Japsa Documentation
Release v15.8-Ekka

Minh Duc Cao

July 29, 2015

Japsa (*JAva Package for Statistical Sequence Analysis*) is a package for analysis of biological sequences data, written in Java. The package contains ready-to-run analysis tools, together with the Java library for further development.

Contents:

DEPENDENCIES

Japsa has the following dependencies, some of which are included in the package.

- Java Runtime Environment (java) >=1.6

- Jfreechart >= 1.0.19 (http://www.jfree.org/jfreechart/) and Jcommon (http://www.jfree.org/jcommon/)– included

- colloquial.jar, now java-arithcode (https://github.com/bob-carpenter/java-arithcode) – included

- common-math.jar >=3.3.0 (http://commons.apache.org/proper/commons-math/) –included

- htsjdk >=1.126 – included

- sam >=1.84 – included. This will be replaced by htsjdk above

- guava >=16.0 – included

- jhdf5 >= 18 – included

- JRI – included. Dependency on JRI will be removed in the future

- HDF-Java https://www.hdfgroup.org/products/java/release/download.html – needed for npReader

- R and rJava – needed only for speciesTyping

Japsa is provided with a ready to run package at every stable release. These pre-built releases are compiled with javac 1.6 to ensure compatibility. If you wish to use the latest version of Japsa, or use japsa compiled with your version of Java, you will need to build from source, which requires:

- Java Development Kit (javac) >= 1.6

- make

INSTALLATION

There are two methods to install Japsa in your computer:

2.1 1. Install from the pre-compiled package

2.2 2. Obtain source code and compile

First download the latest source code:

```
git clone https://github.com/mdcao/japsa
cd japsa
make -f Makefile.main install [INSTALL_DIR=~/.usr/local] [JLP=/usr/lib]
```

which will install Japsa to the directory specified by INSTALL_DIR (e.g., *~/.usr/local* or */usr/local* if you have root privilege). If not specified, INSTALL_DIR is defaulted to */usr/local*. Directive JLP specifies path to libjhdf5 and libjri.so, and only needed for npReader and npSpeciesTyping.

To uninstall Japsa, run the following in the japsa directory:

```
make -f Makefile.main uninstall [INSTALL_DIR=~/.usr/local]
```

INDICES AND TABLES

- genindex
- modindex
- search