

GitLab as a Collaborative Working Environment - part 2

Introductory Course

Mihai Lefter

Department of Human Genetics



Outline

Time	Activity	Contents
09:00	Lecture 1	Introduction, version control.
09:30	Practical 1	GitLab: groups, projects, and file handling.
09:50	Break	
10:00	Lecture 2	GitLab: issues, labels, milestones,
10:20	Practical 2	and the issue board.
10:40	Break	
10:50	Lecture 3	GitLab: wiki, markdown, extras.
11:20	Practical 3	
11:50	Final questions	
12:00	Closing	

Issues

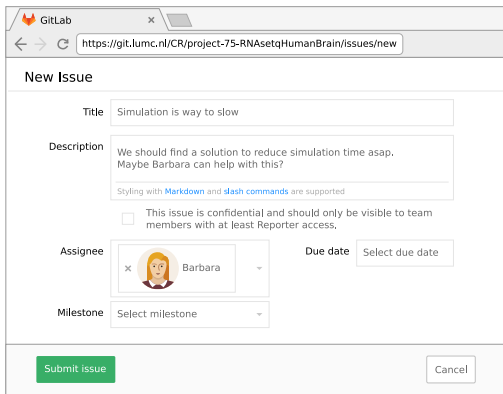
Allow you to signalize problems and to delegate their solving to project members.

You can make issues and:

- Assign them to people.
- Leave them general.
- Have discussions in them.
- File them under milestones.



Example: issue creation



GitLab

https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/issues/new


New Issue

Title: Simulation is way too slow

Description: We should find a solution to reduce simulation time asap. Maybe Barbara can help with this?

Styling with [Markdown](#) and [slash commands](#) are supported

☐ This issue is confidential and should only be visible to team members with at least Reporter access.

Assignee:  Barbara

Due date: Select due date

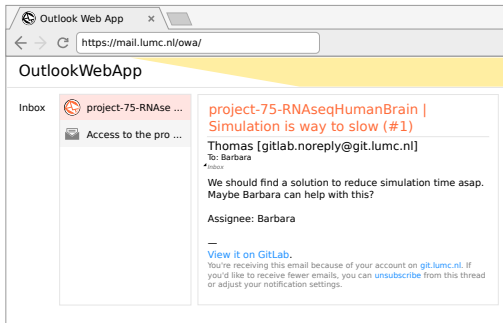
Milestone: Select milestone

Submit issue Cancel



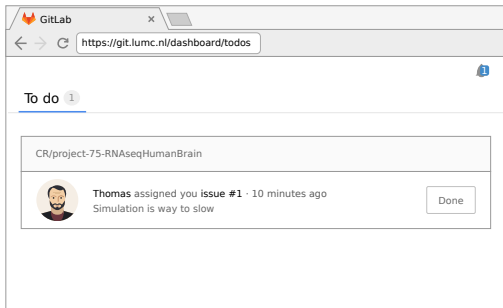
Creates a general issue and assigns it to Barbara.

Example: issue assignment email notification



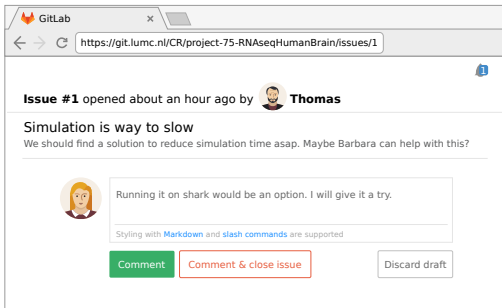
Receives email with the new issue created and assigned to her.

Example: the issue appears as a To do



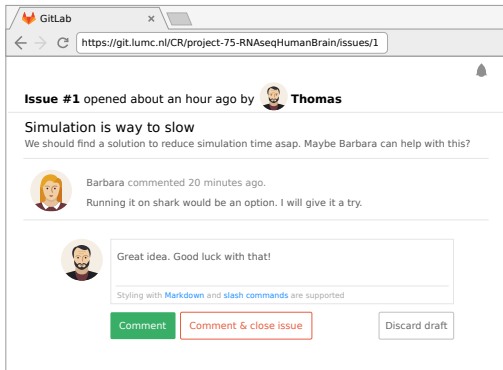
Logs in to GitLab. The issue appears also as a To do notification.

Example: issue reply



Uses the issues discussion option to reply.

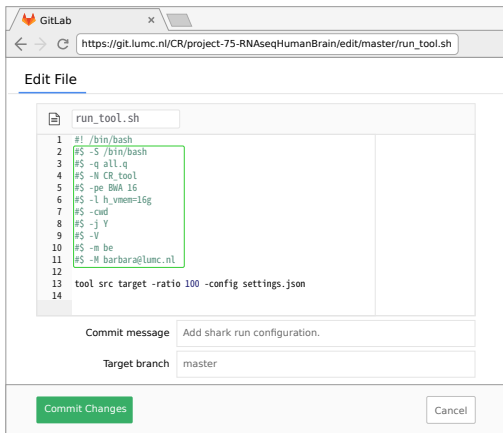
Example: issue reply again



Replies back to Barbara.

