



CEPLAS

Cluster of Excellence on Plant Sciences

ARCify your research project

October, 2024

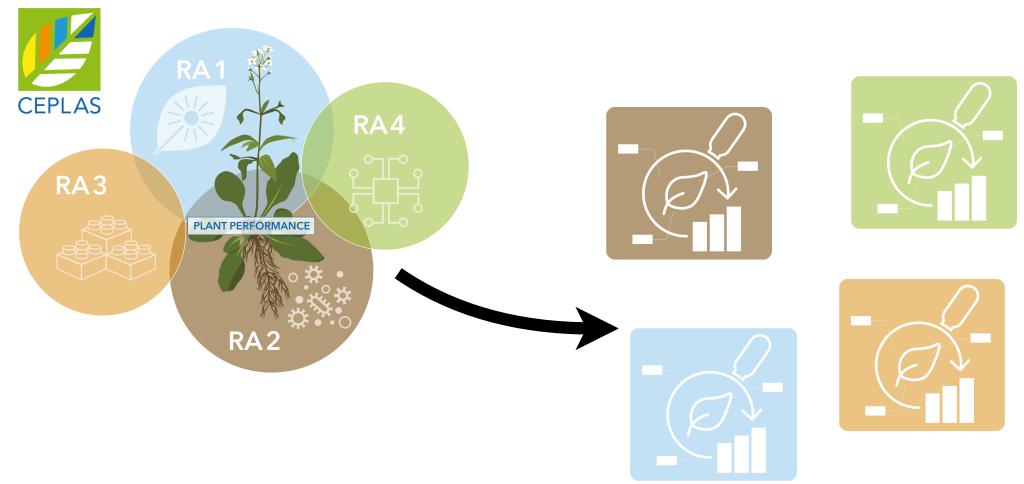
Dominik Brilhaus (CEPLAS)

Sabrina Zander (MibiNet)



Goals

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



House-keeping

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



Training Materials

Slides are shared via [DataPLANT knowledge base](#)

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.

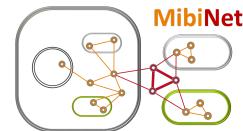
1. Slack Workspace for ad hoc support
2. Monthly user meeting (2nd Friday of the month)

→ [Details](#).



trr_341

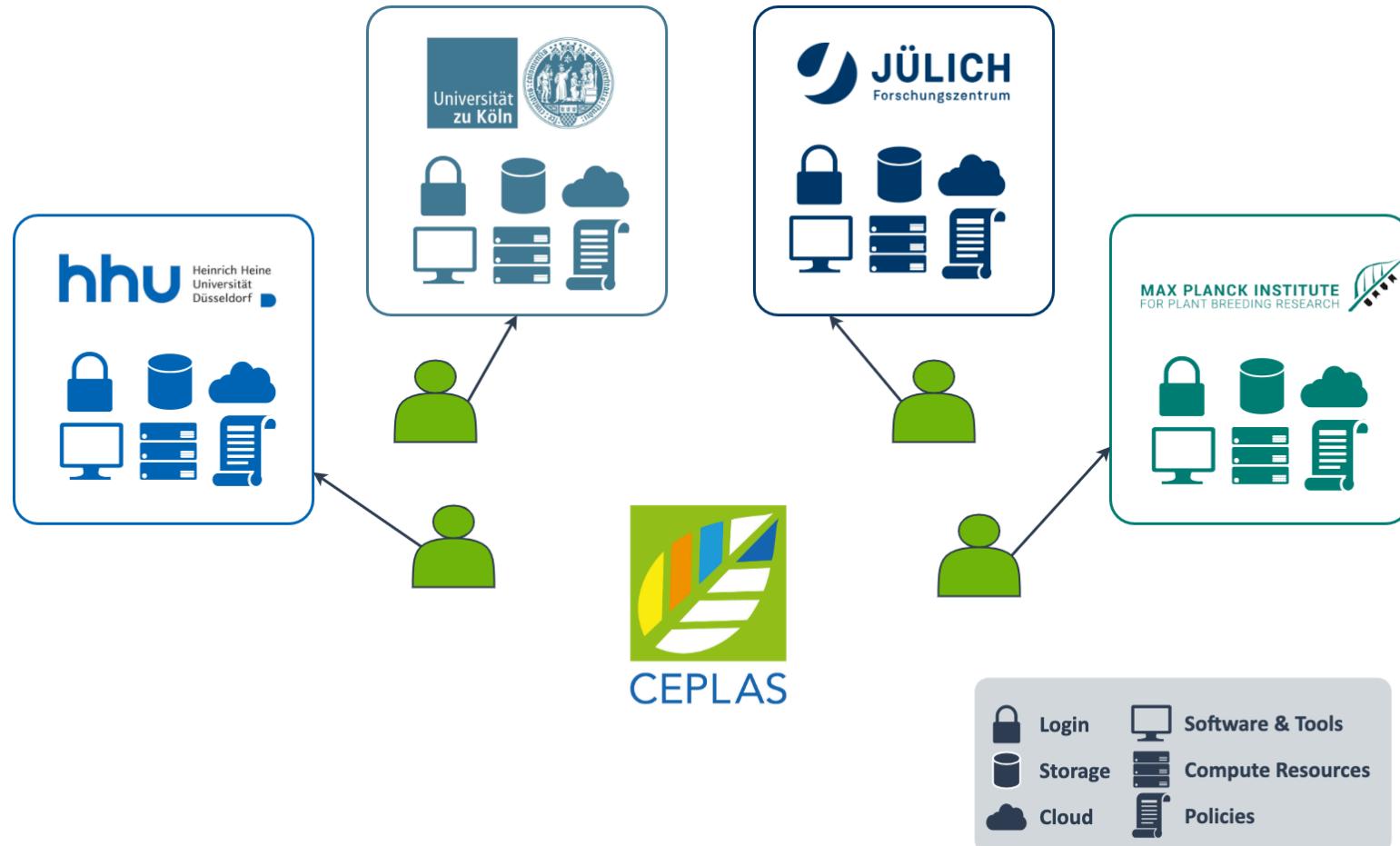
plant
ecological
genetics



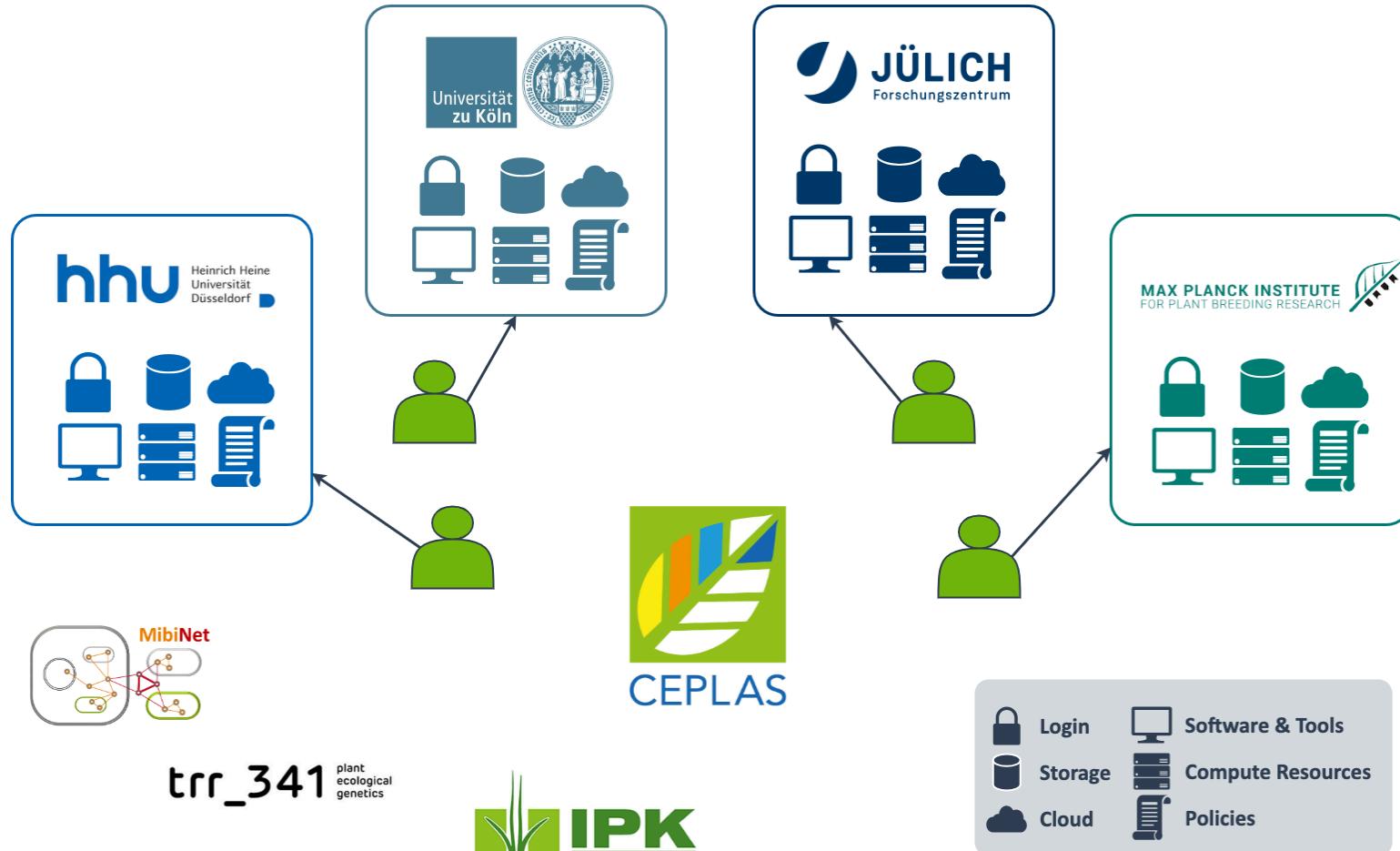
CEPLAS – One cluster, four locations



Data silos impede collaboration

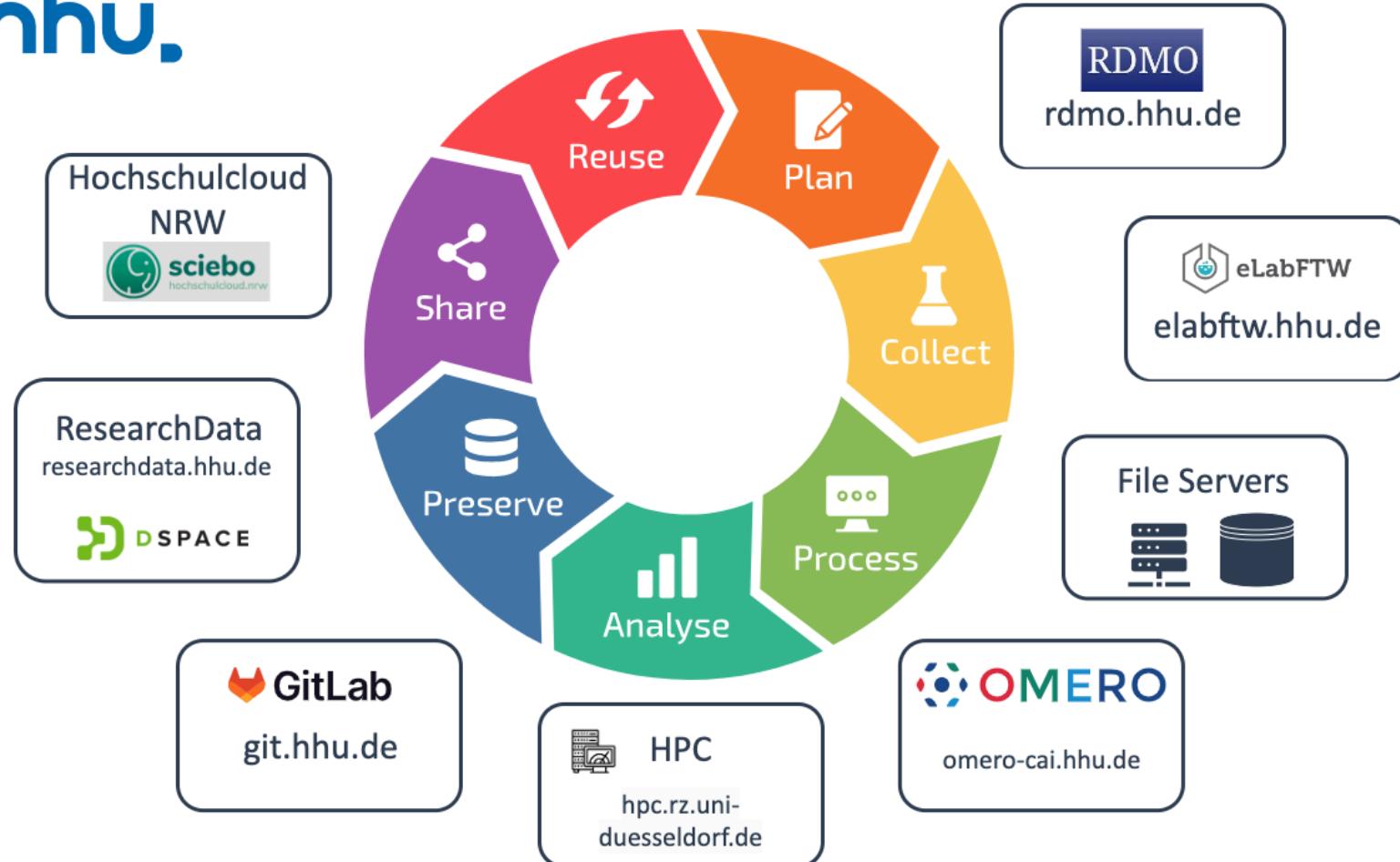


Data silos impede collaboration



Missing interfaces impede collaboration

hhu.



Data Stewardship between DataPLANT and the community

Community



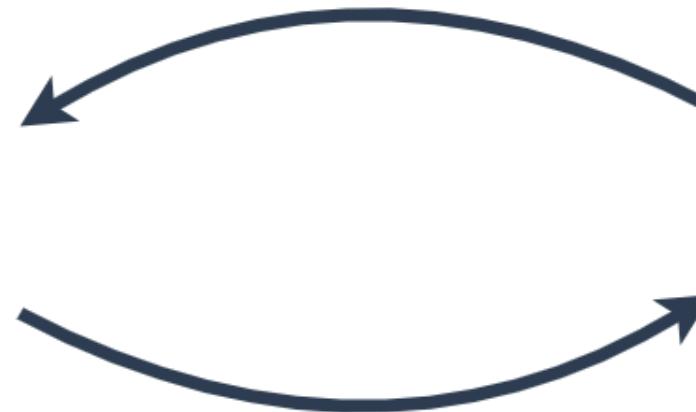
CEPLAS

Domain experts
User experience
Training

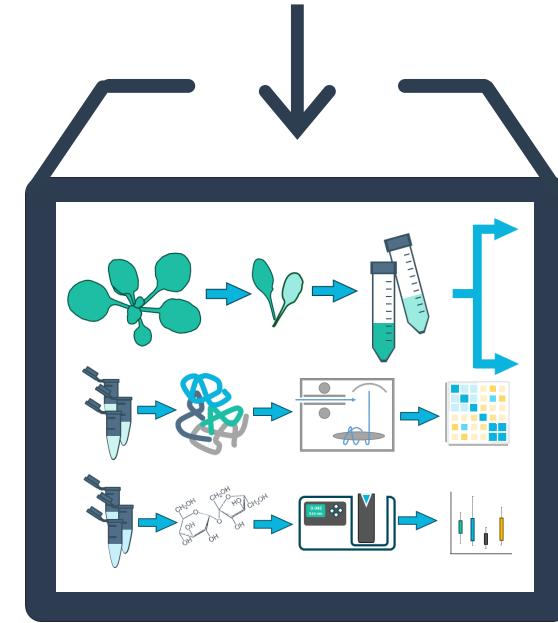
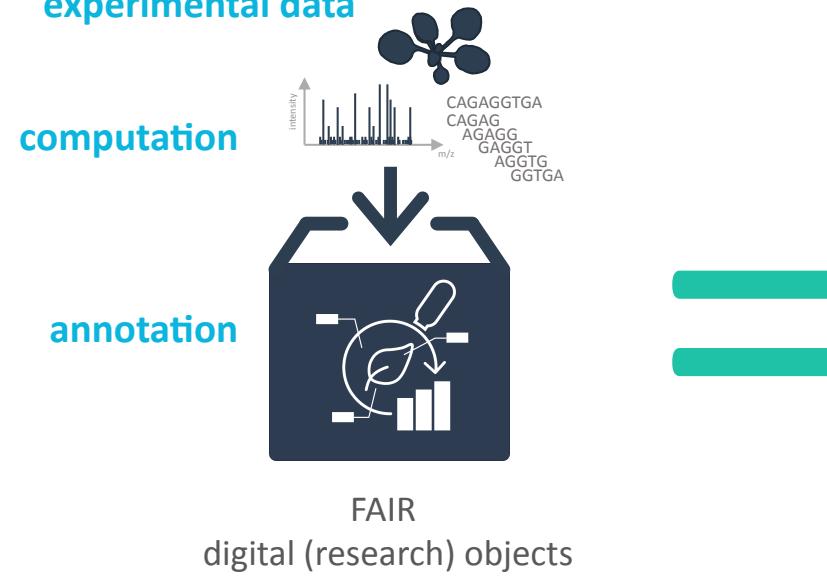
nfdi4plants



Service provider
Developers
Tech experts

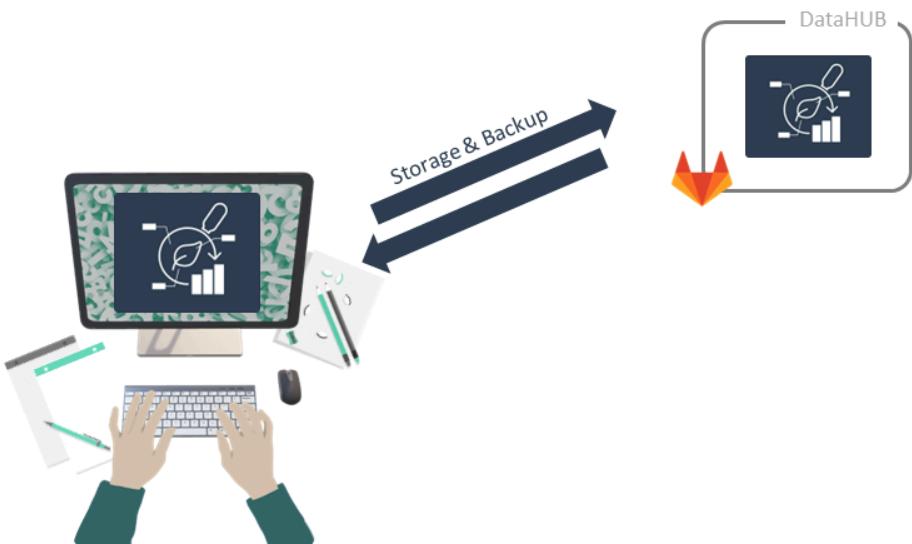


Annotated Research Context (ARC)

