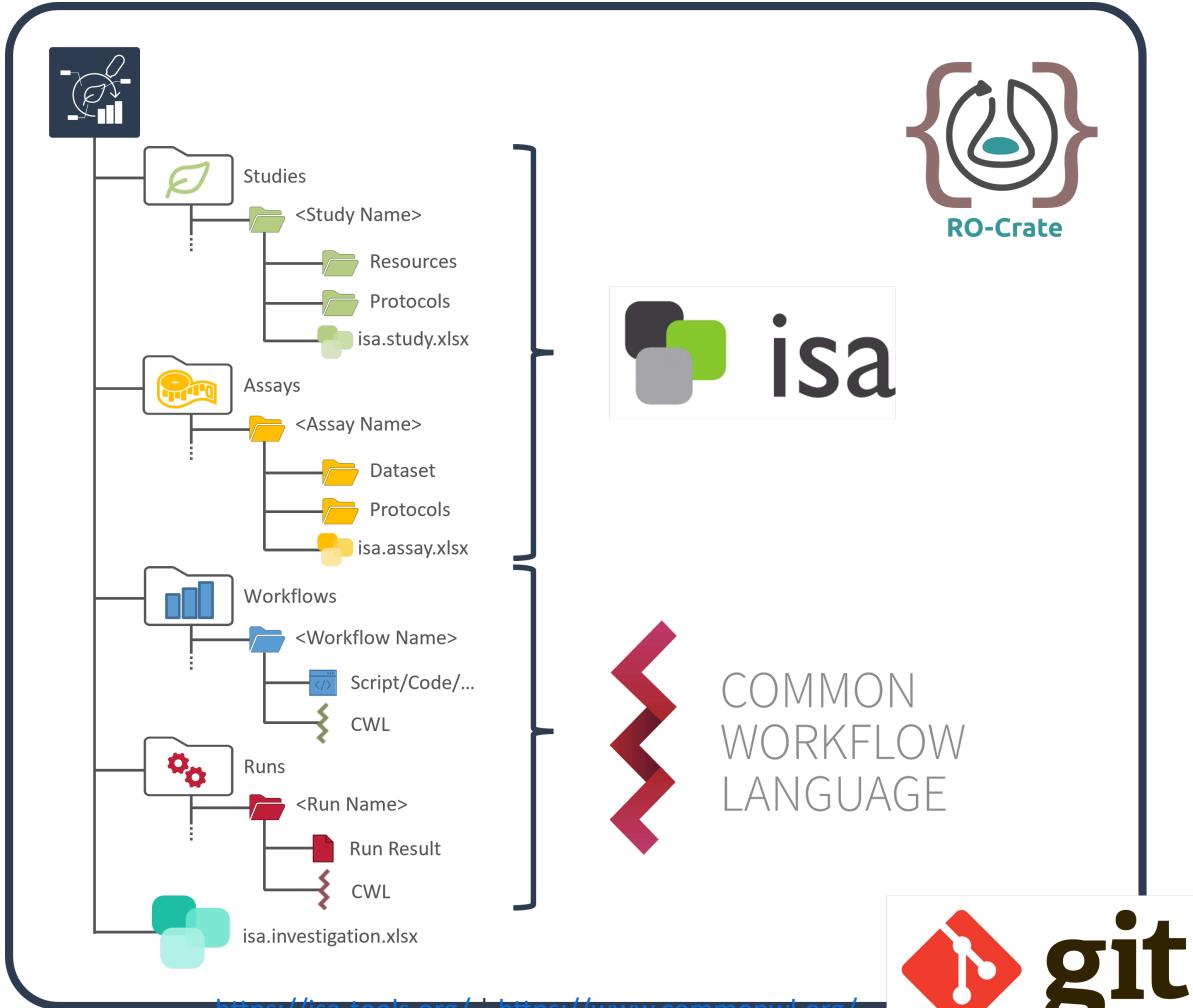
 Stop after step **Describing the Investigation**

