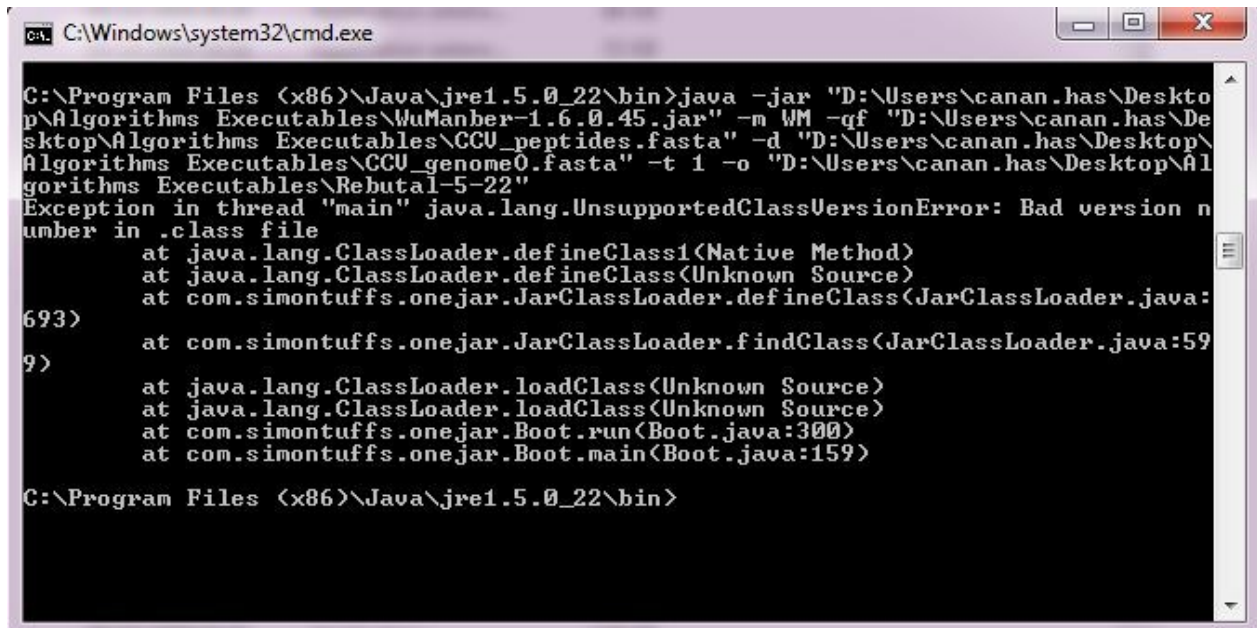


Lelantos Executable Switches

WuManber implementation

Wu-Manber console application is a JAVA implementation. Therefore, it must be sure that JAVA is installed on the path. Wu-Manber implementation was compiled in two Java versions; 1.6 and 1.7. For 1.6 implementation, the minimum Java version must be 1.6 and for 1.7 implementation, the minimum version must be 1.7. At below Java installations, below error will be retrieved:

A screenshot of a Windows command prompt window. The title bar reads "C:\Windows\system32\cmd.exe". The command prompt shows the following text:

```
C:\Program Files (x86)\Java\jre1.5.0_22\bin>java -jar "D:\Users\canan.has\Desktop\Algorithms Executables\WuManber-1.6.0.45.jar" -m WM -qf "D:\Users\canan.has\Desktop\Algorithms Executables\CCU_peptides.fasta" -d "D:\Users\canan.has\Desktop\Algorithms Executables\CCU_genome0.fasta" -t 1 -o "D:\Users\canan.has\Desktop\Algorithms Executables\Rebutal-5-22"
Exception in thread "main" java.lang.UnsupportedClassVersionError: Bad version number in .class file
    at java.lang.ClassLoader.defineClass1(Native Method)
    at java.lang.ClassLoader.defineClass(Unknown Source)
    at com.sinontuffs.onejar.JarClassLoader.defineClass(JarClassLoader.java:693)
    at com.sinontuffs.onejar.JarClassLoader.findClass(JarClassLoader.java:599)
    at java.lang.ClassLoader.loadClass(Unknown Source)
    at java.lang.ClassLoader.loadClass(Unknown Source)
    at com.sinontuffs.onejar.Boot.run(Boot.java:300)
    at com.sinontuffs.onejar.Boot.main(Boot.java:159)

C:\Program Files (x86)\Java\jre1.5.0_22\bin>
```

