

DataPLANT Tool-Workshop

April, 2024

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Dominik Brilhaus, CEPLAS

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 knowledge base](#)

Resources – join the open source movement



DataPLANT (nfdi4plants)

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...

Continuous support

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

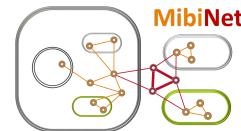
1. Slack Workspace for ad hoc support
2. Monthly user meeting (2nd Friday of the month)

→ [Details](#).



trr_341

plant
ecological
genetics



Introduce yourself

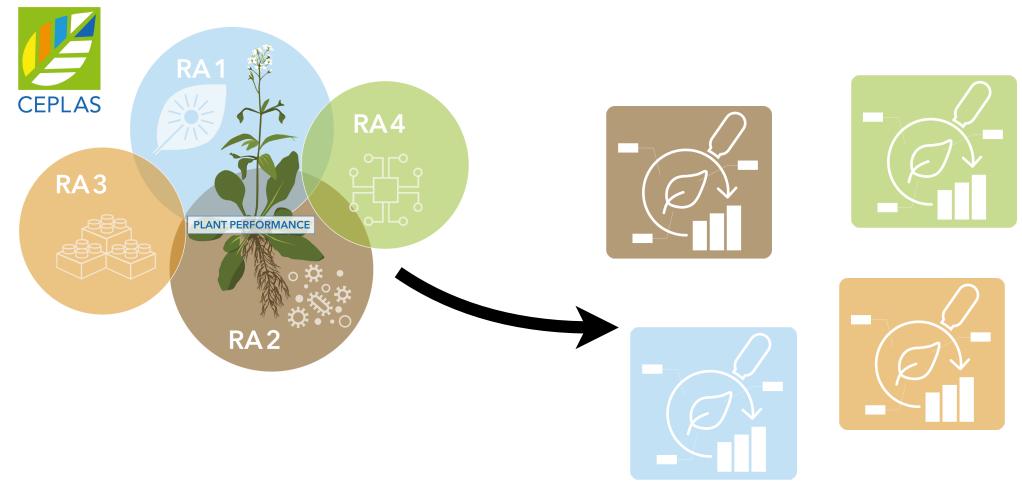
- Lab
- MibiNet / CEPLAS / TRR / ?
- Used code / programming language before
- Experience with Git / GitLab / GitHub?
- Have an ORCID
- My motivation / expectation
- My favorite lab assay

Let's draw a typical lab workflow



BYOD – Goals

- Move existing datasets into ARCs
- Share them via the DataHUB
- First few steps into ARCs
- You or collaborators can pick them up from there



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> <pre>graph LR; F[Findable] --- B1[Bar]; A[Accessible] --- B1; I[Interoperable] --- B1; R[Reusable] --- B1; Rep[Reproducibility] --- B2[Bar]; Rep --- Checkmark[✓];</pre>	<p>Added-value to the research community</p> <p>Compliance with funding policies</p> <p>Receive due credit</p> <p>Saves time & workload</p> <p>FAIR</p> <p>Time wasted</p>
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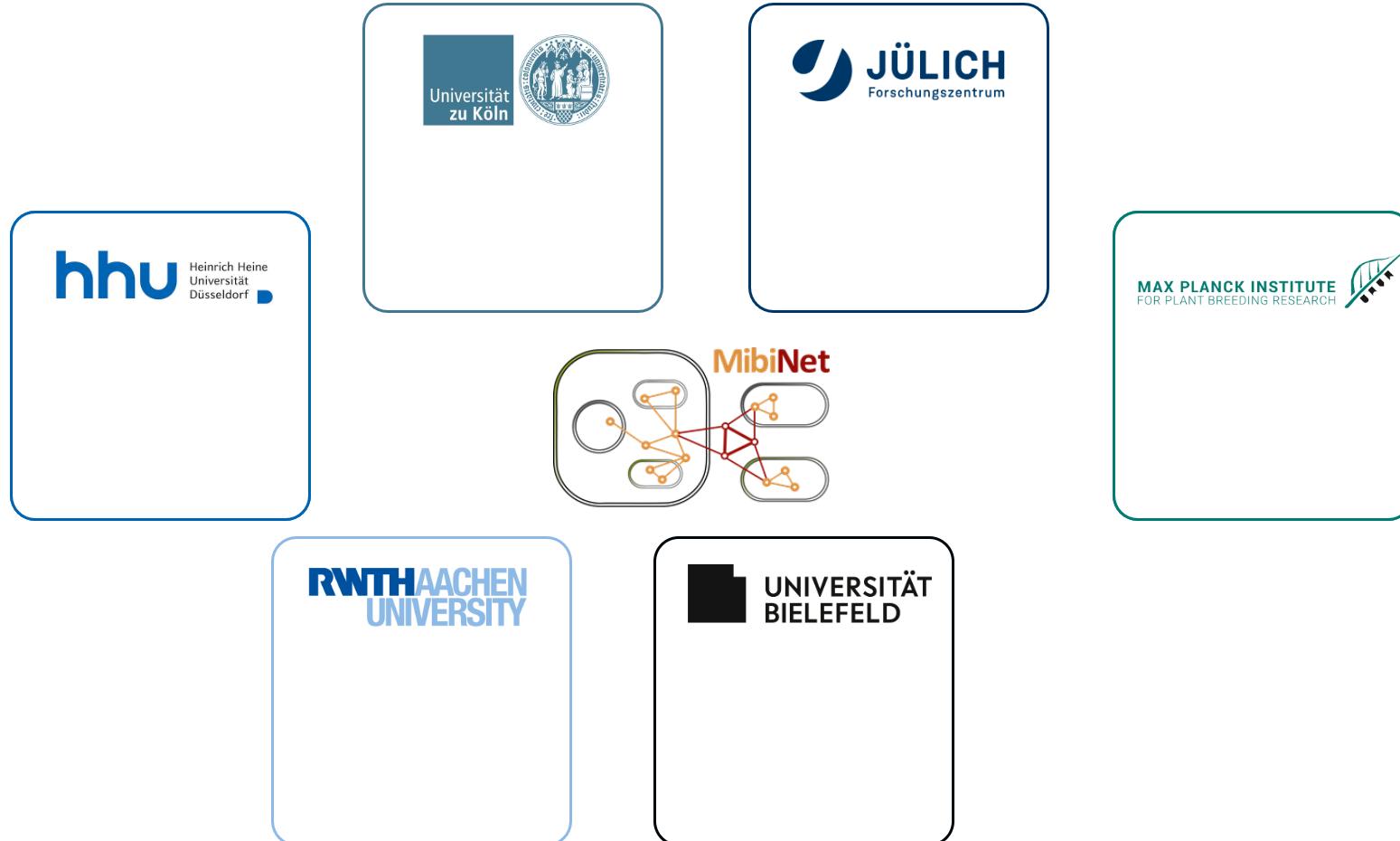
Is your data FAIR?

Findable | Accessible | Interoperable | Reusable

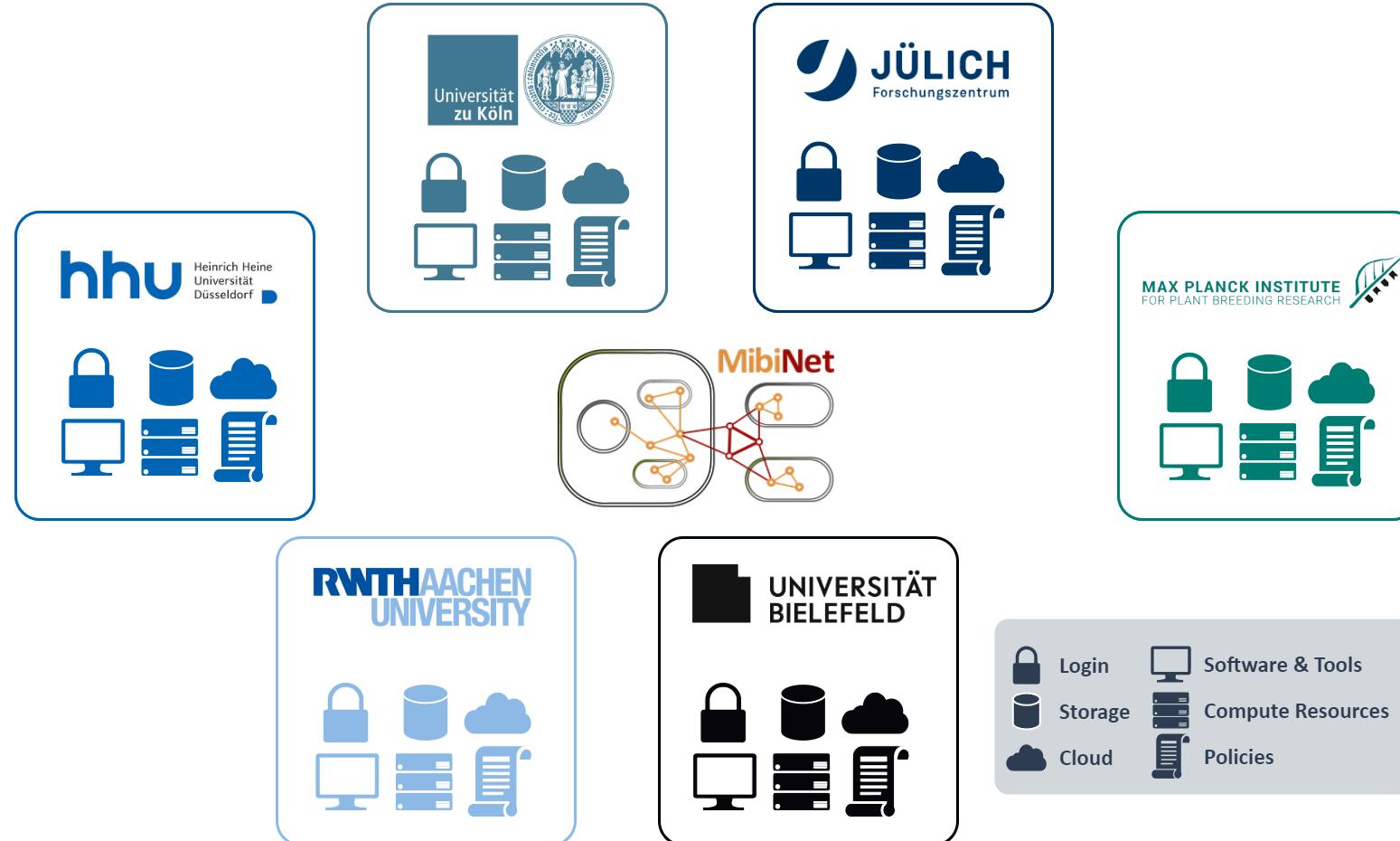
- Where do you store your data?
- How do you annotate your data?
- How do you share your data?
- What tools do you use to analyse your data?
- How do you reuse other people's data?



MibiNet – One SFB, six locations

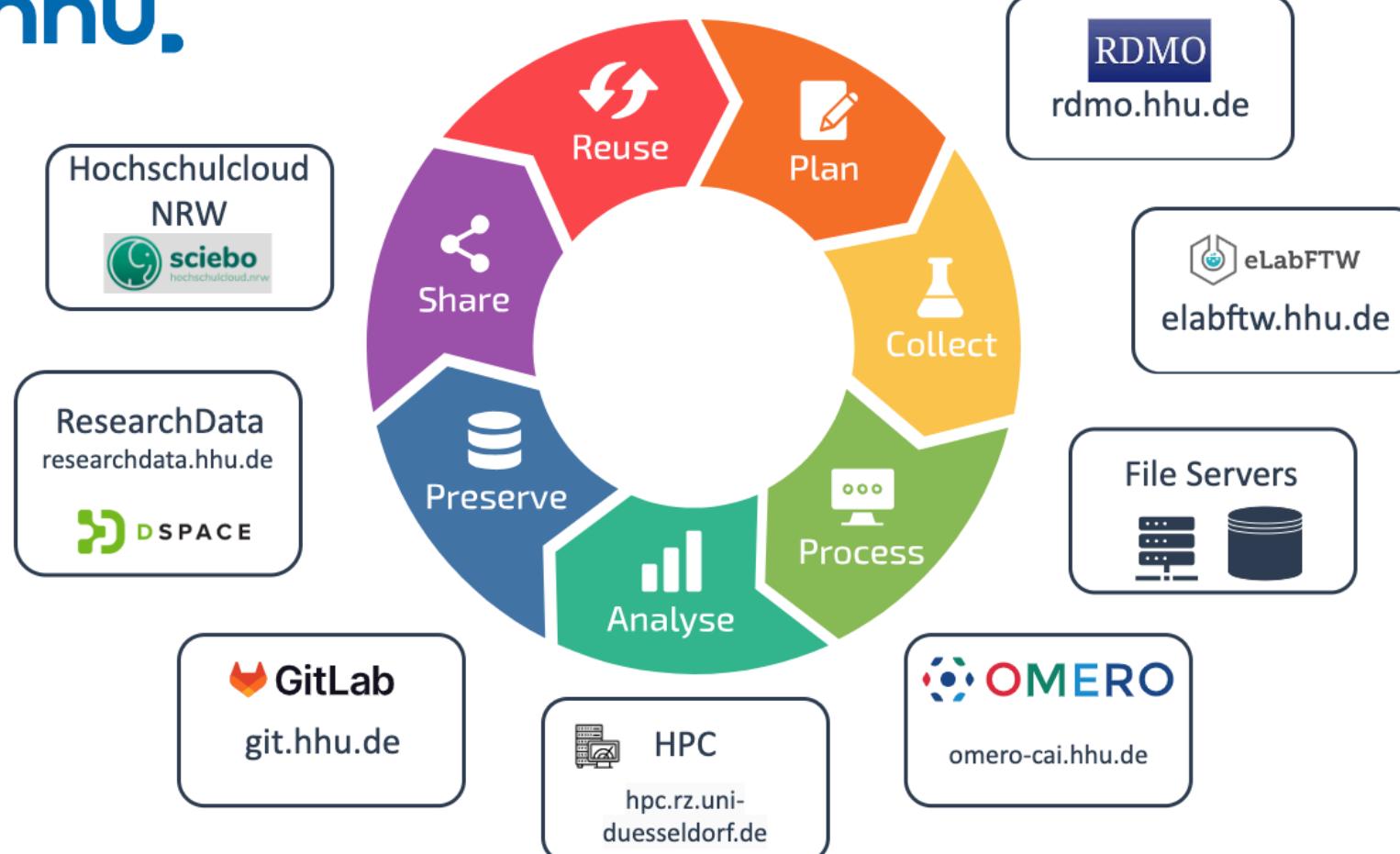


Data silos impede collaboration



Missing interfaces impede collaboration

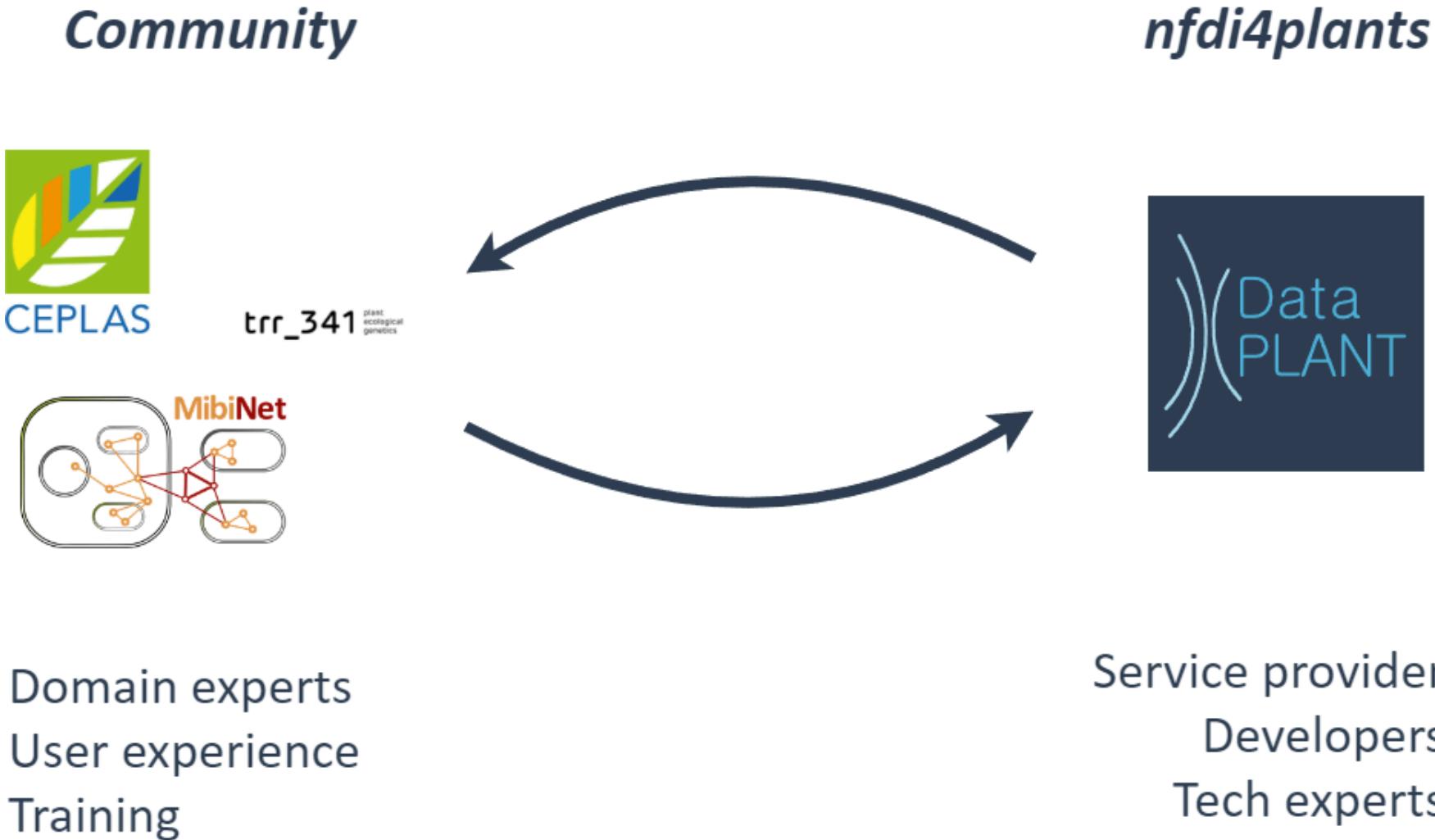
hhu.



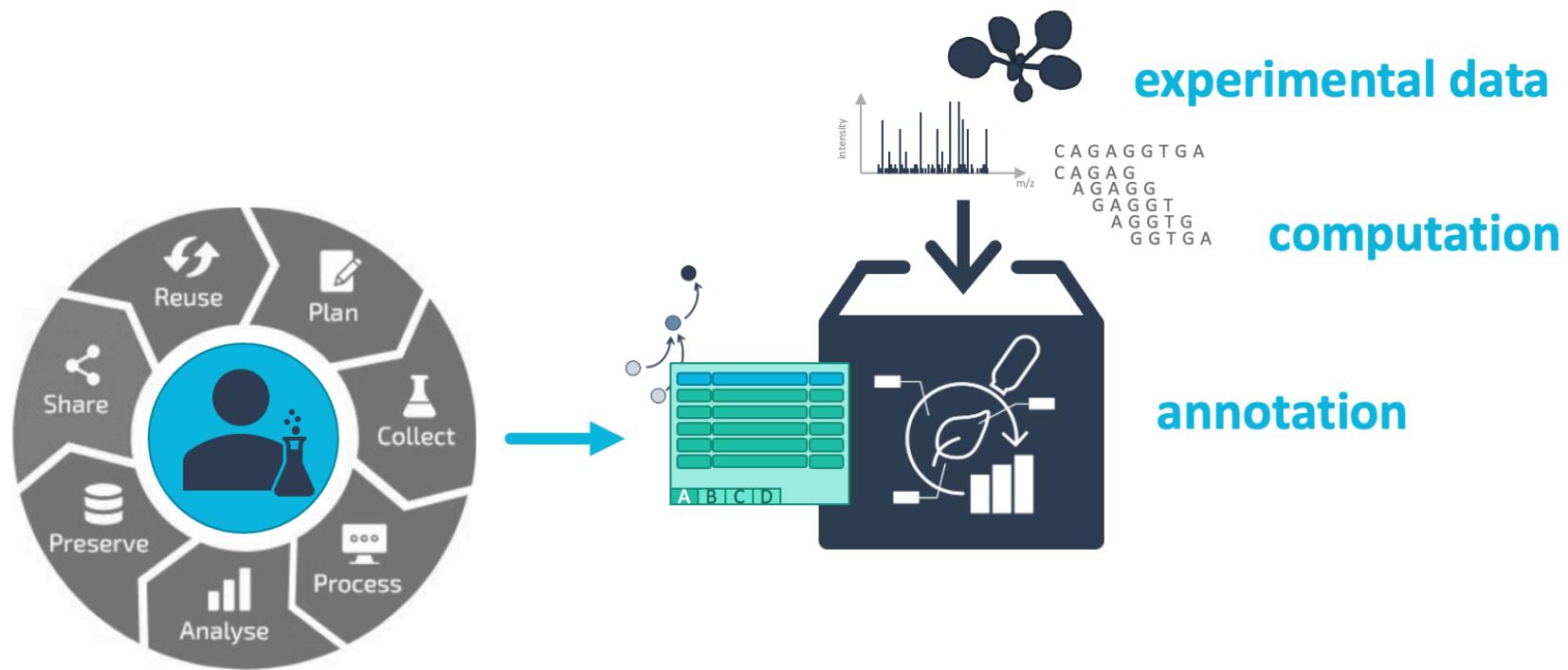
MibiNet connection to NFDIs



Data Stewardship between DataPLANT and the community

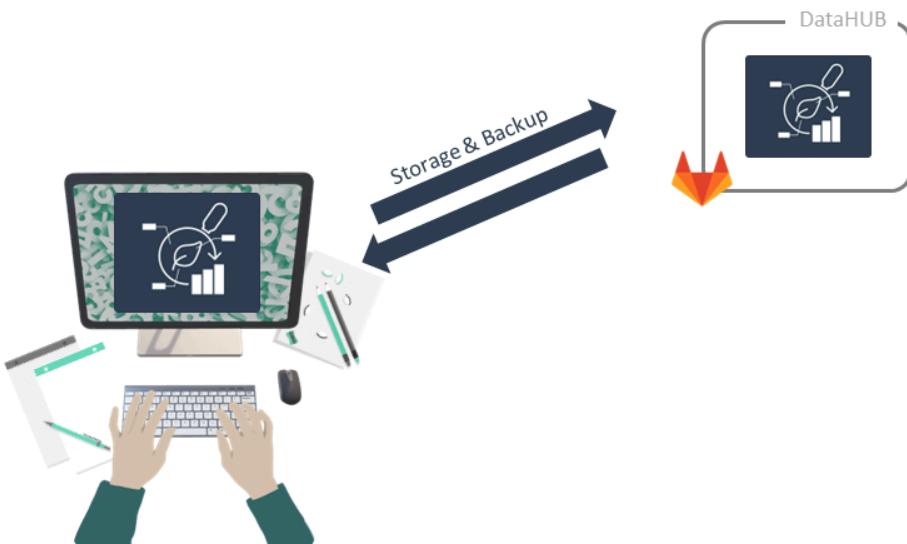


Annotated Research Context (ARC)