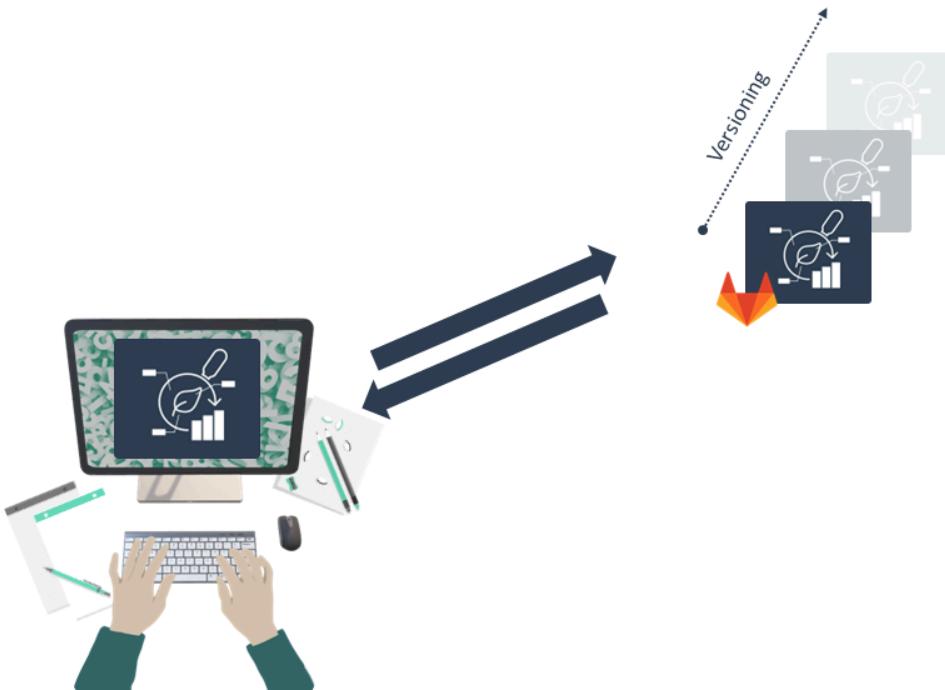


Your entire investigation in a single unified bag

You can store your ARC in the DataHUB



ARCs are versioned



You can invite collaborators



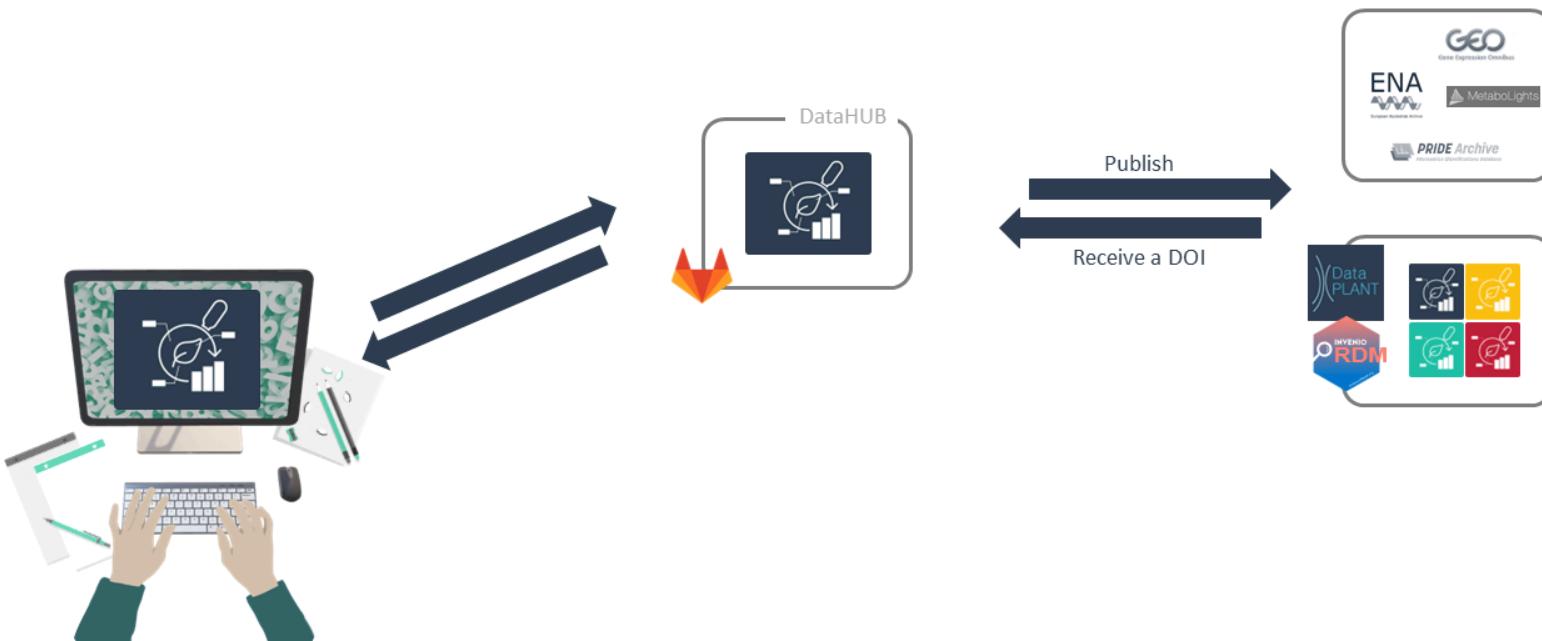
Collaborate and contribute



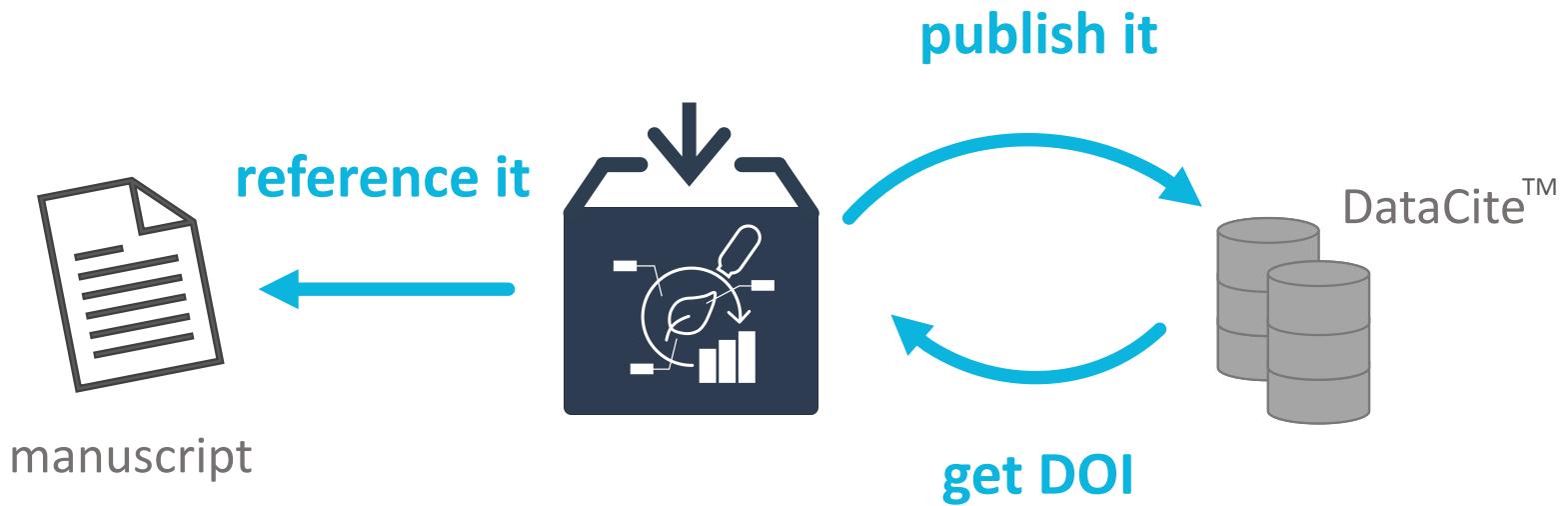
Reuse data in ARCs



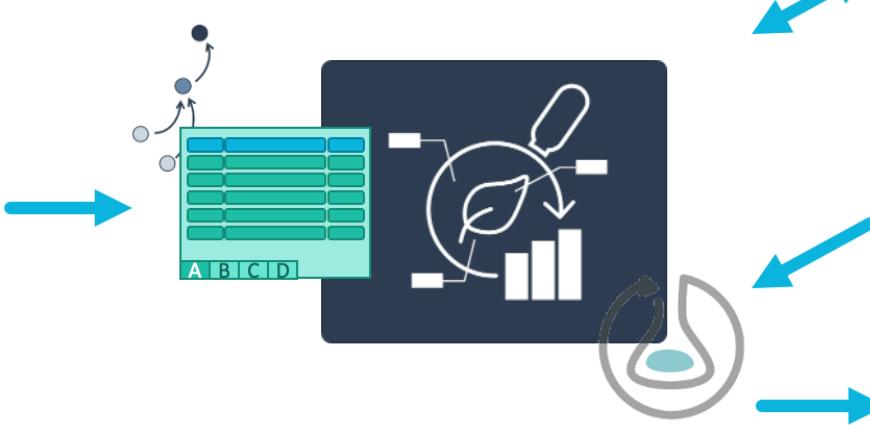
Publish your ARC



Publish your ARC, get a DOI



ARC as single-entry point



specialized endpoints

ENA
European Nucleotide Archive

GEO
Gene Expression Omnibus

PRIDE Archive
Proteomics Identifications database

EBI: MetaboLights

BioImage Archive

dataset search

Google

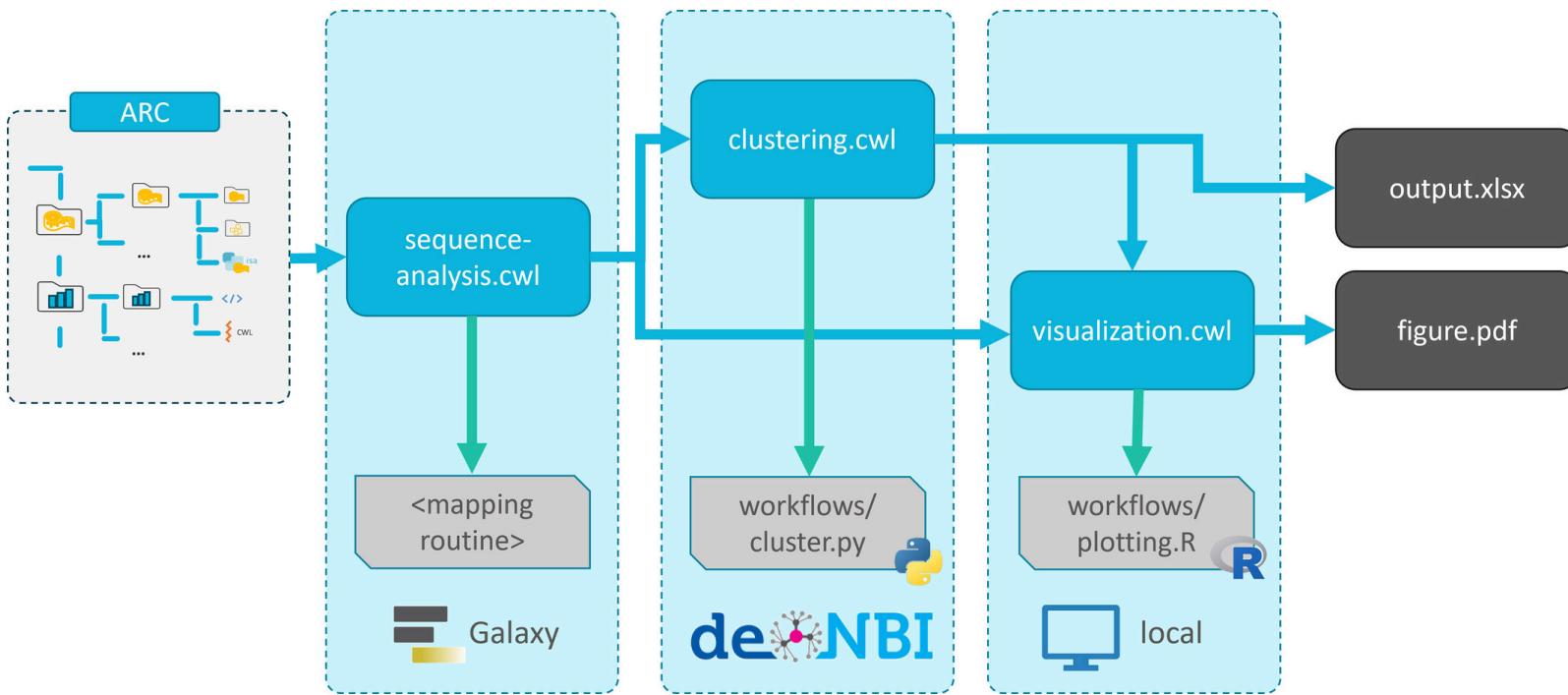
OpenAIRE

The Dataverse® Project

INVENIO

data publication

Data analysis and workflows



Galaxy integration: Extra value for plant research

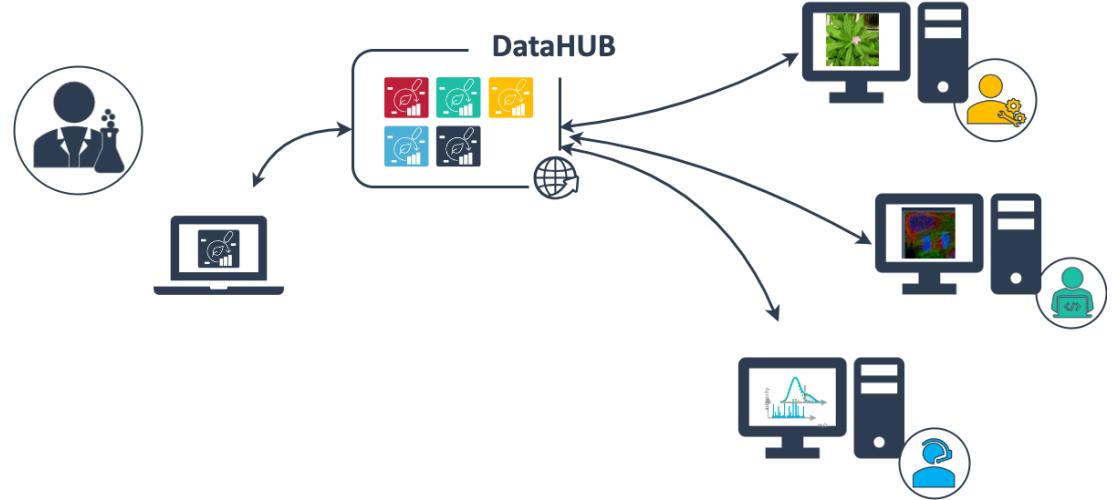


e.g. <https://plants.usegalaxy.eu>

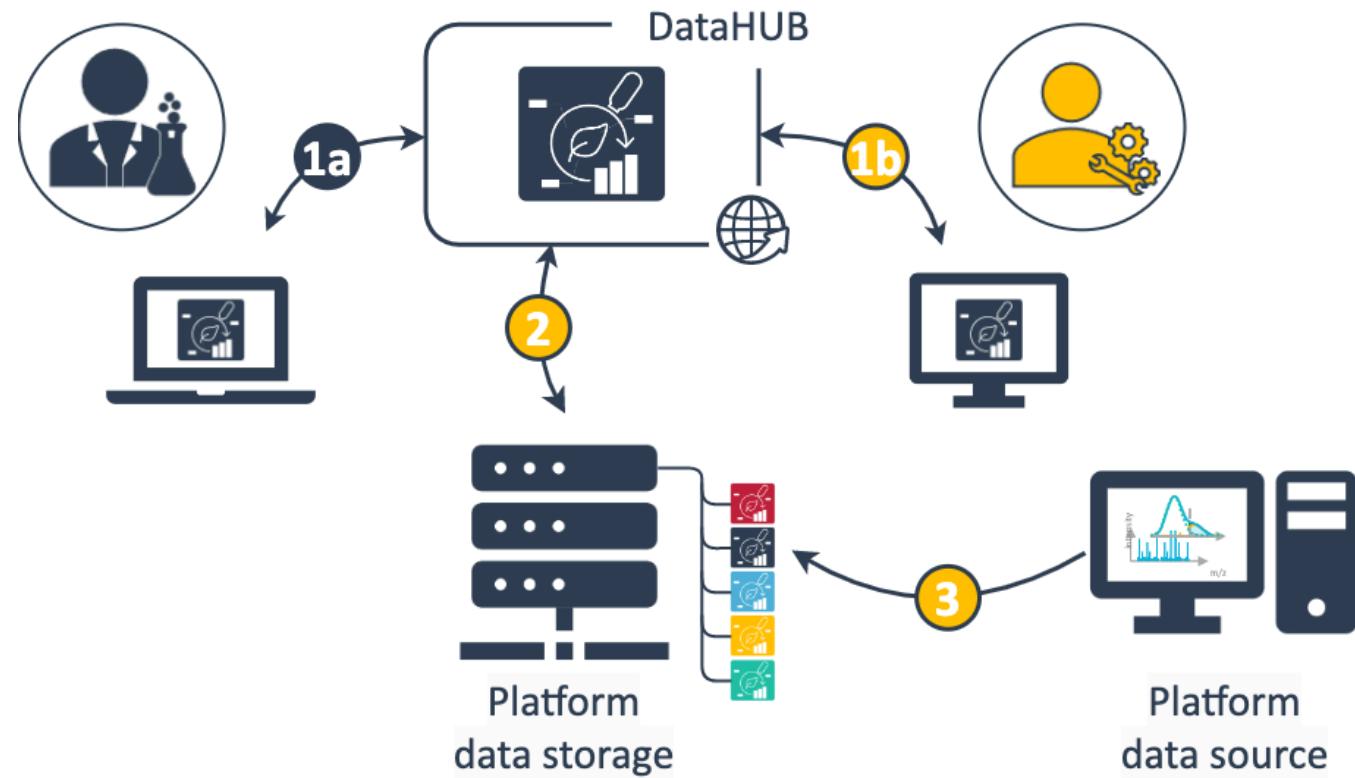
- Full ARC compatibility
- Automated metadata generation
- Specialized tools and workflows for ‘omics processing and analysis
- Public repository compatibility
- Galaxy teaching resource for data analysis

Enabling platforms

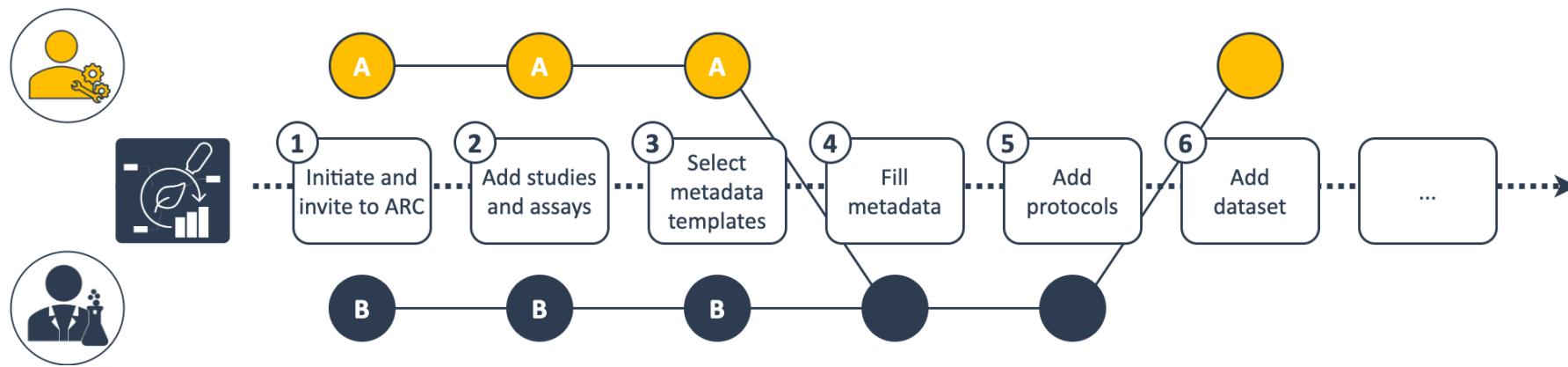
- Streamlined exchange of (meta)data
- Communication and project management



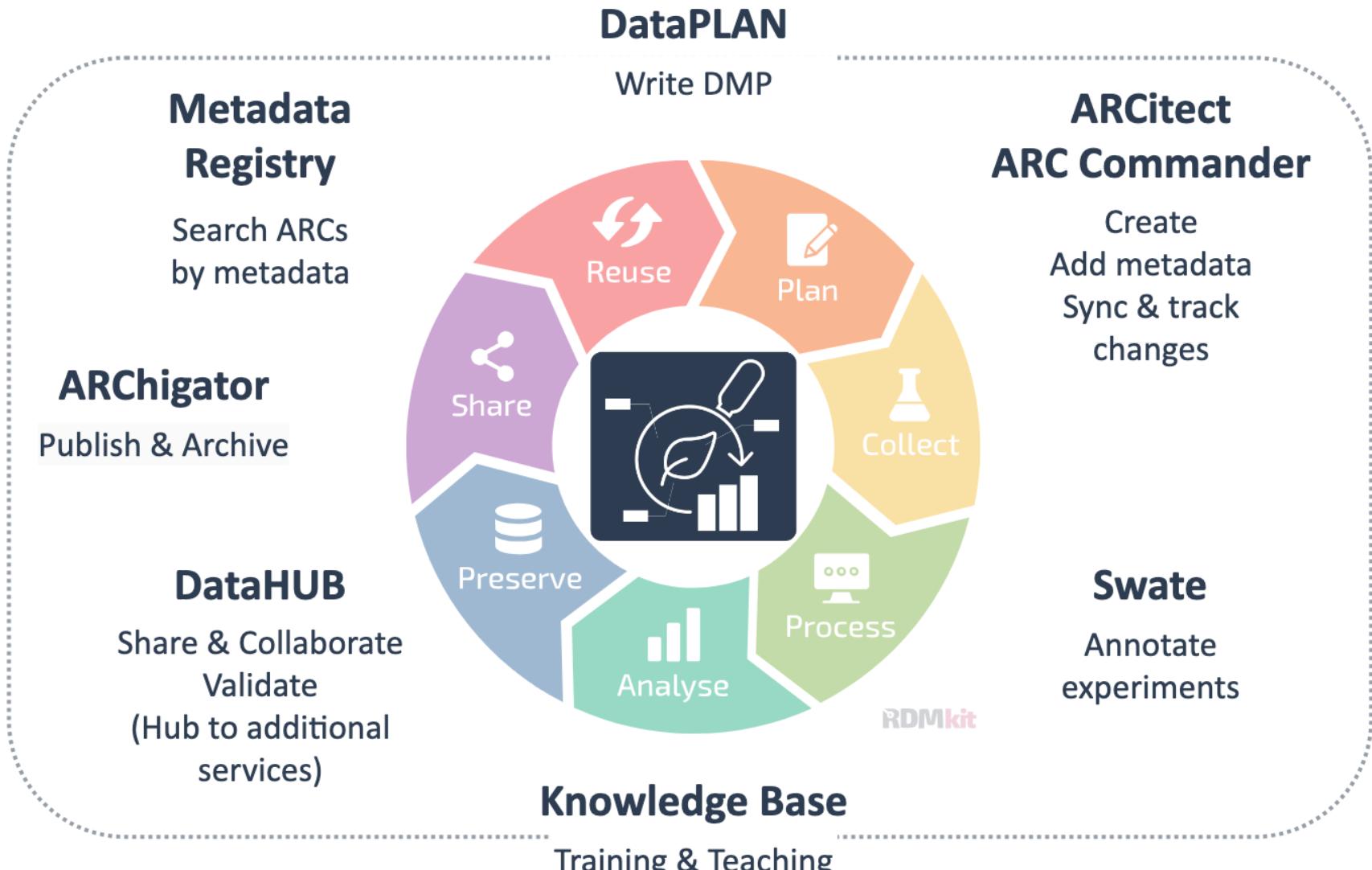
Streamlined data exchange



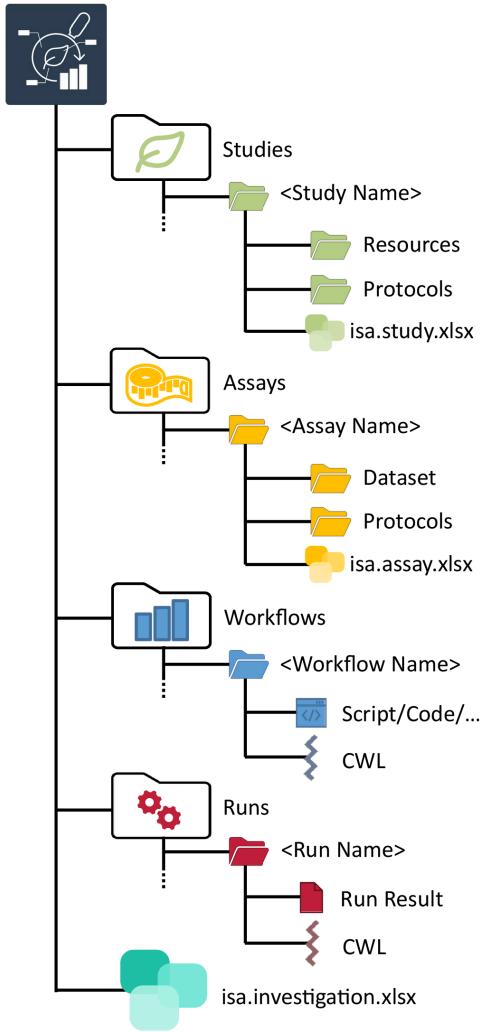
Meet your collaborators in an ARC



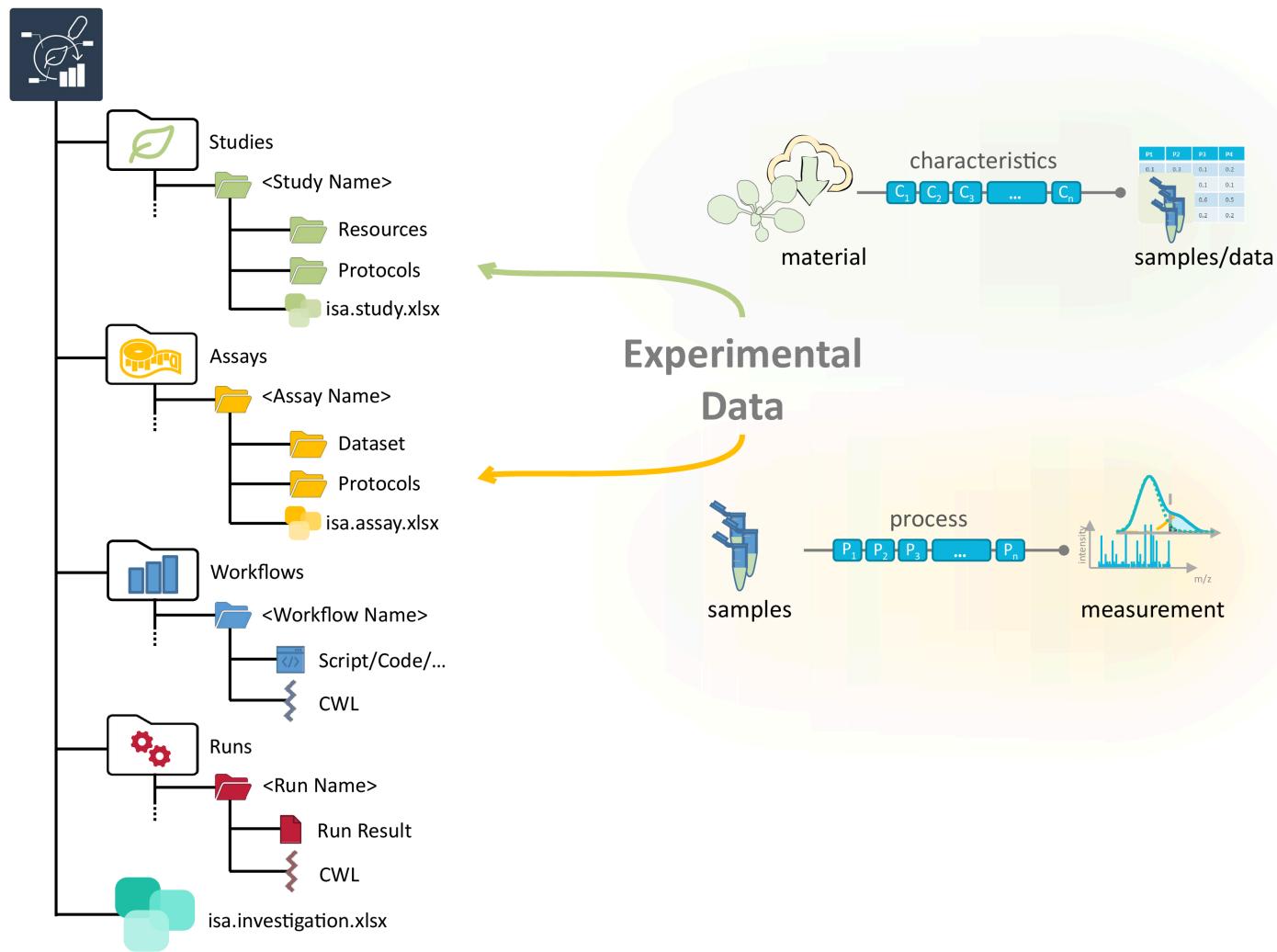
The ARC ecosystem



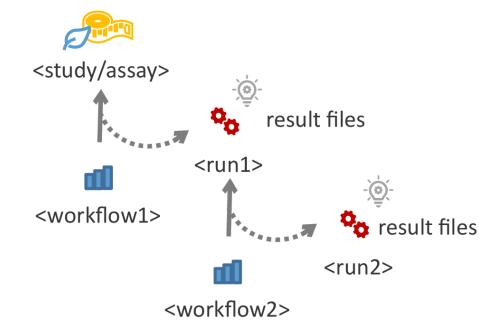
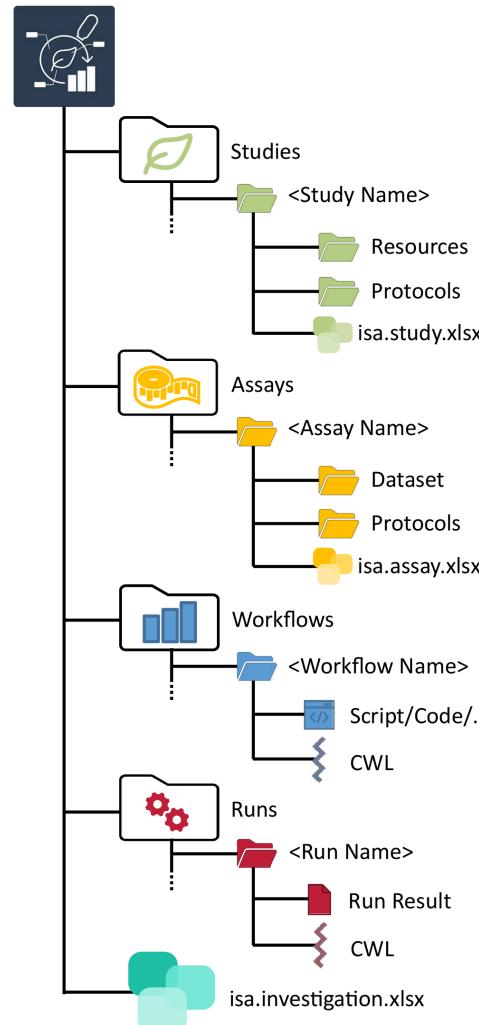
What does an ARC look like?



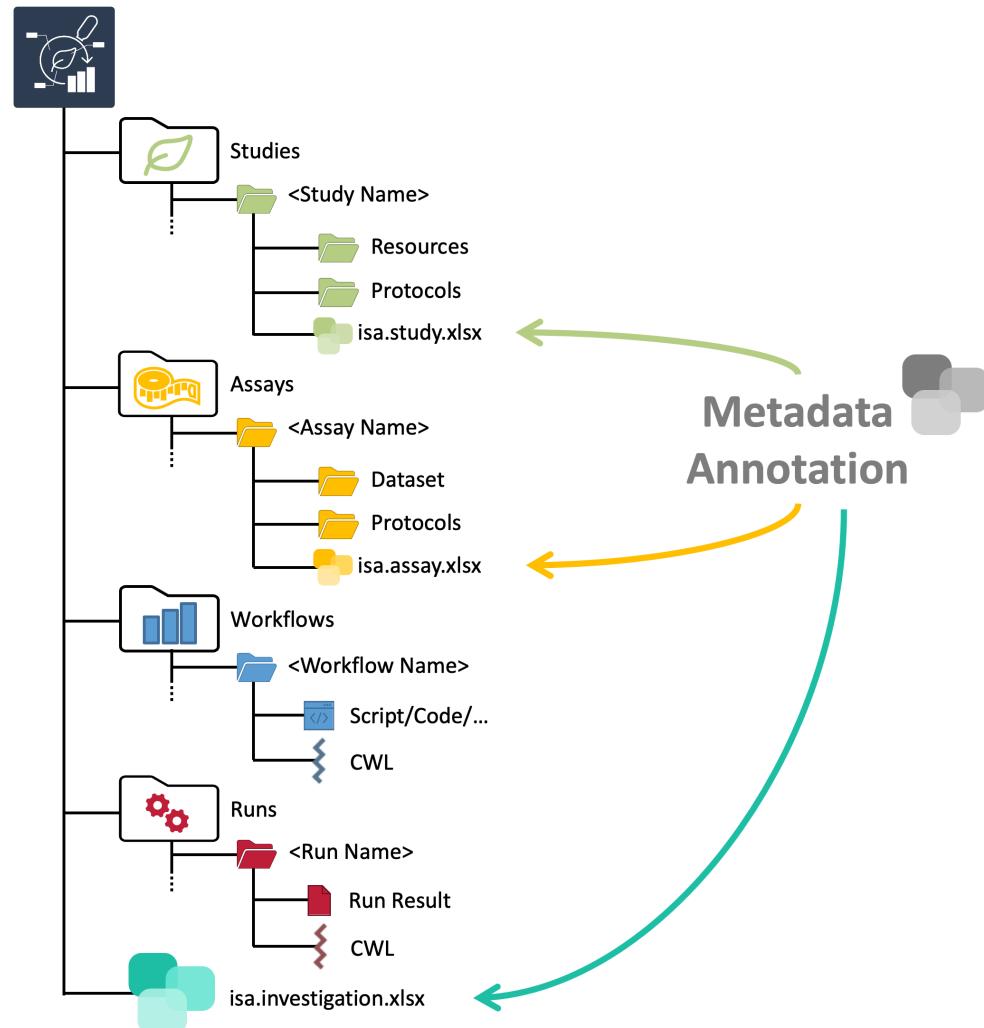
ARCs store experimental data



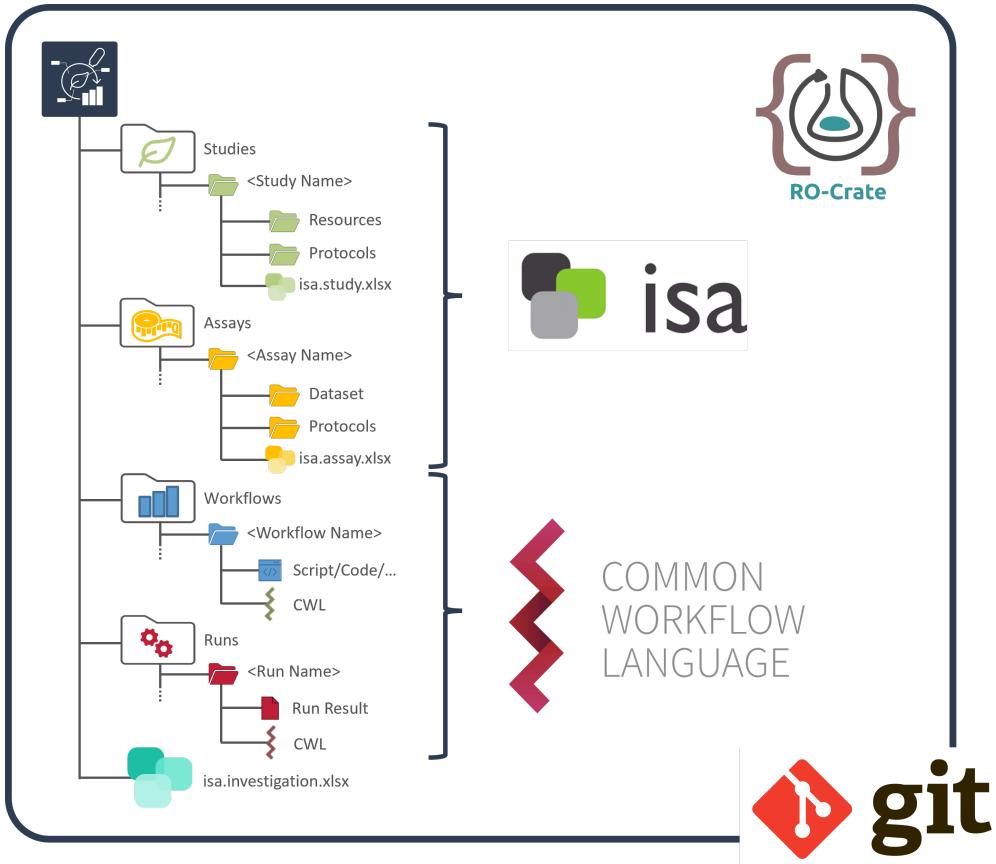
Computations can be run inside ARCs



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

Hands-on demo

ARCitect installation

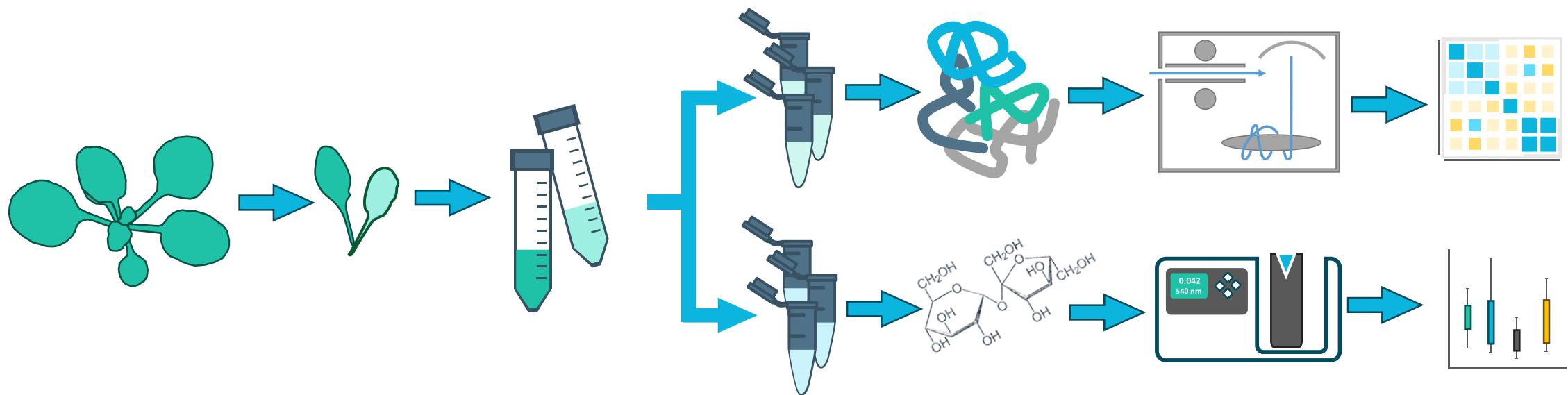
Please install version **v0.0.48** (or later) of the ARCitect:

<https://github.com/nfdi4plants/ARCitect/releases/latest>

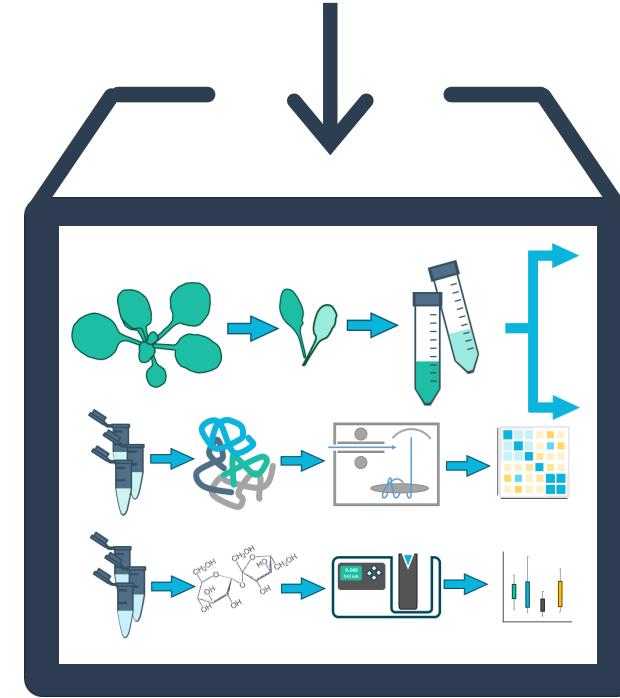
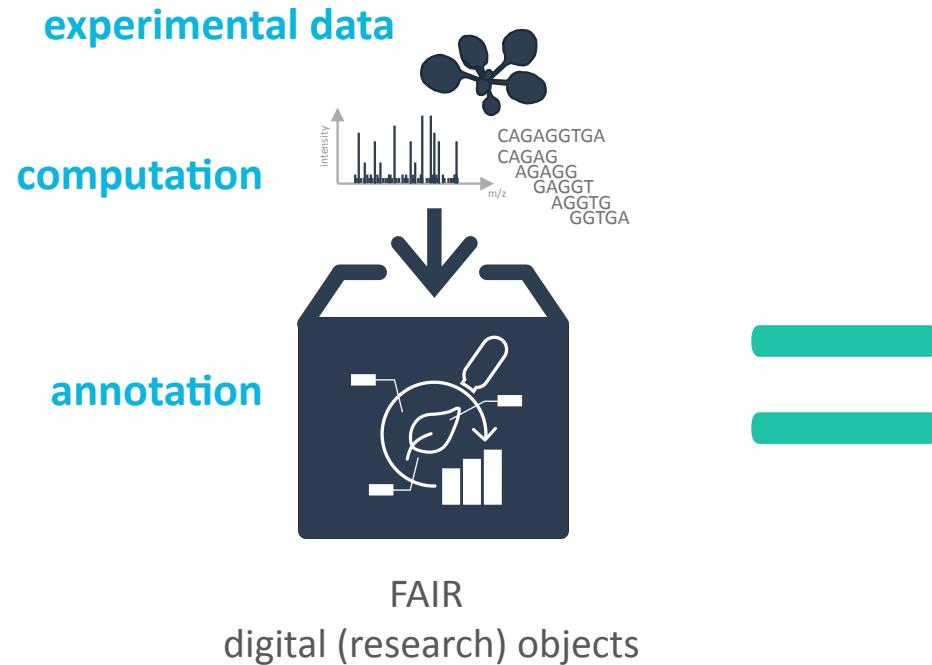
Download the demo data