For the errors other than `UnsupportedClassVersionError`, please contact with us.

```
Command Prompt
Z:\Users\Canan Has\Desktop\LelantosFinalSubmission\LelantosBinaries>java -jar WuManber.jar
Please review the usage of the program:
*****
*                               LELANTOS WuManber v.1.0                               *
*                               Canan Has & Jens Allmer                               *
*                               Izmir Institute of Technology                         *
*****
* Wu-Manber search algorithm for exact string search of                             *
* peptides on six frame translation of given nucleotide sequence or                 *
* amino acid sequence.                                                              *
* The program was compiled on JDK 1.7. Please be sure your java version is 1.7.    *
*                                                                                      *
*-----*
* Switches:                                                                        *
* -m [method <required>]: WM: Wu-Manber                                           *
* Input peptide sequences must be given either as FASTA, mzIdentML or string      *
* -qf [path to query input file <required>]: query file in FASTA format           *
* -qs [query sequence]: input peptide sequence as string.                         *
* -qm [path to query input file <required>]: query file in mzid format             *
* -d [path to sequence file <required>]: sequence file in FASTA format either     *
*     nucleotide sequence or aminoacid sequence.                                  *
* -o [path to output filename <required>]:                                        *
* GFF3 file includes the mapping result                                           *
* When memory size is not enough to handle search for large files, file can be    *
* read and processed partially as chunks                                          *
* Codon usage for translation can be set via NCBI codon table file.               *
* If table is given, name of codon usage must be set with -s switch.             *
* -ut [NCBI codon table <optional>]: given as text file.                         *
```

Suffix Array implementation

Suffix array implementation is developed in C++ as part of SeqAn library. It has Linux and Windows executables in our website. Please make sure that missing C++ dependencies in computer might cause problems. In that case, please report your problem to us.

```
Command Prompt
C:\Users\Canan Has\Dropbox\lelantos_gui\suffix_tree_mapping>win_suffix_array_map
ping.exe -help
suffix_array_mapping - This program searches for exact query matches using a suf
fix array index.
=====
SYNOPSIS
    suffix_array_mapping [OPTIONS] -is SAMPLEFILE -ir REFERENCE -t TYPE [dna, pe
ptide] -o OUTFILE
DESCRIPTION
    This program determines the locations of the input queries in the reference
using a suffix array index.
    -h, --help
        Displays this help message.
    --version
        Display version information.
    -is, --inputSample IN
        Name of the multi-FASTA input. Valid filetypes are: fasta, fa, and fna
.
    -t, --inputType STR
        The type of the input. One of dna and peptide.
    -ir, --inputRefs IN
        Name of the multi-FASTA input. Valid filetypes are: fasta, fa, and fna
.
    -o, --outputFileName OUT
        Name of the output file. Valid filetype is: gff.
    -oI, --outputIndexName OUT
        Name of the index to store.
    -s0, --storeOnly
        Stop after storing the index.
    -th, --threads NUM
        The number of threads to be used.
    -bf, --bufferSize NUM
        The number of reads stored in a buffer before writing them to disk.
    -gc, --geneticCode NUM
        There are several different genetic codes available taken from NCBI: 1
- Canonical, 2 - VertMitochondrial, 3
- YeastMitochondrial, 4 - MoldMitochondrial, 5 - InvertMitochondrial,
6 - Ciliate, 9 -
FlatwormMitochondrial, 10 - Euplotid, 11 - Prokaryote, 12 - AltYeast,
13 - AscidianMitochondrial, 14 -
AltFlatwormMitochondrial, 15 - Blepherisma, 16 - ChlorophyceanMitochon
drial, 21 - TrematodeMitochondrial, 22
- ScenedesmusMitochondrial, 23 - ThraustochytriumMitochondrial, 24 - P
terobranchiaMitochondrial, 25 -
Gracilibacteria
VERSION
    suffix_array_mapping version: 0.1
    Last update Feb 2015
C:\Users\Canan Has\Dropbox\lelantos_gui\suffix_tree_mapping>
```