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

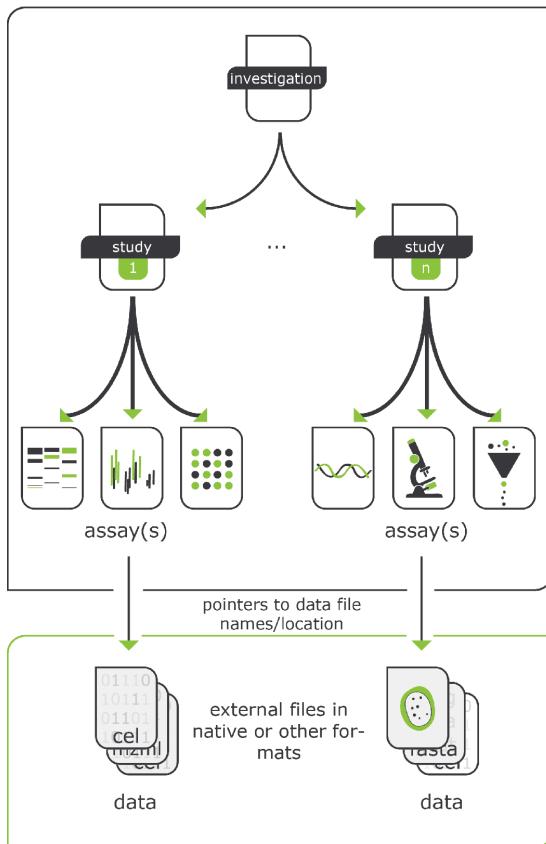
ARCs come with comprehensive metadata



ARC builds on standards



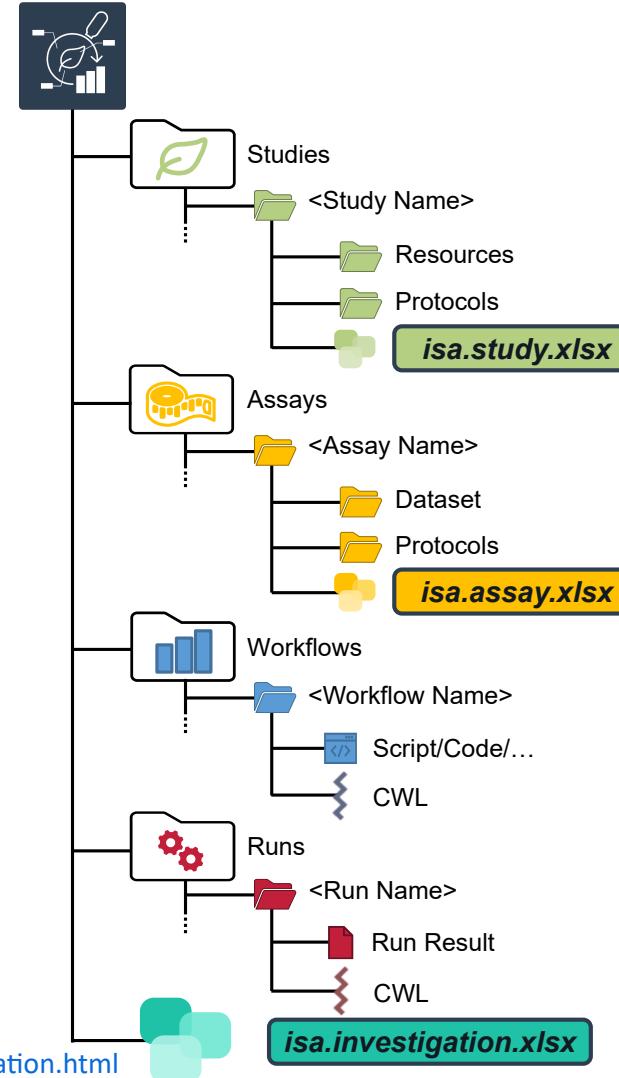
ARC builds on ISA



Investigation
Overall goals
Scientific context

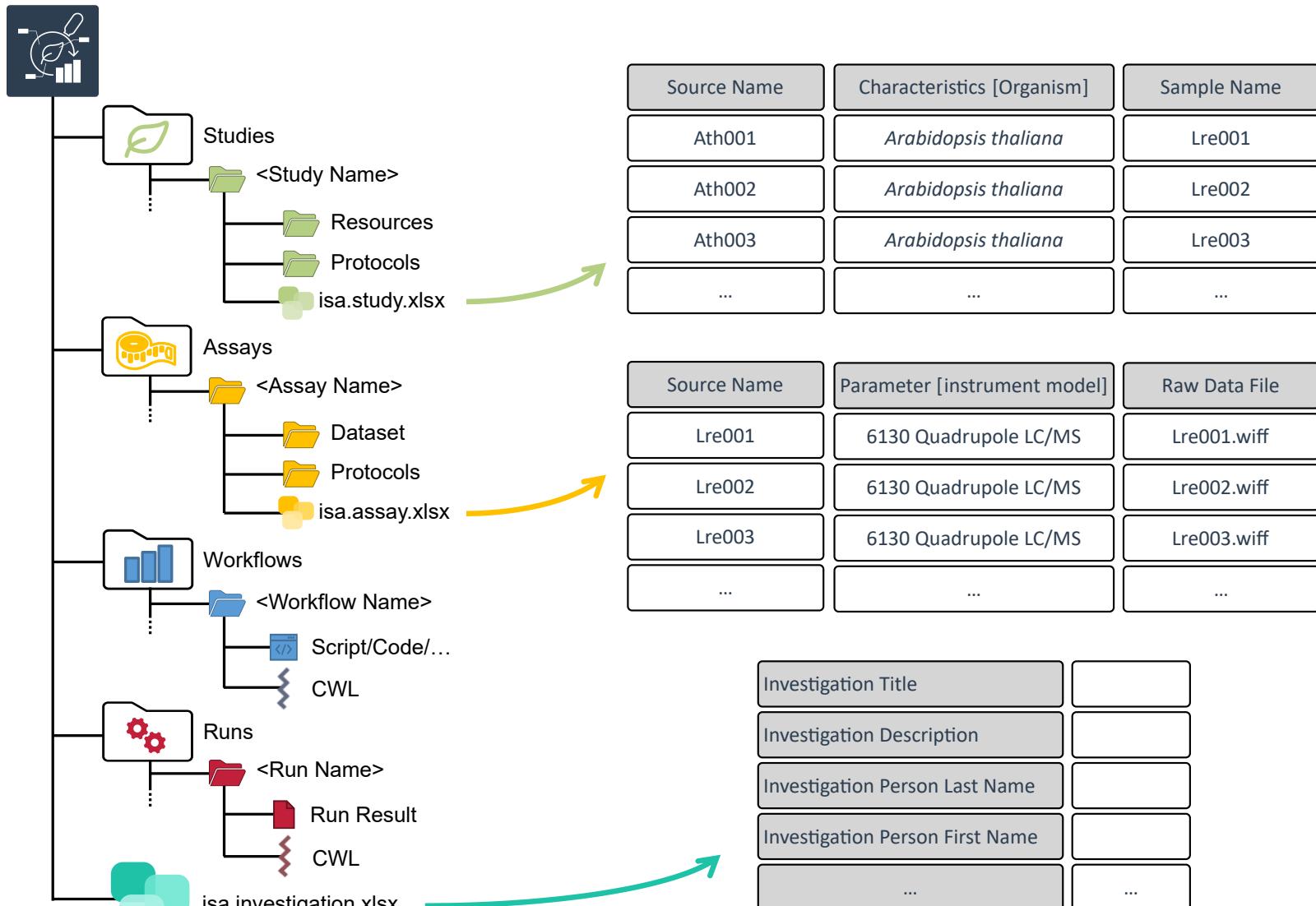
Study
Experimental design

Assay
Leading to (raw) data



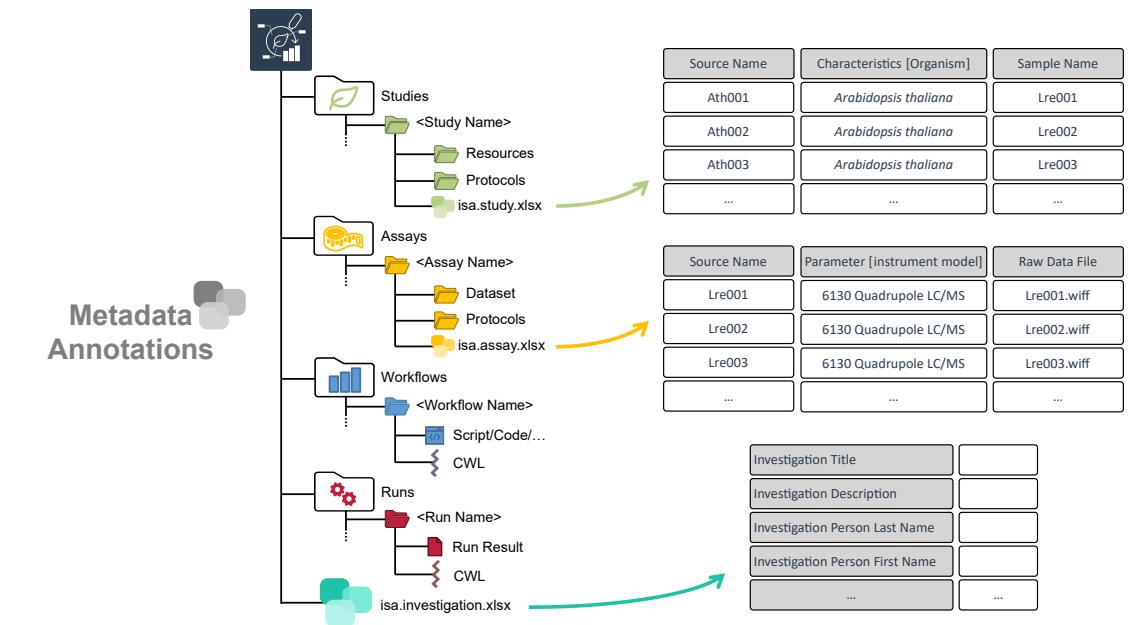
ARC builds on ISA to connect data

Metadata Annotations

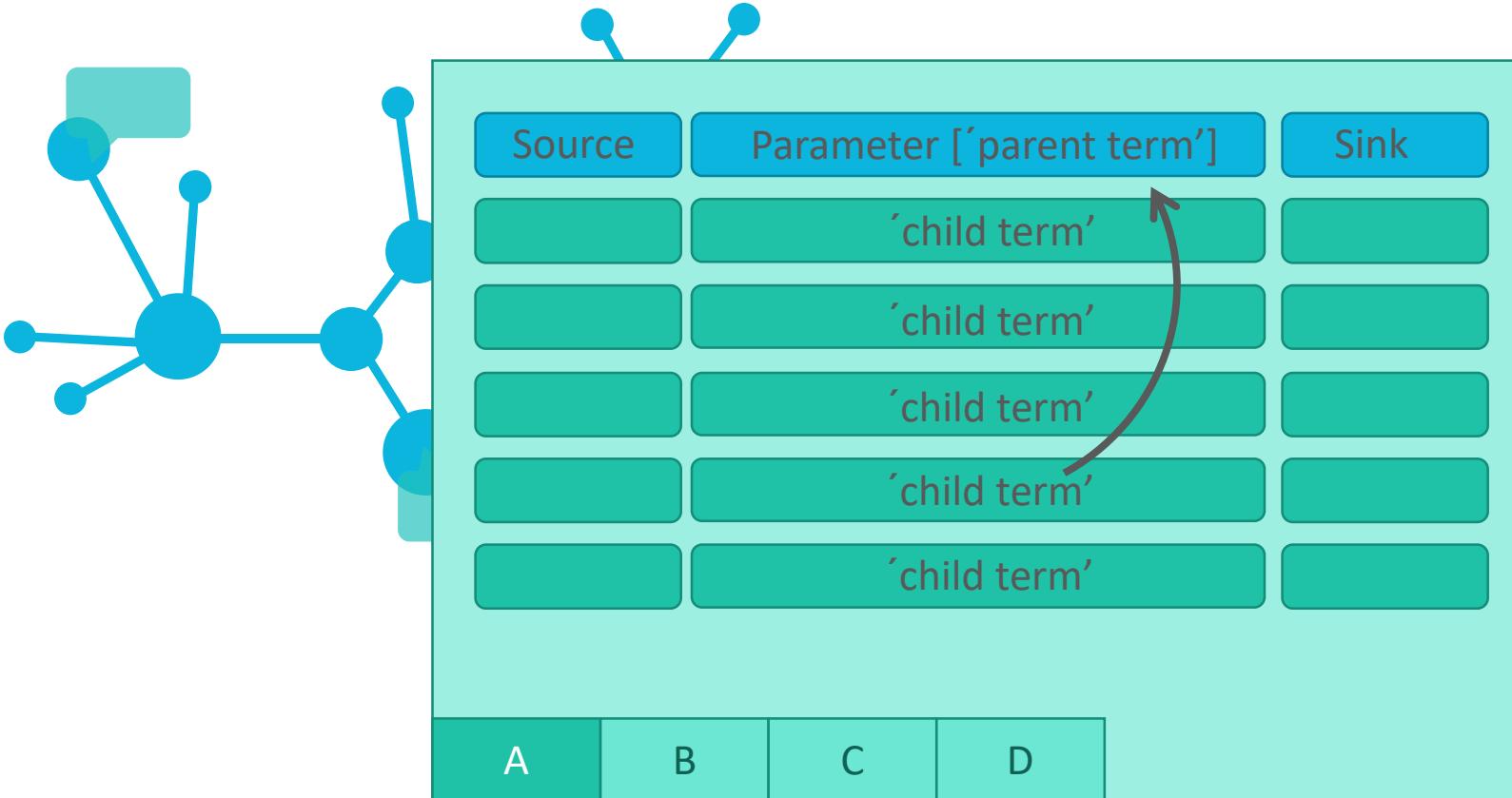


ARC builds on ISA to link data

- 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 with the 'Widgets' view open. The main table displays experimental data with columns for Input [Source Name], Characteristic [organism], Factor [watering exposure], and Output [Sample Name]. A 'Factor' column is highlighted in blue. Arrows point from labels 'Input', 'Characteristic', 'Factor', 'Output', and 'Sidebar' to their respective corresponding columns in the table. A 'New Parameter' dialog box is also visible on the right side.

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

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 with a table on the left and a search panel on the right.

Table 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

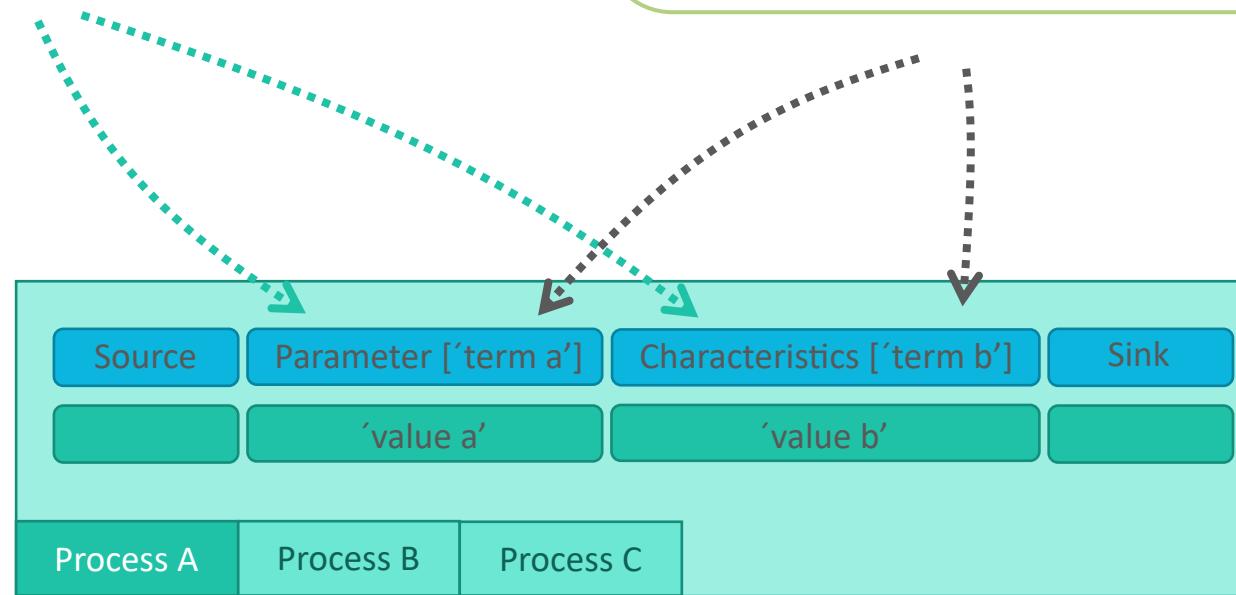
Search Panel:

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

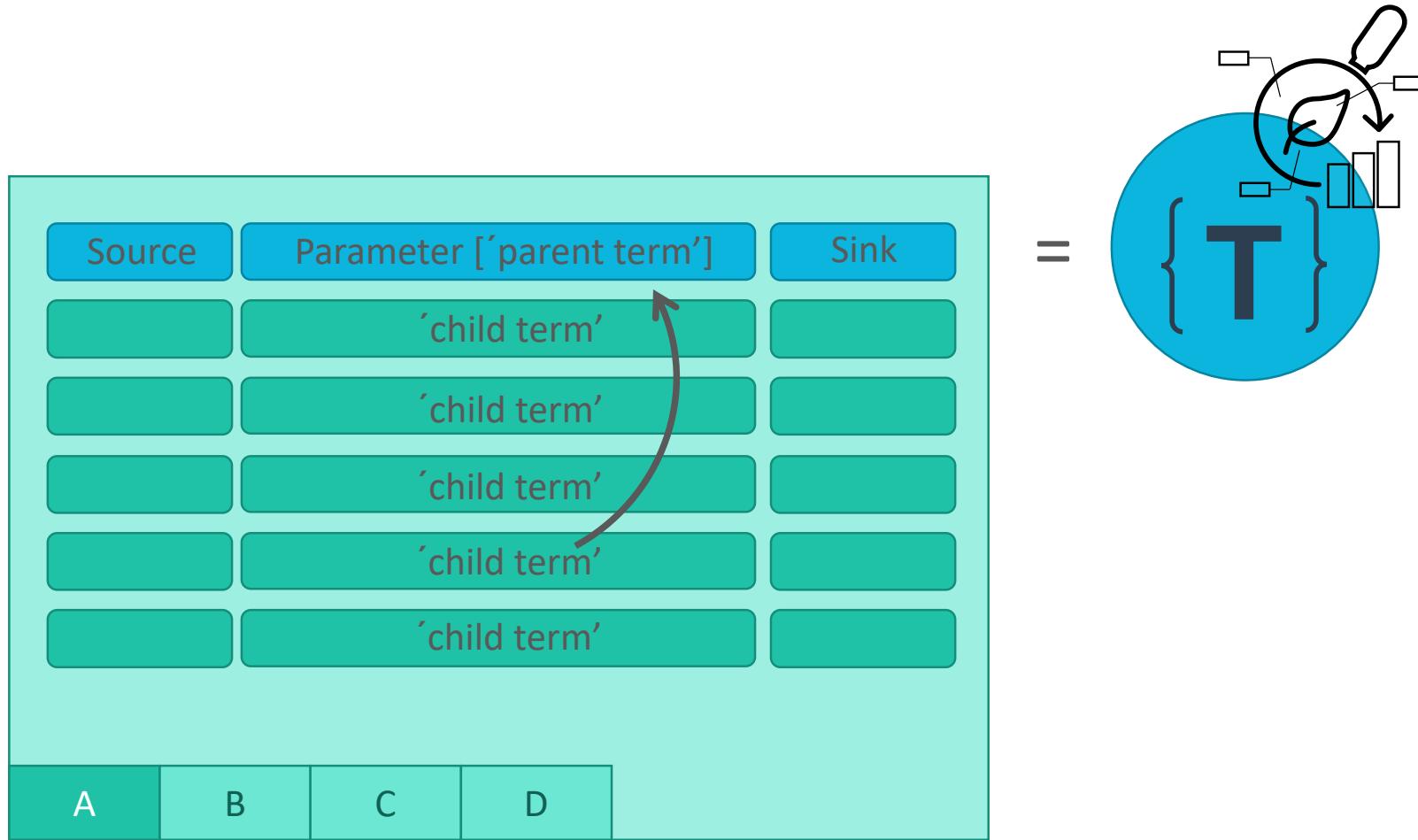
Parent: Organism, MIAPPE:0041 [Use advanced search](#)

[Fill selected cells with this term](#)

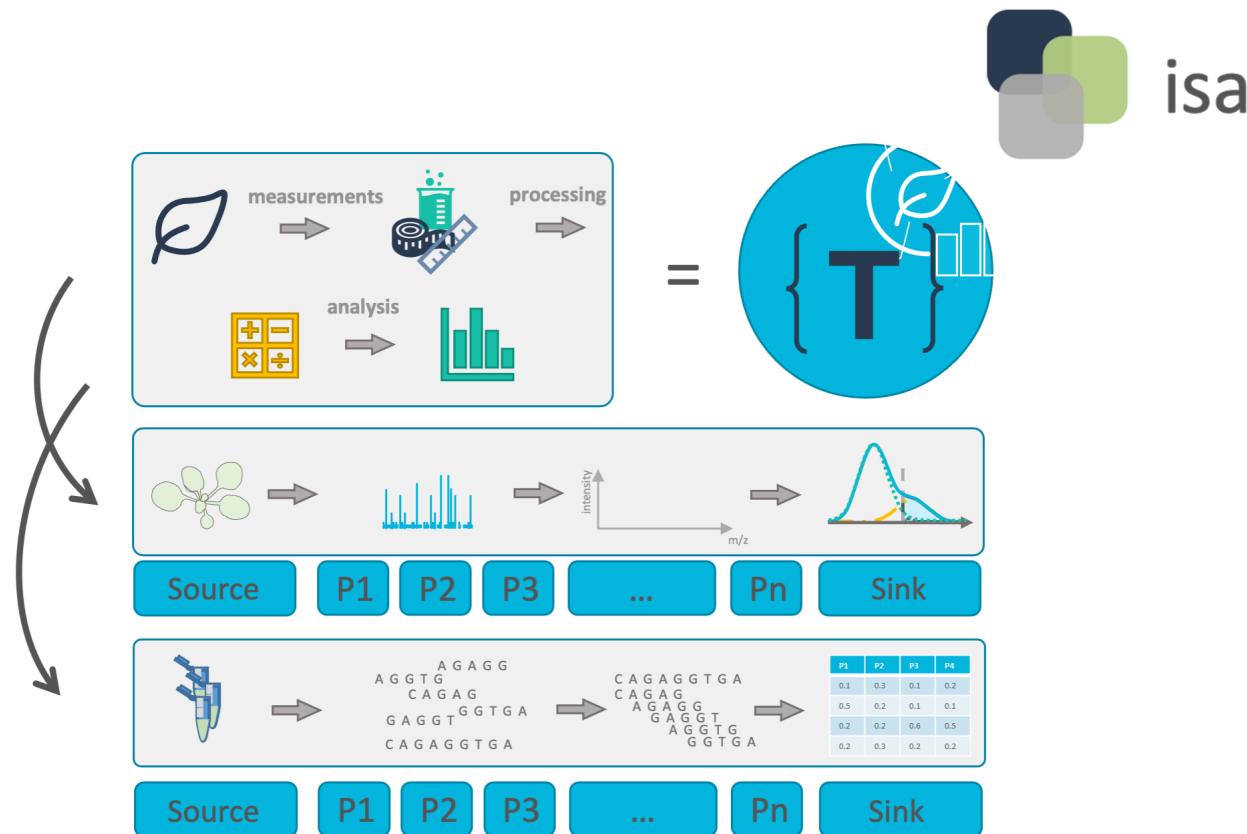
Hierarchical combination of ontologies



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

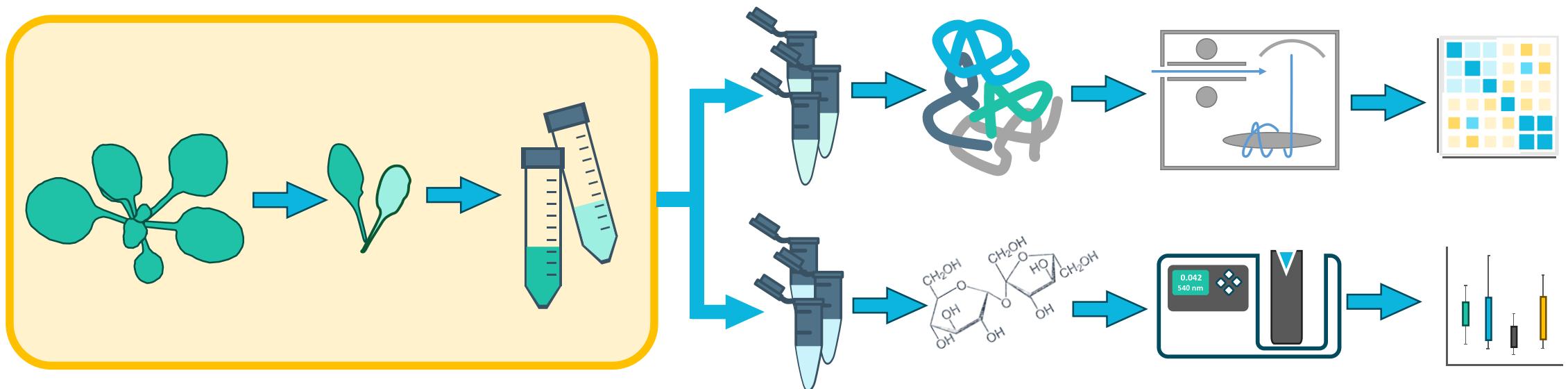
The screenshot shows the Swate web application interface. At the top, there is a dark header bar with several small icons. Below it is a light gray search bar containing two input fields: "Search by template name" and "Search for tags". Underneath the search bar is a dropdown menu labeled "Select community" with "DataPLANT official" selected. The main content area is a table with the following columns: "Template Name", "Community", and "Template Version". The table lists several templates, each with a "curated" status indicator and a dropdown arrow:

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

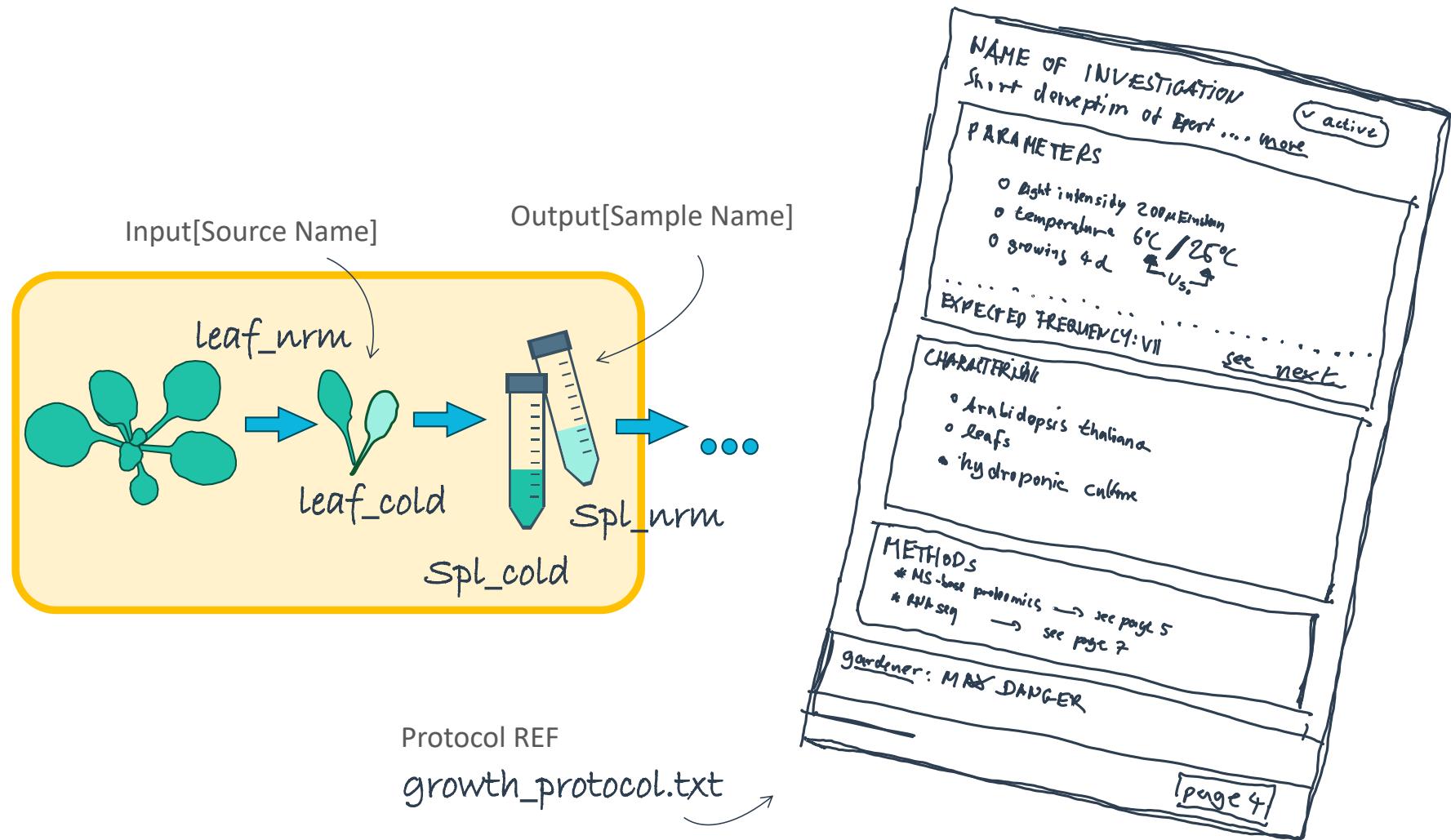
Hands-on part 2: Start Here guide, study & assay part

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

Divide and conquer for reproducibility



Identifying the 'study' part



A table-based organization schema

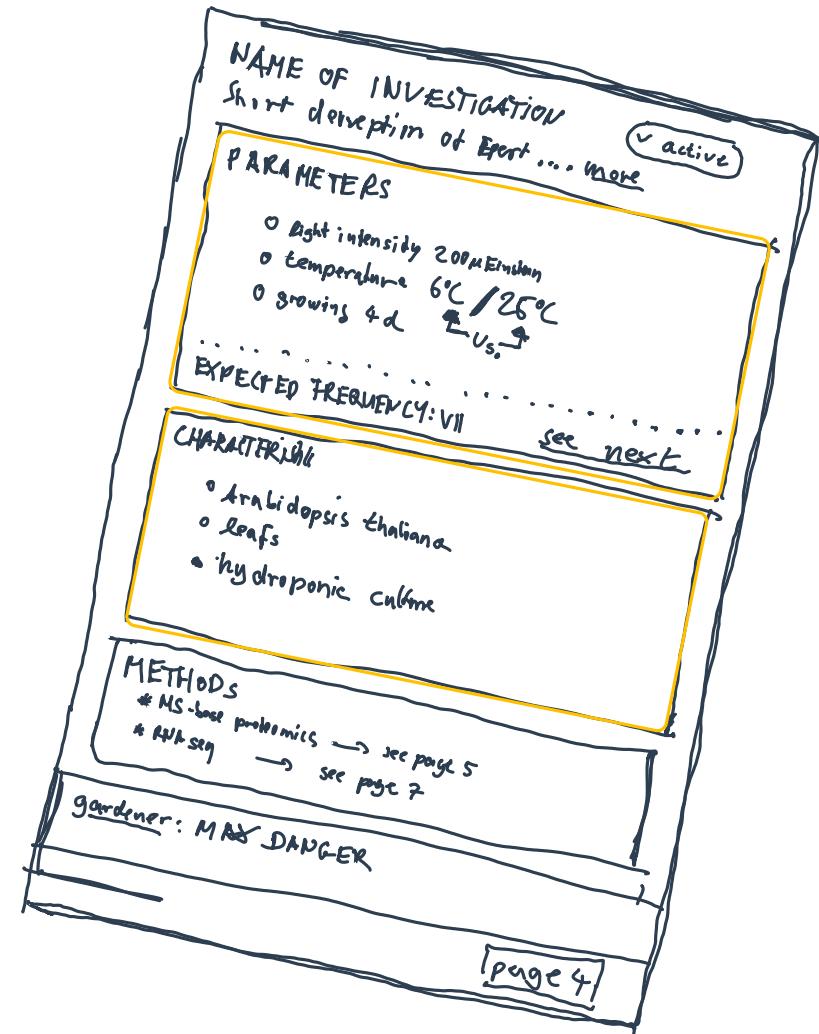
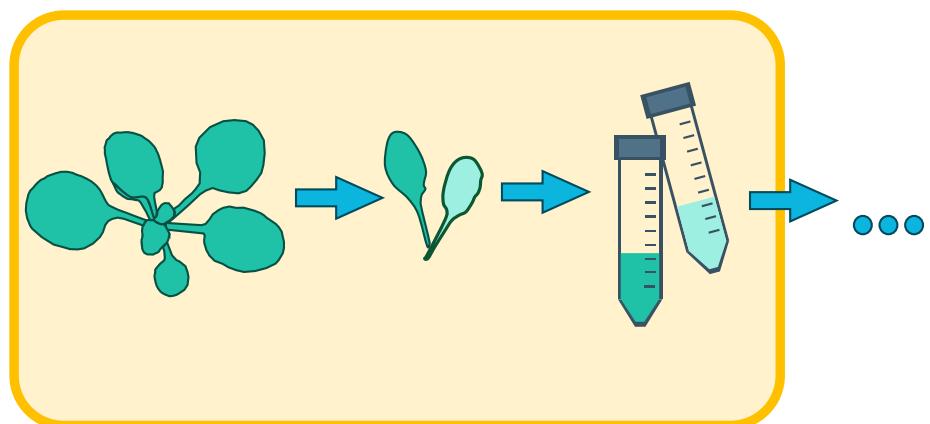
Input[Source Name]		Output[Sample Name]
leaf_nrm		spl_nrm
leaf_cold		spl_cold
A	B	C
D		

Referencing a protocol

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

- 💡 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

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?

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.

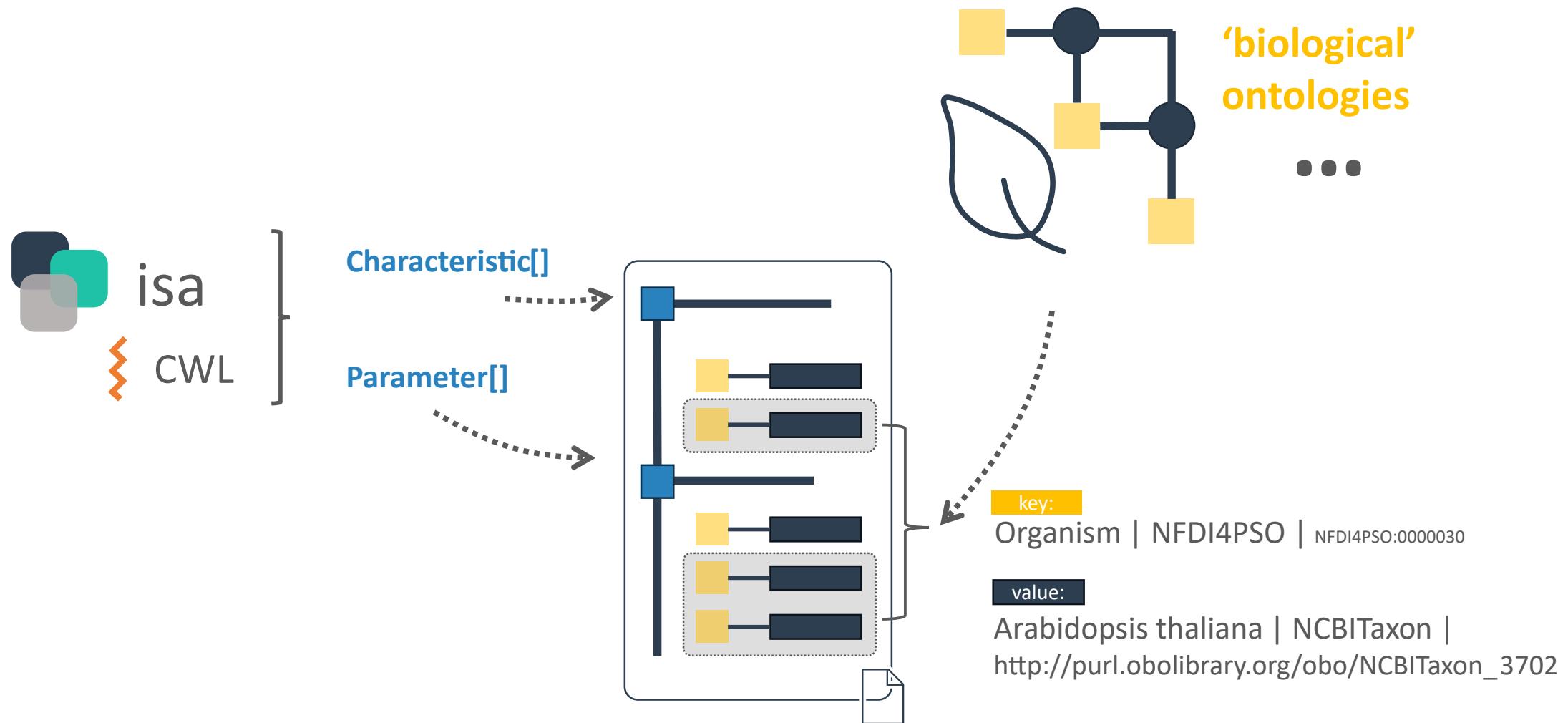
FOLLOW US

X

EMBL-EBI 2023 Licensing

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

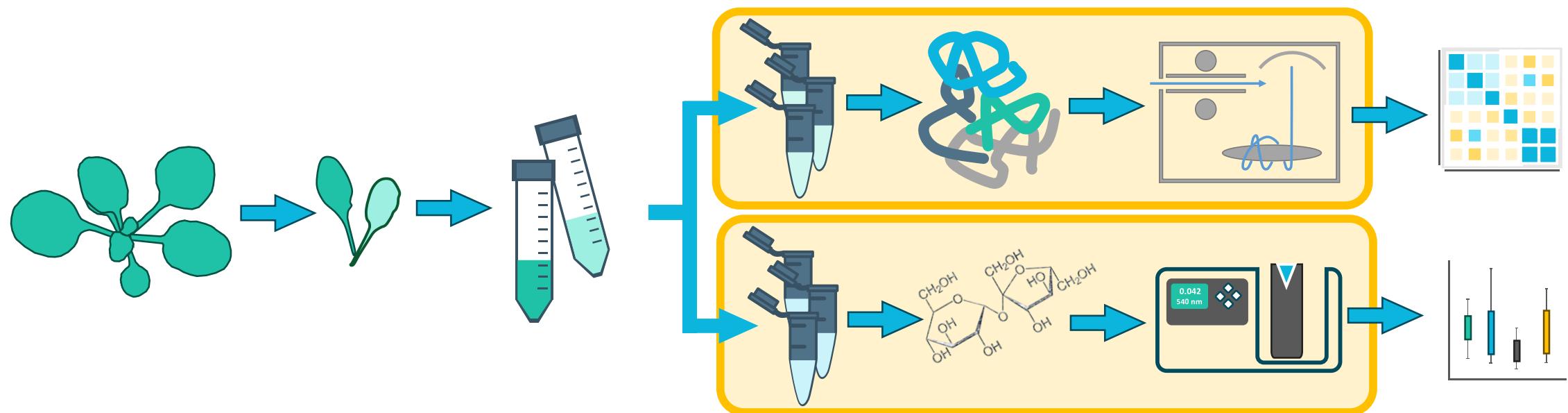
Parameters []