Email notification not shown.

Example: edit file directly on GitLab



The screenshot shows the GitLab web interface for editing a file. The browser address bar displays the URL: `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/edit/master/run_tool.sh`. The page title is "Edit File". Below the title, the file name "run_tool.sh" is shown in a text box. The file content is displayed in a code editor with line numbers 1 through 14. Lines 2 through 11 are highlighted with a green box. The code content is as follows:

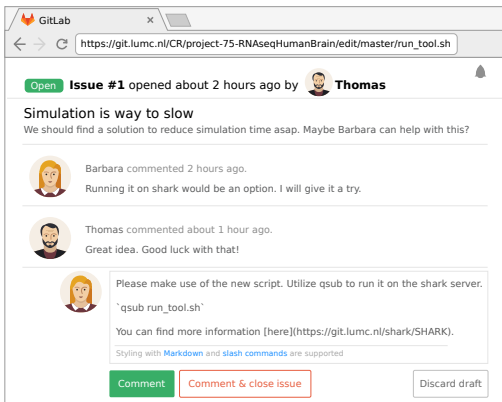
```
1 #!/bin/bash
2 # $ -S /bin/bash
3 # $ -q all.q
4 # $ -N CR_tool
5 # $ -pe BWA 16
6 # $ -l h_vmem=16g
7 # $ -cwd
8 # $ -j Y
9 # $ -V
10 # $ -m be
11 # $ -M barbara@lumc.nl
12
13 tool src target -ratio 100 -config settings.json
14
```

Below the code editor, there are two input fields: "Commit message" with the value "Add shark run configuration." and "Target branch" with the value "master". At the bottom of the form, there are two buttons: "Commit Changes" (highlighted in green) and "Cancel".

Edits the file
using the GitLab
interface.



Example: close issue



The screenshot shows a web browser window with the GitLab logo and a tab. The address bar displays the URL: `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/edit/master/run_tool.sh`. The page content shows an issue titled "Issue #1 opened about 2 hours ago by Thomas". The issue description is "Simulation is way to slow" with the text "We should find a solution to reduce simulation time asap. Maybe Barbara can help with this?". There are three comments: Barbara commented 2 hours ago with the text "Running it on shark would be an option. I will give it a try."; Thomas commented about 1 hour ago with the text "Great idea. Good luck with that!"; and Barbara commented with the text "Please make use of the new script. Utilize qsub to run it on the shark server. `qsub run_tool.sh`". Below the comments, there is a note: "You can find more information [here](https://git.lumc.nl/shark/SHARK). Styling with Markdown and slash commands are supported". At the bottom of the issue page, there are three buttons: "Comment" (green), "Comment & close issue" (red, highlighted), and "Discard draft" (white).



Replies with solution and closes the issue.

Email notification not shown.

Issues extras

- You can reassign an issue.
- You can reopen an issue.
- You can still make comments in closed issues.
- You can upvote/downvote issues or add emojis.
- You can categorize issues with labels (detailed later).

Todos

A chronological list of things that are waiting for your input.

Todos allow you to see where:

- You should spend your time.
- Your team members need help.
- You need to take some action.
- You need to keep an eye on.

Note that Todos are personal.



Todos triggering

A Todo is triggered when:

- An issue is assigned to you.
- You are @mentioned in an issue.
 - Be it the description or in a comment.

You can also manually add an issue to your Todos list.

Note that there is just one Todo per issue.

Todos dismissal

Any of the following action to the corresponding issue will mark your Todo as Done:

- Changing the assignee.
- Changing the milestone.
- Adding/removing a label.
- Commenting on the issue.

You can also manually mark the Todo as done.

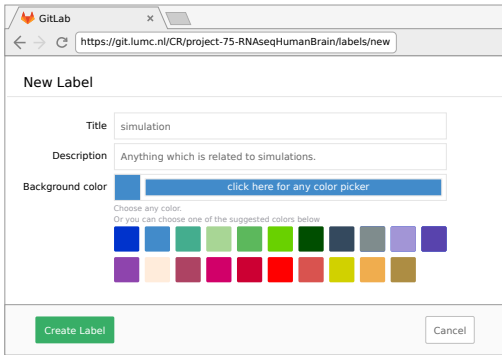
Todos are only marked as **Done** if the action is coming from you.

Labels

- Categorize and filter issues based on descriptions.
- They can have different colors.
- Predefined labels are available.
- You can prioritize labels.
- You can subscribe to be notified when a label gets added to an issue.



