SeqDEAS

Manual

1. Installation

(Installer will be set up when software is done)

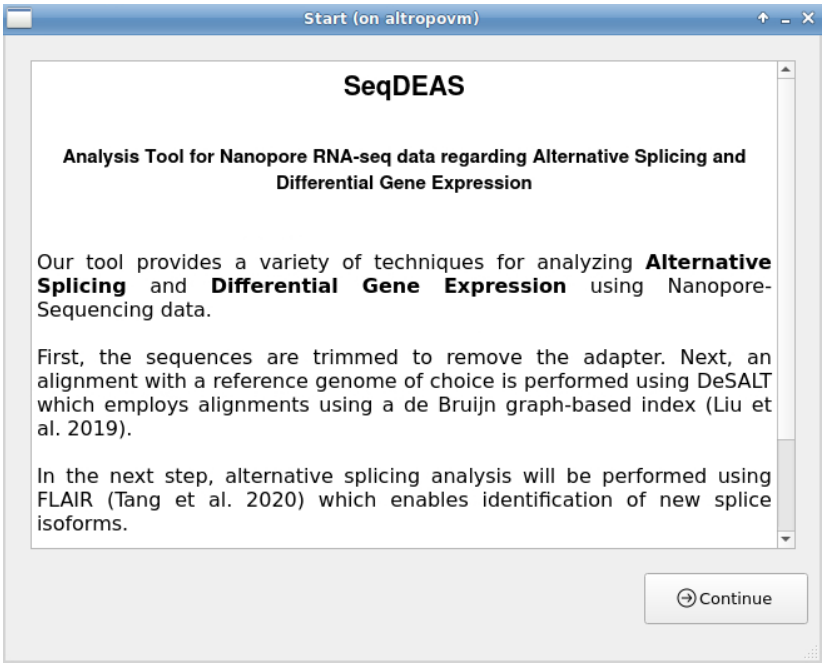
1.1. Git clone project: https://github.com/anbergander/splivardet.git

1.2. Install software packages from requirements.txt

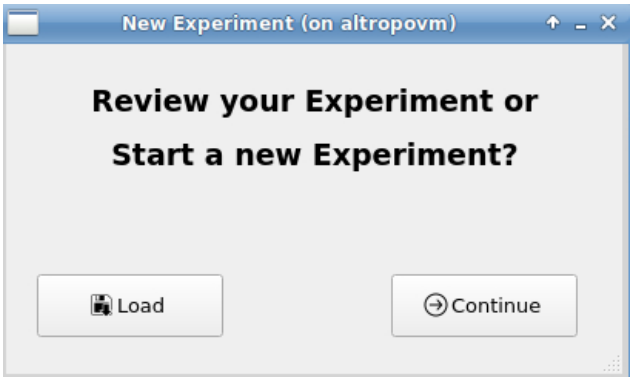
1.3. Run project via terminal or pycharm

2. Software

2.1. Start Window will show up; Press Continue for the next window.

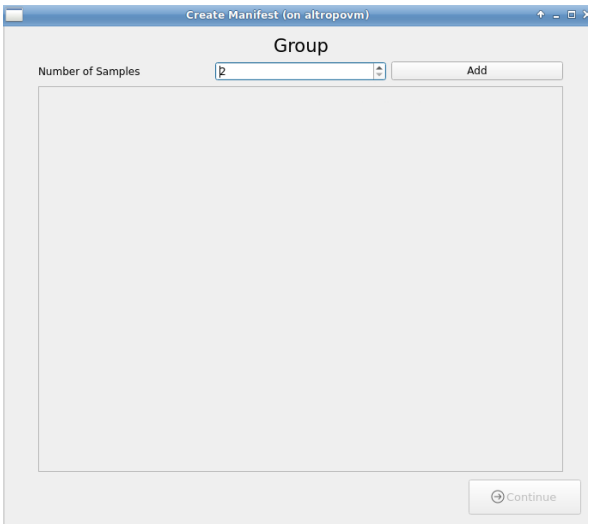


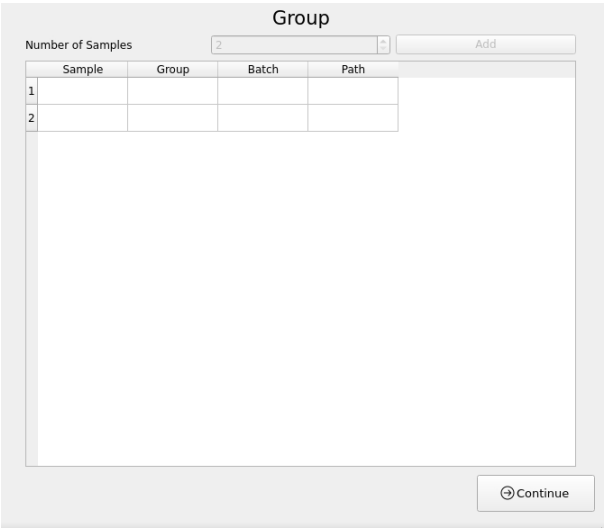
2.2. Decide whether you want to review an experiment or start a new one



