

A photograph of a yellow concrete ledge with two metal handrails, set against a bright blue background. The handrails are made of dark metal and are mounted on the ledge. The concrete has some visible cracks and texture. The blue background is a solid, vibrant color.

STOCKS Training: The embedded Electronic Lab Notebook

Charles Girardot

Genome Biology Computational Support (GBCS)

Your ELN is composed of experiments organized into projects

Welcome, Charles Girardot

STOCKS v1.27.0 (v1.22.0)

Import datasets ▾

- CONSUMABLES
- EQUIPMENT
- STORAGE EQUIPMENT
- SPECIMEN
- BIOMATERIALS
- PROTOCOLS**
 - Project
 - Experiment
 - Study
- ASSAYS
- DATASET MANAGEMENT

You have ongoing experiments!
[View your dashboard](#)

WELCOME TO
STOCKS

Search...

GET SUPPORT

- [Read the documentation](#)
- [Chat with us](#)
- [Email us](#)

BROUGHT TO YOU BY

GBCS

- The ELN is primarily composed of **Experiments** that belong to **Projects**
- The **Protocols** are tightly related to the ELN

The ELN's experiment

An experiment ...

- reflects the execution of one (or more) protocol
- contains all the details not always described in the protocol
 - results and conclusions (pictures, tables...)
- belongs to one project

Main features:

- Word-like embedded text editor
- Insert list, tables & image (png, jpeg)
- Attach documents
- Link any items from lab inventory
- Share
- Freeze and electronic timestamping (IP protection)
- Export as PDF or Archive
- Link Samples (both **In** and **Out**)

EXPERIMENTS

Final selection and analysis of ChIP-seq NC14 samples

This experiment is frozen and has been digitally signed for IP purposes. Unfreezing the experiment to further edit it, should be considered an exceptional action.

Project: Gaby Project

Completed on: 2020-01-16 14:38:32

Status: ✓ (completed)

Created on: 2020-01-13 09:39:19

condition	R1	R2	Input1	Input2	IDR 1%	IDR 5%
BEAF	chro1	chro2	chro1	chro2	2847	3251
CP190	rep1	rep2	rep1.24M	rep2.7M	4396	4933
CTCF	chro2	rep4	chro2	rep3.20M	1494	1858

2. Signal over IDR Peaks

Individual Replicate (RPGC Input Sub) signal over IDR Peaks at 1% & 5% cutoff. IDR peaks are NOT merged here i.e. a heatmap is available for each IDR peak group (ie common regions will appear in different heatmaps). Heatmaps are sorted according to region IDR score ie with the strongest at the top.

Observation :

- CTCF rep3 replicate clearly shows lower signal compared to Chro2 replicate
- Cp190 rep1 replicate clearly shows lower signal compared to rep2 replicate
- BEAF signal is equivalent for both replicate
- Bottom regions of the 5% maps have signal that poorly distinguishes from bg ; suggesting to use the IDR 1%

Maps at 1% cutoff

Item details

ID	4176124a-5f9f-453d-a903-b9e254ff0376
Deleted	✗ no

Embed pictures in your notes

Project: Type to search Project

Completed on: 2020-10-14 17:06:32

Status: COMPLETED

Created: 2020-

Topology in early Dm embryo (Gaby Project, Furlong Lab)

Layout: A4 Full Width

Edit Insert Format Table

Paragraph B I U [List icons] [Color icons] [Link icon] [Image icon]

This note is related to:

- [Analysis of Gaby ChIP-seq 6-8h CP190, BEAF and CTCF from Bing](#)
- [Binding of CTCF, Cp190, BEAF w.r.t DEGs ; DiffBind NC14 vs 68h](#)
- [Gaby Insulator Project Meeting 23.09.2020](#)

Running usual DiffBind WF on Galaxy (with input) gives us very weird MA plots:

- The situation of CTCF is particularly dramatic and suggests that something goes wrong with the normalization.
- CP190 is also skewed for lower concentration values.
- Although BEAF looks OK, there is still a weird asymmetry with an absence of significant regions for average concentration > 10 in the NC14 (reds)

BEAF NC14 vs 6-8h (DEseq2) Up: 423 Down: 444 NS

CTCF NC14 vs 6-8h (DEseq2) Up: 1015 Down: 606 NS

CP190 NC14 vs 6-8h (DEseq2) Up: 238 Down: 129 NS

Embed an image

Upload a new Image

all_maplot.png 987 KB Upload complete tap to undo

Choose from attachments

all_maplot.png

all_maplot.png width in pixels 580 Remove copy from attachments Cancel Embed image

- No direct copy-paste

Reference any STOCKS items

1. Put water in the boiler and turn it on.
2. Meanwhile, grab a cup of tea
3. Put a bag of tea in the cup.
4. Finally pour boiling water into the cup
5. Remove the tea bag after 2 minutes

Insert a link

STOCKS items Web URL

Consumables Specimen Equipment Storage Equipment Biomaterial Lab Notebook Protocols Assays Data Management

+ New other tea

1 - 6 of 6 (1 selected)


<input type="checkbox"/>	Name	Code	Origin/Vendor	Catalogue #	Description	Storage Condition
<input type="checkbox"/>	Earl-Grey Tea Bag	—	—	—	—	—
<input checked="" type="checkbox"/>	Green Tea Bag	—	—	—	—	—
<input type="checkbox"/>	Herbal Tea	—	—	—	—	—
<input type="checkbox"/>	Oolong Tea Bag	—	—	—	—	—
<input type="checkbox"/>	Tea spoon	—	—	—	—	—
<input type="checkbox"/>	Tea tongs 7.5cm	—	—	—	—	—

+ Add link(s) Cancel

Estimated Completion Date 2022-07-21

1. Put water in the boiler and turn it on.
2. Meanwhile, grab a cup of tea
3. Put a bag of tea in the cup.
• [Green Tea Bag](#)
4. Finally pour boiling water into the cup
5. Remove the tea bag after 2 minutes.
6. Add a spoon of sugar.
7. Ready.

Here is a typical water boiler:



038c842f-0f27-4510-b4dd-6573718e37d0

Linked items 1


[Green Tea Bag](#)

Insertion of many links at once possible

An advanced permission/sharing system

- Permissions (View, Edit, Delete) can be granted to groups or individuals
- Public Items can be **viewed** by anyone **who can log in** STOCKS

Permissions

 Public item

	View	Edit	Delete	
Groups				
<input type="text" value="Add group"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="button" value="Add"/>
Computational Support Genome Biology	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
Users				
<input type="text" value="Add user"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="button" value="Add"/>
girardot	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	

- Sharing your experiment in **Edit** mode is most likely **NOT** a good idea
 - STOCKS does NOT track individual edits
 - Only share experiments where authorship is NOT an issue

Export experiment as PDF

EXPERIMENTS

Analysis of ChIP-seq NC14 Dec 2019 batch, comparison wi... [Edit](#) [Copy URL](#) [Clone](#) [PDF](#) [Unfreeze](#) [Delete](#)

This experiment is frozen and has been digitally signed for IP purposes. Unfreezing the experiment to further edit it, should be considered an exceptional action.

- Print out when needed at the bench
- Act as a report to e.g. email

Project
Topology in early Dm embryo (Gaby Project, Furlong Lab)

1. Processing

Ran usual galaxy WF for PE chip-seq dm6

2. Sample Description

Sample	
Input_NC14_rep1	input for "_rep1" sam
Input_NC14_rep2	input for "_rep2" sam
Input_NC14_rep3	input for "_rep3" and samples ; no input v generated for the rep chromatin prep

1/12 Analysis of ChIP-seq NC14 Dec 2019 batch, comparison with No...

