

Open research data management with the ~~STOCKS~~ LabID platform

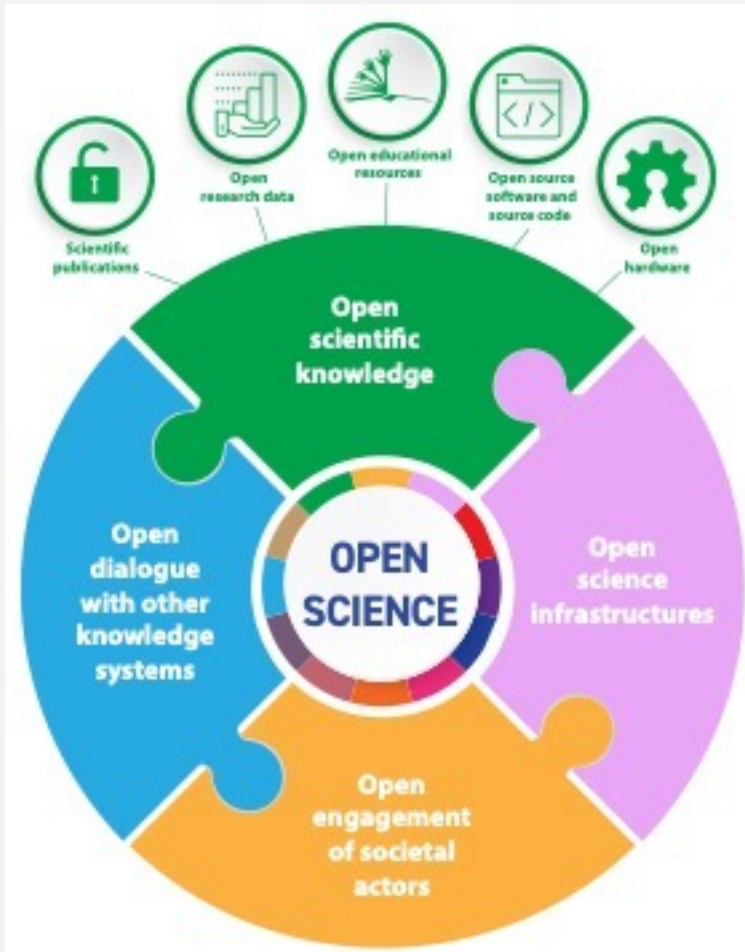
Charles Girardot
EMBL, Heidelberg
DeiC 2023, Kolding

Lab ID

Integrated Data



Open Science accelerates scientific progress and innovation

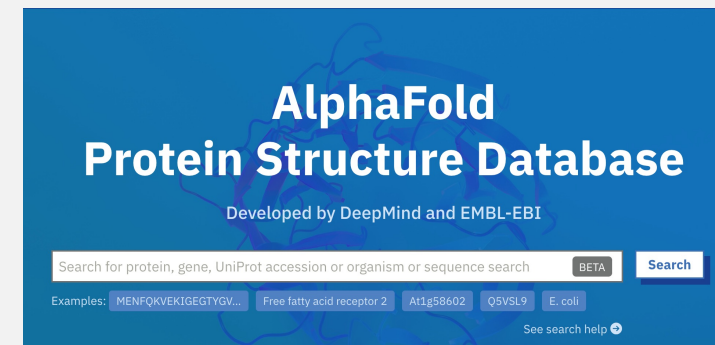


UNESCO Recommendations on Open Science (2021)

- Facilitates Knowledge Dissemination
- Encourages Reproducible Science
- Allows Fairer Science by sharing tools and data (lowers \$ barrier)
- Helps building Public Trust and Engagement
- Compliancy with Funding Agency Policies

“AlphaFold was trained on all known 200,000 protein structures in the Protein Data Bank – an archive that is the result of decades of work of thousands of molecular biologists around the globe.”

*Prof. Dr. Patrick Cramer, Max Planck Society President
(German AI Award Ceremony, Berlin, 28/9/2023)*

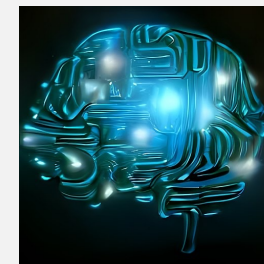
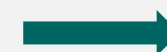


Open Science == Open **Data** + Open **Source** + Open **Access**

Data Management as a prerequisite of Open Data



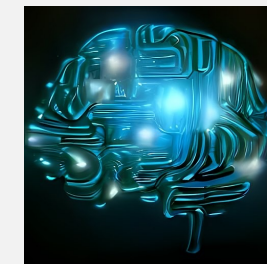
- Curated
- Structured
- FAIR



Data Management as a prerequisite of Open Data



- Curated
- Structured
- FAIR



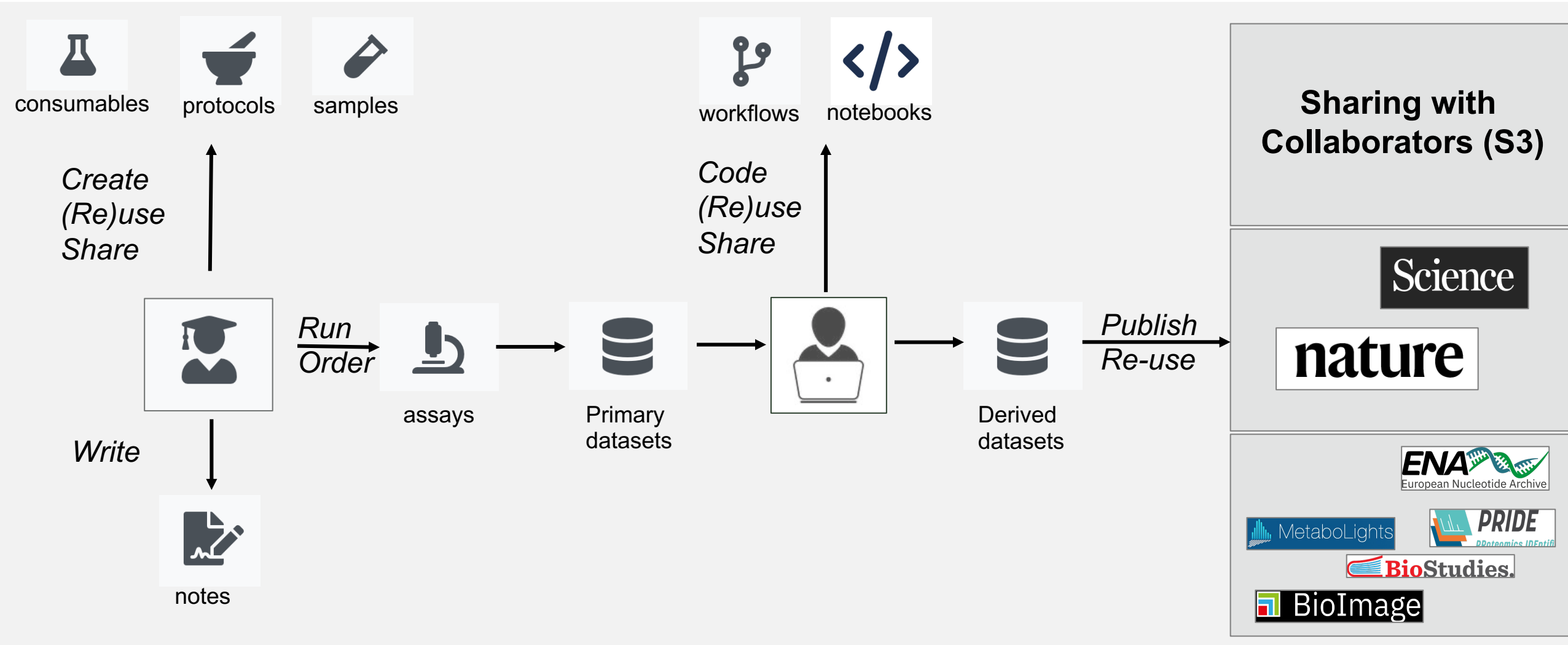
- Unpublished
- Actively Analyzed
- Waiting ... (lost?)
- Data stored ... somewhere



