



# User manual, Java assembly review

MSc Applied Bioinformatics,  
Marie Schmit

The java version used is Java 1.8.

Run the application with an IDE like Netbeans or in the terminal with java -jar.

When the app opens, select the fasta file of interest and click “confirm”. The statistics of the file should appear. This might take some time, depending on the length of the file. To add gtf file content, click on the menu Choose New file -> Choose gtf File and browse the gtf file of interest. Again, click “Confirm”. The button “view” in the menu redirects to the statistics screen. When a contig or a scaffold is selected in the “List of contigs, information appear in the panel “contig / scaffold metrics”.



- 1- General statistics on the assembly
- 2- Scaffolds overview. The gap sequences (“NNN” in the fasta file) are in salmon.
- 3- Appears when gtf file is loaded. Table of gtf file content. The size of the cloumns can be changed to better se their content.
- 4- Each bar represents a contig length. The salmon bar corresponds to the N50.
- 5- List of contigs or scaffold. Select one element of the list to see its information on the panel contig/scaffold metrics.
- 6- Length and GC content of the selected scaffold or contig.
- 7- Sequence of the selected scaffold or contig.
- 8- Graphical overview of selected scaffold or contig. Each salmon bar corresponds to a gap (sequence of “NNN” in the fasta file). One larger bar can represents two or three gaps if they are very close to each other in comparison to the whole scaffold size (used as scale).