Summary

Name	Analysis of ChIP-seq NC14 Dec 2019 batch, comparison with Nov2019 Batch
ID	680b03eb-f334-4a4f-8add-4fa39f500797
Project	Topology in early Dm embryo (Gaby Project, Furlong Lab)
Status	COMPLETED
Completed	Jan. 13, 2020, 8:28 p.m.
Frozen	True
Freeze date	June 17, 2020, 3:34 p.m.
Modified	June 17, 2020, 3:34 p.m.
Created	Dec. 19, 2019, 4:41 p.m.
Modified by	Charles Girardot (girardot)
Created by	Charles Girardot (girardot)
Owner	Charles Girardot (girardot)
Owned by Group	Computational Support Genome Biology

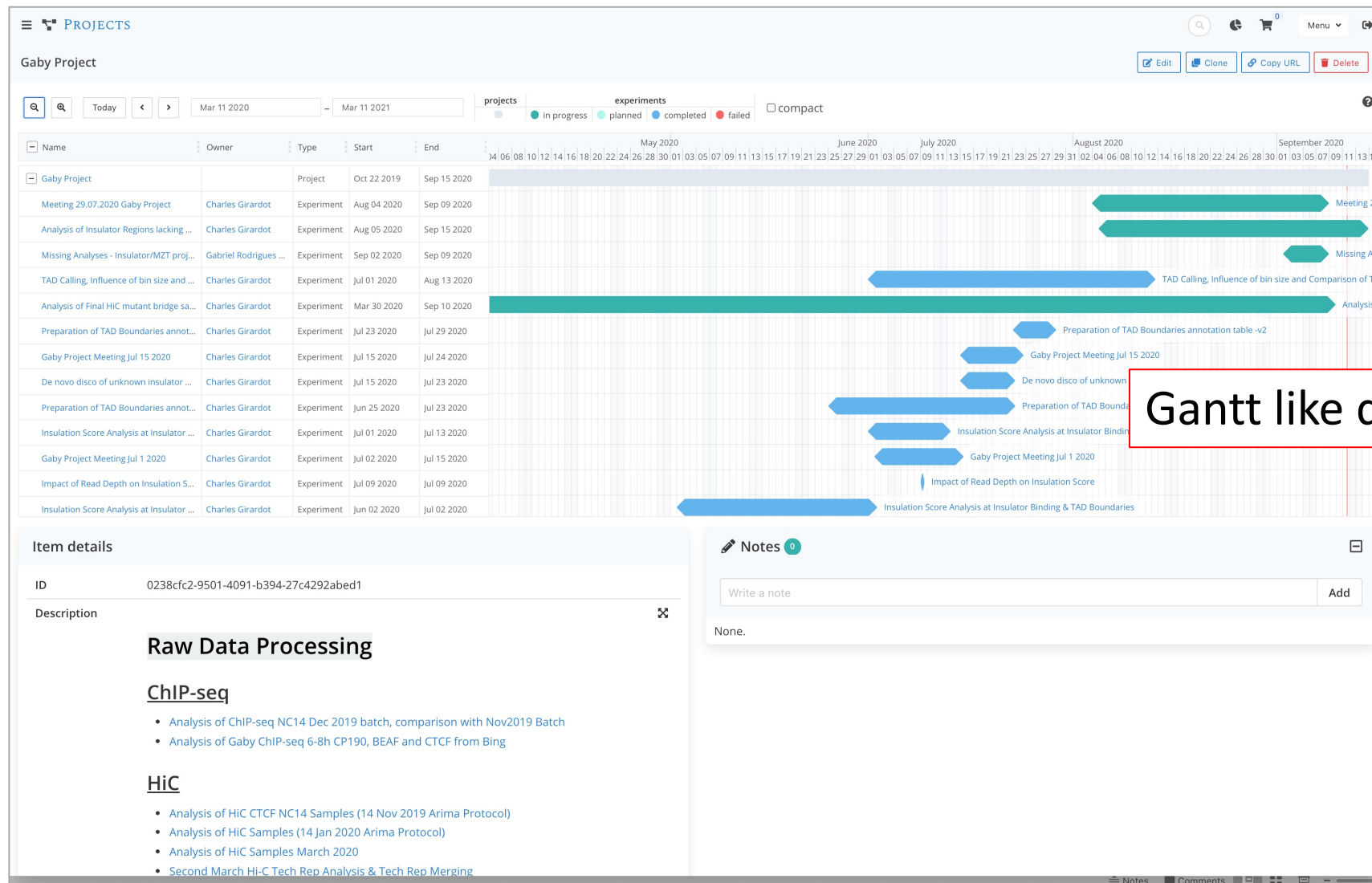
Description

1. Processing
Ran usual galaxy WF for PE chip-seq dm6.

2. Sample Description

Sample		
Input_NC14_rep1	input for "_rep1" samples	this was over-fixed (needed for cp190)
Input_NC14_rep2	input for "_rep2" samples	this was over-fixed (needed for cp190)
Input_NC14_rep3	input for "_rep3" and "_rep4" samples ; no input was generated for the rep4 chromatin prep	normal protocol

Projects group related experiments



Gantt like display of all experiments

Protocols have similar characteristics as experiments

=> A protocol describes how to perform an experiment

PROTOCOLS - EXTRACTION

Nuclei extraction and counting

Summary
Nuclei extraction from fixed embryos.

Prepare in advance:

- Pre-chill centrifuge for falcon tubes to 4°C.
- Pre-chill HB buffer (27ml/sample) and PBT (4ml/sample) to 4°C. Add complete protease inhibitor (PI) before use.
 - For less than 0.5g/sample of embryos use 7 ml douncer and 4 ml HB buffer.
- Miracloth, two pieces/sample.
- Nitex 20µm, in water. 1 piece/sample

Nuclei Isolation

1. Transfer 0.5-1.2 g of embryos to 15 ml douncer on ice, add 10 ml HB buffer and let thaw for a few minutes.

Item details

