



USER GUIDE

NGSReadsTreatment

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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>

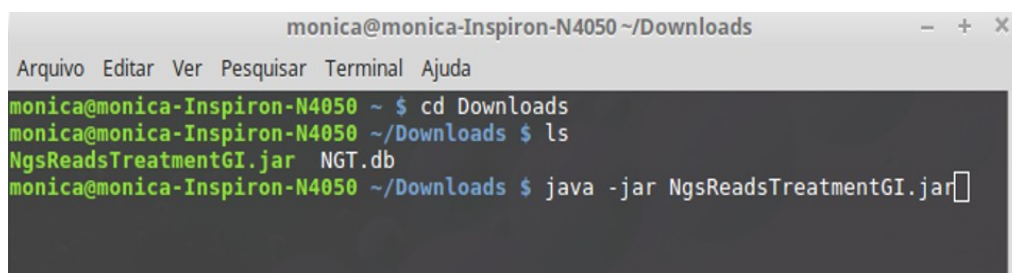
Artigo II. EXECUTION - GRAPHICAL INTERFACE

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.

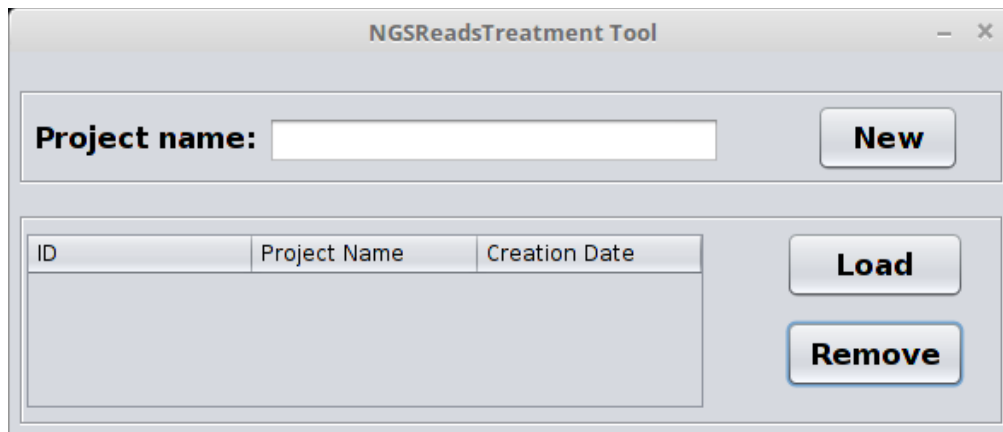
```
java -jar NgsReadsTreatmentGI.jar
```



```
monica@monica-Inspiron-N4050 ~/Downloads
Arquivo Editar Ver Pesquisar Terminal Ajuda
monica@monica-Inspiron-N4050 ~ $ cd Downloads
monica@monica-Inspiron-N4050 ~/Downloads $ ls
NgsReadsTreatmentGI.jar NGT.db
monica@monica-Inspiron-N4050 ~/Downloads $ 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.



The screenshot shows a window titled "NGSReadsTreatment Tool". It features a "Project name:" label followed by a text input field. To the right of the input field is a "New" button. Below the input field is a table with three columns: "ID", "Project Name", and "Creation Date". The table is currently empty. To the right of the table are two buttons: "Load" and "Remove".

