

RE java and snpEff

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First of all:

I am exceedingly proud of you! You totally rocked this email! You gave me like 99% of what I needed to think about this problem effectively without me having to ask a single question! I hope that you notice your improved computer literacy and allow yourself to feel some pride as well. You deserve it.

So on to the snpEff stuff:

when i run "which java" i get:

```
mariangelabonizzoni@dhcp-v106-224 17:31:49 ~:
which java
/usr/bin/java
```

when i call java, i get the help menu.

When i call java -version, i get the java version as:

```
mariangelabonizzoni@dhcp-v106-224 17:31:53 ~:
java -version
java version "1.8.0_25"
Java(TM) SE Runtime Environment (build 1.8.0_25-b17)
Java HotSpot(TM) 64-Bit Server VM (build 25.25-b02, mixed mode)
```

When i call which snpEff, i get:

```
which snpEff
/usr/local/bin/snpEff
```

snpEff is supposedly a java program to be run through java -jar snpEff.jar, but when i do it, i always get the message:

```
mariangelabonizzoni@dhcp-v106-224 17:33:18 ~:
java -jar snpEff.jar
Error: Unable to access jarfile snpEff.jar
```

I tried to run this command with many different variants, like going into /user/local/bin or from /user/bin or using instead of sniper.jar the whole path to the program, but i always get the same message.

interestingly, when i simply type snpEff, i get the help menu. As follows

```
snpEff
Error: Missing command

snpEff version SnpEff 3.6c (build 2014-05-20), by Pablo Cingolani
Usage: snpEff [command] [options] [files]

Run 'java -jar snpEff.jar command' for help on each specific command

Available commands:
    [eff]                               : Calculate effect of variants. Default: eff
(no command or 'eff').
    build                               : Build a SnpEff database.
    XXXXXXXXXXXX
    -ud , -upDownStreamLen <int> : Set upstream downstream interval length
(in bases)
```

My reply:

Yes.

I am fairly certain that the correct way to call snpEff is to omit the java -jar call and simply call snpEff directly. The reason for this is that it has been installed in /usr/local/bin which is almost always in the user's \$PATH variable by default. The way that it is installed the java -jar portion is implied and the computer takes care of it behind the scenes.

The help text is an unfortunate confusion: for **for sure**. But again, I am quite proud that you basically figured this out without my help at all. Very nice work, Dr!

The genome data files:

the big problem that i have is that i have to build a genomic database because the organism that i want to study is not supported (it is an asian mosquito). i downloaded the required genome sequences and annotation file in GTF from vectorbase and i followed (i think i did) the instruction in the "create database" from the snpEff menu page. but i keep getting the same message as: genome not found. see below. i tried i do not know many different options to change the name of the files, to run the command from different folders, to change the configuration file for snpEff, i always get the same message. like the genome file is not seen. it is driving me crazy!!!! any idea? I wrote to the snpEff developers, but they have not had the courtesy to reply yet. any suggestion would be great!!! thanks

```
snpEff build -gtf22 /Volumes/Seagate_Exp_1/snpEff/data/AsinC2.1
java.lang.RuntimeException: Property:
'/Volumes/Seagate_Exp_1/snpEff/data/AsinC2.1.genome' not found
```

```
    at ca.mcgill.mcb.pcingola.interval.Genome.<init>(Genome.java:92)
    at ca.mcgill.mcb.pcingola.snpEffect.Config.readGenomeConfig(Config.java:513)
    at ca.mcgill.mcb.pcingola.snpEffect.Config.readConfig(Config.java:476)
    at ca.mcgill.mcb.pcingola.snpEffect.Config.init(Config.java:377)
    at ca.mcgill.mcb.pcingola.snpEffect.Config.<init>(Config.java:99)
    at
ca.mcgill.mcb.pcingola.snpEffect.commandLine.SnpEff.loadConfig(SnpEff.java:236)
    at
ca.mcgill.mcb.pcingola.snpEffect.commandLine.SnpEffCmdBuild.run(SnpEffCmdBuild.java:256)
    at ca.mcgill.mcb.pcingola.snpEffect.commandLine.SnpEff.run(SnpEff.java:685)
    at ca.mcgill.mcb.pcingola.snpEffect.commandLine.SnpEff.main(SnpEff.java:118)
```

My reply:

Ok. This is a bit more complicated. I am going to have to try looking through the `snpEff.config` file that they mention. It looks like this file is how you set up all the locations of things that you will need to organize to let `snpEff` know how to build its databases. Did you configure this file yet? If so, would you send me the file so I have a place to start?

Gus