

Learning objectives

1. Become familiar and comfortable with Linux command line
2. Get initiated into *bash* scripting
3. Become familiar with Linux administration
4. Learn read alignment
5. Learn to call, compare and annotate variants

Learning objectives

6. Become familiar with R language
7. Manipulate variant calling data in R
8. Learn to build Phylogenetic trees
9. Start working with epidemiological data in R

What is the best way to learn?

- Practice, practice, ... Install Linux and start using it for work or even everyday computing
- Type commands in the terminal, do not copy them from the slides
- Trial and error make mistakes and try to fix them
- Google is your best friend, formulate questions and google the answers. Everyone is doing it!

What is the best way to learn?

- Regarding R ..., abandon Excel and do all of your statistical analysis in R
- Same principle as for Linux apply to learning R

What are good online resource about bioinformatics?

- Biostars forum: <https://www.biostars.org/>
- Seqanswers: <https://www.seqanswers.com/>
- <https://www.reddit.com/r/bioinformatics/>
- Again, google, there is absolutely a ton of great resources online
- Books: read this post <https://www.biostars.org/p/181/>
- Josh Starmer StatQuest youtube channel <https://www.youtube.com/@statquest>

How to ask questions online?

- Read the rules of the community and follow them
- Read the manual before asking software-related question
- Do not cross-post