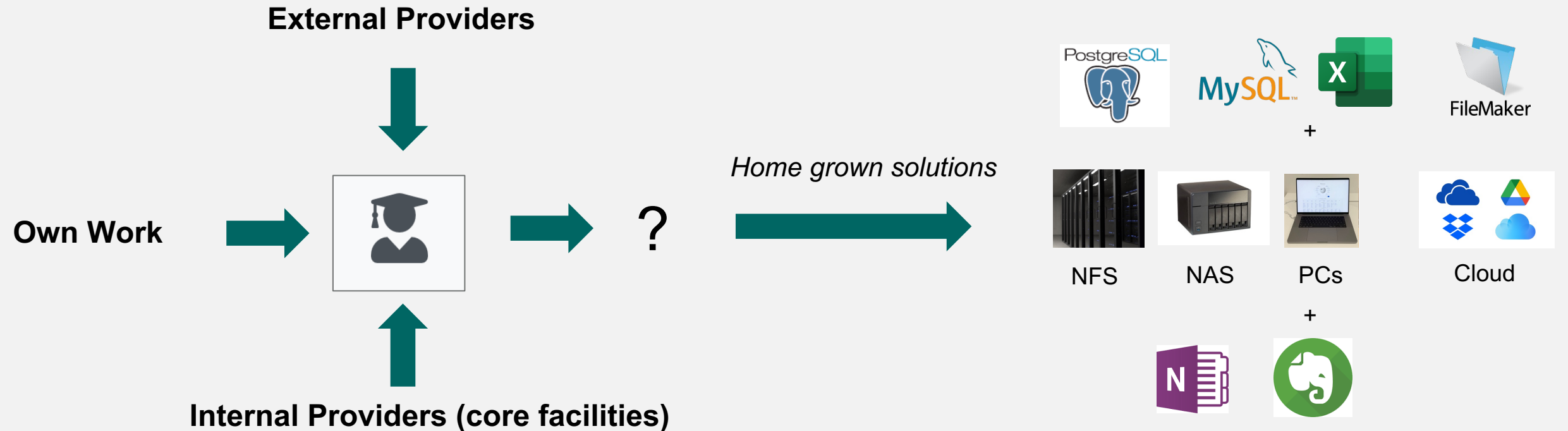
- Data explosion (size & technology)
- Bioinformaticians don't grow on trees
- How to share (meta)data with collaborators (e.g. AI)?
- Need of powerful Data Management tools

Open Data == Managed and FAIR Data from Day 1

Capturing high-quality (meta)data from creation to dissemination

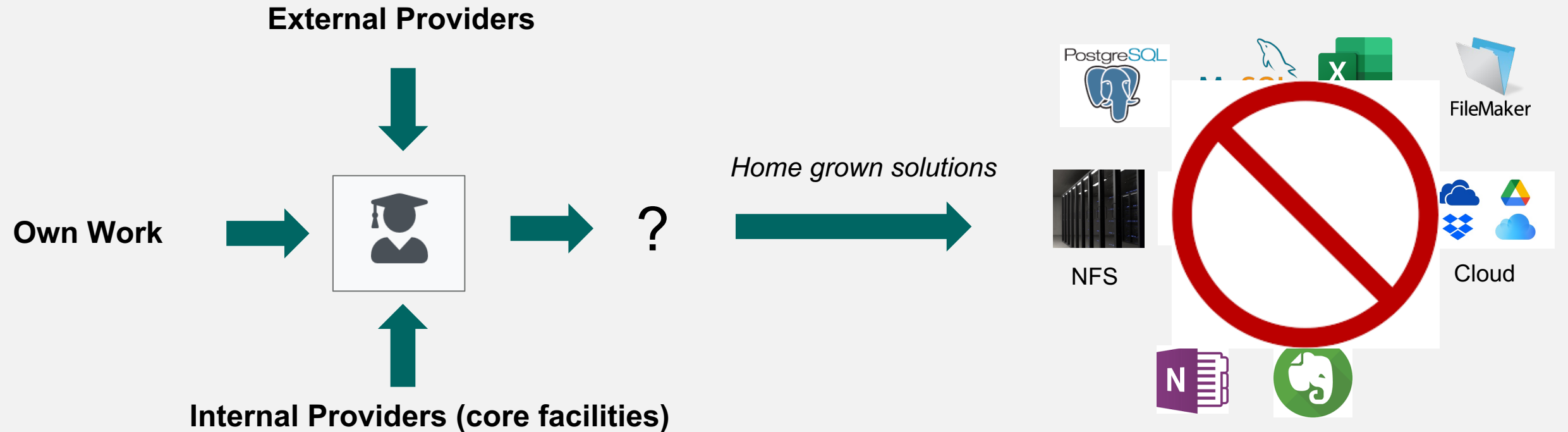


Data is often scattered in many places and solutions



- Users/Groups often left alone: home grown solutions
- Labs use more and more technologies (multi-omics, imaging assays)
- Data scattered in different places, registered in different systems
- X Difficult to collate all data together and keep information up to date

One place to manage all your data!



- X DM is often perceived as a burden
- X Exposing users to multiple systems is not the right answer
- ✓ Offer a system with **low entry level** that users **use frequently**

Lab Integrated Data: One-stop shop for managing all your data

- FAIR scientific Data Management solution
- Aims at covering your everyday DM needs
- Open Source
 - ❖ <https://gitlab.com/lab-integrated-data>
- Documentation & Online Training
 - ❖ <https://grp-gbcs.embl-community.io/labid-user-docs/>
- Demo Server
 - ❖ <https://labid-demo.embl.de/>

The screenshot shows the Lab ID web application interface. At the top left, it says "Welcome, Charles Girardot" and displays the "Lab ID Integrated Data" logo with the version "v23.10.0 (v23.10.0)". A navigation menu on the left lists categories: CONSUMABLES, EQUIPMENT, STORAGE EQUIPMENT, SPECIMEN, BIOMATERIALS, PROTOCOLS, LAB NOTEBOOK, ASSAYS, and DATASET MANAGEMENT. The main content area features a green announcement banner stating "STOCKS is becoming «Lab Integrated Data» (Lab ID)" and providing details about the name change and open-source availability. Below the banner, there's a "WELCOME TO Lab ID" section with a search bar. A "GET SUPPORT" section offers links for "READ THE DOCUMENTATION", "CHAT WITH US", and "EMAIL US". A small "You have ongoing experiments!" notification is visible in the top right. The footer includes "GBCS · 2018-present" and social media icons.