Example: create a label



The screenshot shows the 'New Label' form in a web browser. The browser's address bar displays the URL: `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/labels/new`. The form has the following fields:

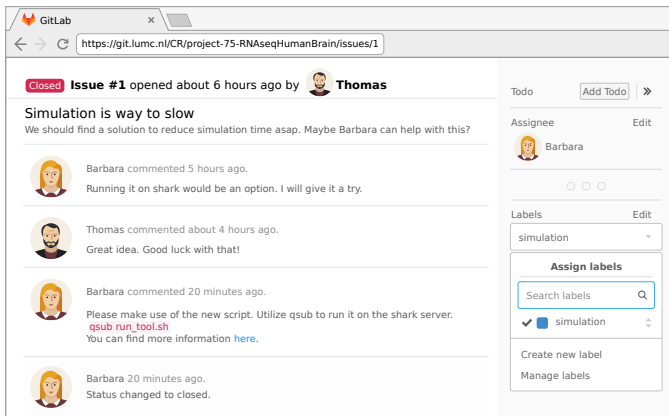
- Title:** A text input field containing the word 'simulation'.
- Description:** A text input field containing the text 'Anything which is related to simulations.'
- Background color:** A color selection interface. It features a blue square icon, a button labeled 'click here for any color picker', and a grid of 20 suggested color swatches. Below the grid, it says 'Choose any color. Or you can choose one of the suggested colors below'.

At the bottom of the form, there are two buttons: a green 'Create Label' button and a white 'Cancel' button.



Creates a new label to be assigned to simulation related issues.

Example: assign label to issue



The screenshot shows a GitLab web interface for a project named 'project-75-RNAseqHumanBrain'. The issue is titled 'Simulation is way to slow' and is marked as 'Closed'. It was opened by Thomas about 6 hours ago. The issue description states: 'We should find a solution to reduce simulation time asap. Maybe Barbara can help with this?'. There are four comments: Barbara commented 5 hours ago suggesting 'shark' and offering a try; Thomas commented about 4 hours ago saying 'Great idea. Good luck with that!'; Barbara commented 20 minutes ago asking to use a new script 'qsub_run_tool.sh' and providing a link; and a final comment from Barbara 20 minutes ago stating 'Status changed to closed.' The right sidebar shows the 'Assign labels' section with a search bar and a list of labels, where 'simulation' is selected and checked.



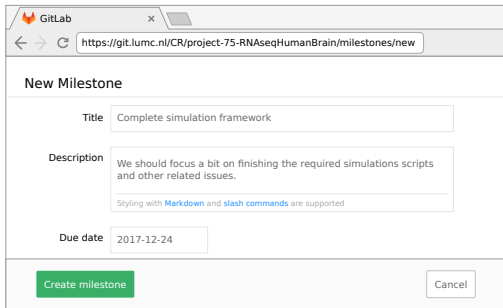
Assigns the "simulation" label to the closed "Simulation is way to slow" issue.

Milestones

- Allow you to organize issues into a cohesive group and, optionally, to set a due date.
- Milestones are usually created per-project.
- You can create a milestone for several projects in the same group simultaneously.



Example: create milestone

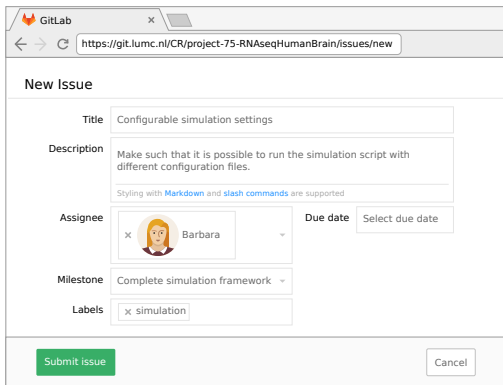


A screenshot of a web browser window showing the GitLab interface for creating a new milestone. The browser's address bar displays the URL `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/milestones/new`. The page title is "New Milestone". The form contains three main sections: "Title" with the text "Complete simulation framework", "Description" with the text "We should focus a bit on finishing the required simulations scripts and other related issues." and a note "Styling with [Markdown](#) and [slash commands](#) are supported", and "Due date" with the date "2017-12-24". At the bottom of the form are two buttons: a green "Create milestone" button and a white "Cancel" button.



Creates a new milestone to push things a bit :).