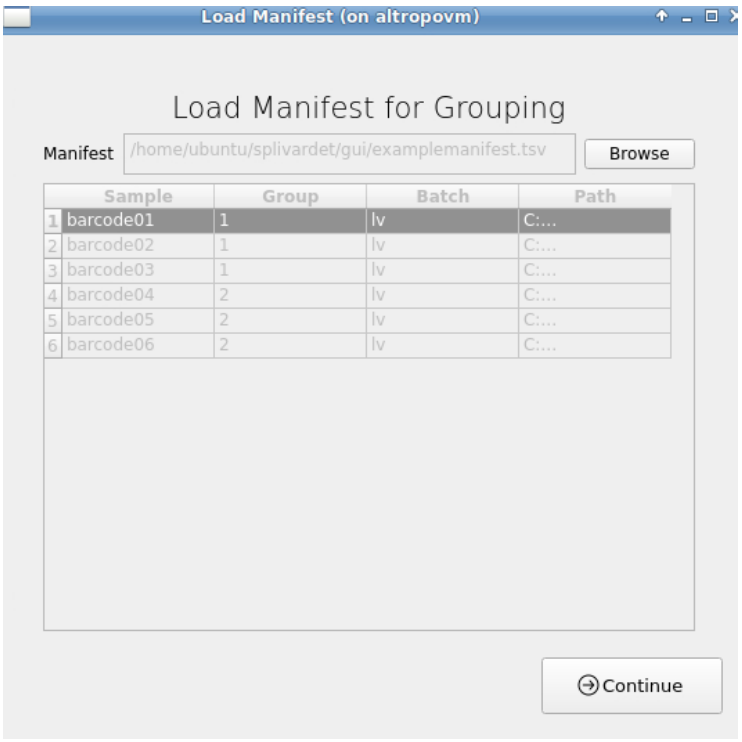
2.3. In case: you decided to start a new experiment: you will be asked to create a manifest

2.4. In case: you decided to create a new manifest you need to enter the number of samples and click ADD. Then, you need to fill out the table and press CONTINUE. A manifest in TSV formate will be generated