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

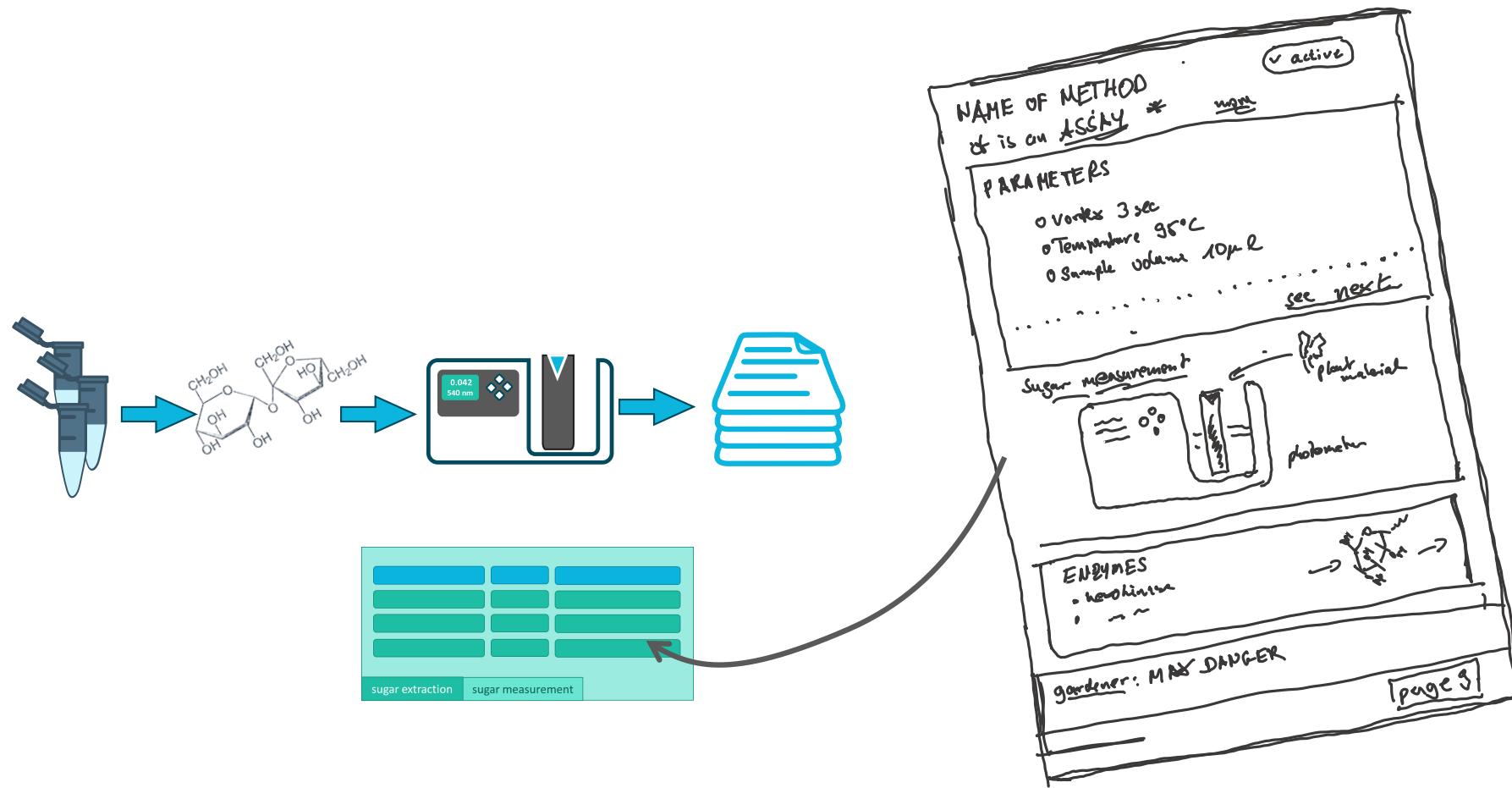
Characteristics []

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

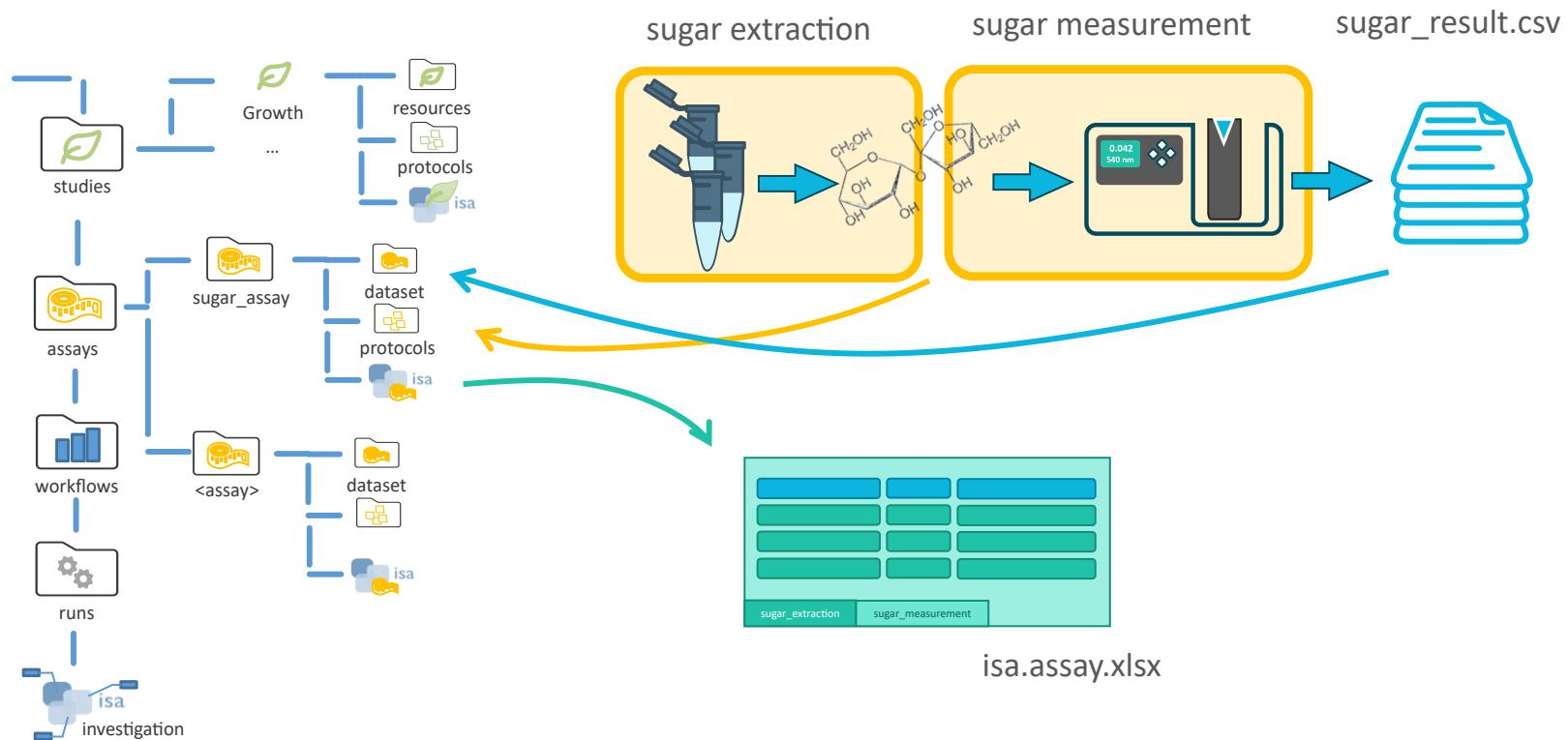
Identifying assays



Assay for sugar measurement



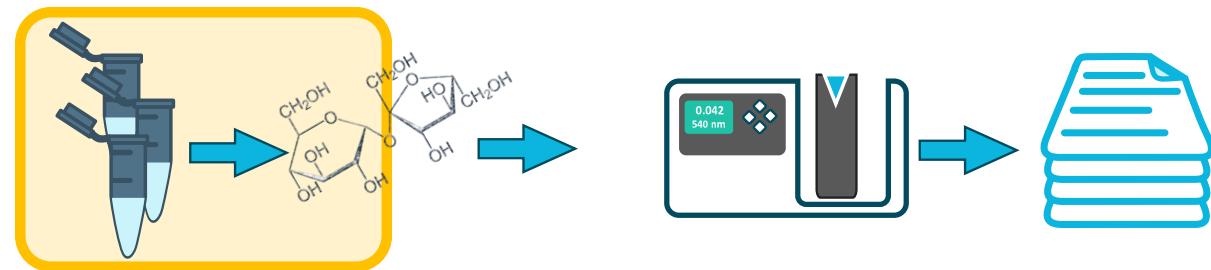
Separating different assay elements



Isolating the lab processes in an assay

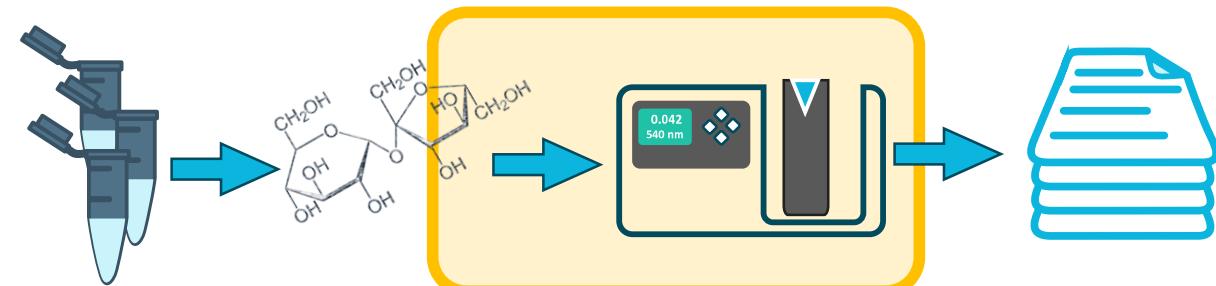
Parameteterization: sugar extraction

- 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



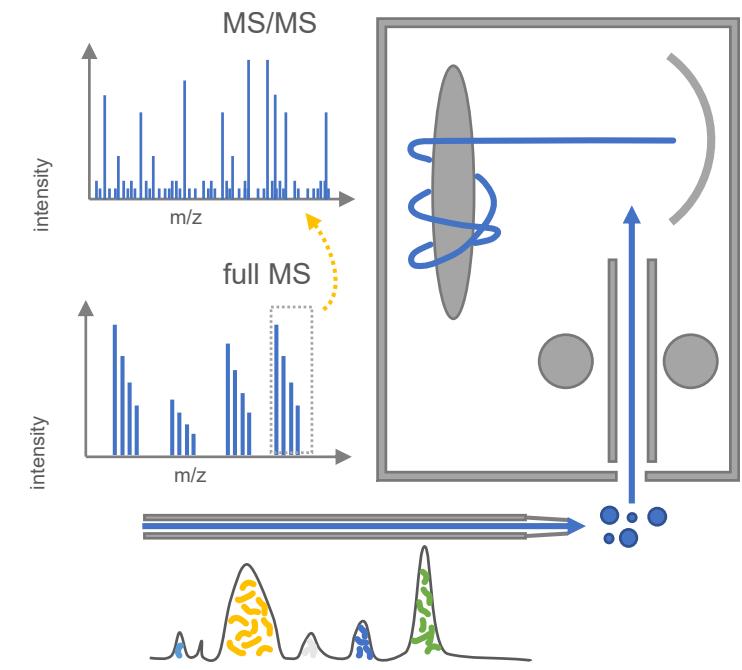
Save time using standard methods and SOPs

Parameter []