Example: create issue under milestone




GitLab

https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/issues/new


New Issue

Title Configurable simulation settings

Description Make such that it is possible to run the simulation script with different configuration files.
Styling with [Markdown](#) and [slash commands](#) are supported

Assignee  Barbara **Due date** Select due date

Milestone Complete simulation framework

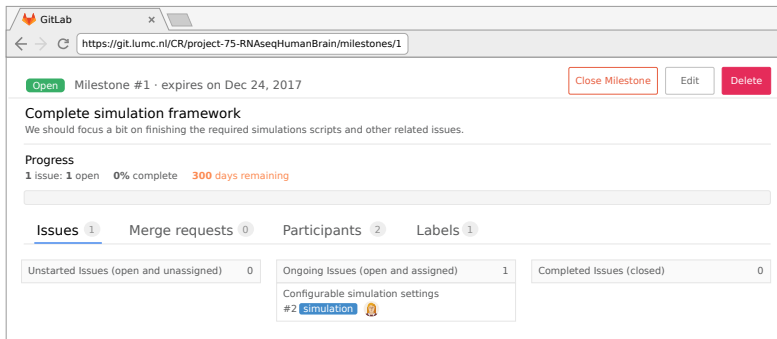
Labels 

Submit issue **Cancel**



Creates an issue for the new milestone utilizing the "simulation" label.

Example: milestone summary



The screenshot shows a web browser window with the GitLab logo and a tab titled 'x'. The address bar displays the URL: `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/milestones/1`.

At the top, there is a green 'Open' button, the text 'Milestone #1 · expires on Dec 24, 2017', and three buttons: 'Close Milestone' (outlined in red), 'Edit', and 'Delete' (pink).

The main content area has the title 'Complete simulation framework' and a description: 'We should focus a bit on finishing the required simulations scripts and other related issues.'

Below this is a 'Progress' section showing '1 issue: 1 open', '0% complete', and '300 days remaining' in red text. A progress bar is shown below this information.

There are four tabs: 'Issues' (with a count of 1), 'Merge requests' (0), 'Participants' (2), and 'Labels' (1). The 'Issues' tab is selected.

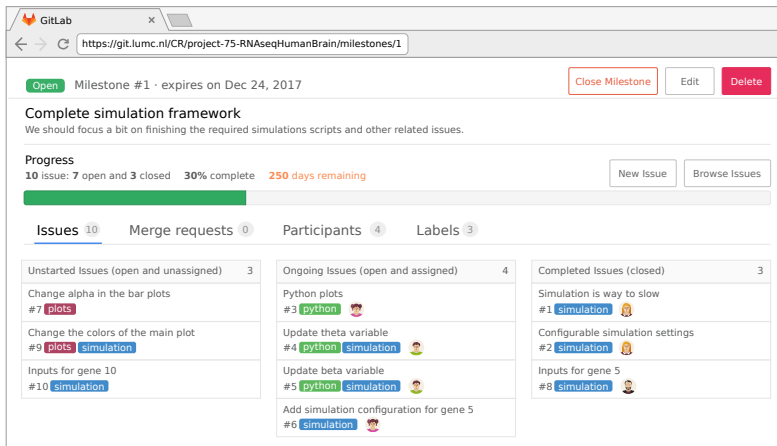
Under the 'Issues' tab, there are three summary boxes:

- Unstarted Issues (open and unassigned)**: 0
- Ongoing Issues (open and assigned)**: 1
 - Configurable simulation settings
 - #2 [simulation](#) (with a person icon)
- Completed Issues (closed)**: 0

Example: skip some steps



Example: milestone summary after fast forward



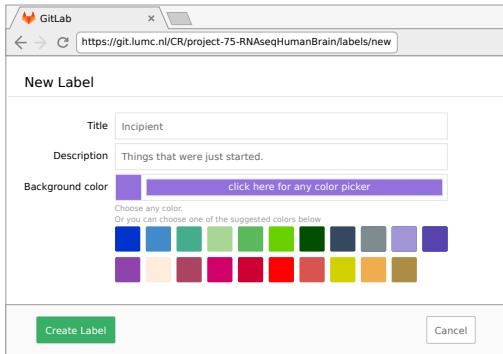
The screenshot shows a GitLab web interface for a milestone titled "Milestone #1 · expires on Dec 24, 2017". At the top right are buttons for "Close Milestone", "Edit", and "Delete". The main heading is "Complete simulation framework" with a description: "We should focus a bit on finishing the required simulations scripts and other related issues." Below this is a "Progress" section showing "10 issue: 7 open and 3 closed", "30% complete", and "250 days remaining". A green progress bar is partially filled. To the right of the progress bar are buttons for "New Issue" and "Browse Issues". Below the progress bar are tabs for "Issues 10", "Merge requests 0", "Participants 4", and "Labels 3". The "Issues" tab is active, showing three columns: "Unstarted Issues (open and unassigned) 3", "Ongoing Issues (open and assigned) 4", and "Completed Issues (closed) 3".

Unstarted Issues (open and unassigned) 3	Ongoing Issues (open and assigned) 4	Completed Issues (closed) 3
Change alpha in the bar plots #7 plots	Python plots #3 python	Simulation is way to slow #1 simulation
Change the colors of the main plot #9 plots simulation	Update theta variable #4 python simulation	Configurable simulation settings #2 simulation
Inputs for gene 10 #10 simulation	Update beta variable #5 python simulation	Inputs for gene 5 #8 simulation
	Add simulation configuration for gene 5 #6 simulation	

Issue board

- Organize issues using lists.
- Labels are utilized for lists creation.
- Lists types:
 - Custom: the ones you create based on your labels.
 - Default: **Open** and **Closed**.
- Available also for projects, but also for groups.

