

Navigating large biological datasets using simple bioinformatic tools, 2.5 hp

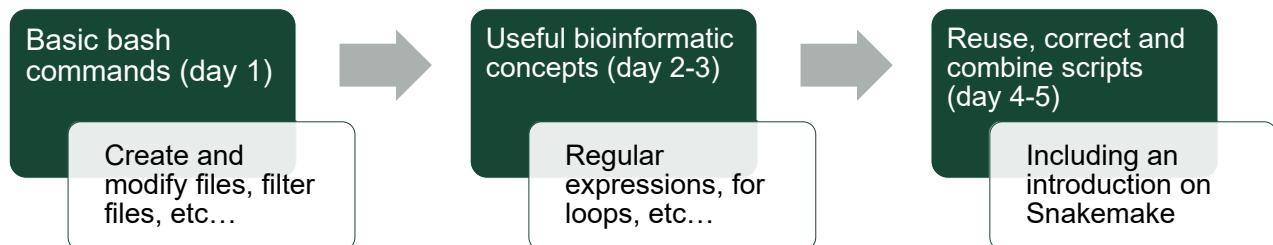
April 17-21, 2023 at Ultuna

Do you have a set of genes and want to know if they are on the same scaffold? Do you want to extract all the sequences of a specific genus from a big multifasta file? Are you performing transcriptomic analyses and need to quickly turn a list of transcript names into gene or protein names? Or do you just need to deal with an overwhelming dataset such as an extremely long BLAST output? All these operations can be completed quickly and painlessly by learning a very small number of bioinformatic concepts. However, biologists today still spend a lot of time to extract meaningful information from complex datasets such as BLAST outputs, annotation files, or sequence files.

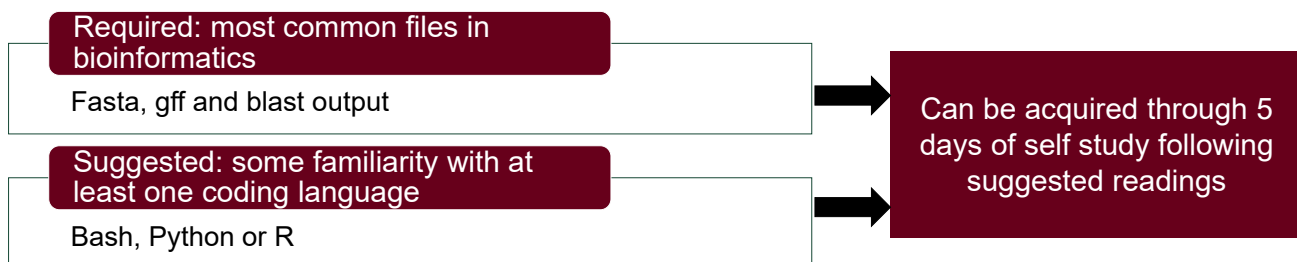
In this course you will learn to independently write **simple but powerful scripts** to automate your analysis and **spend the least amount of time repeating the same operations**. Such skills are useful for scientists working with genetic information in plant, animal, microbial, and soil sciences.

Register to the course by writing to edoardo.piombo@slu.se at the latest by March 20th.

Content



Prior knowledge/Entry requirements



Questions? Contact the course leader:

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