

PM17 - Software Dependencies

Javier Perales-Paton

jperales@cnio.es

Quick manual installation (root user in Ubuntu 16)

1. Install **Java (version 1.7 or 1.8) in ubuntu**.

When the installation is finished, check that Java is correctly installed:

```
participant@machine:~$ java -version
openjdk version "1.8.0_151"
OpenJDK Runtime Environment (build 1.8.0_151-8u151-b12-0ubuntu0.16.04.2-b12)
OpenJDK 64-Bit Server VM (build 25.151-b12, mixed mode)
```

2. Install **python**

```
sudo apt-get install python-dev
```

3. Get the library **libmysqlclient**

```
sudo apt-get install libmysqlclient-dev
```

4. **Perl Modules ::**

Rubioseq built on perl modules which must be correctly installed. If one of these is missing, the pipeline will get a crash.

- DBI
- DBD::mysql
- XML::LibXML
- Carp
- FindBin
- File::Basename
- File::Spec
- File::Copy
- Getopt::Long
- Class::Inspector

```
sudo cpan DBI DBD::mysql XML::LibXML Carp FindBin File::Basename
```

```
sudo cpan File::Spec File::Copy Getopt::long Class::Inspector
```

- Bioperl :: Finally, Install Bioperl using CPAN and root permissions following these instructions: <http://bioperl.org/INSTALL.html> . So,

```
sudo cpan
```

```
cpan> force install CJFIELDS/BioPerl-1.6.924.tar.gz
```

```
cpan> exit
```

```
 #(This will take ~ 10 minutes. Please, wait until it is finished)
```

5. Python modules : Numpy, Scipy and pysam

```
sudo pip install Numpy
```

```
sudo pip install Scipy
```

```
sudo pip install pysam
```

6. Third-party Software component for the pipeline:

6.1. First, define the PATH to install the rest of the Software:

```
mkdir /home/$USER/Software
```

6.2. Get IGV browser from:

http://data.broadinstitute.org/igv/projects/downloads/2.4/IGV_2.4.3.zip

Download it into the directory `/home/$USER/Software` . Then, unzip the file:

```
cd /home/$USER/Software
```

```
unzip /home/$USER/Software/IGV_2.4.3.zip
```

6.3. Get RubioSeq v3.8.1 from the source:

<https://sourceforge.net/projects/rubioseq/files/SourceVersions/RUbioSeq3.8.1.tgz/download>

Please, download it into the user's Software directory (`/home/$USER/Software`). Then, decompress the file by executing in the terminal:

```
tar xzvf /home/$USER/Software/RUbioSeq3.8.1.tgz
```

Download the **Installer for RubioSeq dependencies**. It is a **Bash script** which you may download it into `/home/$USER/Software` from:

https://sourceforge.net/projects/rubioseq/files/Installation_bundle/RUbioSeq3.8.1/install-rubiose-q-bundlev3.8.bash/download

Next, execute in the terminal the following command:

```
bash /home/$USER/Software/install-rubioseq-bundlev3.8.bash /home/$USER/Software/
```

You are going to see these series of messages while the bash script is running:

```
INFO: Checking dependencies [programs]
INFO: Detected python interpreter: python2 (Python 2.7.12)
INFO: Checking dependencies [C/C++ development libraries]
INFO: Checking dependencies [Perl libraries]
INFO: Checking dependencies [Python libraries]
INFO: Destination directory for RUBioSeq is /home/jperales/Software/
INFO: Temporal directory (for downloads, compilations, etc...) is
/tmp/rubioseq.A3eFwFEt
INFO: Running install_autoconf
INFO: Running install_automake
INFO: Running install_pkgconfig
INFO: Running install_samtools
INFO: Running install_picard
INFO: Running install_fastqc
INFO: Running install_bwa
INFO: Running install_bfast bwa
INFO: Running install_gatk
INFO: Running install_bioperl
INFO: Running install_contra
INFO: Running install_mac
INFO: Running install_ccat
INFO: Running install_bedtools
INFO: Running install_bedgraphtobigwig
ERROR: install_bedgraphtobigwig died downloading sources. See log file at
/tmp/rubioseq.A3eFwFEt/logs/install_bedgraphtobigwig_log.txt
(Please, ignore the last ERROR).
```