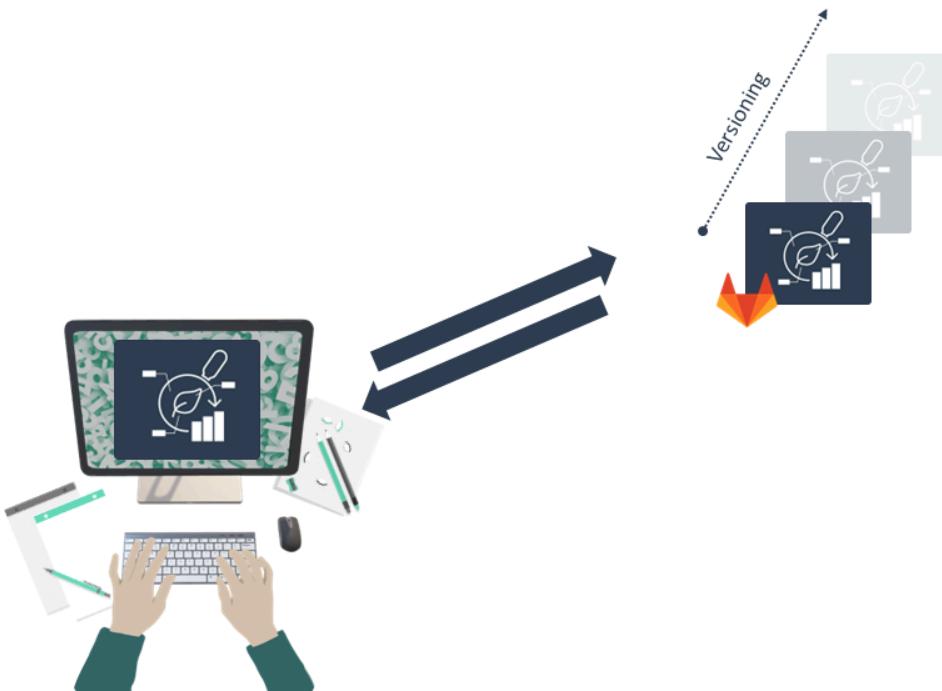


Your entire investigation in a single unified bag

You can store your ARC in the DataHUB



ARCs are versioned



You can invite collaborators



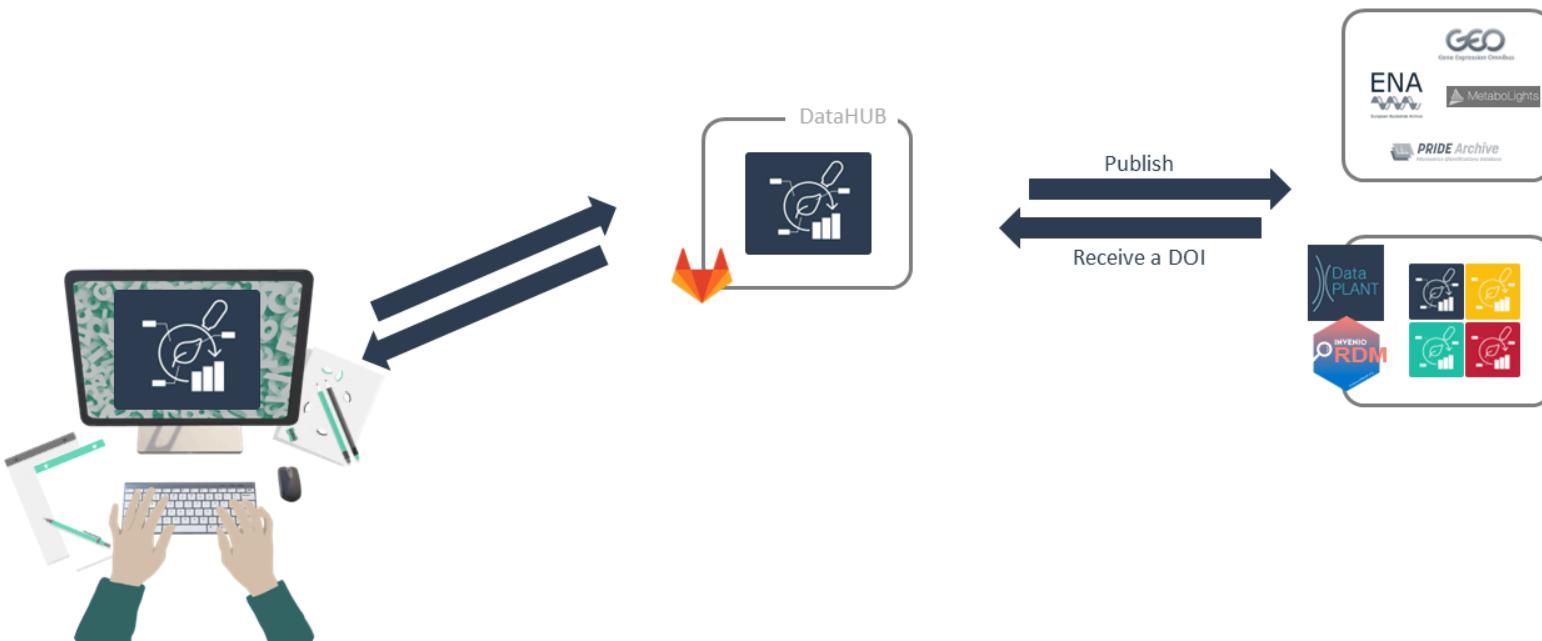
Collaborate and contribute



Reuse data in ARCs



Publish your ARC



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

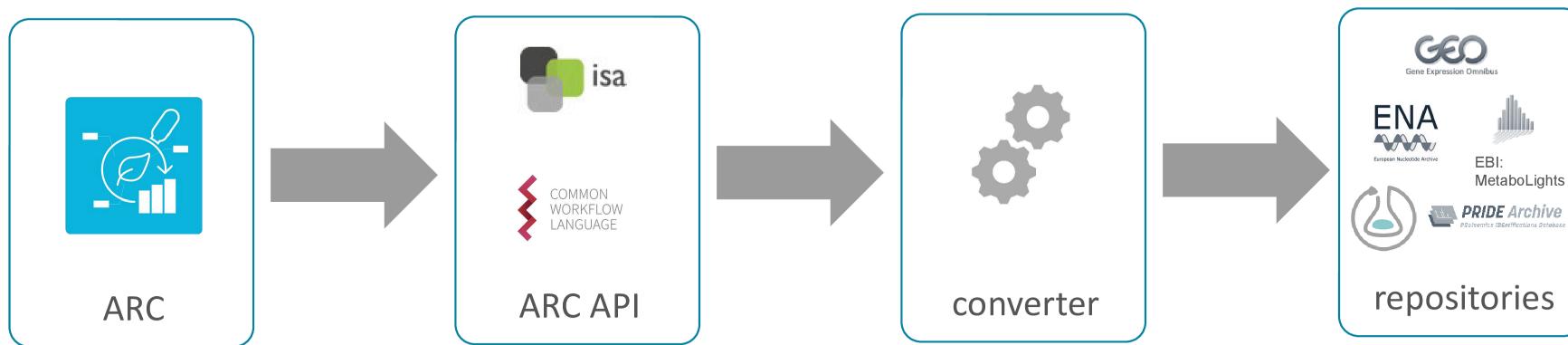
OpenAIRE

The Dataverse® Project

INVENIO

data publication

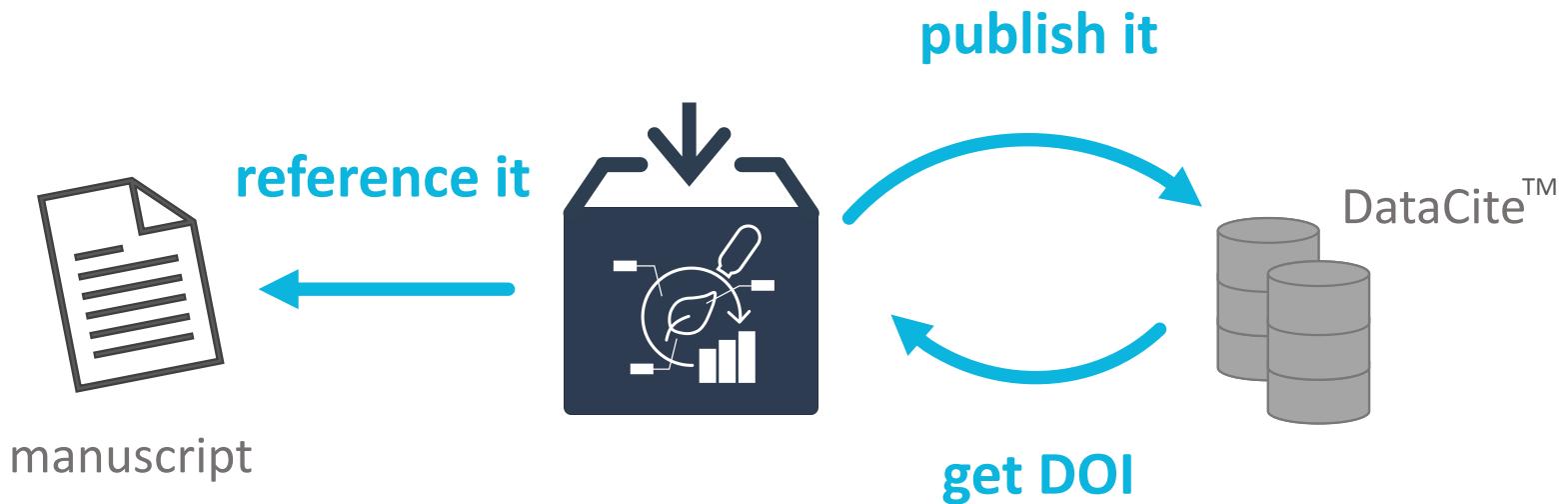
From ARC to repositories



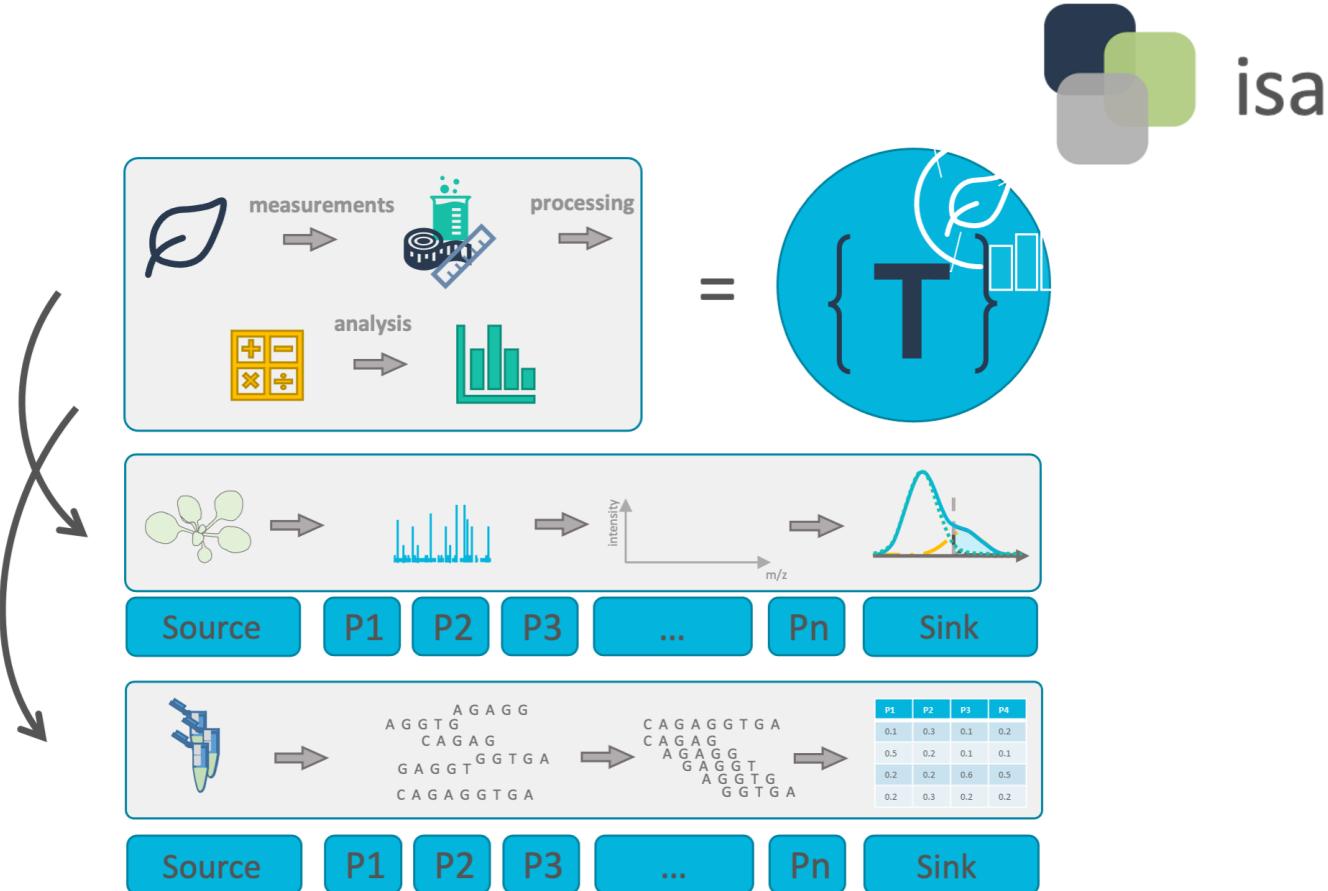
Moving from paper to data publications



Publish your ARC, get a DOI

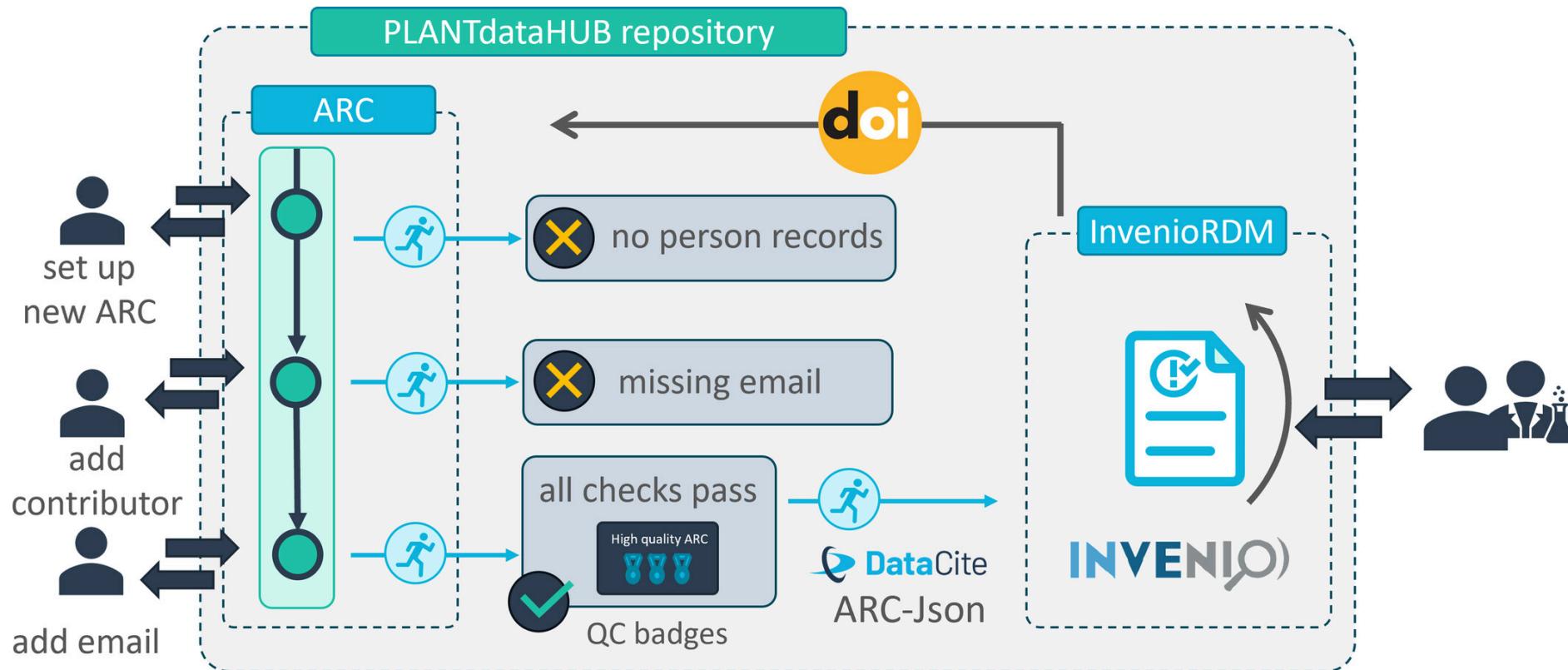


Metadata templates

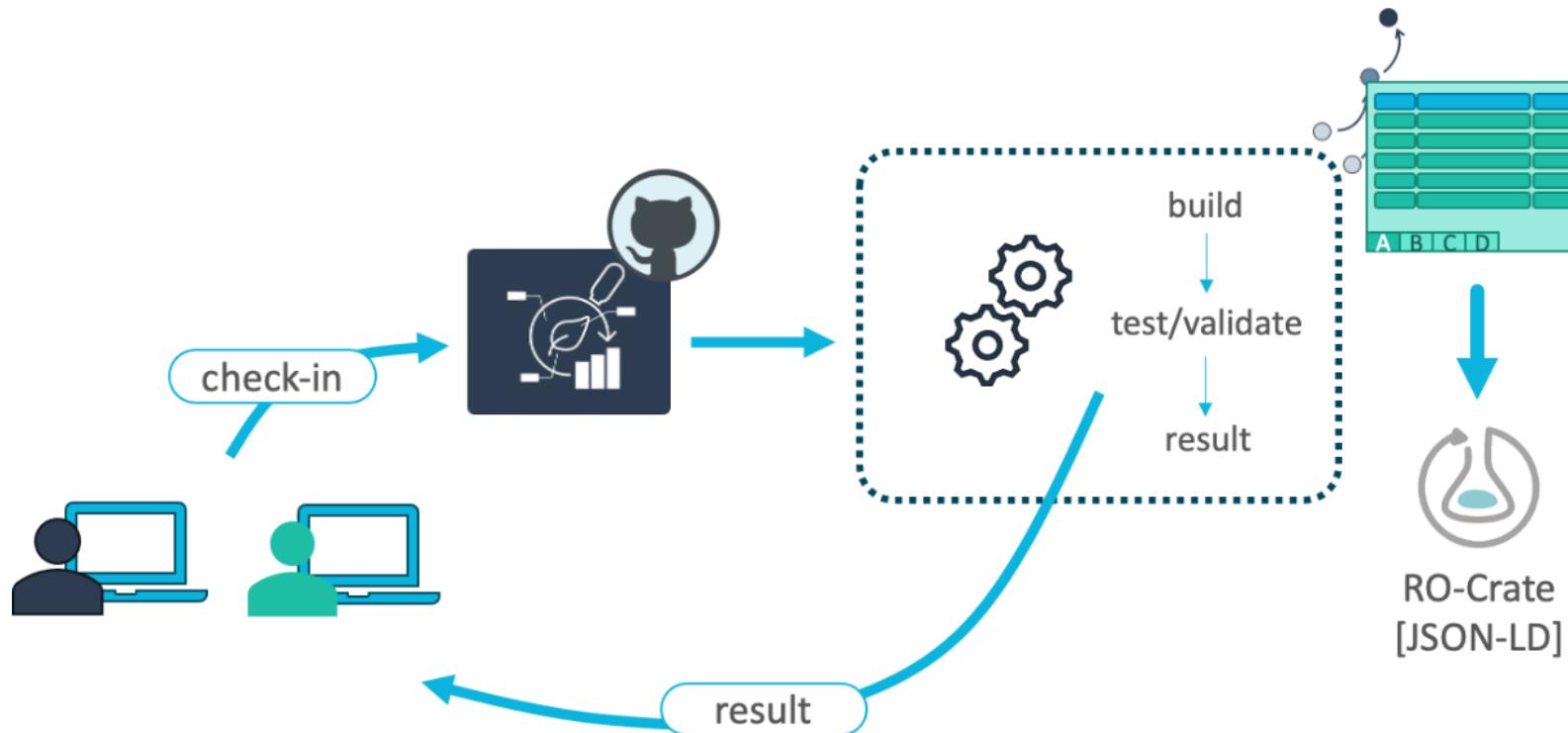


Facilities and labs can define their common workflows as templates

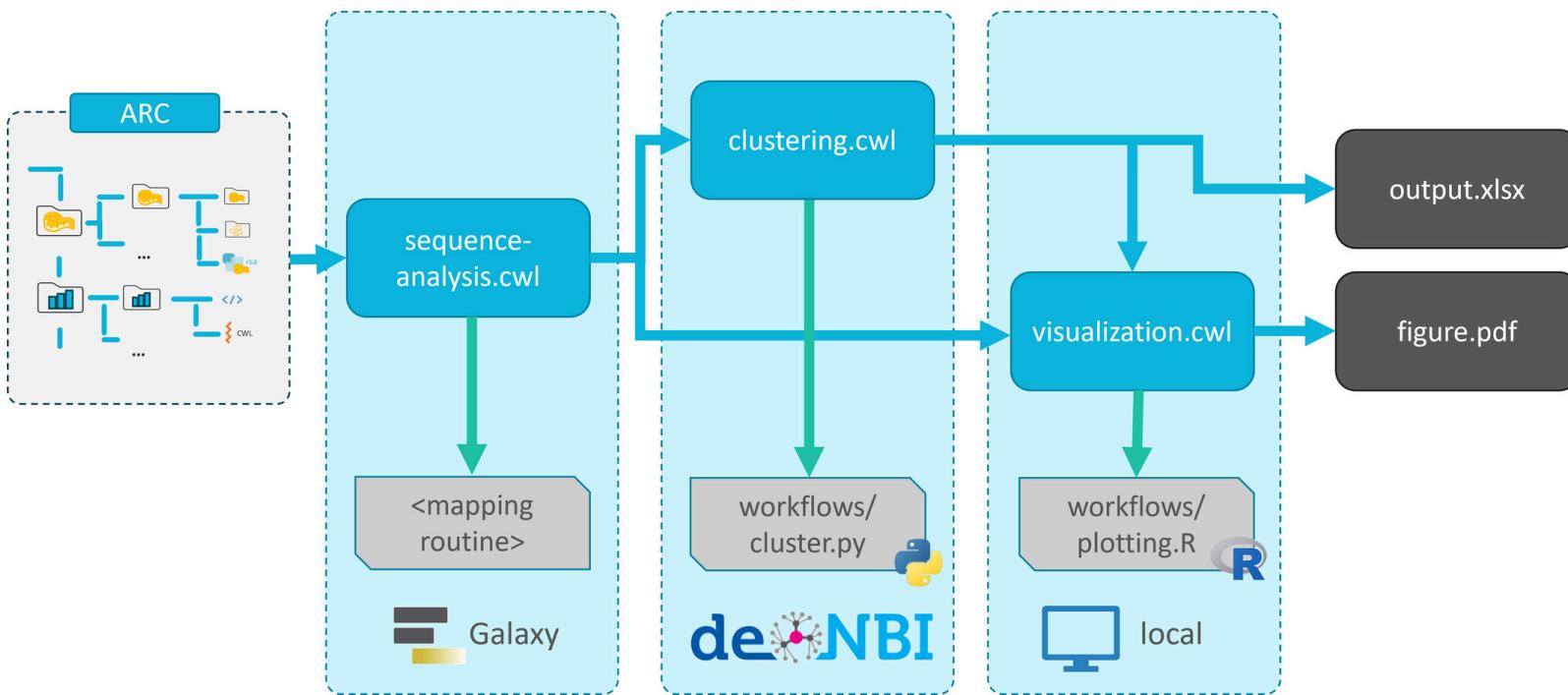
Validate & publish



Learning from Open-Source-Software development



Data analysis and workflows



Galaxy integration: Extra value for plant research

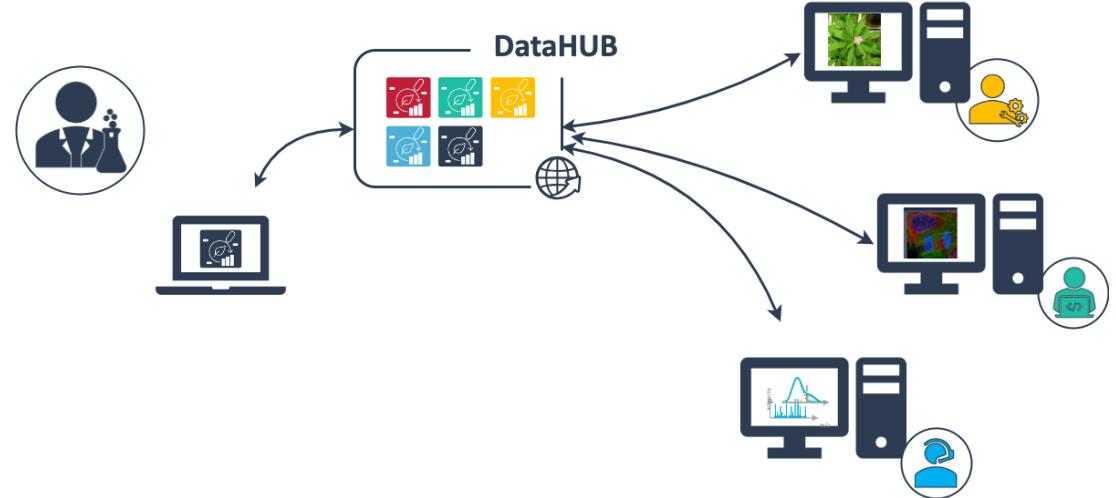


e.g. <https://plants.usegalaxy.eu>

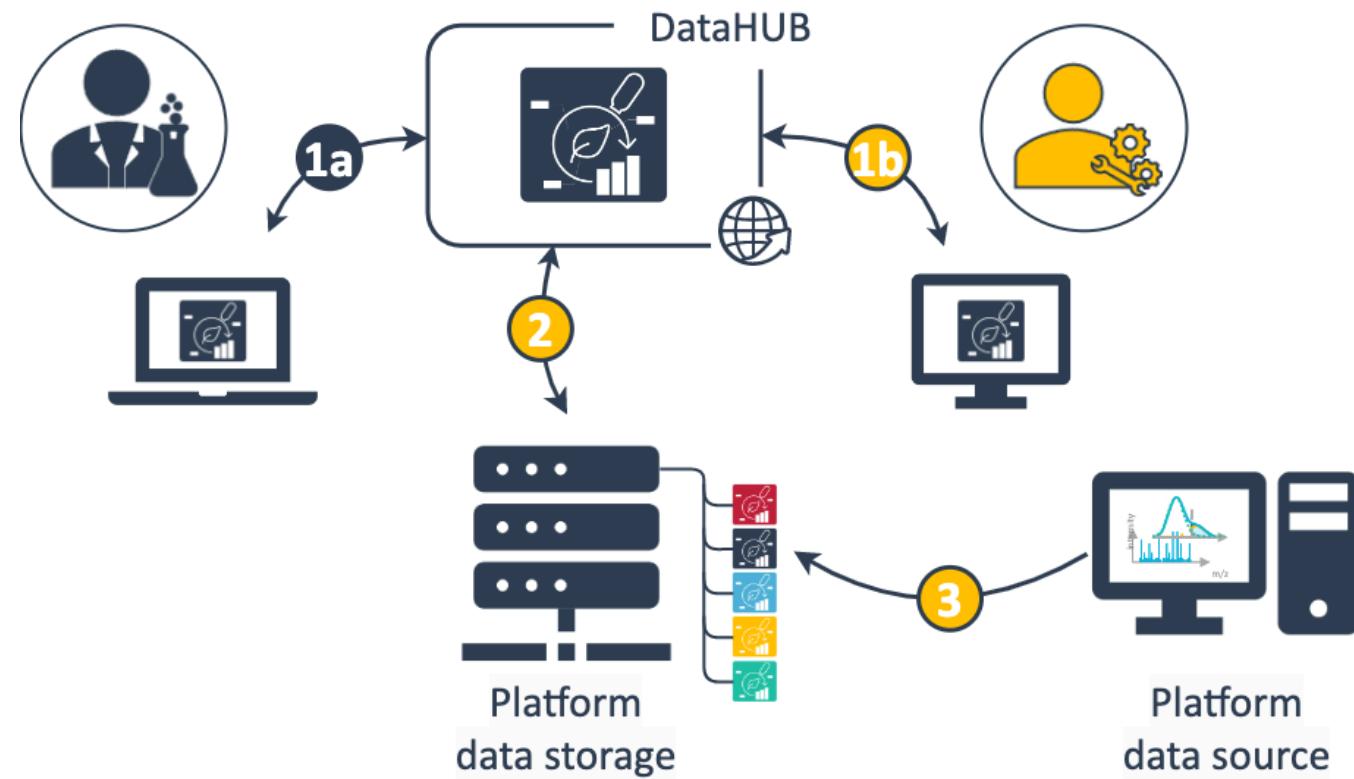
- Full ARC compatibility
- Automated metadata generation
- Specialized tools and workflows for ‘omics processing and analysis
- Public repository compatibility
- Galaxy teaching resource for data analysis

Enabling platforms

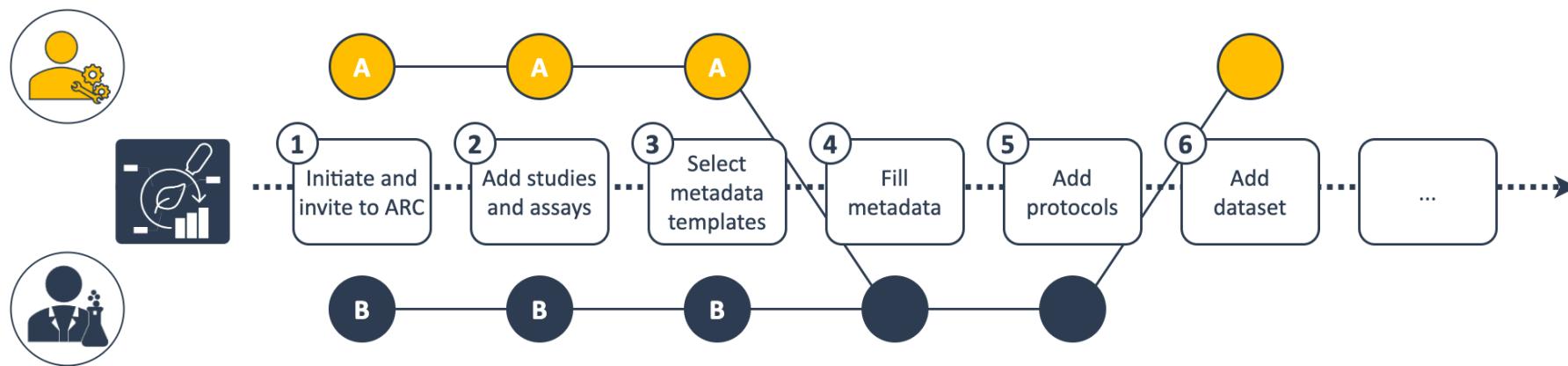
- Streamlined exchange of (meta)data
- Communication and project management