Figure 2. Project window

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



The screenshot shows the same window as Figure 2, but the text input field now contains the text "primeiroteste". The "New" button is still visible to the right of the input field. The table below remains empty, and the "Load" and "Remove" buttons are still present to the right of the table.

Figure 3. Creating project

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

The screenshot shows a window titled "NGSReadsTreatment Tool". Inside, there is a section labeled "Reads". Under this section, there are two input fields: "Tag1:" and "Tag2:". The "Tag1:" field contains the text "ome/monica/Documentos/reads/SRR2000272_raw_1.fastq" and has a "Find" button to its right. The "Tag2:" field contains the text "ome/monica/Documentos/reads/SRR2000272_raw_2.fastq" and has an "Add" button to its right. Below these fields is a section labeled "List of Reads". This section contains a large, empty rectangular box with a header "Reads" at the top left. To the right of this box is a "Remove" button. At the bottom right of the window is a "Next" button.

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.

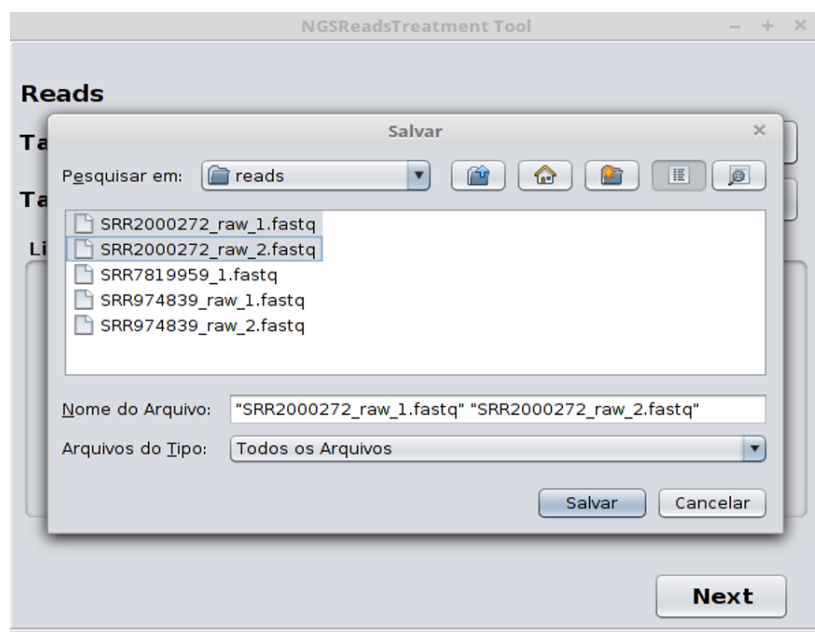


Figure 5. Selecting paired-end reads

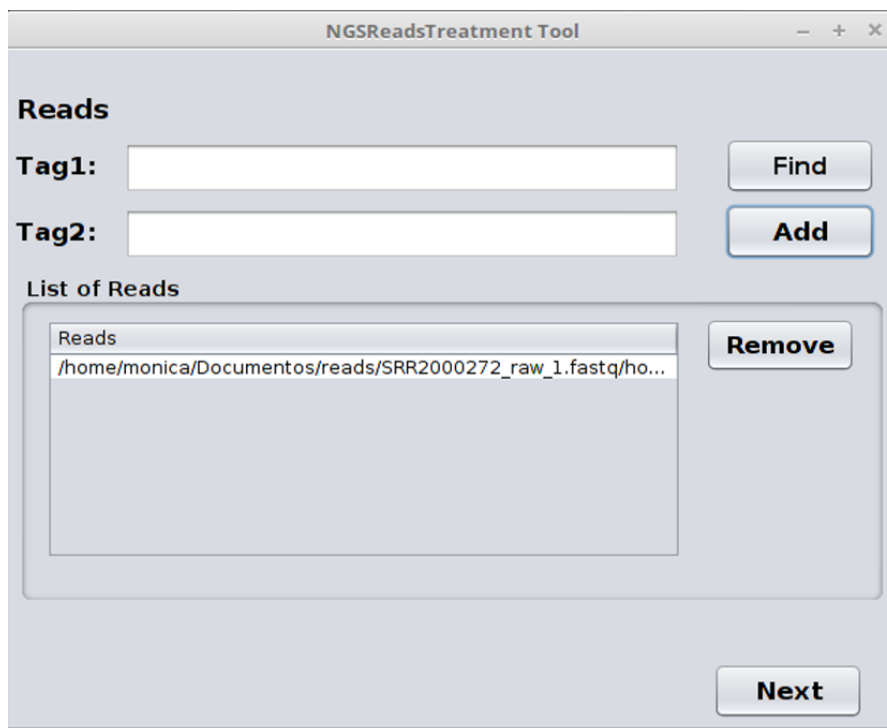


Figure 6. Adding reads

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.

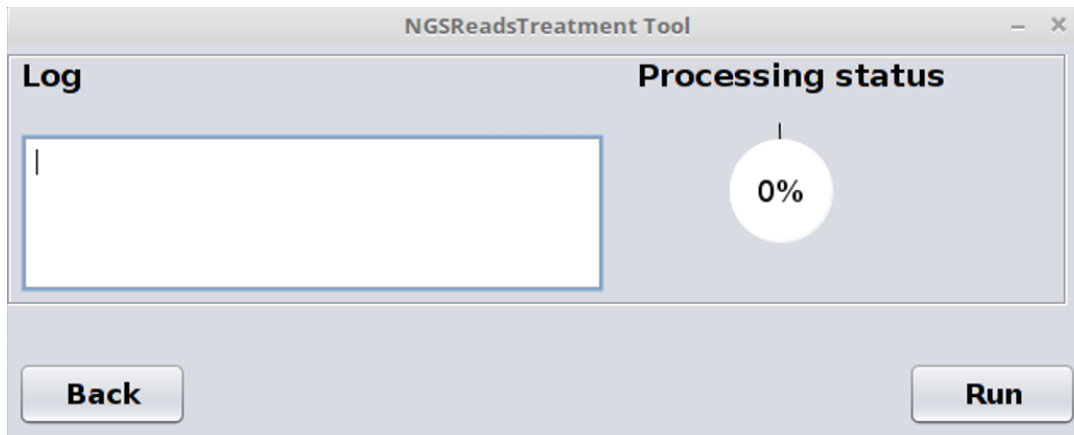


Figura 7. Run screen

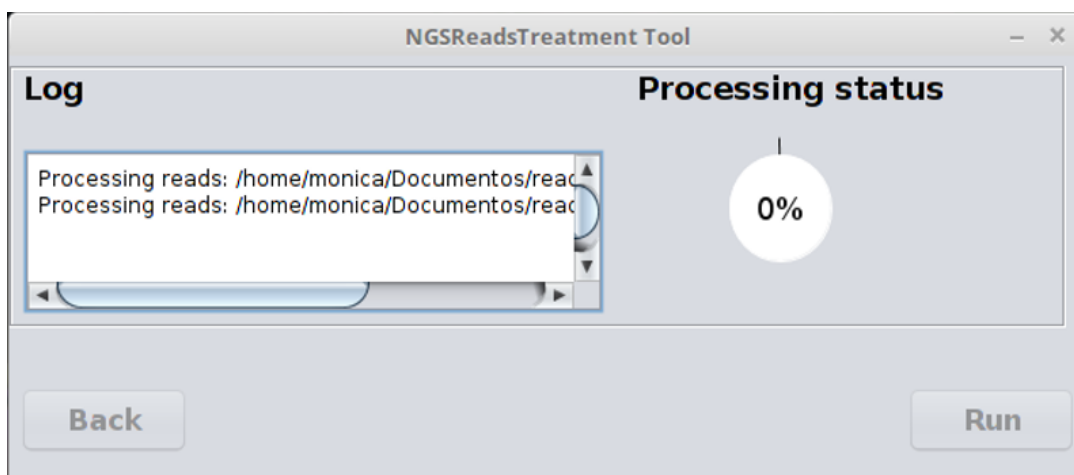


Figura 8. Running example



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.

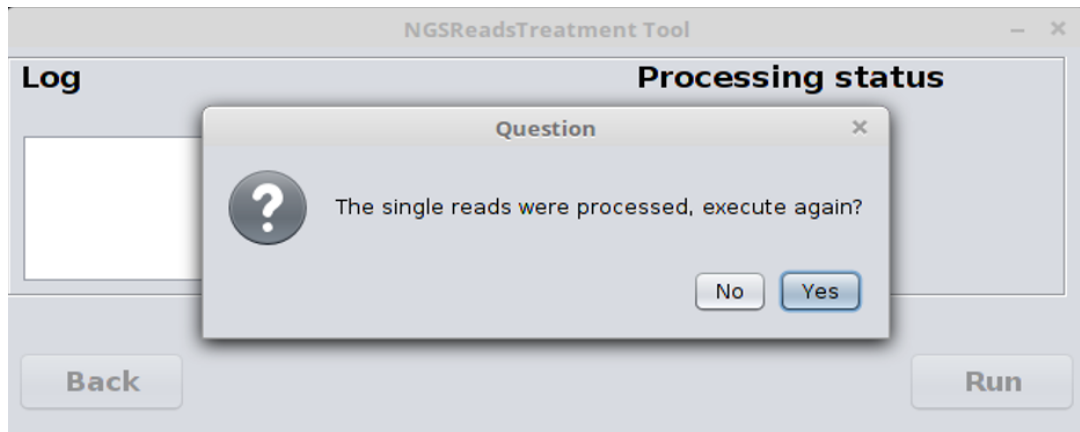


Figura 9. Running with *already processed reads*

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>
```