

Finding Repeats

Task Name: find-repeats

Searches for repeats in sequences and saves the regions found as annotations.

Parameters:

in — semicolon-separated list of input files. [String, Required]

out — output file with the annotations. [String, Required]

name — name of the annotated regions. [String, Optional, Default: "repeat_unit"]

min-length — minimum length of the repeats. [Number, Optional, Default: 5]

identity — percent identity between repeats. [Number, Optional, Default: 100]

min-distance — minimum distance between the repeats. [Number, Optional, Default: 0]

max-distance — maximum distance between the repeats. [Number, Optional, Default: 5000]

inverted — if *true*, searches for the inverted repeats. [Boolean, Optional, Default: false]

Example:

```
ugene find-repeats --in=murine.gb --out=murine_repeats.gb --identity=99
```