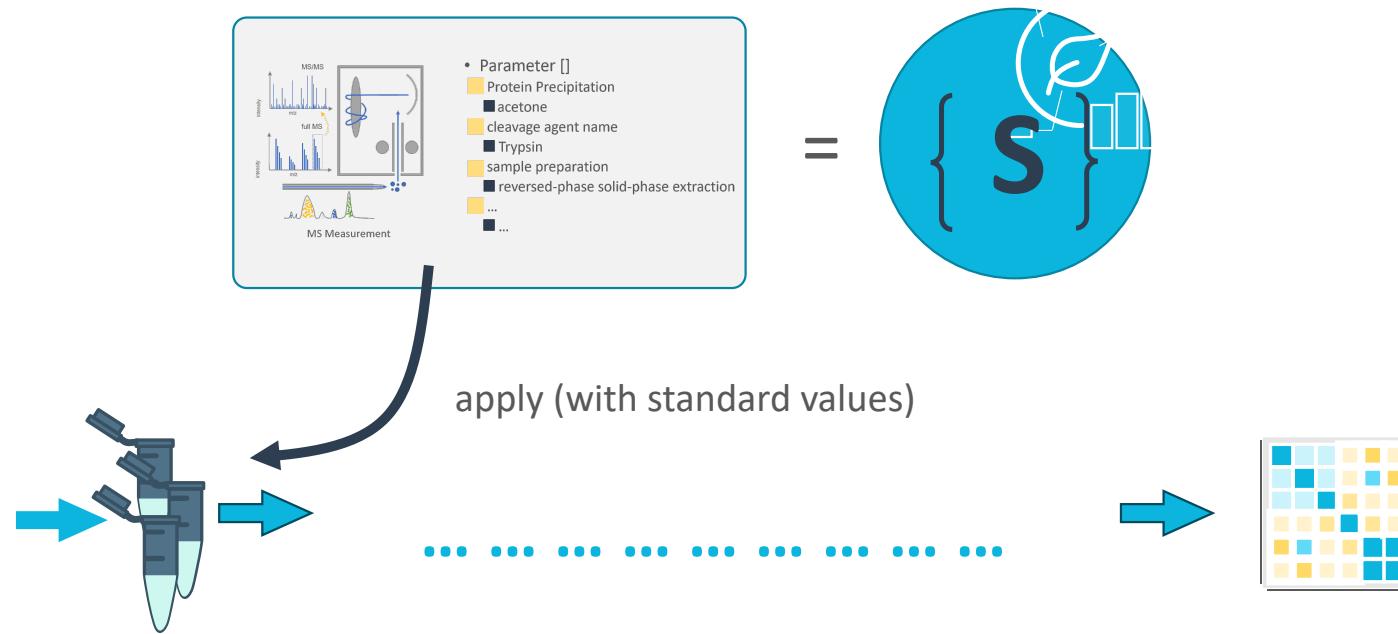
- █ Protein Precipitation
 - █ acetone
- █ cleavage agent name
 - █ Trypsin
- █ sample preparation
 - █ reversed-phase solid-phase extraction
- ...

Component []

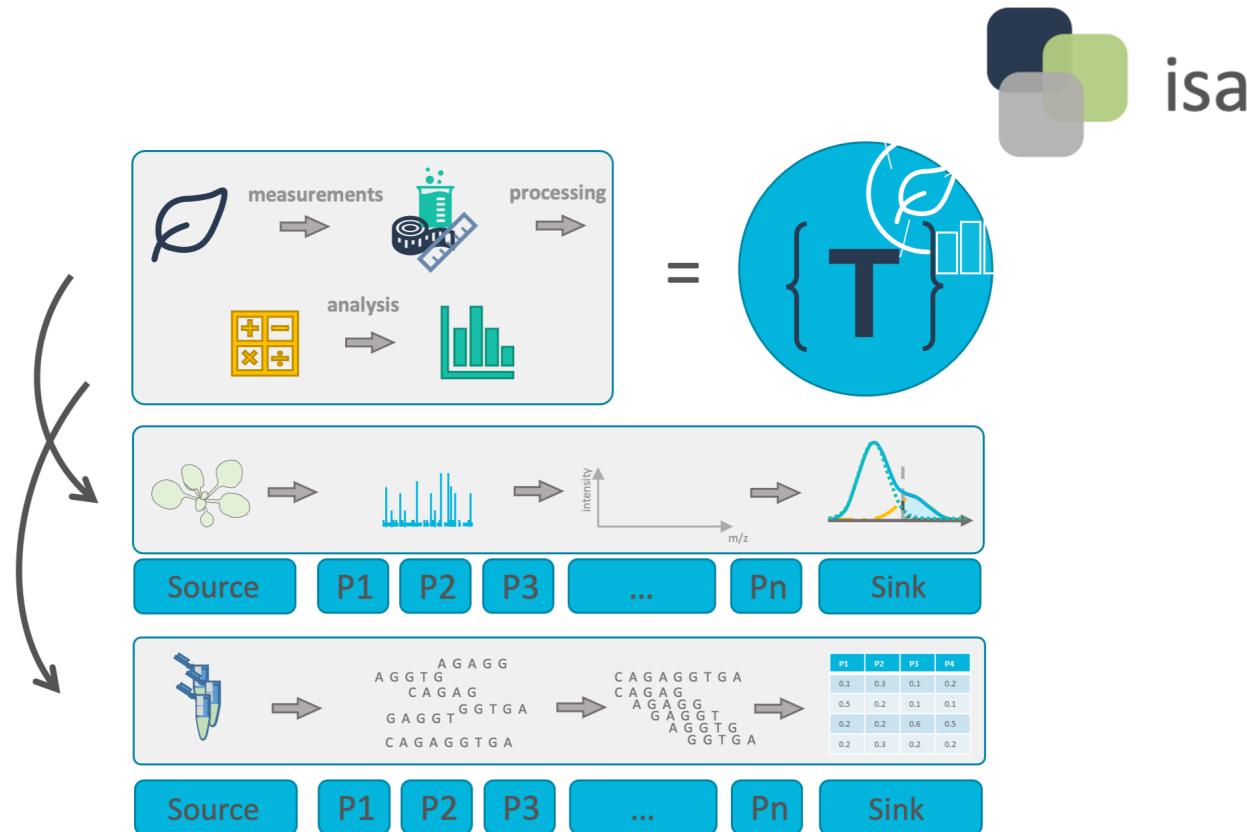
- █ chromatography instrument model
 - █ nanoElute2
- █ chromatography column model
 - █ PepSep C18 1.9 μ , 25cm x 75 μ m
- ...
...



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)

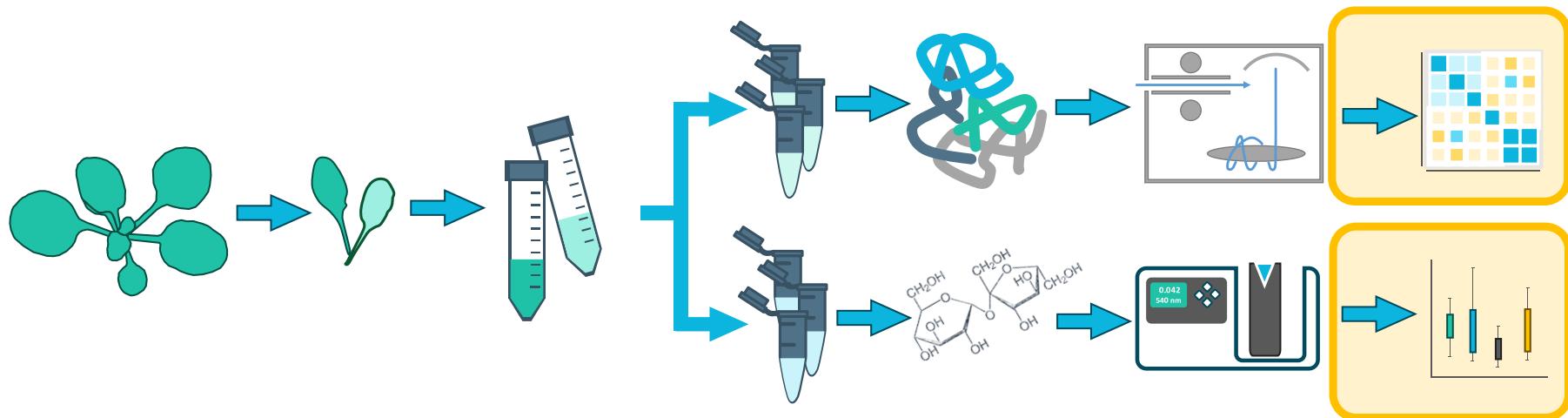
Continue the [Start Here](#) guide in the DataPLANT knowledge base.



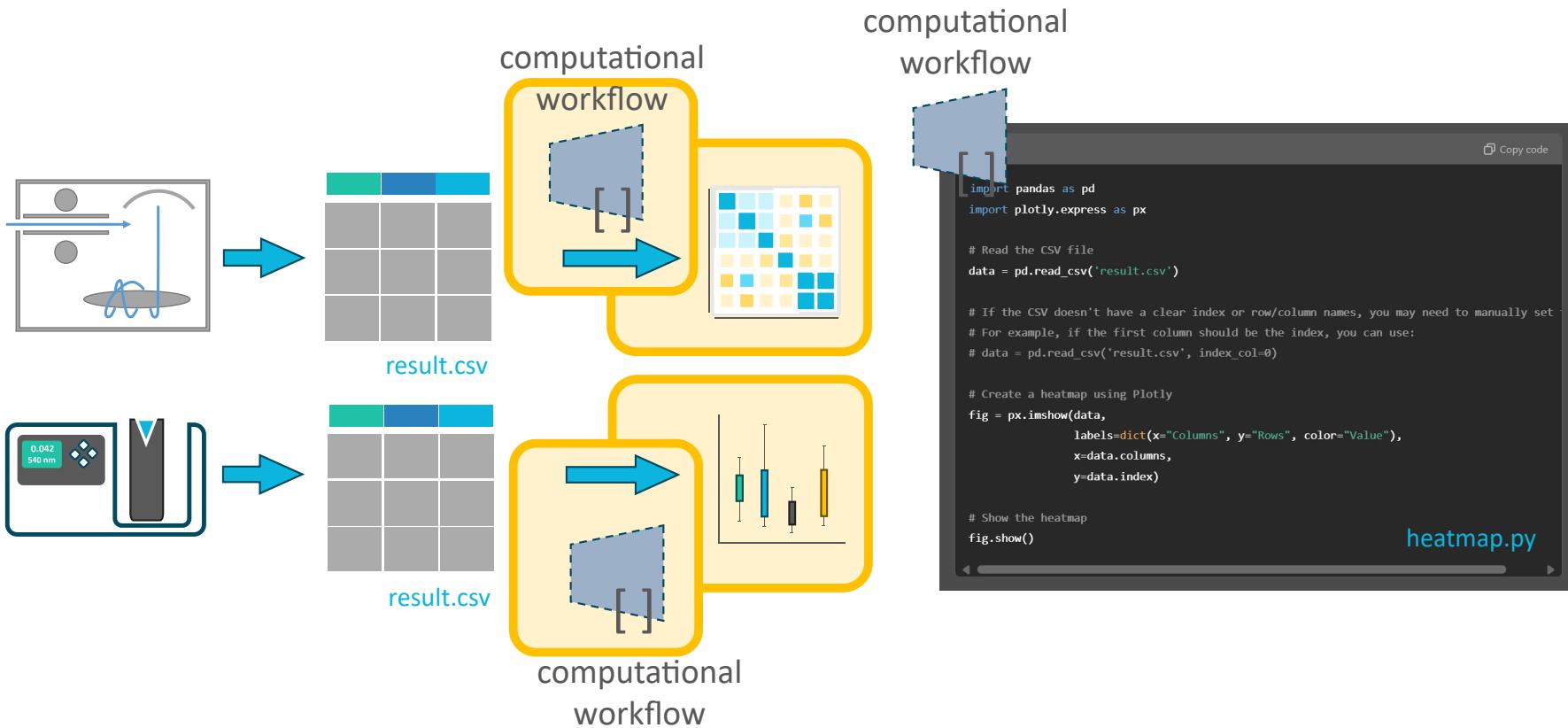
Stop after step [Add assay data](#)