<https://uni-duesseldorf.sciebo.de/s/C7ms3QA6q7OZnU2>

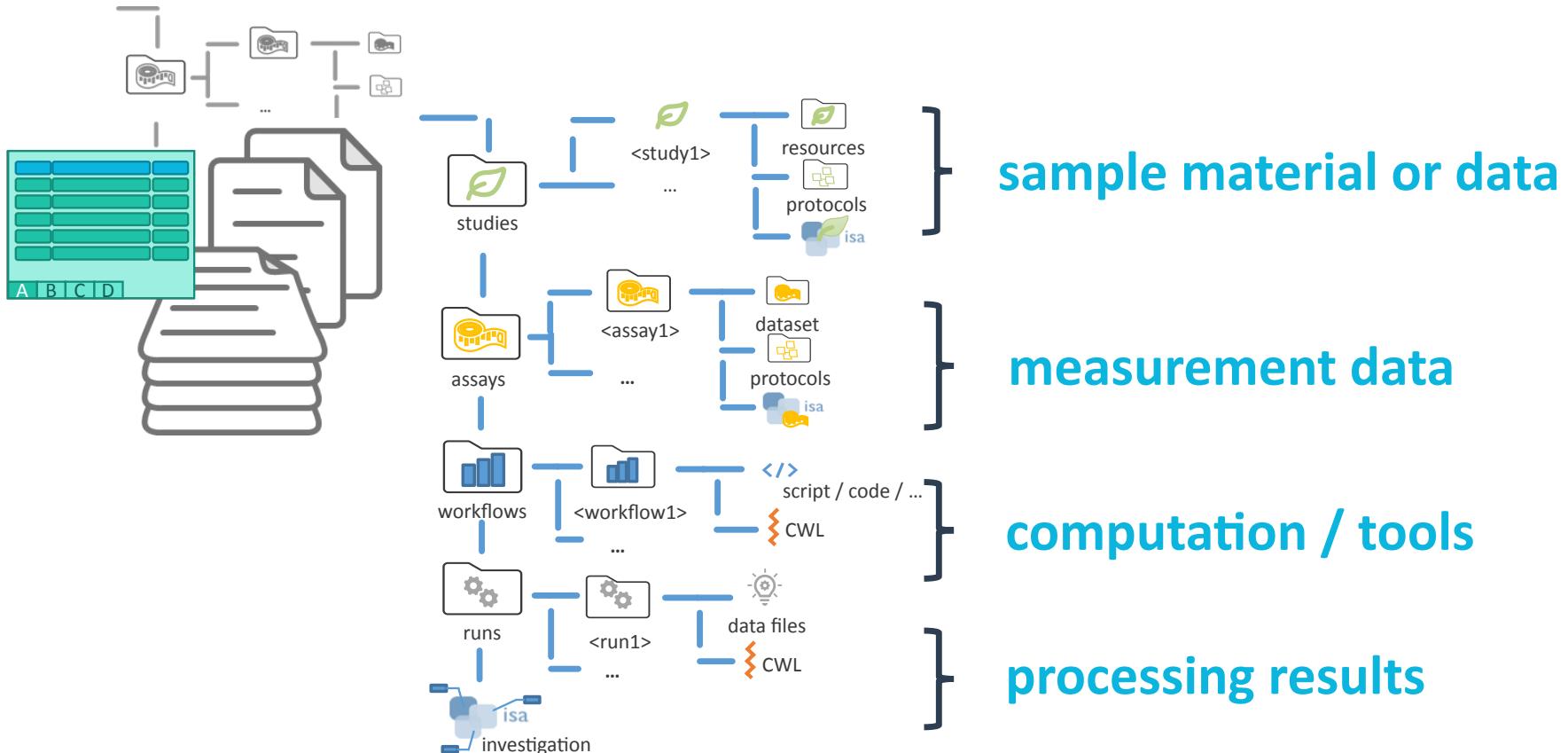
A small prototypic project



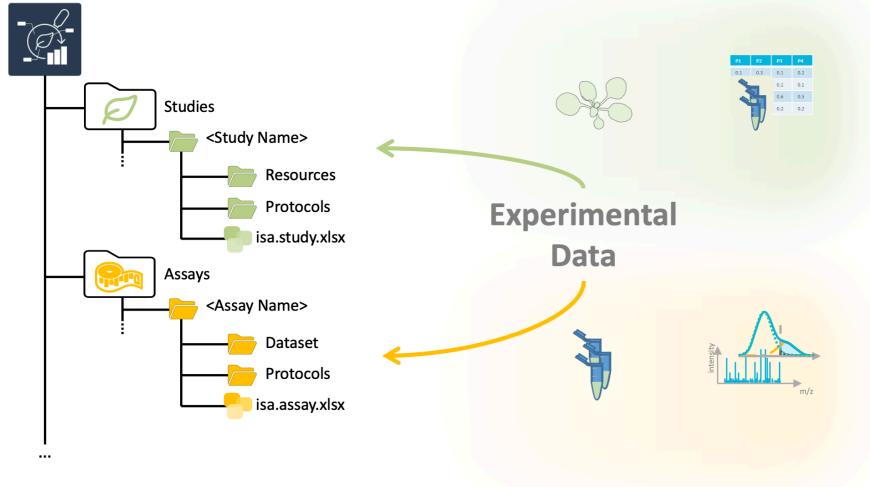
ARC: Annotated research context



The ARC scaffold structure



Sort Demo data in an ARC



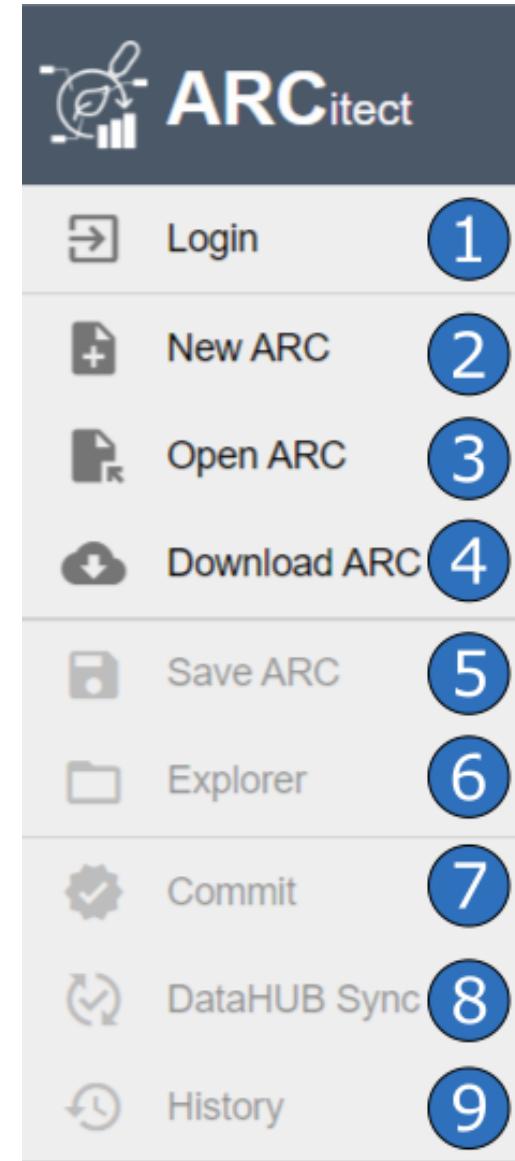
Experimental
Data

metabolomics_data
150112_56.D
150112_62.D
150112_66.D
150115_12.D
150115_14.D
150115_16.D
gcms_samplelist.tsv
method_gcms.txt
sample_submission_gcms.csv
methods
Illumina_libraries.txt
metabolite_extraction.txt
plant_material.txt
RNA_extraction.txt
rnaseq_data
DB_097_CAGATC_L001_R1_001.fastq.gz
DB_099_CTTGTA_L001_R1_001.fastq.gz
DB_103_AGTCAA_L001_R1_001.fastq.gz
DB_161_GTCCGC_L001_R1_001.fastq.gz
DB_163_GTGAAA_L001_R1_001.fastq.gz
DB_165_GTGAAA_L002_R1_001.fastq.gz
NGS_SampleSheet.xlsx

Initiate the ARC folder structure

1. Open ARCitect
2. Create a **New ARC** (2)
3. Select a location and name it

TalinumPhotosynthesis



Your ARC's name

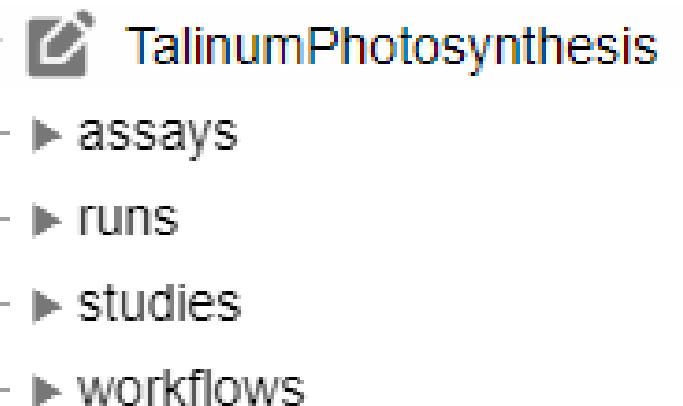
💡 By default, your ARC's name will be used

- for the ARC folder on your machine
- to create your ARC in the DataHUB at
<https://git.nfdi4plants.org/<YourUserName>/<YourARC>>
(see next steps)
- as the identifier for your investigation

💡 Make sure that no ARC exists at

<https://git.nfdi4plants.org/<YourUserName>/<YourARC>> .

Otherwise you will sync to that ARC.



Add a description to your investigation

C:/Users/Sabrina/Desktop/Workshops ARCs
/TalinumPhotosynthesis

TalinumPhotosynthesis

- assays
- runs
- studies
- workflows
-  .gitignore

1.34 KB

Identifier

Title

Description

This is a very interesting investigation about life and photosynthesis

Add contributors

- you could also add the contacts directly via ORCID

Contacts

Your First Name Your Last Name

Your ORCID

6/10 ▾

First Name

Last Name

Your First Name

Your Last Name

Mid Initials

ORCID

Your ORCID

Search

Affiliation

Address

Your Affiliation

Email

Phone

Fax

yourEmailAdress@uni.de

Roles

1.

Author



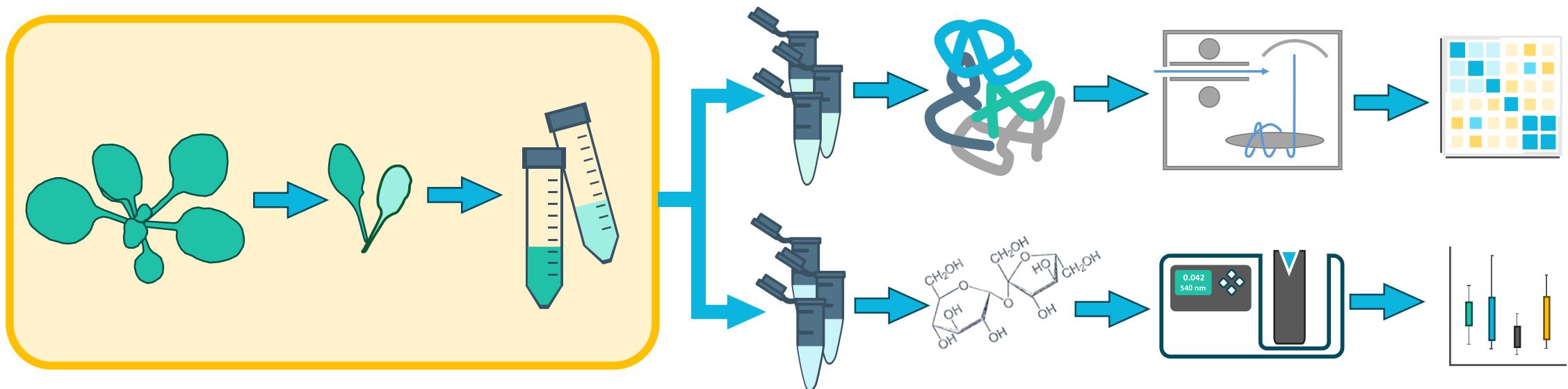
NCIT

NCIT:C42781

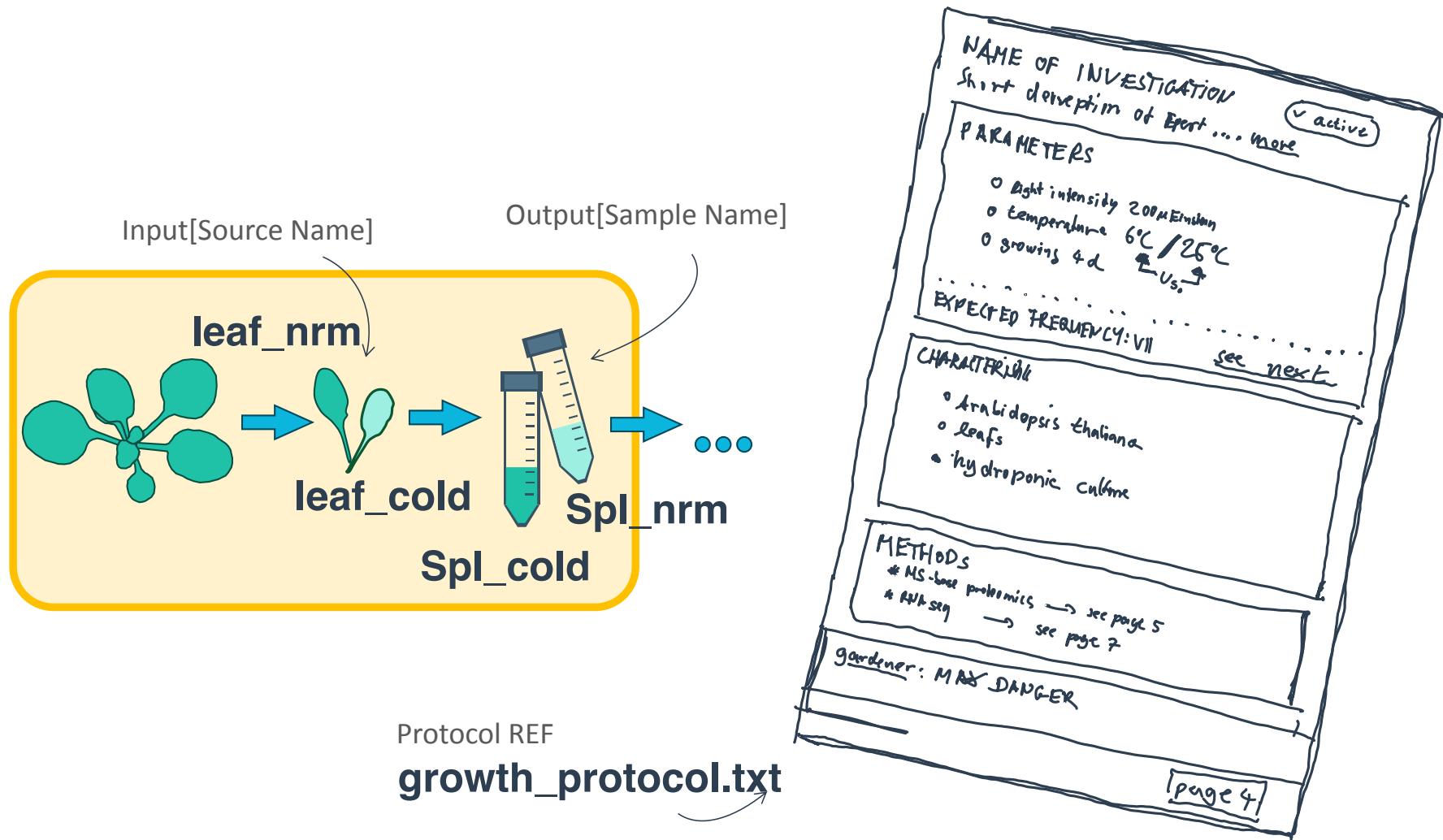


Delete

Divide and conquer for reproducibility



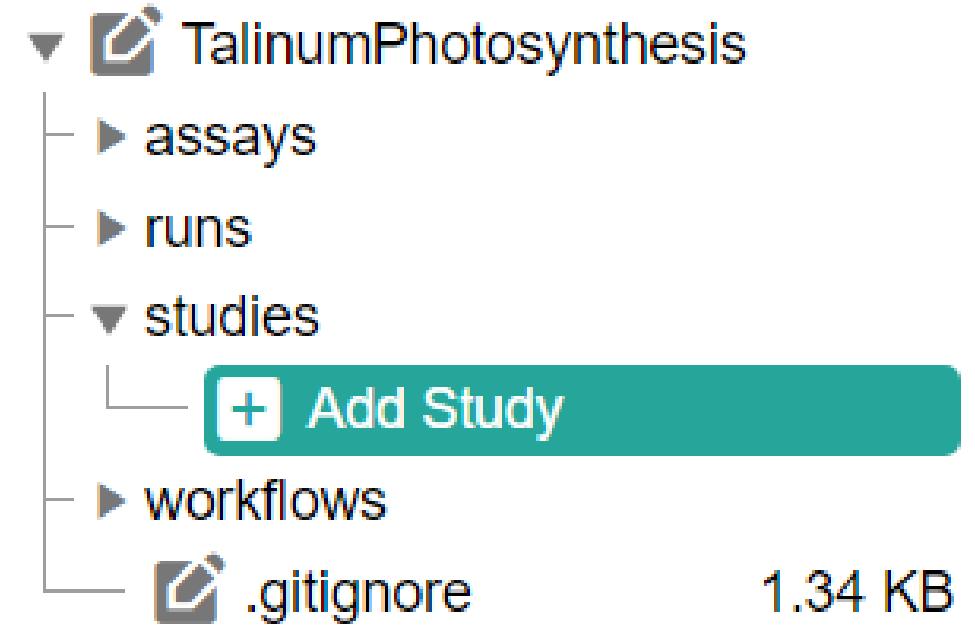
Identifying the 'study' part



Add a study

by clicking "Add Study" and entering an identifier for your study

Use **talinum_drought** as an identifier



Study panel

In the study panel you can add

- general metadata,
- people, and
- publications
- data process information

Identifier
talinum_drought

Description

Contacts

Publications

Submission Date
tt.mm.jjjj --:--

Public ReleaseDate
tt.mm.jjjj --:--

Study Design Descriptors

Let's annotate the plant samples

1. Check out the lab notes

```
studies/talinum_drought/protocols/plant_material.txt
```

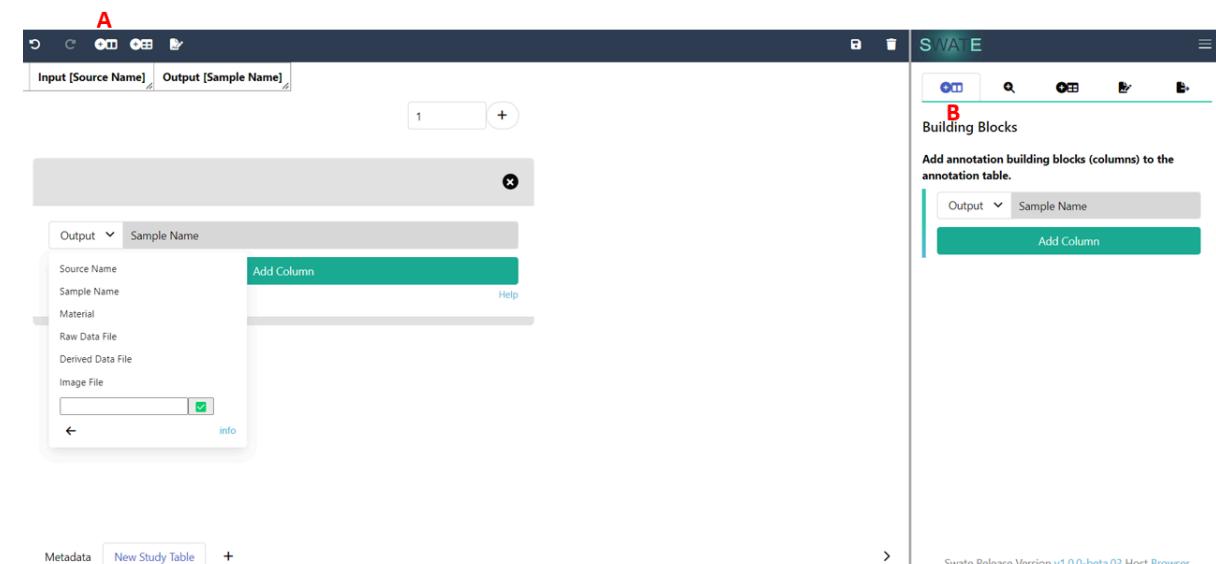
2. Select the study talinum_drought

3. Add a new table sheet at the bottom

Create an annotation table

1. Create a annotation table by adding **Building blocks** via the widget (A) or the sidebar (B)
2. Add an *Input* (Source Name) and *Output* (Sample Name) column

 Each table can contain only one *Input* and one *Output* column



A table-based organization schema

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

Fill out source name and sample name

Transfer the sample ids from the protocol.

1. Invent names for **Source Name** (we do not have this information)
2. Use the sample names from the protocol (DB_*) as **Sample Name**

Add protocols

You can either

- directly write a **new protocol** within the ARCitect or
- import an existing one from your computer

Create or Import Protocol

Protocol Name



NEW PROTOCOL



IMPORT PROTOCOL

CANCEL

Link the protocol to the isa table

1. In the *Building Blocks* tab, select *More* -> *Protocol REF*.
2. Click  *Add Column*.
3. Add the name of the protocol file (`plant_material.txt`) to the *Protocol REF* column.

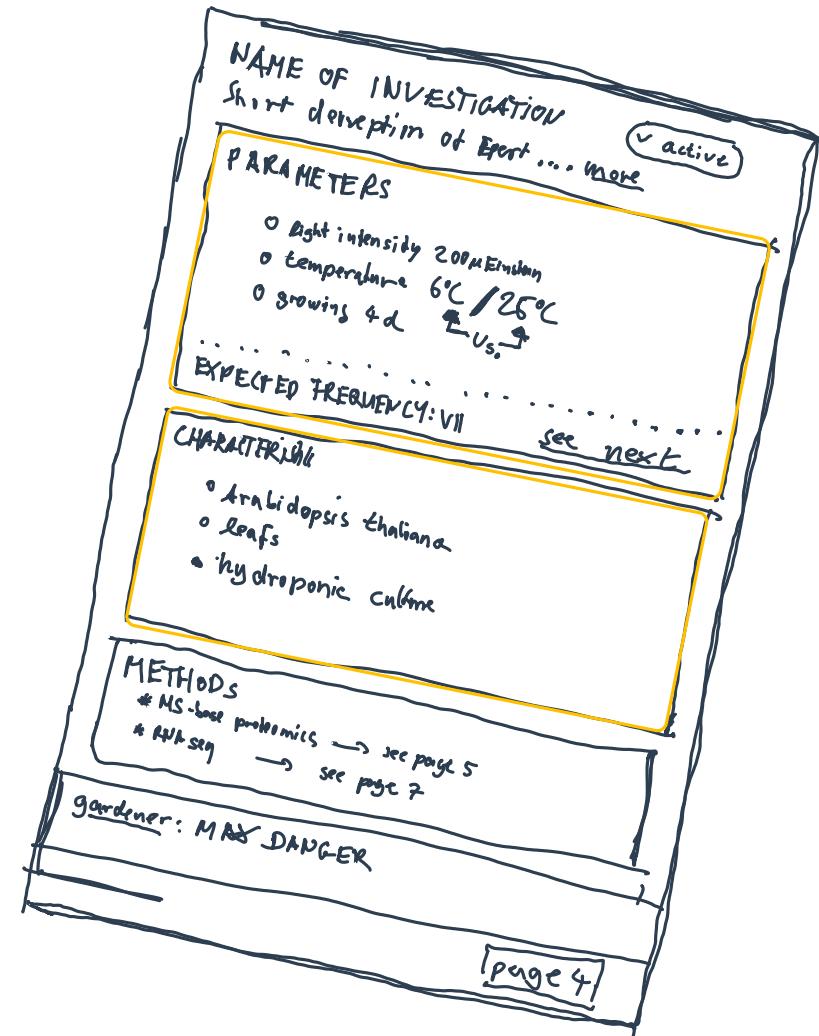
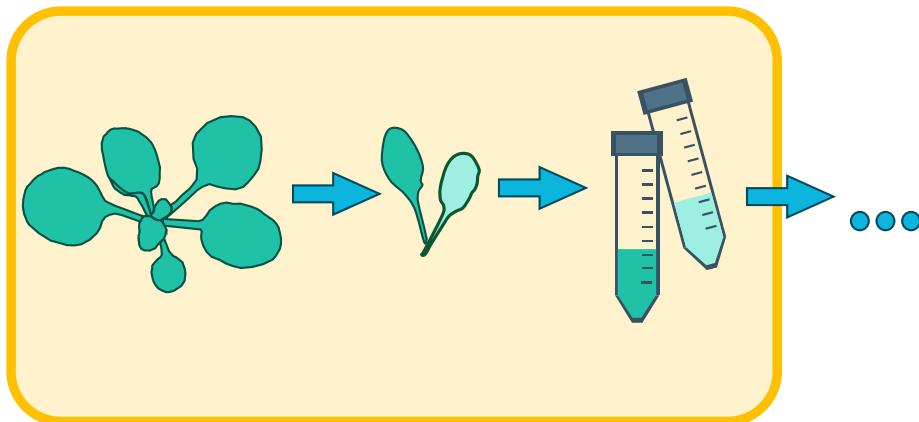
Referencing a protocol

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
D		

- 💡 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](#)

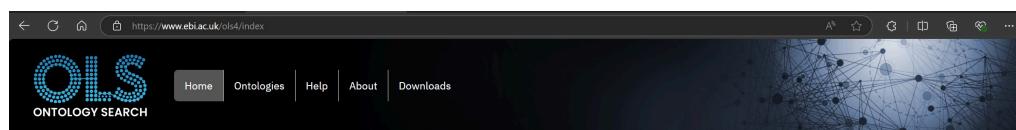
temperature [PATO:0000146](#)

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?

Data Content
Updated 4 Oct 2024 Fri 17:50(+02:00)

- 265 ontologies
- 8,598,500 classes
- 45,471 properties
- 687,188 individuals

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.

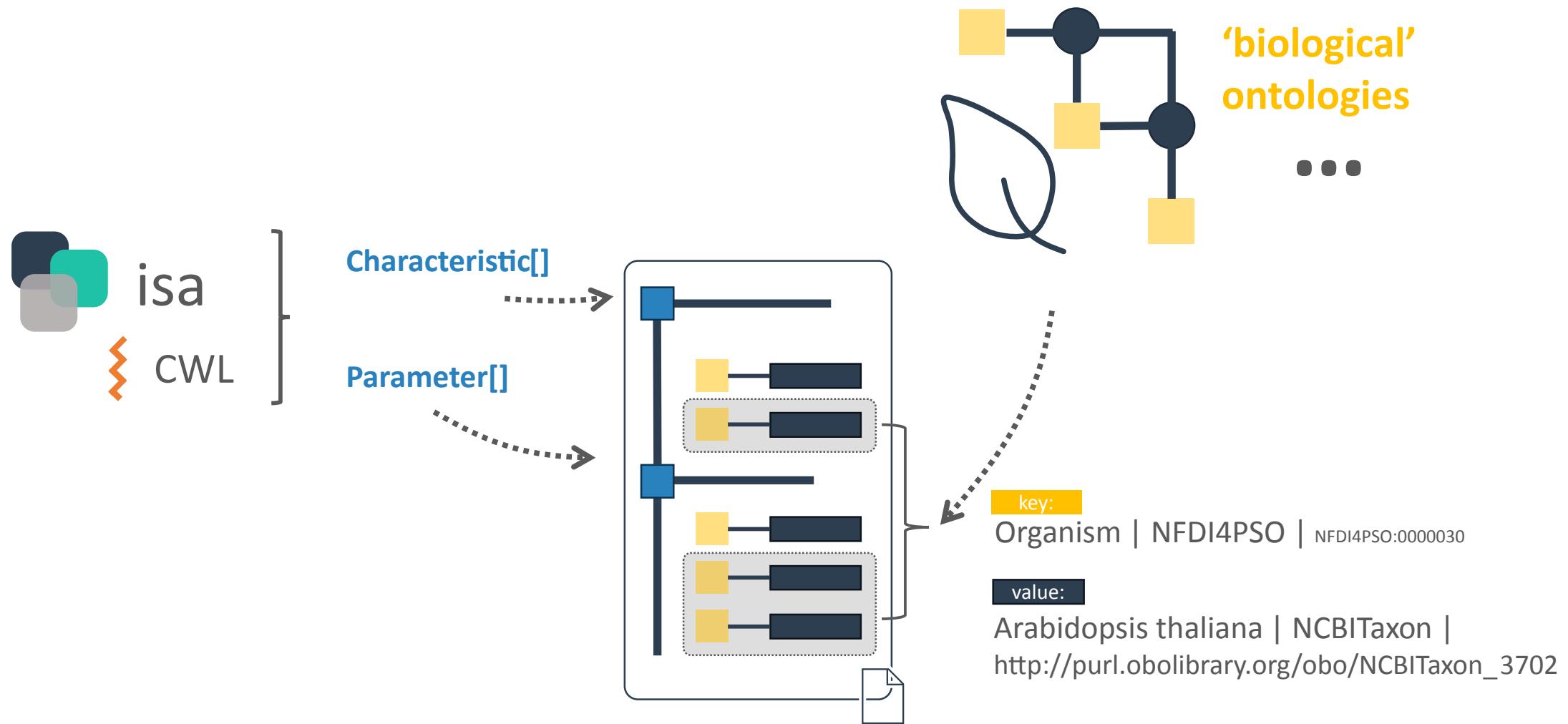
Related Tools
In addition to OLS the SPOT team also provides the OxO and ZOOMA services. OxO provides cross-ontology mappings between terms from different ontologies. ZOOMA is a service to assist in mapping data to ontologies in OLS.

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

EMBL-EBI 2023 Licensing

Finding the metadata vocabulary and descriptors



Finding the metadata vocabulary and descriptors

Parameters []

- 
- 
- 
-  Light intensity 200 μ 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

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 a software interface for managing annotation building blocks. At the top, there's a toolbar with various icons. Below it is a header bar labeled "Widgets". The main area contains a table with six rows of data:

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 rewetted	reC3_01
DB_163	Talinum fruticosum	✓ 12 days drought + 2 days rewetted	reC3_02
DB_165	Talinum fruticosum	✓ 12 days drought + 2 days rewetted	reC3_03

Annotations are present in the "Factor" column:

- Row 1: "Factor" is highlighted with a blue box, and "Input" is annotated below it.
- Row 2: "Factor" is highlighted with a blue box, and "Characteristic" is annotated below it.
- Row 3: "Factor" is highlighted with a blue box, and "Output" is annotated below it.
- Row 4: "Factor" is highlighted with a blue box, and "Input" is annotated below it.
- Row 5: "Factor" is highlighted with a blue box, and "Characteristic" is annotated below it.
- Row 6: "Factor" is highlighted with a blue box, and "Output" is annotated below it.

To the right of the table is a "New Parameter" dialog box with tabs for "Parameter", "Factor", "Characteristic", "Component", "More", and "Output". The "Parameter" tab is selected. The "Sidebar" button is located at the bottom right of the dialog. The sidebar itself is visible on the far right, showing sections for "Metadata", "plant_material", and "+".

