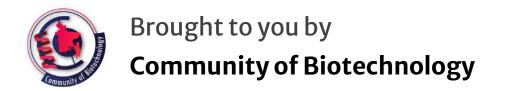
# Software in Genomics and How to Install them

Instructor

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### Virtual Environment

- create an isolated environment for programming projects
- avoid conflicts between multiple versions of the same or different software
- can be imagined as folders where all of your project-specific packages and tools are
- just like folders, you can create and delete them once a project is completed
- eliminates the hassle of painful installation process
- save disk space of your computer
- can be created with multiple tools such as **conda**, virtualenv or pyenv

### Conda

- 1. Package, dependency and virtual environment management for any language
- 2. Runs on Windows, Linux, MacOS
- 3. Quick installation
- 4. 7500+ Python, R, C/C++ based packages
- 5. Easy to update packages
- 6. Remove when the project is finished
- 7. Saves disk space and your time

\*\*\*Although conda works on all operating systems, most bioinformatics software only work on Linux and MacOS

### Install:Conda

### **Anaconda**

- Complete data science toolkit with conda packages
- Takes ~3GB disk space with more than intended packages

#### Download

<a href="https://www.anaconda.com/products/individual#windows">https://www.anaconda.com/products/individual#windows</a>

### Miniconda

- Minimal conda installer with only necessary default packages
- 2. Takes ~400MB disk space
- 3. Install any package later when needed

#### Download

https://docs.conda.io/en/latest/miniconda. html

### **Conda Commands**

#### See all environments

conda info -e

#### **Create an environment**

conda create -n <env-name> python=3.8 -y

### **Activate an environment**

conda activate <env-name>

#### **Deactivate current environment**

conda deactivate

### **Delete an environment**

conda env remove -n <env-name>

### Install a package

conda install <package-name> -y

#### **Cheat sheet**

https://docs.conda.io/projects/conda/en/latest/user-guide/cheatsheet.html

## Conda in Google Colab (For non-Linux users)

### Setup conda in Google Colab

!pip install condacolab

import condacolab

condacolab.install()

#### **Run Conda**

!conda

### **Google Colab**

https://colab.research.google.com

### **Create an environment**

!conda create -n <env-name> python=3.8 -y

### **Activate Environment**

!source activate <env-name>

#### **Deactivate Environment**

!source deactivate

\*\*\*Every tool might not work in Colab

# **fastQC**

A quality control tool for high throughput sequence data

### **Installation**

conda install -c bioconda fastqc -y

### **Installation URL**

https://anaconda.org/bioconda/fastqc

### trimmomatic

A flexible read trimming tool for Illumina Next Generation Sequencing data

### **Installation**

conda install -c bioconda trimmomatic -y

### **Installation URL**

https://anaconda.org/bioconda/trimmomatic

### **BWA**

Burrows-Wheeler Aligner (BWA) is a software package for mapping low-divergent sequences against a large reference genome, such as the human genome

### **Installation**

conda install -c bioconda bwa -y

### **Installation URL**

https://anaconda.org/bioconda/bwa

### samtools

Tools for dealing with SAM, BAM and CRAM files

### **Installation**

conda install -c bioconda samtools -y

### **Installation URL**

https://anaconda.org/bioconda/samtools

### bedtools

A powerful toolset for genome arithmetic

### **Installation**

conda install -c bioconda bedtools -y

### **Installation URL**

https://anaconda.org/bioconda/bedtools

# **SeqKit**

A cross-platform and ultrafast toolkit for FASTA/Q file manipulation

### **Installation**

conda install -c bioconda seqkit -y

### **Installation URL**

https://anaconda.org/bioconda/seqkit

# megahit

An ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph

### **Installation**

conda install -c bioconda megahit -y

### **Installation URL**

https://anaconda.org/bioconda/megahit

### quast

**Quality Assessment Tool for Genome Assemblies** 

### **Installation**

conda install -c bioconda quast -y

### **Installation URL**

https://anaconda.org/bioconda/quast

# Thank you