Hands-on part 3: Data

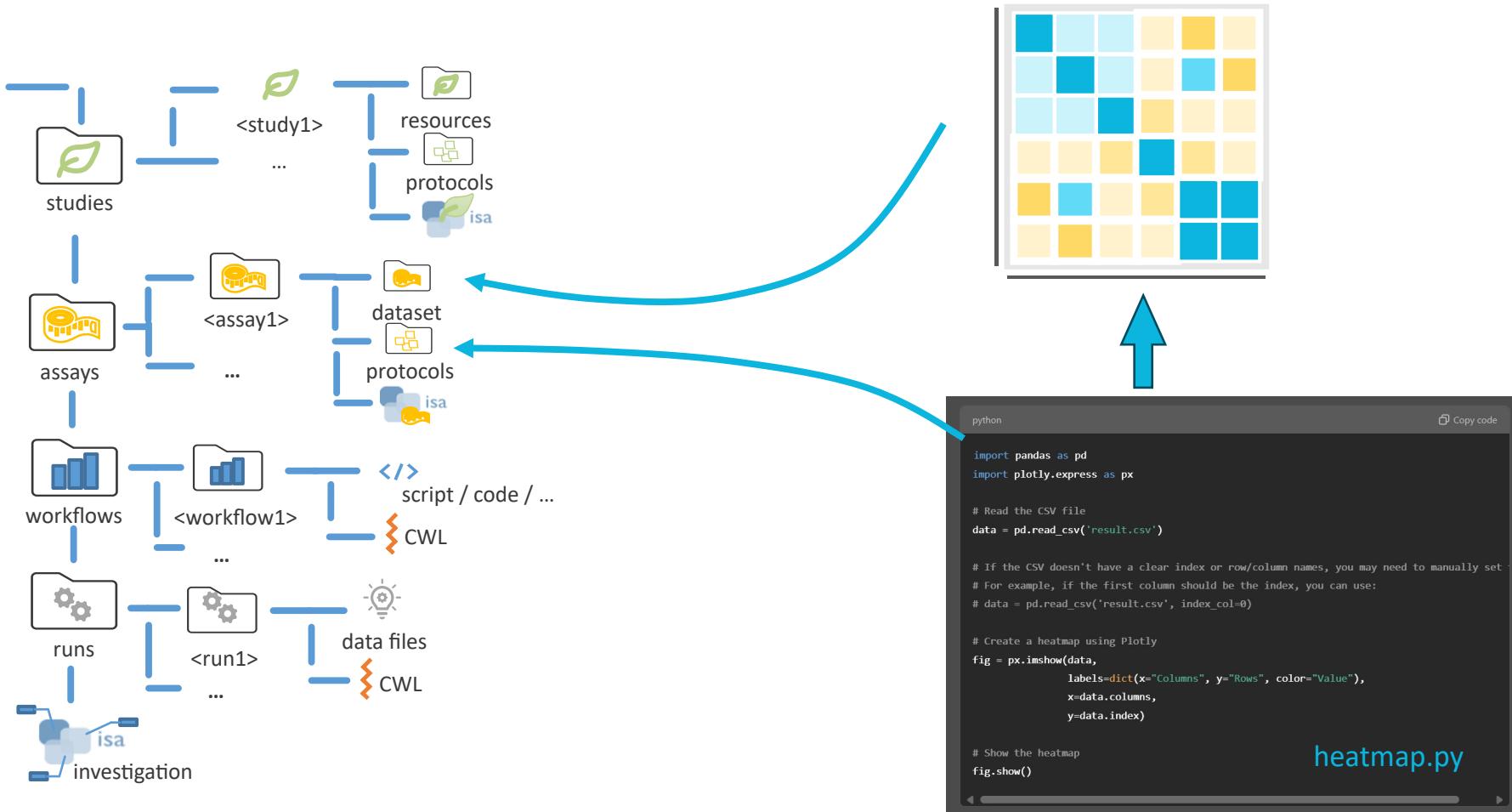
Options to annotate the data analysis



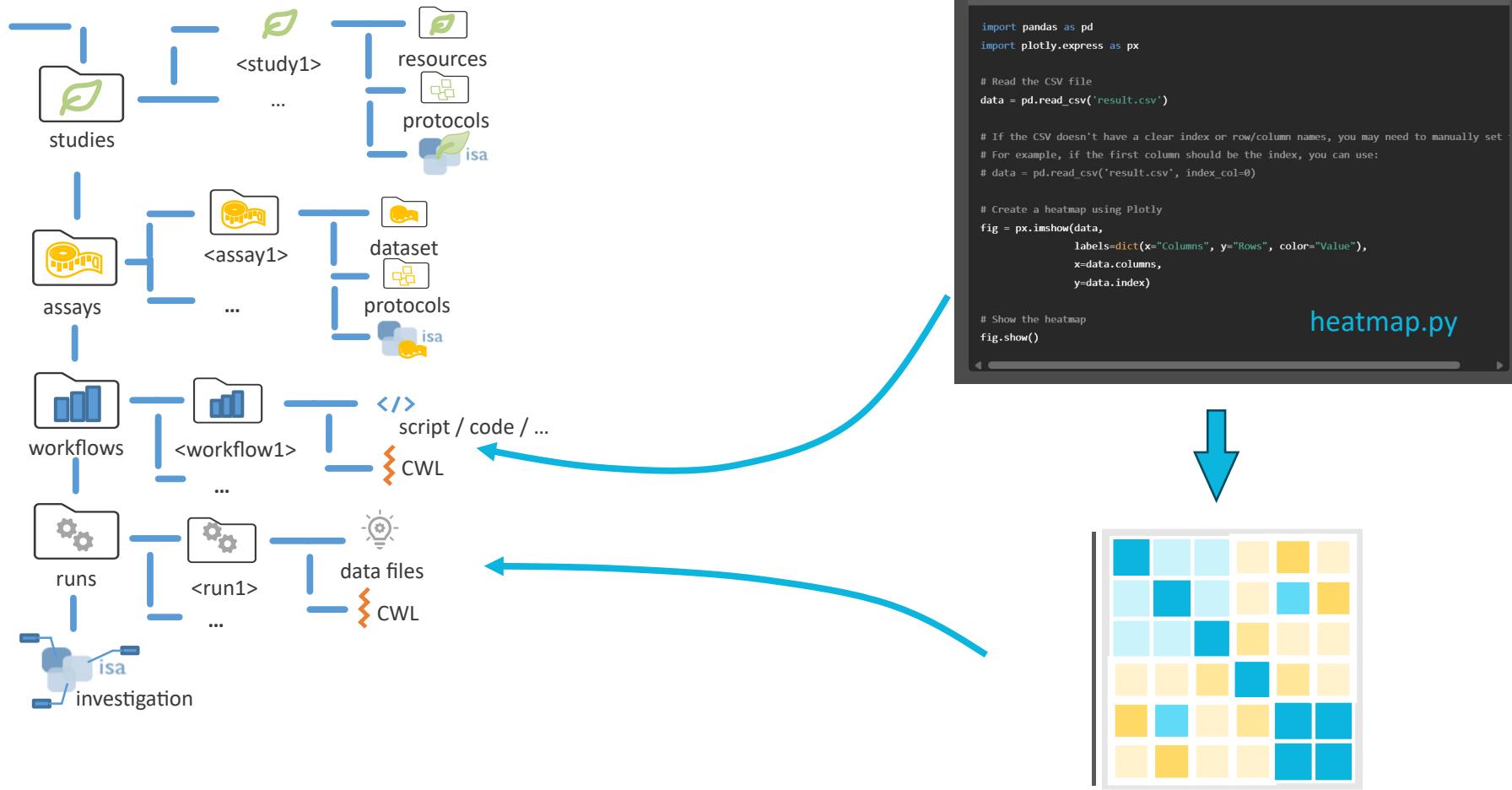
A computational workflow is like a protocol



Option I: Create a virtual assay



Option II: Create a workflow and run



Use CWL to wrap your workflow

CWL workflow document (*.cwl)

```
graph LR; A["CWL workflow document (*.cwl)"] --> B["CWL job parameter (*.yaml)"]; B --> C["CWL runner"]; C --> D["output folder"]
```

1 → 2 → 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]

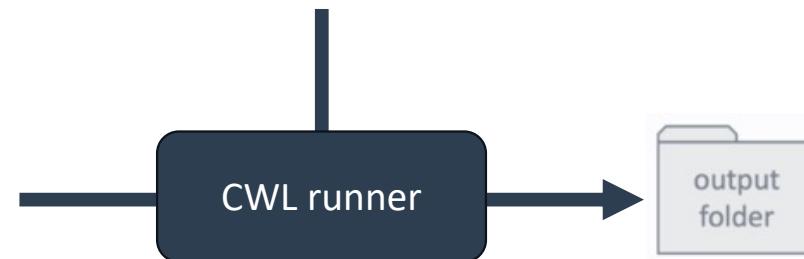
    compile:
      run: arguments.cwl
      in:
        src: untar/extracted_file
        out: [classfile]
```

CWL
tool descriptors (*.cwl)

CWL job parameter (*.yaml)

```
job
yaml

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



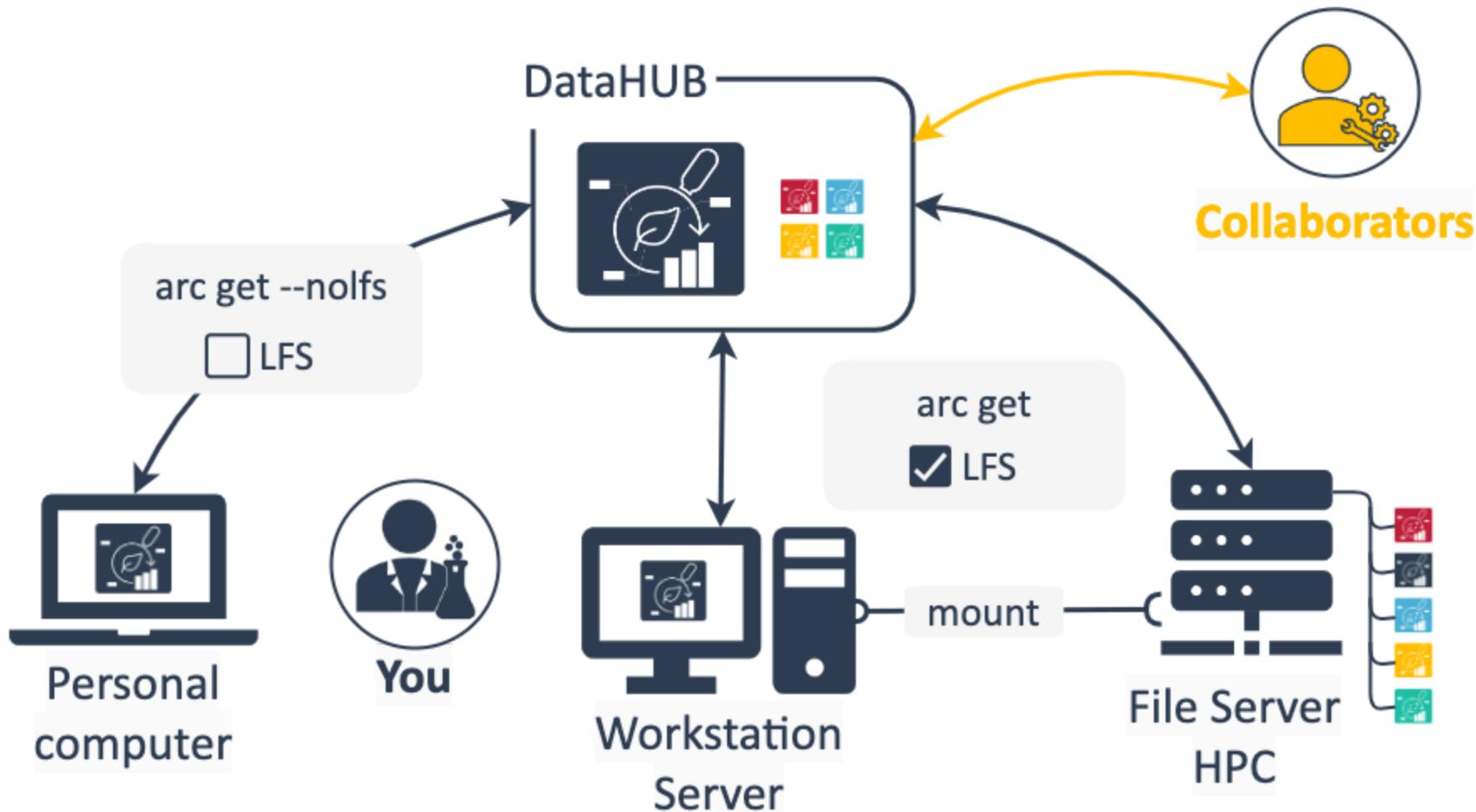
Hands-on part 3: Data

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

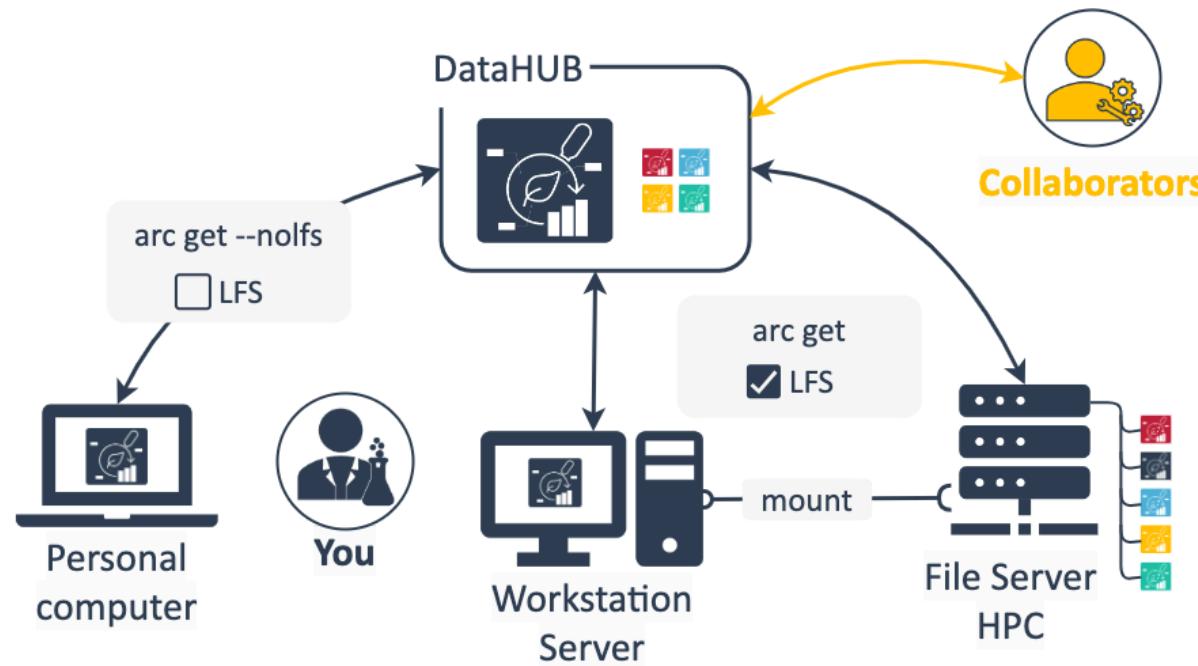
-  We will skip the **Add a datemap** step
-  Do the **Data analysis** step and stop