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

Add Characteristics

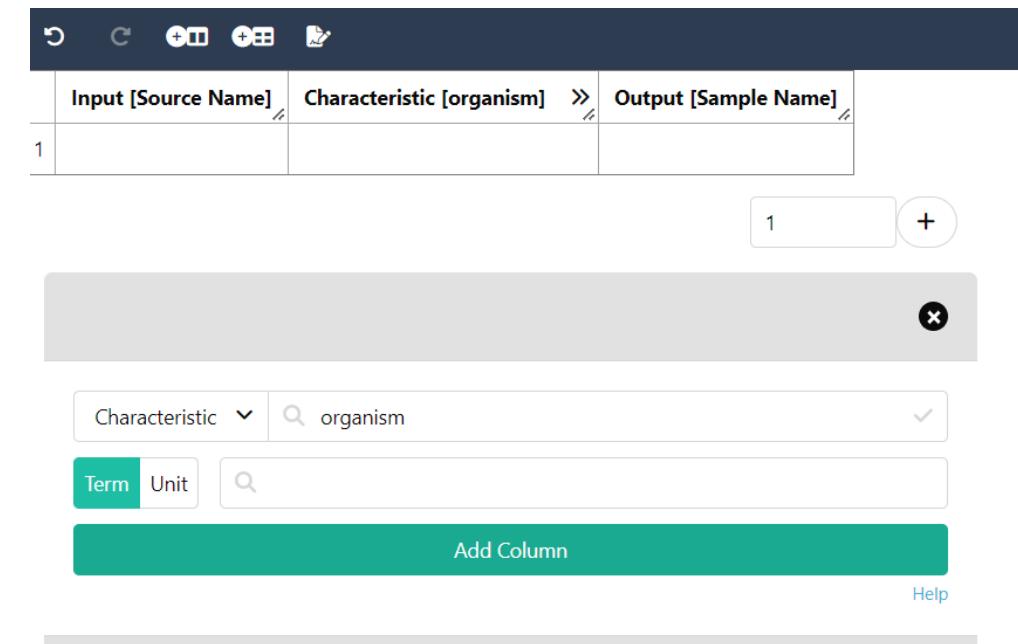
1. Select *Characteristic* from the drop-down menu

2. Enter **organism** in the search bar. This search looks for suitable *Terms* in our *Ontology* database.

3. Select the Term with the id **OBI:0100026** and,

4. Click **Add Column**

 This adds four columns to your table, one visible and **three** hidden.



The screenshot shows the 'Add Column' dialog in the ARCitect interface. The dialog has three columns: 'Input [Source Name]', 'Characteristic [organism]', and 'Output [Sample Name]'. The 'Characteristic [organism]' column contains a search bar with the term 'organism'. Below the search bar are buttons for 'Term' and 'Unit', a search icon, and a large green 'Add Column' button. The 'Input' and 'Output' columns are currently empty. At the top of the dialog, there are standard window controls (minimize, maximize, close) and a toolbar with icons for copy, paste, and other functions.

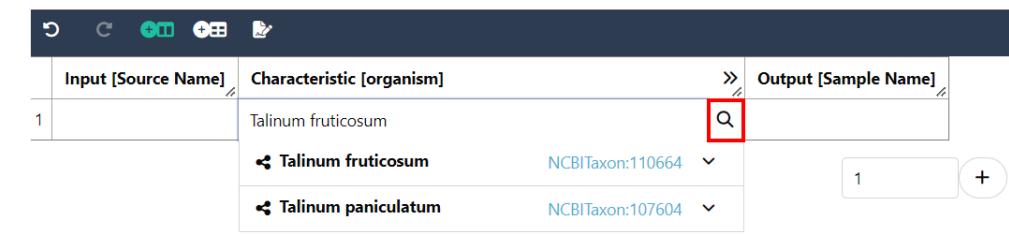
Insert ontology terms

1. Insert values by selecting any cell below

Characteristic [organism]

2. Use free text or use the magnifying glass to activate *Term* search

3. Write "Talinum fruticosum" and enable *Term* search
4. Select the hit



Add a Parameter building block with a unit

1. In the *Building Blocks* widget, select *Parameter*, search for `light intensity exposure` and select the term with id `PEC0:0007224`.
2. Check the box for *Unit* and search for `microeinsteins per square meter per second` in the adjacent search bar.
3. Select `U0:0000160`.
4. Click Add Column.

 This also adds four columns to your table, one visible and **three** hidden.

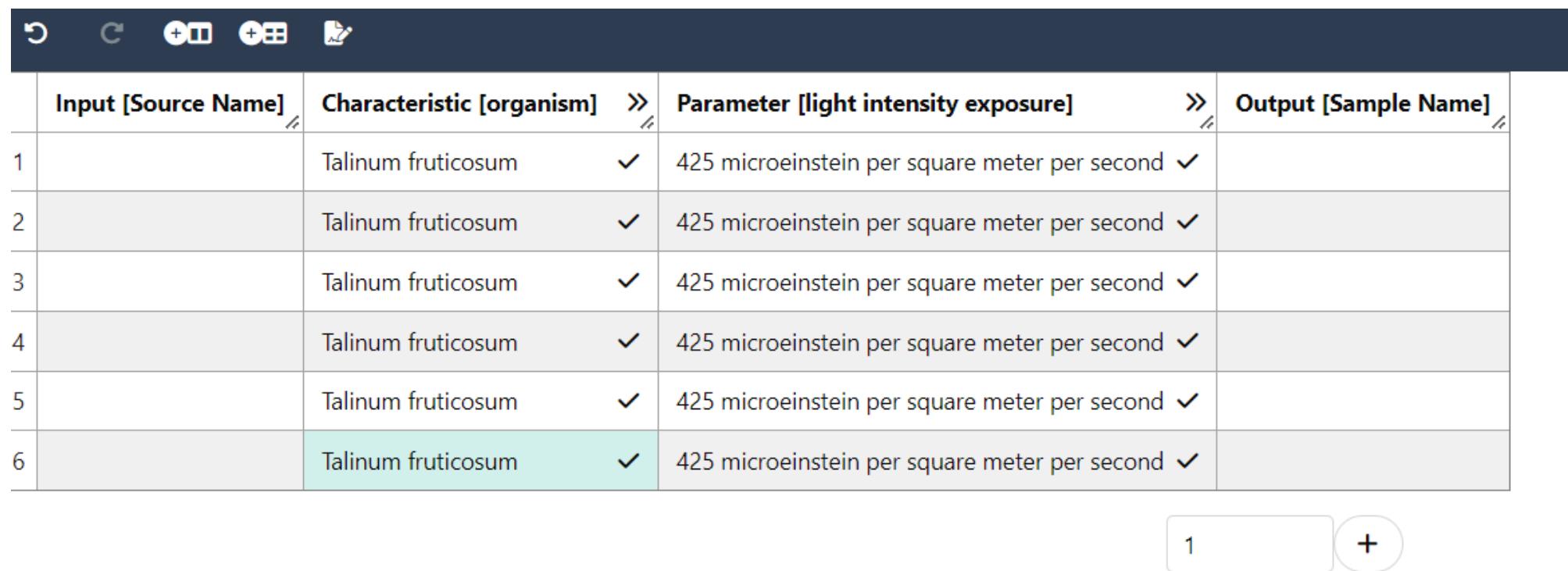
Insert unit-values

In the annotation table, select any cell below **Parameter [light intensity exposure]** and add "425" as light intensity.

 You can see the numbers being complemented with the chosen unit, e.g. 425 microeinstein per square meter per second

Your annotation table is growing

At this point. Your table should look similar to this:



Input [Source Name]	Characteristic [organism]	Parameter [light intensity exposure]	Output [Sample Name]
1	Talinum fruticosum	425 microeinsteins per square meter per second	
2	Talinum fruticosum	425 microeinsteins per square meter per second	
3	Talinum fruticosum	425 microeinsteins per square meter per second	
4	Talinum fruticosum	425 microeinsteins per square meter per second	
5	Talinum fruticosum	425 microeinsteins per square meter per second	
6	Talinum fruticosum	425 microeinsteins per square meter per second	

1 +

Exercise

Try to add suitable *Building Blocks* for other pieces of metadata from the plant growth protocol (`studies/talinum_drought/protocols/plant_material.txt`).

Add a factor building block

1. In the *Building Blocks* widget, select *Factor*, search for `watering exposure` and select the term with id `PEC0:0007383`.
 2. Click `Add Column`.
 3. Add the drought treatment ("no water for 12 days", "re-water for 2 days") to the respective samples
-  There are different options to add the drought treatment.

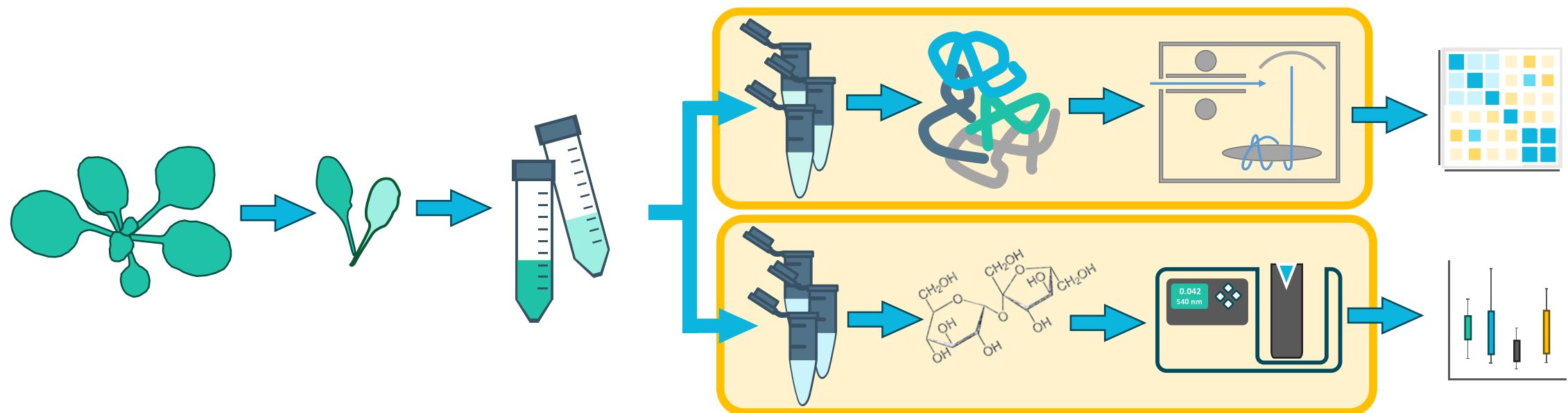
Showing ontology reference columns

Use double pointed quotation mark to un-hide hidden columns.

- 💡 You can see that your organism of choice was added with id and source Ontology in the reference (hidden) columns.

Characteristic [organism]	Unit	TSR (OBI:0100026)	TAN (OBI:0100026)
Talinum fruticosum	-	NCBITaxon	NCBITaxon:110664

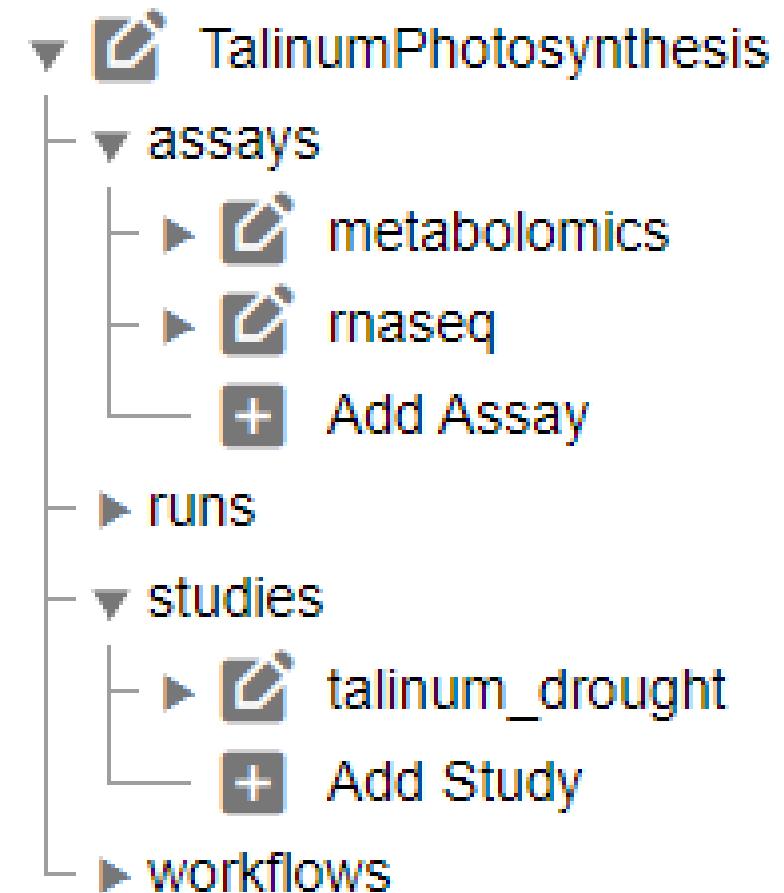
Identifying assays



Add an assay

by clicking "Add Assay" and entering an identifier for your assay

Add two assays with **rnaseq** and **metabolomics** as an identifier



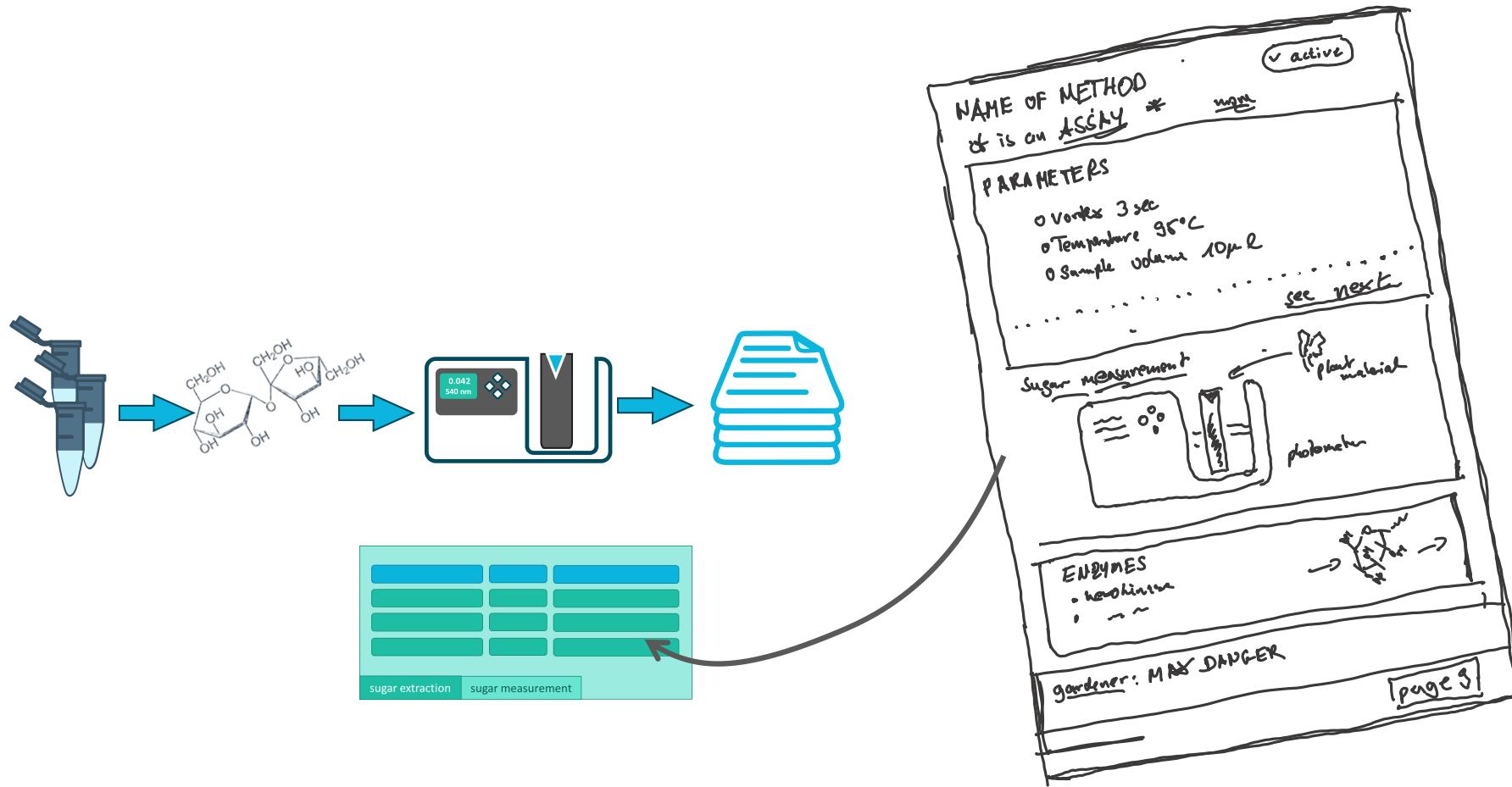
Add information about your assay

In the assay panel you can define the assay's

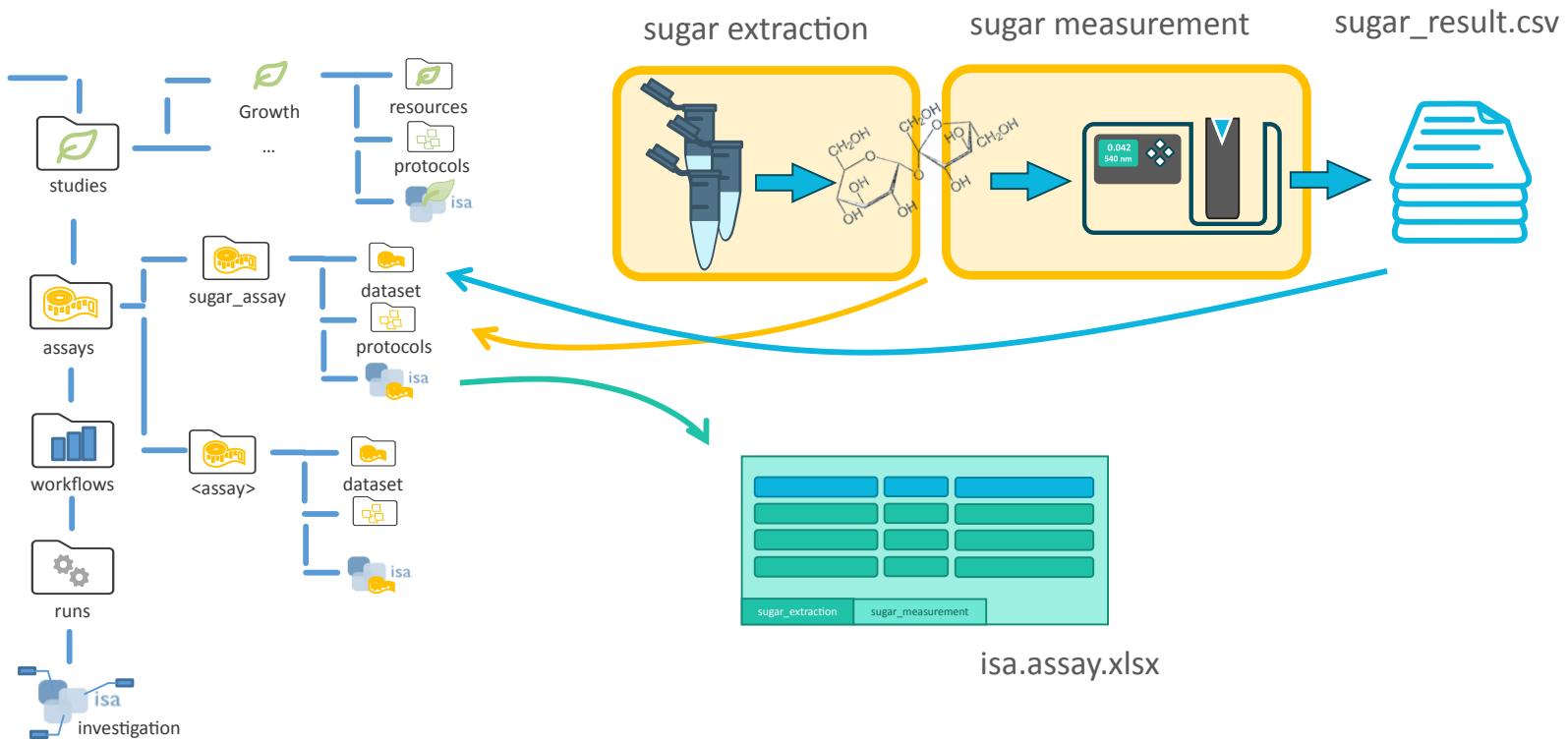
- measurement type
- technology type, and
- technology platform

Identifier		
rnaseq		
Measurement Type		
Term Name	TSR	TAN
<input type="text"/>	<input type="text"/>	<input type="text"/>
Technology Type		
Term Name	TSR	TAN
<input type="text"/>	<input type="text"/>	<input type="text"/>
Technology Platform		
Term Name	TSR	TAN
<input type="text"/>	<input type="text"/>	<input type="text"/>
Performers		
<input type="button" value="+"/>		
Comments		
<input type="button" value="+"/>		

Assay for sugar measurement



Separating different assay elements



Parametric description of the lab process

sugar extraction

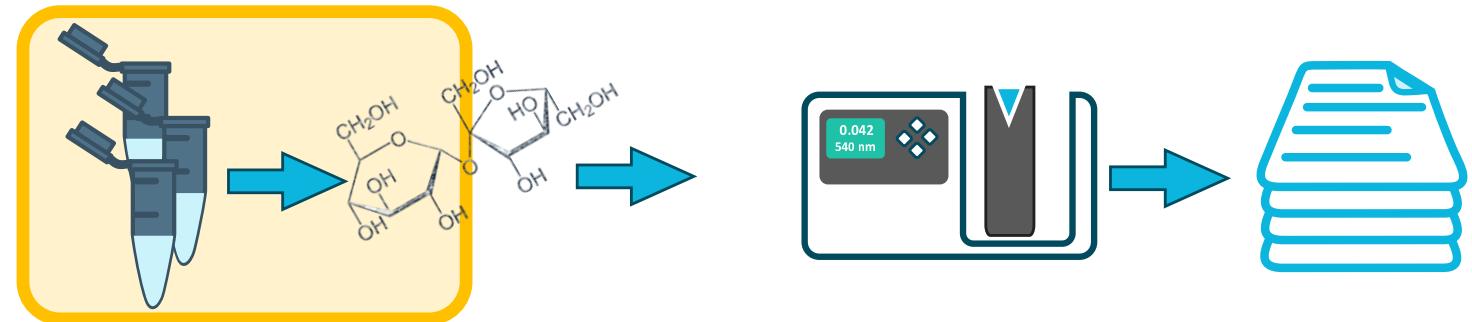
- Parameter []

- Temperature

- 95 °C

- Vortex Mixer

- 3 s



Parametric description of the lab process

- Parameter []

- technical replicate

- 1-3

- sample volume

- 10 µl

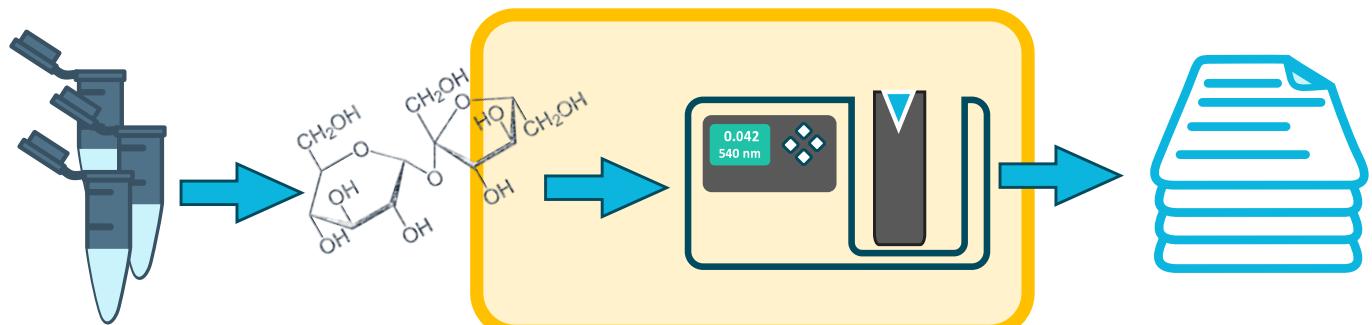
- Buffer

- 190 µl

- Cycle

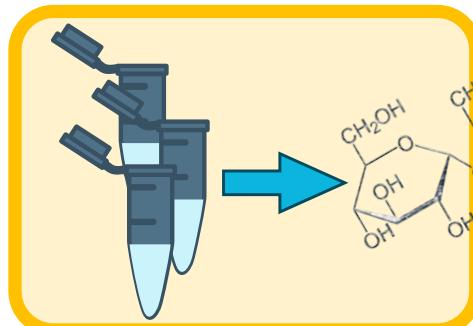
- 5

sugar measurement

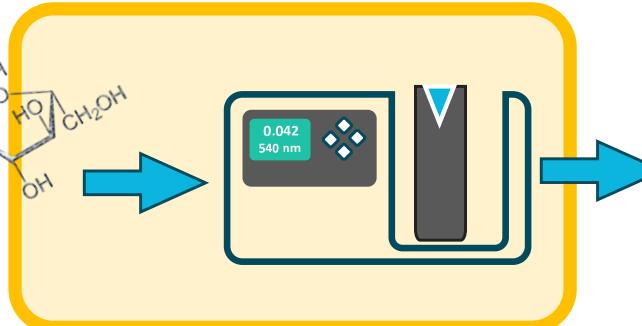


Isolating the lab processes in an assay

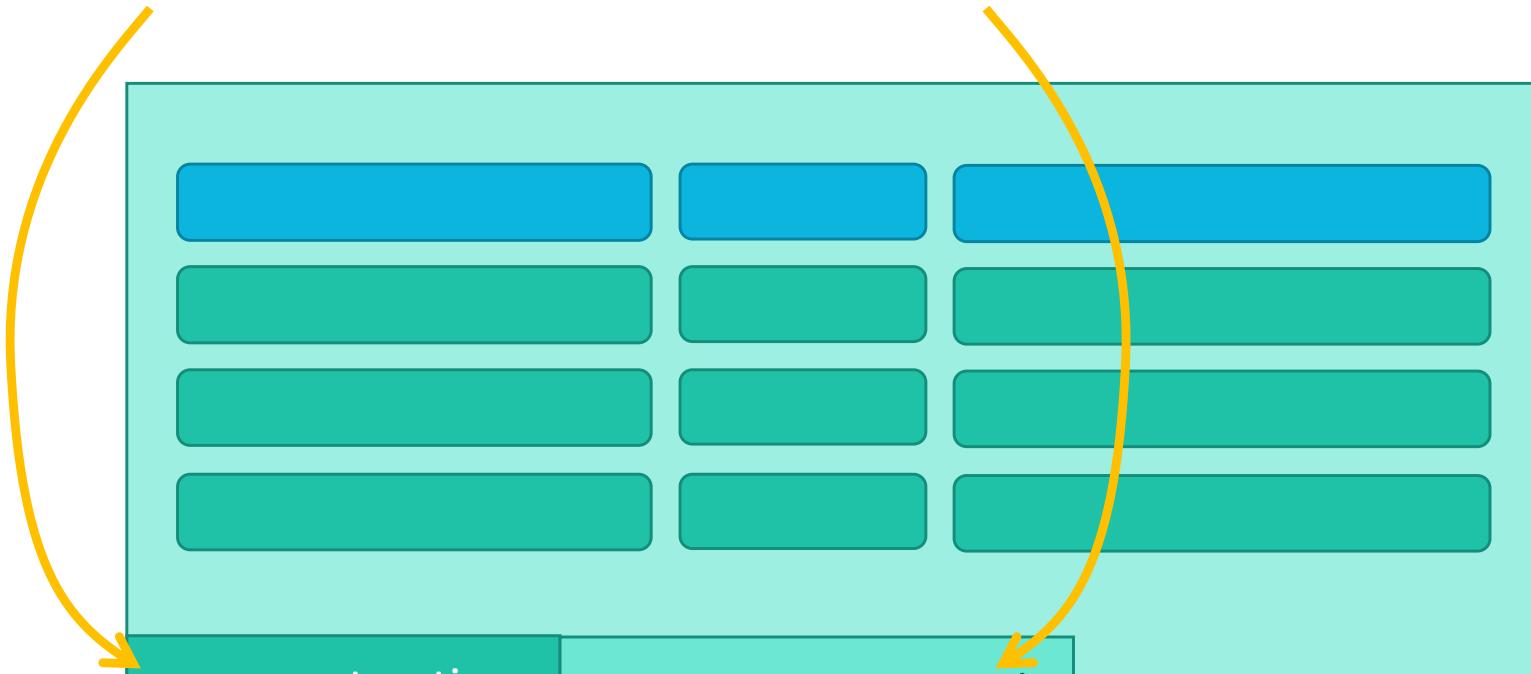
sugar extraction



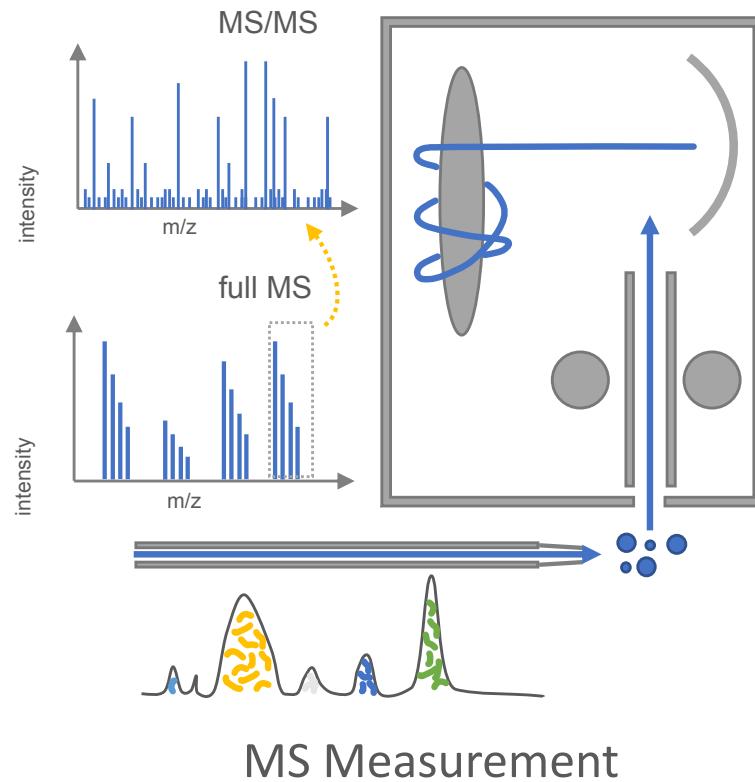
sugar measurement



sugar_result.csv

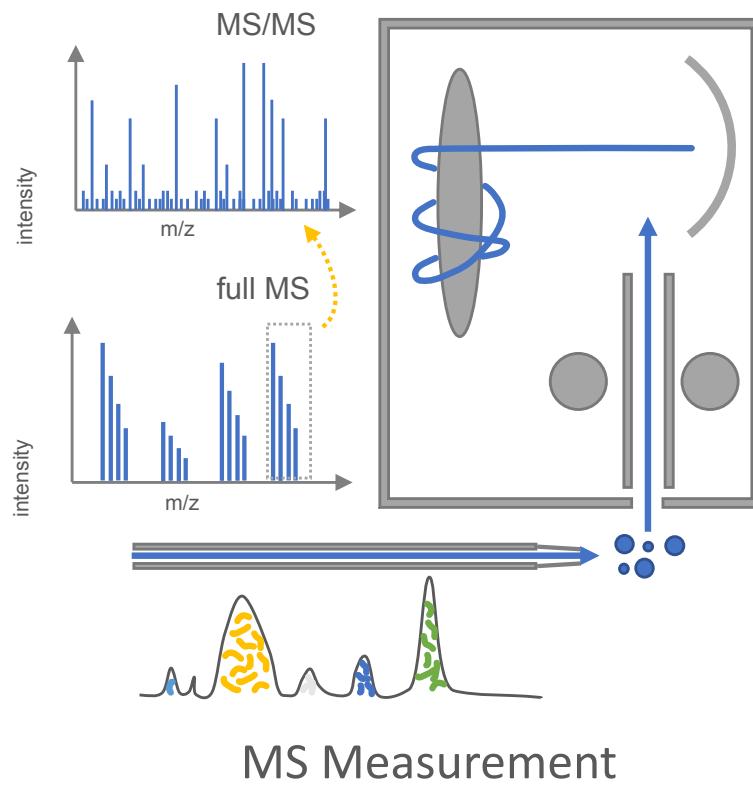


Save time using standard methods and SOPs



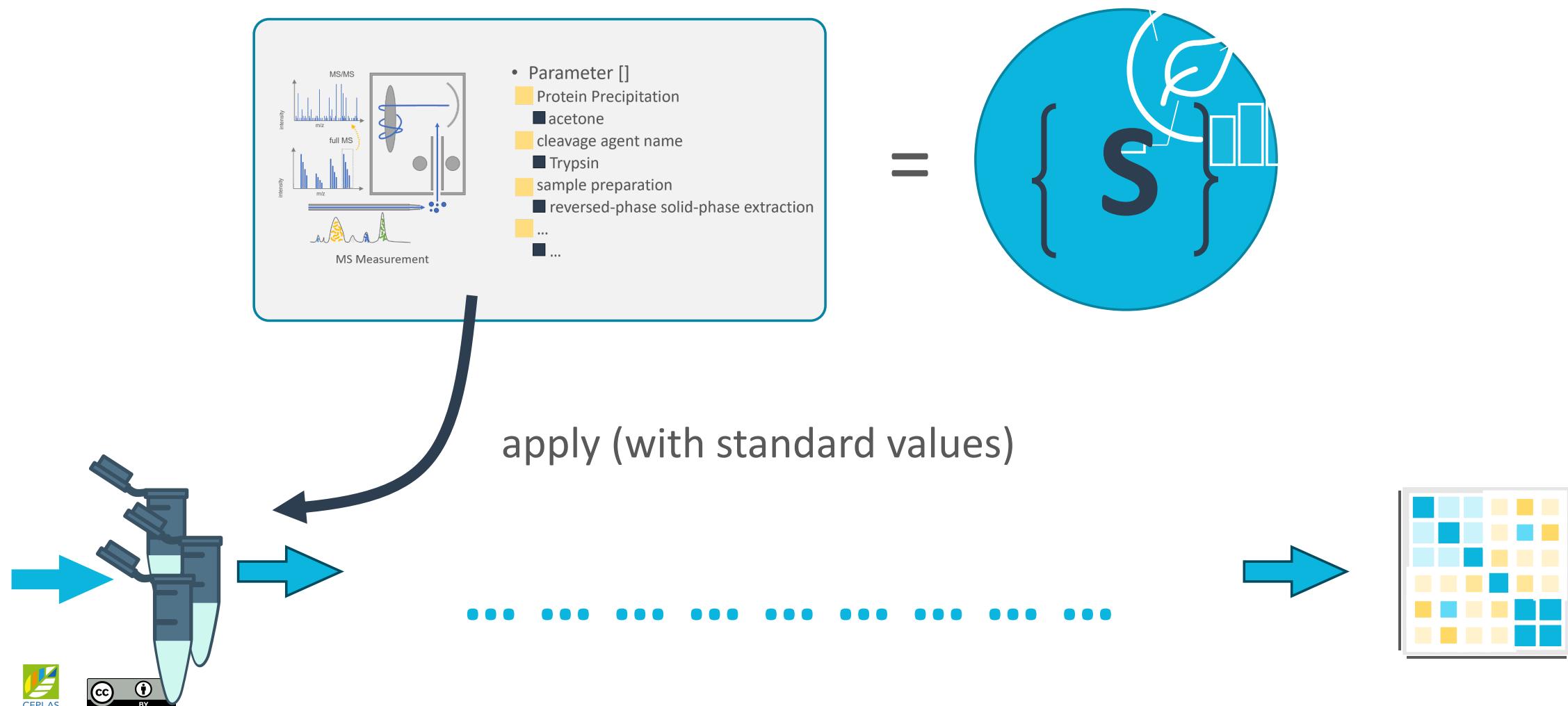
- Parameter []
 - Protein Precipitation
 - acetone
 - cleavage agent name
 - Trypsin
 - sample preparation
 - reversed-phase solid-phase extraction
 - ...
 - ...