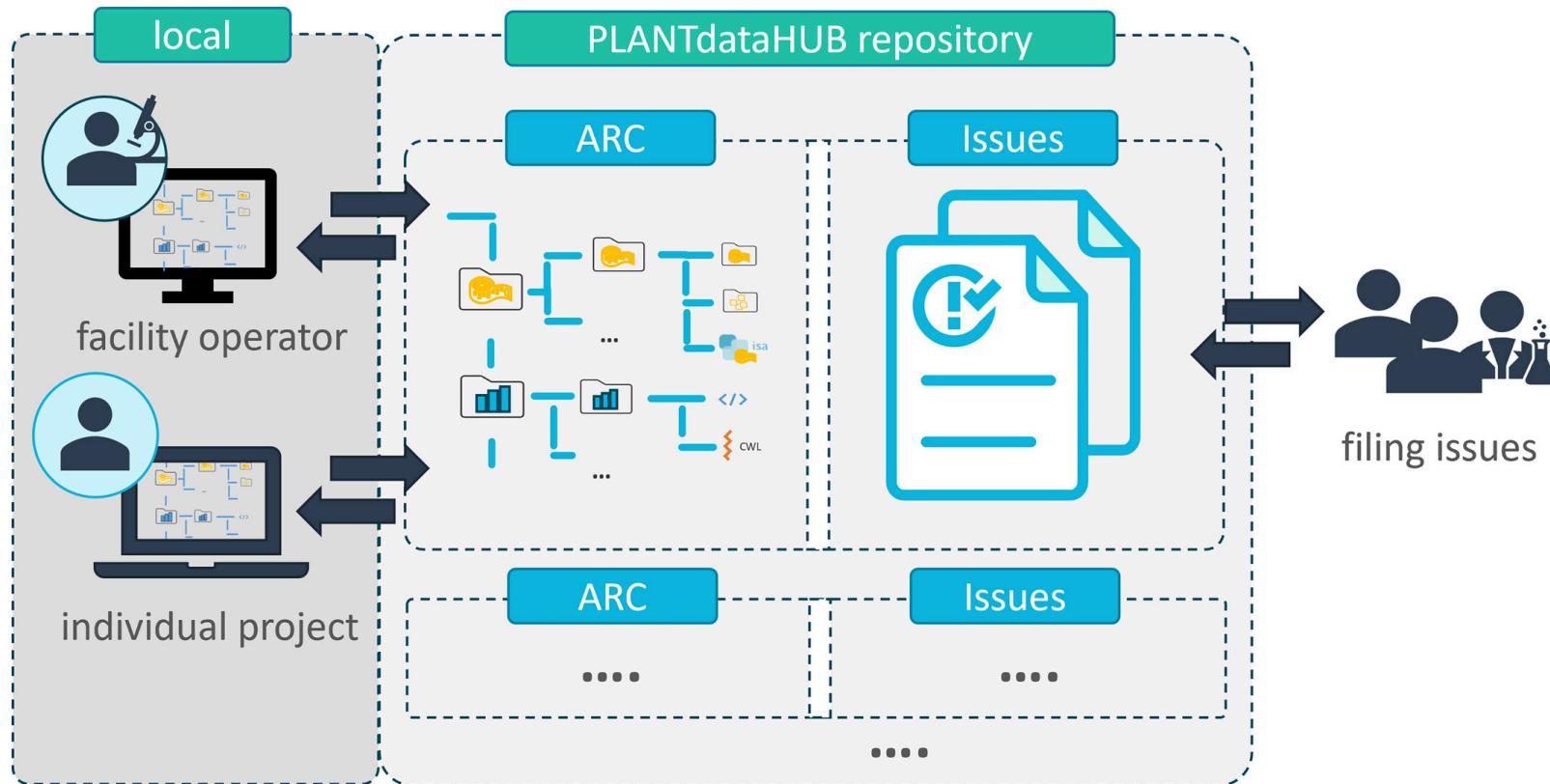
Streamlined data exchange



Meet your collaborators in an ARC

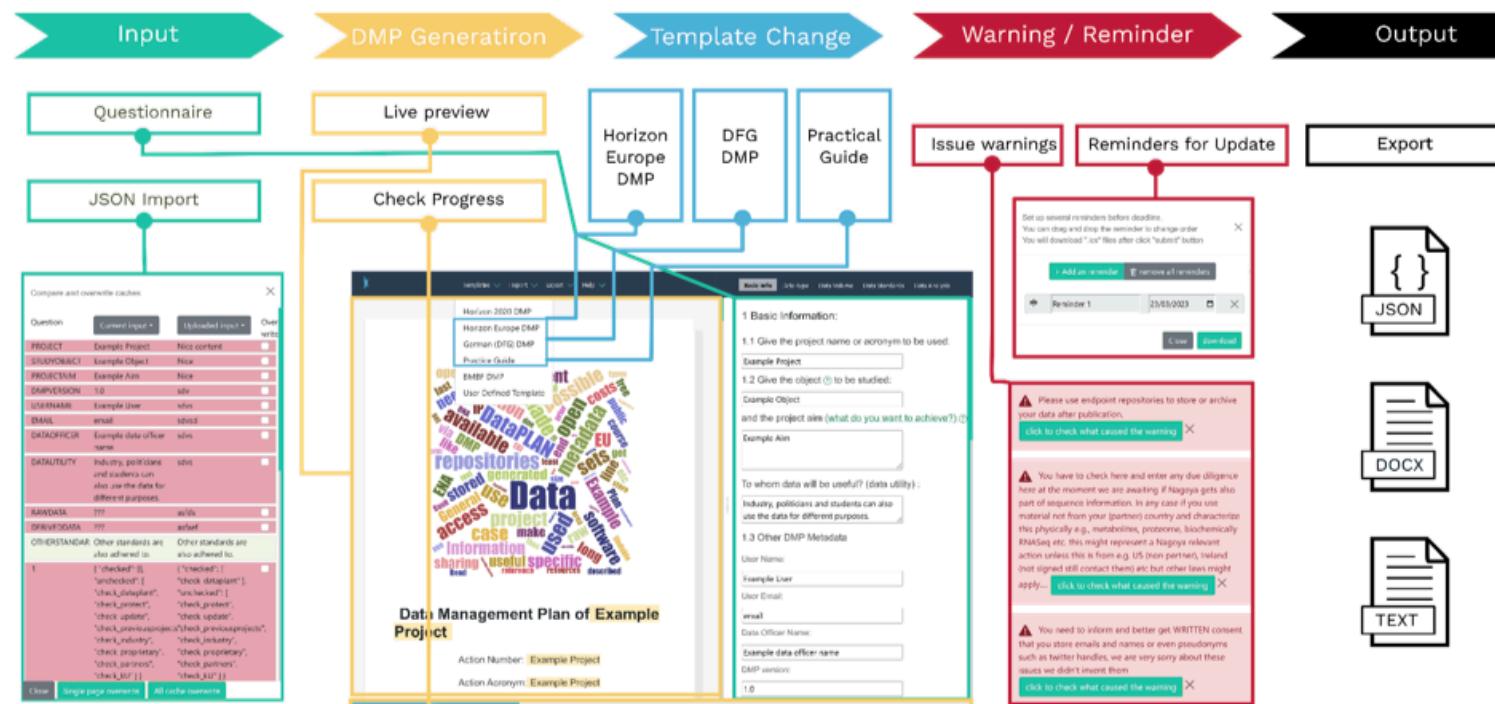


Project management



DataPLAN – a DataPLANT DMP generator

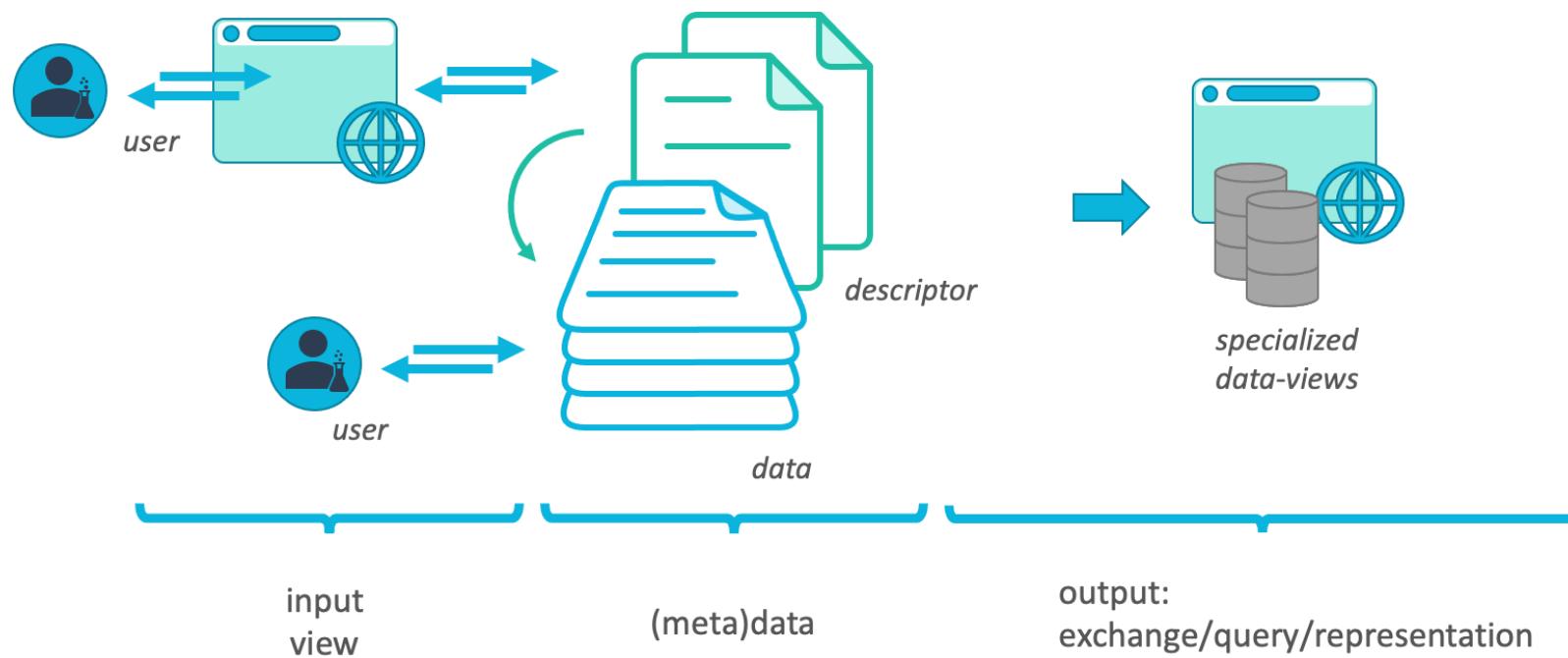
<https://dmpg.nfdi4plants.org>



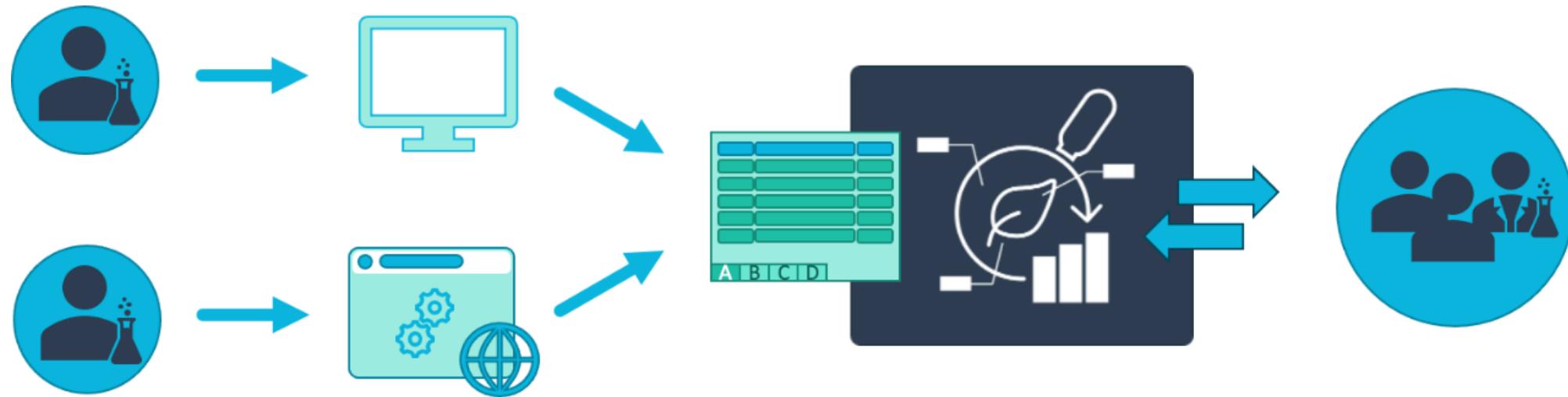
Zhou et al. (2023), DataPLAN: a web-based data management plan generator for the plant sciences, bioRxiv 2023.07.07.548147; doi: <https://doi.org/10.1101/2023.07.07.548147>

Everything is a file

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

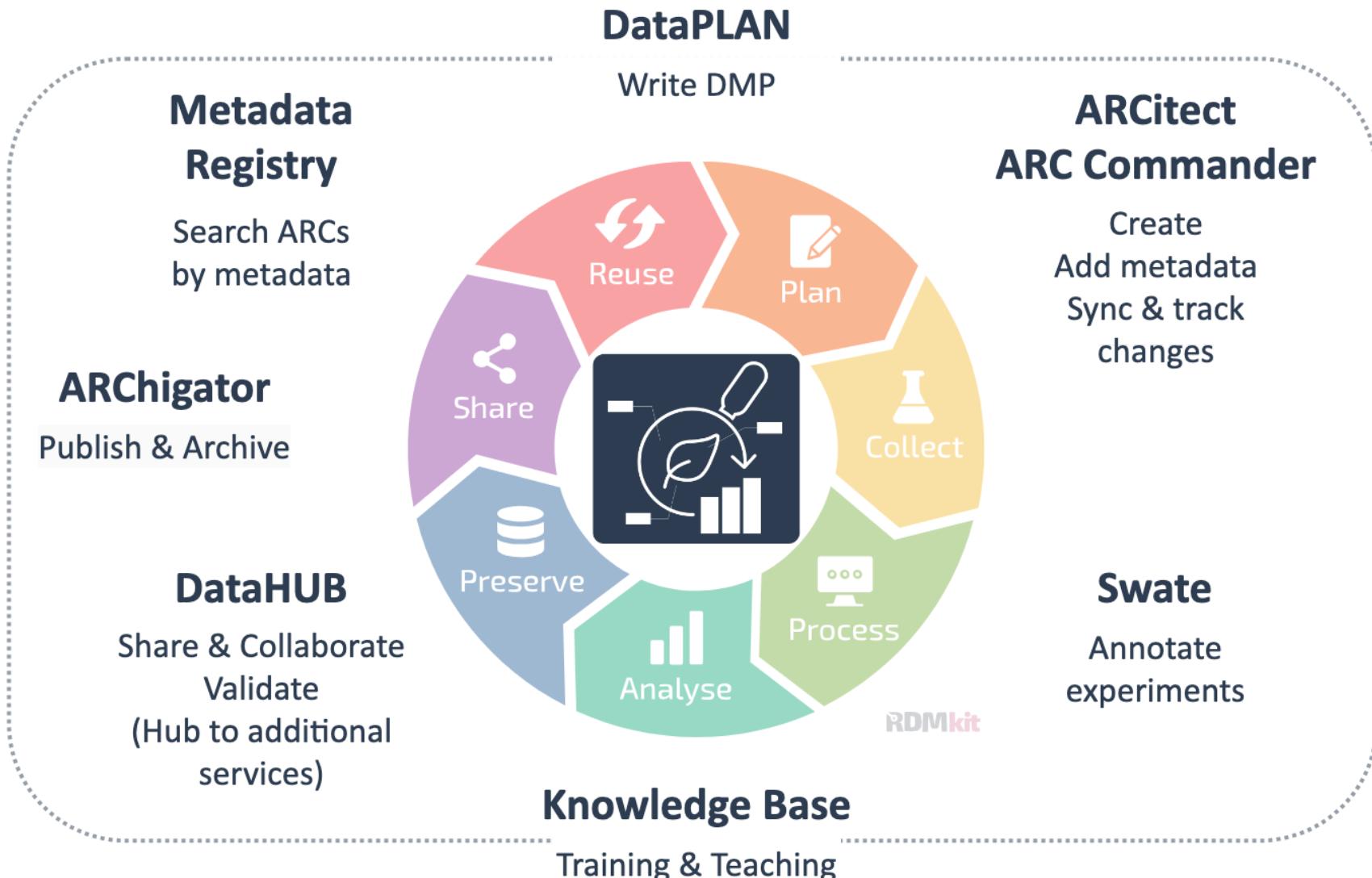


No technical lock-in

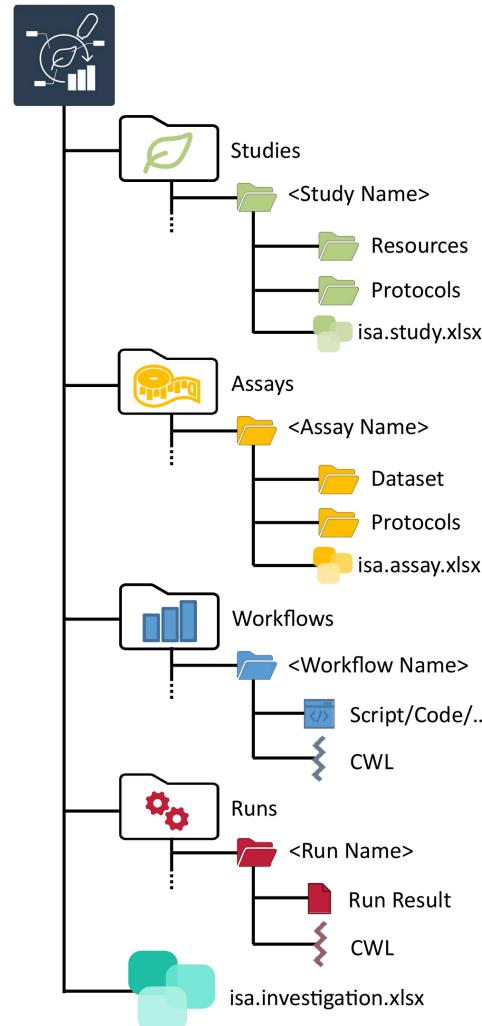


(Meta)data transparency with tool assistance but **no technical lock-in**

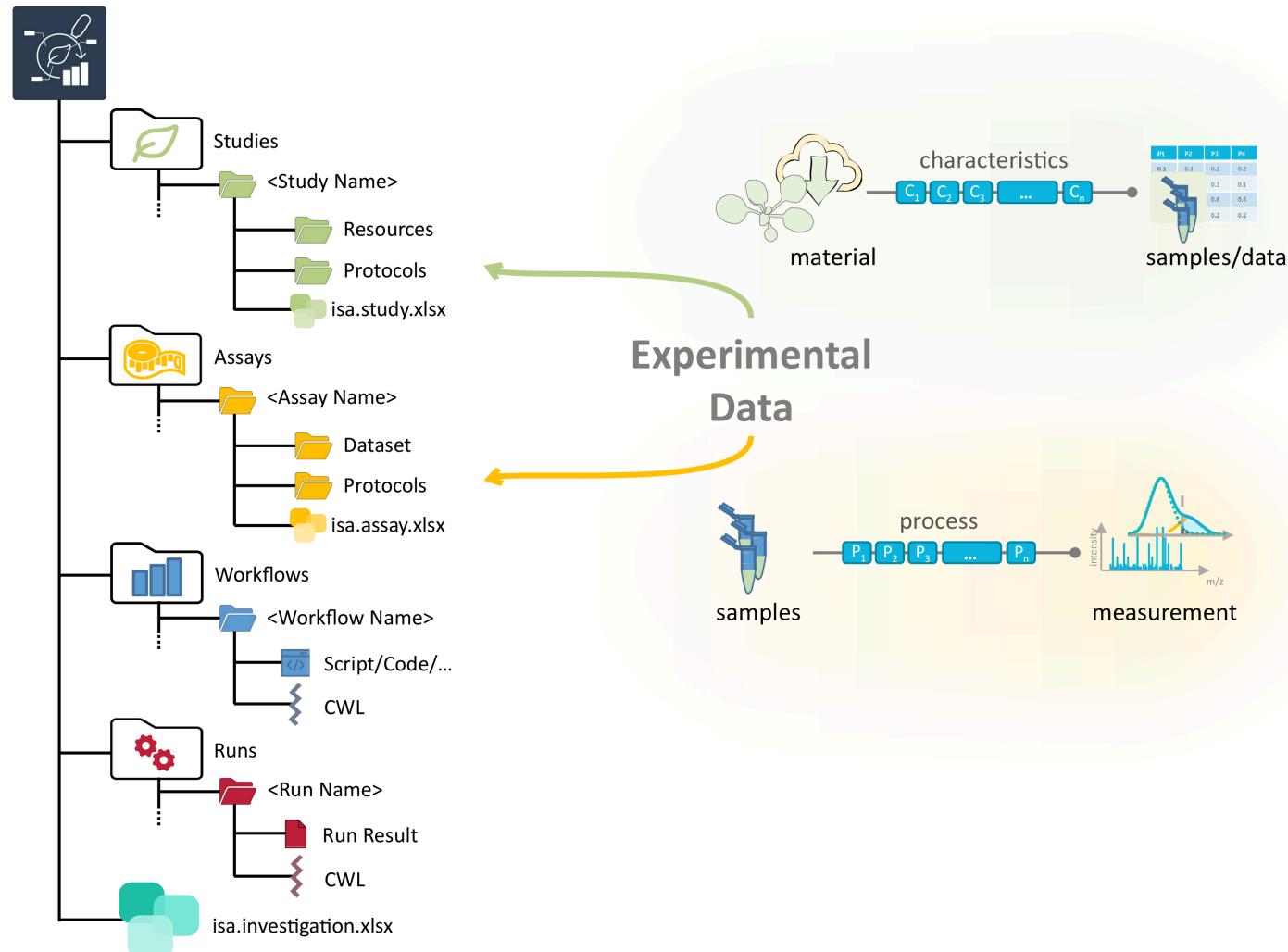
The ARC ecosystem



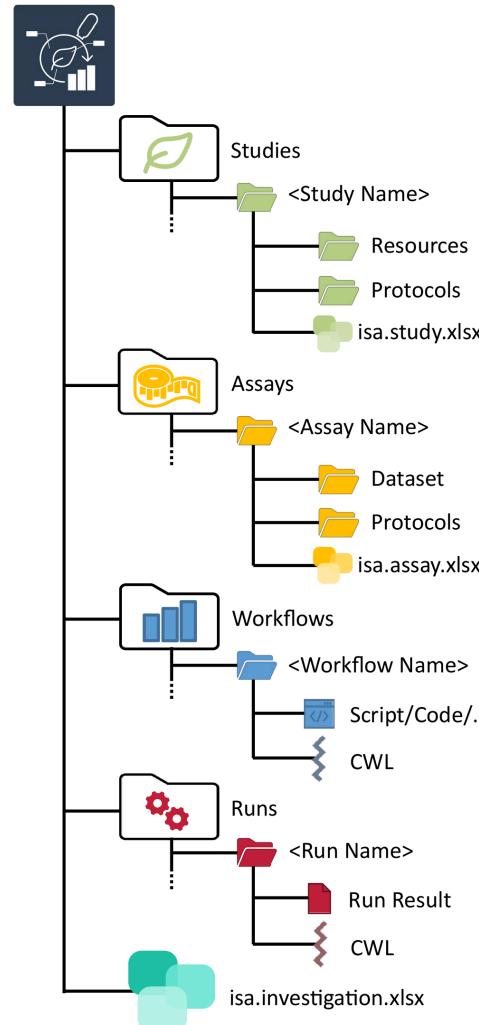
What does an ARC look like?



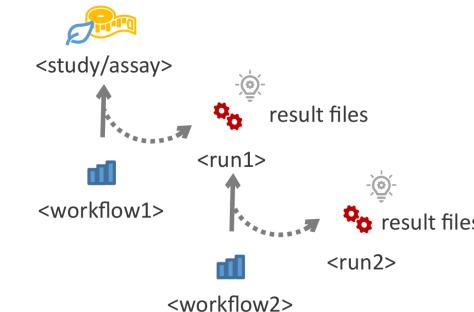
ARCs store experimental data



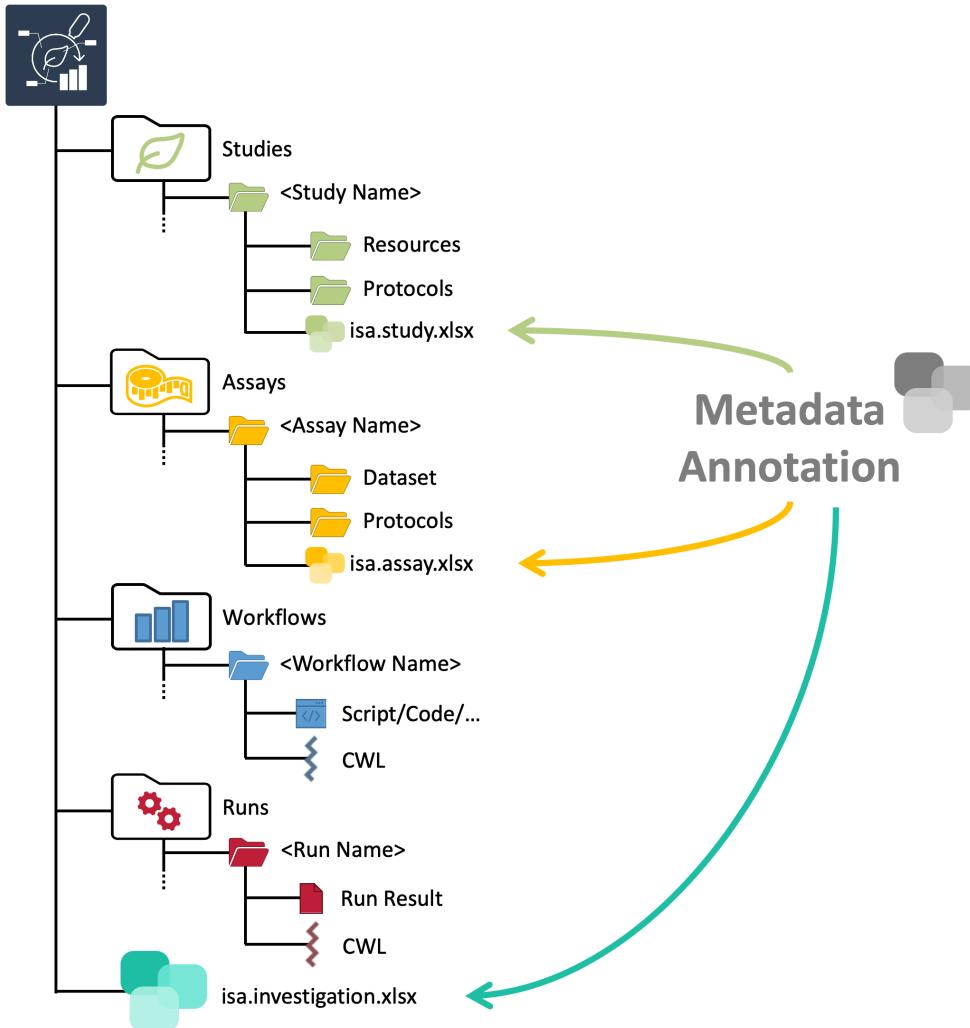
Computations can be run inside ARCs



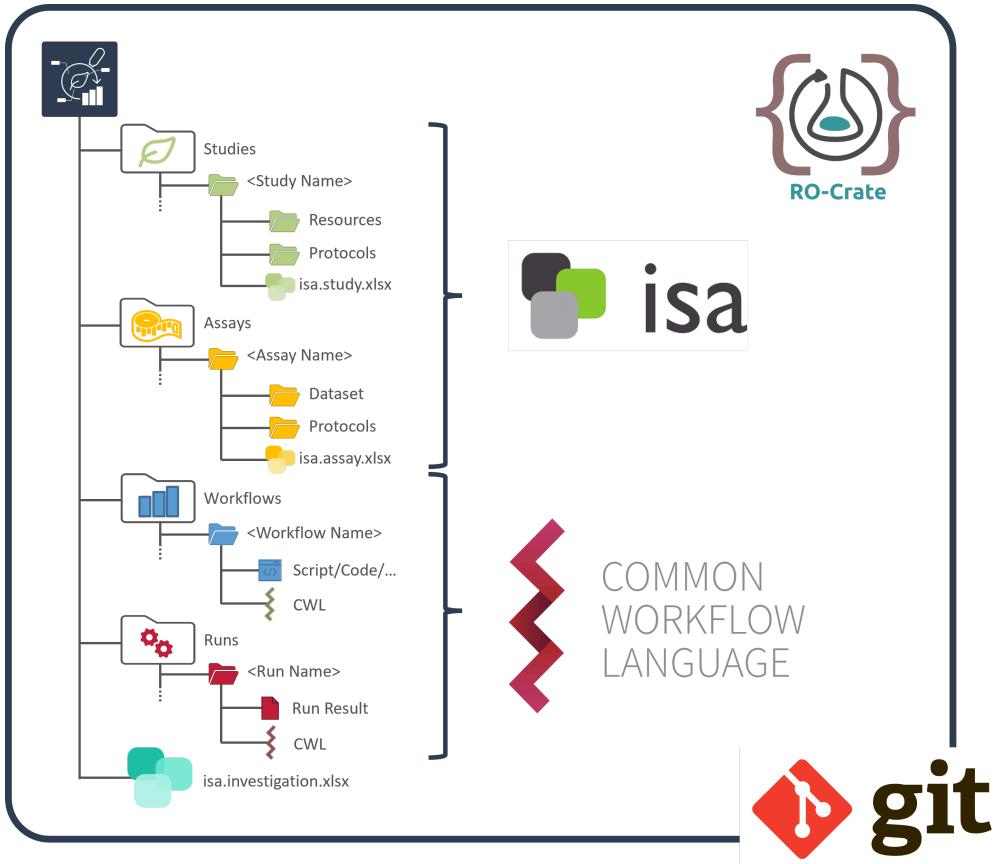
Data analysis
Computation



ARCs come with comprehensive metadata

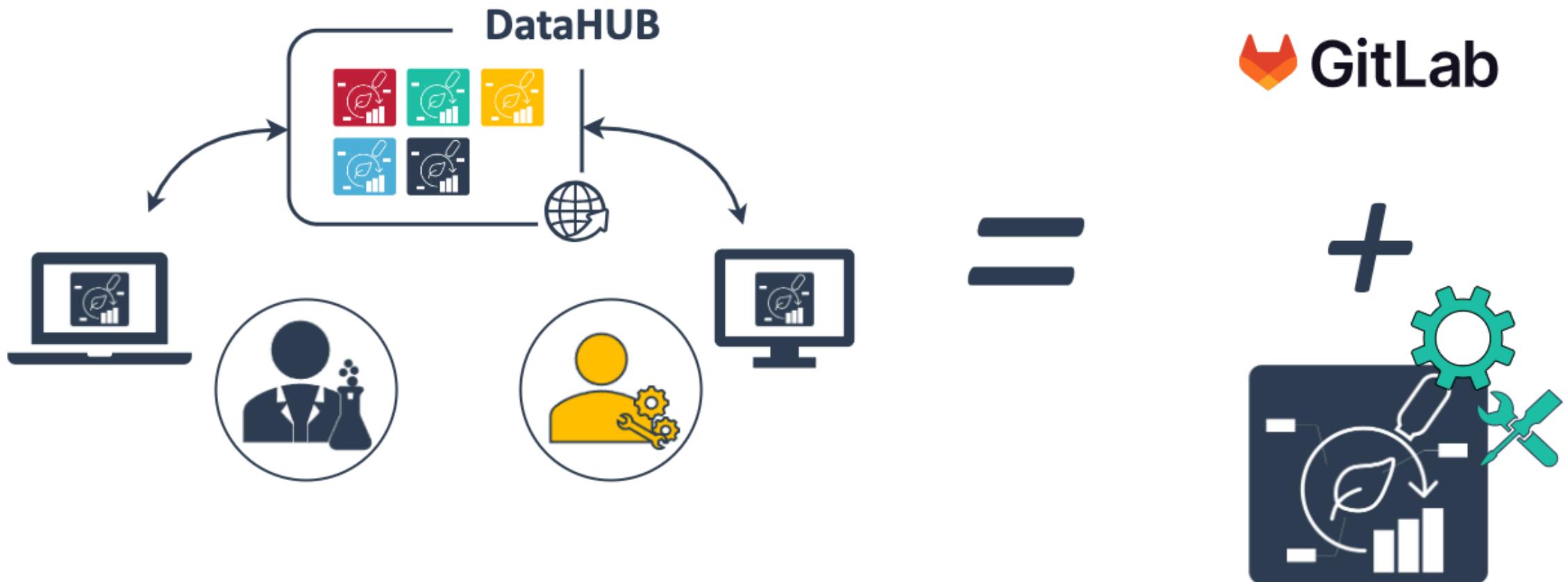


ARC builds on standards

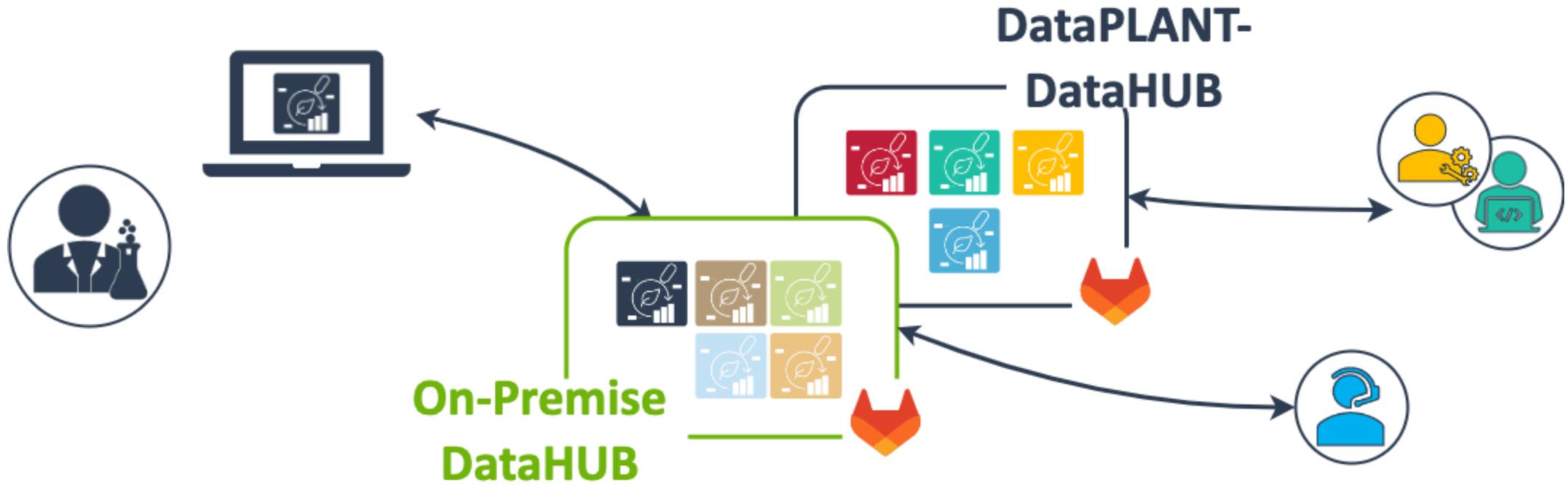


- RO-Crate: standardized exchange
- ISA: structured, machine-readable metadata
- CWL: reproducible, re-usable data analysis
- Git: version control

