NGSREADSTREATMENT

USER GUIDE

NGSReadsTreatment

Version 1.1 de 09/10/2018

SUMMARY

PRESENTATION

NGSReadsTreatment is a tool for removing redundancy from reads for any NGS platform based on the probabilistic structure of the cuckoo filter. Still able to handle single-end and paired-end reads. Available for Windows and Linux operating systems.

Artigo I. REQUIREMENTS FOR RUNNING

JDK Package Available in:

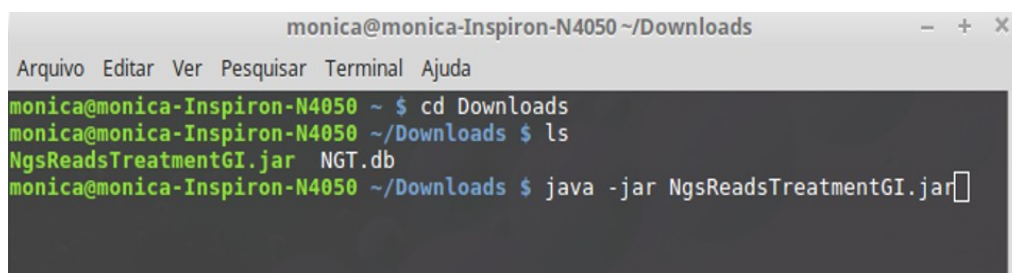https://www.oracle.com/technetwork/java/javase/downloads/index.html)

Artigo II. EXECUTION - GRAPHICAL INTERFACE

To run NGSReadsTreatment, you must first verify the requirements described in item 1. After these validations, follow the steps described below:

Step 01 - Download tool: The tool is available in https://sourceforge.net/projects/ngsreadstreatment/

Step 02 - Start Application: To run the tool follow the example below, it is also demonstrated in Figure 1.
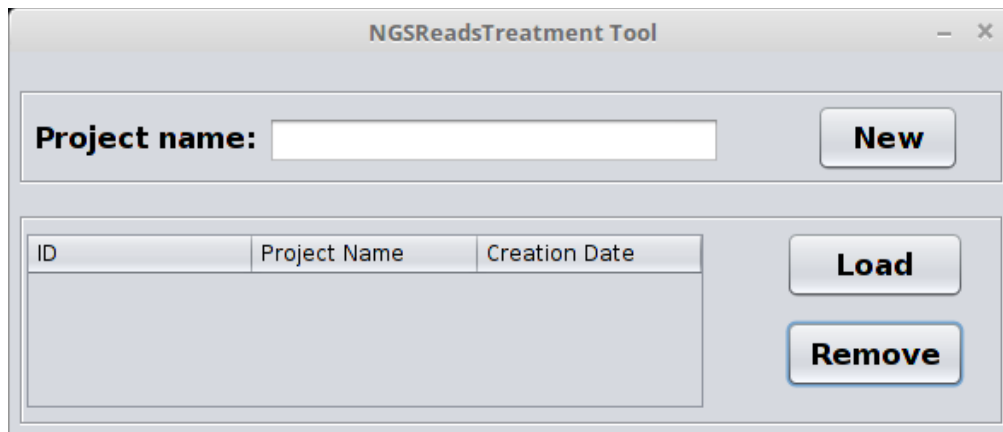
```
java -jar  NgsReadsTreatmentGI.jar
```


Figure 1. Graphic Interface Execution

The graphic system is project oriented. So the first screen that appears is the projects screen Figure 2, in which the user can create a new project or load a previously created project.

Figure 2. Project window

Step 03 - Creating a Project: Enter a name for your project and click the NEW button.

Figure 3. Creating project

Step 04 - Adding Reads Files: Click on the "Find" button and browse your files to add the reads.

Figure 4. Finding reads

⚠️ **Warning**: The reads added can be paired-end or single-end. To add paired-end reads, press the CTRL key on your keyboard and select the two read files (Tag1 and Tag2) to be used, whereas in the single-end the user should add only one tag (Figure 5).

