

Searching in Biological Databases (Task 2)

Alex-Alex-Helena

7 oktober, 2021

Introduction

The purpose of this task is to play around with querying different types of biological databases using R. In the following, some questions will be answered using queries.

Question 1:

Retrieve the genome of a cat via its *scientific name* or *taxonomic identifier* from *NCBI Taxonomy*. Then read the file.

This information will be retrieved using the library `biomartr`. The documentation can be found [here](#)

Question 2:

Find the allele names in the Applied Biosystem identifier allelic ladder (from the `sequinr` library)

Question 3:

We have the [Uniprot](#) code of a human transcription factor: Q01196. We must (a) identify the name of the protein; and (b) find molecular pathways where this protein is participating in both KEGG and REACTOME and compare them.