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

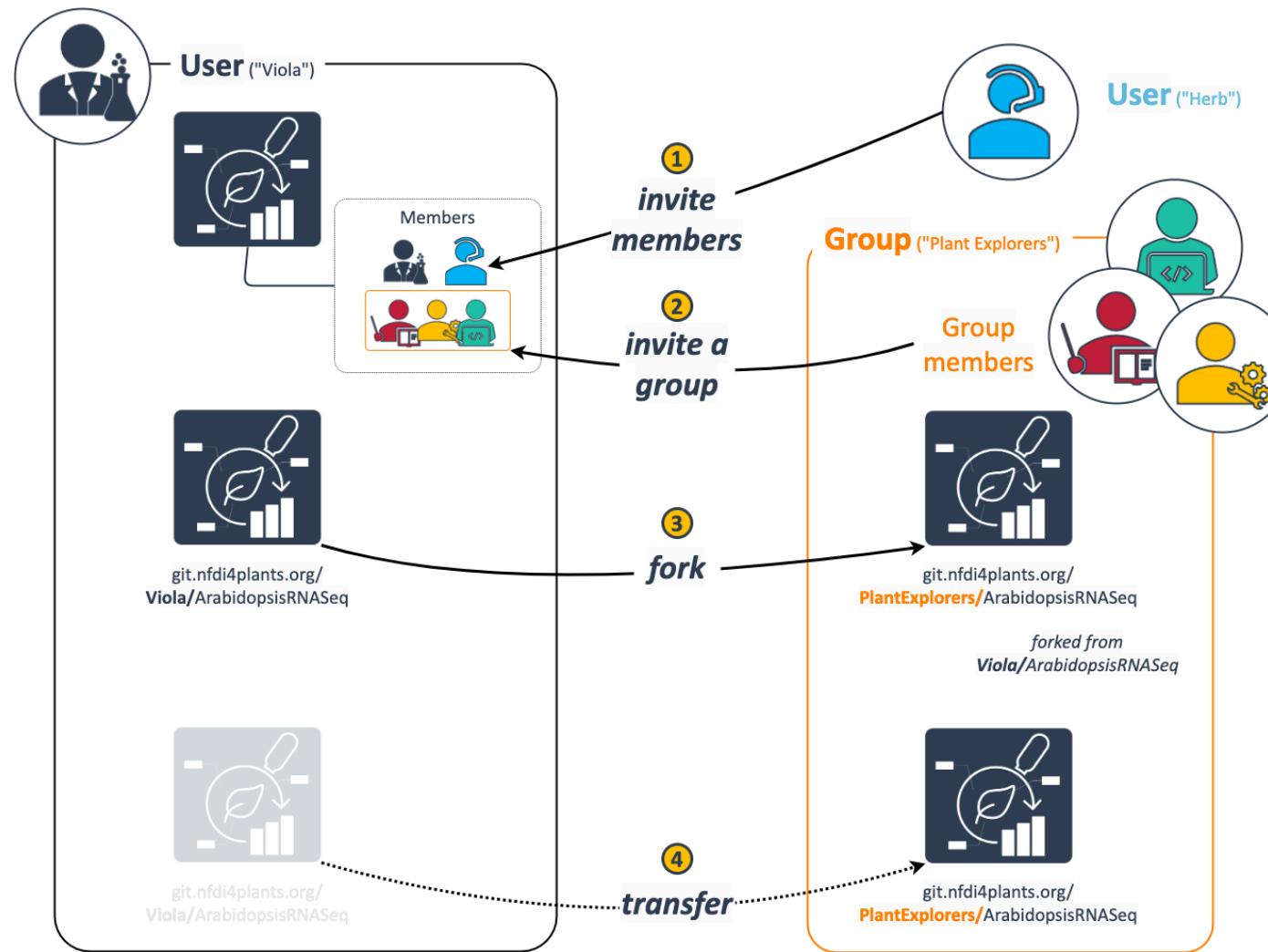
Project = ARC

- 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	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

 **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 in GitLab. It includes a search bar, navigation links, and buttons for 'Import from a project', 'Invite a group', and 'Invite members'. A table lists four members with their accounts, source, max role, expiration date, and activity details.

Account	Source	Max role	Expiration	Activity
Adriano Nunes-Nesi @hunesnesi	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

The screenshot shows the 'Samuilov-2018-BOU-PSP' page in ARCIct. It includes a sidebar with navigation links like 'Login', 'New ARC', and 'Explorer'. The main area displays investigation contacts with their names, ORCID IDs, scores, and dropdown menus.

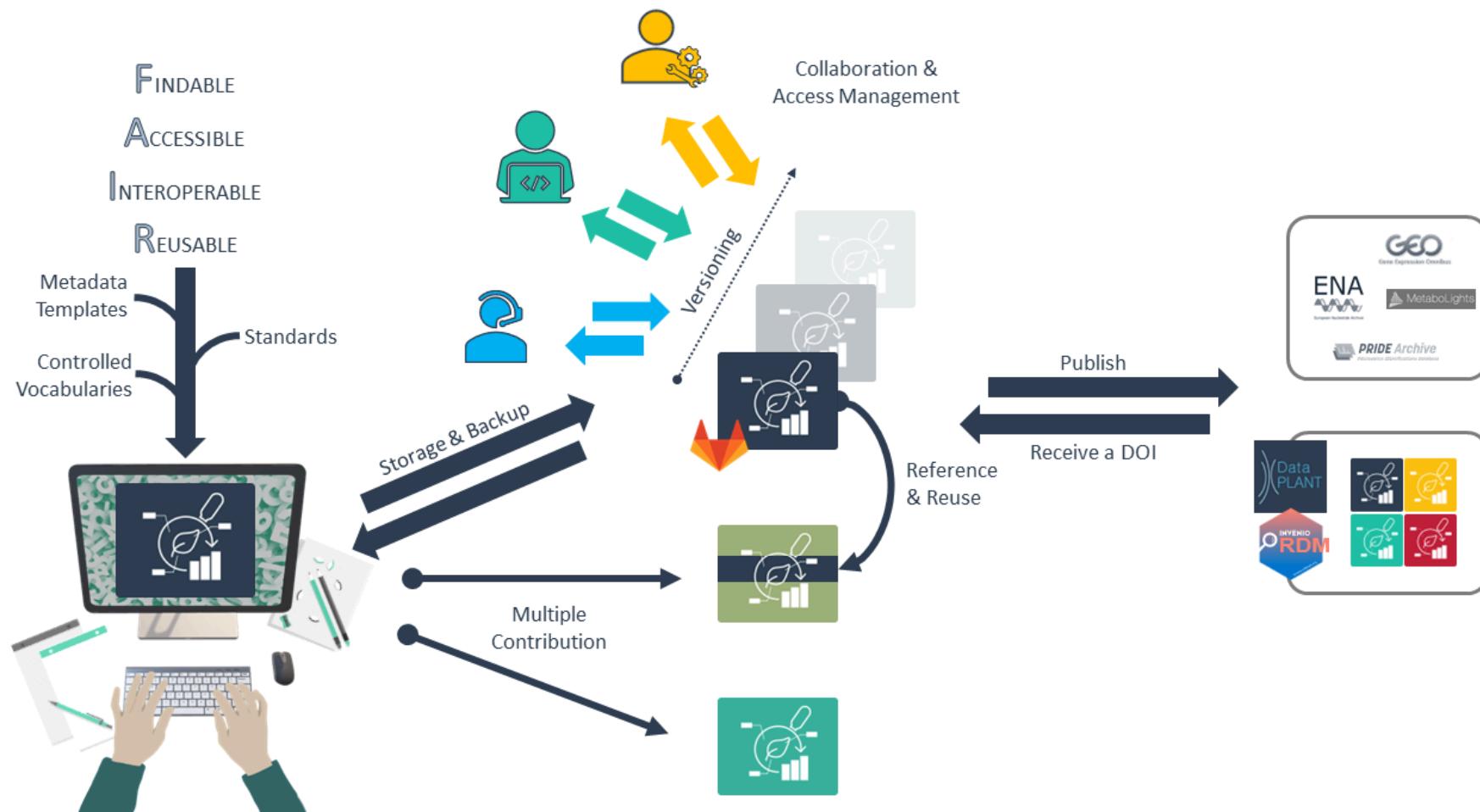
Contact	Score	Actions
Sladjana Samuilov <orcid>	4/10	▼
Nadine Rademacher <orcid>	3/10	▼
Samantha Flachbart <orcid>	3/10	▼
Leila Arab <orcid>	3/10	▼
Saleh Alfarraj <orcid>	3/10	▼
Franziska Kuhnert <orcid>	3/10	▼
Stanislav Kopriva <orcid>	3/10	▼
Andreas P. M. Weber <orcid>	4/10	▼
Tabea Mettler-Altmann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

ARCIct: Investigation Contacts

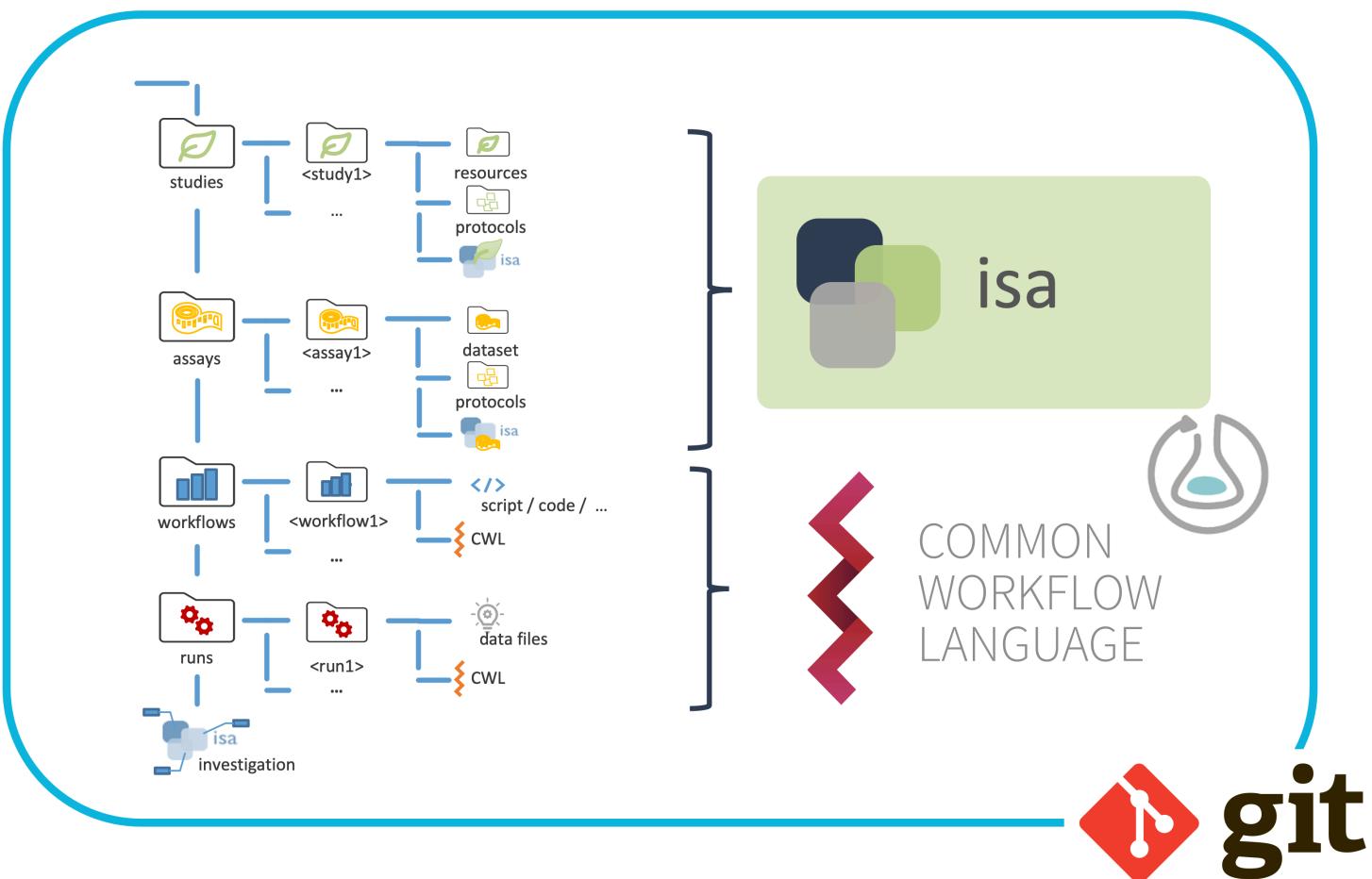
Investigation contacts are not automatically invited as members to the ARC.