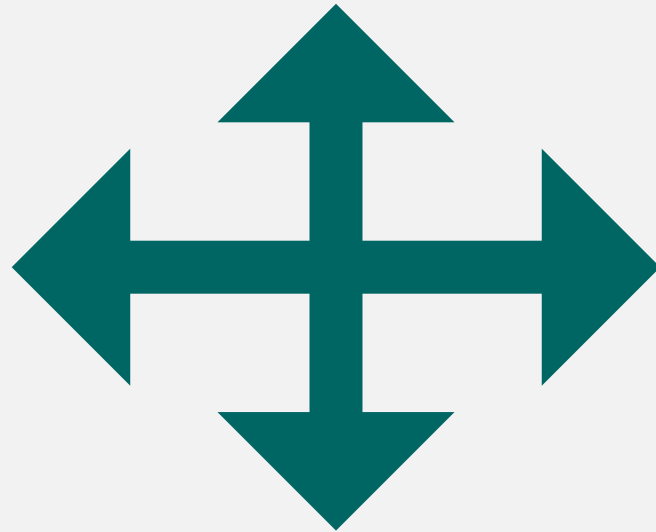
LabID articulates around 4 interconnected modules

Lab Collection Management

(Consumables, Equipment, Storage)

Dataset Management

(Assays, Datasets & Studies)



Biomaterial Management

(Sample & Specimen, Biobanking)

Electronic Lab Notebook (ELN)

(Project, Experiment & Protocols)

Searchable, customizable and extendable lab collections

The screenshot displays the 'Lab ID Integrated Data' interface for 'STORAGE EQUIPMENT - FREEZER'. The left sidebar shows a navigation menu with categories: CONSUMABLES, EQUIPMENT, and STORAGE EQUIPMENT (selected). Under STORAGE EQUIPMENT, there are sub-categories: Tower, Cabinet, Cryogenic, Freezers (selected), Fridges, Drawer, Shelf, Rack, Compartment, and Box. The main content area shows a table of freezer records. The table has columns for Name, Code, Stock locations, Origin/Vendor, and Catalogue #. A search bar at the top contains the text 'trec'. The table lists 13 records, all of which are 'TREC -80C Freezer' units from 'Eppendorf' with 'U535 Innova' as the catalogue number. The interface includes various UI elements like a search bar, filters, and a table with expandable rows.

Name	Code	Stock locations	Origin/Vendor	Catalogue #
TREC -80C Freezer 1	trec-80-freezer-1	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 10	trec-80-freezer-10	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 11	trec-80-freezer-11	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 12	trec-80-freezer-12	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 13	trec-80-freezer-13	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 2	trec-80-freezer-2	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 3	trec-80-freezer-3	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 4	trec-80-freezer-4	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 5	trec-80-freezer-5	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 6	trec-80-freezer-6	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova

- Consumables, Equipment & Storage Equipment
- Extensive **search and filtering** options
- Customizable table views
- New **types** can be added **without coding** (Admin UI)

Searchable, customizable and extendable lab collections

The screenshot shows the LabID interface for 'STORAGE EQUIPMENT - FREEZER'. It features a search bar with 'trec' entered, a table with columns for Name, Code, Stock locations, Origin/Vendor, and Catalogue #, and a sidebar with navigation options like Tower, Cabinet, Cryogenic, and Freezers.

Name	Code	Stock locations	Origin/Vendor	Catalogue #
TREC -80C Freezer 1	trec-80-freezer-1	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 10	trec-80-freezer-10	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 11	trec-80-freezer-11	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 12	trec-80-freezer-12	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 13	trec-80-freezer-13	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 2	trec-80-freezer-2	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 3	trec-80-freezer-3	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 4	trec-80-freezer-4	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 5	trec-80-freezer-5	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova
TREC -80C Freezer 6	trec-80-freezer-6	9A E-1 Bio Hub Storage	Eppendorf	U535 Innova

The screenshot shows the detailed view for 'Halo-H2B-N-10'. It includes fields for ID, Vector, Vector Size, Antibiotic Resistance, Insert details, Insert Size, Insert 5p RE, Insert 3p RE, Insert sequence, Code, Origin/Vendor, Catalogue #, Lot #, Concentration/Amount, Expiration date, Description, Storage Conditions, Location, and Breadcrumb. It also features sections for Annotations, Attachments, Notes, and Orders.

Item details

ID: 2bb864f2-7fe3-44d2-aacc-6b06ca5cae9f

Vector: N-10

Vector Size: 5226 bp

Antibiotic Resistance: kanamycin

Insert details: H2B-Halo

Insert Size: 1287 bp

Insert 5p RE: —

Insert 3p RE: —

Insert sequence: —

Code: 2-33

Origin/Vendor: Deo Lab (Bego)

Catalogue #: —

Lot #: —

Concentration/Amount: 352.15 ng/µl

Expiration date: —

Description: * We removed TOMM20 (NheI and BamHI) and inserted H2B (amplified from plasmid 1-25 with restriction enzymes NheI and BamHI for ligation with T4 DNA Ligase)

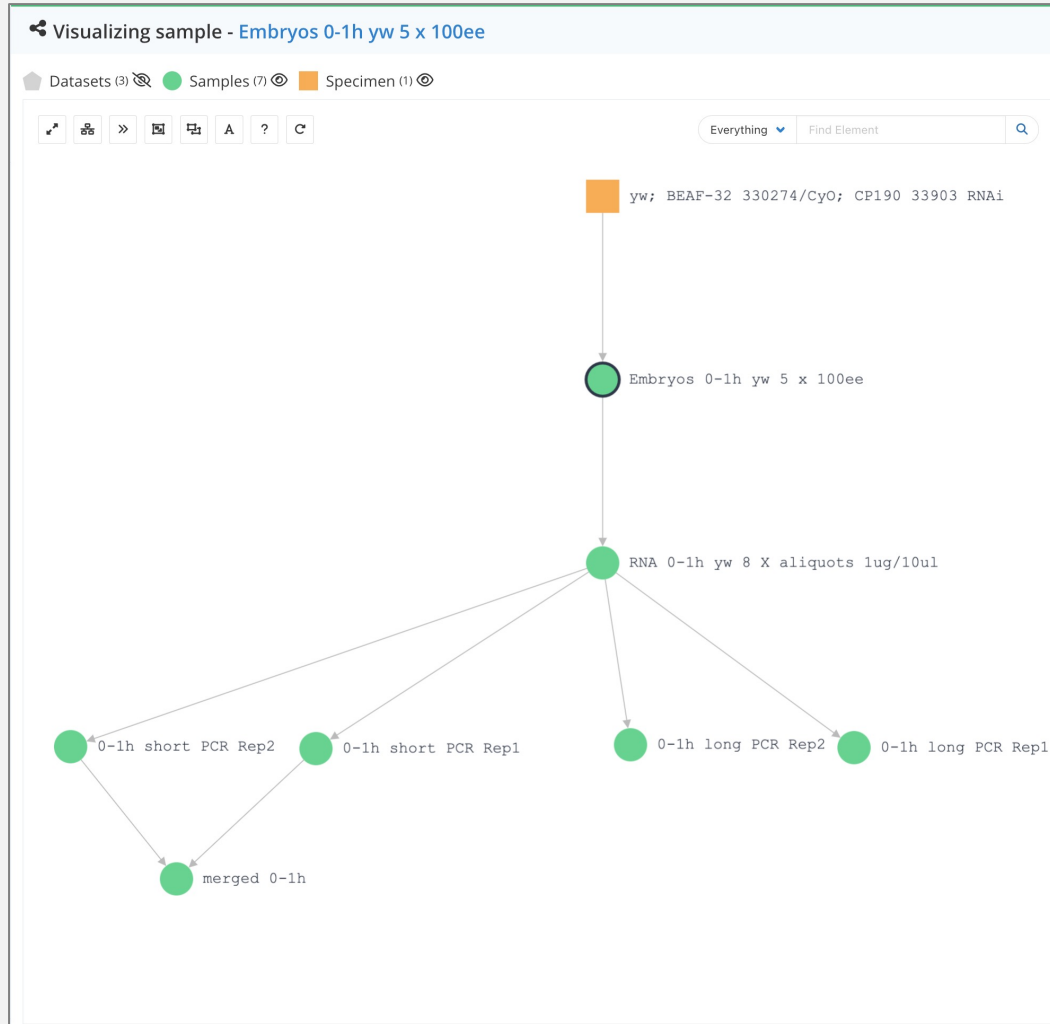
Storage Conditions: —

Location: -80 Freezer:2-33, V314 Equipment Room > Box:2-33

Breadcrumb: —

- **Customizable** Item Properties (text, number, CVs, item type...)
- Detailed Item **Location**
- Annotations, **Attachments** & Notes (Orders)
- Fine grained **sharing** (per user or group)
- **Batch** create & edit

