

Intro: Conda

Conda Introduction

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- Conda is an open-source package and environment management system
- Runs on Windows, macOS, and Linux
- It allows you to easily create, manage, and share environments and packages for different programming languages and tools

Intro: Conda Installation

- Conda can be downloaded from the official website
 - (<https://docs.conda.io/en/latest/miniconda.html>)
- Run the installation on CLI

```
wget https://repo.continuum.io/miniconda/Miniconda3-latest-Linux-x86_64.sh  
chmod +x Miniconda-latest-Linux-x86_64.sh  
. ./Miniconda-latest-Linux-x86_64.sh
```

Intro: Create Conda environment

- Self-contained directory with necessary files, libraries and dependencies for a specific project
- Use the `conda create` command and specify the name of the env and packages you want to install
- Example command:
 - `conda create --name myenv python=3.9 #Creates a new environment myenv with python version 3.9`

Intro: Activate conda environment

- Use the `conda activate` and `conda deactivate` commands
- Example commands:
 - `conda activate myenv` #activates `myenv` environment
 - `conda deactivate` #deactivates `myenv` environment

Intro: Install conda packages

- You can install packages in the conda environment
- Use `conda install` command
- Example command:
 - `conda install pandas` #installs Pandas library in the active environment

Intro: Managing environments

- List all your conda environment with `conda env list` command
- To delete the environment use `conda env remove`
- Example commands:
 - `conda env remove --name myenv` #removes the myenv environment
 - `Conda env export > environment.yml` #exports the current environment to a YAML file
 - `Conda env create -f environment.yml` #creates a new environment with packages and dependencies listed in the YAML file

For more information please checkout:

- You can learn more about Conda by checking out the official documentation (<https://docs.conda.io/projects/conda/en/latest/user-guide/getting-started.html>)

Practical: Install programs using conda

- **Install the following programs in `bioinfo-tools` environment**

	Tools	Version
1.	seqtk	1.3
2.	bioawk	1.0
3.	fastqc	0.12.1
4.	orthofinder	2.5.4
5.	mafft	7.520
6.	iqtree	2.2.0.3
7.	fastq-scan	1.0.1