**What is NCBIFEcth**

**BioJava** is an open-source project dedicated to providing a Java framework for processing biological data. It provides analytical and statistical routines, parsers for common file formats and allows the manipulation of sequences and 3D structures

Biojava.org

External source from BioJava

Besides building your very own database-driven sequence repository, most users will need to fetch sequences from public datasources.

A primary source of sequence information is [NCBI](http://www.ncbi.nlm.nih.gov/).

**How does NCBI fetch work**

From its very beginning, Biojava was able to get sequences from NCBI with wrapper objects and methods

**Why was NCBIFetch used?**

Best approach to retrieve sequences from NCBI and to write them in a readable file to our program.

It intergraded well.

BioJava methods are specific to bioinformatics processes.