



VIR-MINION

Vir-MinION Installation Manual

The current document contains the useful information to install and configure Vir-MinION on local machine. The pipeline has been tested on Linux Ubuntu 20.04, NVIDIA GE Force 3080.

Create the folder for the packages:

```
sudo mkdir /usr/share/NANOPORE-PKGs
```

Installation of ONT-Guppy

```
wget https://mirror.oxfordnanoportal.com/software/analysis/ont-guppy_5.0.13_linux64.tar.gz
sudo cp -Rf ont-guppy /usr/share/NANOPORE-PKGs
```

Insert the following line in the `.bashrc` file:

```
#Export path for NANO
export PATH=$PATH:/usr/share/NANOPORE-PKGs/ont-guppy/bin
```

Load the environment

```
source .bashrc
```

Installation of Nanofilt/NanoQC/NanoPlot/NanoStat

```
pip install nanopack
```

Add the following `PATH` to the `.bashrc`

```
/home/virmion/.local/bin
```

Installation of Anaconda

```
wget -c https://repo.anaconda.com/archive/Anaconda3-2020.02-Linux-x86_64.sh
sudo mkdir /opt/Anaconda3
sudo bash Anaconda3-2020.02-Linux-x86_64.sh -u
PATH --> /opt/Anaconda3 [multiusers]
Do you wish the installer to initialize Anaconda3 by running conda init? YES
```

Add the following `PATH` to the `.bashrc`

```
/opt/Anaconda3/bin
```

Installation of NGSspeciesID

```
conda create -n NGSspeciesID python=3.6 pip
```

[If it is the first time activating the conda shell:

```
conda init bash
```

```
logout bash and login again]
```

```
conda activate NGSspeciesID  
conda install --yes -c conda-forge -c bioconda medaka==0.11.5 openblas==0.3.3 spoa racon minimap2  
pip install NGSspeciesID
```

Installation of Kraken2

```
sudo apt install kraken2
```

Installation of Krona-tools

```
cd Krona-master/KronaTools  
sudo ./install.pl  
mkdir taxonomy  
./updateTaxonomy.sh  
./updateAccessions.sh  
mv Krona-master/KronaTools /usr/share/NANOPORE-PKGs/
```

Add the following line in .bashrc

```
/usr/share/NANOPORE-PKGs/Krona-master/KronaTools/scripts
```

Installation of MEGAHIT

```
conda install -c bioconda megahit
```

Installation of FLYE

```
git clone https://github.com/fenderglass/Flye  
cd Flye  
make
```

To run assembly with Flye (test)

```
python ../Flye/bin/flye --nano-raw /mnt/DATA_MDPI/3G/Ippy_RCA_minion.fasta --out-dir ass_flye --threads  
8
```

Installation of KAIJU

```
cd /usr/share/NANOPORE-PKGs/  
git clone https://github.com/bioinformatics-centre/kaiju.git  
cd kanji/src  
make  
cd .. ; mkdir kaijudb ; cd kaijudb  
../bin/kaiju-makedb -s viruses
```

Add the following line to .bashrc

```
/usr/share/NANOPORE-PKGs/kaiju/bin
```

Installation of the SCRIPTS used by Vir-MinION

```
mkdir /usr/share/NANOPORE-PKGs/  
copy the scripts in this folder: VirMinION-Pipe_V0.1.sh taxonomy.sh
```

Add the following line to the .bashrc

```
/usr/share/NANOPORE-PKGs/scripts
```

Locate the correct path of conda.sh

```
/opt/Anaconda3/etc/profile.d/conda.sh
```

Set it in the VirMinION-Pipe_V0.1.sh

DATABASES

It supposed you already have copies of the databases on your local machine

Installation of KRAKENVIRAL/KAIJU

```
sudo mkdir /usr/share/DBs
cp -Rf /mnt/DBs/KrakenViral/ . [from local copy on HD]
cp -Rf /mnt/DBs/Kaiju/ . [from local copy on HD]
```

CONFIGURE THE CORRECT PATH

The following variable have to be correctly configured according to the local path on your installation.

```
taxonomy.sh:
KrakenViralDB="/usr/share/DBs/KrakenViral"
kaijuNodes="/usr/share/NANOPORE-PKGs/kaiju/kaijudb/nodes.dmp"
kaijuNames="/usr/share/NANOPORE-PKGs/kaiju/kaijudb/names.dmp"
kaijuDB="/usr/share/NANOPORE-PKGs/kaiju/kaijudb/viruses/kaiju_db_viruses.fmi"
```

Be sure the PATH variable is correctly set in your .bashrc:

```
#Export path for NANO
export PATH=$PATH:/usr/share/NANOPORE-PKGs/ont-
guppy/bin:/home/virmion/.local/bin:/opt/Anaconda3/bin:/usr/share/NANOPORE-PKGs/Krona-
master/KronaTools/scripts:/usr/share/NANOPORE-PKGs/kaiju/bin:/usr/share/NANOPORE-PKGs/scripts
```