Save time using standard methods and SOPs

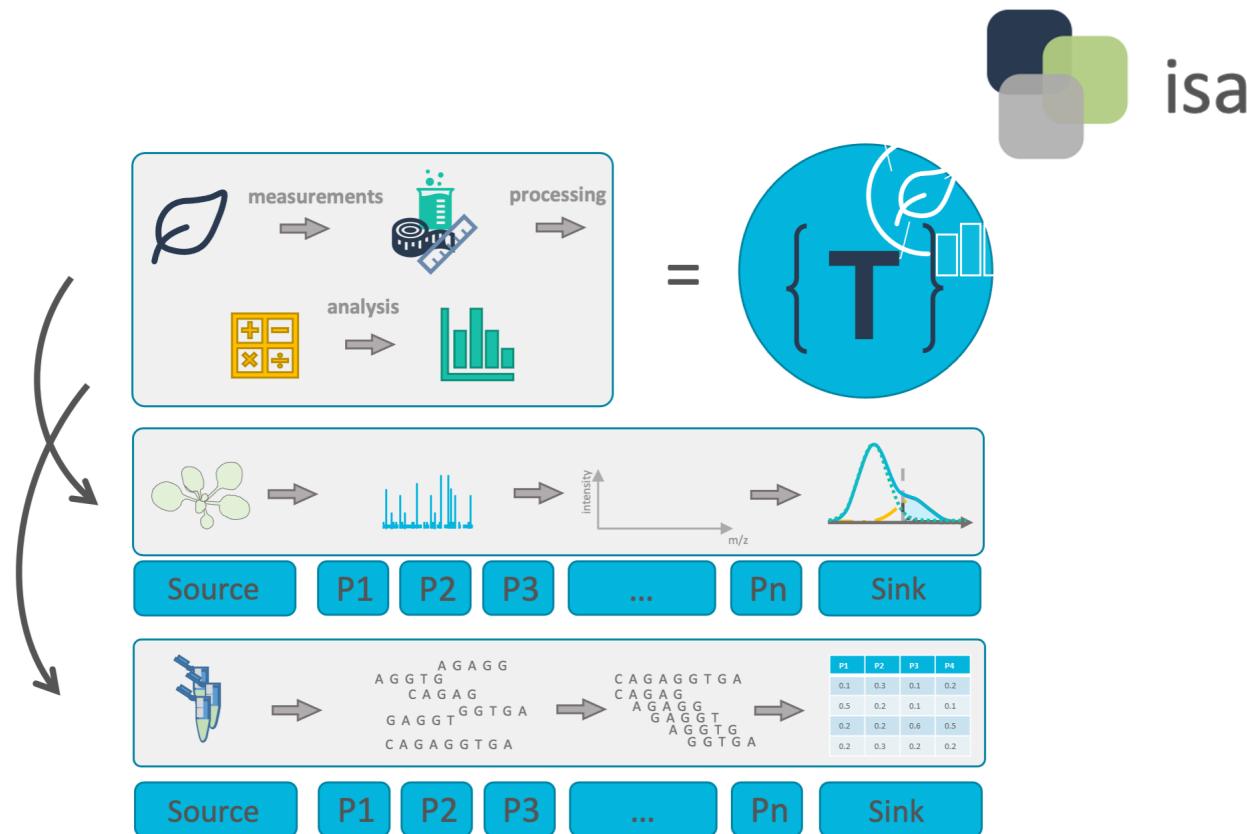


- Component []
 - chromatography instrument model
 - nanoElute2
 - chromatography column model
 - PepSep C18 1.9u, 25cm x 75um
 - ...
 - ...
 - ...
 - ...

Applying standard procedures to sample record



Realization of lab-specific metadata templates



Facilities can define their most common workflows as templates

Import templates from a database

- DataPLANT curated
- Community templates

The screenshot shows a user interface for managing templates. 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 these are dropdown menus for "Select community" and "DataPLANT official". 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. The templates listed are: 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), and Genome assembly (curated, 1.1.7). A vertical scrollbar is visible on the right side of the table.

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

Let's annotate the RNA Seq assay

Open the lab notes assays/rnaseq/protocols/

Use a template

1. Open the *Templates* widget in the Bar

💡 Here you can find DataPLANT and community created workflow annotation templates

2. Search for **RNA extraction** and click **select**

- You will see a preview of all *Building Blocks* which are part of this template.

3. Click **Add template** to add all *Building Blocks* from the template to your table

The screenshot shows the 'Templates' widget interface. At the top, there are search bars for 'Search by template name' and 'Search for tags', both with placeholder text and magnifying glass icons. Below that is a dropdown menu labeled 'Select community' with 'DataPLANT official' selected. The main area is a table with columns for 'Template Name', 'Community', and 'Template Version'. The table lists several templates, each with a 'curated' status indicator and a dropdown arrow. The listed templates are: DNA extraction (1.1.7), Data Processing (PRIDE minimal) (1.0.0), GEO - Minimal information RNA assays (1.0.1), GEO - Minimal information RNA extraction (1.0.0), GEO - Minimal information computational analysis (1.0.0), GEO - Minimal information plant growth (1.0.0), and Genome assembly (1.1.7). A vertical scroll bar is visible on the right side of the table.

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

Remove Building blocks

If there are any *Building Blocks* which do not fit to your experiment you can use right click --> "Delete Column" to remove it including all related (hidden) reference columns.

Move Building blocks

If the order of the *Building Blocks* should be adjusted you can use right click --> "Move Column"

Move Column×

Preview1ApplyUpdate TableSubmit

Index	Column
0	Input [Source Name]
1	Characteristic [Organism]
2	Factor [watering exposure]
3	Output [Sample Name]

Replace multiple names

Right click --> "Update Column" can be used to replace names in batches

 this only works on Input columns

Update Column ×

	Regex	Replacement
	DB	sample

Preview

	Before	After
0	DB_097	sample_097
1	DB_099	sample_099
2	DB_103	sample_103
3	DB_161	sample_161
4	DB_163	sample_163

Submit

New process, new worksheet

1. Add a new sheet to the `assays/rnaseq/isa.assay.xlsx` workbook.
2. Add the template "RNASeq Assay"

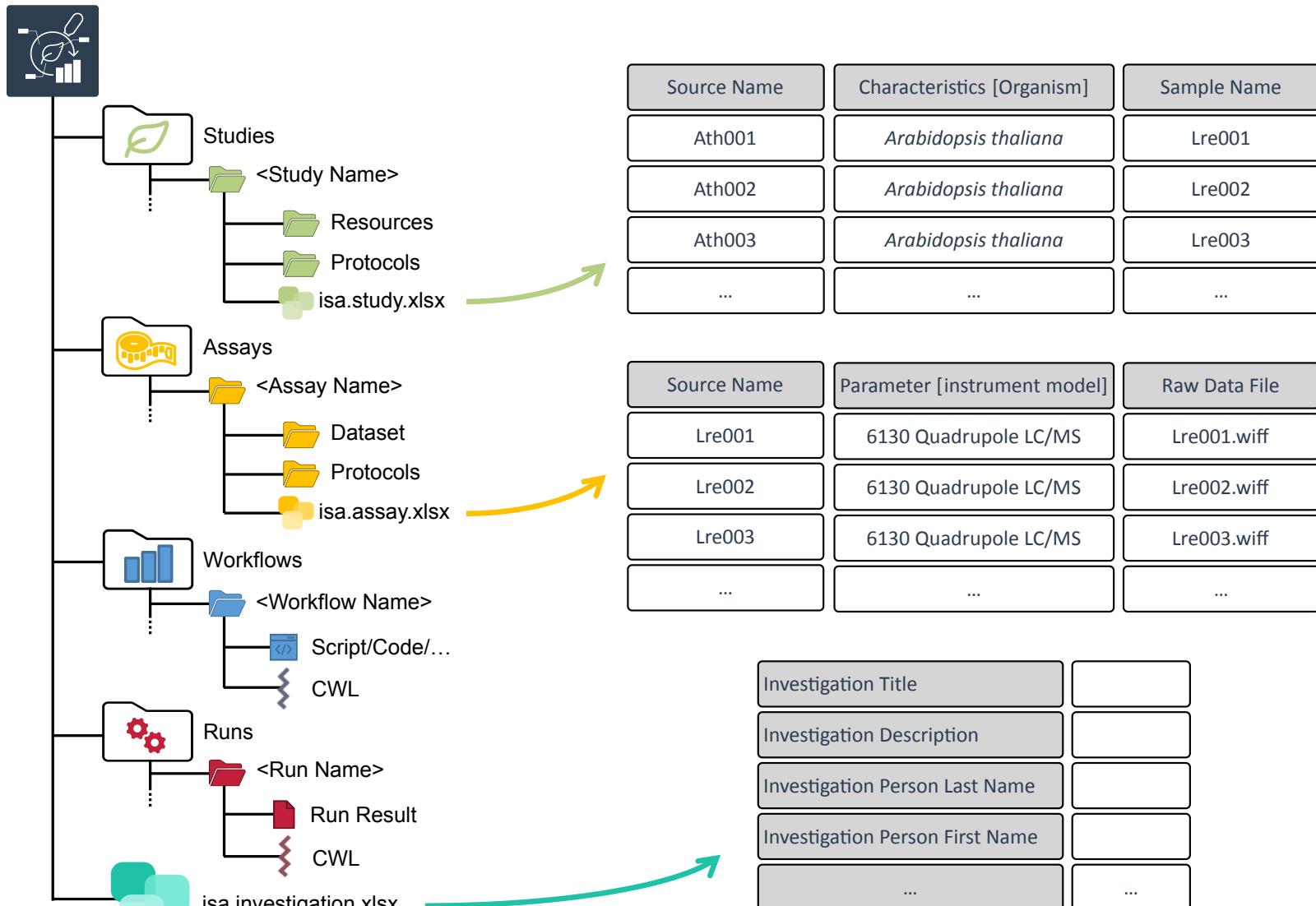
Exercise

Try to fill the two sheets with the protocol details:

- assays/rnaseq/protocols/RNA_extraction.txt and
- assays/rnaseq/protocols/Illumina_libraries.txt

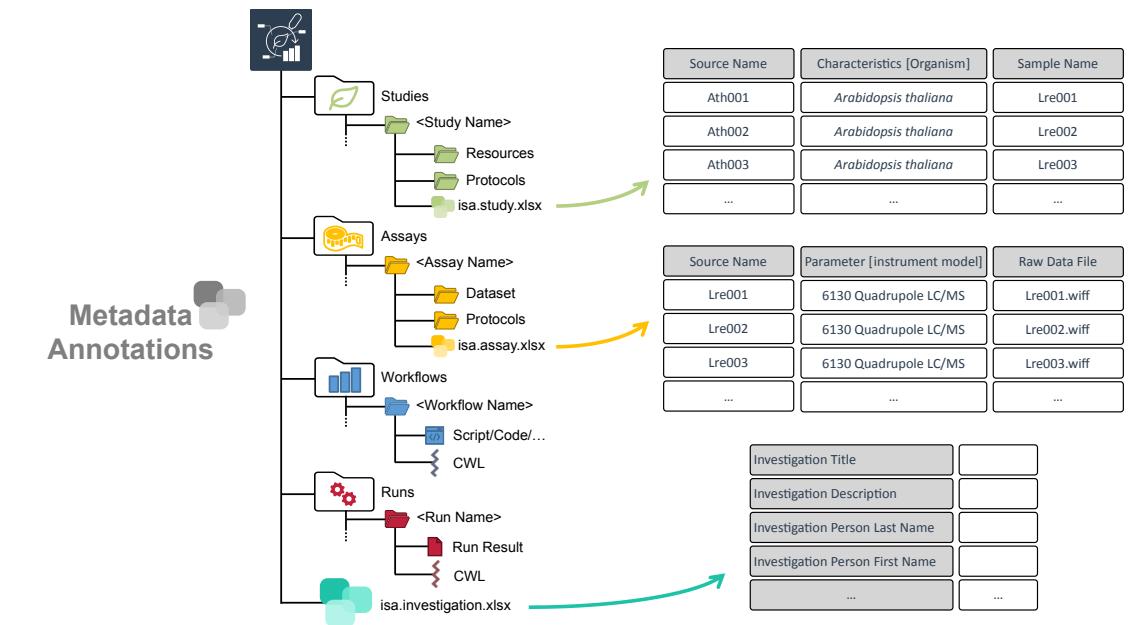
ARC builds on ISA to connect data

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
- ...



Link samples across studies and assays

1. Use the **Output [Sample Name]** of studies/talinum_drought/isa.study.xlsx as the **Input [Sample Name]** to **rna-extraction**.
2. Use the **Output [Sample Name]** of **rna-extraction** as the **Input [Sample Name]** to **illumina-libraries**.

Seeds –Plant growth→ Leaves –RNA Extraction→ RNA –Illumina→ fastq files

Link dataset files to samples

1. In the *Building Blocks* widget select *Output -> Raw Data File*.

2. Click **Add Column**.

 You see a warning about a changed output column.

3. Click **Continue**.

4. Go to the *File Picker* tab and click **Pick file names**.

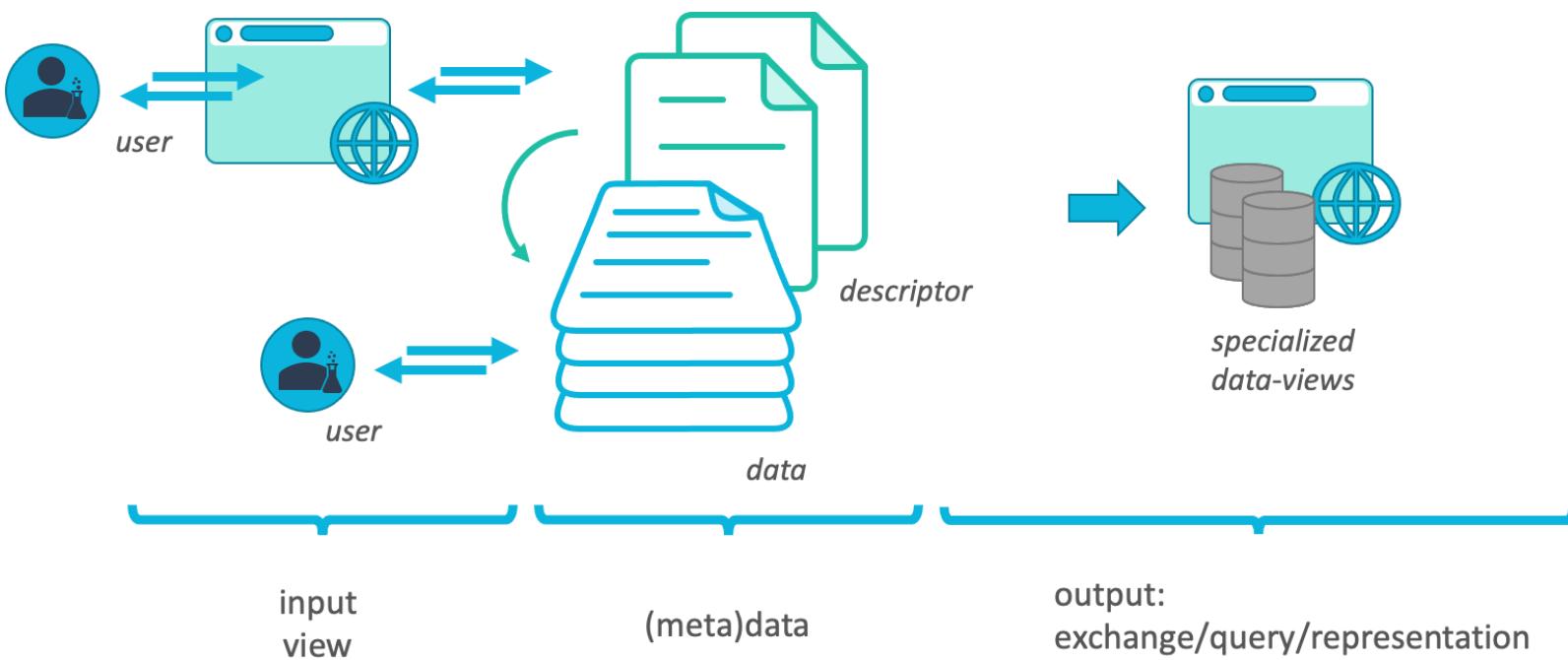
5. Select and open the *fastq.gz files from the dataset folder.

6. Copy / paste them to the **Raw Data File**.

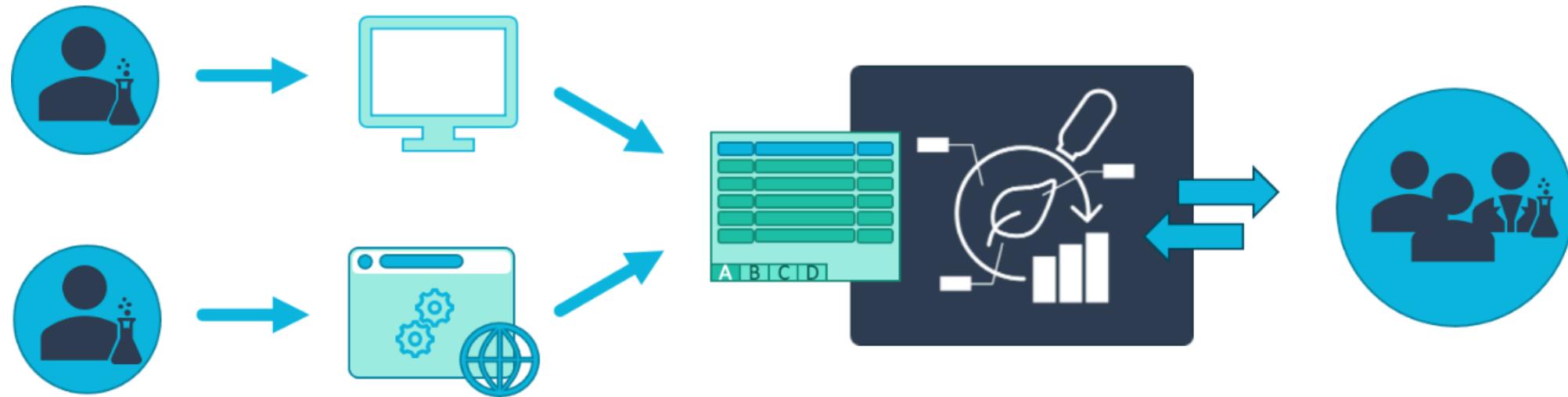
 This allows you to link your samples to the resulting raw data files.

Everything is a file

The ARC is a **data-centric** approach to RDM



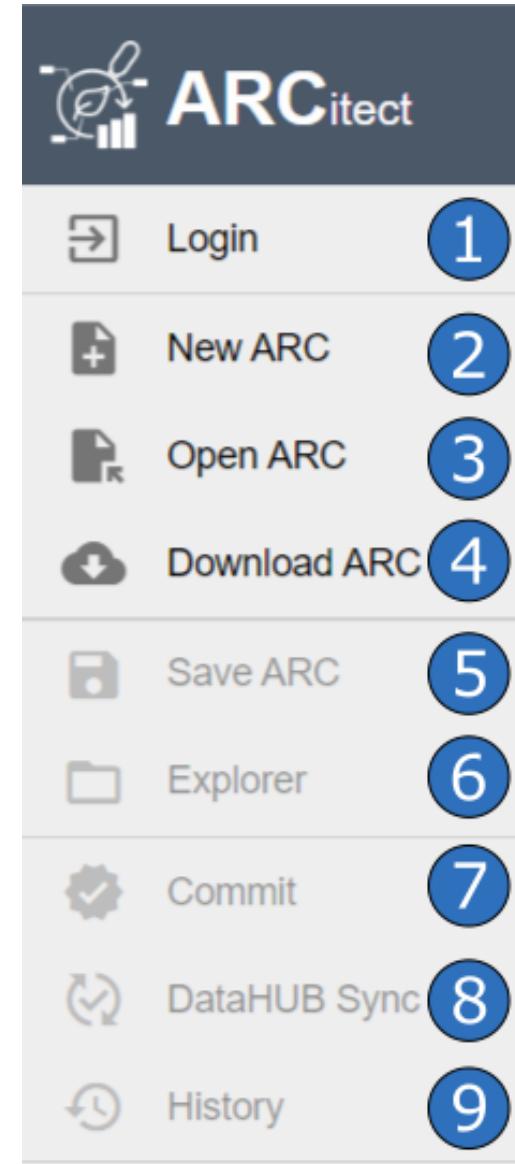
No technical lock-in



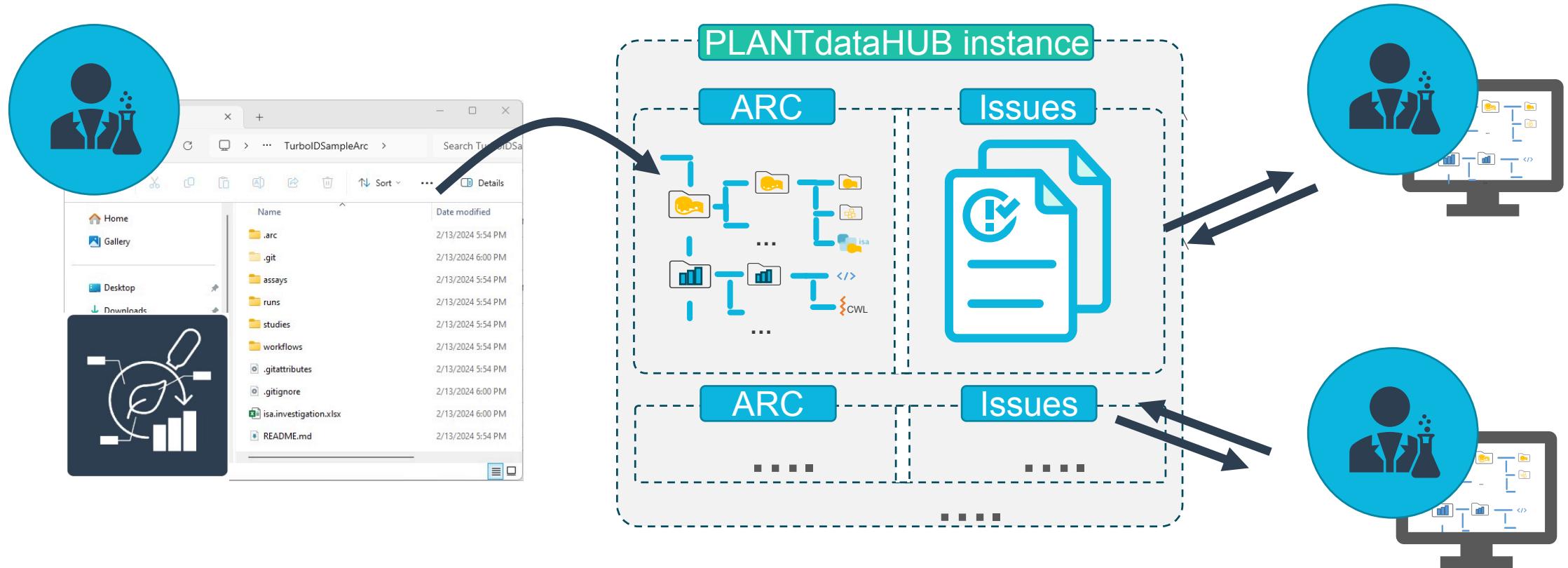
(Meta)data transparency with tool assistance but **no technical lock-in**

Explorer

The **Explorer (6)** button directly opens your ARC locally



Using the DataHUB to collaborate



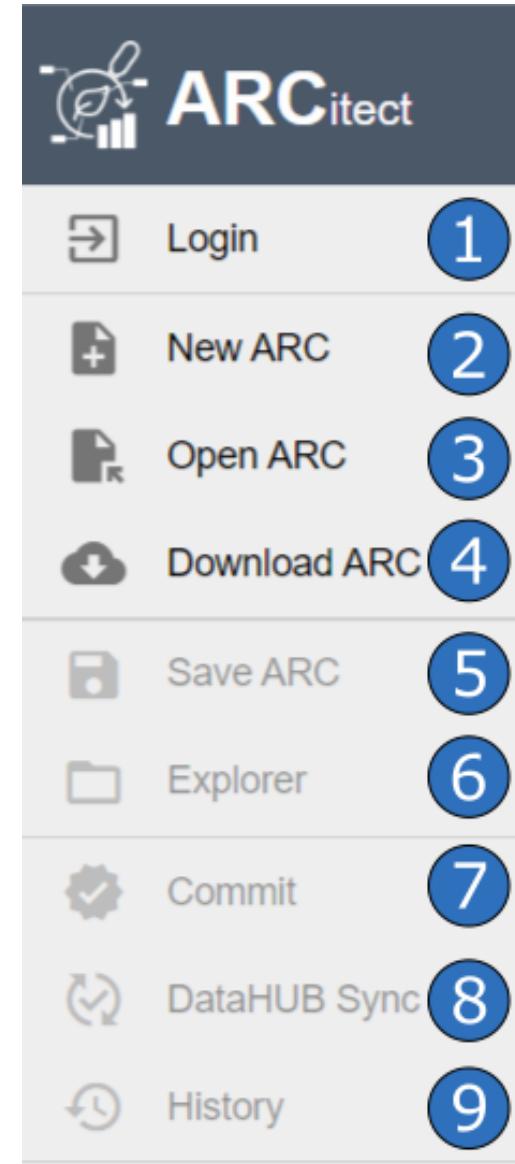
Login to DataHUB

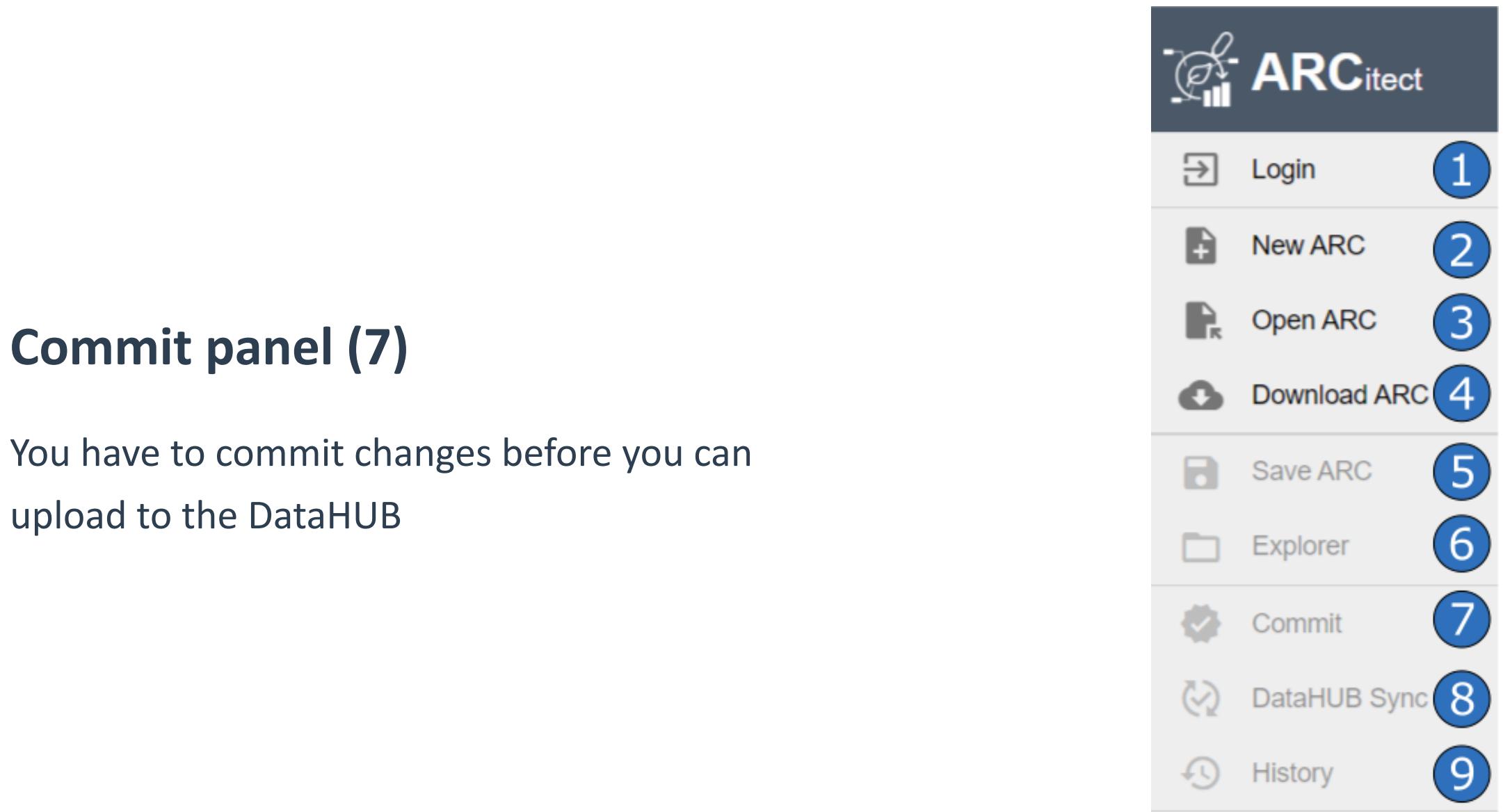
1. Login to DataHUB (1)
2. Select `git.nfdi4plants.org` as Host