ID	d392aee0-a8f8-4a2b-bca6-502735ac5c13
Type	EXTRACTION
Parent protocol	—
Modified	2022-09-20 12:05:19
Modified by	girardot
Created by	girardot
Owner	girardot
Owned by Group	Furlong Group
Permissions	View Edit Delete

Annotations 0

Linked items 0

Attachments 1

Drag & Drop your files or [Browse](#)

Powered by PQINA

[HB_buffer.xlsx](#) 9.81 kB
Uploaded by girardot on 4 Mar '19, 17:20

Like experiments:

- Formatted text with images, tables
- ...
- Linked Items
- Permissions/Sharing
- Attachments

- Copy-paste from e.g. word documents usually works but is not guaranteed (double check !!)

Protocols type and summary to support data deposition

Welcome, Charles Girardot!

STOCKS
version 1.17.5

- CONSUMABLES
- SPECIMEN
- EQUIPMENT
- STORAGE
- SAMPLES
- LAB NOTEBOOK
- PROTOCOLS**
- Biochemistry
- Buffer
- Data Analysis
- Extraction**
- Fixation
- Culture & Growth
- Labeling
- Library Preparation
- Molecular Biology
- Sequencing
- Other
- All
- Workflows

PROTOCOLS - **EXTRACTION**

Nuclei extraction and counting

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- Different **protocol types**
 - ✓ Match public repo types
 - ✓ More types can be added by your admin
- **Summary:** unstructured text used for submission to public repositories
 - ✓ Experiments content are not submitted to public repositories

Protocol versioning to reflect technological development

Create a submission folder

- ssh to the server as you
- sudo su admin
- create a new submission folder on the group share
 - mkdir Data_Submissions/<MY_SUBMISSION_FOLDER>/
- create a eg 'fastq' subfolder for ngs data submission
 - mkdir Data_Submissions/<MY_SUBMISSION_FOLDER>/fastq/
- Go in this folder
 - cd Data_Submissions/<MY_SUBMISSION_FOLDER>/fastq/