Then click "Add" button to add the reads. Only one set of reads per organism may be added each time (Figure 6).
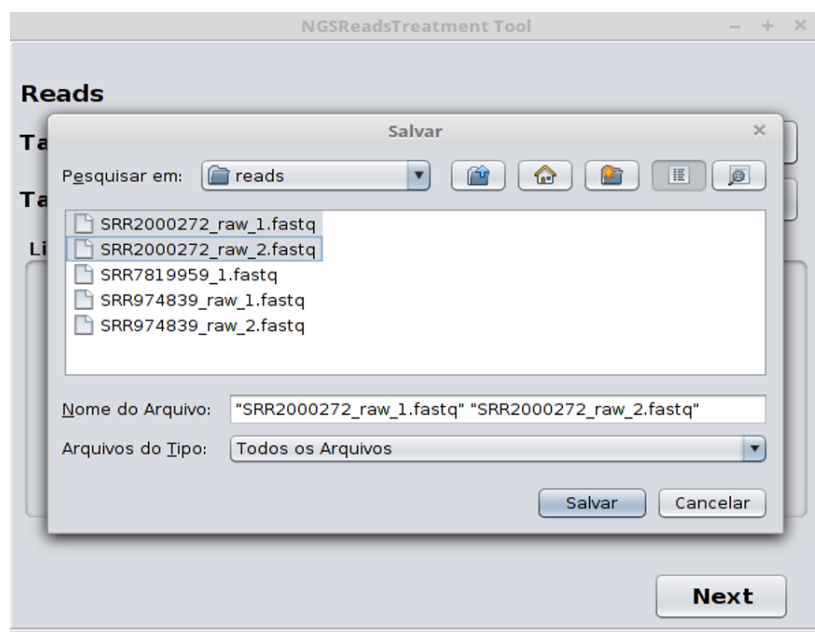
After add the reads, click in the "Next" button.