Accurately reflect your sample processing workflow



- **Graphical Lineage** of relationships
- **Unlimited** step number
- **Merge & Split** supported
- **Specimen** are your living collections (fly lines, cell lines ...)
- **Samples** may derive from **Specimen**

A rich sample model fitting most situations

The screenshot displays a web application interface for managing biomaterial samples. The main content area is divided into several sections:

- Annotations:** A table listing key attributes such as InitialTimePoint (egg laying), StrainOrLine (yw), Compound Dose (400 mg), IndividualGeneticCharacteristics (wild-type), Compound (ibuprofen), and Age (0-1h).
- Attachments:** A section for uploading files, currently empty with a 'Drag & Drop your files or Browse' instruction.
- Notes:** A section for adding notes, currently empty with a 'Write a note' input field and an 'Add' button.
- Lineage Graph:** A visual representation of the sample's lineage, showing a flow from a specimen to a sample and then to multiple aliquots.

The sidebar on the left provides detailed information about the sample:

- ID:** 4acba913-8e17-4d75-934c-231d80e9819
- Name:** Embryos 0-1h yw 5 x 100ee
- Code:** XYZ-3345
- Project:** Wonderful microscope project
- Status:** CREATED, Sample QC PASSED
- Organism:** Drosophila melanogaster (Fly)
- Material Type:** whole organism (Whole Organism)
- Description:** —
- Storage Locations:** 1. Tube A12-, Furlong Freezer 2 (-20) in V320 Furlong Laboratory
- Locations paths:** V320 Furlong Laboratory > Furlong Freezer 2 (-20) > Tube:-
- Workflow:** Fly Growth Protocol, Fly embryo collection
- Sample Preparation:** Is Control (no), Is Single Cell (no), Use Screen Position (no)
- Sample Lineage:** Derives from Specimen (yw; BEAF-32 330274/CyO; CP190 33903 RNAi), Children (RNA 0-1h yw 8 X aliquots 1ug/10ul)
- Link to ELN:** Used in Experiments (yw RNA extraction for smth seq), Produced by Experiment (yw embryo collection for RNA extraction)
- Sharing:** —
- Ownership and Lifecycle:** —

- **Samples** have **code**, **project** and **location**
- Samples may be linked to **protocols**
- Samples can be **annotated**
- **Activable sections** for **control**, **single-cell** and **plated** samples
- Connection to **ELN**

Describe protocols with details and share with your lab

PROTOCOLS - LABELING

Fixation and staining - version 2

Summary
Fixation in 3.7 % PFA in 100 % EtOH, staining with DAPI and Phalloidin

Fixation and Staining of sponges in PFA

- gemmules are grown in glass bottom dishes
- under the hood: prepare fixative
 - 3.7 % (P)FA [37 % stock solution]
 - 100 % ice-cold EtOH
 - e.g.: 720 uL EtOH + 80 uL PFA
- remove all of the FLW from the sponges
- add 200 uL of the fixative directly to the glass bottom (sponges should be covered)
 - otherwise, use more fixative --> 1 mL
- incubate for 30 min - 1 h at 4 oC
- wash 3 x with 5 mL PBS
 - keep third washing step for 10 min
- remove PBS
- add 200 uL of staining solution
 - e.g.: DAPI, Phalloidin, antibody staining

Item details

ID	1f76b3b6-1f8a-4e8a-8bad-211e868df7c3
Type	LABELING
Parent protocol	Fixation and staining
Modified	2023-10-27 18:16:23

- **Protocols** are **cooking recipes**
- **Rich text** formatting
- Embed **tables and images**
- **Attach** documents e.g. excel table
- Export to **PDF**
- **Protocols** may be **versioned** (“Clone”)
- **Protocols** act as templates for **Experiments**

An experiment is an entry in your ELN

PROTOCOLS - LABELING

Fixation and staining - version 2

Summary
Fixation in 3.7 % PFA in 100 % EtOH, staining with DAPI and Phalloidin

Fixation and Staining of sponges in PFA

- gemmules are grown in glass bottom dishes
- under the hood: prepare fixative
 - 3.7 % (P)FA [37 % stock solution]
 - 100 % ice-cold EtOH
 - e.g.: 720 uL EtOH + 80 uL PFA
- remove all of the FLW from the sponges
- add 200 uL of the fixative directly to the glass bottom (sponges should be covered)
 - otherwise, use more fixative --> 1 mL
- incubate for 30 min - 1 h at 4 oC
- wash 3 x with 5 mL PBS
 - keep third washing step for 10 min
- remove PBS
- add 200 uL of staining solution
 - e.g.: DAPI, Phalloidin, antibody staining

Item details

ID	1f76b3b6-1f8a-4e8a-8bad-211e868df7c3
Type	LABELING
Parent protocol	Fixation and staining
Modified	2023-10-27 18:16:23

EXPERIMENTS

Fixation and staining - version 2 - 2023-10-27 18:22:52

Project
Wonderful microscope project

Estimated Completion Date
2023-11-03

Status
(in progress)

Created on
2023-10-27 18:22:52

Fixation and Staining of sponges in PFA

- gemmules are grown in glass bottom dishes
- under the hood: prepare fixative
 - 3.7 % (P)FA [37 % stock solution]
 - 100 % ice-cold EtOH
 - e.g.: 720 uL EtOH + 80 uL PFA
- remove all of the FLW from the sponges
- add 200 uL of the fixative directly to the glass bottom (sponges should be covered)
 - otherwise, use more fixative --> 1 mL

It worked

Item details

ID	c6208f09-1a4c-43c1-838b-34685912bb7
Deleted	no
Summary	—
Start date	2023-10-27
Completed	—
Frozen	no

