

Installing Roary and Prokka on Ubuntu

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In the [last article](#) on Bioinformatics Review, the utilization of Roary [1] and Prokka [2] was explained to create a pangenome from isolated genome sequences. This article is about installing these both packages on Ubuntu.

In order to install Roary and Prokka, you need to install some dependencies such as ncbi-blast+, cd-hit, and so on. These are explained in the following sections. So, let's start.

1. Installing dependencies

Open the terminal (Ctrl+T) and type the following commands:

```
$ sudo apt-get update
```

```
$ sudo apt-get upgrade
```

It's better to upgrade the system before installing new software.

After that, start installing the dependencies.

```
$ sudo apt-get install bedtools ncbi-blast+ mcl cd-hit mafft prank fasttree parallel
```

```
$ sudo perl -MCPAN -e shell
```

```
> install Array::Utils
```

Similarly, install the following modules:

```
Bio::Perl Exception::Class File::Basename File::Copy File::Find::Rule File::Grep File::Path File::Slurper  
File::Spec File::Temp File::Which FindBin Getopt::Long Graph Graph::Writer::Dot List::Util  
Log::Log4perl Moose Moose::Role Text::CSV PerlIO::utf8_strict Devel::OverloadInfo  
Digest::MD5::File
```

Or install all of them at once:

```
$ sudo cpanm Array::Utils Bio::Perl Exception::Class File::Basename File::Copy File::Find::Rule  
File::Grep File::Path File::Slurper File::Spec File::Temp File::Which FindBin Getopt::Long Graph  
Graph::Writer::Dot List::Util Log::Log4perl Moose Moose::Role Text::CSV PerlIO::utf8_strict  
Devel::OverloadInfo Digest::MD5::File
```

2. Installing Roary from source

You can install Roary from the source. First, download the latest software from here (<https://github.com/sanger-pathogens/Roary/tarball/master>) and then go into the directory where you have downloaded the software (let's say, *Downloads*).

```
$ cd Downloads
```

```
$ tar xvzf sanger-pathogens-Roary-xxxx.tar.gz
```

```
$ cd sanger-pathogens-Roary-db
```

Now, open your bashrc file, type the following lines at the end of the file:

```
$ sudo gedit ~/.bashrc
```

```
$ export PATH=/home/user/Downloads/sanger-pathogens-Roary-db/bin
```

```
$ export PERL5LIB=/home/user/Downloads/sanger-pathogens-Roary-db/lib
```

Check whether it has been installed or not:

```
$ roary -w
```

It will print the version.

3. Installing Prokka

Open the terminal and type the following commands:

```
$ sudo apt-get install libdatetime-perl libxml-simple-perl libdigest-md5-perl git default-jre bioperl
```

```
$ sudo cpan Bio::Perl
```

```
$ git clone https://github.com/tseemann/prokka.git $HOME/prokka
```

```
$ $HOME/prokka/bin/prokka --setupdb
```

Click [here](#) to read more about the further usage of Prokka.

References

1. Page, A. J., Cummins, C. A., Hunt, M., Wong, V. K., Reuter, S., Holden, M. T., ... & Parkhill, J. (2015). Roary: rapid large-scale prokaryote pan genome analysis. *Bioinformatics*, 31(22), 3691-3693.
2. Seemann, T. (2014). Prokka: rapid prokaryotic genome annotation. *Bioinformatics*, 30(14), 2068-2069.

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