Please Select a DataHub

Host
`git.nfdi4plants.org`

LOGIN **CANCEL**





Commit panel (7)

You have to commit changes before you can upload to the DataHUB

Commit your changes

If you are logged in, the **Commit panel** shows

- your DataHUB's *Full Name* and *eMail*

It allows you to

- track changes of the ARC with git
- add a commit message
- use different branches

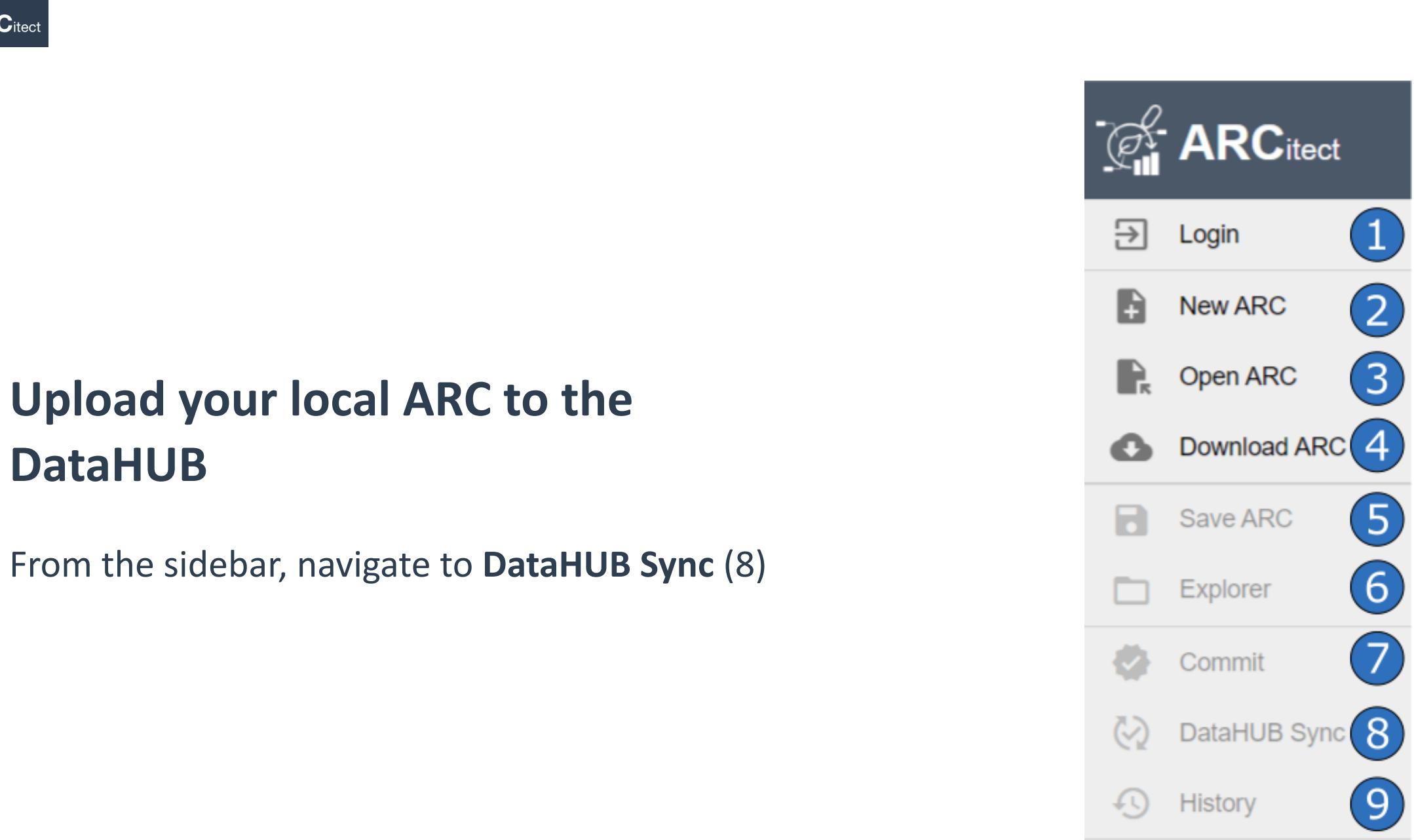
The screenshot shows the 'Commit Changes' panel. At the top, it says 'Commit Changes' and 'Track changes of the ARC with git'. Below that, there are fields for 'Name' (Sabrina Zander) and 'eMail' (sabrina.zander@uni-duesseldorf.de). There are dropdowns for 'Branch' and 'Commit Message'. A field for 'Large File Storage Limit in MB' is set to 1. Below these, a section titled 'Changes' shows a message 'No changes to commit'. At the bottom are two buttons: 'RESET' and 'COMMIT'.

History panel (9)

In the History panel you can inspect your ARCs history with all commits

The screenshot shows a 'History' panel with a title 'Inspect ARC history'. Below the title is a circular icon with a clock and a downward arrow. The main area displays a vertical timeline of commits, each marked with a teal circle. The commits are listed from top to bottom:

- 08.04.2024 12:44 - SABRINA ZANDER (SABRINA.ZANDER@UNI-DUESSELDORF.DE)
add data and protocols to rnaseq
- 08.04.2024 12:43 - SABRINA ZANDER (SABRINA.ZANDER@UNI-DUESSELDORF.DE)
add assay rnaseq
- 08.04.2024 12:43 - SABRINA ZANDER (SABRINA.ZANDER@UNI-DUESSELDORF.DE)
add study talinum_drought
- 08.04.2024 12:43 - SABRINA ZANDER (SABRINA.ZANDER@UNI-DUESSELDORF.DE)
add contributors
- 08.04.2024 12:42 - SABRINA ZANDER (SABRINA.ZANDER@UNI-DUESSELDORF.DE)
add description to investigation
- 08.04.2024 12:41 - SABRINA ZANDER (SABRINA.ZANDER@UNI-DUESSELDORF.DE)
set up new ARC



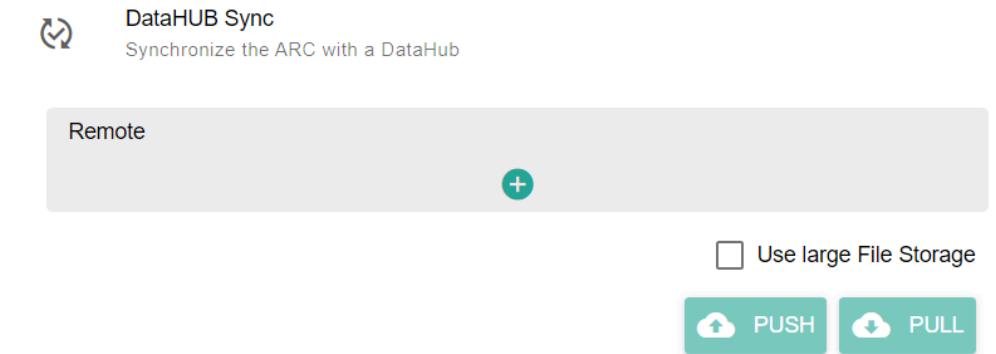
Upload your local ARC to the DataHUB

From the sidebar, navigate to **DataHUB Sync** (8)

DataHUB Sync

The DataHUB Sync panel allows you to

- sync the changes to the DataHUB: **Push**
- sync from the DataHUB: **Pull**, and
- change the Remote for the synchronization



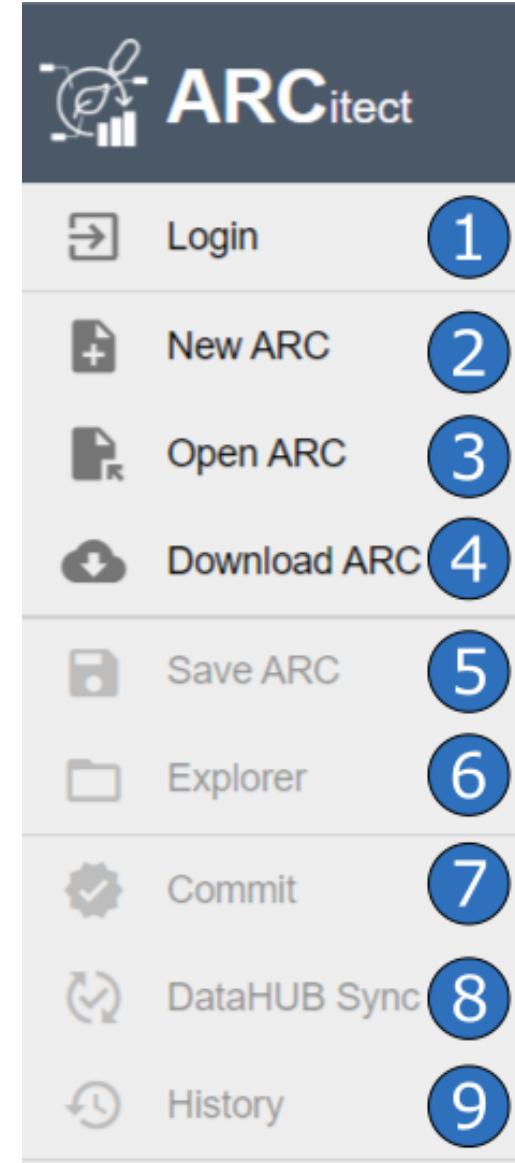
Check if your ARC is successfully uploaded

1. [sign in](#) to the DataHUB
2. Check your projects

Backup Slides

Download the demo data

1. Open the ARCitect
2. Login (1) to your DataHUB account
3. Navigate to Download ARC (4)

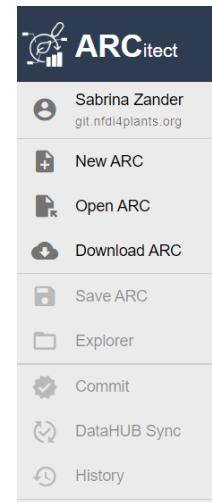


Download the demo data

4. Search for **Talinum-CAM-Photosynthesis**

5. Click the download button, select a location and open the ARC.

6. Open the downloaded ARC



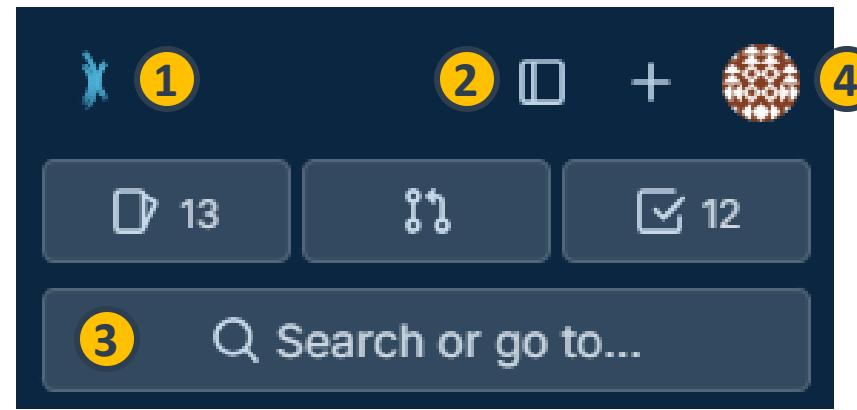
Open ARC

A screenshot of the 'Download ARC' interface. It shows a search bar with 'Talinum-CAM-Photosynthesis' and a green 'C' button. Below the search bar, there is a list item for 'Talinum-CAM-Photosynthesis [2023-10-11T09:24:10.208Z] Teaching'. To the right of this list item are a search icon and a download icon.

This is basically the ARC we created in the last session.

DataHub Hands-On

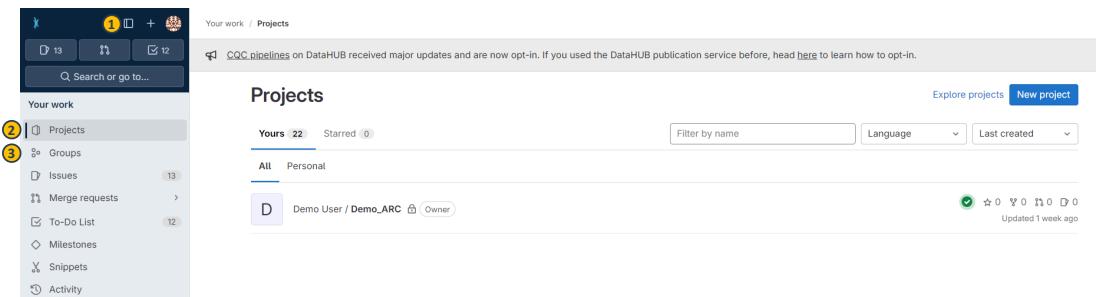
Navigation Bar



1. navigate directly to the [projects panel](#) via the icon in the top-left (1)
2. open the [hamburger Menu](#) (2)
3. use the search field (3) to find ARCs, users and groups
4. open the [avatar Menu](#) (4)

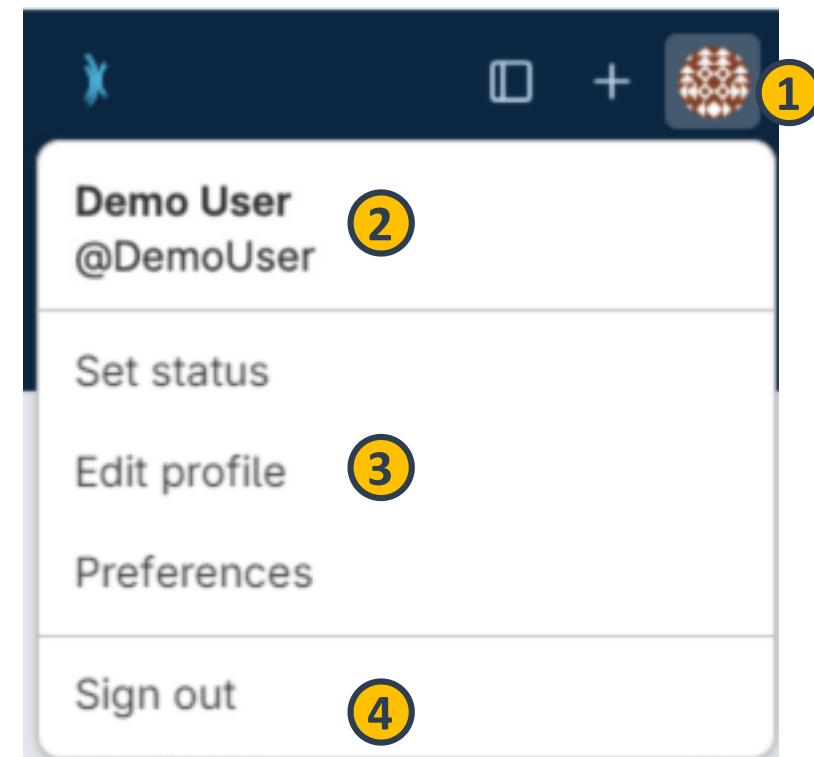
Hamburger Menu

1. From the hamburger menu (1) you can
2. navigate to the **projects** (2)
3. or **groups** (3) panels



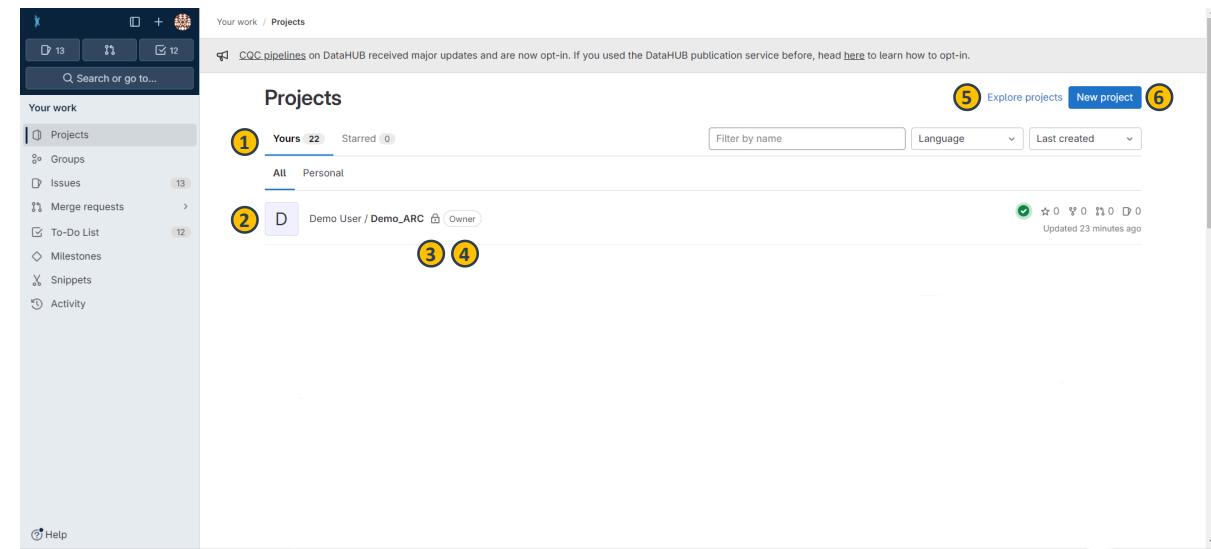
Avatar Menu

1. In the avatar menu (1) you can
2. find your profile name and user name (2),
3. navigate to the [user settings](#) (3)
4. or sign out (4) of the DataHUB.



Projects Panel

1. Choose a tab (1) to see only your ARCs, or explore other publicly available ARCs.
2. The main panel (2) lists all ARCs
3. Here you can also see, the visibility level (3), and
4. your permission or role (4) for the listed ARC.



ARC Panel

The ARC Panel is the main working area for your ARC.

The screenshot shows the ARC Panel interface for a project named "Demo_ARC".

- Left Sidebar:** Contains navigation links numbered 1 through 8.
 - 1 Manage
 - 2 Plan
 - 3 Code
 - 4 Settings
 - 5 Help
- Project Header:** Shows the project name "Demo_ARC" with a lock icon (5), a branch dropdown (main) (6), a plus sign (7), and a "Code" button (8).
- Project Information:** Includes a pipeline status (passed) and a "Publish ARC" button.
- File List:** Shows a recent commit "arc init" by "Demo User" (authored 4 minutes ago). Below it is a table of files with their last commit and update times.

Name	Last commit	Last update
assays	arc init	4 minutes ago
runs	arc init	4 minutes ago
studies	arc init	4 minutes ago
workflows	arc init	4 minutes ago
.gitignore	arc init	4 minutes ago
isa.investigation.xlsx	arc init	4 minutes ago
- Bottom Navigation:** Includes DataPLANT and CEPLAS logos, and Creative Commons BY license information.

ARC Panel – sidebar

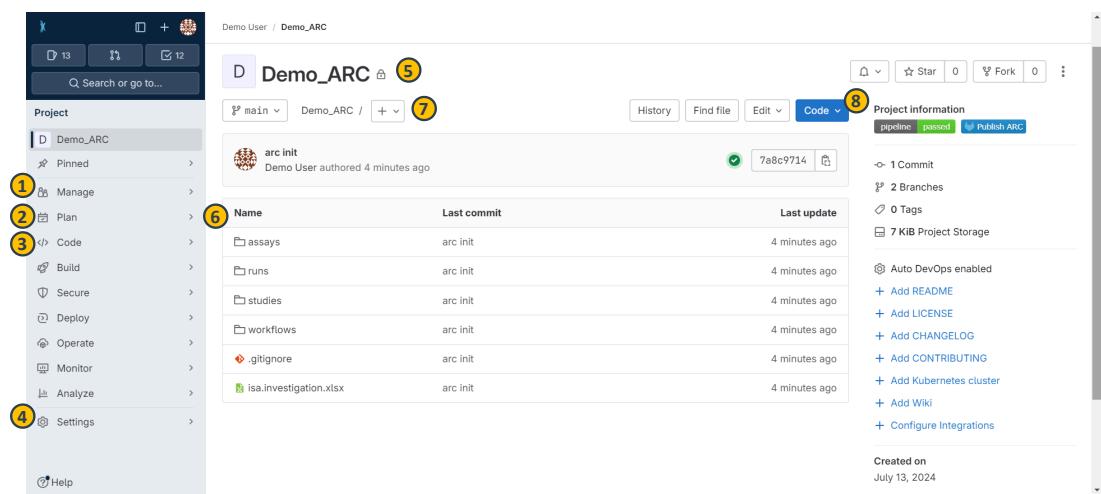
1. access the project information (1), e.g.
invite members to the ARC
2. follow the progress of your ARC
repository (2),
3. organize tasks in issue lists and boards
(3),
4. take notes in a wiki to your ARC (4),
5. adapt the **settings** (5) of the ARC.

The screenshot shows the DataHUB interface. On the left is a sidebar with various project management options: Manage (1), Plan (2), Code (3), Build (4), Secure (5), Deploy (6), Operate (7), Monitor (8), Analyze (9), Settings (10), and Help (11). The main area displays project details for 'Demo User / Demo_ARC'. It includes a header with project name, pipeline status (passed), and repository stats (1 commit, 2 branches, 0 tags, 7 KB storage). Below this is a table of files and their last commits:

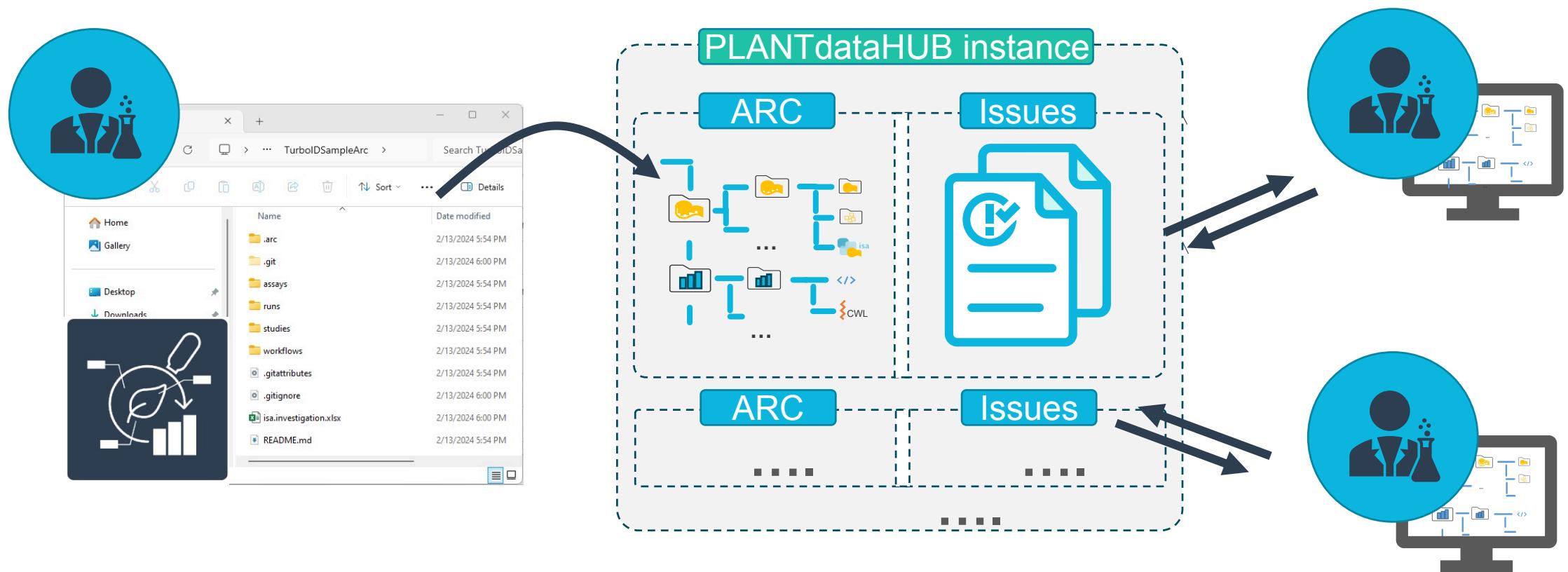
Name	Last commit	Last update
assays	arc init	4 minutes ago
runs	arc init	4 minutes ago
studies	arc init	4 minutes ago
workflows	arc init	4 minutes ago
.gitignore	arc init	4 minutes ago
isa.investigation.xlsx	arc init	4 minutes ago

ARC Panel – main panel

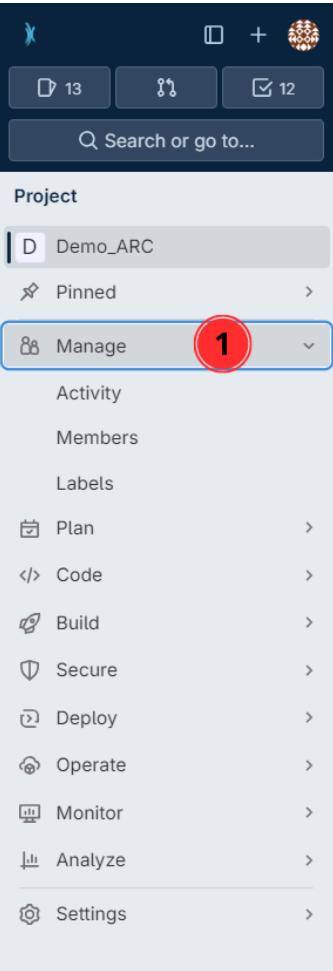
6. see the ARC's name and visibility level (6),
7. follow the ARC's commit history (7),
8. see files contained in your ARC just like on your computer (8),
9. add new files or directories (9), and
10. download or clone your ARC (10).



Collaborate and share



1. Click on Project Information in the left navigation panel



The screenshot shows the DataHUB project management interface. On the left, a sidebar lists various project management sections: Project, Pinned, Manage (highlighted with a red circle), Activity, Members, Labels, Plan, Code, Build, Secure, Deploy, Operate, Monitor, Analyze, and Settings. The main content area displays the 'Demo_ARC' project details. At the top, there's a message about CQC pipelines. Below it, the project name 'Demo_ARC' is shown with a lock icon, and a 'Code' dropdown menu is open. A commit history table lists files like 'assays', 'runs', 'studies', 'workflows', '.gitignore', and 'isa.investigation.xlsx' with their last commits and update times. To the right, a 'Project information' section provides metrics such as 1 Commit, 2 Branches, 0 Tags, 21 KiB Project Storage, and various enablement options like Auto DevOps, Wiki, README, LICENSE, CHANGELOG, CONTRIBUTING, Kubernetes cluster, and Integrations. It also shows the creation date as July 13, 2024.

Demo User / Demo_ARC

CQC pipelines on DataHUB received major updates and are now opt-in. If you used the DataHUB publication service before, head [here](#) to learn how to opt-in.

D Demo_ARC

main Demo_ARC / +

History Find file Edit Code

Project information

pipeline passed [Publish ARC](#)

Name	Last commit	Last update
assays	arc init	1 week ago
runs	arc init	1 week ago
studies	arc init	1 week ago
workflows	arc init	1 week ago
.gitignore	arc init	1 week ago
isa.investigation.xlsx	arc init	1 week ago

-o 1 Commit
2 Branches
0 Tags
21 KiB Project Storage

Auto DevOps enabled
Wiki
+ Add README
+ Add LICENSE
+ Add CHANGELOG
+ Add CONTRIBUTING
+ Add Kubernetes cluster
+ Configure Integrations

Created on
July 13, 2024

2. Click on Members

The screenshot shows the DataHUB interface for the project 'Demo_ARC'. On the left, a sidebar lists various project sections: Pinned, Manage (with a red circle '1'), Activity, Members (with a red circle '2'), Labels, Plan, Code, Build, Secure, Deploy, Operate, Monitor, Analyze, and Settings. The 'Members' section is currently selected. The main area displays the 'Project members' page, which includes a message about CQC pipelines, three buttons ('Import from a project', 'Invite a group', 'Invite members'), and a table showing one member: 'Demo User (@DemoUser) [It's you]'. The table columns are Account, Source, Max role, Expiration, and Activity. The member is a 'Direct member by Demo User' with 'Owner' role, expiration on Sep 27, 2023, and activity from Jul 13, 2024, to Jul 21, 2024.

Account	Source	Max role	Expiration	Activity
Demo User @DemoUser [It's you]	Direct member by Demo User	Owner	8+ Sep 27, 2023 ✓ Jul 13, 2024 ✗ Jul 21, 2024	

3. Click on Invite members

The screenshot shows the DataHUB interface for a project named 'Demo_ARC'. The left sidebar has a 'Members' tab selected (labeled 2). The main area shows 'Project members' with one member listed: 'Demo User @DemoUser' (labeled 1). A red circle labeled 3 highlights the 'Invite members' button in the top right corner of the member list.

Account	Source	Max role	Expiration	Activity
Demo User @DemoUser <i>It's you</i>	Direct member by Demo User	Owner	8+ Sep 27, 2023 ✓ Jul 13, 2024 ✗ Jul 21, 2024	⋮

4. Search for potential collaborators

Invite members X

You're inviting members to the **Demo_ARC** project.

