Workshop Guidelines

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Contents

Please follow the guidelines below and install required tools packages, and software before you come to the workshop (If you have your personal laptops please bring them. Otherwise contact ITU-1 to install required software before the work shop)

<u>**Quick Guide (for detailed explanation see below)**</u>

Install MiKTeX

https://miktex.org/download

Install R

https://cran.r-project.org/mirrors.html

Install R studio

https://www.rstudio.com/products/rstudio/download/#download

Install R markdown

Refer

https://rmarkdown.rstudio.com/authoring_quick_tour.html

or

https://www.youtube.com/watch?v=QaKCirYknS8

<u>**All above steps are explained in this document (Detailed Explanation)**</u>

https://medium.com/@sorenlind/create-pdf-reports-using-r-r-markdown-latex-and-knitr-on-windows-10-952b0c48bfa9

<u>**Install following R packages**</u>

Tidyverse

https://cran.r-project.org/web/packages/tidyr/README.html

ggplot2

https://ggplot2.tidyverse.org/

dplyr

https://www.r-project.org/nosvn/pandoc/dplyr.html

Bioconductor

https://www.bioconductor.org/install/

data.table

https://github.com/Rdatatable/data.table/wiki/Installation

rttracklayer

https://bioconductor.org/packages/release/bioc/html/rtracklayer.html

Important

Before you come to the work shop please be familiar with basics of R. Then we can skip the basics and do some more… But I will try to give a brief introduction.

You can follow this document as a reference.

https://github.com/jmonlong/HGSS_Rworkshops/blob/master/Intro-Rbasics-2016/HGSS-Workshop-Rintro-2016.pdf

Linux for Windows (Cygwin)

Follow below steps only if you use a windows computer.

Install cygwin

http://www.cygwin.com/install.html

install these tools using the options presented at the installation

gawk

less

grep

sed

emacs

nano

install bedtools

https://www.reddit.com/r/bioinformatics/comments/46sz57/installing_bedtools_on_windows_using_cygwin/