Enable conda env for the admin user

- enable the stocks client
 - > `conda activate /home/stocks/stocks-client-env`
- reinit the env with admin but make sure first to clean up

Item details

ID	18293e2a-94be-4356-83dc-5c5d9fccef5
Type	OTHER
Parent protocol	Fastq File Transfer to ArrayExpress [Admin version]

Annotations 0

—

Linked items 0

—

- Reflect technical improvements
- Keep previous versions untouched
 - Important when protocols were already used and referenced

Protocols act as templates to create experiments

PROTOCOLS - EXTRACTION

Nuclei extraction and counting

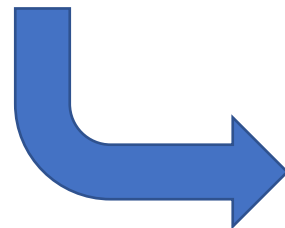
Summary
Nuclei extraction from fixed embryos.

Prepare in advance:

- Pre-chill centrifuge for falcon tubes to 4°C.
- Pre-chill HB buffer (27ml/sample) and PBT (4ml/sample) to 4°C. Add complete protease inhibitor (PI) before use.
 - For less than 0.5g/sample of embryos use 7 ml douncer and 4 ml HB buffer.
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Nuclei Isolation

1. Transfer 0.5-1.2 g of embryos to 15 ml douncer on ice, add 10 ml HB buffer and let thaw for a few minutes.



- Create a new experiment
- Copy the protocol content (incl. images) into the experiment
- Duplicates all attachments
 - E.g. excel spreadsheet to compute quantities ...

Protocols should not be changed once used in production

- An experiment must be self-contained
 - Always “Derive Lab Note” from protocol
 - Force you to make sure protocols are uploaded
- Protocols may be linked from different places
 - Never modify a protocol that might have been used by someone
 - Make protocols read-only once released for production.
 - Make a new version if changes should be done

Experiment freezing enables IP protection



Change status



Freeze



Experiment Creation

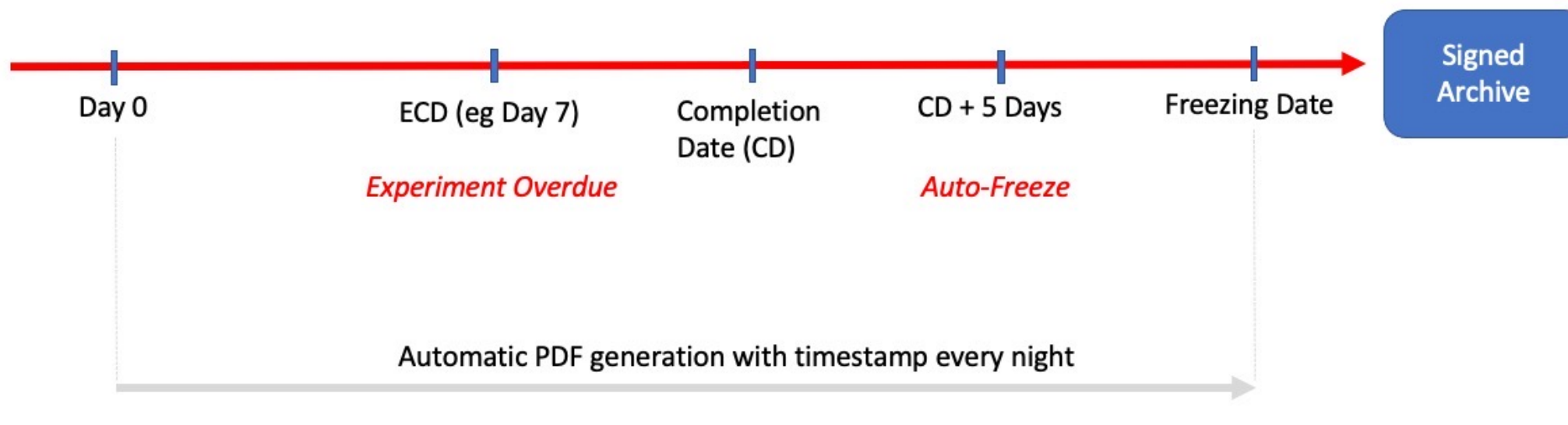
- Status: "in progress" or "planned"
- Creation Date set
- Expected Completion Date (ECD)