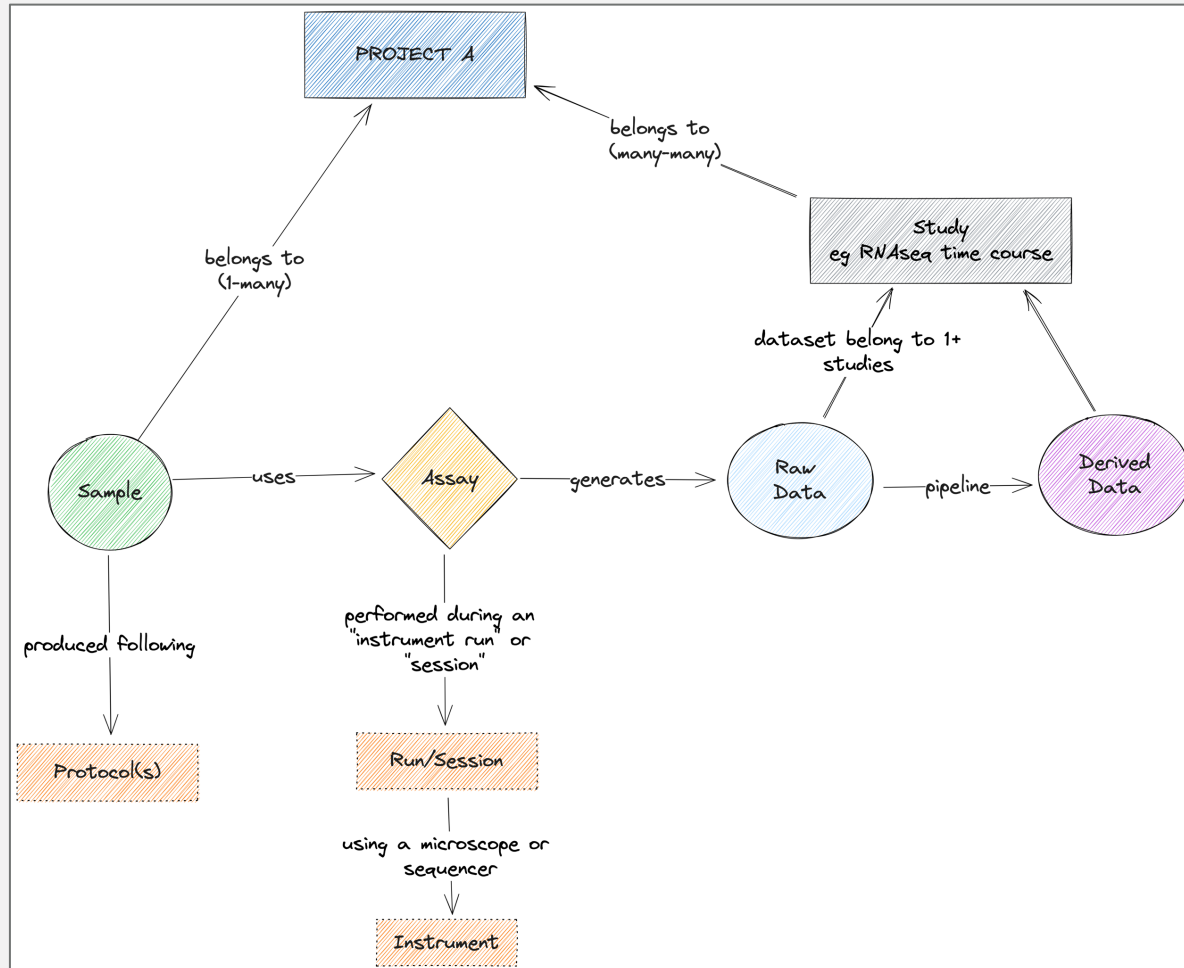
Linked items 5

- 0-Nitrophenyl β-D-Galacto-Pyranoside
- 0.3% alcian blue in 70% ethanol
- 10 mM Alexa Fluor™ 405 NHS Ester in DMSO
- Aatl
- Accl

Attachments 2

- **Experiments** represent a particular lunch
- Experiments are grouped into **Projects**
- Experiments have a **life-cycle**
- **Frozen experiment** are electronically **timestamped**

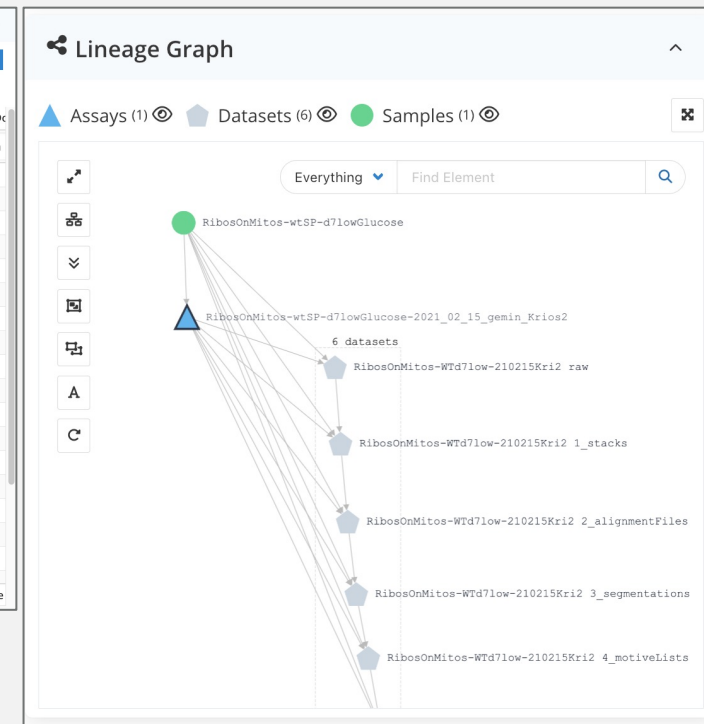
Performing an Assay generates (raw) Datasets



- **Raw** data is generated by **Assays**
- **Raw & Derived** are organized into **Studies**
- A Study groups **datasets** of the **same technology** (e.g. sequencing) and **experiment type** (e.g. ChIP-seq) that may come from **multiple assays**
- **Similar to the ISA model (MAGE-TAB)**

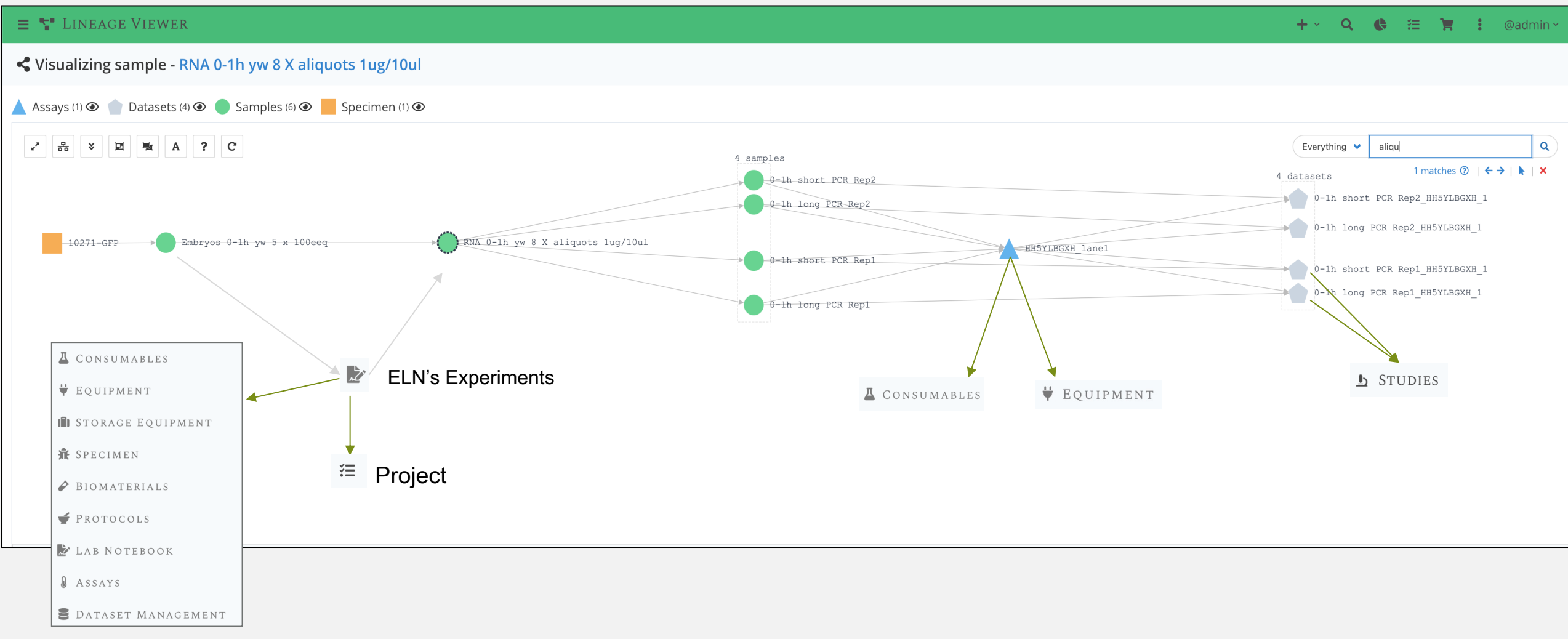
Flexible dataset granularity and composition

