Virtual environment

Installation

If you are using usegalaxy, conda is already installed. Skip the installation and continue with practice.

1. Get the conda installer

```
#Find the miniconda version you want to install in https://docs.conda.io/en/latest/miniconda.html, right click and copy link.
#Use "wget" + link to download file
#Example
mkdir program
cd program
wget https://repo.anaconda.com/miniconda/Miniconda3-py38_23.5.2-0-Linux-aarch64.sh
```

2. Run the installer

```
bash Miniconda3-py38_23.5.2-0-Linux-aarch64.sh
```

3. Refresh the shell

```
#Refresh the shell
source ~/.bashrc

#You should see "(base) username@host" in your terminal.
#The parenthesis shows you which environment you are currently in.
```

Practice

1. Create a conda environment named training, with python 2.7 as the default python.

```
conda create -n training python=2.7
```

2. Check what other environment is available

```
conda env list
```

3. Activate the environment

```
conda activate training
```

4. Check the python version

```
python --version
#or
python
quit()
```

5. Install R version 3.5

```
conda install -c bioconda rbase=3.5
```

6. Delete the python package

```
conda remove python=2.7
```

7. Verify the uninstallation

```
#try to run python
python
```

8. Deactivate the environment

```
conda deactivate training
```

9. Delete the environment

```
conda remove -n training -all
```

Prepare conda environment for NGS analysis

1. Create an environment named training with python 3.7 as the main python.

```
conda create -n training python=3.7
```

2. Activate the environment with `conda activate`

3. Install package called micromamba (https://mamba.readthedocs.io/en/latest/user_guide/micromamba.html).

```
conda install -c conda-forge micromamba
```

4. Install the remaining packages using micromamba.

```
micromamba install -c conda-forge -c bioconda \
blast \
minimap2 \
bowtie2 \
seqkit \
fastp \
trimmomatic \
fastqc \
bcftools=1.17 \
samtools=1.17 \
deepTools \
nanoplot=1.41 \
freebayes \
iVar \
nanofilt \
medaka \
lofreq
```

Information for each package:
blast: https://www.ncbi.nlm.nih.gov/books/NBK279690/
minimap2: https://github.com/lh3/minimap2
bowtie2: https://github.com/BenLangmead/bowtie2

seqkit: https://github.com/shenwei356/seqkit
fastp: https://github.com/OpenGene/fastp
trimmomatic: http://www.usadellab.org/cms/?page=trimmomatic
fastqc: https://github.com/s-andrews/FastQC
bcftools: https://github.com/samtools/bcftools
samtools: https://github.com/samtools/samtools
deepTools: https://github.com/deeptools/deepTools
nanoplot: https://github.com/wdecoster/NanoPlot GitHub - wdecoster/NanoPlot: Plotting scripts for long read sequencing data
iVar: https://andersen-lab.github.io/ivar/html/
nanofilt: https://github.com/wdecoster/nanofilt
medaka: https://github.com/nanoporetech/medaka
lofreq: https://github.com/CSB5/lofreq