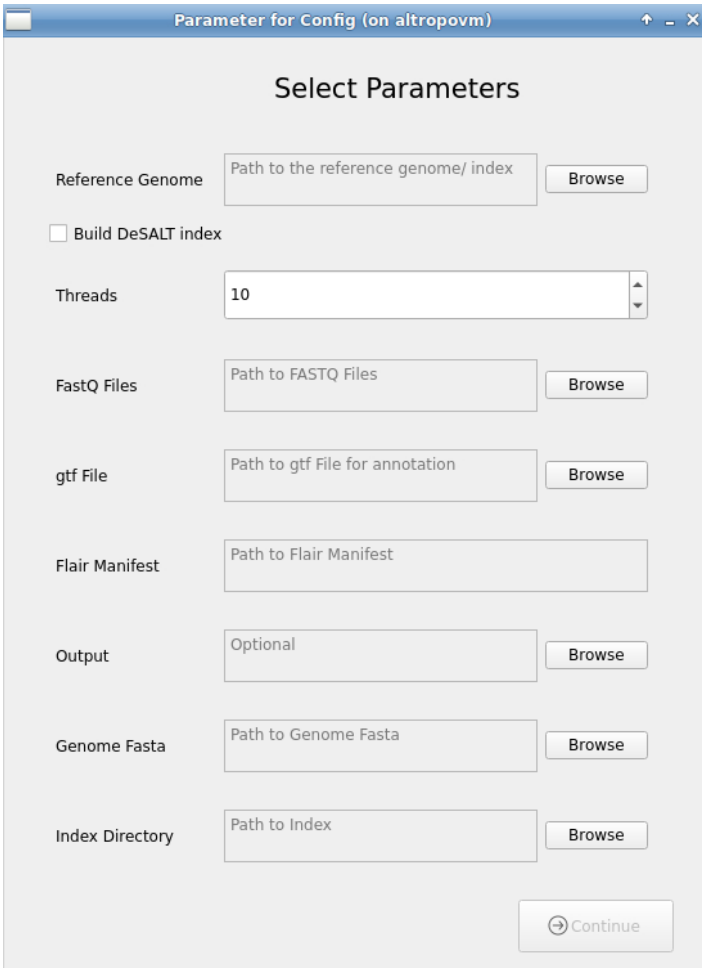




2.5. In case you decided to load a manifest, load your manifest by BROWSING



2.6. Next you need to fill out the parameter form. All fields need to be filled except for the output path. Then press CONTINUE

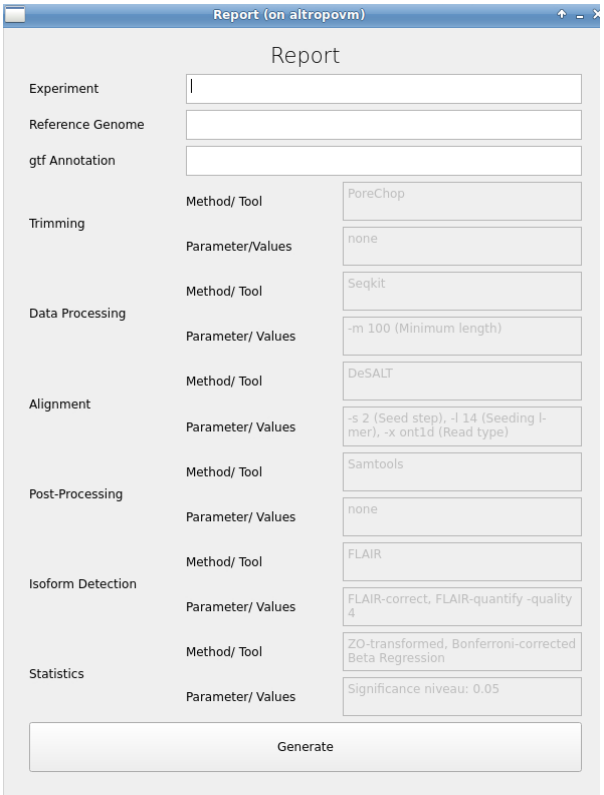


2.7. You will be asked to start the run

2.8. Press the START Button to start.

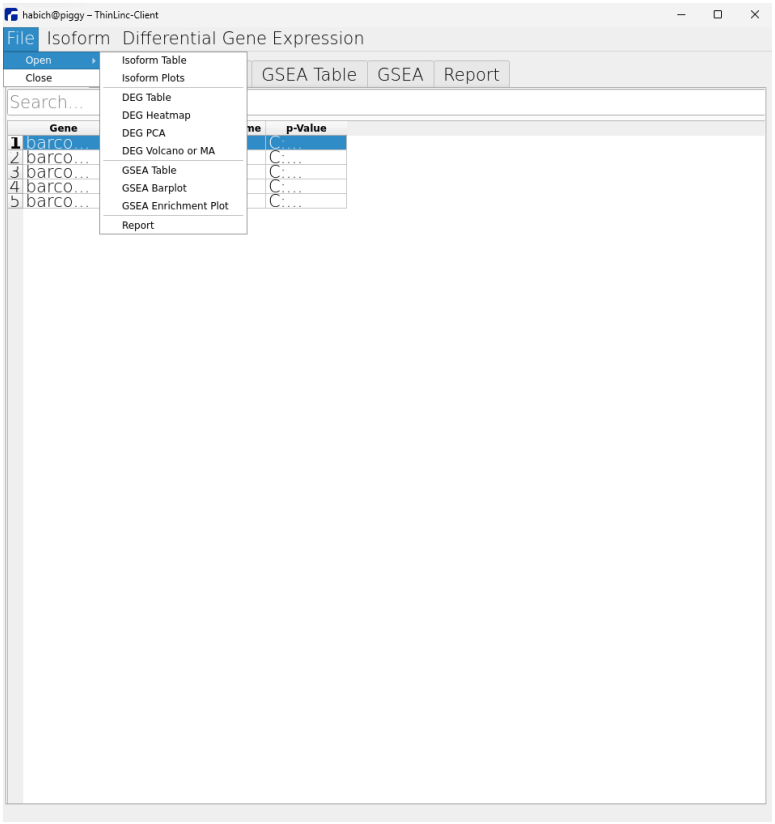
2.9. After the run is done: a CONTINUE button will be disabled.