Username, name or email address 4

Select members or type email addresses

Select a role

Guest ▼

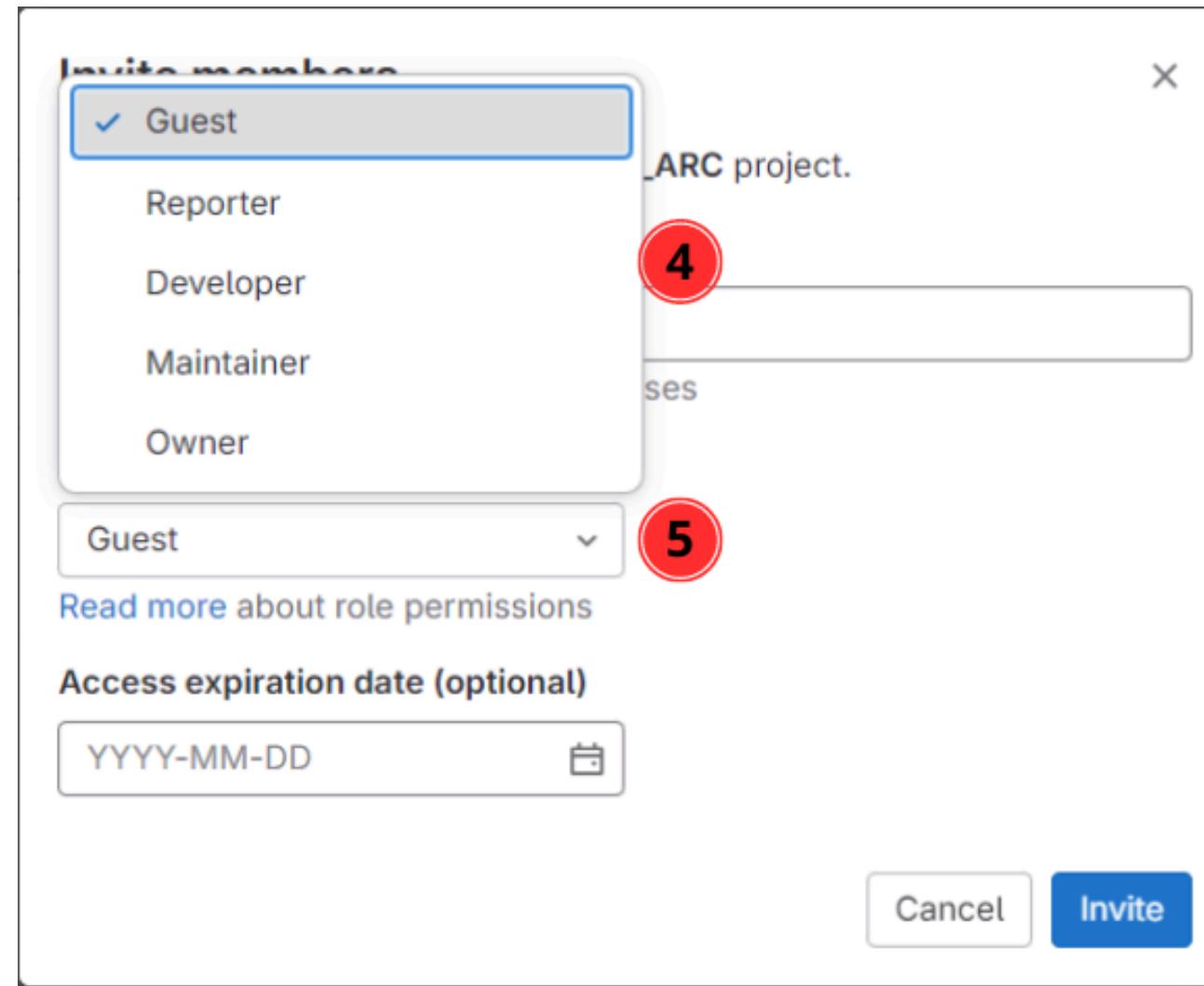
[Read more](#) about role permissions

Access expiration date (optional)

YYYY-MM-DD ▼

Cancel Invite

5. Select a role



Choosing the proper role

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

Permissions & Roles

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

Guest – Can only see the ARC's wiki

Reporter – Can read, but not add or edit data

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

Maintainer – Developer permissions + can add new members

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

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

Projects and Groups are not the same

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

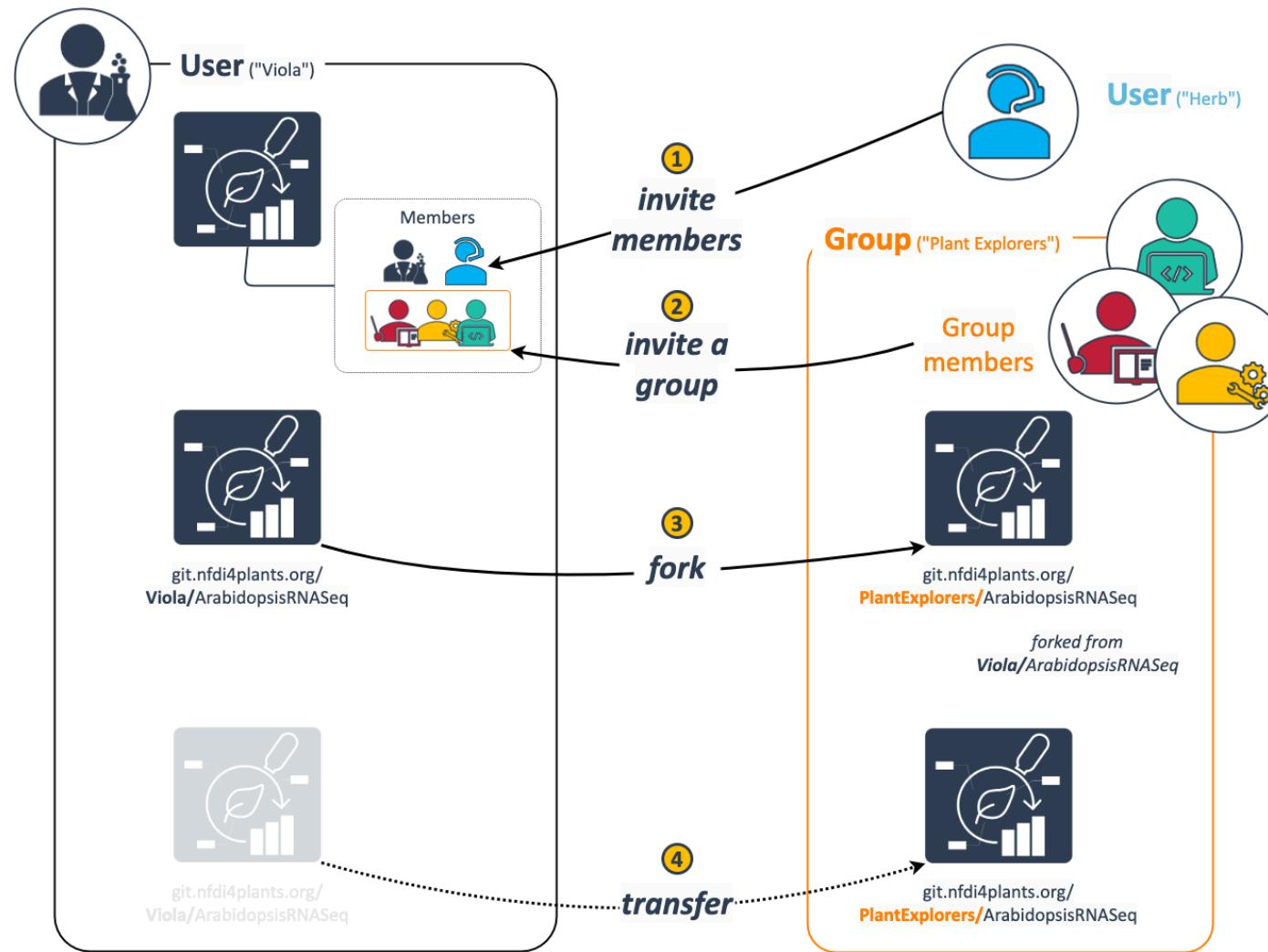
Project = ARC

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

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

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

Options to share an ARC via the DataHUB



Namespaces

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

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

 **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**.

ARC DataHUB members // ARC Investigation contacts

The screenshot shows the 'Members' section of a GitLab project named 'Samuilov-2018-BOU-PSP'. It lists four members with their accounts, sources, roles, expiration dates, and activity details.

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

DataHUB: ARC members

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

The screenshot shows the 'Investigation Contacts' section of the ARCTect interface. It displays a list of contacts with their names, ORCID IDs, and scores.

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

ARCTect: Investigation Contacts

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

Version control

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

The screenshot shows the DataHUB interface with the following numbered callouts:

- 1** Manage: Project management menu.
- 2** Plan: Plan section.
- 3** Code: Code section.
- 4** Settings: Settings menu.
- 5** Demo_ARC: Project name in the header.
- 6** Name: Column header for the file list table.
- 7** History: History tab in the repository view.
- 8** Project information: Project information sidebar.

Demo User / Demo_ARC

D Demo_ARC **5**

main Demo_ARC / **7**

arc init Demo User authored 4 minutes ago **8**

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

Project information

- pipeline passed
- Published ARC**

-o 1 Commit
2 Branches
0 Tags
7 KiB Project Storage

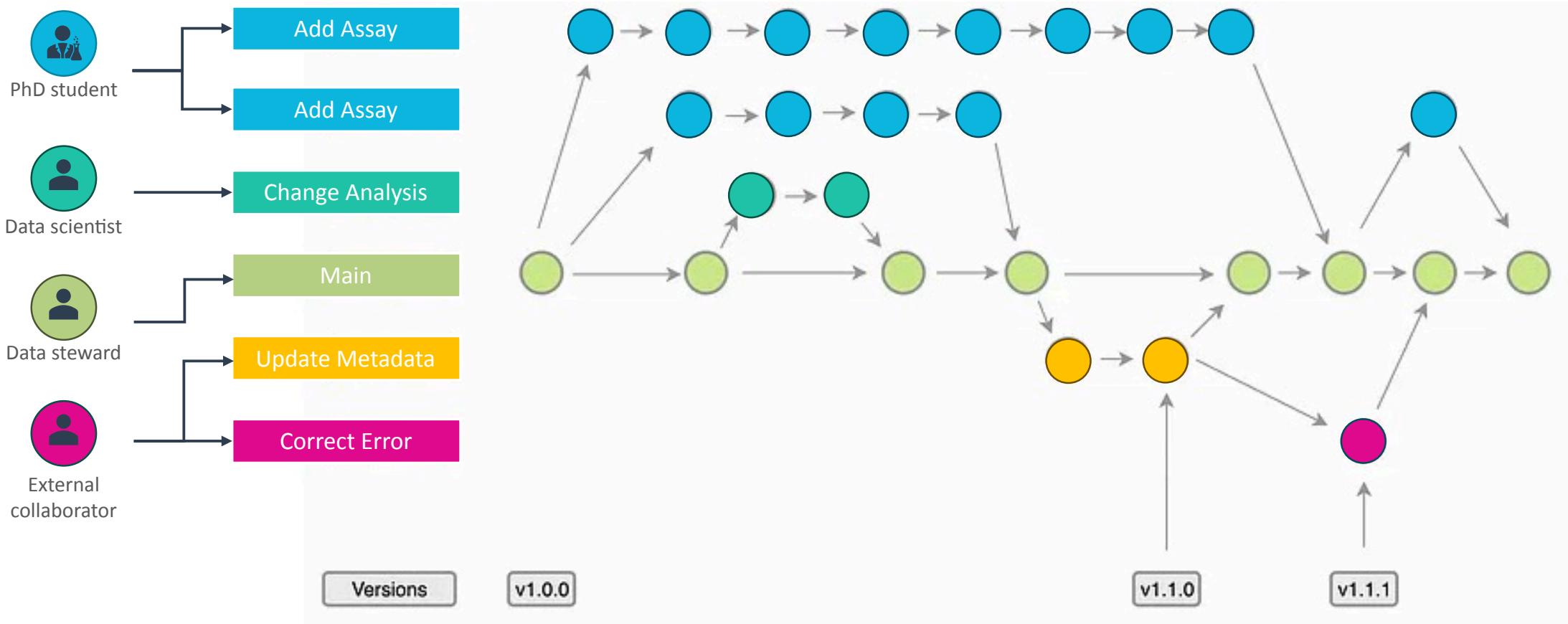
Auto DevOps enabled

+ Add README
+ Add LICENSE
+ Add CHANGELOG
+ Add CONTRIBUTING
+ Add Kubernetes cluster
+ Add Wiki
+ Configure Integrations

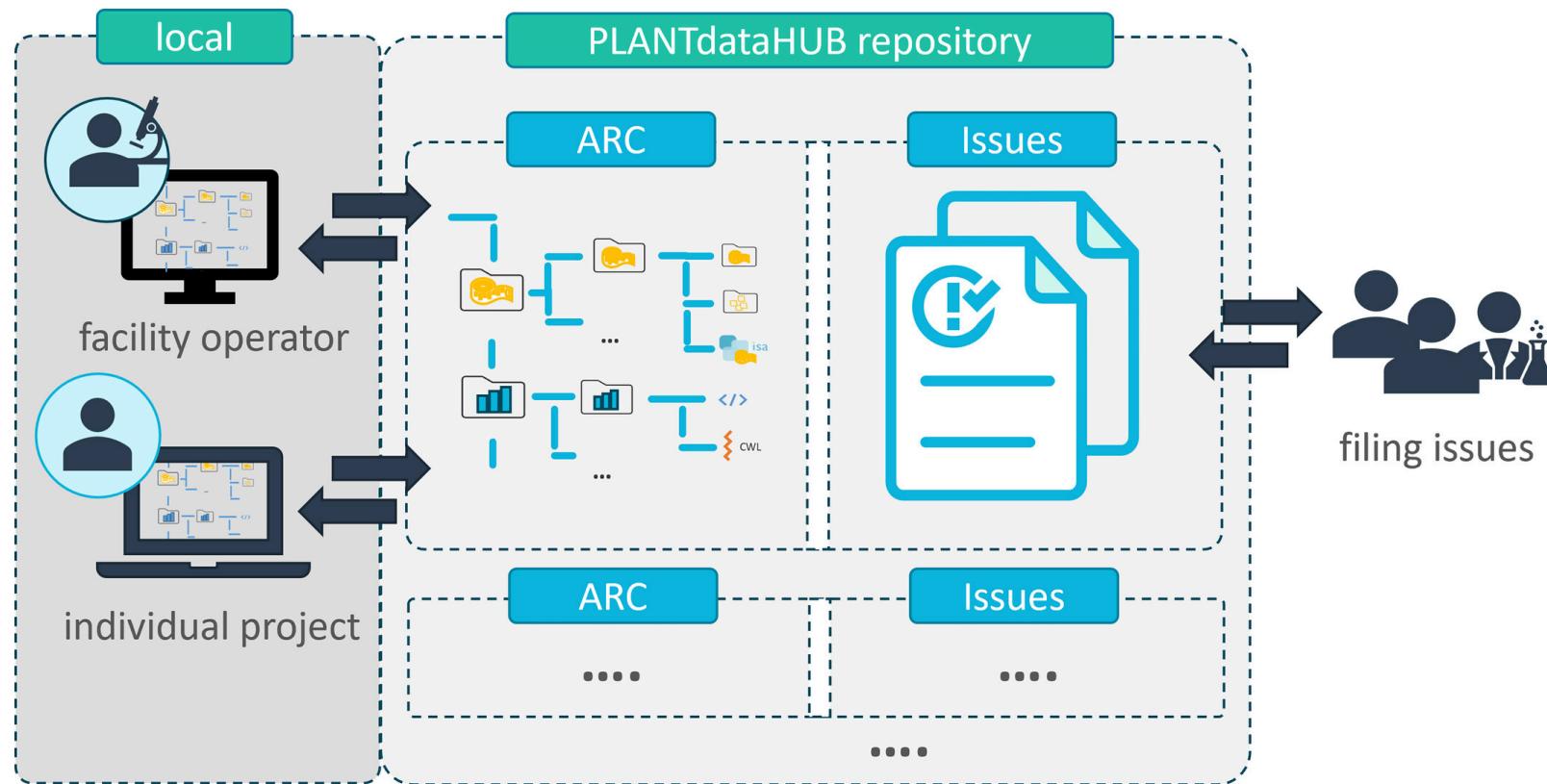
Created on July 13, 2024

Data PLANT **CEPLAS** **CC BY**

Collaboration Workflows



Project management



Project Management

Add issues to your ARC (3)

The screenshot shows the DataHUB Project Management interface. On the left, there is a sidebar with various project management options: Manage (1), Plan (2), Code (3), Build, Secure, Deploy, Operate, Monitor, Analyze, Settings (4), and Help. The main workspace is titled "Demo User / Demo_ARC". It displays a file tree under "arc init" with the following structure:

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

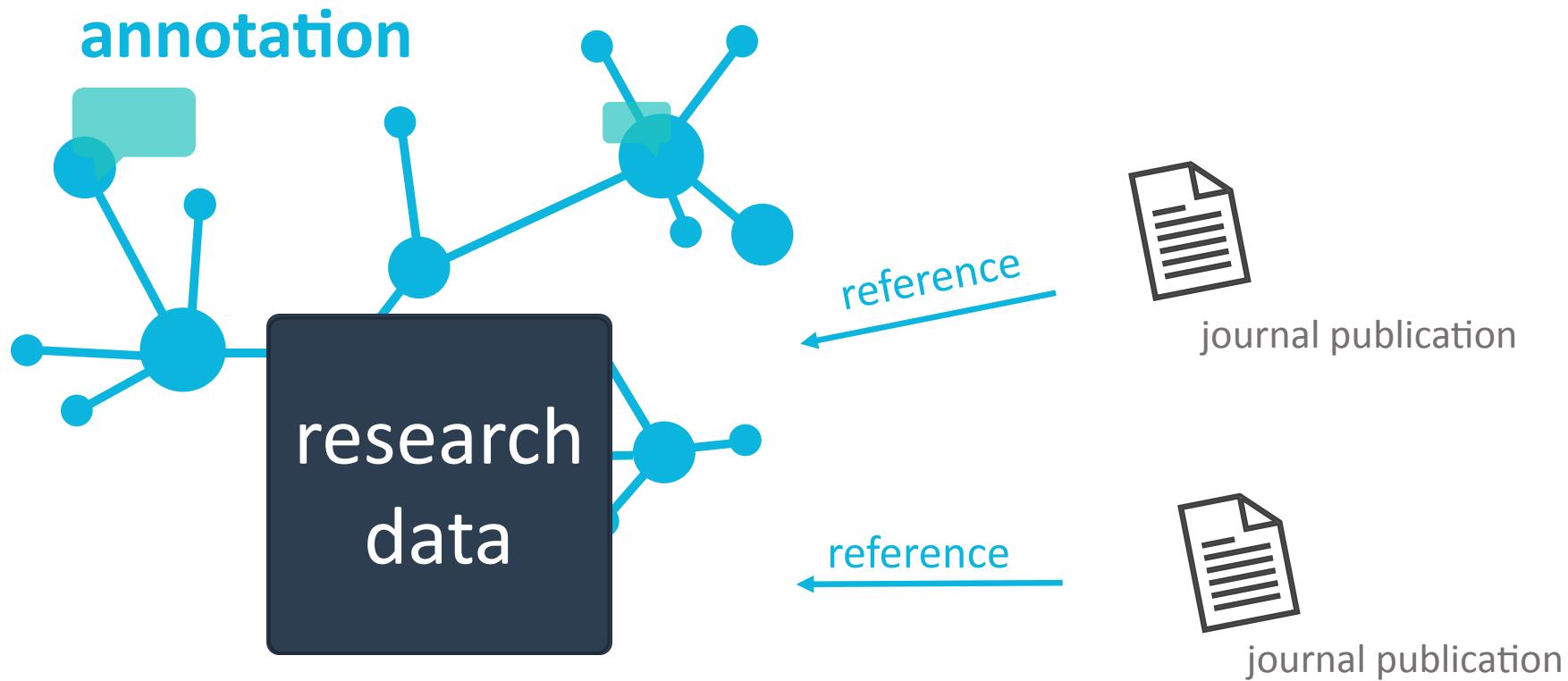
At the top right, there are buttons for History, Find file, Edit, Code (selected), and Project information. The Project information section shows a green "pipeline passed" status and a blue "Publish ARC" button. Below this, it lists 1 Commit, 2 Branches, 0 Tags, and 7 KiB Project Storage. There are also links to Auto DevOps enabled and various integration options like Add README, Add LICENSE, etc.

ARCs come with their own wiki space

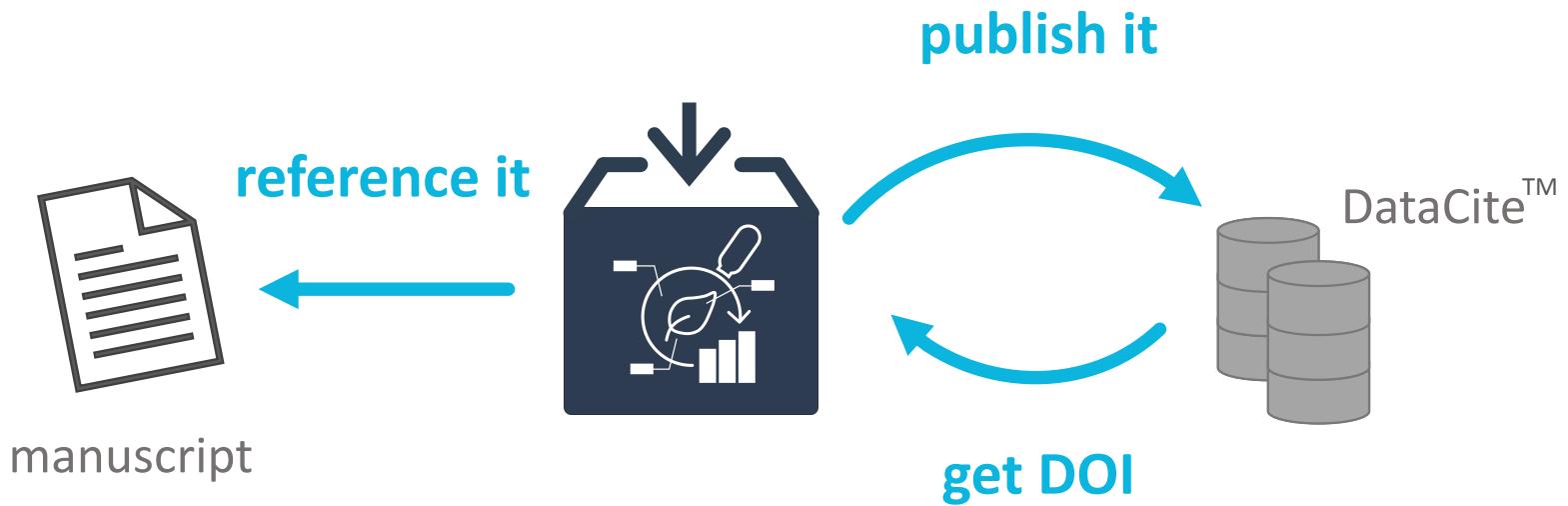
- directly associated to your ARC
- same access rights as your ARC
- share meeting minutes or ideas with collaboration partners
- keep ARC clean of files that are not considered "research data"

The screenshot shows the DataHUB interface. On the left, a sidebar for the 'Demo_ARC' project is visible, featuring sections for Project (with 'Demo_ARC' pinned), Manage, Plan, Issues (0), Issue boards, Milestones, and Wiki. The Wiki section is currently selected. The main content area displays a 'Home' page for the 'Wiki' of 'Demo_ARC'. The page header includes the URL 'Demo User / Demo_ARC / Wiki / Home'. A note at the top states: 'QC.pipelines on DataHUB received major updates and are now opt-in. If you used the DataHUB publication service before, head [here](#) to learn how to opt-in.' Below this, there's a 'Home' section with an 'Edit' button, followed by a 'Meeting Schedule' section listing events: '2024-06-12 Kick-off', '2024-06-27 Proposal discussion', and '2024-07-04 Discuss RNA-seq pipeline'. At the bottom, there's an 'Ideas and drafts' section with a single item: 'Golden Gate protocol'.

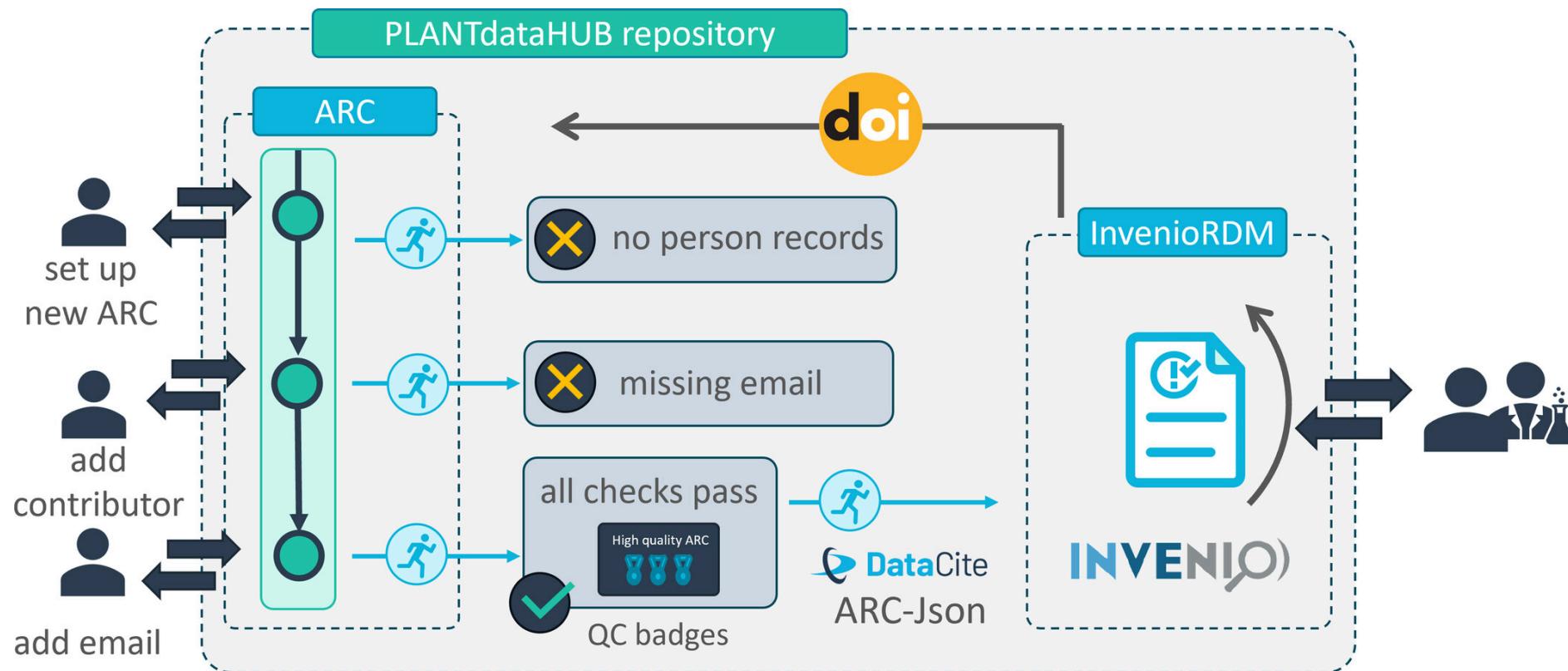
Moving from paper to FAIR data publication



Publish your ARC, get a DOI



Validate & publish



Validation towards publication

 **Ru_ChlamyHeatstress** 

 add validation_packages.yml
Kevin Schneider authored 2 months ago

History Find file Code

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

 README.md

Project information

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

Chlamydomonas abiotic stress
proteomics + 1 more

pipeline passed invenio 10/10

-o 55 Commits
2 Branches
0 Tags

 README
Auto DevOps enabled

Created on
July 11, 2022





Chlamydomonas reinhardtii heat stress time course experiment

Receive a DOI

Published September 7, 2023 | Version v1

Dataset  Open

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

Zhang, Ningning¹; Mattoon, Erin¹; McHargue, Will¹ ; Venn, Benedict² ; Zimmer, David² ; Pecani, Kresti³; Jeong, Jooyeon¹; Anderson, Cheyenne¹; Chen, Chen⁴; Berry, Jeffrey¹; Xia, Ming¹; Tzeng, Shin-Cheng¹ ; Becker, Eric¹; Pazouki, Leila¹; Evans, Bradley¹; Cross, Fred³; Cheng, Jianlin⁴; Czymmek, Kirk¹ ; Schröda, Michael⁵ ; Mühlhaus, Timo² ; Zhang, Ru¹ 

Show affiliations

Style APA

1
Citation

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

Description

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

Files

arc-summary.md

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

File contents:

