

Elements of Computational Biology

Subject 15: Distance phylogenetics: UPGMA and NJ

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December 19, 2016

1 Algorithms

1.1 UPGMA

1.2 NJ

1.3 Comparing topology

2 Usage

Application can be downloaded from Github and compiled using **Maven**.

Listing 1: Building project

```
git clone git@github.com:MiSSLab/BioComp15.git
mvn package
```

Created Java archive can be run using **JRE**. Sample data can be found in directory **resources/**.

Listing 2: Running project using data1.matrix

```
java -jar -Dfilename="resources/data1.matrix" \
    target/distance-phylogenetics-jar-with-dependencies.jar
```

3 Data formats

3.1 Input

Application requires CSV data format and quadratic matrix of distances.

Listing 3: Example data file content

```
0,8,8,5,3
8,0,3,8,8
8,3,0,8,8
5,8,8,0,5
3,8,8,5,0
```

3.2 Output