The DataPLANT DataHUB – a GitLab *Plus*

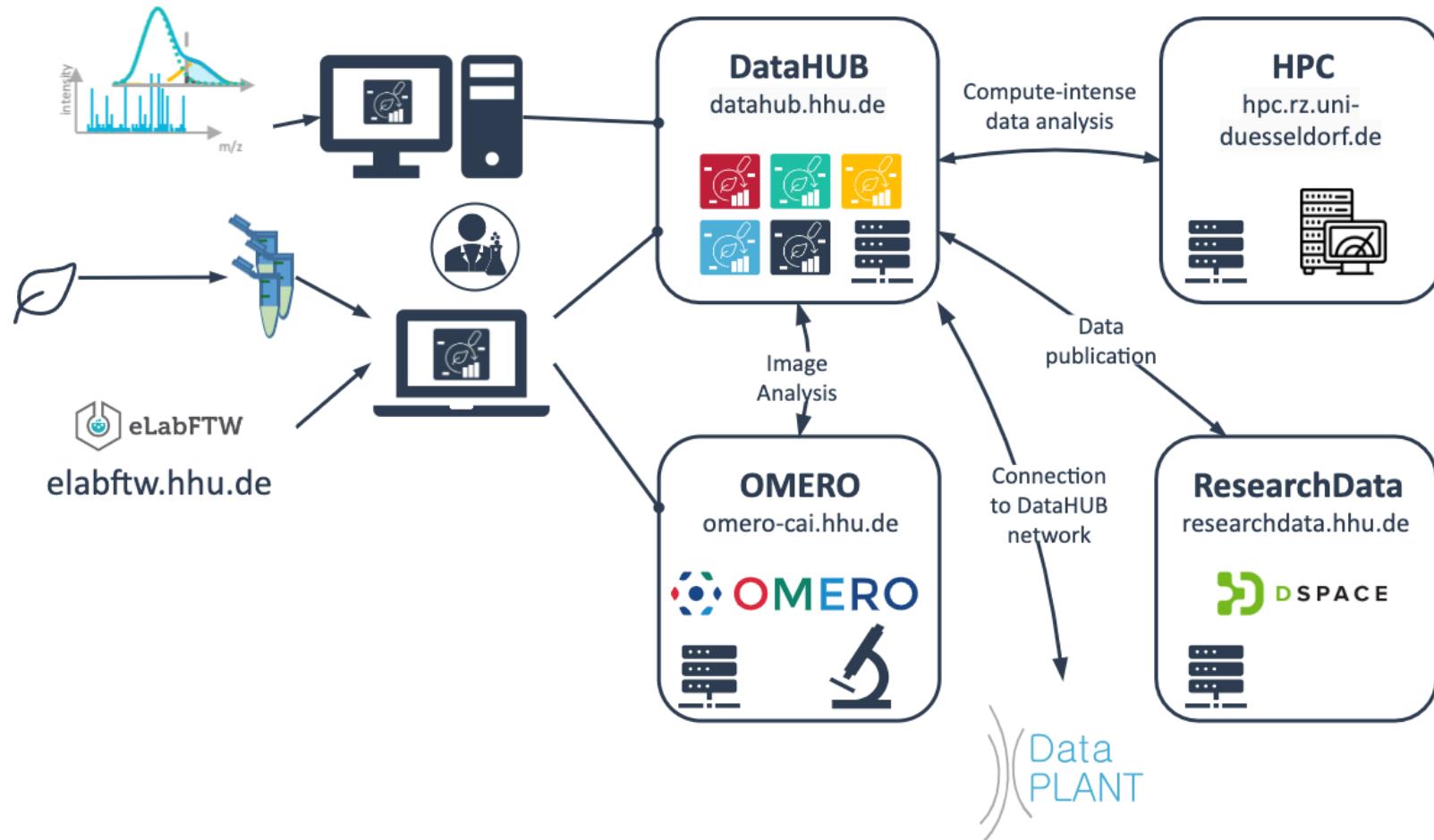


On-premise DataHUBs



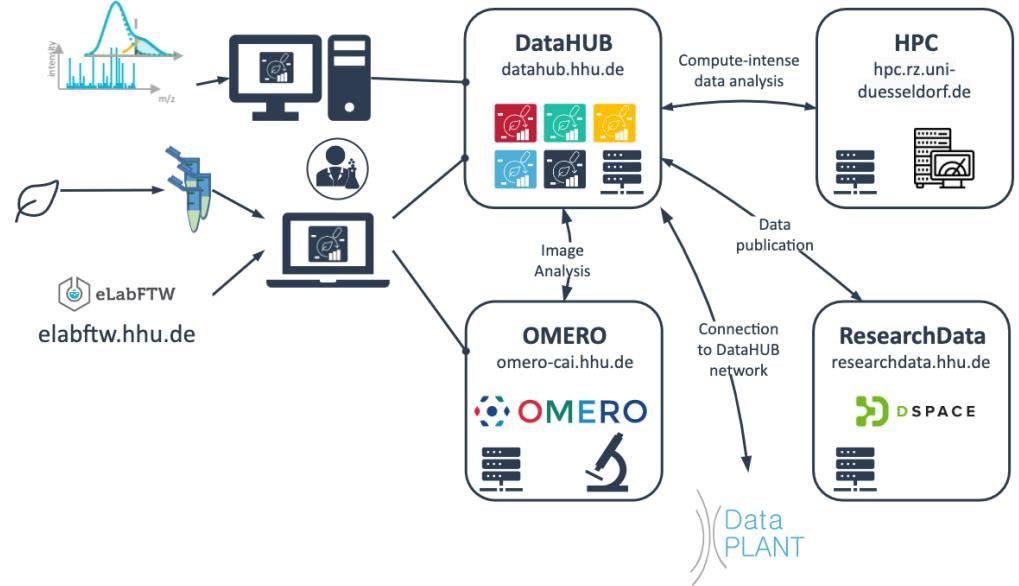
ARC services are available as on-premise option

HHU-DataHUB

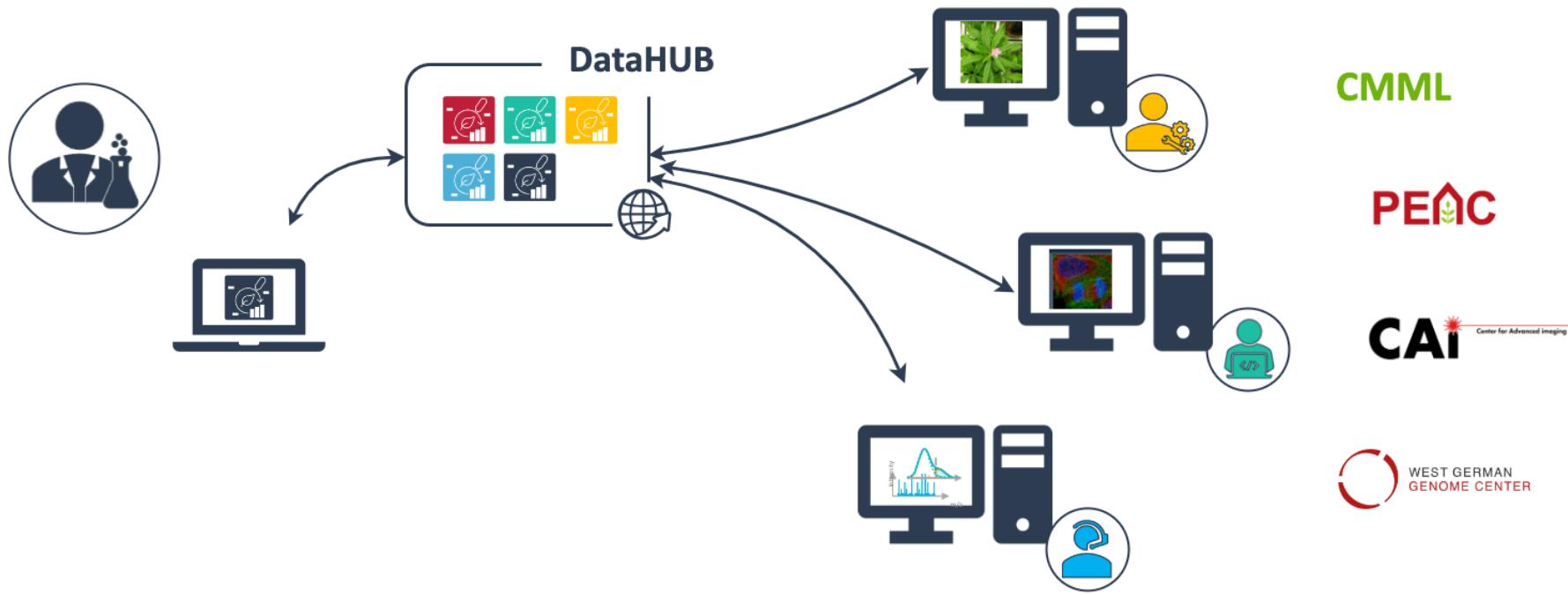


HHU-DataHUB

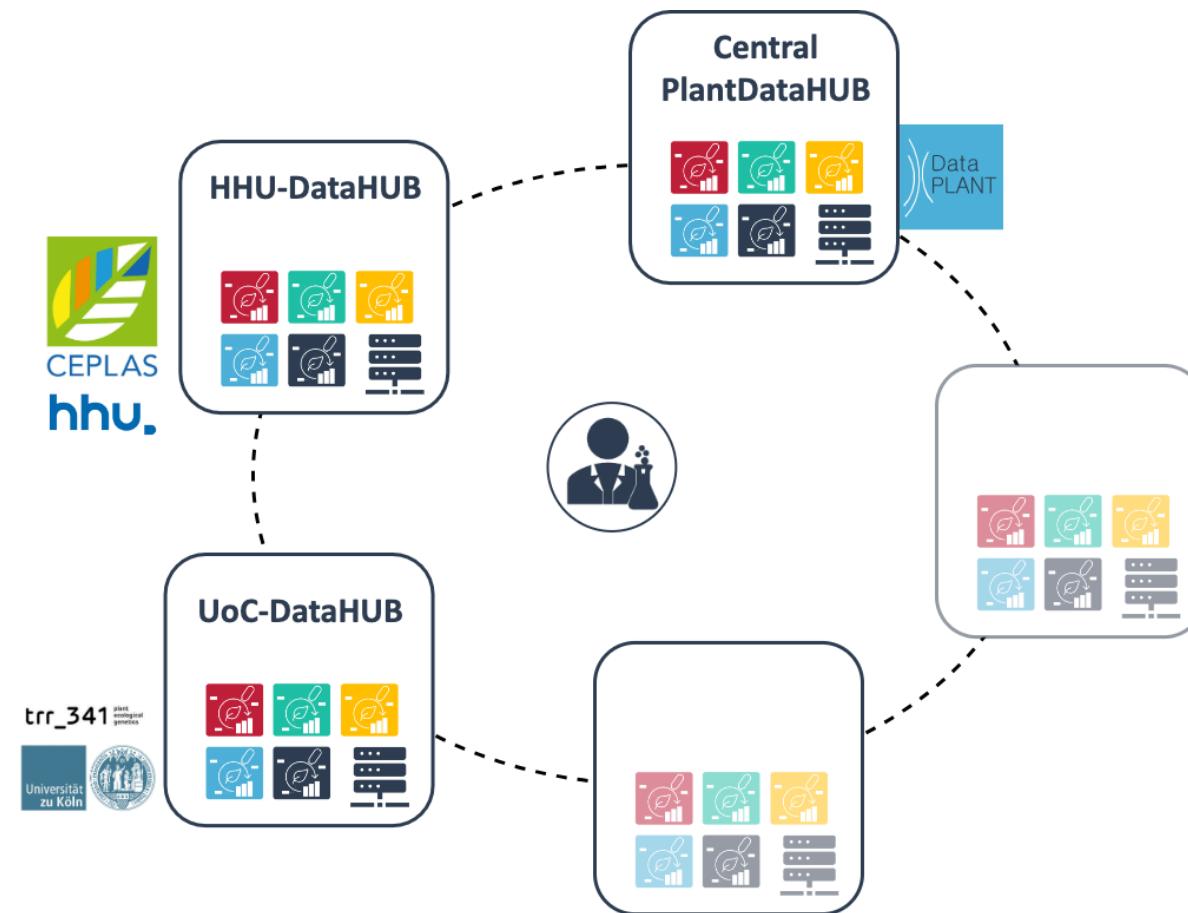
- FAIR data along the research data cycle
- Structured exchange of (meta)data
- Local (long-term) storage, backup, version control
- Integration of existing services and infrastructure
- External collaboration



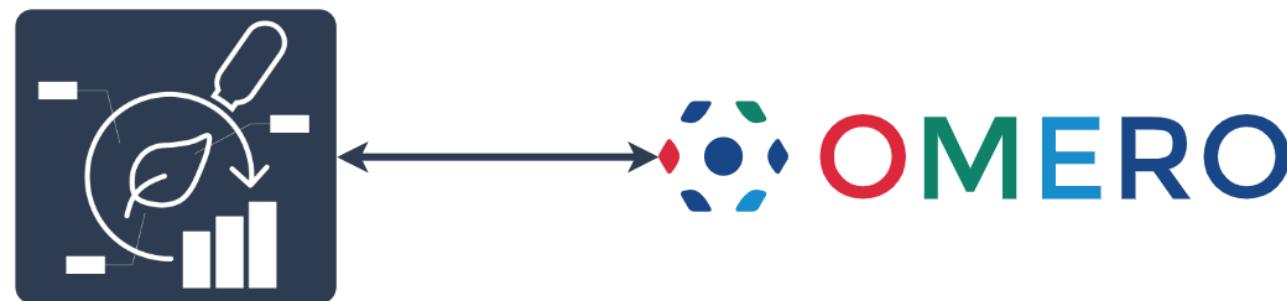
HHU-DataHUB – Node for platforms



Embedded into an RDM network



CEPLAS collaborates with DataPLANT and NFDI4BIOIMAGE



ARCitect Hands-on

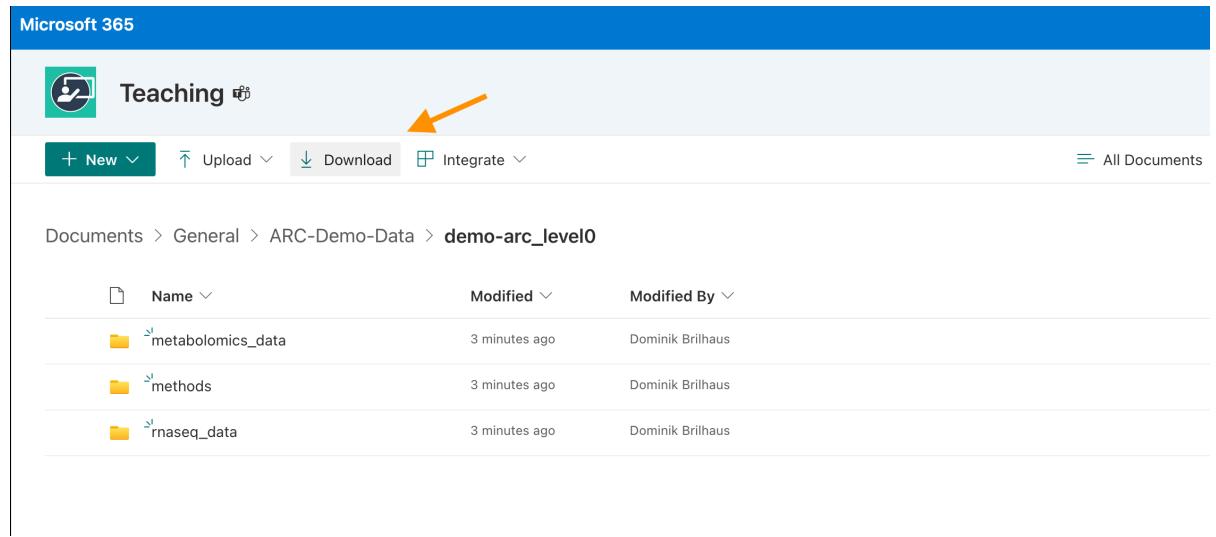
ARCitect installation

Please install version **v0.0.31** (or later) of the ARCitect:

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

Download the demo data

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



Microsoft 365

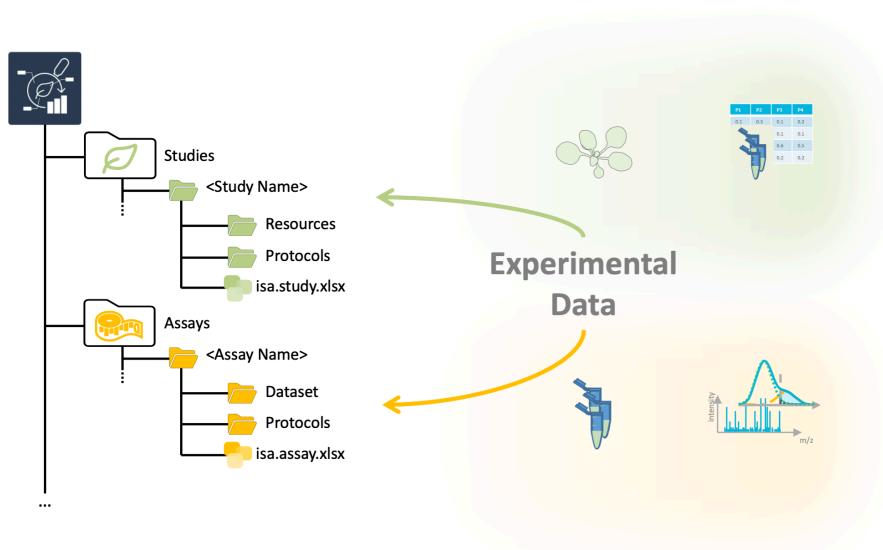
Teaching

+ New ▾ Upload ▾ Download ▾ Integrate ▾ All Documents

Documents > General > ARC-Demo-Data > **demo-arc_level0**

Name	Modified	Modified By
metabolomics_data	3 minutes ago	Dominik Brilhaus
methods	3 minutes ago	Dominik Brilhaus
rnaseq_data	3 minutes ago	Dominik Brilhaus

Sort Demo data in an ARC



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

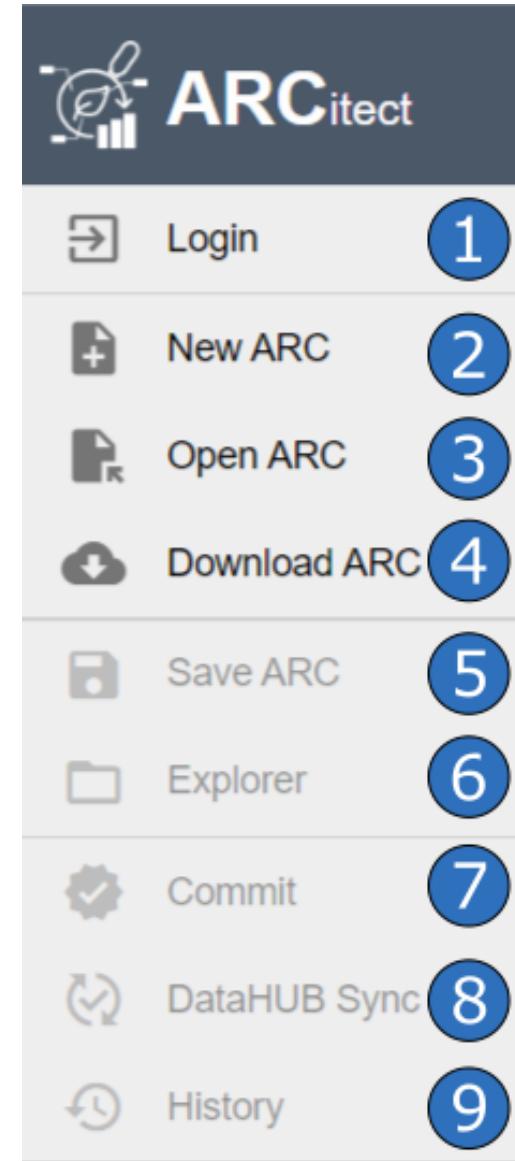
Open ARCitect

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

Please Select a DataHub

Host
git.nfdi4plants.org

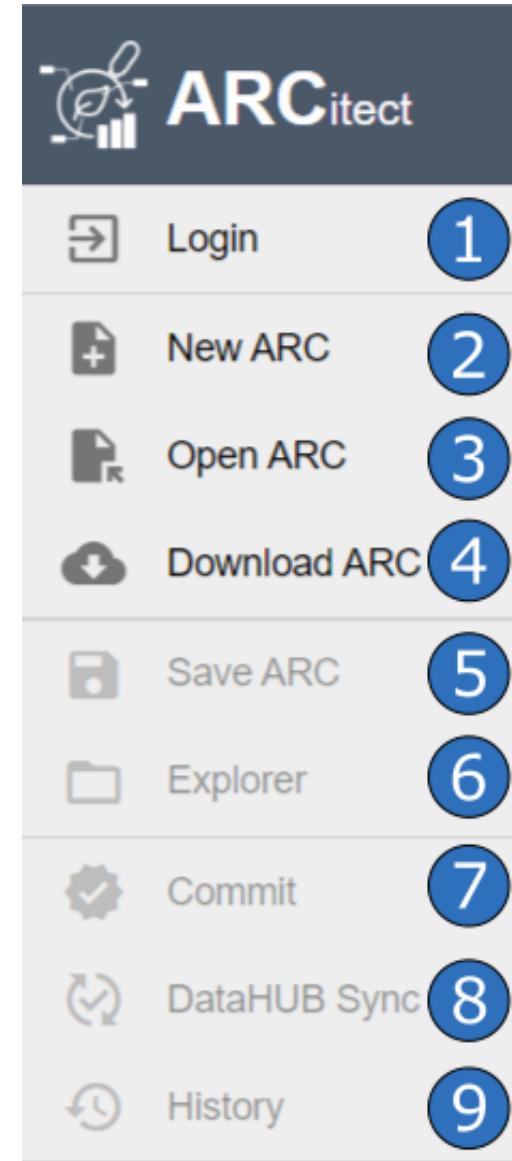
LOGIN CANCEL



Initiate the ARC folder structure

1. Create a **New ARC** (2)
2. 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.
-  [TalinumPhotosynthesis](#)
 - ► assays
 - ► runs
 - ► studies
 - ► workflows

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 a contributor

- you could also add the contacts directly via ORCID

Contacts

Your First Name Your Last Name 6/10

Your ORCID

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

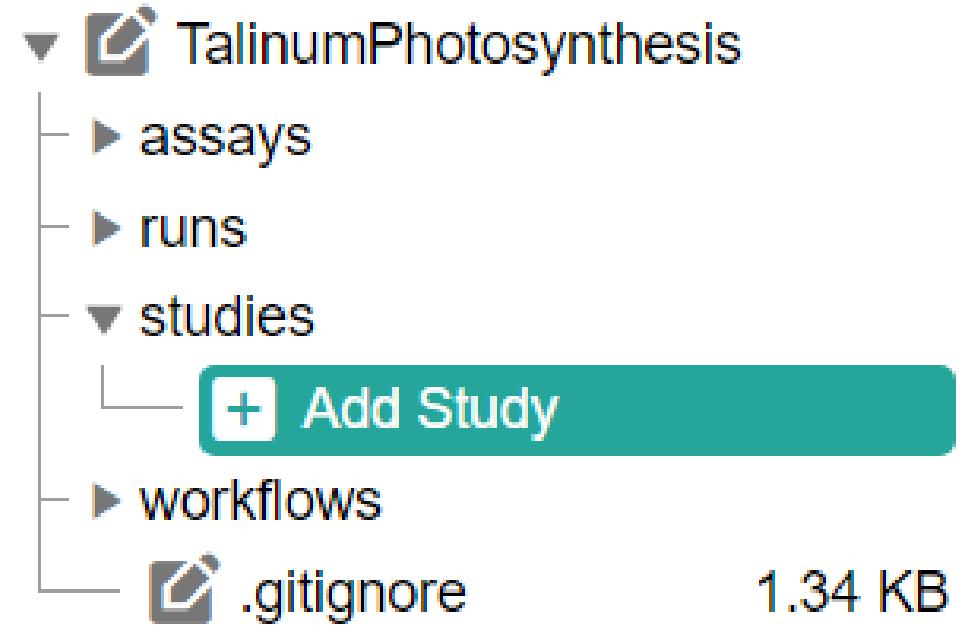
1. Author NCIT NCIT:C42781 X

+ Delete

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 Release Date
tt.mm.jjjj --:--

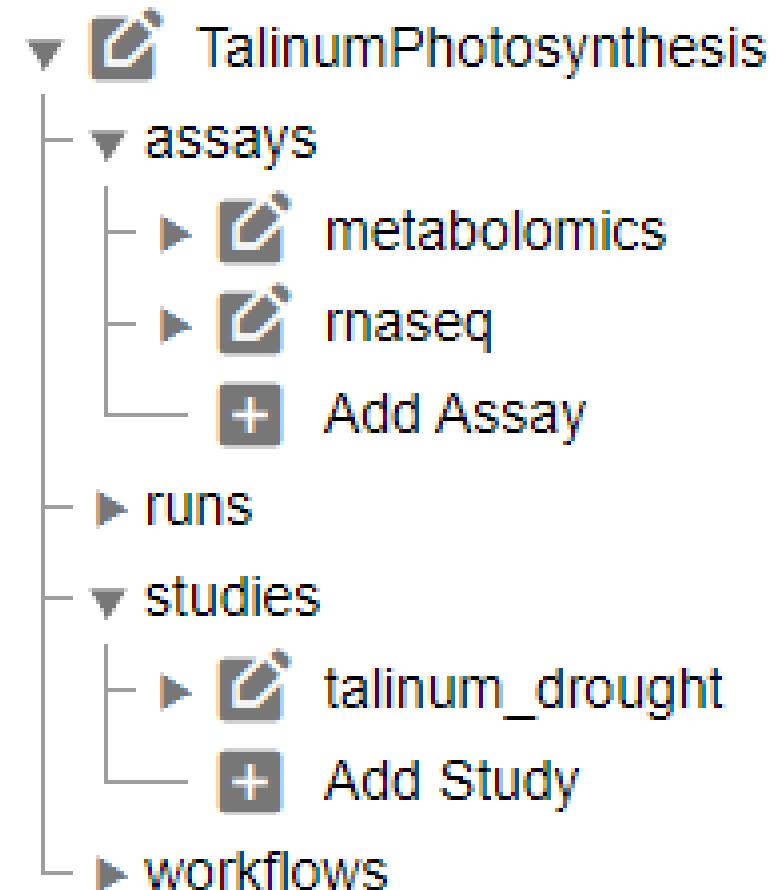
Study Design Descriptors

+

Add an assay

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

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



Link your assay to a study

You can either

- link your new assay to an existing study in your ARC or
- create a new one

Link your assays to your
talinum_drought study

Add Assay

Add Assay
rnaseq

Study Identifiers
talinum_drought 

talinum_drought

 ADD ASSAY CANCEL

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="+"/>		

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

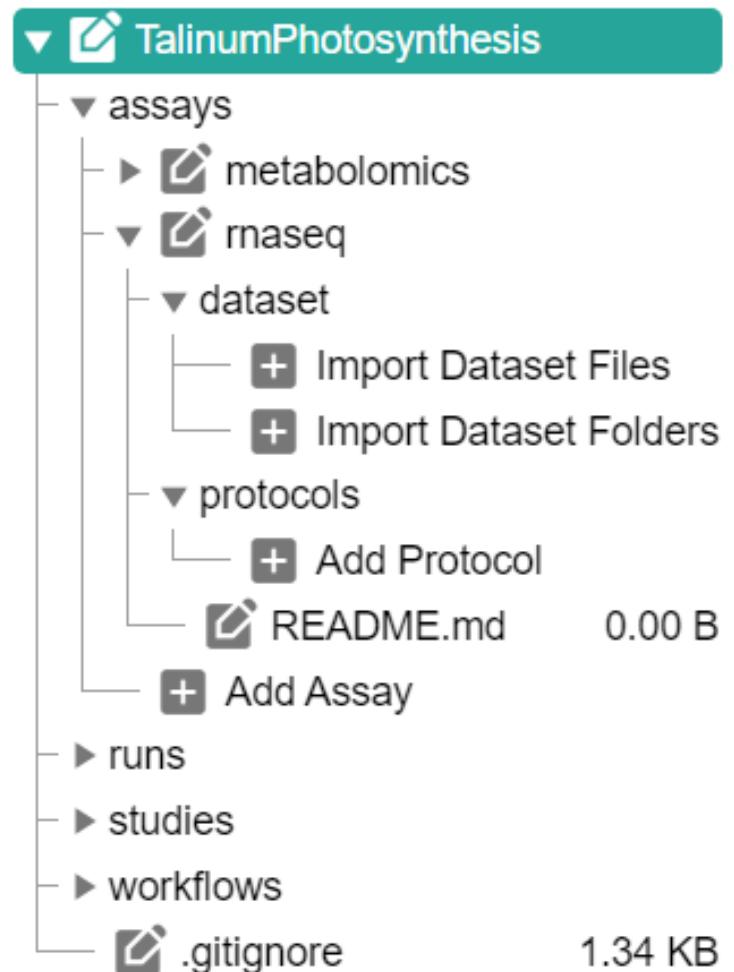
Add protocols and datasets

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.