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

2

Edit

New version

Share

Versions

Version v1 Sep 7, 2023
10.60534/9e5jx-75d83

Details

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

Resource type
Dataset

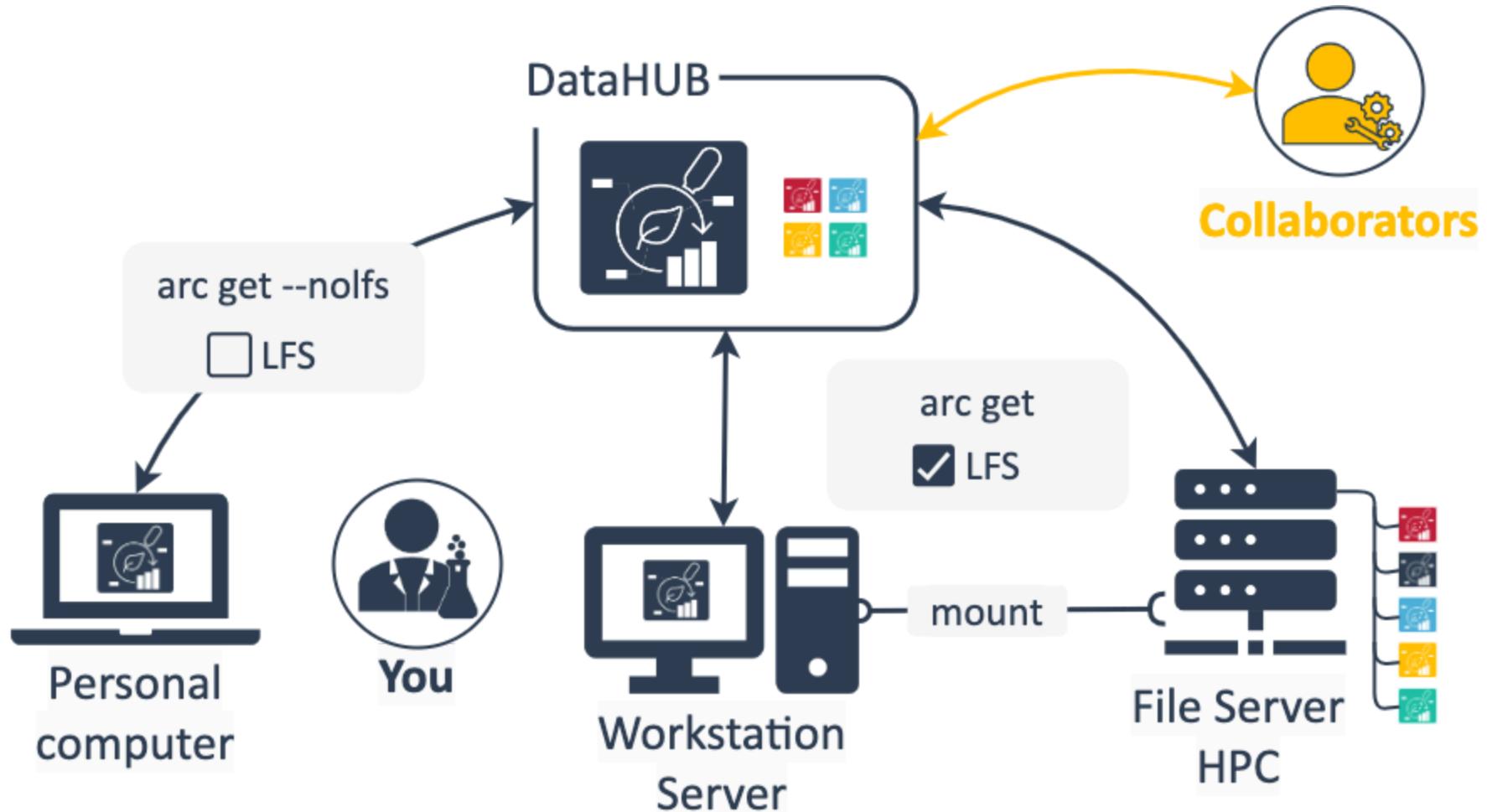
Publisher
DataPLANT

Export

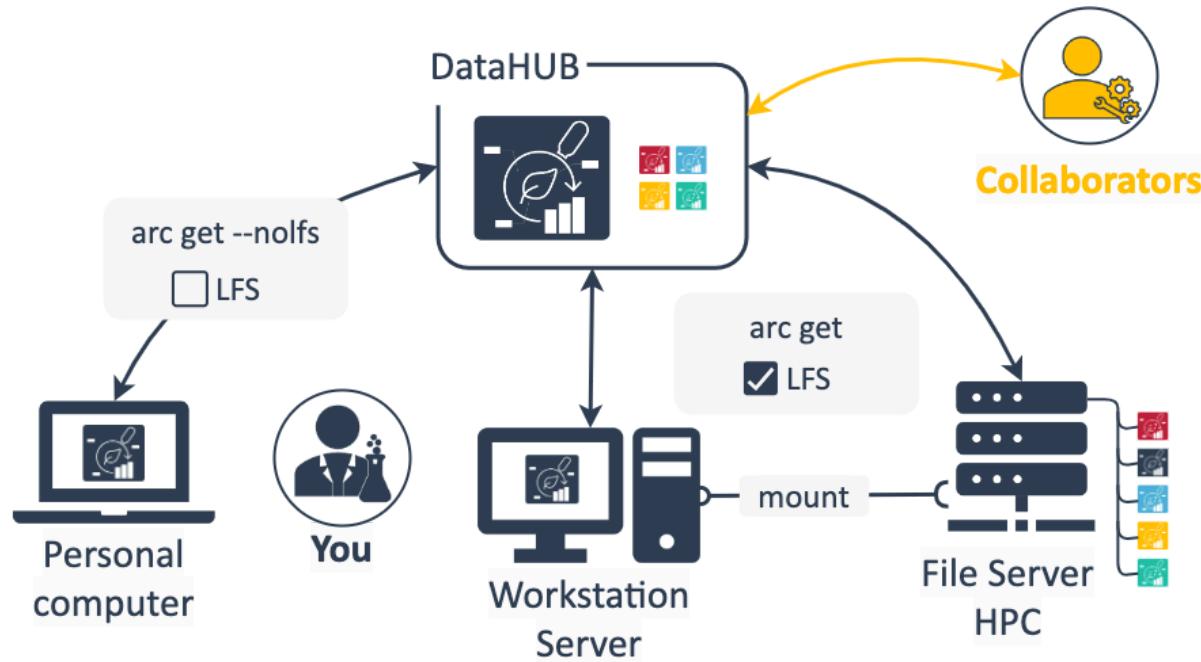
JSON Export

Backup

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

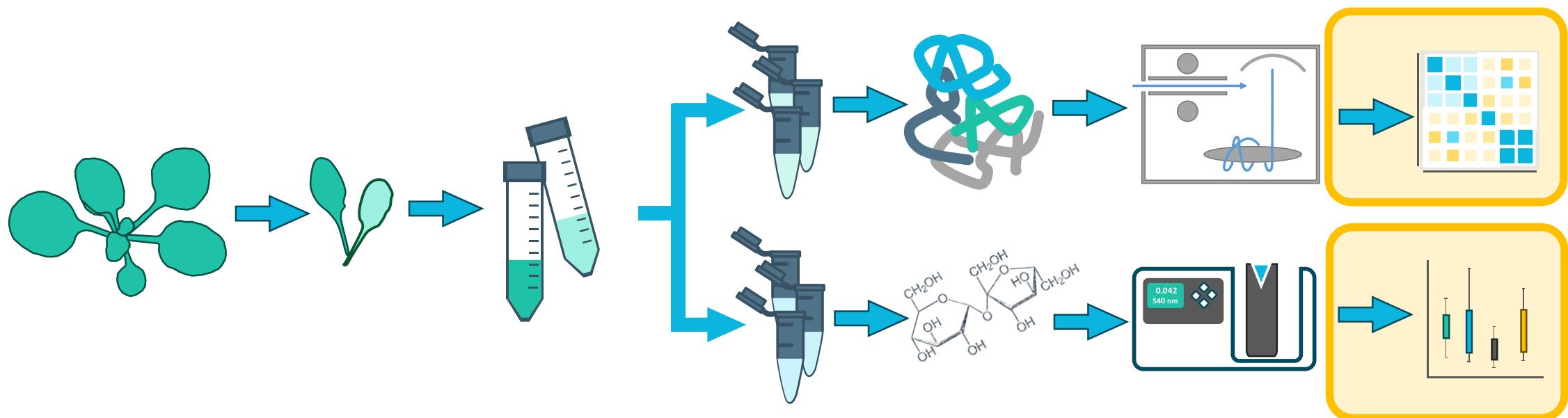
FileShare

- mount to local machine, sync ARC from there

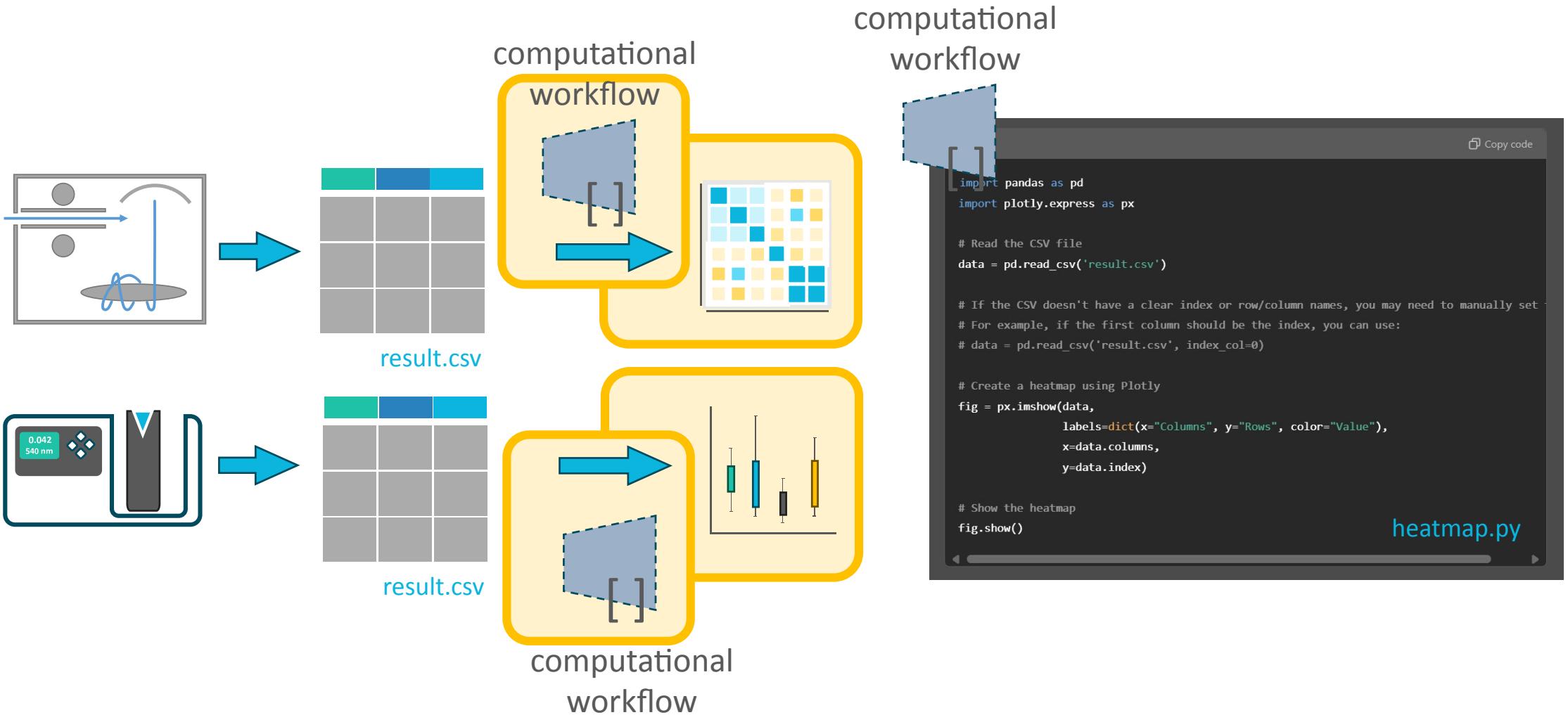
HPC

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

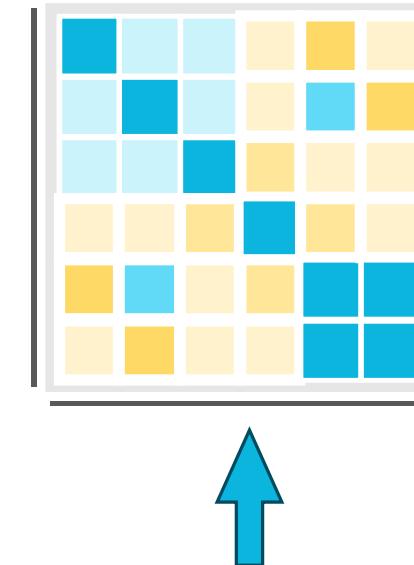
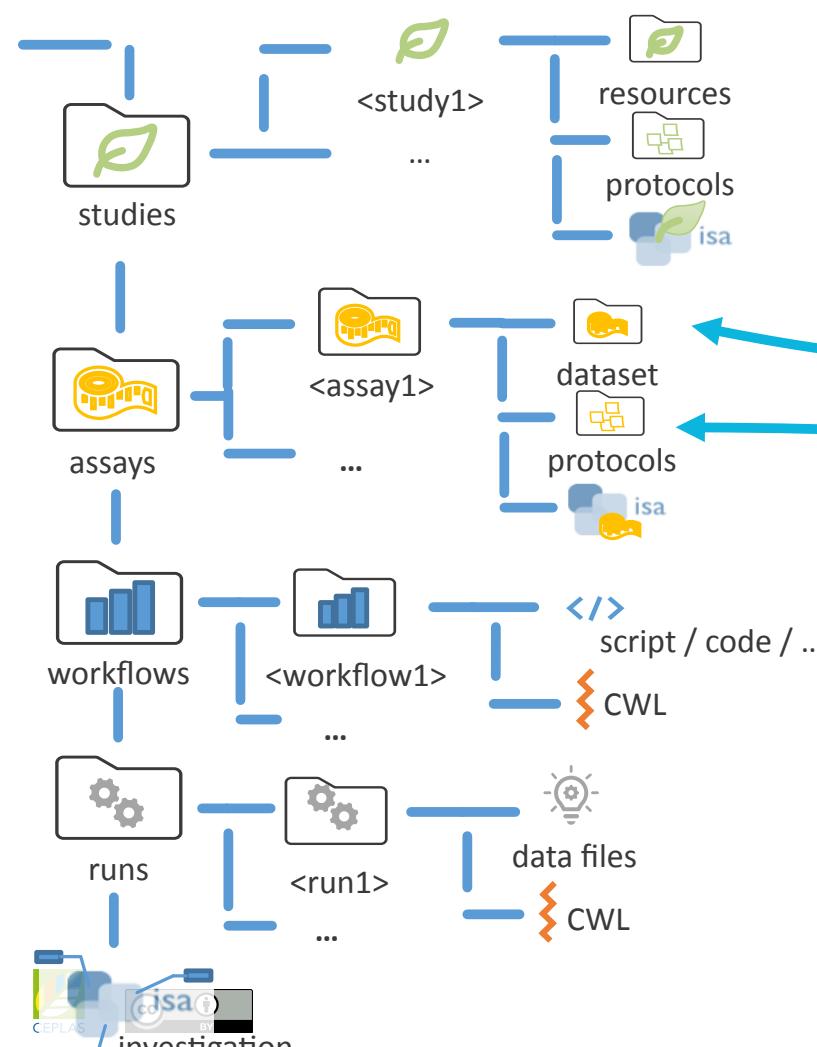
Options to annotate the data analysis



A computational workflow is like a protocol



Option I: Create a virtual assay



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

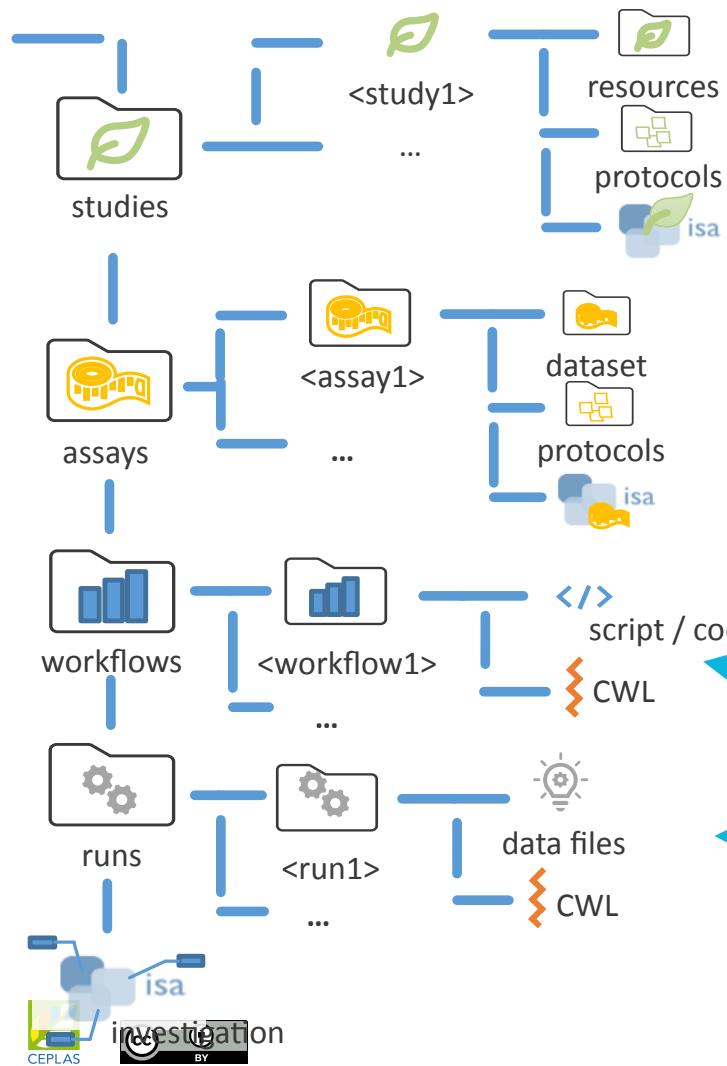
# Read the CSV file
data = pd.read_csv('result.csv')

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

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

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

Option II: Create a workflow and run



```
python
Copy code

import pandas as pd
import plotly.express as px

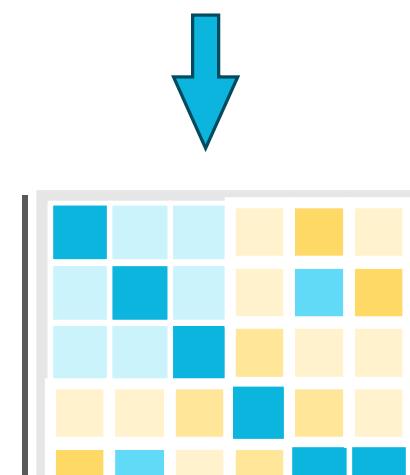
# Read the CSV file
data = pd.read_csv('result.csv')

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

```
graph TD; A[1] --> B[2]; B --> C[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 job parameter (*.yaml)

```
job yaml

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

CWL
tool descriptors (*.cwl)

CWL runner

output
folder

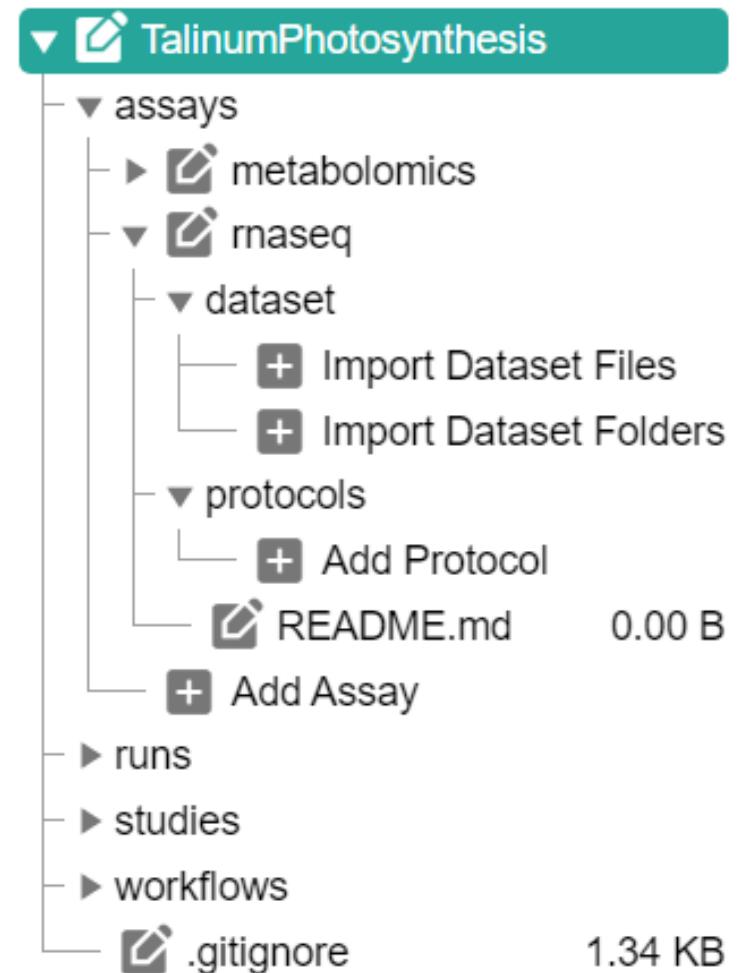
Add datasets

In the file tree you can

- **import dataset files or folders** and
- **protocols** associated to that dataset.

 **Import Dataset** allows to import data from any location on your computer into the ARC.

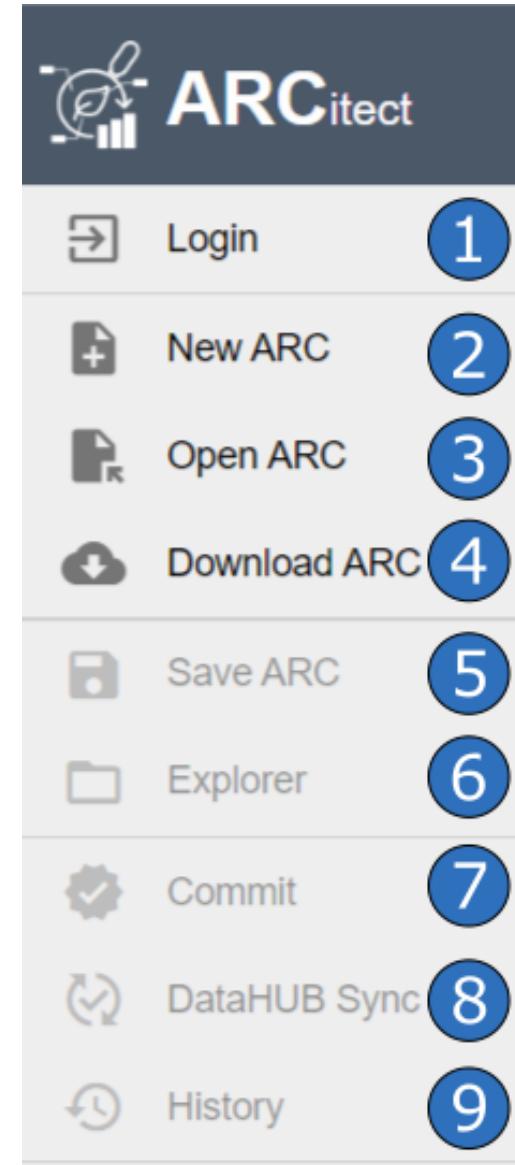
 Depending on the file size, this may take a while. Test this with a small batch of files first.



Backup Slides

Download the demo data

1. Open the ARCitect
2. Login (1) to your DataHUB account
3. Navigate to Download ARC (4)

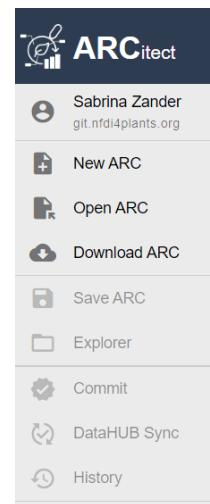


Download the demo data

4. Search for **Talinum-CAM-Photosynthesis**

5. Click the download button, select a location and open the ARC.

6. Open the downloaded ARC

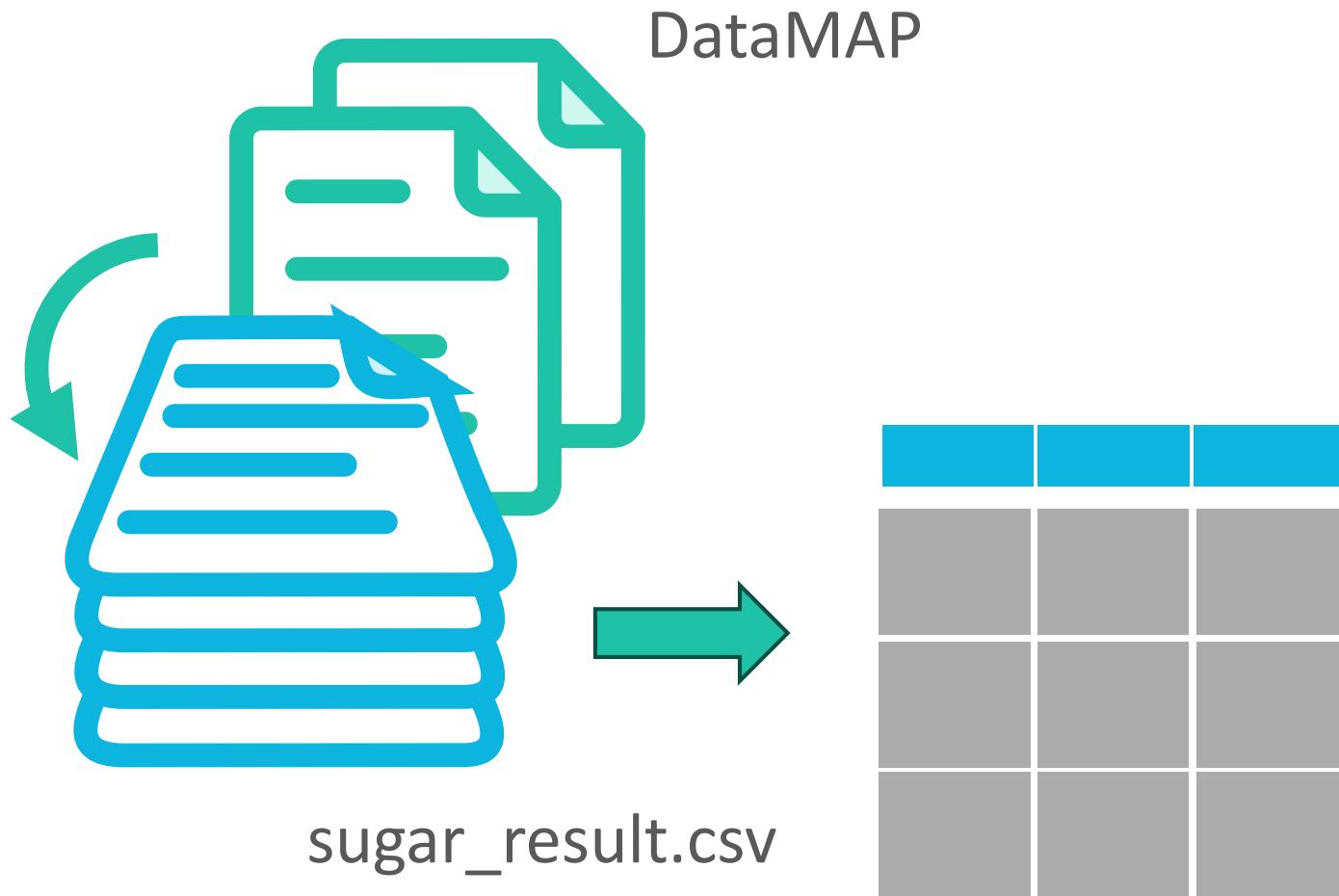


Open ARC

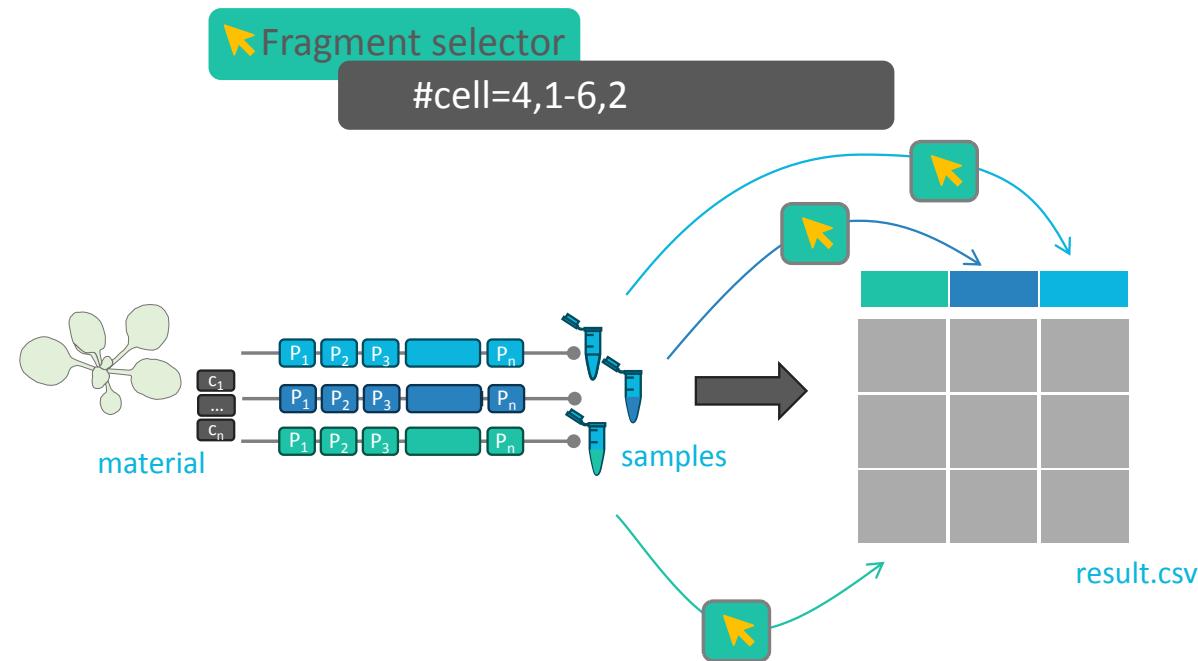
A screenshot of the 'Download ARC' page from the DataHUB. The top bar shows 'Download ARC' and 'Download ARCs from the nfdi4plants DataHUB'. The search bar contains 'Talinum-CAM-Photosynthesis'. Below the search bar, there are checkboxes for 'LFS' and 'Host git.nfdi4plants.org'. A green button labeled 'C' is visible. The main list displays one item: 'Talinum-CAM-Photosynthesis [2023-10-11T09:24:10.208Z] Teaching'. To the right of the list are a search icon and a download icon.

This is basically the ARC we created in the last session.

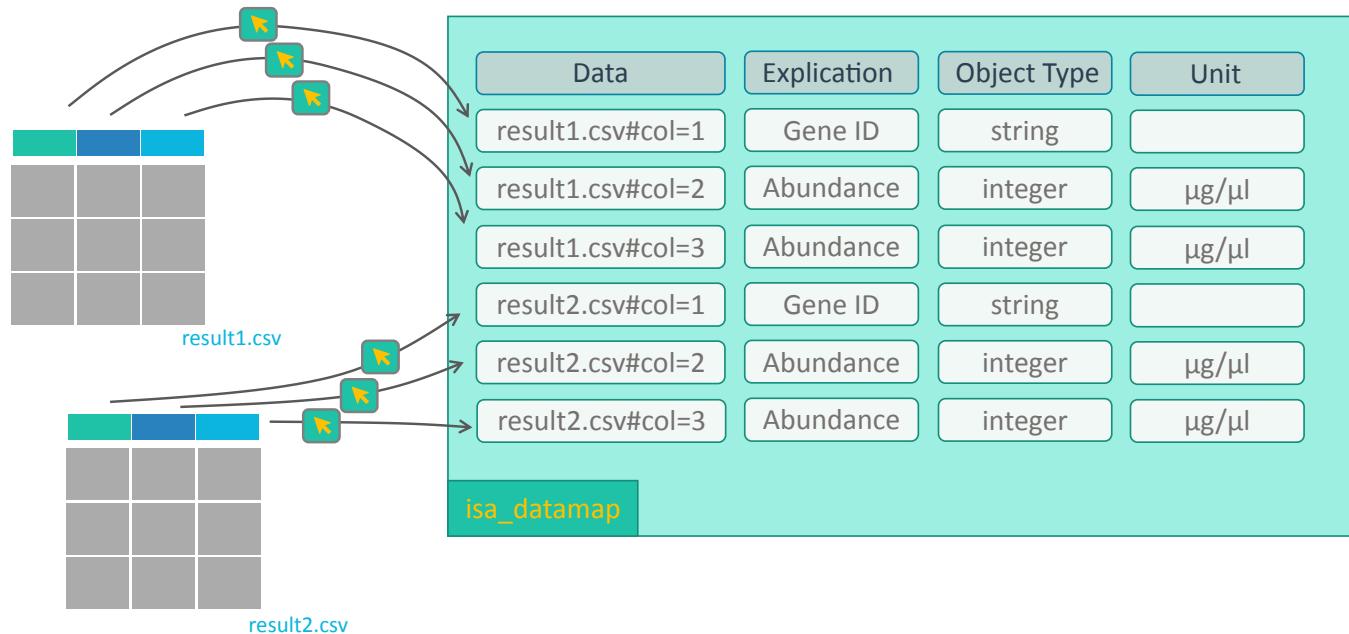
Annotation of the result data points



Point into results - Fragment selectors



DataMAP: Annotation for the fragment selectors



Contributors

If not referenced otherwise, figures and slides presented here were created by members of DataPLANT (<https://nfdi4plants.org>).

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