2.10. Next, you can generate a report for the run with the important steps in PDF formate. You can fill out the experiment name, the reference genome and the annotation



2.11. Click GENERATE to go to the main window

2.12. Main Window will appear

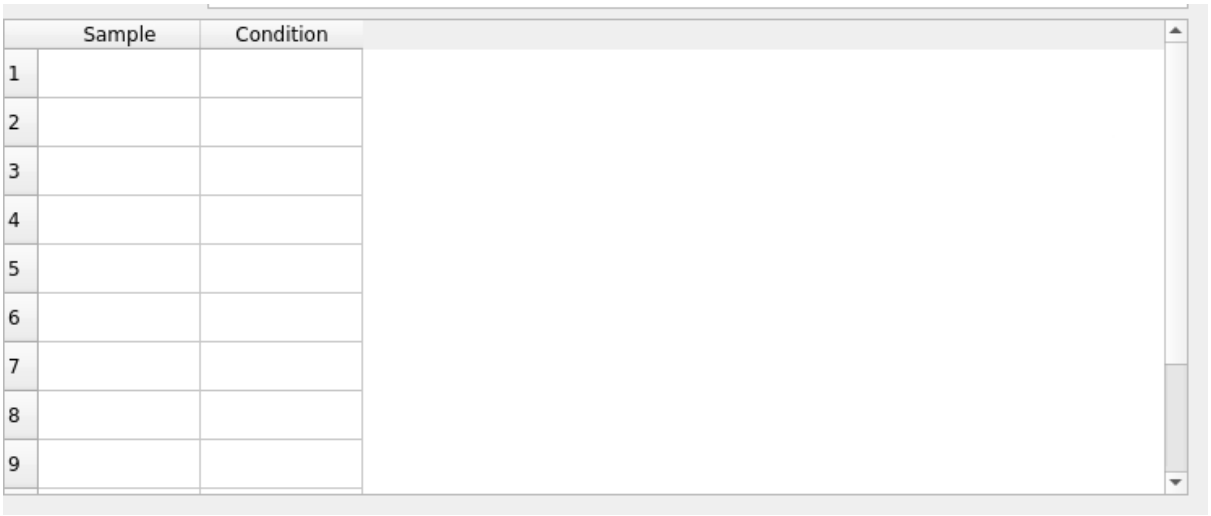


2.13. Here you have a various choices to display data from your experiment or start a DEG or GSEA in case you have count data generated

2.14. For the DEG, click Differential Gene Expression; then perform DEG Analysis

2.15. In order to perform a DEG, you need to enter your count table, an output path, the factors you are interested in and optionally a list of genes you want to see in the volcano plot. The list for the genes and factors you should be separated by “,”

2.16. Enter the number of samples and factors and click CREATE METADATA TABLE for creating your own metadata table. Fill out the table before you click START in order to perform the DEG



2.17. After finishing a message will show up. Close all windows

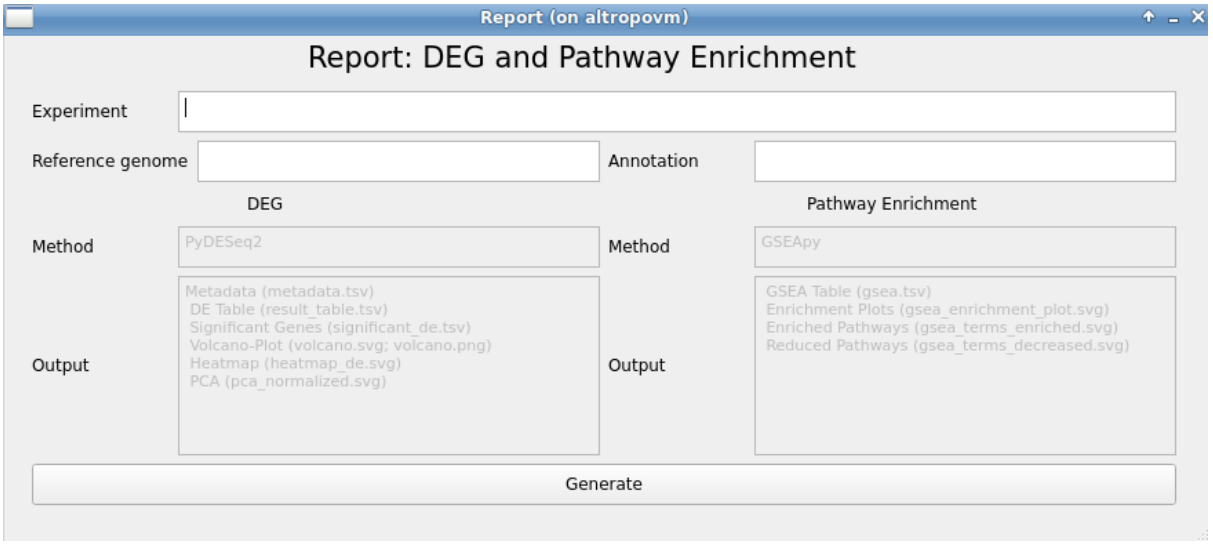
2.18. For the GSEA, click Differential Gene Expression; then perform GSEA