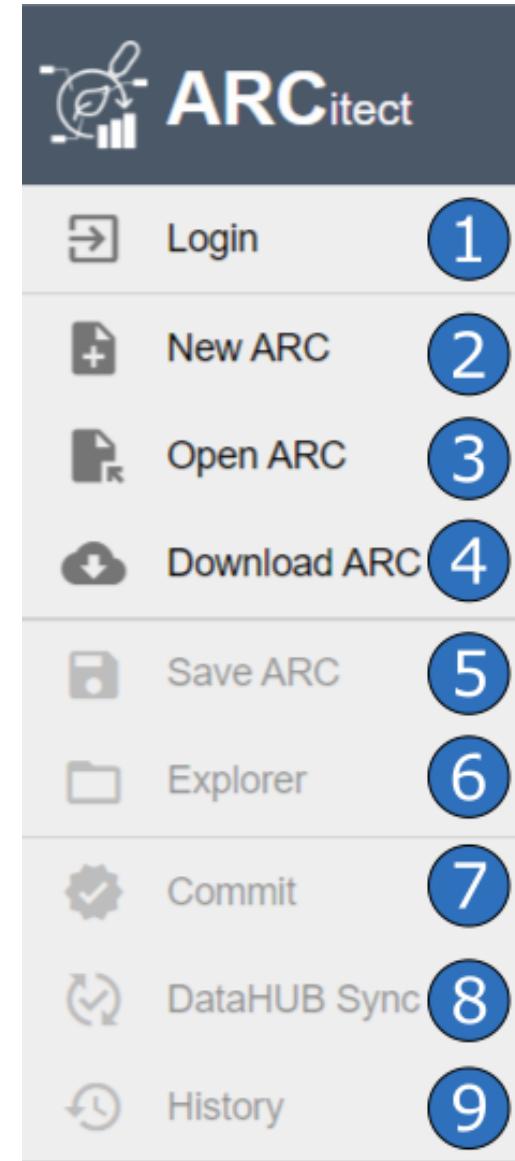


Sort Demo Data to your ARC

- 💡 protocols and multiple datasets can directly be imported via ARCitect

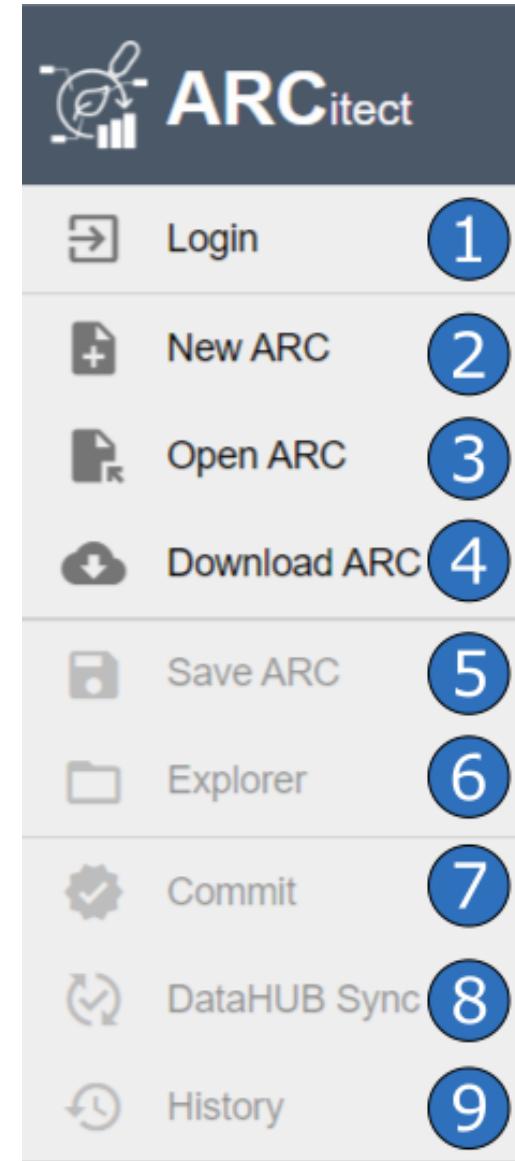
Explorer

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



Commit panel (7)

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



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 DataHUB Commit panel. At the top, there is a header with a gear icon and the text "Commit Changes" and "Track changes of the ARC with git". Below this, there are input fields for "Name" (Sabrina Zander) and "eMail" (sabrina.zander@uni-duesseldorf.de). There are also fields for "Branch" and "Commit Message". A section labeled "Large File Storage Limit in MB" shows the value "1". Below these fields is a "Changes" section with a trash bin icon and the text "No changes to commit". At the bottom right are two buttons: "RESET" and "COMMIT" (highlighted in green).

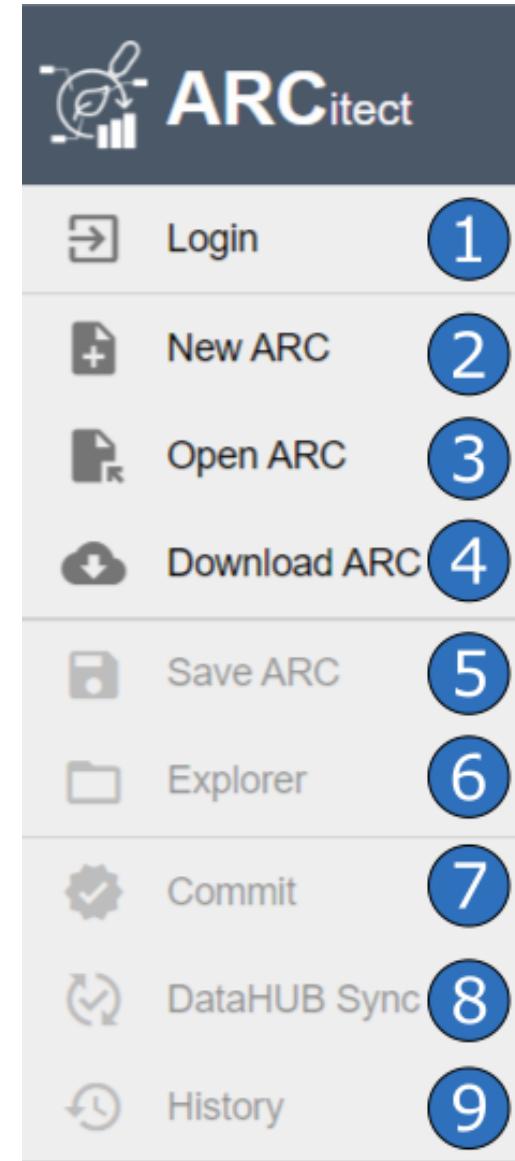
History panel (9)

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

 History	Inspect ARC history
	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

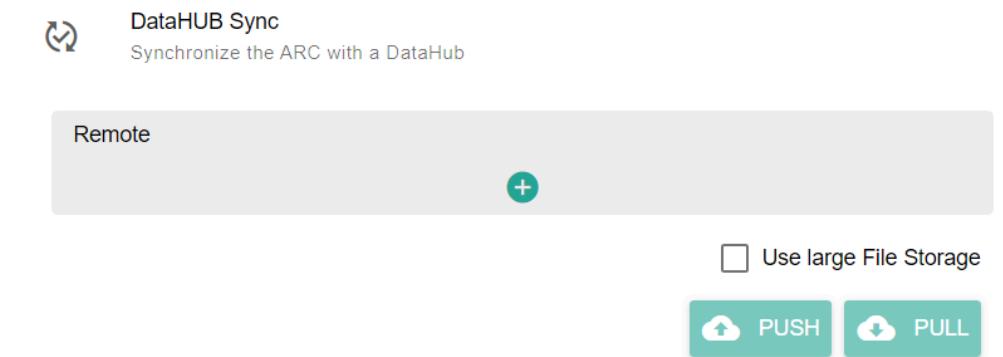
From the sidebar, navigate to **DataHUB Sync** (8)



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

Your ARC is ready

 Initiated an ARC

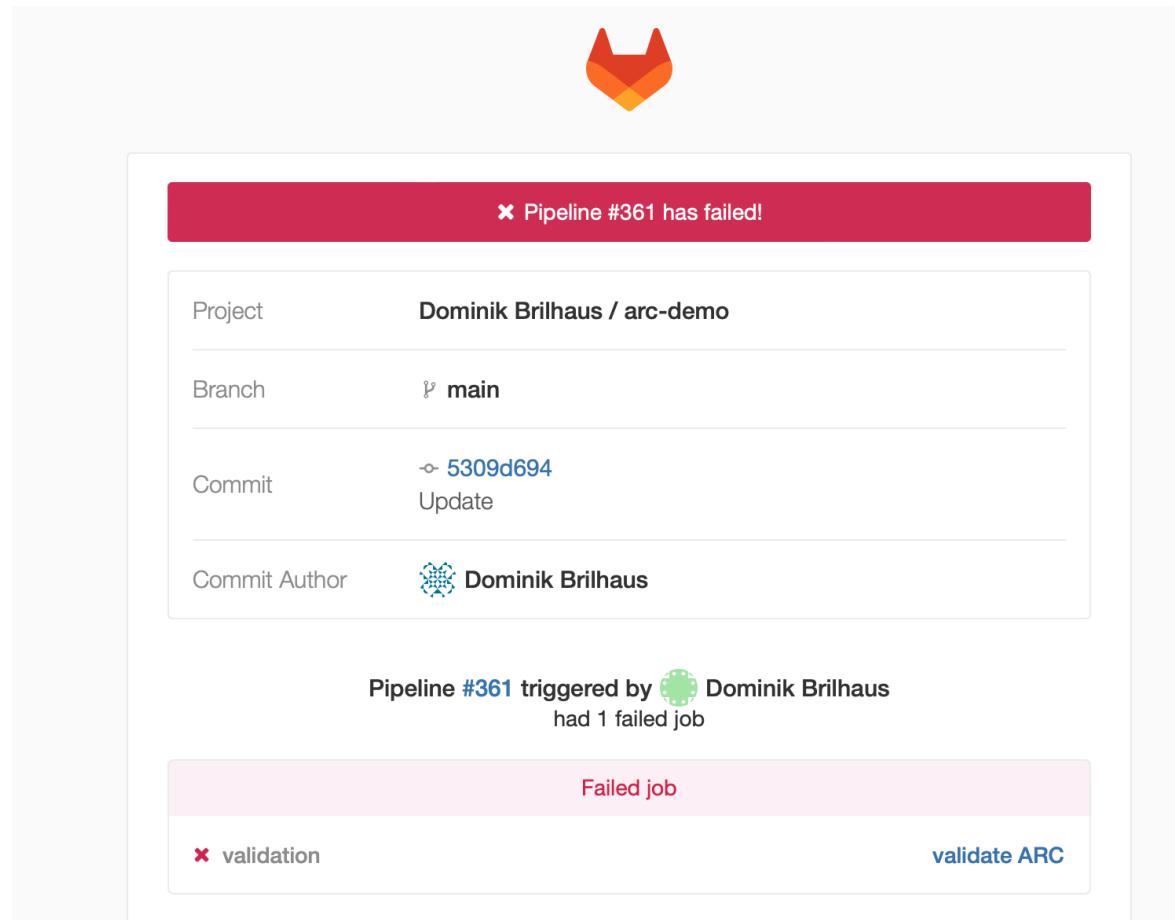
 Structured and ...

 ... annotated experimental data

 Shared with collaborators



Received two emails from "GitLab" about a failed pipeline?

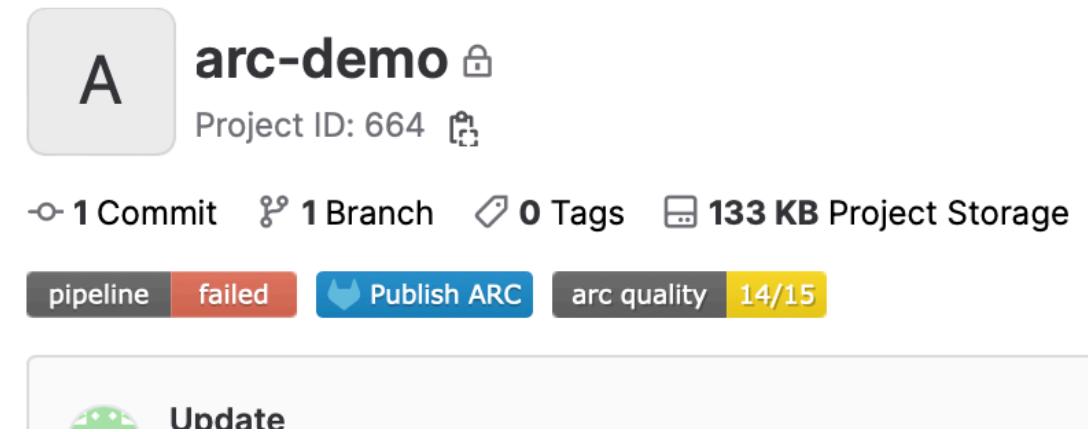


🔥 Don't worry 😊

Pipeline Failed

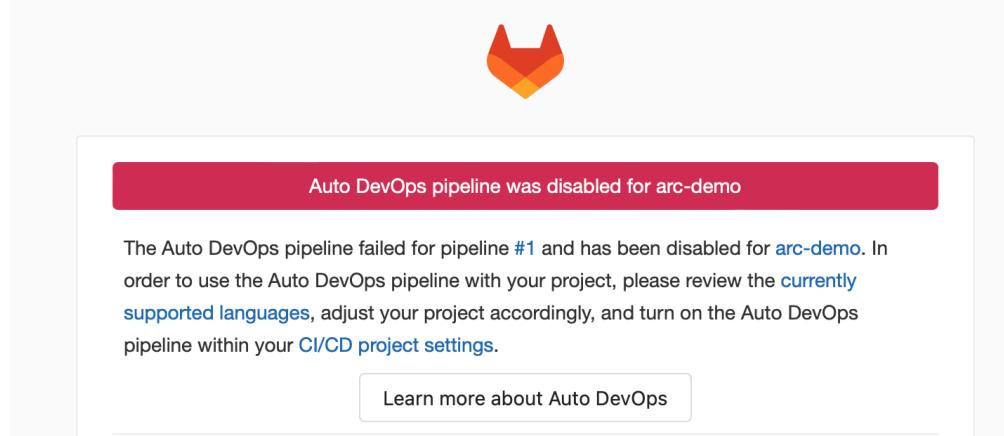
- a "continuous quality control" (CQC) pipeline validates your ARC
- This fails if one of the following metadata items is missing:

```
Investigation Identifier
Investigation Title
Investigation Description
Investigation Person Last Name
Investigation Person First Name
Investigation Person Email
Investigation Person Affiliation
```



Pipeline Failed

If the pipeline has failed once, it is disabled by default



The screenshot shows a GitHub Auto DevOps pipeline status page. At the top, there's a large orange and yellow logo. Below it, a red banner displays the message "Auto DevOps pipeline was disabled for arc-demo". The main content area contains text explaining the failure: "The Auto DevOps pipeline failed for pipeline #1 and has been disabled for [arc-demo](#). In order to use the Auto DevOps pipeline with your project, please review the [currently supported languages](#), adjust your project accordingly, and turn on the Auto DevOps pipeline within your [CI/CD project settings](#)." A button at the bottom right says "Learn more about Auto DevOps".

Reactivate the CQC pipeline

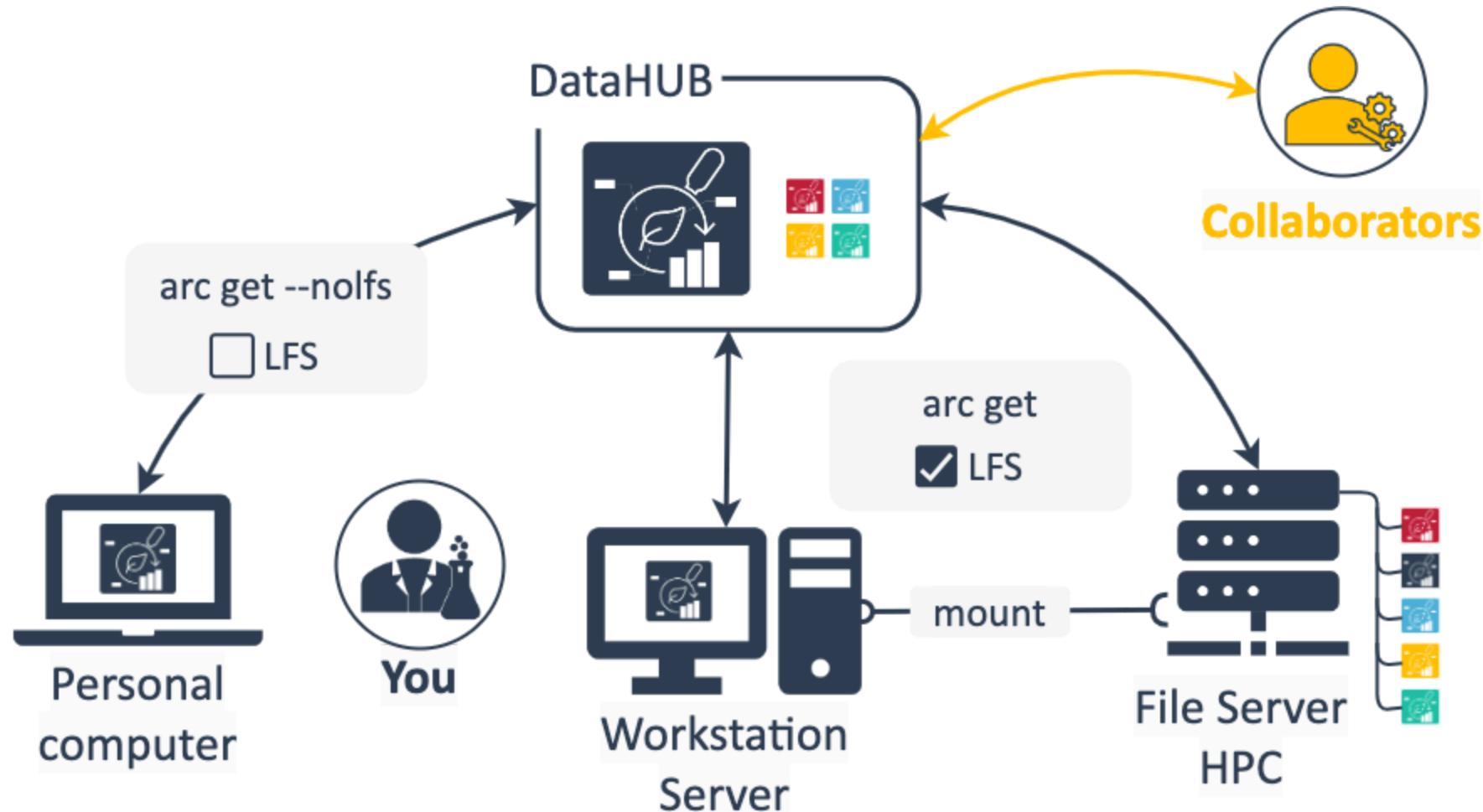
To reactivate it and let the DataHUB validate your ARC again:

1. navigate to CI/CD setting `<arc-url>/-/settings/ci_cd`
2. expand "Auto DevOps"
3. check box "Default to Auto DevOps pipeline"
4. Save changes

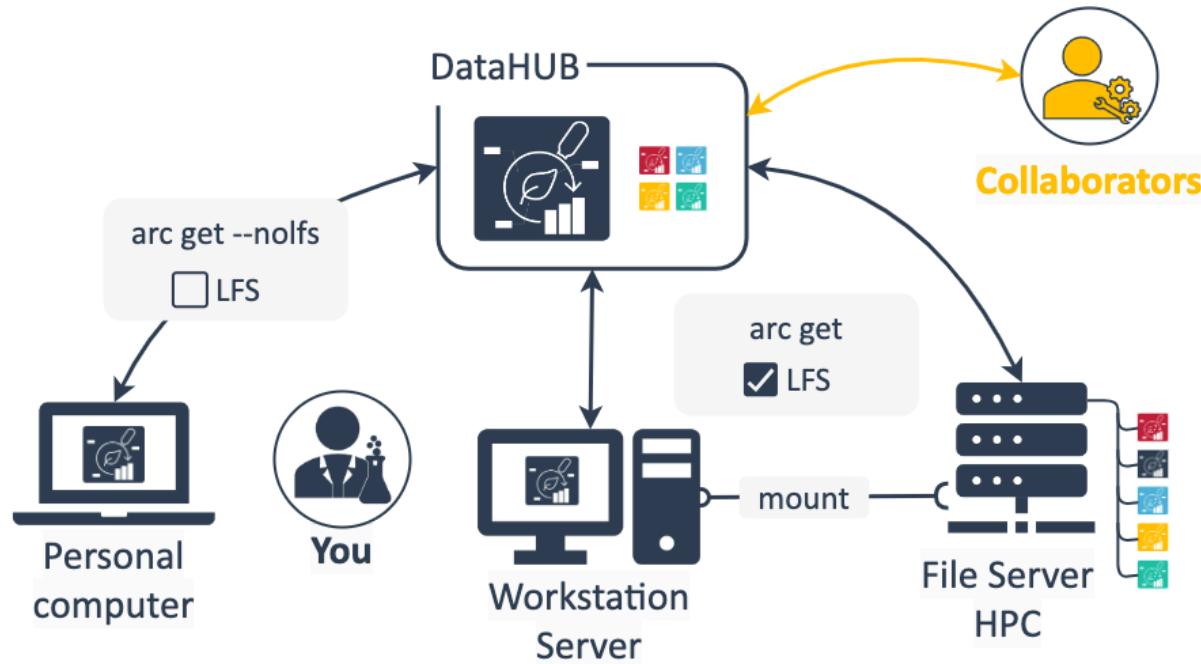
The screenshot shows the GitLab CI/CD settings interface. On the left, a sidebar lists various project management and development tools: Security & Compliance, Deployments, Packages and registries, Infrastructure, Monitor, Analytics, Wiki, Snippets, Settings (selected), General, Integrations, Webhooks, Access Tokens, Repository, Merge requests, CI/CD (selected), Packages and registries, Monitor, and Usage Quotas. The main content area is titled "Auto DevOps" with a "Collapse" button. It includes a sub-section "Default to Auto DevOps pipeline" with a checked checkbox labeled "instance enabled". Below it, there's a note about adding a Kubernetes cluster integration or creating an AUTO_DEVOPS_PLATFORM_TARGET CI variable. Another section, "Deployment strategy", contains three radio buttons: "Continuous deployment to production" (selected), "Continuous deployment to production using timed incremental rollout", and "Automatic deployment to staging, manual deployment to production". A "Save changes" button is at the bottom of this section. Further down, sections for "Runners" and "Artifacts" are partially visible with "Expand" buttons.

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

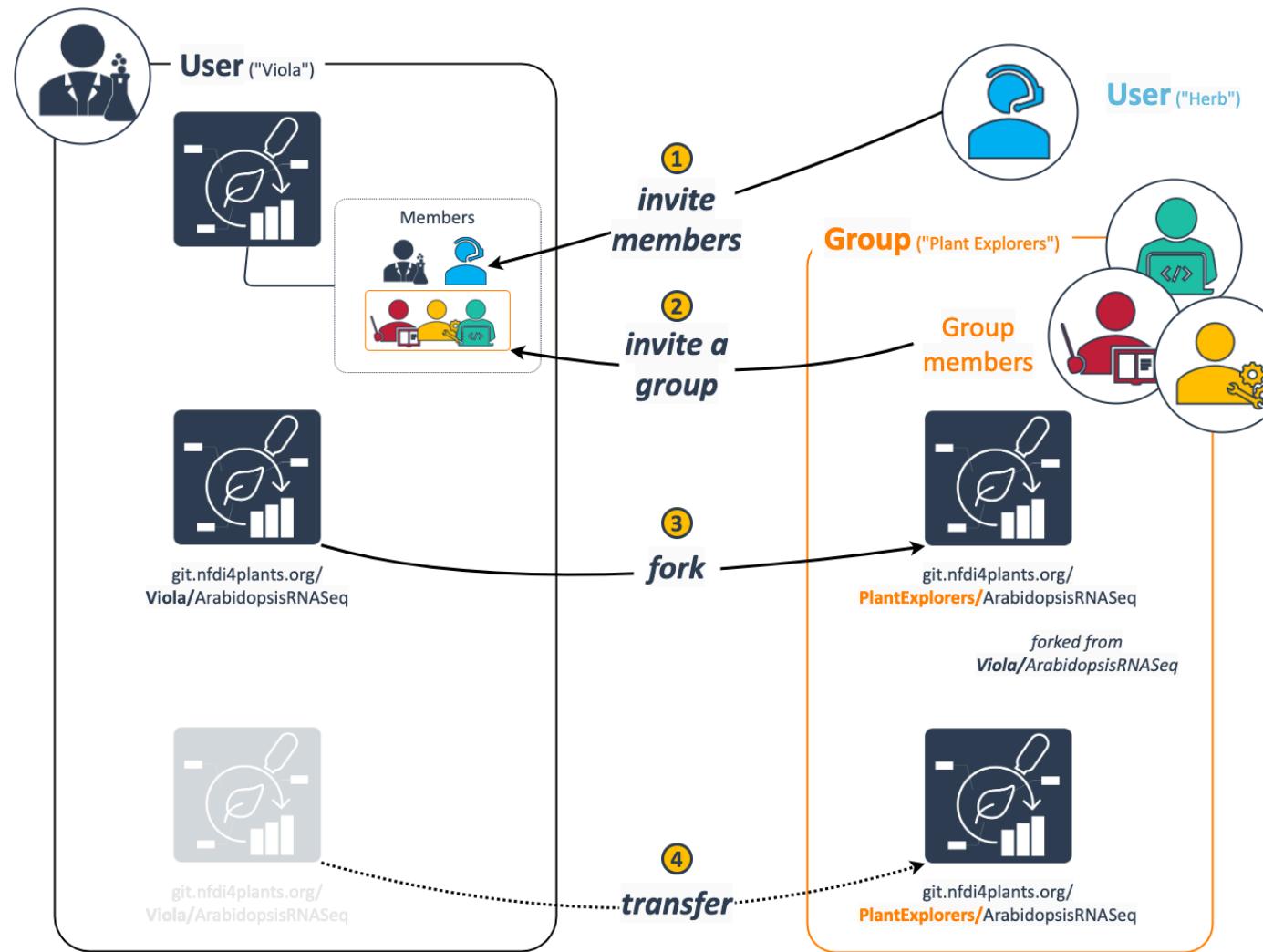
Project = ARC

- 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' page for the 'Samuilov-2018-BOU-PSP' project in the 'HHU Plant Biochemistry' group on GitLab. The page title is 'Project members'. It displays a table of members with columns: Account, Source, Max role, Expiration, and Activity. The table includes four rows:

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

Below the table are buttons for 'Import from a project', 'Invite a group', and 'Invite members'. A sidebar on the left shows navigation links for the project.