When the bash script have finished, the structure of the **Software** directory
(/home/\$USER/Software) must look like this. Please, check if these directories and files
exists:

```
/home/$USER/Software/BEDTools-Version-2.16.2
/home/$USER/Software/bfast-bwa-ed42c18ea7f48af862935be52f1c072b1d5609cc
/home/$USER/Software/bwa-0.7.10
/home/$USER/Software/CCAT3.0
/home/$USER/Software/CONTRA.v2.0.3
/home/$USER/Software/FastQC
/home/$USER/Software/GATK-3.4-0
/home/$USER/Software/IGV_2.4.3.zip
/home/$USER/Software/install-rubioseq-bundlev3.8.bash
/home/$USER/Software/MACS2-2.0.10.20130712
/home/$USER/Software/picard-tools-1.107
/home/$USER/Software/RUBioSeq3.8.1
/home/$USER/Software/RUBioSeq3.8.1.tgz
/home/$USER/Software/samtools-0.1.19
```

Check (☑) that every single component of the pipeline is correctly installed :

- ☐ bfast+bwa

```
/home/$USER/Software/bfast-bwa-ed42c18ea7f48af862935be52f1c072b1d5609cc/bin/bfast
```

```
participant@machine:~$ /home/$USER/Software/bfast-bwa-ed42c18ea7f48af862935be52f1c072b1d5609cc/bin/bfast
BFAST:  the blat-like fast accurate search tool
Version: 0.7.0b git:Revision: undefined$
Contact: bfast-help@lists.sourceforge.net
```

- ☐ bwa

```
/home/$USER/Software/bwa-0.7.10/bwa
```

```
participant@machine:~$ /home/$USER/Software/bwa-0.7.10/bwa
Program: bwa (alignment via Burrows-Wheeler transformation)
Version: 0.7.10-r789
Contact: Heng Li <lh3@sanger.ac.uk>
```

- ☐ CONTRA

```
python /home/jperales/Software/CONTRA.v2.0.3/contra.py
```

```
participant@machine:~$ python /home/$USER/Software/CONTRA.v2.0.3/contra.py -h
Usage: contra.py [options]
```

- ☐ FastQC

```
perl /home/$USER/Software/FastQC/fastqc -v
```

```
participant@machine:~$ perl /home/$USER/Software/FastQC/fastqc -v
FastQC v0.10.1
```

- ☐ GATK

```
java -jar /home/$USER/Software/GATK-3.4-0/GenomeAnalysisTK-3.4-0/GenomeAnalysisTK.jar --version
```

```
participant@machine:~$ java -jar /home/$USER/Software/GATK-3.4-0/GenomeAnalysisTK-3.4-0/GenomeAnalysisTK.jar --version
3.4-0-g7e26428
```

- ☐ PICARD-TOOLS

```
java -jar /home/jperales/Software/picard-tools-1.107/MarkDuplicates.jar --version
```

```
participant@machine:~$ java -jar /home/$USER/Software/picard-tools-1.107/MarkDuplicates.jar --version
1.107(1667)
```

- ☐ RUBioSeq 3.8.1

```
perl /home/$USER/Software/RUBioSeq3.8.1/RUBioSeq.pl
```

```
participant@machine:~$ perl /home/$USER/Software/RUBioSeq3.8.1/RUBioSeq.pl

RUBioSeq.pl --analysis analysisType --config config_file [--level level_number]

Getting help:
[--help]
Analysis Types:
variantCalling : Variant Calling Workflow.(default)
cnvCalling: CNV Calling Workflow.
CHIPseq: CHIPseq workflow.
methylationCalling : Methylation Calling Workflow.
Example:
./RUBioSeq.pl --analysis variantCalling --config /dir/config.xml --level 3

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```

6.4. Please remove the installers and temporary files:

```
rm /home/$USER/Software/RUBioSeq3.8.1.tgz
```

```
rm /home/$USER/Software/install-rubioseq-bundlev3.8.bash
```

```
rm /home/$USER/Software/IGV 2.4.3.zip
```

That's all! Thank you very much for your time.

```
# version 1.0
```