2.19. For the GSEA, enter your DEG data and the output path before clicking START.

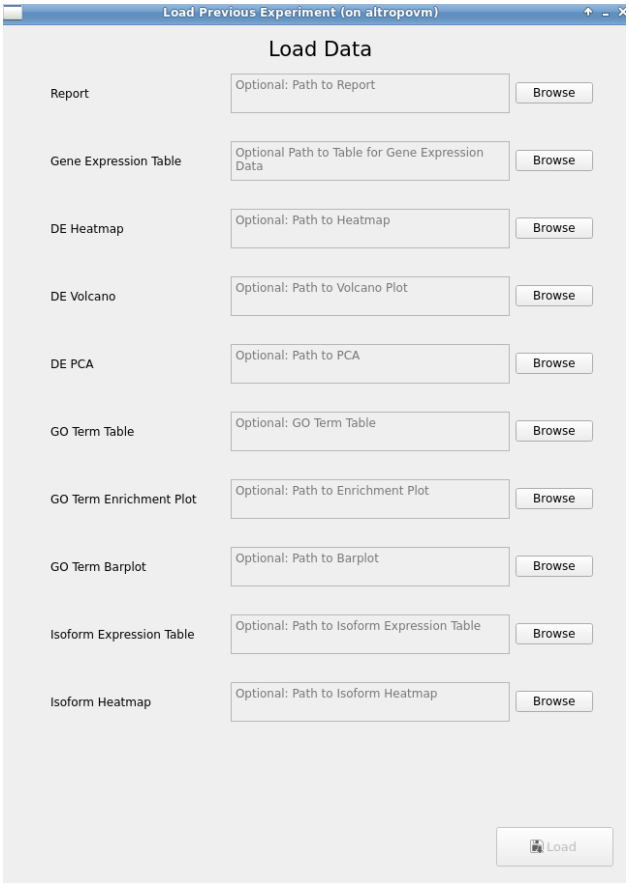
2.20. After finishing a message will show up

2.21. In order to create a report for the DEG click Differential Gene Expression > Create Report for DEG

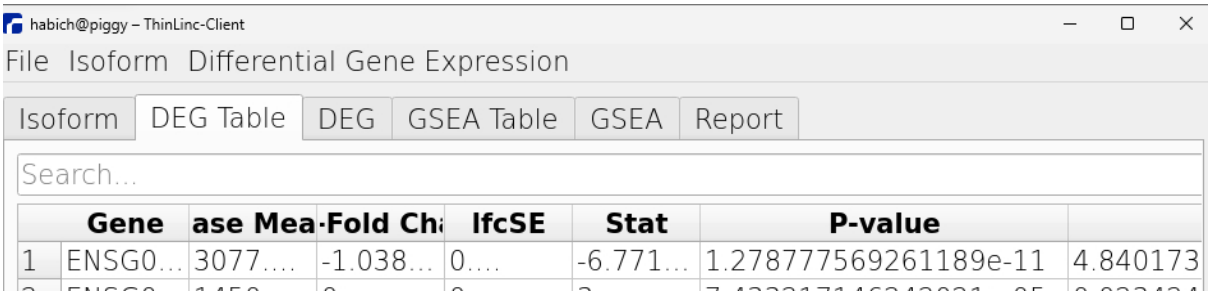
2.22. Enter your Experiment name, Annotation and Reference Genome and click GENERATE. You will obtain a report in PDF formate



2.23. In case you decided to load your data in step 2.2, you will be seeing this window



2.24. Fill out the data you want to load and click LOAD. Then you will see your data in the main menu having the same functions as before.



2.25. Close the window either by clicking X or File > Close