DataHUB: ARC members

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

The screenshot shows the 'Samuilov-2018-BOU-PSP' project in the 'ARCIctect' interface. The left sidebar lists project files: '_publications', 'assays', 'runs', 'studies', 'workflows', '.gitignore', 'LICENSE', and 'README.md'. The right panel is titled 'Investigation Contacts' and lists ten contacts with their names, GitHub handles, and scores (e.g., 4/10, 3/10). Each contact has a dropdown arrow next to it.

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

ARCIctect: Investigation Contacts

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

DataHub Hands-On

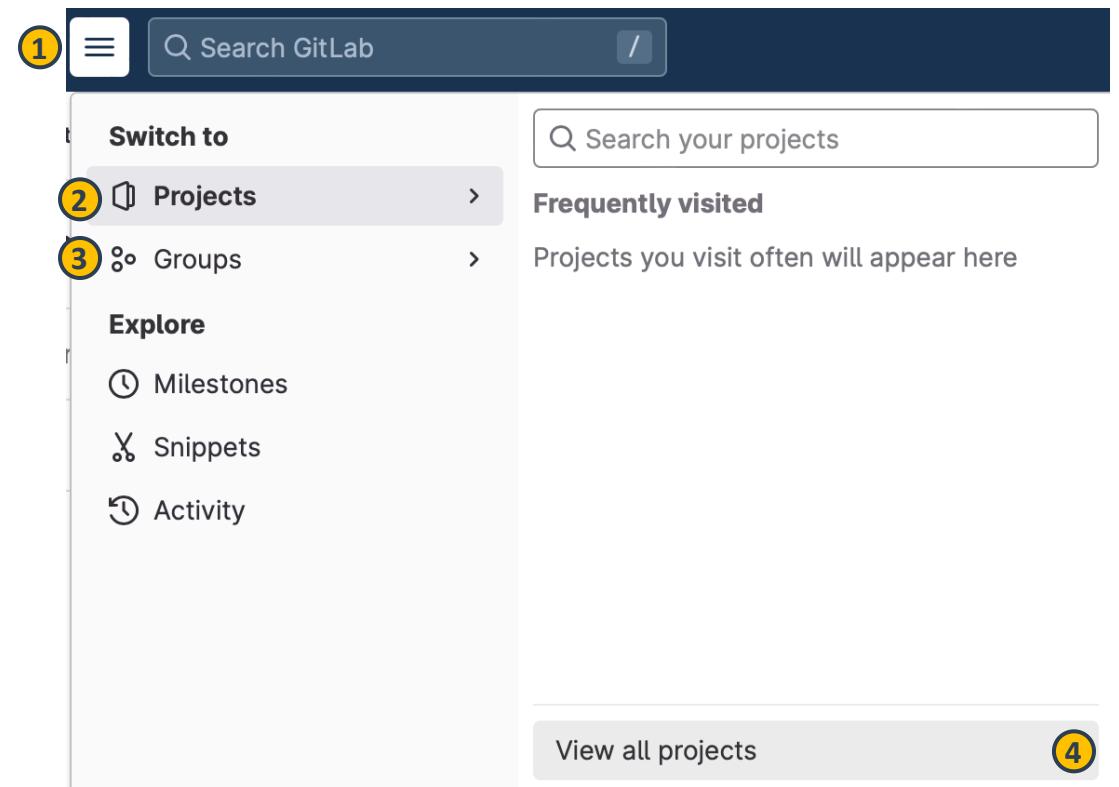
Navigation Bar



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)

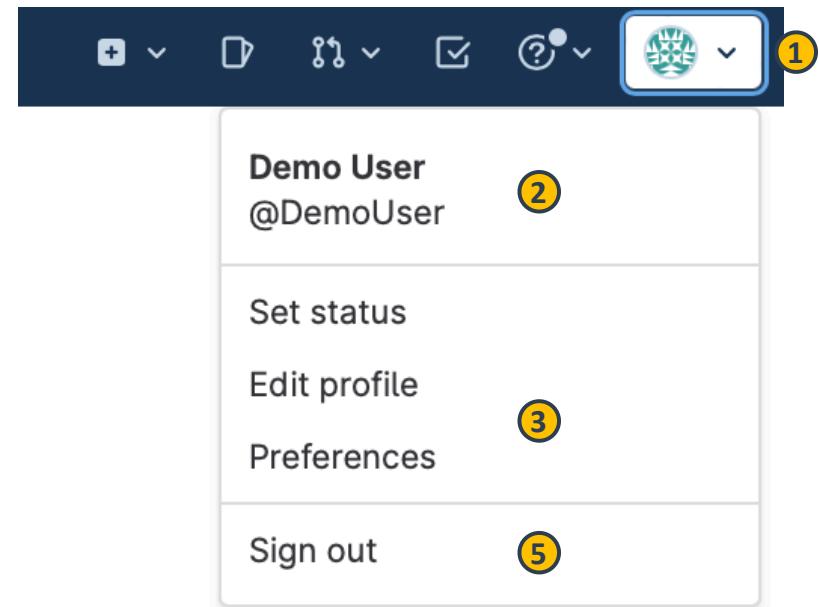
Hamburger Menu

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

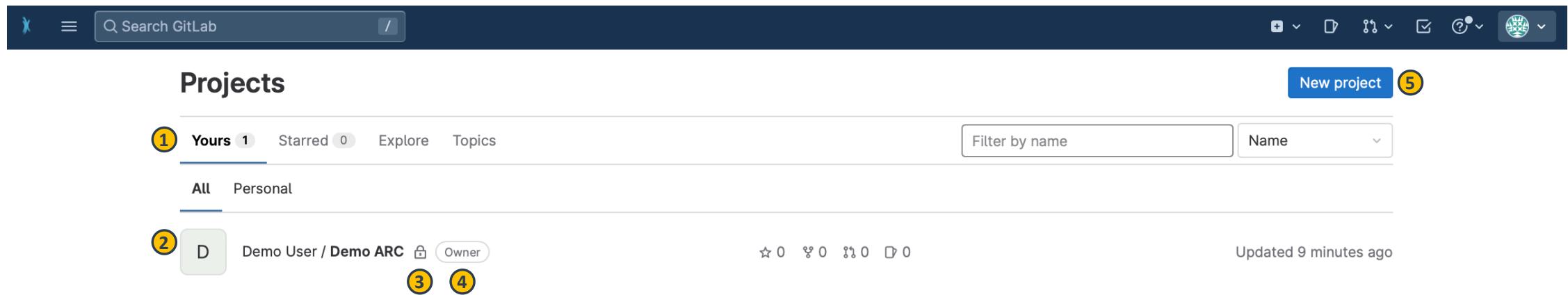


Avatar Menu

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.
5. You can create a **New Project** in the top-right corner (5).

ARC Panel

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

The screenshot shows the ARC Panel interface for the 'Demo ARC' project. The left sidebar contains navigation links numbered 1 through 5:

- Project information (1)
- Repository (2)
- Issues (3) - 0
- Merge requests (4) - 0
- CI/CD
- Security & Compliance
- Deployments
- Packages and registries
- Infrastructure
- Monitor
- Analytics
- Wiki (4)
- Snippets
- Settings (5)

The main workspace displays the 'Demo ARC' project details:

- Demo ARC** (Project ID: 494) - 6 notifications
- 1 Commit, 1 Branch, 0 Tags, 51 KB Project Storage
- create investigation (authored just now by Demo User)
- Branch selector: main / demo-arc / + (9)
- Action buttons: Find file, Web IDE, Clone (10), Add README, Add LICENSE, Add CHANGELOG, Add CONTRIBUTING, Add Kubernetes cluster, Configure Integrations
- File list (8): .arc, assays, runs, studies, workflows. Last commit: create investigation, arc init, arc init, arc init, arc init. Last update: just now, 1 minute ago, 1 minute ago, 1 minute ago, 1 minute ago.

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 ARC Panel interface. On the left is a sidebar with the following items, each numbered:

- 1 Project information
- 2 Repository
- 3 Issues
- 4 Wiki
- 5 Settings

The main area displays a repository named "Demo ARC". It shows basic statistics: 1 Commit, 1 Branch, 0 Tags, and 51 KB Project Storage. Below this is a "create investigation" section. The repository navigation bar includes "main" and "demo-arc /". A "Find file" and "Web IDE" button are also present. The "Clone" button has a count of 10. At the bottom, there is a table showing recent commits:

Name	Last commit	Last update
.arc	create investigation	just now
assays	arc init	1 minute ago
runs	arc init	1 minute ago
studies	arc init	1 minute ago
workflows	arc init	1 minute 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).

The screenshot shows the ARC Panel interface. On the left is a sidebar with the following items:

- 1 Project information
- 2 Repository
- 3 Issues
- 4 Merge requests
- 5 CI/CD
- 6 Security & Compliance
- 7 Deployments
- 8 Packages and registries
- 9 Infrastructure
- 10 Monitor
- 11 Analytics
- 12 Wiki
- 13 Snippets
- 14 Settings

The right side displays the project details for "Demo ARC". It includes:

- Demo User > Demo ARC
- D Demo ARC (6)
- Project ID: 494
- 1 Commit, 1 Branch, 0 Tags, 51 KB Project Storage
- create investigation (Demo User authored just now)
- main / demo-arc / (with a yellow circle around it)
- Find file, Web IDE, Clone (10)
- Auto DevOps enabled, Add README, Add LICENSE, Add CHANGELOG, Add CONTRIBUTING, Add Kubernetes cluster, Configure Integrations
- A table showing recent commits:

Name	Last commit	Last update
.arc	create investigation	just now
assays	arc init	1 minute ago
runs	arc init	1 minute ago
studies	arc init	1 minute ago
workflows	arc init	1 minute ago

Collaborate and share



Invite collaborators

- Unless changed, your ARC is set to private by default.
- To collaborate, you can invite lab colleagues or project partners to your ARC by following the steps on the subsequent slides.
- To get started [sign in](#) to the DataHUB and open the ARC you want to share.

1. Click on Project Information in the left navigation panel

The screenshot shows the GitLab web interface. The left sidebar contains a list of project management sections: Quickstart, Project information (which is highlighted with a red border and has a red circled '1' icon), Activity, Labels, Members, Repository, Issues (0), Merge requests (0), CI/CD, Security & Compliance, Deployments, Packages & Registries, Infrastructure, Monitor, Analytics, Wiki, Snippets, and Settings. The main content area shows the activity feed for the 'Quickstart' project, with a single event from 'User Name' (@username) created at '1 minute ago'. The top navigation bar includes a 'Menu' icon, search bar, and various user and project management icons.

2. Click on Members

The screenshot shows the 'Members' page in the GitLab interface. The left sidebar has a red box around 'Project information' (labeled 1) and another red box around 'Members' (labeled 2). The main content area shows the title 'Project members' and a message: 'You can invite a new member to **Quickstart** or invite another group.' Below this is a table with one row of data.

Account	Source	Access granted	Max role	Expiration	Created on	Last activity
User Name It's you @username	Direct member	2 minutes ago by User Name	Owner	Expiration date <input type="button" value="calendar icon"/>	14 Feb, 2022	4 Nov, 2022

3. Click on Invite members

The screenshot shows the 'Members' page in the GitLab interface. On the left, there's a sidebar with various project management options like Quickstart, Project information (highlighted with a red box and circled 1), Activity, Labels, Members (highlighted with a red box and circled 2), Repository, Issues (0), Merge requests (0), CI/CD, Security & Compliance, Deployments, Packages & Registries, Infrastructure, Monitor, Analytics, Wiki, Snippets, and Settings. The main area is titled 'Project members' and displays a table of current members. At the top right of this area are three buttons: 'Import from a project', 'Invite a gr...', and 'Invite members' (highlighted with a red box and circled 3). The table has columns for Account, Source, Access granted, Max role, Expiration, Created on, and Last activity. One member is listed: 'User Name' (highlighted with a blue circle), with a note 'It's you @username'. The 'Access granted' column shows '2 minutes ago by User Name'. The 'Max role' column shows 'Owner'. The 'Expiration' column has a 'Expiration date' button. The 'Created on' column shows '14 Feb, 2022'. The 'Last activity' column shows '4 Nov, 2022'.

4. Search for potential collaborators

The screenshot shows the GitLab interface for a project named 'Quickstart'. On the left sidebar, under 'Project information', the 'Members' tab is selected (marked with a red box and number 2). In the main content area, the 'Project members' section displays one member: 'Cristina Martins Rodrigues' (Activity: 0, Labels: 0). Below this, there is a modal dialog titled 'Invite members' (marked with a red box and number 4) which is overlaid on the page. The dialog contains fields for 'Username or email address' (with a placeholder 'Select members or type email addresses'), 'Select a role' (set to 'Guest'), and an 'Access expiration date (optional)' field. At the bottom of the dialog are 'Cancel' and 'Invite' buttons. The top right of the main page has buttons for 'Import from a project', 'Invite a group' (marked with a red box and number 3), and 'Invite members'.

5. Select a role

The screenshot shows the GitLab 'Project members' page for the 'Quickstart' project. The sidebar on the left is visible with various project management options like 'Activity', 'Labels', 'Members' (highlighted with a red box and number 2), 'Repository', 'Issues', 'Merge requests', 'CI/CD', 'Security & Compliance', 'Deployments', 'Packages & Registries', 'Infrastructure', 'Monitor', 'Analytics', 'Wiki', 'Snippets', and 'Settings'. The main area shows 'Project members' (1 member) and an 'Invite members' dialog is open. The dialog has a text input field for 'Username or email address' (empty) and a dropdown menu for 'Select a role' (set to 'Guest', highlighted with a red box and number 5). Other role options include 'Reporter', 'Developer', 'Maintainer', and 'Owner'. Buttons for 'Cancel' and 'Invite' are at the bottom right of the dialog. The top right of the screen shows standard GitLab navigation icons.

Choosing the proper role

Guests

Have the least rights. They will not be able to see the content of your ARC (only the wiki page).

Reporters

Have **read access** to your ARC. This is recommended for people you ask for consultancy.

Developers

The choice for most people you want to invite to your ARC. Developers have **read and write access**, but cannot maintain the project on the DataHUB, e.g. inviting others.

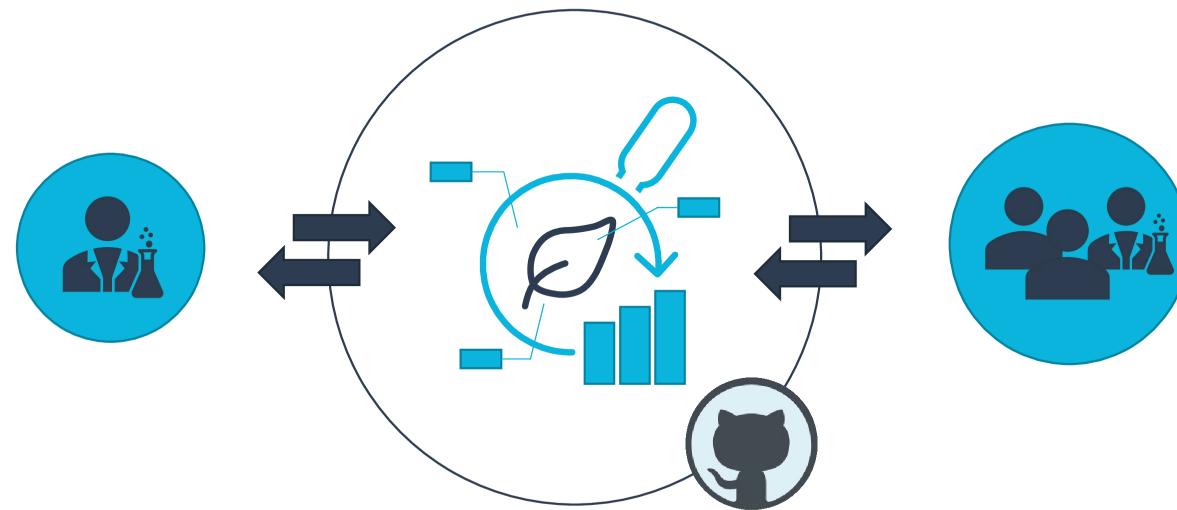
Maintainers

Gives the person the same rights as you have (except of removing you from your own project). This is recommended for inviting PIs or group leaders allowing them to add their group members for data upload or analysis to the project as well.

A detailed list of all permissions for the individual roles can be found [here](#)

Congratulations!

You have just shared your ARC with a collaborator.



Version control

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

The screenshot shows the 'Demo User > Demo ARC' interface. On the left, a sidebar lists project management features: Project information (1), Repository (2), Issues (3), Merge requests (0), CI/CD, Security & Compliance, Deployments, Packages and registries, Infrastructure, Monitor, Analytics, Wiki (4), Snippets, and Settings (5). The main area displays the 'Demo ARC' project details: Project ID: 494, 1 Commit, 1 Branch, 0 Tags, and 51 KB Project Storage. A recent commit is shown: 'create investigation' by Demo User authored just now, with commit hash 3c538706. Below this is a file browser showing 'main / demo-arc /' with a '+' button (9). A row of buttons includes Auto DevOps enabled, Add README, Add LICENSE, Add CHANGELOG, Add CONTRIBUTING, Add Kubernetes cluster, and Configure Integrations. At the bottom is a table of files with their last commits and update times.

Name	Last commit	Last update
.arc	create investigation	just now
assays	arc init	1 minute ago
runs	arc init	1 minute ago
studies	arc init	1 minute ago
workflows	arc init	1 minute ago

Project Management

Add issues to your ARC (3)

The screenshot shows the 'Demo User > Demo ARC' interface. On the left, a sidebar lists project management features with numbered callouts:

- 1 Project information
- 2 Repository
- 3 Issues (highlighted with a yellow circle)
- 4 Wiki
- 5 Settings

The main area displays the 'Demo ARC' project details:

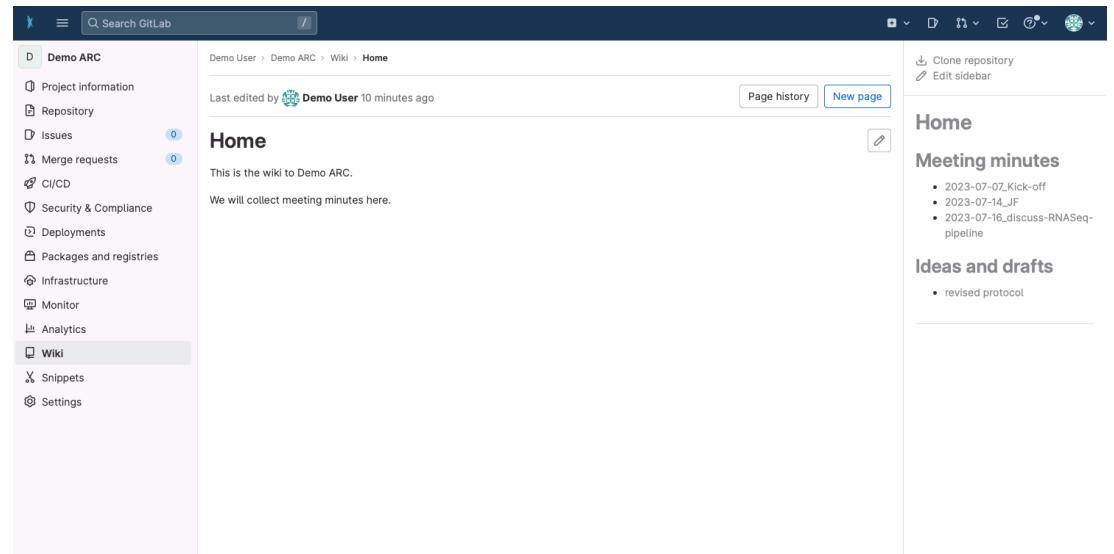
- Demo ARC (Project ID: 494)
- 6 Issues (highlighted with a yellow circle)
- 7 1 Commit, 1 Branch, 0 Tags, 51 KB Project Storage
- create investigation (authored just now by Demo User)
- main / demo-arc / (highlighted with a yellow circle) 9
- Auto DevOps enabled
- Add README
- Add LICENSE
- Add CHANGELOG
- Add CONTRIBUTING
- Add Kubernetes cluster
- Configure Integrations

A commit history table is shown:

Name	Last commit	Last update
.arc	create investigation	just now
assays	arc init	1 minute ago
runs	arc init	1 minute ago
studies	arc init	1 minute ago
workflows	arc init	1 minute ago

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"



Publish your ARC with a few clicks

The screenshot shows a bioRxiv project page for 'Ru_ChlamyHeatstress'. The project icon features a green cell with a鞭毛 (flagella) and a red thermometer icon. The project ID is 122. The page displays 53 commits, 1 branch, 0 tags, and 293.9 GB of project storage. Topics include Chlamydomonas, abiotic stress, proteomics, and more. A summary states: "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." At the bottom, there are three numbered steps: 1. pipeline (passed), 2. Publish ARC (button), and 3. arc quality (301/301).

Ru_ChlamyHeatstress

Project ID: 122

53 Commits 1 Branch 0 Tags 293.9 GB Project Storage

Topics: Chlamydomonas, abiotic stress, proteomics, + 1 more

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

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

Receive a DOI

Published September 7, 2023 | Version v1

Dataset  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 

1

Citation

Style APA

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

2

Description

hosted on: <https://git.nfdi4plants.org/projects/122>

Files

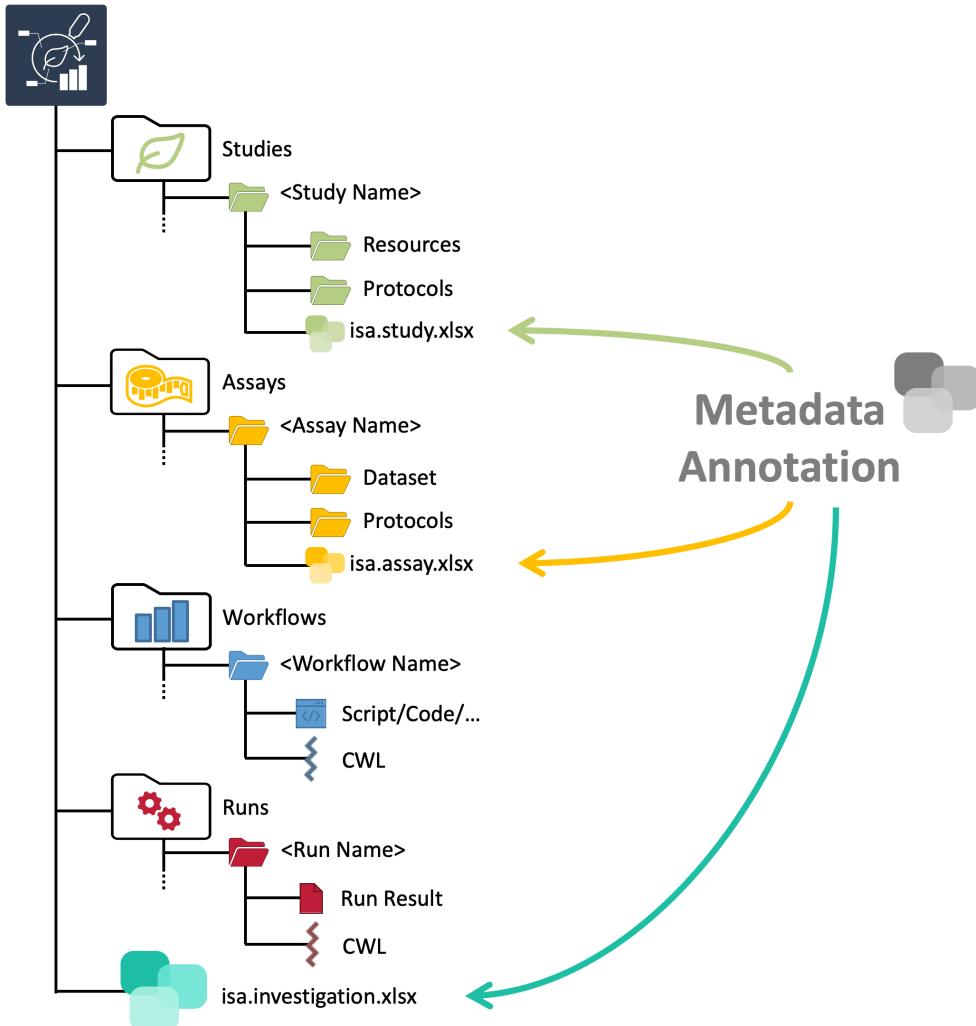
arc-summary.md

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

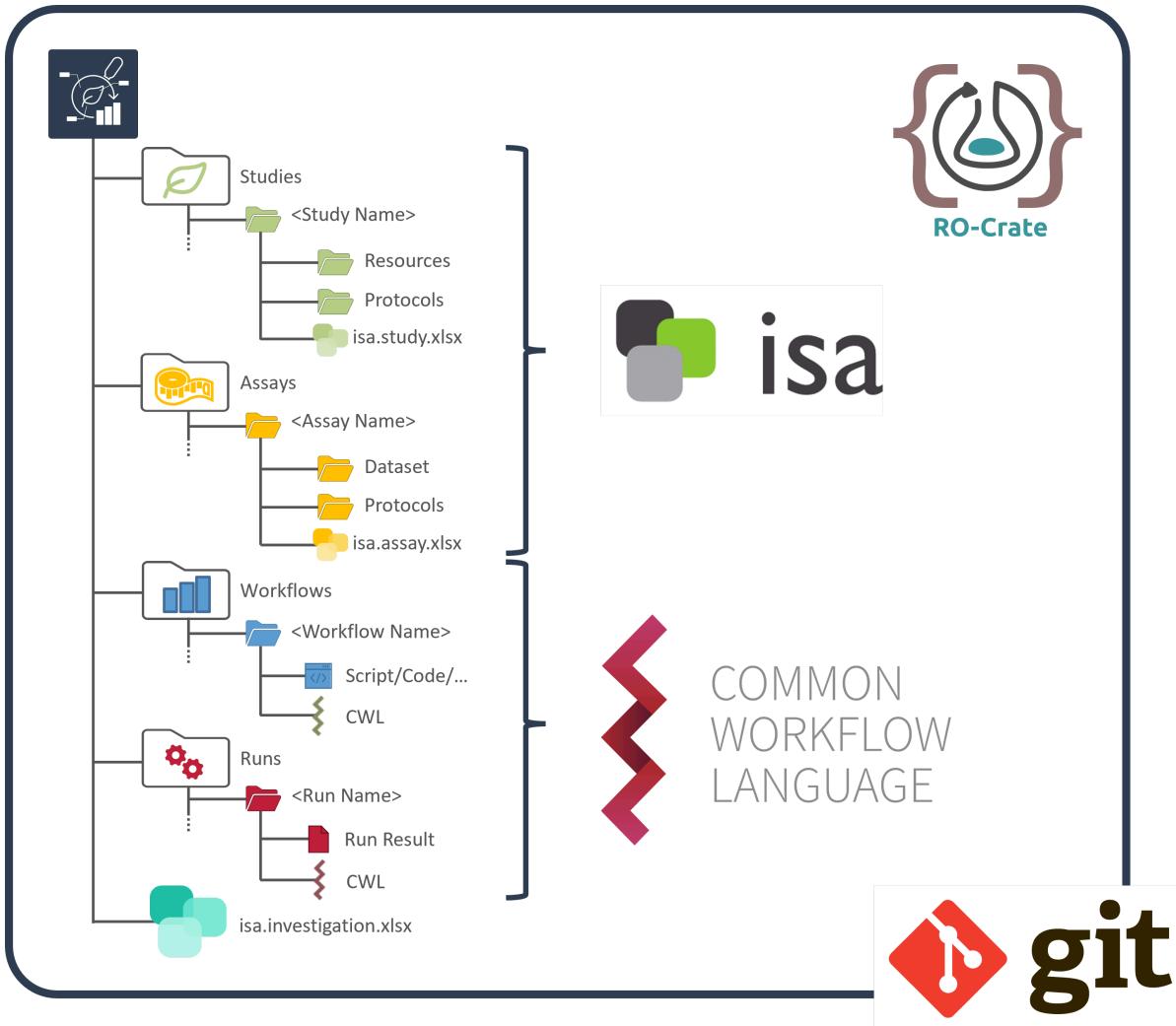
File contents:

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

ARCs come with comprehensive metadata

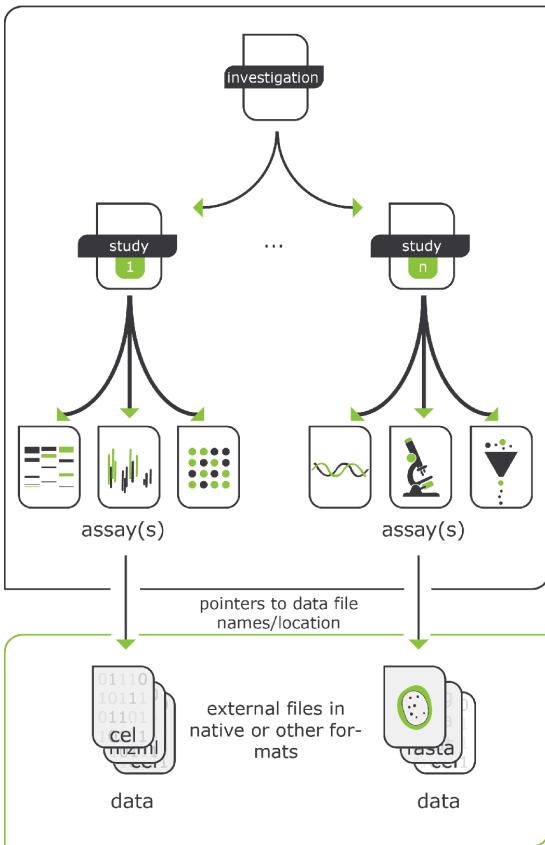


ARC builds on standards



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

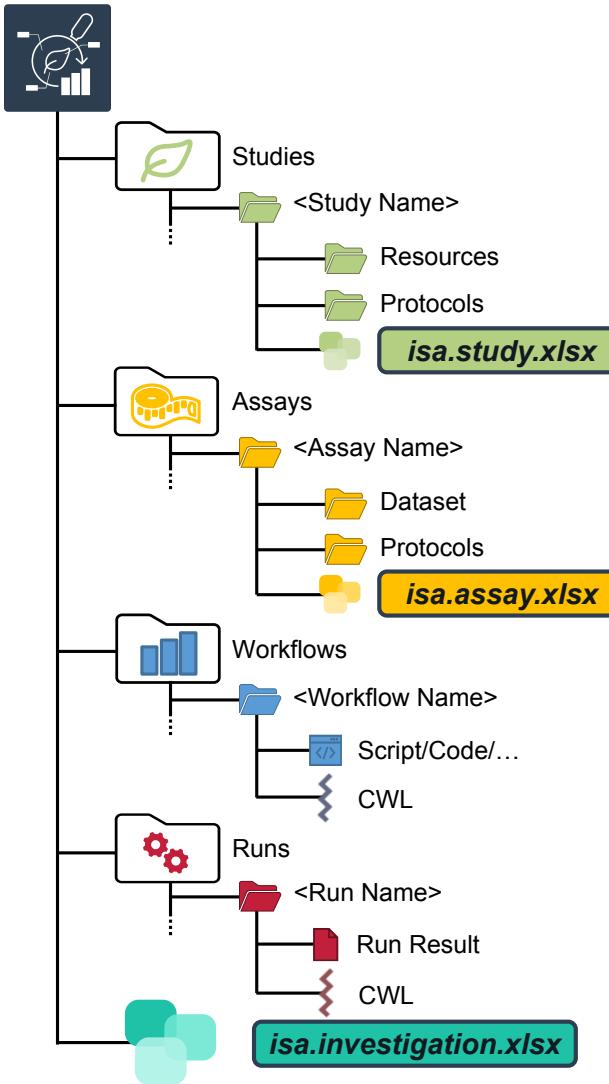
ARC builds on ISA



Investigation
Overall goals
Scientific context

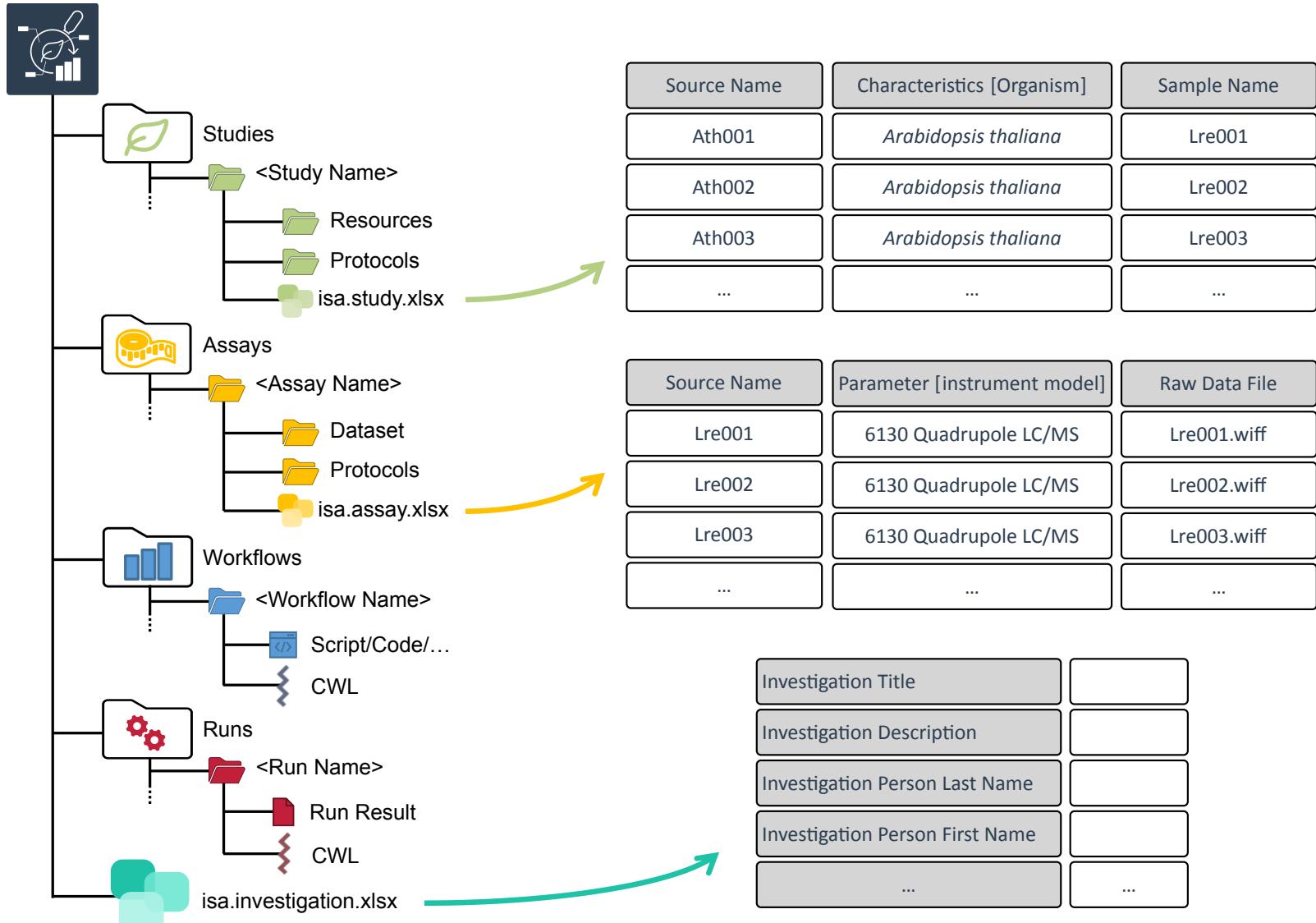
Study
Experimental design

Assay
Leading to (raw) data



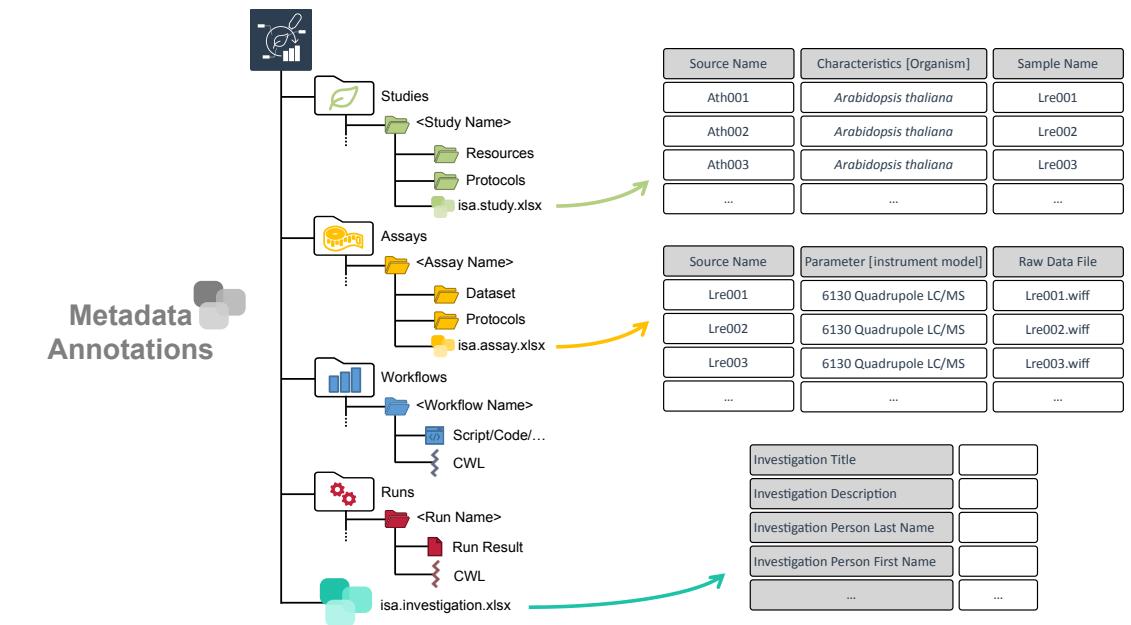
ARC builds on ISA to connect data

Metadata Annotations

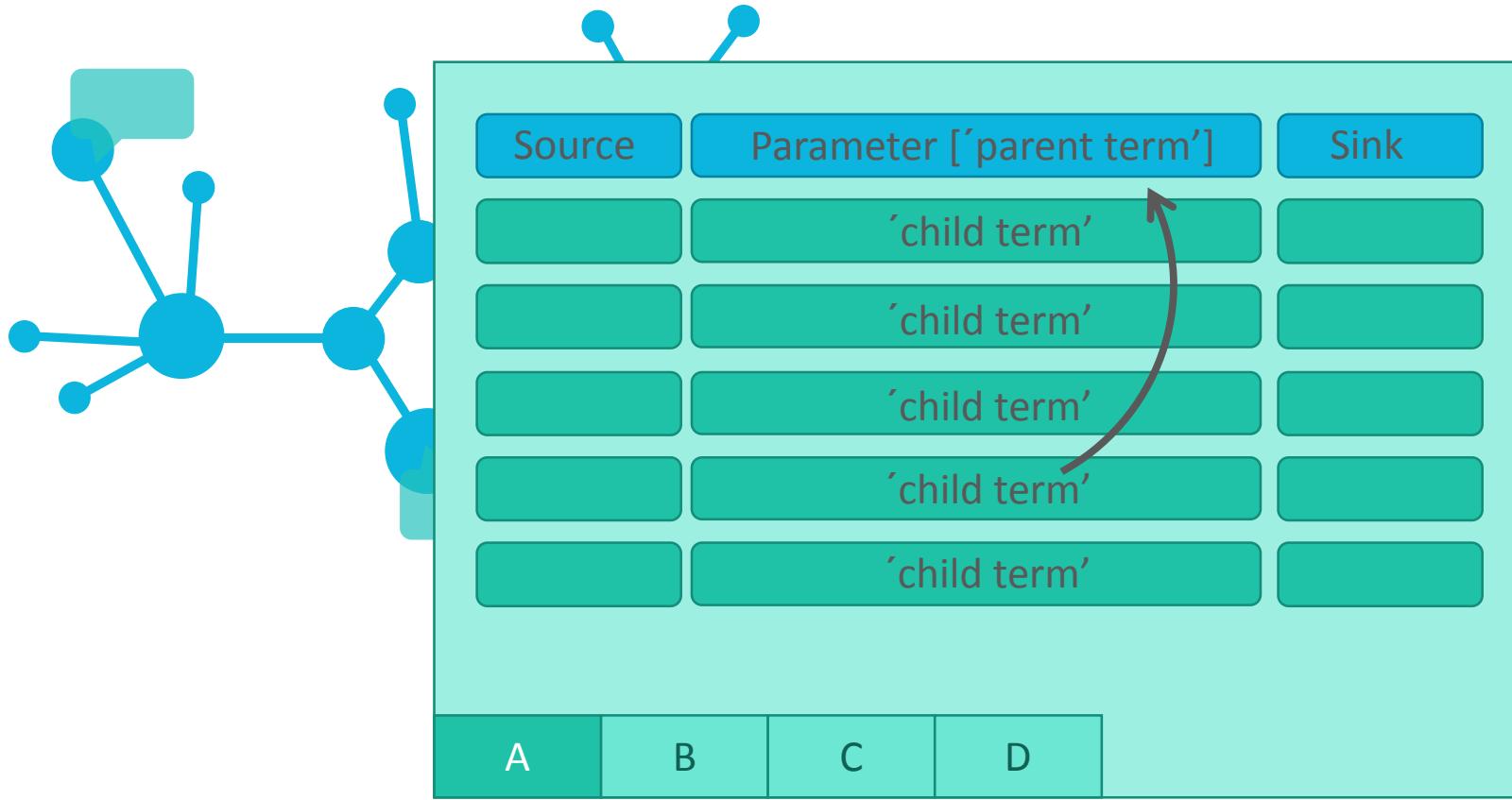


ARC builds on ISA to link data

- 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 is a navigation bar with tabs: Metadata, plant_material, and a plus sign.

On the right, a modal window titled "New building blocks" is open. It contains a search bar with the placeholder "instrument model" and a green "Add Column" button. A dropdown menu lists categories: Input, Parameter, Factor, Characteristic, Component, More, and Output. A "Help" link is also present.

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' tab selected. The main area displays a table of data with the following columns: Input [Source Name], Characteristic [organism], Factor [watering exposure], and Output [Sample Name]. The data rows are as follows:

	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 rewetared	reC3_01
5	DB_163	Talinum fruticosum	✓ 12 days drought + 2 days rewetared	reC3_02
6	DB_165	Talinum fruticosum	✓ 12 days drought + 2 days rewetared	reC3_03

Annotations with blue boxes and arrows point to specific elements:

- Input**: Points to the 'Input [Source Name]' column header.
- Characteristic**: Points to the 'Characteristic [organism]' column header.
- Factor**: Points to the 'Factor [watering exposure]' column header.
- Output**: Points to the 'Output [Sample Name]' column header.
- New Parameter**: Points to a floating 'New Parameter' dialog box.
- Sidebar**: Points to the sidebar on the right side of the interface.

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

Ontology term search

The screenshot shows the Swate interface with a search results table and an ontology search sidebar.

Table Data:

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

Search Sidebar:

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

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

[Fill selected cells with this term](#)

Metadata plant_material +

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

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

Fill your table with ontology terms

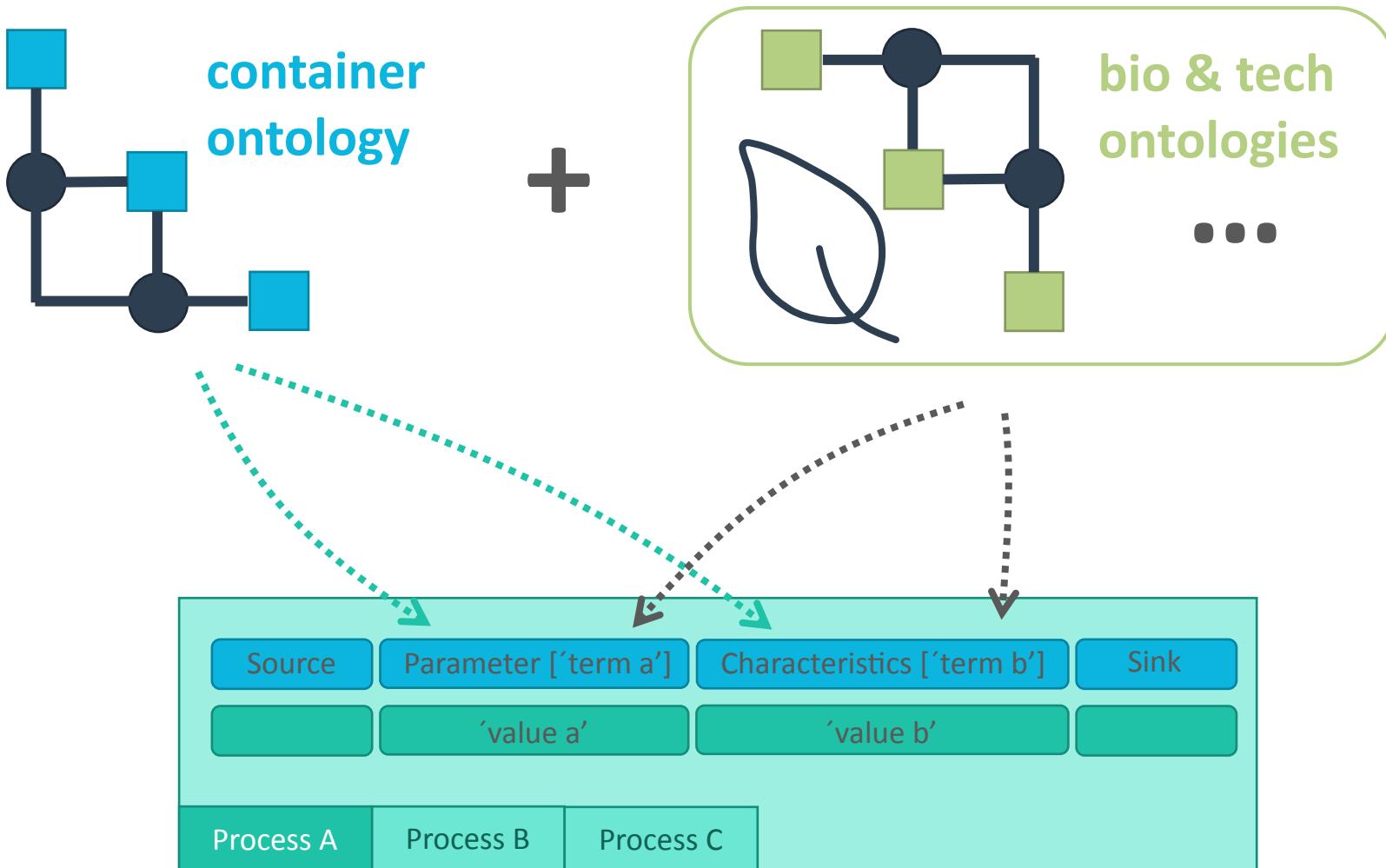
The screenshot shows the Swate interface. On the left, there is a table with six rows of data:

	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

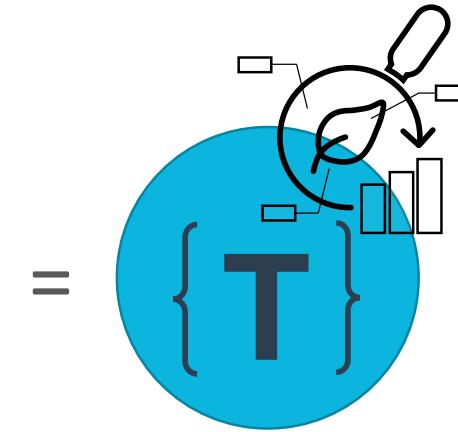
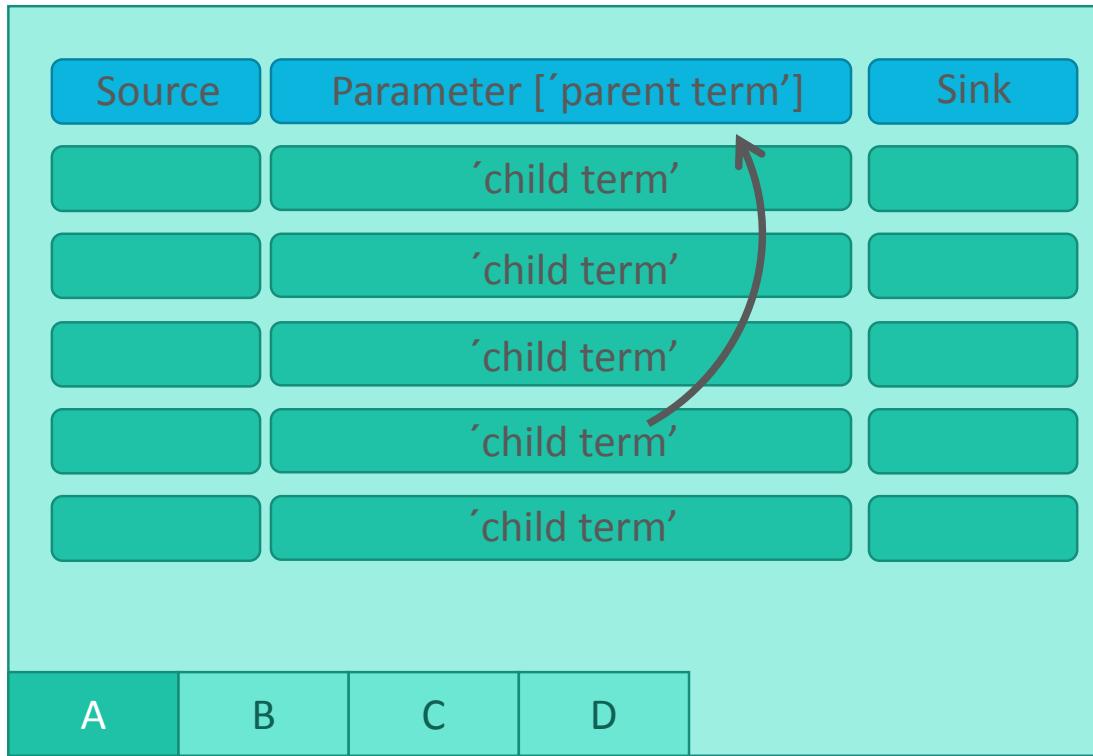
On the right, there is an "Ontology term search" panel with the following fields:

- Search bar: Talinum fruticosum
- Parent: Organism, MIAPPE:0041
- Use advanced search
- Fill selected cells with this term

Hierarchical combination of ontologies

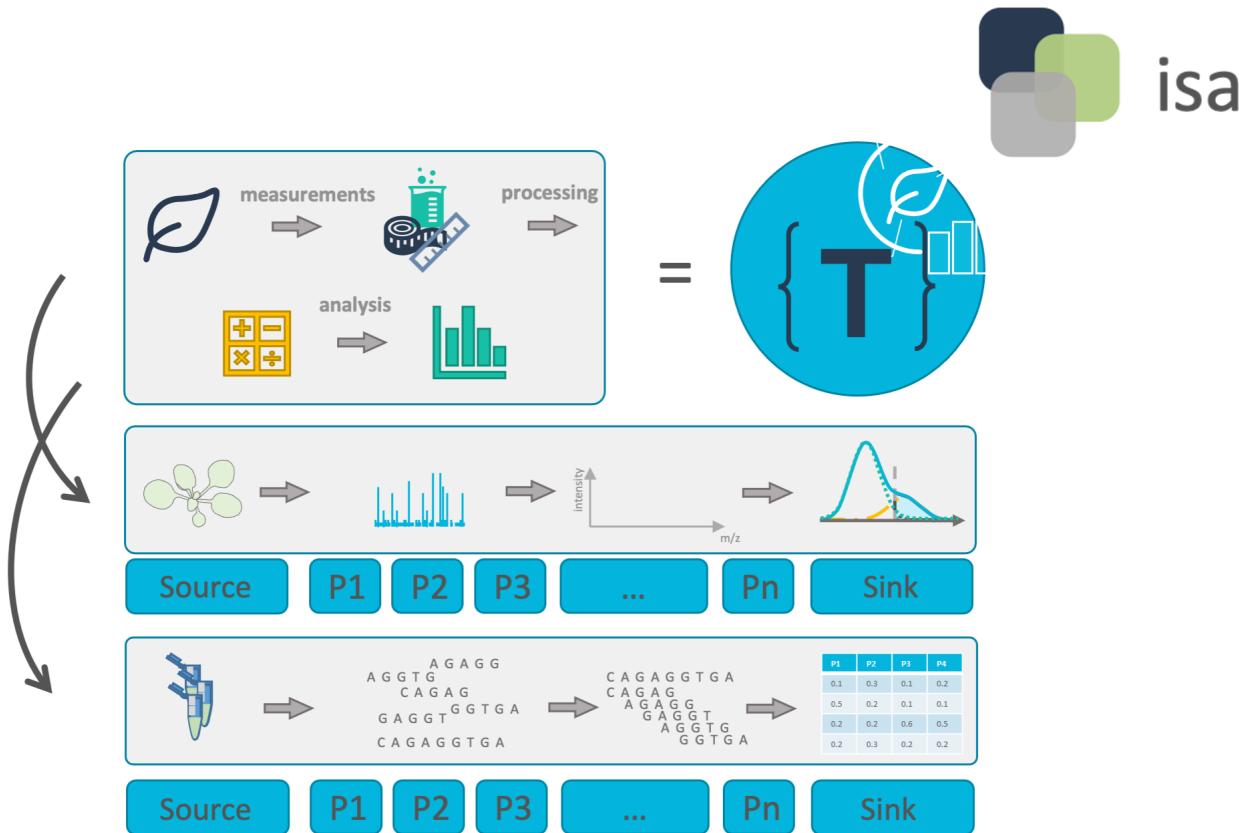


Checklists and Templates



Metadata standards or repository requirements can be represented as 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 these is a dropdown menu labeled "Select community" set to "DataPLANT official". The main content area is a table listing various templates. The columns are "Template Name", "Community", and "Template Version". Each row contains a link icon at the end. The data in the table is as follows:

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

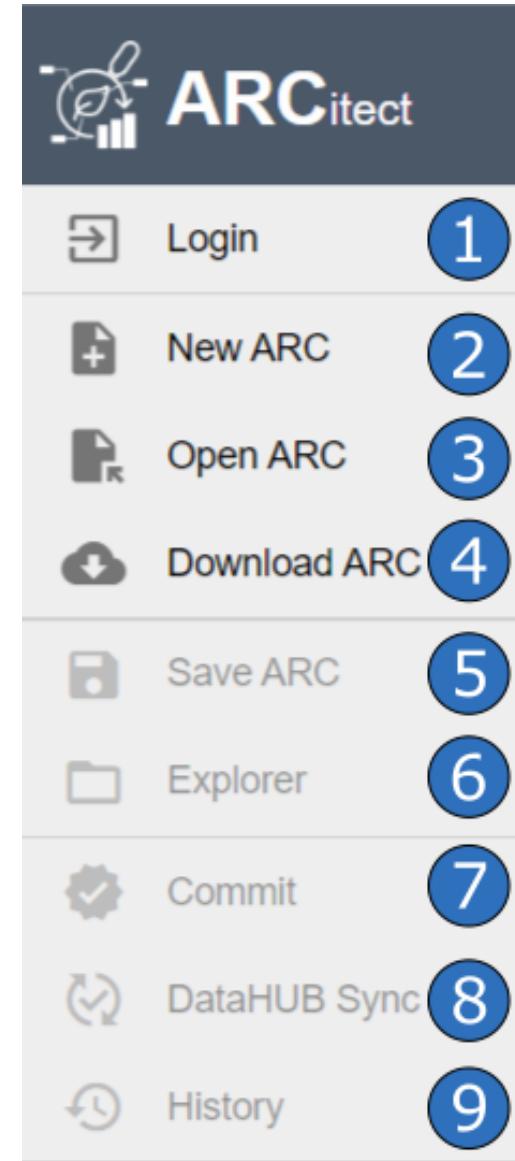
Swate hands-on with demo data

Goals

- Get familiar with ISA metadata and Swate
- Annotate data in your ARC

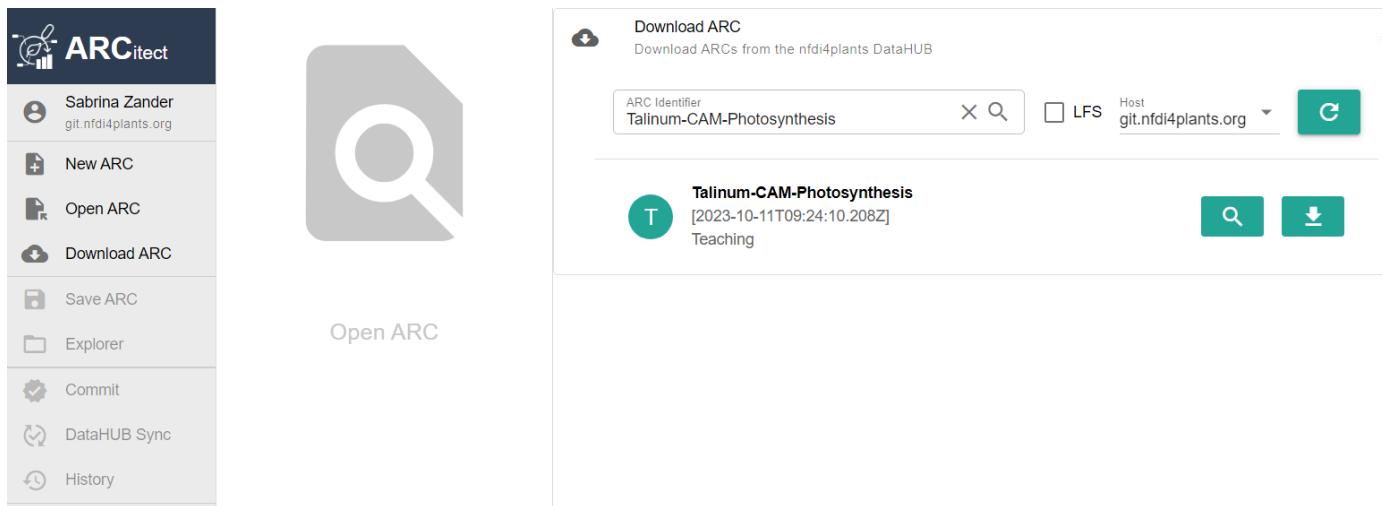
Download the demo data

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



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

Alternative: Use Swate standalone

Open [Swate standalone](#) in web browser

 Alternatively, you can use Swate as [Excel Plugin](#), but this is outdated

Swate Overview

The screenshot shows the Swate software interface with a table of experimental data and a 'New Parameter' dialog box.

