



LEARN PYTHON & R FOR BIOINFORMATICS

Introduction

R is a language and environment for statistical computing and graphics. R provides a wide variety of statistical (linear and nonlinear modelling, classical statistical tests, time-series analysis, classification, clustering) and graphical techniques, and is highly extensible.

R in Bioinformatics:

R is rapidly becoming the most important scripting language for both experimental- and computational biologists. R is one of the most widely-used and powerful programming languages in bioinformatics. R especially shines where a variety of statistical tools are required (e.g. RNA-Seq, population genomics, etc.) and in the generation of publication-quality graphs and figures.

R Installation

Steps:

- Open an internet browser search for 'download R'.

- Click on this link <https://cran.r-project.org/bin/windows/base/>
- Click on hyperlink "Download R 3.6.2 for Windows "
- Open the download file and select the language and installation path.
- Install the R.
- Complete the setup process.
- Search for the R on your laptop or PC.
- Open the R studio.

Summary:

In this video we talked about R language and its importance in Bioinformatics. We also discussed the process to install the R language.