

Background

We provide gene annotation for the human genome.

The latest assembly available is GRCh38 but some users still use the previous assembly, GRCh37, and want to convert coordinates between the two assemblies.

You can find more information about genome assemblies here:

<https://www.genome.gov/12011238/an-overview-of-the-human-genome-project/>

For this exercise, we use the latest Ensembl release, 104.

Ensembl Perl API

The Ensembl Perl API is used to generate annotation as well as access it programmatically.

You can find more information about it here:

http://www.ensembl.org/info/docs/api/core/core_tutorial.html

Exercise

Using the Perl API on the latest human data for Ensembl release 104, convert coordinates on chromosome 10, from 25.000 to 30.000 to the same region in GRCh37.

Alternatives

Describe at least one other way of retrieving the same information, along with its advantages and disadvantages.