Widgets: The main area displays a table with columns: Input [Source Name], Characteristic [organism], Factor [watering exposure], and Output [Sample Name]. The table contains 6 rows of data. A 'New Parameter' dialog box is open on the right, listing categories like Parameter, Factor, and Output.

Input: Points to the 'Input [Source Name]' column in the table.

Characteristic: Points to the 'Characteristic [organism]' column in the table.

Factor: Points to the 'Factor [watering exposure]' column in the table.

Output: Points to the 'Output [Sample Name]' column in the table.

New Parameter: Points to the 'New Parameter' dialog box.

Sidebar: Points to the sidebar area at the bottom right.

	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

Metadata: plant_material +

Let's annotate the plant samples first

1. Check out the lab notes

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

ARCitect

2. Select the study `talinum_drought`

3. Add a new table

Swate standalone

Import the empty

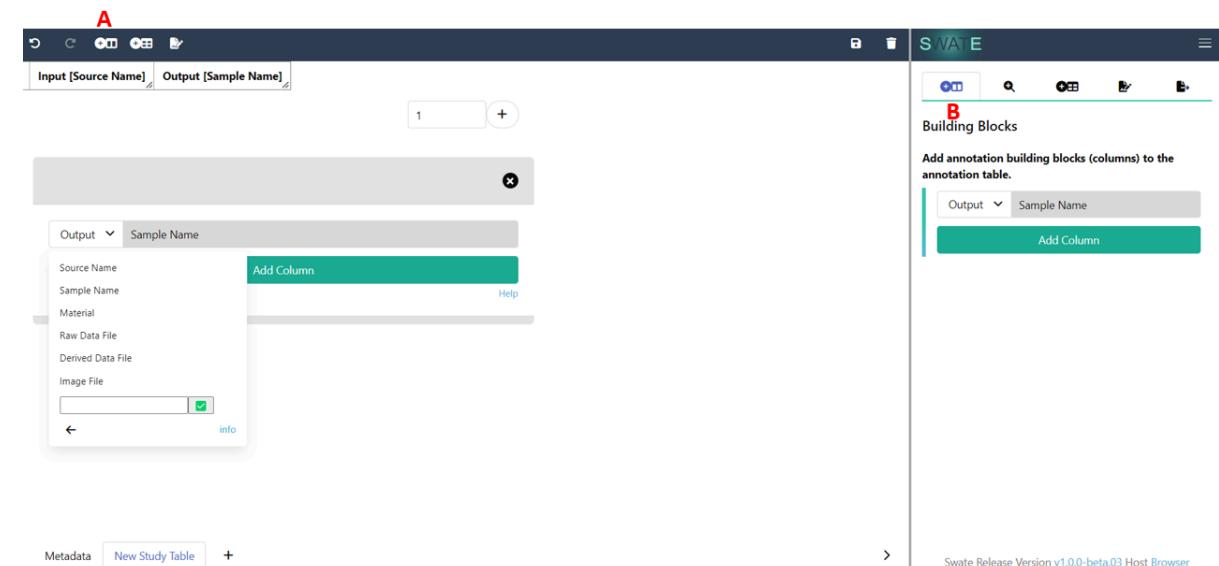
```
studies/talinum_drought/isa.study.xlsx
```



Create an annotation table

Create a Swate annotation table by adding **Building blocks** via the widget (A) or the sidebar (B)

- 💡 Each table can contain only one *Input* and one *Output* column
- 💡 different *Input* and *Output* options:
Source Name , Sample Name ,
Material , Raw Data File ,
Derived Data File , Image File



Add more Building blocks

1. Add an *Input* (Source Name) and *Output* (Sample Name) column

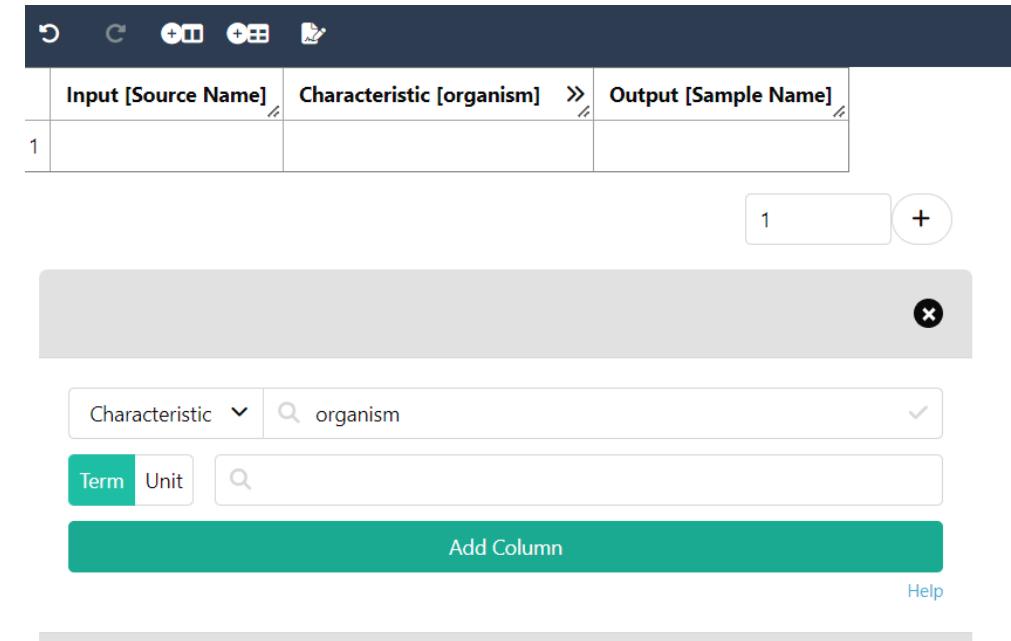
2. Select *Characteristic* from the drop-down menu

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

4. Select the Term with the id OBI:0100026 and,

5. Click Add Column

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



The screenshot shows a software interface for managing building blocks. At the top, there is a toolbar with various icons. Below it is a table with three columns: 'Input [Source Name]', 'Characteristic [organism]', and 'Output [Sample Name]'. The first row contains the number '1' under the 'Input' column. To the right of the table is a counter '1' and a '+' button. Below the table is a search bar with the placeholder 'Characteristic' and a dropdown arrow, followed by a search input field containing 'organism' with a checkmark. Underneath the search bar are two buttons: 'Term' (highlighted in green) and 'Unit', and a magnifying glass icon. At the bottom is a teal-colored button labeled 'Add Column'.

Insert values to annotate your data

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

Input [Source Name]	Characteristic [organism]	Output [Sample Name]
1	Talinum fruticosum	<input type="text"/>
	↳ Talinum fruticosum NCBITaxon:110664	<input type="button" value="x"/>
	↳ Talinum paniculatum NCBITaxon:107604	<input type="button" value="x"/>

Add a 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 `microeinsteин 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 to annotate your data

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

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

Your ISA 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.

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

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 (DB_*) as **Sample Name**

Let's annotate the RNA Seq data

1. Navigate to the demo ARC.
2. Open the lab notes `assays/rnaseq/protocols/RNA_extraction.txt` in a text editor.
3. Import the empty `assays/rnaseq/isa.assay.xlsx` workbook in Swate.

Use a template

1. Open the *Templates* widget in the Bar

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

1. Search for **RNA extraction** and click

select

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

2. Click **Add template** to add all *Building Blocks* from the template to your table, which do not exist yet.

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 ×

Preview Update Table

1 Apply Submit

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

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.

Your ISA table is ready 

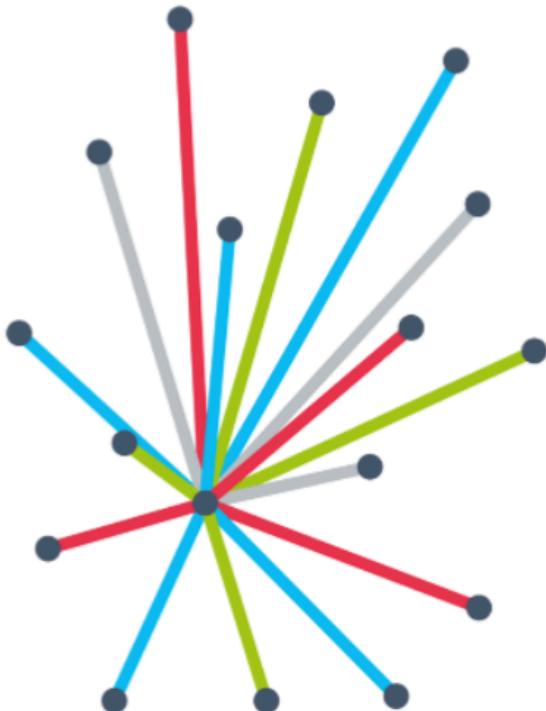
Go ahead, adjust the *Building Blocks* you want to use to describe your experiment as you see fit.

Insert values using Swate Term search and add input and output.

Known issues with ARCitect and Swate (April 2024)

 Swate Desktop outdated

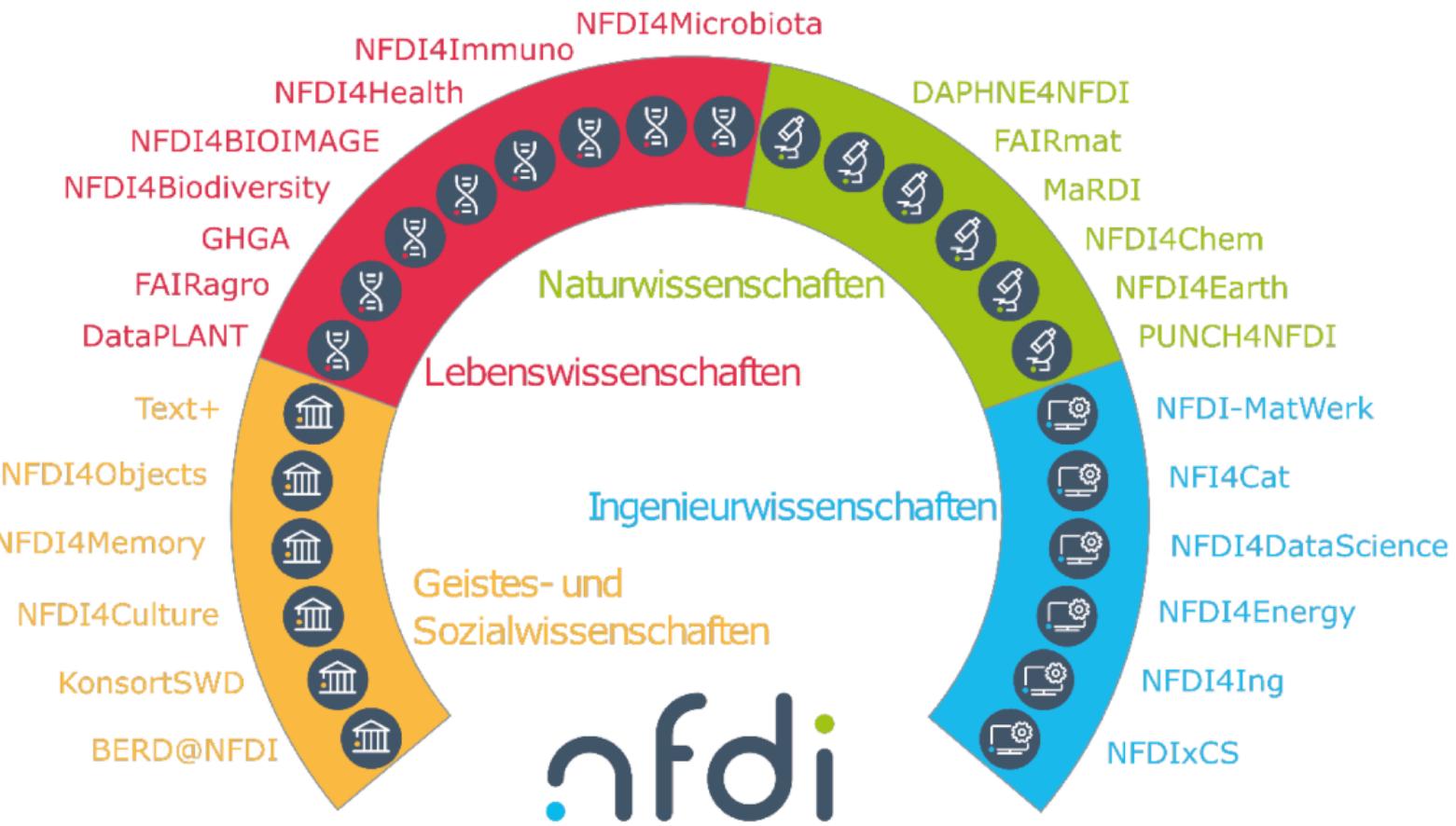
NFDI – Nationale Forschungsdaten Infrastruktur



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

nfdi.de

NFDI consortia



nfdi.de

NFDI sections

-  **Section-metatada** (Meta)data, Terminologies, Provenance
-  **Section-infra** Common Infrastructures
-  **Section-edutrain** Training and Education
-  **Section-ELSA** Ethical, Legal and Social Aspects
-  **Section-industry** Industry Engagement

nfdi.de

Base4NFDI



www.base4nfdi.de

What is Base4NFDI?

- Base4NFDI is a joint initiative of all 26 NFDI-**consortia**.
 - Our goal is to establish reliable NFDI-wide **basic services** for **FAIR** research data management.
 - Such basic and technical services will **benefit all communities and domains**.
 - We ensure **interoperability** with national and international infrastructures and engage with science policy bodies.

What is a basic service?

A **basic service** is a technical-organizational solution which typically includes:

- storage and computing services
 - software, processes and workflows
 - personnel support for different service desks



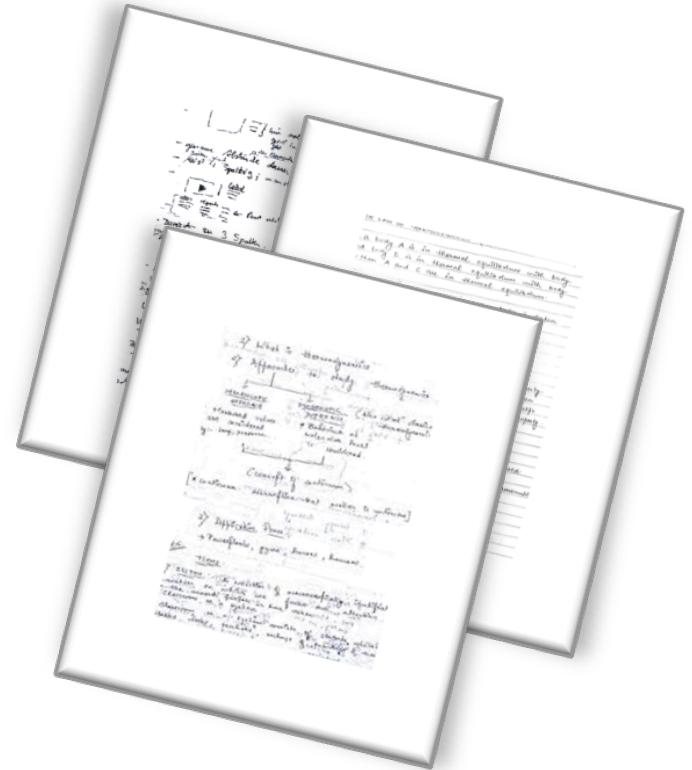
Basic services under development



Electronic Lab Notebooks (ELNs)

ELN ≈ Digital Protocol Editors

- Documenting daily lab routine
 - Lab methods & protocols
 - Lab inventory (biologicals, chemicals, instruments)
 - Local sharing & collaboration
 - Backup (locally)



ELNs help to digitalize research documentation

Are ELNs FAIR?

FAIR indicator*	ELN
Findable	
F1. (Meta)data are assigned a globally unique and persistent identifier.	
F2. Data are described with rich metadata (defined by R1 below).	
F3. Metadata clearly and explicitly include the identifier of the data they describe.	
F4. (Meta)data are registered or indexed in a searchable resource.	
Accessible	
A1. (Meta)data are retrievable by their identifier using a standardised	

Findable

FAIR indicator*	elabFTW
F1. (Meta)data are assigned a globally unique and persistent identifier.	 / 
F2. Data are described with rich metadata (defined by R1 below).	
F3. Metadata clearly and explicitly include the identifier of the data they describe.	 / 
F4. (Meta)data are registered or indexed in a searchable resource.	

Accessible

FAIR indicator*	elabFTW
A1. (Meta)data are retrievable by their identifier using a standardised communications protocol	●
A1.1 The protocol is open, free, and universally implementable	● / ●
A1.2 The protocol allows for an authentication and authorisation procedure, where necessary	?
A2. Metadata are accessible, even when the data are no longer available	?

Interoperable

FAIR indicator*	elabFTW
I1. (Meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.	●
I2. (Meta)data use vocabularies that follow FAIR principles.	●
I3. (Meta)data include qualified references to other (meta)data.	●

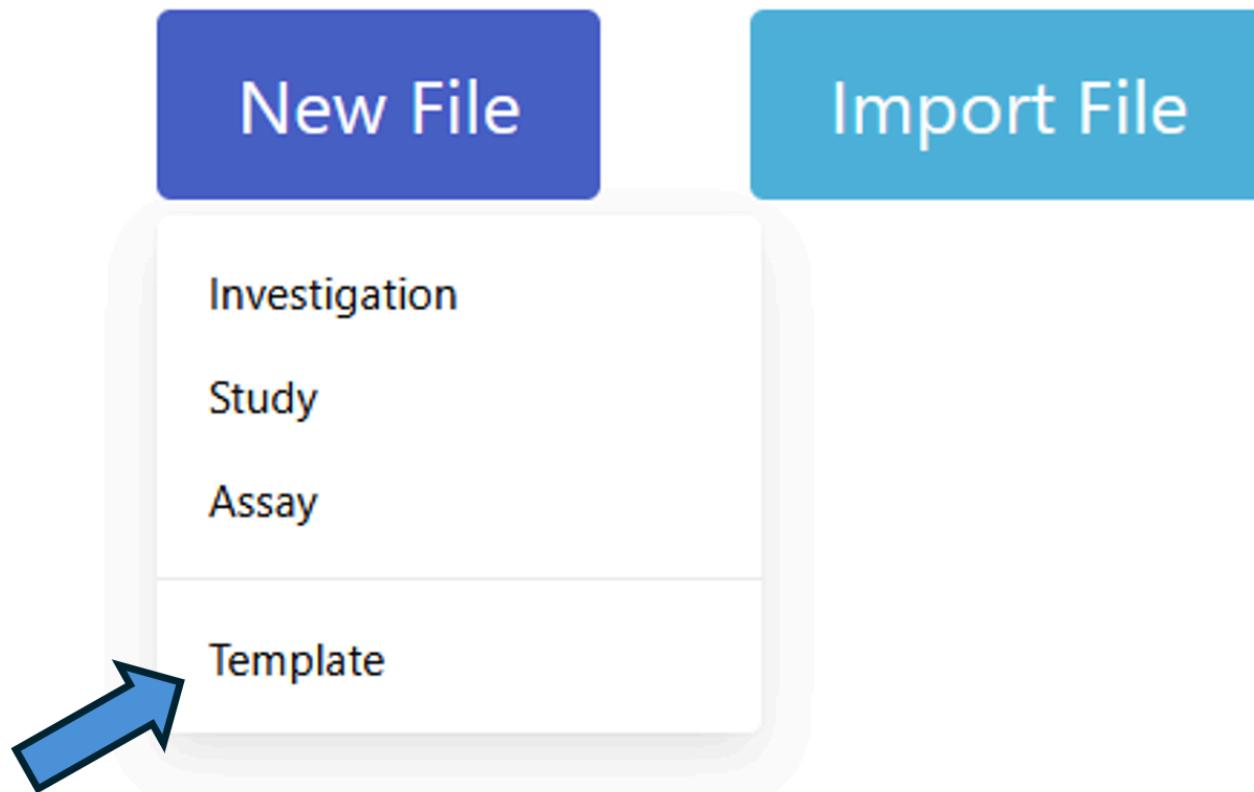
Reusable

FAIR indicator*	elabFTW
R1. (Meta)data are richly described with a plurality of accurate and relevant attributes	●
R1.1. (Meta)data are released with a clear and accessible data usage license	●
R1.2. (Meta)data are associated with detailed provenance	●
R1.3. (Meta)data meet domain-relevant community standards	●

Creating Swate Templates

Create or open a Swate template

Open [Swate-alpha](#). To create a new template click "New File" and select "Template". If you want to edit an existing template, click "Import" and select the respective file.



Add Template Metadata

- Once you open a new template, you will see a "Metadata" sheet.
- Enter a name for the template
- Add a description about the template

 Do not change the **Identifier**

Template Metadata

Key	Definition	Tip 
Identifier		<p>Do not change this field. It maps your template to a database entry</p> <p></p>
Name	This is the first info Swate users see about your template	<p>Try using a short, descriptive and human readable name. Capitalize the first letter of the first word.</p>
Description	Here you can describe your template.	<p>Users interested in your template can read this in Swate, but not in the database.</p>

Template Metadata Example

Example template metadata and how it helps in Swate's template search

Identifier		
a927fd4c-851f-4a69-8aa0-fc680f495a64		
Guid should contain 32 digits with 4 dashes following: xxxxxxxx-xxxx-xxxx-xxxx-xxxxxxxxxxxx. Allowed are a-f, A-F and numbers.		
Name		
DNA extraction		
Description		
Template to describe the extraction of DNA.		
Organisation		
DataPLANT		
Version		
1.1.7		
Last Updated		
21.03.2024, 02:53		
Tags		
1. Term Name	TSR	TAN
<input type="text" value="extraction"/>	<input type="text" value="OBI"/>	<input type="text" value="OBI:0302884"/>

Template Name	Community	Template Version	
DNA extraction	curated	1.1.7	▼

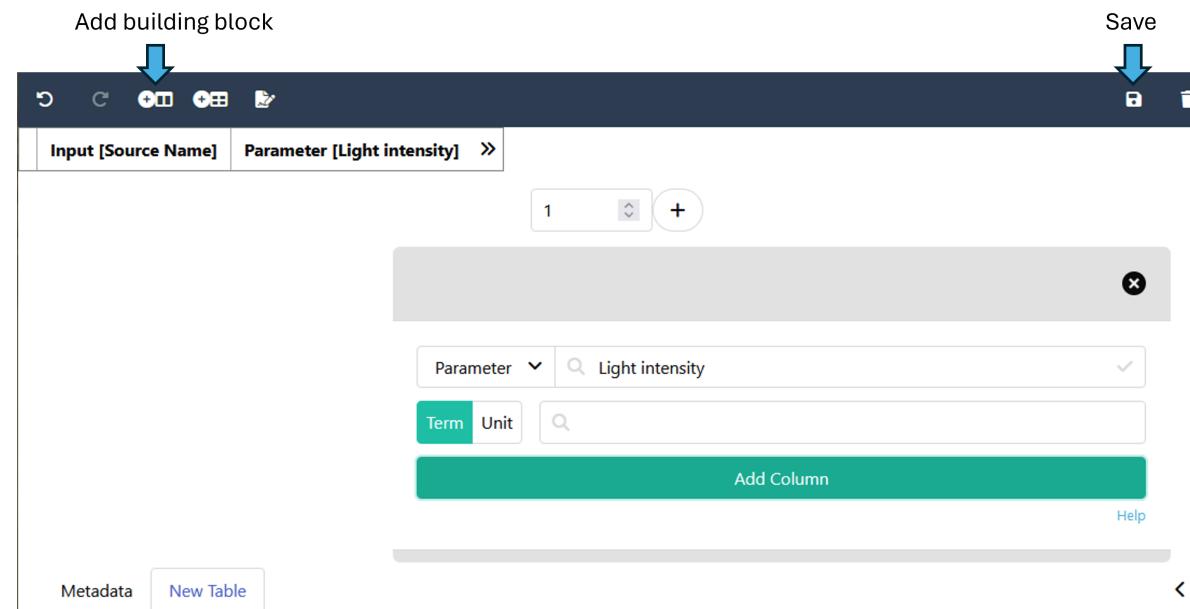
Template to describe the extraction of DNA.
Author: Angela Kranz, Dominik Brilhaus
Created: 2024/03/19
Organisation: DataPLANT

[extraction](#) [DNA](#)

select

Add building blocks

- To add building blocks to the actual template, switch from the "Metadata" sheet to the "New Table" sheet on the bottom left.
- Using the "Add Building Block" button, you can add your desired building blocks with or without a unit.



Recommendations for template design

- Keep the template as concise as possible
- If you miss a term or ontology, please follow the [DPBO contribution guide](#) to let us know
- If you add a template to address a missing method, try to add building blocks that cover experimental procedures (as Parameters) and features of the sample (as Characteristics) that the experimenter would use when working on an experiment of that type
- The typical order of the columns is: **Input** -> (all the Parameters and Characteristics in between in chronological order) -> **Output** -or- **Raw Data File** -or- **Derived Data File**. Try to think about in which order the experimenter in the lab will do their work. Try to match this chronological order from left to right. This step is optional and only meant to increase readability.

Recommendations for template design (continued)

- Avoid using the building block type `Factor` in templates. Any given characteristic or parameter in one study or assay can become a factor in another study or assay depending on the experimental context or scientific question.
- Background info on your template can be shared alongside the template via the [Swate-templates GitHub repository](#)

Recommendations for endpoint repository templates

- Please follow the following naming pattern: "Repository" - "Assay", e.g. MetaboLights - MS measurement
- The endpoint repository tag should be added ONLY in the "Endpoint repository" category in the metadata sheet
- By default repository templates should contain **only mandatory** information. In this case, please add "mandatory" as a tag.
- Optional or recommended information can be added with an extension template that contains only the optional/recommended information. In this case, please add "-extension" to the template name.
- If applicable, templates should be split into different assays.
- Templates should be checked for validity of requirements every ~ 6 months.

Save your template

- You can download and save your template as xlsx-file by clicking on the disc symbol in the top right corner.
- Please adjust the name of the file to correspond to the name of the template, but use underscores instead of spaces.
- Save the file in a suitable folder within your local clone of the Swate templates repository.

Your template is ready for upload



- Well done! You created a new template.
- You can now submit your template via GitHub
- Once your pull request is merged, you will receive an Email from "Swobup Commit Report"

GitHub Workflow to add or edit templates

1. (Recommended) [Create an issue](#) with background information about the template you want to add. This also serves as a place for discussion.
2. [Fork the Swate-templates repository](#).
3. (Recommended) Create a feature branch (e.g. "template-xy") on your fork.
4. [Clone](#) your fork-branch
5. Add/update **ONE** template ([see steps below](#))
6. Commit, push and [sync](#) your branch.
7. Open a [pull request](#)

 You can **reference your issue** typing `#` in the pull request's commenting dialog

Known pitfalls with Swate Templates

- Opening and saving a Swate template .xlsx file with a program other than Microsoft Excel (e.g. LibreOffice, python script, R script) often destroys the template (backend). Please, avoid to upload this file into the GitHub repository.

Contributors

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