Elements of Computational Biology
Subject 15: Distance phylogenetics: UPGMA and NJ

Agata Radys, Paweł Cejrowski, Łukasz Myśliński

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1 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
```

2 Data format

Application requires `CSV` data format and quadratic matrix of distances.

Listing 3: Example data file

```
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
```