

PM16 - Software Dependencies

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Quick manual installation (root user in Ubuntu (linux))

1. Install **java 1.7** (<http://www.webupd8.org/2012/01/install-oracle-java-jdk-7-in-ubuntu-via.html>)

```
sudo add-apt-repository ppa:webupd8team/java
```

```
sudo apt-get update
```

```
sudo apt-get install oracle-java7-installer
```

2. Install **python**

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

3. Get the library **libmysqlclient**

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

4. **Perl Modules ::**

Rubioseq is based 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 C/CJ/CJFIELDS/BioPerl-1.6.923.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:

During the class, we will learn to install all these third-party software to set up the pipeline.

Define the PATH to install **the rest of the Software**:

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

Download and compile every single component from the repository. You can do this in one single command as follows:

- 6.1.) Download into `/home/$USER/Software` the **bundle-installer of RUBioSeq** from:

https://sourceforge.net/projects/rubioseq/files/Installation_bundle/RUBioSeq%2B/

Execute the following command in a terminal

```
bash /home/$USER/Software/rubioseq-bundle-installer.sh /home/$USER/Software/  
# (ignore the error about BioPerl)
```

- 6.2) Install **CONTRA**. Download it into `/home/$USER/Software` Then, untar this file:

<https://www.dropbox.com/s/oxraj31fqyvyir6/CONTRA.v2.0.3.tar?dl=0>

```
cd /home/$USER/Software  
tar xvf CONTRA.v2.0.3.tar
```

- 6.3) Install **RUBioSeq+**. Download it into `/home/$USER/Software` Then, untar the file:

<http://sourceforge.net/projects/rubioseq/files/SourceVersions/RUBioSeq%2B.tgz/download>

```
cd /home/$USER/Software  
tar zxvf RUBioSeq+.tgz  
cd /home/$USER/Software/RUBioSeq+  
tar zxvf RUBioSeq3.7.tgz
```

- 6.4) Install **ngsCAT**. Download it into `/home/$USER/Software`:

https://www.dropbox.com/s/p9kxiyvi0mvpz59/ngsCAT_setup_ubuntu.sh?dl=0

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

```
sudo bash /home/$USER/Software/ngsCAT_setup_ubuntu.sh /home/$USER/Software
```

- 6.5) Download this particular R script (targetedRegionCoverage.R) into
/home/\$USER/Software
<https://www.dropbox.com/s/lce7hwscp8q0id4/targetedRegionCoverage.R?dl=0>

The directory structure must keep like this. Please, check these directories and files:

/home/participant/Software/bfast-bwa-ed42c18ea7f48af862935be52f1c072b1d5609cc

/home/participant/Software/bwa-0.7.10

/home/participant/Software/CONTRA.v2.0.3

/home/participant/Software/FastQC

/home/participant/Software/GATK-3.1-1-g07a4bf8

/home/participant/Software/picard-tools-1.107

/home/participant/Software/RUBioSeq+

/home/participant/Software/samtools-0.1.19

/home/participant/Software/ngscat.v0.1

/home/participant/Software/targetedRegionCoverage.R

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

```
# version 1.0
```