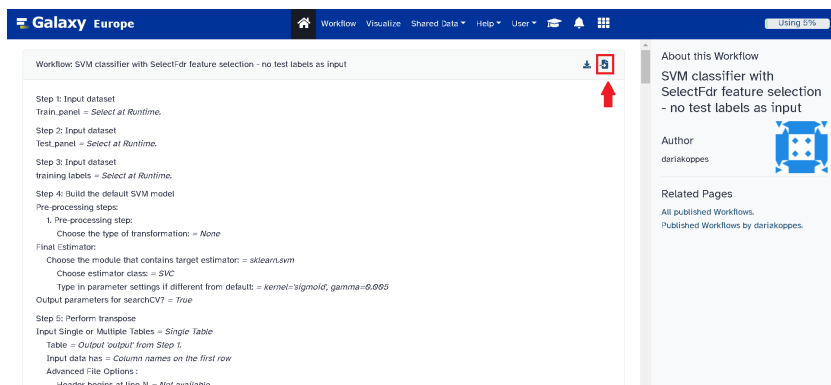


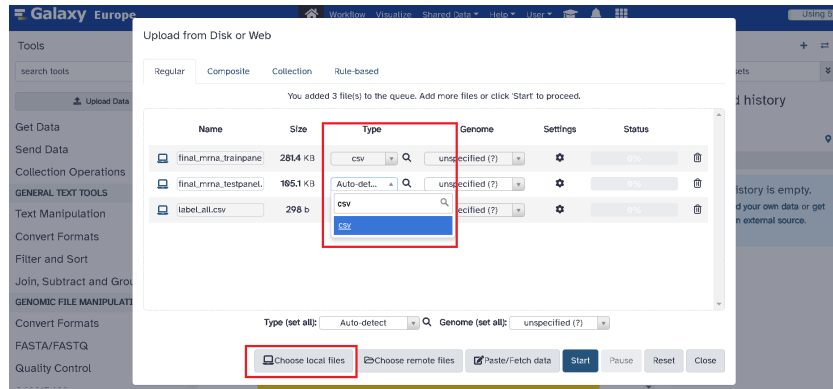
Manual to run the workflows in Galaxy

1. Create an account on the European Galaxy server: <https://usegalaxy.eu>.
2. Follow the 'Galaxy 101 for everyone' tutorial to get familiar with the basics of working with Galaxy. Link: <https://training.galaxyproject.org/training-material/topics/introduction/tutorials/galaxy-intro-101-everyone/tutorial.html>
3. Follow the steps in the tutorial to create a new history.
4. Leave the Galaxy tab open and go back to this paper to click on one of the workflow links provided in Table 9 above.
5. The link will open the following page:



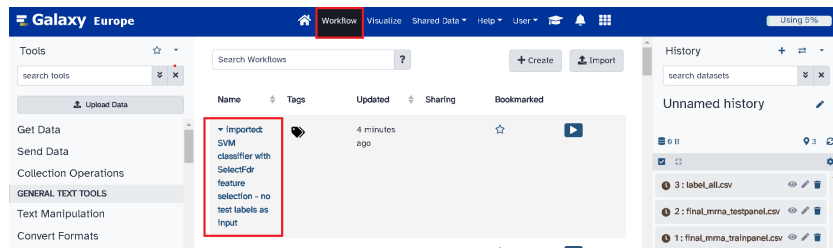
Click on the import workflow button highlighted in red. Afterwards, click on **Return to previous page**.

6. Click on the home button in the top menu bar to see the main page of Galaxy with your new made history.
7. Upload the data that you want to use in the history by clicking on **Upload data** at the top of the tool panel.
8. Click on **Choose local files** and select your datasets. Make sure you change the type of the datasets to csv.



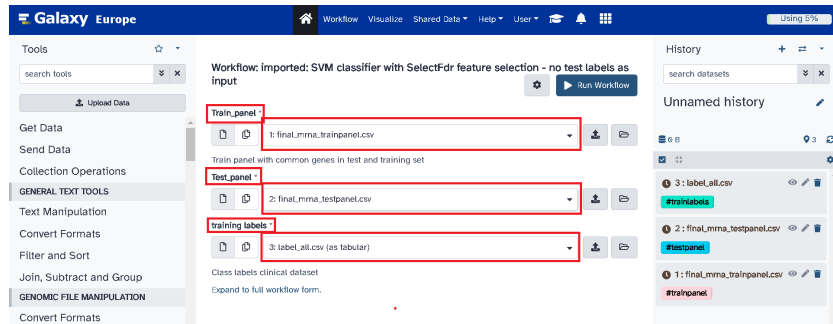
Afterwards click **Start** and the datasets will appear in your history.

9. Add tags such as training and test panel to your dataset, as explained in the training tutorial, to keep your history organised.
10. Click on **Workflow** in the top menu bar where you should see the title of the workflow you uploaded.

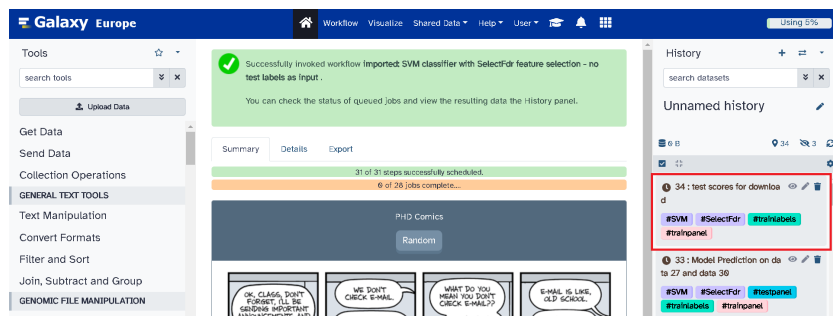


Note: If you click on the title and chose edit this will open the workflow editor of Galaxy where you can see the graphical representation of the workflow.

11. To run the workflow click on the play button visible in the previous screenshot.
12. This will open the workflow form where you need to specify which file to use for each workflow input. Make sure your training set file corresponds with the input called train.panel etc.



13. Click on the **Run Workflow** button.
14. All outputs for the tools used in the workflow are shown in your history in grey. Once they all turned green the workflow is done running.



15. You can inspect the different outputs by clicking on them to expand a small summary view or click on the eye symbol for details.
 - The repeated nested cross-validation accuracy scores in csv format are visible in the output called: *test scores for download*. Once downloaded they can be used in the *Code_for_graphics.ipynb* file in the Github page of this research to make the repeated nested cross-validation plots.
 - The genes that were left after feature selection in csv format are visible in the output called: *selected features for download*
 - The predicted class labels for the test set in tabular format are visible in the output called: *Model prediction on data .. and data ..*. They can be further used in the *Code_for_graphics.ipynb* file to make the Kaplan-Meier plots.
 - The hyperparameters used to fit the model are visible in the output called: *Fitted estimator or estimator skeleton on data .., data .., and others*
16. To download an output, click on it to expand the small summary view. Then click on the **save file** symbol to download the output on your local computer and use for further analysis using python notebooks.

17. Your first workflow is run!