Experiment Completion

- Status: "Completed" or "Failed"
- Completion Date (CD) set

Experiment Freeze

- Frozen == True
- Archive digitally time-stamped



The many dates of an experiment

The screenshot displays an experiment management interface. At the top, the title is "Preparing a much better coffee with a french press". Below the title, there are action buttons: Edit, Copy URL, Clone, PDF, Freeze, and Delete. The project name is "Tea Project".

Key dates and status are highlighted in yellow boxes:

- Estimated Completion Date: 2022-07-27
- Status: (in progress)
- Created on: 2022-07-20 11:50:50

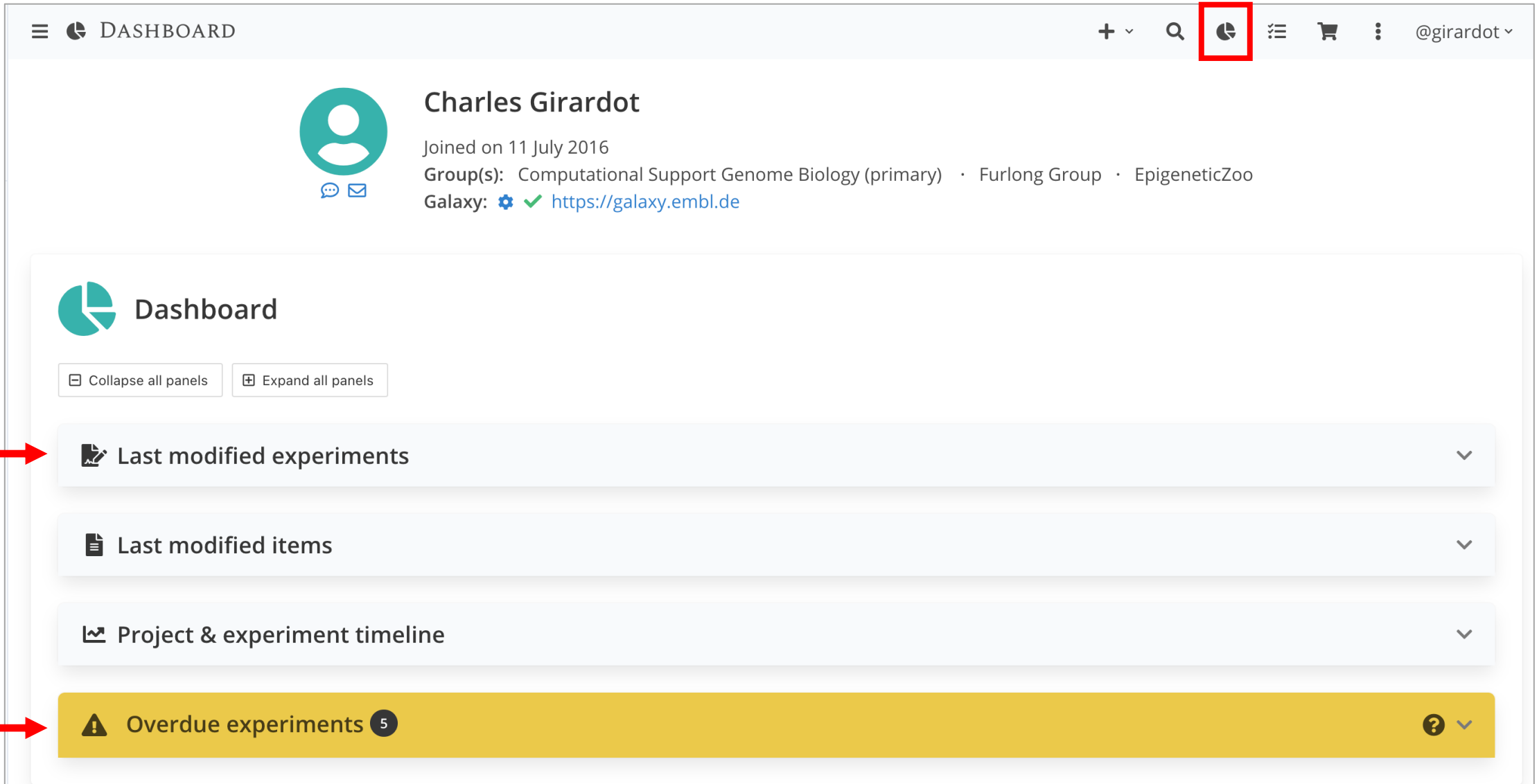
The main content area shows a step: "Step 1: Measure your coffee. The standard ratio is approximately 2 tablespoons of coffee per 6 ounces of water. Don't be afraid to add a few".

