



- **Quast compares the preliminary assembly to a known genome from the same species.**
- **Also, identifies functional sequences, like genes and RNAs.**

Preliminary assembly

The reference .fasta file.

```
quast.py prelim_assembly.fasta -R ebola_ref.fasta \
-G ebola_ref_genes.gff -o output_folder -glimmer
```

List of genes in the reference.

Output folder
containing results

Provide list of gene locations in
the preliminary assembly.