Example: issue board lists creation



The screenshot shows a web browser window with the GitLab logo in the tab and the URL `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/labels/new`. The page title is "New Label". It contains three input fields: "Title" with the value "Incipient", "Description" with the value "Things that were just started.", and "Background color" with a purple color swatch. Below the color swatch is a link "click here for any color picker" and a grid of 20 suggested color swatches. At the bottom are two buttons: "Create Label" (green) and "Cancel" (white).


GitLab

https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/labels/new


New Label

Title: Incipient

Description: Things that were just started.

Background color:  [click here for any color picker](#)

Choose any color.
Or you can choose one of the suggested colors below

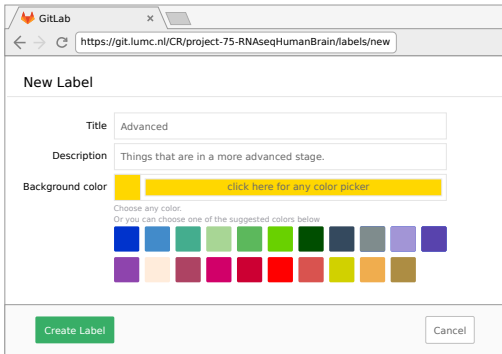


Create Label Cancel



Creates a first label to be used as list on the issue board.

Example: issue board lists creation



The screenshot shows the 'New Label' form in a web browser. The browser's address bar displays the URL: `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/labels/new`. The form has the following fields:

- Title:** A text input field containing the word 'Advanced'.
- Description:** A text input field containing the text 'Things that are in a more advanced stage.'
- Background color:** A color selection interface. It features a yellow color bar with the text 'click here for any color picker'. Below this, it says 'Choose any color. Or you can choose one of the suggested colors below' and displays a grid of 20 color swatches in two rows.

At the bottom of the form, there are two buttons: a green 'Create Label' button and a grey 'Cancel' button.



Creates a second label to be used as list on the issue board.

Example: issue board lists creation

The screenshot shows the GitLab Issue Board interface for the project `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/board`. The board is titled "Issue Board" and features a filter bar with dropdowns for Author, Assignee, Milestone, and Label, along with a "Reset filters" link and a "Filter by name ..." input. There are two green buttons: "Add list" and "Add issues".

The board is divided into three main sections:

- Open (6 issues):**
 - Inputs for gene 10 (#10) with labels `simulation` and an assignee icon.
 - Update theta variable (#4) with labels `python` and `simulation`, and an assignee icon.
 - Update beta variable (#5) with labels `python` and `simulation`, and an assignee icon.
 - Add simulation configuration for ... (#6) with label `simulation` and an assignee icon.
 - Change alpha in the bar plots (#7) with label `plots`.
 - Change the colors of the main plot (#9) with labels `plots` and `simulation`.
- Welcome to your issue board!**

Add the following default lists to your Issue Board with one click:

 - To do (orange square)
 - Doing (green square)

Starting out with the default set of lists will get you right on the way to making the most of your board.

[Add default lists](#)

Nevermind, I'll use my own
- Closed (4 issues):**
 - Python plots (#3) with label `python` and an assignee icon.
 - Simulation is way to slow (#1) with label `simulation` and an assignee icon.
 - Configurable simulation settings (#2) with label `simulation` and an assignee icon.
 - Inputs for gene 5 (#8) with label `simulation` and an assignee icon.

Example: issue board lists creation

The screenshot shows the GitLab Issue Board interface for the project `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/board`. The board is titled "Issue Board" and includes filter buttons for Author, Assignee, Milestone, and Label, along with a "Reset filters" link. There are also buttons for "Filter by name ...", "Add list", and "Add issues".

The board is divided into three main sections:

- Open (6 issues):**
 - Inputs for gene 10 (#10) with labels `simulation` and an assignee icon.
 - Update theta variable (#4) with labels `python` and `simulation`, and an assignee icon.
 - Update beta variable (#5) with labels `python` and `simulation`, and an assignee icon.
 - Add simulation configuration for ... (#6) with label `simulation` and an assignee icon.
 - Change alpha in the bar plots (#7) with label `plots`.
 - Change the colors of the main plot (#9) with labels `plots` and `simulation`.
- Welcome to your issue board!**

Add the following default lists to your Issue Board with one click:

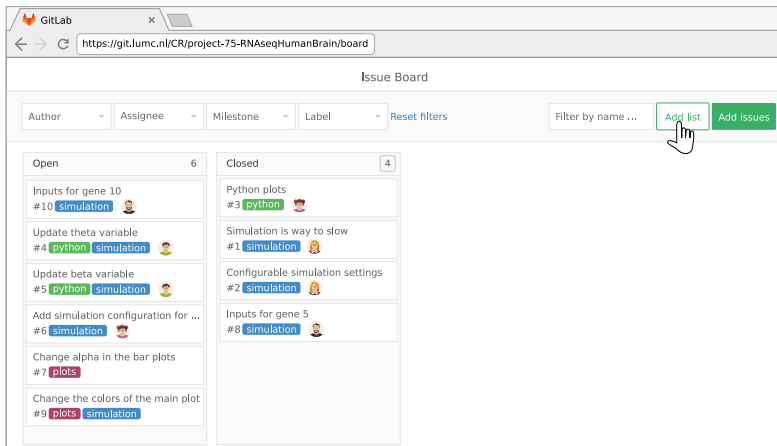
 - To do (orange square)
 - Doing (green square)

Starting out with the default set of lists will get you right on the way to making the most of your board.

[Add default lists](#)

[Nevermind, I'll use my own](#) (with a hand cursor icon pointing to it)
- Closed (4 issues):**
 - Python plots (#3) with label `python` and an assignee icon.
 - Simulation is way to slow (#1) with label `simulation` and an assignee icon.
 - Configurable simulation settings (#2) with label `simulation` and an assignee icon.
 - Inputs for gene 5 (#8) with label `simulation` and an assignee icon.

Example: issue board lists creation



Example: issue board lists creation

The screenshot displays the GitLab Issue Board for the project 'project-75-RNAseqHumanBrain'. The board is organized into two columns: 'Open' with 6 issues and 'Closed' with 4 issues. Each issue is represented by a card showing its title, ID, and associated labels. The 'Open' column includes issues like 'Inputs for gene 10' (#10) with 'simulation' and 'python' labels, and 'Change alpha in the bar plots' (#7) with a 'plots' label. The 'Closed' column includes 'Python plots' (#3) with 'python' and 'plots' labels, and 'Simulation is way to slow' (#1) with a 'simulation' label. On the right, the 'Add list' modal is active, allowing the user to create a new list from existing labels. The modal shows a search bar and a list of labels: 'Advanced' (yellow), 'Incipient' (purple), 'plots' (red), 'python' (green), and 'simulation' (blue). A hand cursor is pointing at the 'Incipient' label, indicating it is being selected for the new list.

Example: issue board lists creation

The screenshot shows the GitLab Issue Board interface. The URL bar indicates the project is `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/board`. The board is titled "Issue Board" and has filters for Author, Assignee, Milestone, and Label, along with a "Reset filters" button. There are buttons for "Filter by name ...", "Add list", and "Add issues".

The board is divided into three columns: "Open" (6 issues), "Incipient" (0 issues), and "Closed" (4 issues). The "Open" column contains issues #10, #4, #5, #6, #7, and #9. The "Closed" column contains issues #3, #1, #2, and #8. Each issue has a title, a number, a label, and an assignee icon.

An "Add list" modal is open, showing a search bar and a list of labels: "Advanced", "Incipient", "plots", "python", and "simulation". A hand cursor is pointing at the "Incipient" label, which is highlighted. Below the list are buttons for "Create new label" and "Manage labels".

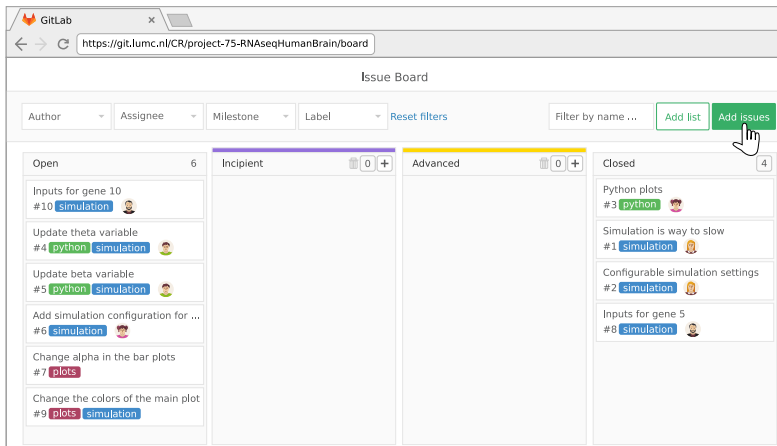
Example: issue board lists creation

The screenshot displays the GitLab Issue Board for the project 'project-75-RNAseqHumanBrain'. The interface includes a top navigation bar with the GitLab logo and a browser address bar showing the URL 'https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/board'. Below the navigation bar, there are filters for Author, Assignee, Milestone, and Label, along with a 'Reset filters' link. To the right of the filters are buttons for 'Filter by name ...', 'Add list', and 'Add issues'.