The "Item details" section on the left lists the following information:

ID	31681fb1-4ed0-4773-8e7b-1205a7cef90e
Deleted	no
Summary	—
Start date	2022-07-20
Completed	2022-07-20 13:58:35
Frozen	no
Freeze date	—
Modified	2022-07-20 14:29:28
Modified by	trainee10
Created by	trainee10
Owner	trainee10
Owned by Group	Tea Lovers
Permissions	—

On the right side, there are sections for "Linked items", "Attachments", "Autogenerated Files", "Embedded images", and "Notes", each with a count of 0. The "Attachments" section includes a "Drag & Drop your files or Browse" button. The "Notes" section has a "Write a note" input field and an "Add" button.

Your dashboard lists ongoing experiments



The screenshot displays the Galaxy dashboard for user Charles Girardot. The top navigation bar includes a hamburger menu, the word "DASHBOARD", a search icon, a red-bordered dashboard icon, a list icon, a shopping cart icon, and the user's name "@girardot". The user profile section shows a teal circular avatar, the name "Charles Girardot", and details: "Joined on 11 July 2016", "Group(s): Computational Support Genome Biology (primary) · Furlong Group · EpigeneticZoo", and "Galaxy: <https://galaxy.embl.de>".

The main dashboard area is titled "Dashboard" and contains two control buttons: "Collapse all panels" and "Expand all panels". Below these are four expandable panels:

- Last modified experiments**: Indicated by a red arrow pointing to the left.
- Last modified items**
- Project & experiment timeline**
- Overdue experiments 5**: Indicated by a red arrow pointing to the left. This panel is highlighted in yellow and includes a question mark icon.

Frozen experiments can be unfrozen !

- Unfreezing is still possible
- Upon unfreezing:
 - Nightly snapshot process restart
 - No automatic freezing! Do not forget to freeze back asap.
- Do not abuse this i.e. it can get expensive in space
- Useful for experiment that last very long (with long waiting period)
 - although creating multiple experiments should be preferred.

Conclusion

- The ELN is a better solution than paper notebook
 - Searchable, editable, shareable ...
 - Accessible from anywhere
- May be used without the other modules
 - Works best together with the lab inventory and protocols
 - Maximized value when also coupled with Biomaterial (samples)
- Sharing in edit/delete should be handled with care
- Once shared and/or used, protocols should not be edited

Thank you for your attention



Jelle Scholtalbers



Matthias Monfort



Nayeem Reza

Questions ?