Name	Type	QC	Samples	Assay	Age	CellLine	Compound	Compound Dose
d4fbfc8e-69e3-482f-befb-156aa1ef803f	free text search	Select option	Select option	free text search	free text search	free text search	free text search	free text search
Single-gastruloid transcriptomics: control vs glycolysis inh...	96t6	single-end fastq	PASSED	96t6	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96t5	single-end fastq	PASSED	96t5	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96t4	single-end fastq	PASSED	96t4	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96t3	single-end fastq	PASSED	96t3	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96t2	single-end fastq	PASSED	96t2	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96t1	single-end fastq	PASSED	96t1	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96c6	single-end fastq	PASSED	96c6	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96c5	single-end fastq	PASSED	96c5	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96c4	single-end fastq	PASSED	96c4	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96c3	single-end fastq	PASSED	96c3	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96c2	single-end fastq	PASSED	96c2	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	96c1	single-end fastq	PASSED	96c1	AAJ2Y7M5_lane1	96h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	48t6	single-end fastq	PASSED	48t6	AAJ2Y7M5_lane1	48h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	48t5	single-end fastq	PASSED	48t5	AAJ2Y7M5_lane1	48h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	48t4	single-end fastq	PASSED	48t4	AAJ2Y7M5_lane1	48h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	48t3	single-end fastq	PASSED	48t3	AAJ2Y7M5_lane1	48h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	48t2	single-end fastq	PASSED	48t2	AAJ2Y7M5_lane1	48h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM
Single-gastruloid transcriptomics: control vs glycolysis inh...	48t1	single-end fastq	PASSED	48t1	AAJ2Y7M5_lane1	48h post-aggregatio	E14, Bra::GFP mESCs	2-Deoxy-D-glucose 6 mM



- A **Dataset** is made of **one or multiple files and/or folder** to accommodate different use cases
- **Derived** datasets may optionally be linked to samples (and assays)
- Datasets can be **accessed and filtered by** assays, studies, projects, samples or annotations
- Actual files/folders are stored in **group-specific, read-only LabID data library** (local network)
- Datasets can be **archived to free up space**

LabID covers the whole data production phases



A growing number of supported assay types & technologies



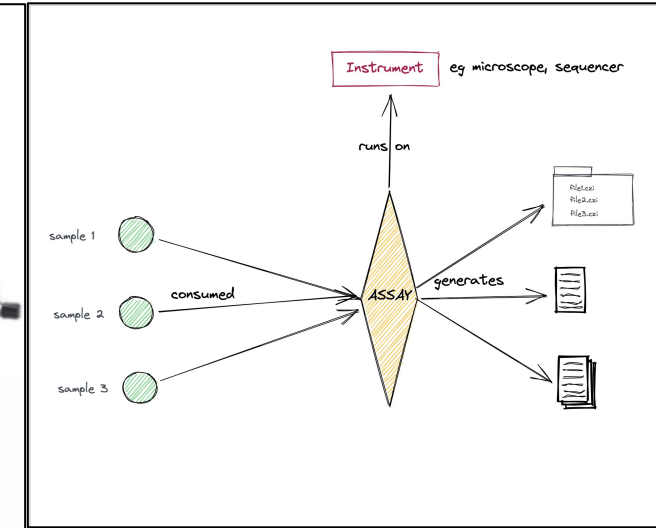
Sequencing



Light Microscopy



Electron Microscopy



Generic

- Assay support: Standards, Formats, Vocabulary & Metadata definition matching CF, users & public repository needs
- Generic Assay to kick in when specific assay type is missing
- ❖ Next: proteomics, metabolomics and flow cytometry

Supporting standards with sub-types and controlled vocabulary

BIOMATERIALS

- Sample
- Sequencing Library
- EM Sample

ASSAYS

- Generic
- Light Microscopy
- Light Microscopy Screen
- Nanopore Sequencing
- Illumina Sequencing
- Transmission EM
- Volume EM
- Instrument Runs

- **Sample** and **Assay sub-types** to support standards' needs
- **Custom properties** can be defined by admin
- **(Custom)Properties & Annotations** can be linked to **controlled vocabulary**

Dox Dox HP_1a

ID	f6b5e90a-6054-492f-bfe6-1fa6b6f65971		
Name	Dox Dox HP_1a		
Code	—		
Project	emBASE Migration - Lancrin Group		
Status	CREATED	Sample QC	PASSED
Organism	Mouse (Mus musculus)	Material Type	cell (Cell)
Description	—		