Hands-on part 4: DataHUB

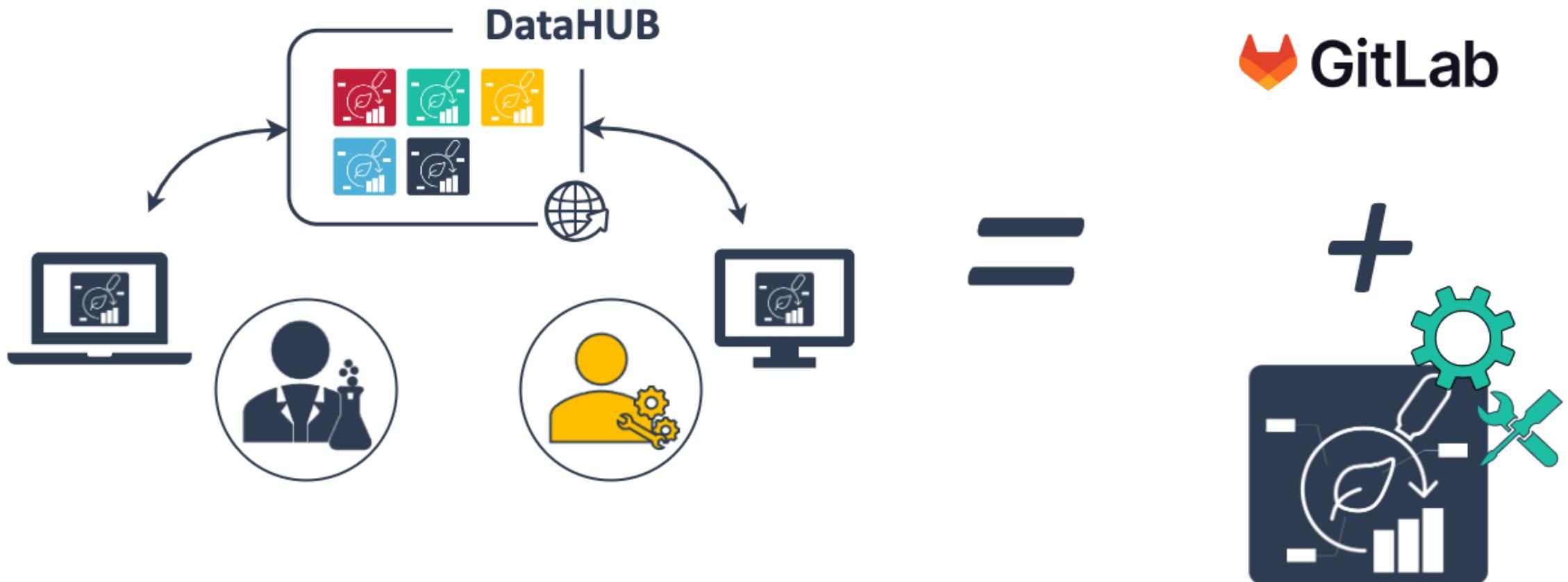
DataHUB overview



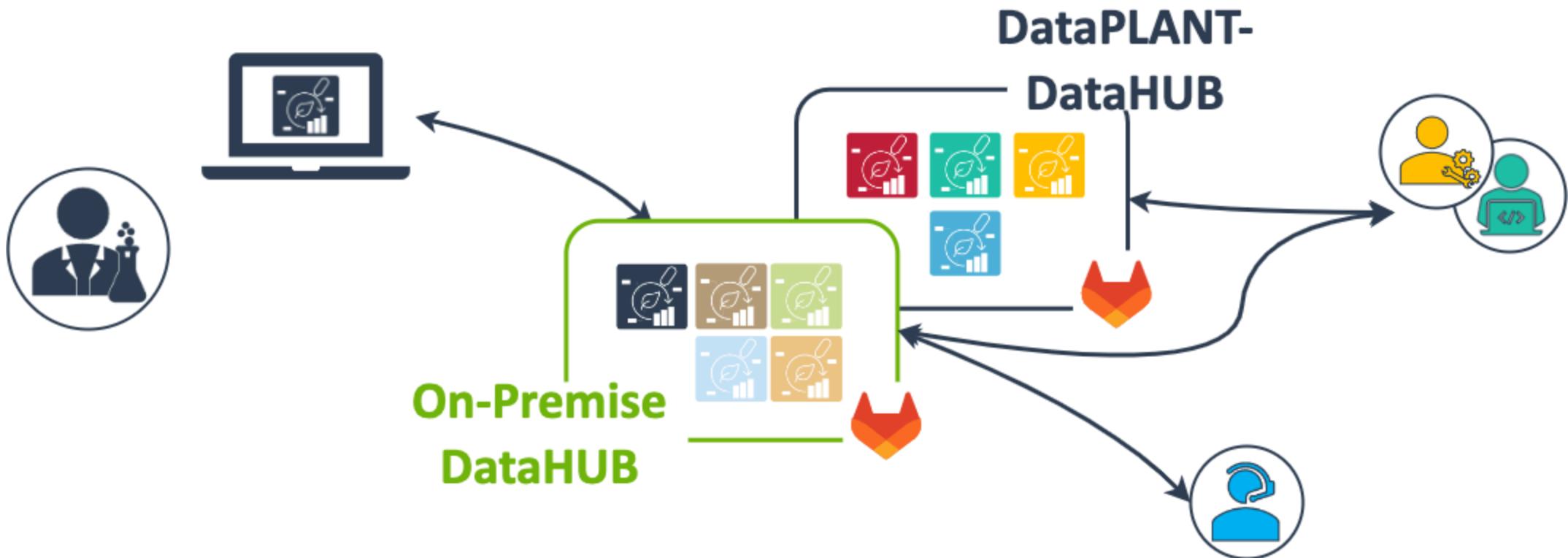
ARC builds on standards + Git



The DataPLANT DataHUB – a GitLab *Plus*

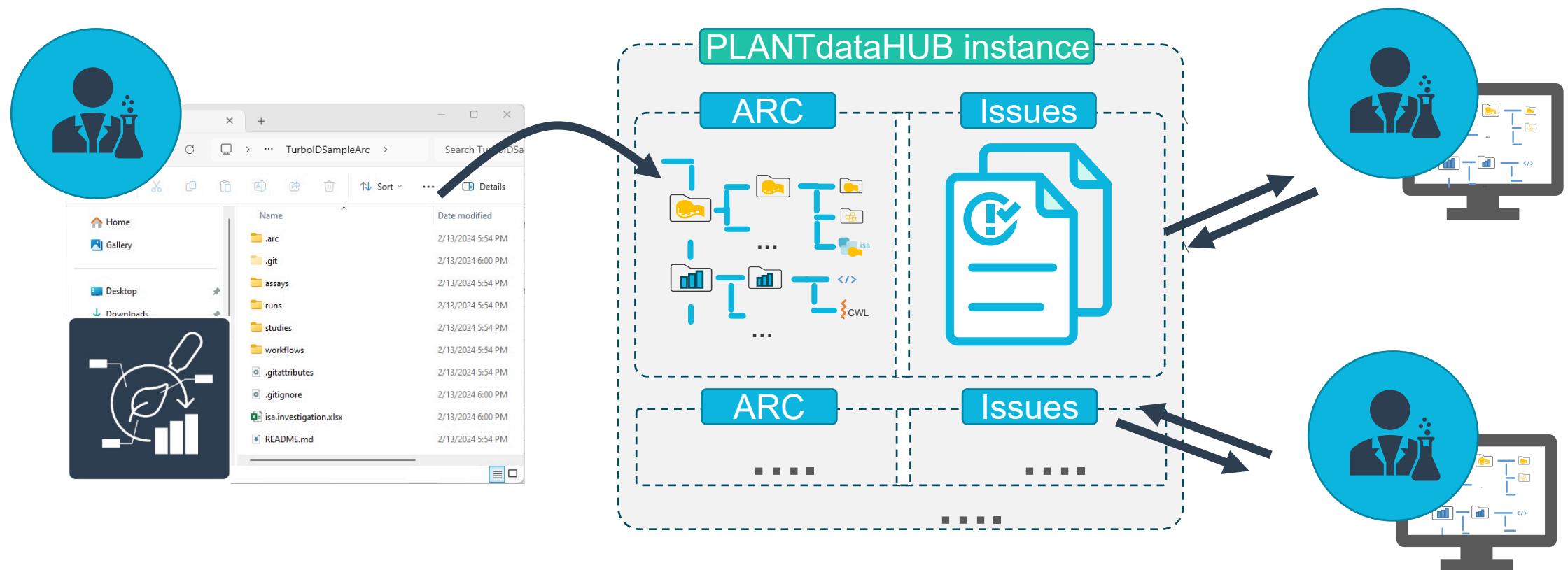


On-premise DataHUBs

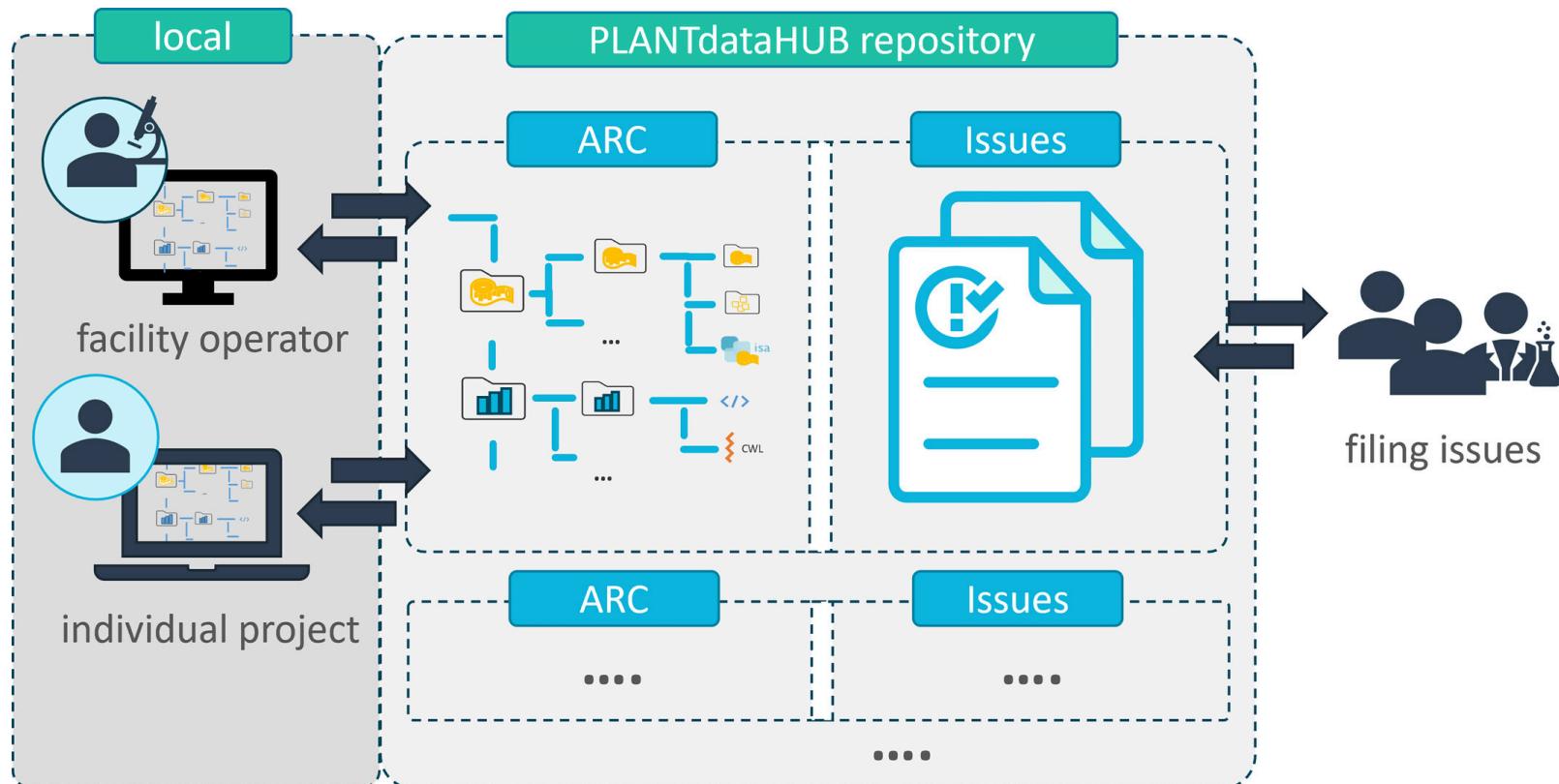


ARC services are available as on-premise option

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 with blue liquid inside, followed by the text "eLabFTW". Below the logo is a horizontal line. The main heading "Über Ihre Institution anmelden" is centered above a dropdown menu. The dropdown menu is currently set to "HHU-IDM" and has a downward arrow indicating it is a selection menu. Below the dropdown is a checkbox labeled "Anmeldung merken" (Remember login) with a checked status. A large teal button labeled "Anmelden" (Login) is positioned below the checkbox. At the bottom left, there are icons for social media sharing (Twitter, LinkedIn, Facebook, and a speech bubble) and a link to "DATENSCHUTZ-BESTIMMUNGEN" (Data Protection). At the bottom right, there is a note stating "Bereitgestellt von eLabFTW" and "Seite generiert in 0.00437 Sekunden" (Page generated in 0.00437 seconds).

Über Ihre Institution anmelden

Wählen Sie einen Identitätsanbieter aus

HHU-IDM

Anmeldung merken

Anmelden

Twitter LinkedIn Facebook DATENSCHUTZ-BESTIMMUNGEN

Bereitgestellt von eLabFTW
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:

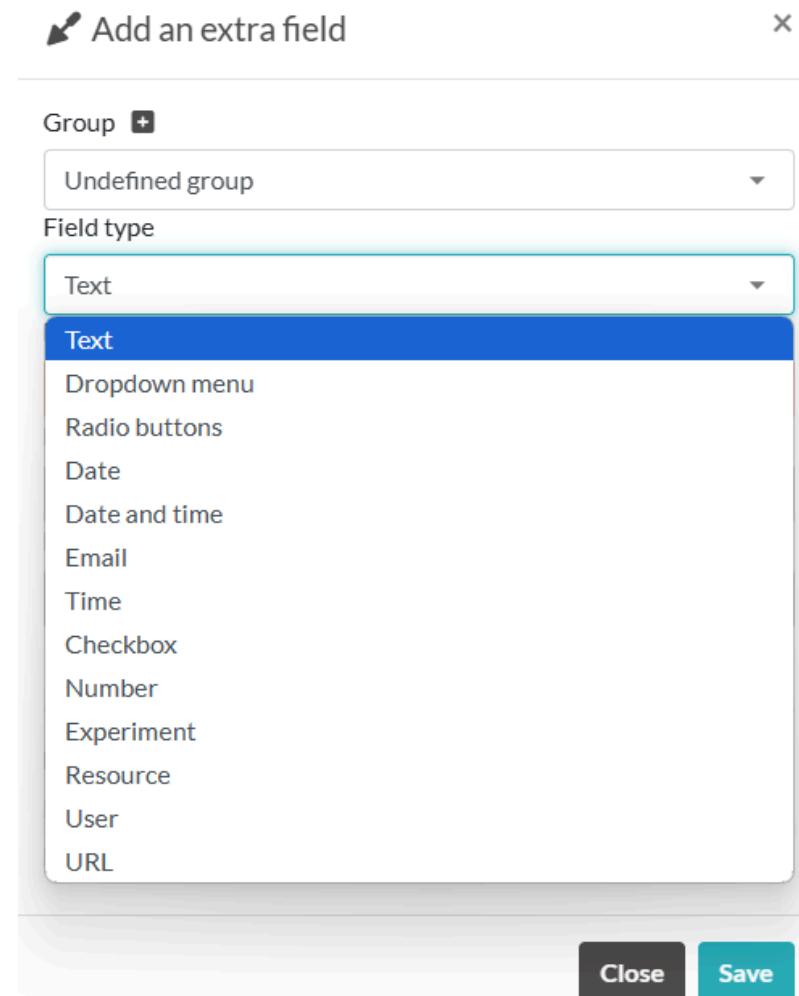
- Investigation ID
- Subgroup
- Organism /part (e.g. A.taliana, leaf, root, mitochondria)
- Goal (strain generation, plasmid genertion)
- Methode (e.g. transformation, western blot, extraction, biolector)
- Genes/ Proteins (e.g. mKate2, eGfp, Rrm4)

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)* Antibiotic used</p> <p>Description Select the antibiotic used</p> <p>Choices Kanamycin Streptomycin 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 https://omero-cai.hhu.de/webclient/?show=dataset-12881</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)* Drug concentration</p> <p>Description Indicate the drug concentration</p> <p>Available units ng/mL µg/mL 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 x

Scope X EQUIPMENT Zeiss AXIO Observer Z1 Inverted Fluorescence Microscope

< > 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 	Custom ID Get next
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

