

INF-BIOx121 2017

Unix/R workshop

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Aug 22, 2017

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INF-BIOx121 - 2017

- ❖ Fundamentals of Molecular Biology Gregor Gilfillan
- ❖ HTS, basic file formats, pre-processing of sequencing data
- ❖ Algorithms Timothy Hughes Arvind Sundaram
Ave Tooming-Klunderud
- ❖ De novo assembly Karin Lagesen
- ❖ RNA-seq analysis Arvind Sundaram
- ❖ Variant calling Timothy Hughes
- ❖ Statistical genomics Borris Simovski

<http://inf-biox121.readthedocs.io/en/2017/>

VMware to access virtual machines

- ❖ Download VMware Horizon client to access UiO VMs
 - ❖ https://my.vmware.com/web/vmware/info?slug=desktop_end_user_computing/vmware_horizon_clients/4_0
- ❖ Link to UiO VM
 - ❖ <https://vdi-apcon-t01.uio.no>

The Unix shell: Setup

- ❖ Download the data set and move it to Desktop

`goo.gl/Y6yXRD`

- ❖ Extract it and you will find a new folder in Desktop

`data-shell`

- ❖ Locate and open Terminal or Command line and type:

`cd`

Terminal shortcuts

- ❖ <http://lifehacker.com/5743814/become-a-command-line-ninja-with-these-time-saving-shortcuts>
- ❖ <https://www.howtogeek.com/howto/ubuntu/keyboard-shortcuts-for-bash-command-shell-for-ubuntu-debian-suse-redhat-linux-etc/>
- ❖ <https://www.marksanborn.net/linux/10-linux-shortcuts-you-cant-live-without/>

R (RStudio)

- ❖ Create a new folder in Desktop

`r-novice-inflammation`

- ❖ Download the data set (goo.gl/fKUXyH) and move it to

`Desktop/r-novice-inflammation`

- ❖ Unzip or extract it and you will find a new folder

`data`

- ❖ Locate and open Terminal or Command line and type:

`cd`

`cd Desktop/r-novice-inflammation/data`

Further reading

- ❖ The Unix Shell

<http://swcarpentry.github.io/shell-novice/>

- ❖ Programming with R

<http://swcarpentry.github.io/r-novice-inflammation/>

- ❖ Python

<http://swcarpentry.github.io/python-novice-inflammation/>

- ❖ Software Carpentry

<https://software-carpentry.org/lessons/>