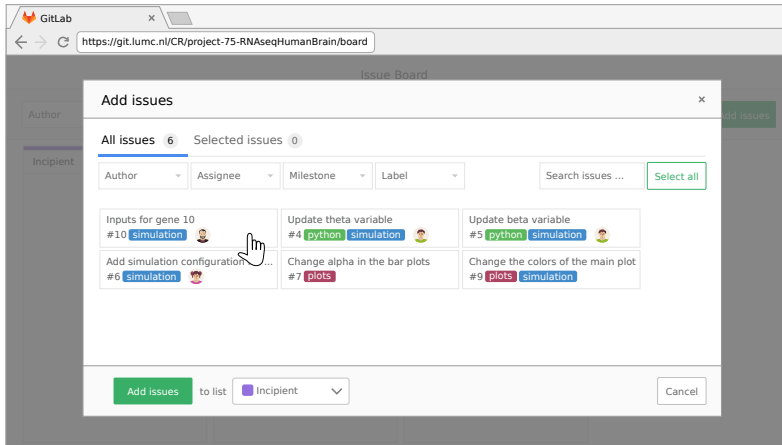
The main area of the board is divided into four columns, each representing a different stage of the issue lifecycle:

- Open (6 issues):** This column contains six issues. The first five issues are related to 'simulation' and have labels 'python' and 'simulation'. The sixth issue is related to 'plots' and has a 'plots' label. The issues are:
 - Inputs for gene 10 (#10 simulation)
 - Update theta variable (#4 python simulation)
 - Update beta variable (#5 python simulation)
 - Add simulation configuration for ... (#6 simulation)
 - Change alpha in the bar plots (#7 plots)
 - Change the colors of the main plot (#9 plots simulation)
- Incipient (0 issues):** This column is currently empty, indicating no issues are in this stage.
- Advanced (0 issues):** This column is also empty, indicating no issues are in this stage.
- Closed (4 issues):** This column contains four issues that have been resolved:
 - Python plots (#3 python)
 - Simulation is way to slow (#1 simulation)
 - Configurable simulation settings (#2 simulation)
 - Inputs for gene 5 (#8 simulation)

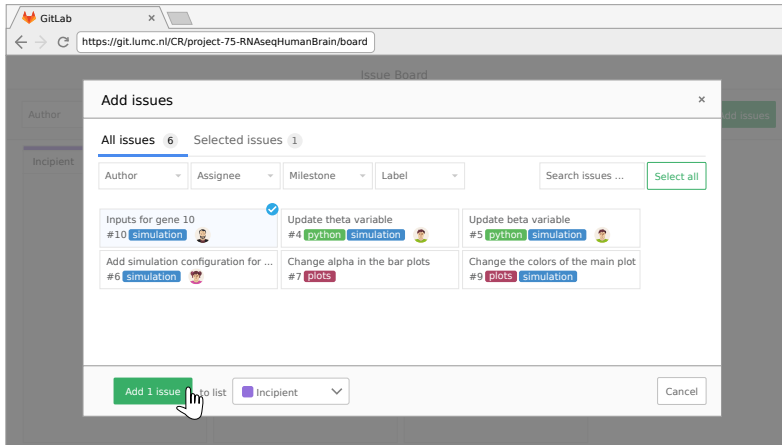
Example: add issues to the custom lists



Example: add issues to the custom lists



Example: add issues to the custom lists



Example: add issues to the custom lists

The screenshot shows the GitLab Issue Board for the project `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/board`. The board is divided into four columns: **Open** (6 issues), **Incipient** (1 issue), **Advanced** (0 issues), and **Closed** (4 issues). Each column has a header with a trash icon, a count, and a plus icon for adding issues.

Open Column Issues:

- #4: Update theta variable (tags: `python`, `simulation`)
- #5: Update beta variable (tags: `python`, `simulation`)
- #6: Add simulation configuration for ... (tag: `simulation`)
- #7: Change alpha in the bar plots (tag: `plots`)
- #9: Change the colors of the main plot (tags: `plots`, `simulation`)

Incipient Column Issue:

- #10: Inputs for gene 10 (tag: `simulation`)

Closed Column Issues:

- #3: Python plots (tag: `python`)
- #1: Simulation is way to slow (tag: `simulation`)
- #2: Configurable simulation settings (tag: `simulation`)
- #8: Inputs for gene 5 (tag: `simulation`)

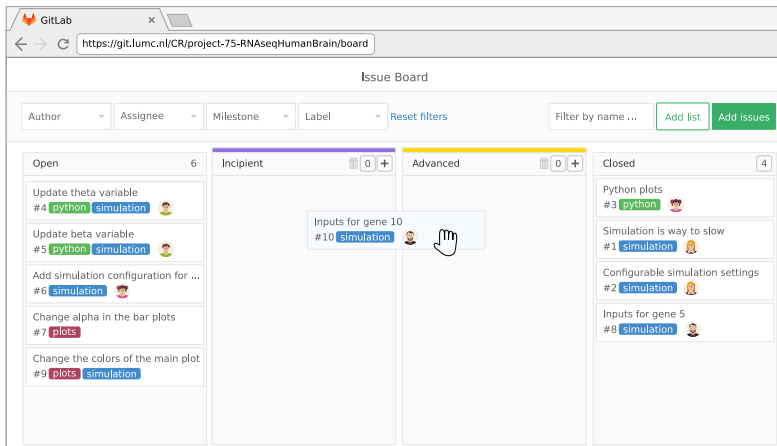
The interface includes filters for Author, Assignee, Milestone, and Label, along with a 'Reset filters' button. There are also buttons for 'Filter by name ...', 'Add list', and 'Add issues'.

