**Genomics and Clinical Microbiology 2024 Software Installation**

Table of Contents

[Introduction to Software Installation 1](#_Toc157521074)

[Software list and their version used in course 1](#_Toc157521075)

[Installation of Inkscape 1](#_Toc157521076)

[Installation of MEGA 2](#_Toc157521077)

[Installation of SplitsTree 2](#_Toc157521078)

[Installation of BLAST+, SPAdes, QUAST and FASTQC (with CONDA) 3](#_Toc157521079)

[Additional Resources and Troubleshooting 4](#_Toc157521080)

## Introduction to Software Installation

This guide provides extensive instructions for software installation on Ubuntu/Windows/MacOS systems, applicable to both virtual machine (VM) and host machine setups, as taught and utilized in the Genomics and Clinical Microbiology 2024 course. For VM installation specifics, please consult the supplementary VM installation guide attached separately. Additionally, valuable troubleshooting links are provided below for additional assistance.

**Note:** The Virtual Machine file (.vdi) contains all the software installed for the course.

## Software list according to course modules

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Module** | **Software** | **Summary** | **Version** | **Website** |
|  | Inkscape | Inkscape is a Free and open source [vector graphics editor](http://en.wikipedia.org/wiki/Comparison_of_vector_graphics_editors) for GNU/Linux, Windows and macOS. | 0.92.4 | <https://inkscape.org/> |
| Constructing phylogenetic trees | MEGA | Sophisticated and user-friendly software suite for analyzing DNA and protein sequence data from species and populations. | 11.0.3 | <https://www.megasoftware.net/> |
| Constructing phylogenetic trees | Splits Tree | SplitsTree is a widely used application for computing unrooted phylogenetic networks from molecular sequence data. | 4.18.3 | **[SplitsTree | University of Tübingen](https://uni-tuebingen.de/en/fakultaeten/mathematisch-naturwissenschaftliche-fakultaet/fachbereiche/informatik/lehrstuehle/algorithms-in-bioinformatics/software/splitstree/)** |
| Introduction to the Linux command line and  BLAST | BLAST+ | The BLAST+ applications can write the query, database, and command-line options for a BLAST search into a "strategy" file. | 2.15.0 | <https://blast.ncbi.nlm.nih.gov/doc/blast-help/downloadblastdata.html> |
| Genome assembly | SPAdes | SPAdes Genome Assembler is an open source tool for de novo sequencing. | 3.15.4 | <https://github.com/ablab/spades> |
| Genome assembly | QUAST | QUAST can evaluate assemblies both with a reference genome, as well as without a reference | 5.2.0 | <https://github.com/ablab/quast> |
| Genome assembly | FastQC | FastQC is used to quality control checks on raw sequence data coming from high throughput sequencing pipelines. | 0.12.1 | <https://github.com/s-andrews/FastQC> |

**Note:** The versions might differ as new releases are enrolled by the software company.

## Installation of Inkscape

**Download Inkscape:**

Visit the Inkscape website (<https://inkscape.org/release/inkscape-1.3.2/>) and download the Windows/MacOS/Ubuntu version of Inkscape.

In Windows and MacOS save the downloaded file and use on-screen instructions to install Inkscape.

**Installing Inkscape on Ubuntu:**

1. Open the Terminal on your Ubuntu system.
2. Add Inkscape Repository: Run the following commands to add the Inkscape repository and update the package lists:

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1. Use the package manager to install Inkscape:

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1. Once the installation is complete, you can launch Inkscape from the application menu or by running Inkscape in the Terminal.

## Installation of MEGA

**Download MEGA:**

Visit the official MEGA website (<https://mega.io/download>) and download the Windows/MacOS version of MEGA Sync Client.

In Windows and MacOS save the downloaded file and use on-screen instructions to install MEGA.

**Installing MEGA on Ubuntu:**

1. Open the Terminal on your Ubuntu system.
2. Add MEGA Repository: Run the following commands to add the MEGA repository and update the package lists:

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1. Use the package manager to install MEGA:

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1. Once the installation is complete, you can launch MEGA from the application menu or by running ‘megasync’ in the Terminal.

## Installation of SplitsTree

**Download SplitsTree:**

Visit the SplitsTree website (<https://www.splitstree.org/>) and download the Windows/MacOS/Ubuntu version of SplitsTree.

In Windows and MacOS save the downloaded file and use on-screen instructions to install SplitsTree.

**Installing SplitsTree on Ubuntu:**

1. Open the Terminal on your Ubuntu system.
2. Download SplitsTree:

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1. Once the installation is complete, you can run SplitsTree by entering the following command in the Terminal:

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## Installation of BLAST+, SPAdes, QUAST and FASTQC (with CONDA)

**Conda Overview:**

Conda is an open-source package management and environment management system that runs on Windows, macOS, and Linux. It simplifies the installation and management of software packages, ensuring dependencies are correctly handled.

**Installation Script:**

Ensure you have Conda installed on your system before running the script.

1. Create a Conda Environment (Optional): If you prefer to create a separate environment for these tools, you can do so by running:

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1. Add Conda Channels: Add necessary channels for accessing bioinformatics packages:

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1. Installations of software and verify:

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**Note:** In order to install individual software, use the command line command “conda install softwareName”. For example: conda install spades.

1. If you created a separate environment, deactivate it:

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**Note:**

* Conda environments provide isolation for different sets of tools, enhancing reproducibility.
* You can customize the script based on your preferences, such as creating a dedicated environment or modifying the channels. Activate the Conda base environment (conda activate base) if you choose not to create a separate environment.
* By using Conda, this script streamlines the installation process, ensuring that the specified bioinformatics tools and their dependencies are correctly configured on your system.
* Save this script to a file (e.g., install\_bioinformatics.sh), make it executable (chmod +x install\_bioinformatics.sh), and run it in your terminal (./install\_bioinformatics.sh). Adjust the script as needed for your specific requirements.

## Additional Resources and Troubleshooting

* Ubuntu Documentation: <https://help.ubuntu.com/>
* Ubuntu Community Support: <https://ubuntu.com/support/community-support>
* Conda Installation: <https://conda.io/projects/conda/en/latest/user-guide/install/index.html>
* Conda Documentation: <https://conda.io/projects/conda/en/latest/user-guide/getting-started.html#managing-python>
* Stack overflow: <https://stackoverflow.com/> (Public Q&A platform for debugging)
* Bioinformatics (BioStars) Forum: <https://www.biostars.org/t/Forum/> (General Bioinformatics queries)