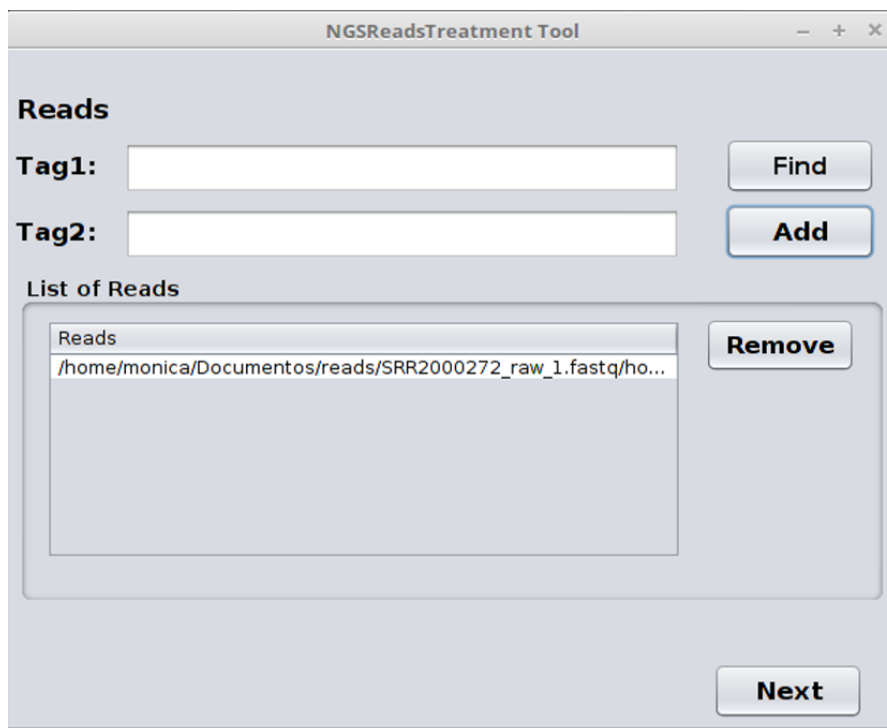
Figure 5. Selecting paired-end reads

Figure 6. Adding reads

Step 05 - Running the Pipeline: To execute you must press the "Run" button, the user can follow the processing by the Log screen and the circular progress bar. On the screen there is also the "Back" button, to return to the previous screen and review / modify the reads added before starting the processing.
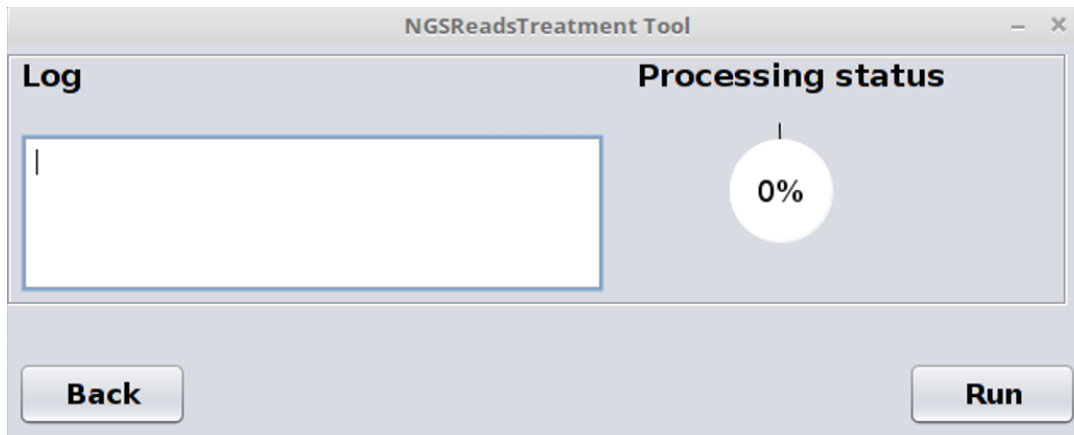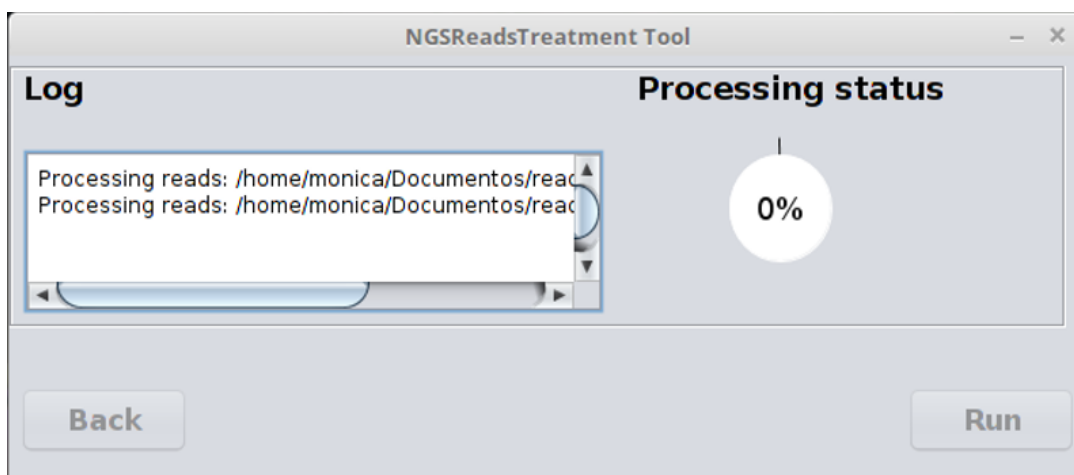

Figura 7. Run screen

Figura 8. Running example

⚠️ **Warning:** In case your reads have already been processed, the screen below will be displayed and you can choose whether to run again or not.
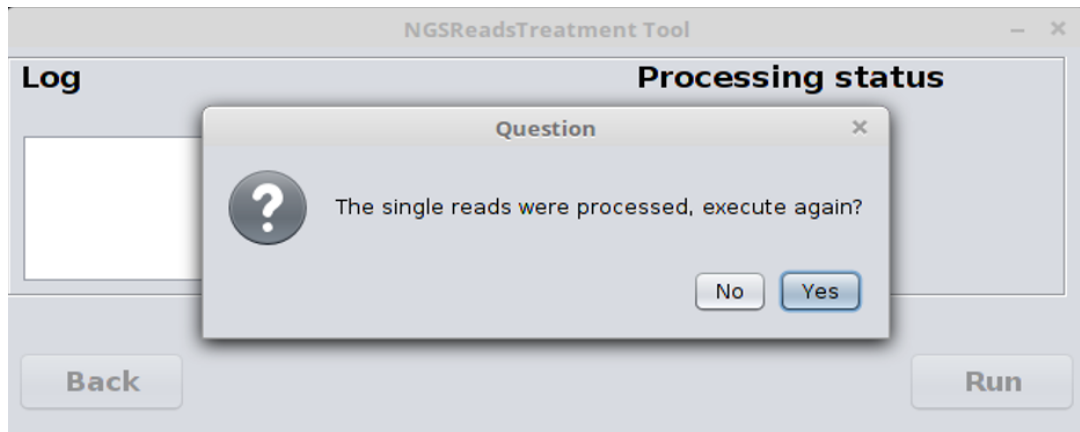

Figura 9. Running with already processed reads

Artigo III.EXECUTION - COMMAND LINE

To run the tool without the graphical interface run the command line below. The user must input the read(s) that they want to process on the line as a parameter.

> *java -jar NgsReadsTreatment.jar PATH<**Single-end**>*
>
> ***OR***
>
> *java -jar NgsReadsTreatment.jar PATH<**Paired tag1**> PATH<**Paired tag2**>*