Order Number order-324 **Custom Property**

Storage Locations —

Locations paths

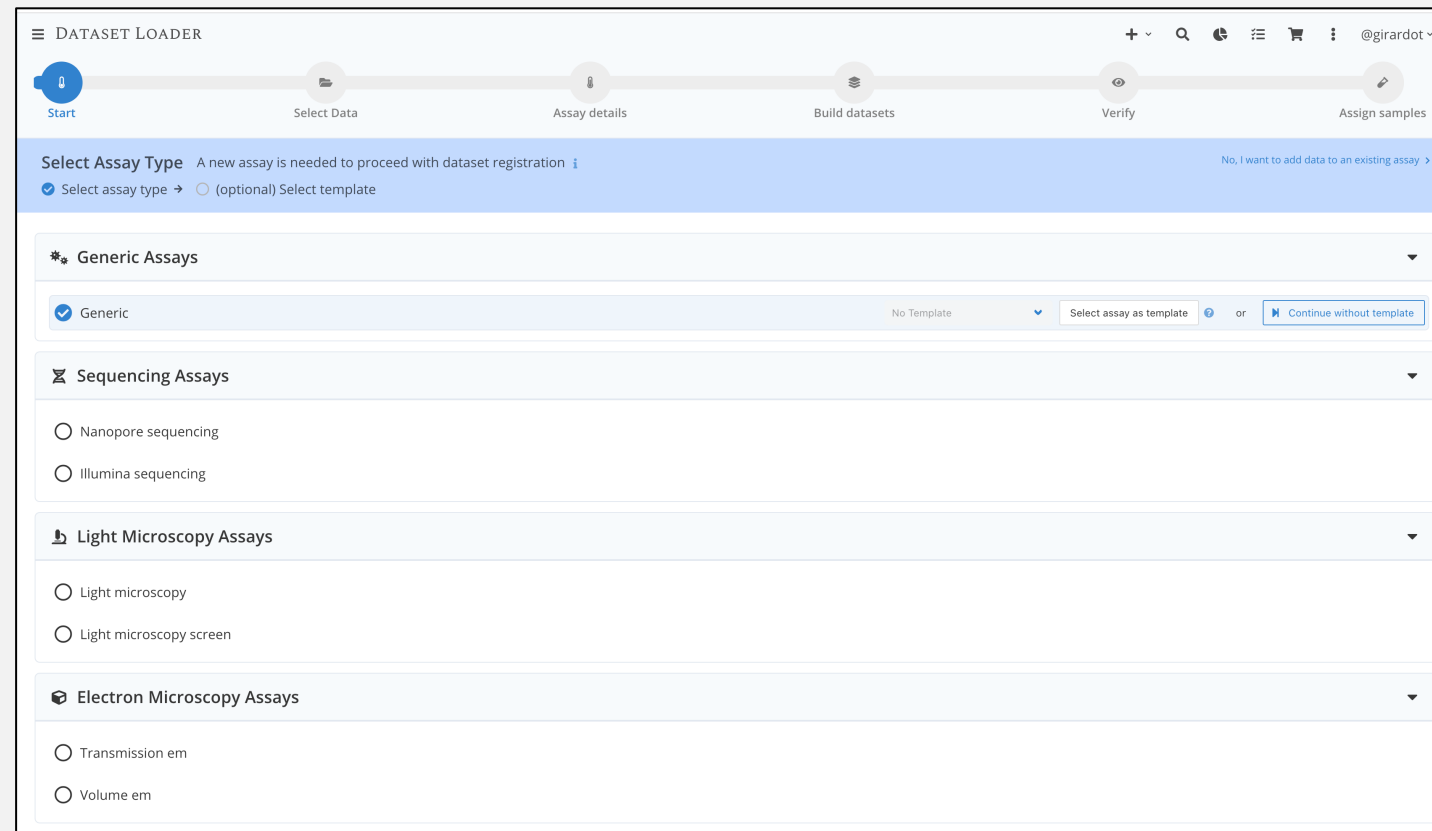
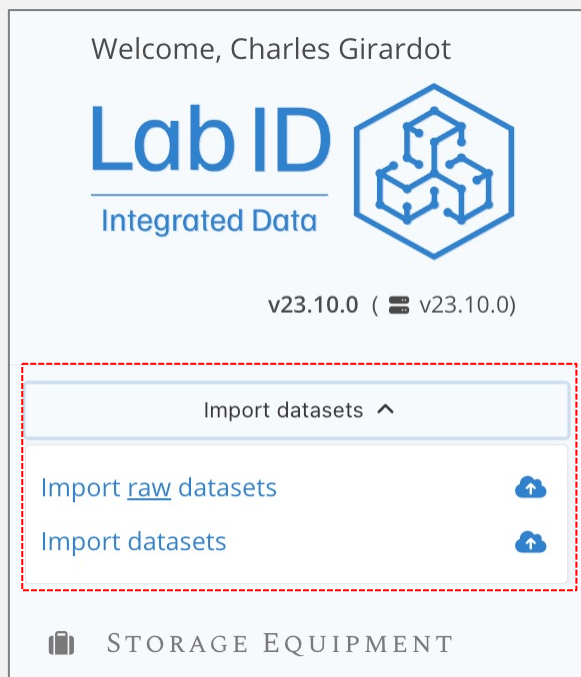
Workflow

- Generation of Tal1Δ/Δ doxycycline-inducible Embryonic Stem Cell (ESC) lines (i3TFs Tal1 Δ/Δ mESCs)
- ↓
- ESC growth, hematopoietic differentiation and cell sorting
- ↓
- RNA-seq

Sequencing Library Preparation ▶

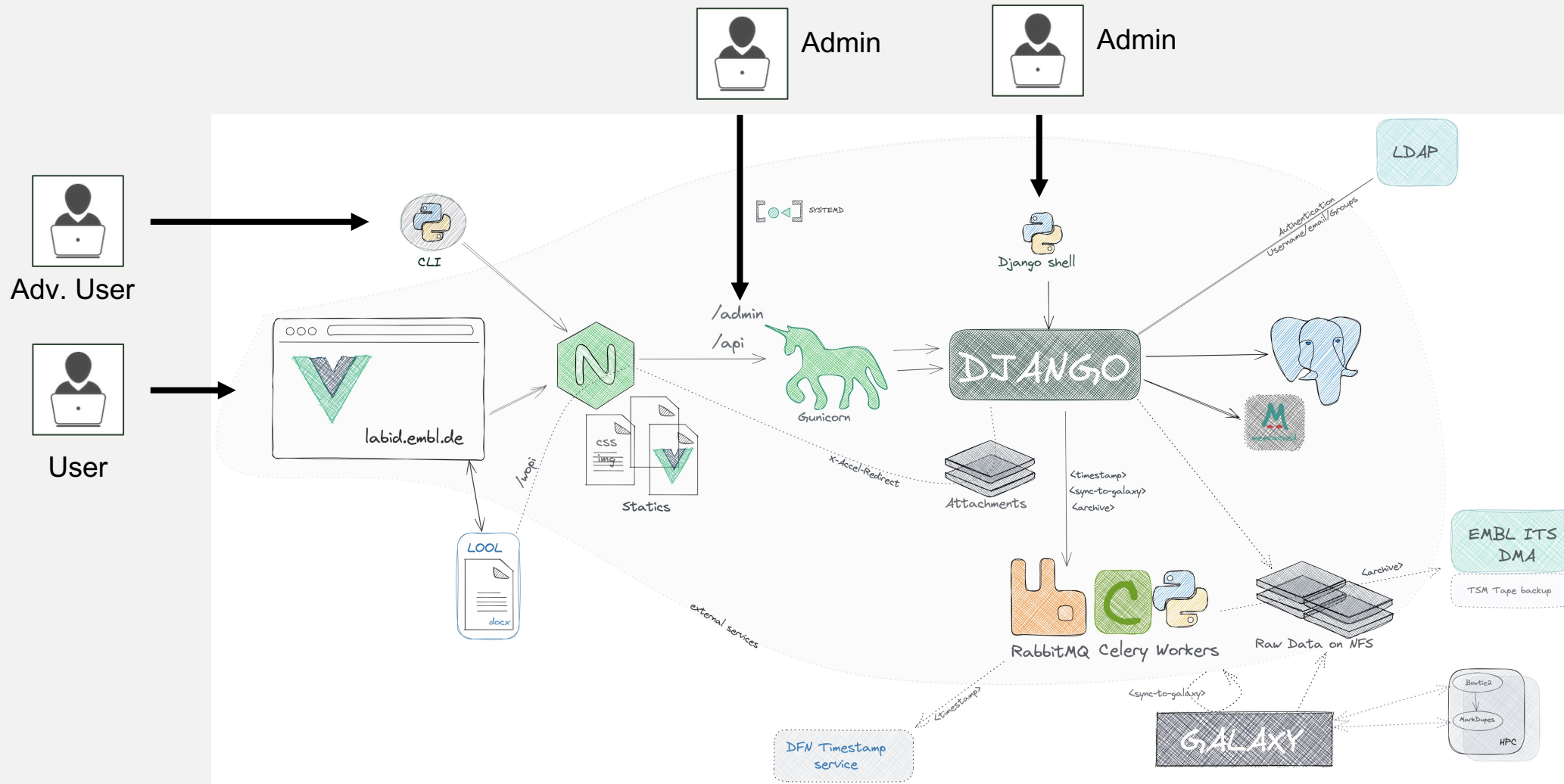
Library Kit Type	—	Orientation	5'-3'-3'-5' (5'-3'-3'-5')
Barcode	GCTCATGA	MINISEQ Support	
Source	TRANSCRIPTOMIC (TRANSCRIPTOMIC)	Strategy	RNA-Seq (RNA-Seq)
Selection	cDNA (cDNA)	RT Primer Type	oligo-dT
Library Strand	—	End Bias	—
Is Control	✗ no	Is Single Cell	✗ no
Use Screen Position	✗ no		

