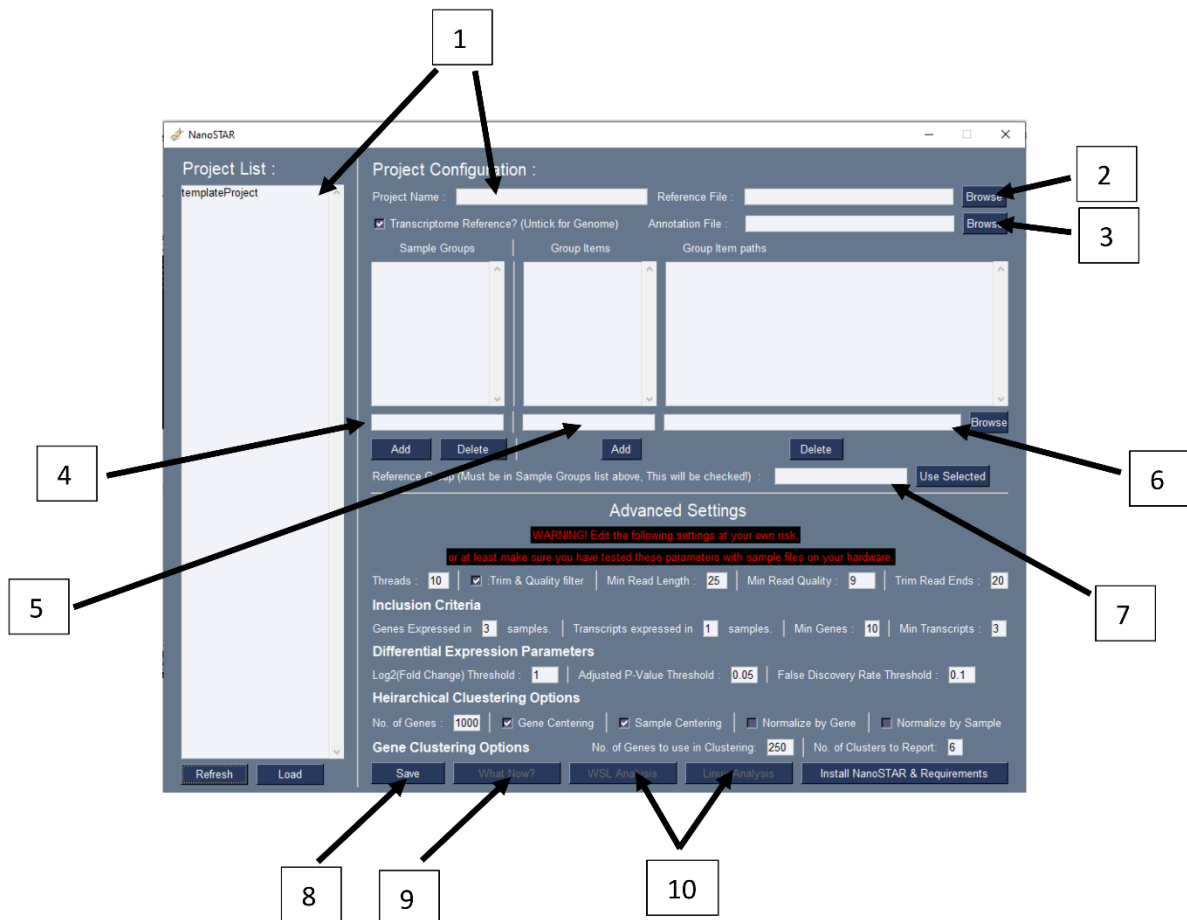




Nanopore Sequenced Transcriptome Analysis Resource

User Guide

To open NanoSTAR, for Windows users double click “NanoSTAR Win Launcher”, whereas Linux users double click “NanoSTAR”. You may get a notification asking if you are sure you wish to run the programme as the publisher is unknown. Allow the programme to run and the NanoSTAR user interface will appear as seen below.



To use NanoSTAR is straightforward and can be split into 10 steps.

1. Project Name and List

Enter a name for the project. If returning to a project, identify the project in the list and click load.

2. Reference File

Click browse and navigate to a .fa, .fna, or .fasta reference file. Genome or transcriptome reference files can be used, and the tick box should be ticked (transcriptome) or unticked (genome) as appropriate.

3. Annotation File

Click browse and navigate to a .gtf or .gff annotation file. This should be the corresponding annotation file to the reference file provided.

4. Sample Groups

Enter group names individually, clicking the Add button for each.

5 & 6. Group Items and Group Item Paths

Click on a sample group. Then individually enter an identifier for each item and browse to the .fastq file associated to that item, clicking the Add button for each.

NOTE: Each item must have a unique name and files can only be used once. If you have called your samples, for example, numbers 1 to 5 in each group, then consider using a prefix here. E.g. A1 to A5, B1 to B5, etc..

Reference Group

Enter the group name of your reference group. Alternatively, select the reference group from the list and click the Use Selected button.

Save

Once all the items have been added correctly click Save. This will move the items into the project folder and populate the config file for running analysis. For larger projects this might take a few minutes.

What Now?

Once the project has been saved click here for extra information before running the analysis.

Analysis

To start analysis, click one of these buttons. NanoSTAR will have auto detected what system is running (Windows or Linux) and only the appropriate button will be available.