Example: issue board list reallocation

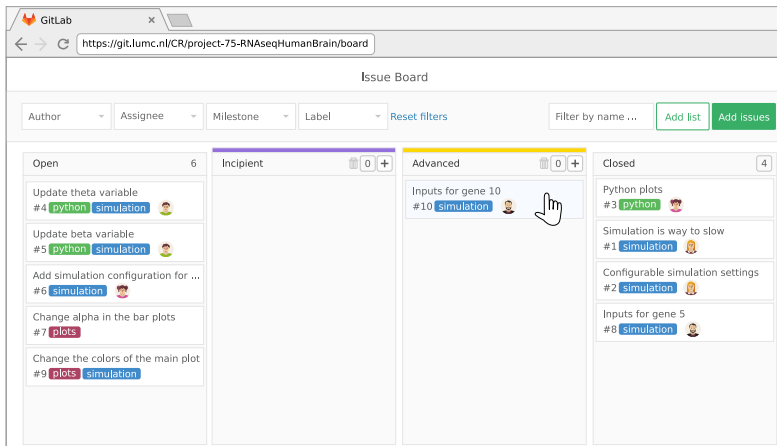
The screenshot shows the GitLab Issue Board interface for the project `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/board`. The board is divided into four columns: Open (6 issues), Incipient (1 issue), Advanced (0 issues), and Closed (4 issues). Each issue card displays its title, ID, labels, and assignee.

Open	Incipient	Advanced	Closed
<p>Update theta variable #4 <code>python</code> <code>simulation</code> </p> <p>Update beta variable #5 <code>python</code> <code>simulation</code> </p> <p>Add simulation configuration for ... #6 <code>simulation</code> </p> <p>Change alpha in the bar plots #7 <code>plots</code></p> <p>Change the colors of the main plot #9 <code>plots</code> <code>simulation</code></p>	<p>Inputs for gene 10 #10 <code>simulation</code> </p>		<p>Python plots #3 <code>python</code> </p> <p>Simulation is way to slow #1 <code>simulation</code> </p> <p>Configurable simulation settings #2 <code>simulation</code> </p> <p>Inputs for gene 5 #8 <code>simulation</code> </p>

Example: issue board list reallocation



Example: issue board list reallocation



Example: issue board list reallocation

The screenshot shows the GitLab Issue Board for the project `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/board`. The board is organized into four columns: **Open** (6 issues), **Incipient** (0 issues), **Advanced** (1 issue), and **Closed** (4 issues). Each column contains issue cards with details such as title, ID, labels, and assignee.

Column	Count	Issues
Open	6	<ul style="list-style-type: none"> Update theta variable #4 (python, simulation) Update beta variable #5 (python, simulation) Add simulation configuration for ... #6 (simulation) Change alpha in the bar plots #7 (plots) Change the colors of the main plot #9 (plots, simulation)
Incipient	0	
Advanced	1	<ul style="list-style-type: none"> Inputs for gene 10 #10 (simulation)
Closed	4	<ul style="list-style-type: none"> Python plots #3 (python) Simulation is way to slow #1 (simulation) Configurable simulation settings #2 (simulation) Inputs for gene 5 #8 (simulation)

Example: skip some steps



Example: issue board after fast forward

The screenshot shows the GitLab Issue Board for the project `https://git.lumc.nl/CR/project-75-RNAseqHumanBrain/board`. The board is organized into four columns: Open, Incipient, Advanced, and Closed. Each column has a header with a trash icon, a count, and a plus icon. The issues are listed below each column header.

Open (6)	Incipient (2)	Advanced (2)	Closed (6)
Switch to Jupyter for analysis #12 plots	Change alpha in the bar plots #7 plots	Add simulation configuration for ... #6 simulation	Python plots #3 python
Write project readme #13 general	Change the colors of the main plot #9 plots simulation	Inputs for gene 10 #10 simulation	Simulation is way to slow #1 simulation
How to handle large files? #14 general			Configurable simulation settings #2 simulation
			Inputs for gene 5 #8 simulation
			Update beta variable #5 python simulation
			Update theta variable #4 python simulation

Practical 2

Issues, labels, milestones, and the issue board.