Generic Data Loader Wizard to support the many flavors of a “dataset”



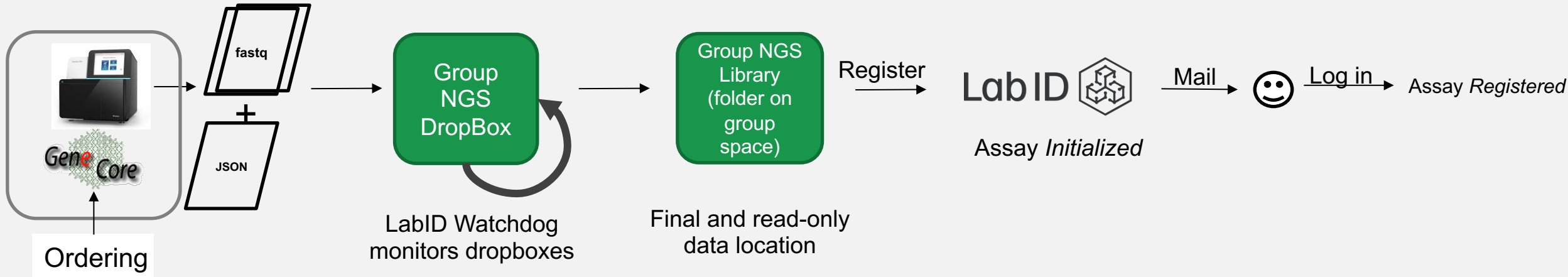
- **Intuitive wizard** to guide user in dataset registration & ensure minimal information is provided
- **Flexible** on Dataset granularity (file, folder) and composition (multiple files per datasets)
- **Derived Datasets** can also be loaded and linked to their parent datasets

LabID offers several clients and use a range of services



➤ The API allows to easily develop your own clients

Automated Data Ingestion



- No data loss
- Information available at GeneCore is passed on
- Enforce minimum information collection: samples, meta-data
- Files are protected from user manipulation (read-only) while accessible for analysis

Data processing using Galaxy Workflow

ATAC-seq of wildtype or Dppa2 knockout ESC upon release of...

Item details

ID: 2735409c-3cc2-47a9-a7d7-799c7eb70695

Project: VC20_007 CnR in Dppa2KO

Design: biological replicate, genotype design

PubMed ID:

Description: Chromatin accessibility was assayed in *wildtype* or *Dppa2* knockout ESC after 26 days of release of the trigger imposed by epigenetic editing. Samples were collected in two clonal *knockout* and *wildtype* lines after sorting at FACS of cells which maintained a repressive Esg1-tdTomato (TOMneg) reporter expression after 26 days of DOX washout (release of the trigger).

Nr. of datasets: 4

Archives:

Modified: 2021-05-11 11:56:49

Modified by: girardot

Created: 2021-05-05 14:34:19

Created by: carlini

Owner: carlini

Owned by Group: Hackett Group

Permissions:

	View	Edit	Delete
Groups			
Hackett Group	✓	✓	
Users			
carlini	✓	✓	✓
girardot	✓	✓	✓

Datasets

Name	Description	Type	QC	Samples
KOB67dWTOMneg_HG7WLBGXG_1		paired-end fastq	PASSED	KOB6_26dDW_TOI
KOC77dWTOMneg_HG7WLBGXG_1		paired-end fastq	PASSED	KOC7_26dDW_TOI
WT126dDW_HG7WLBGXG_1		paired-end fastq	PASSED	WT1_26dDW
WT226dDW_HG7WLBGXG_1		paired-end fastq	PASSED	WT2_26dDW

No data duplication

Galaxy

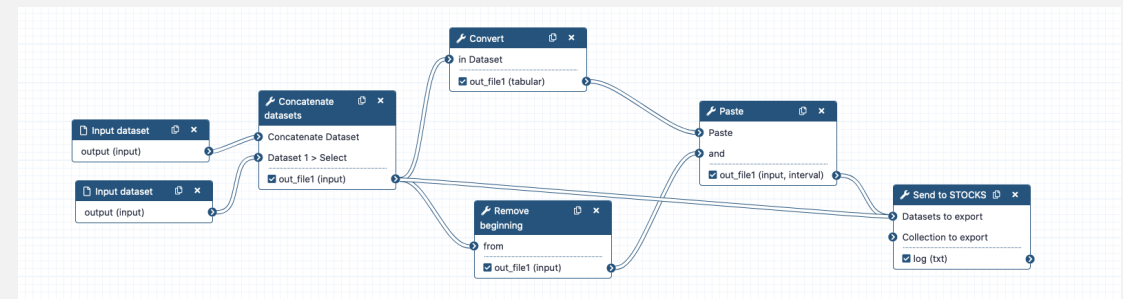
Workflow Visualize Shared Data Admin Help User

Libraries / Hackett Lab / VC20_007 ATAC-seq Dppa2KO

Name	Description	Type	Size	Updated	State
H57WLBGXG_VC20_006-VC20_007_20u002698-1-1_Carlini_JaneKOB67dWTOMneg_1_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	845.3 MB	a year ago	Manage
H57WLBGXG_VC20_006-VC20_007_20u002698-1-1_Carlini_JaneKOB67dWTOMneg_2_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	847.1 MB	a year ago	Manage
H57WLBGXG_VC20_006-VC20_007_20u002698-1-1_Carlini_JaneKOC77dWTOMneg_1_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	241.6 MB	a year ago	Manage
H57WLBGXG_VC20_006-VC20_007_20u002698-1-1_Carlini_JaneKOC77dWTOMneg_2_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	242.5 MB	a year ago	Manage
H57WLBGXG_VC20_006-VC20_007_20u002698-1-1_Carlini_JaneKOB67dWTOMneg_1_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	421.1 MB	a year ago	Manage
H57WLBGXG_VC20_006-VC20_007_20u002698-1-1_Carlini_JaneKOC77dWTOMneg_1_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	1.1 GB	a year ago	Manage
H57WLBGXG_VC20_006-VC20_007_20u002698-1-1_Carlini_JaneKOC77dWTOMneg_2_sequence.txt.gz	uploaded fastqsanger.gz file	fastqsanger.gz	1.1 GB	a year ago	Manage

<https://galaxy.embl.de>

Start ATAC-seq Standard WF



All jobs executed on ITS HPC

Analyzed Data



Remain free

➤ Use what you need

- ✓ Inventory, Biomaterial, Datasets & ELN modules can be use independently

➤ Export about everything you want

- ✓ Export any collections (excel sheets)
- ✓ Export Lab Notebook and Protocols as PDF & static web site
- ✓ Export Studies with all metadata i.e. sample, assay and dataset annotations
- ✓ Datasets remains available on accessible disks

➤ Batch create, edit, share & delete

- ✓ Easily import data using excel spreadsheet

➤ Free and Open Source

- ✓ Published under an open-source MIT license

Thank you for listening



**Jelle
Scholtalbers**



**Matthias
Monfort**



**Nayeem
Reza**



Eileen Furlong



Rainer Pepperkok

Alumni

Markus Fritz
Vincent Schiano de Collela
Frederic Jung
Sajoscha Sauer

LabID Public Repository

❖ <https://gitlab.com/lab-integrated-data>

LabID Demo Server

❖ <https://labid-demo.embl.de/>

Documentation & Online Training

❖ <https://grp-gbcs.embl-community.io/labid-user-docs/>

➤ <https://www.embl.org/gbcs>

Interested? Questions? Get in touch !