SM note 1:
I have installed Ubuntu (Linux OS) on windows computer as a dual boot --- both windows OS and Ubuntu OS can be loaded at start. Such installations of Linux are much more powerful for computation over virtual machine.

Please see guide “2.1_Install_Ubuntu_dual_boot_any_computer.pdf” and “2.2_Install_Ubuntu_different_software.pdf” for detailed installation steps (with screenshots and/or video descriptions where available).
end of SM note 1

SM note 2:
What IDE (integrated development environment) or Editor do I need? How to run/execute Perl script?
Answer: After reviewing multiple options,
IDE point of view Padre and Epic it seems both are good choices for Execution + Syntax and also Edit (ref: https://www.dunebook.com/best-perl-ide-and-editors/). Disadvantage of IDE unlike Editors is that a) IDE are heavy weight applications b) Don’t support multiple languages so got to learn again each time.
Editor point of view that can do not only Edit but also does Execution + Syntax support, github’s Atom is great cause a) Atom is light weight application unlike IDE b) Atom is more amenable to multiple languages and features so there’s the comfort level that comes from using Atom previously.

- For Syntax on Atom: install “language-<program language>” package “language-perl” from withing Atom using >Packages > Settings View > Install Packages/Themes > search package name > click install. This “adds syntax highlighting and snippets to <program language> files in Atom”. The file extension tells atom what language it is, .pl for Perl, .py for Python, .js for JavaScript and .java for Java.
  Perl “language-perl” https://atom.io/packages/language-perl, Python “language-python” https://atom.io/packages/language-python, JavaScript “language-javascript” https://atom.io/packages/language-javascript, Java “language-java” https://atom.io/packages/language-java and other languages too.
- For Execution on Atom: Atom can also execute/run scripts if we install package “script” from withing Atom, to run script file click Packages > Script > Run Script or shortcut Ctrl+Shift+B, output shows in tiny space below script file, if click ‘show in new tab’ icon it shows the output in new tab of Atom.
  Perl https://youtu.be/KzEuTjNwzvk, Python https://youtu.be/QuiquBXdA1o, JavaScript https://youtu.be/Aj7Iah4ksH8, Java https://youtu.be/Wg5Peun14YM and other languages too.
- For Terminal window on Atom: On Atom we can type in terminal window install package “terminal-plus” from withing Atom https://atom.io/packages/terminal-plus.
- Additional IDE features for Atom: Its not essential I think, but additional packages are available on Atom for more IDE type features. To find this type “Atom <language name> IDE” in search engine and follow instructions.

Please see guide “2.3_Install_Atom_Its_More_Than_Just_Text_Editor.pdf” for detailed installation steps (with screenshots and/or video descriptions where available).

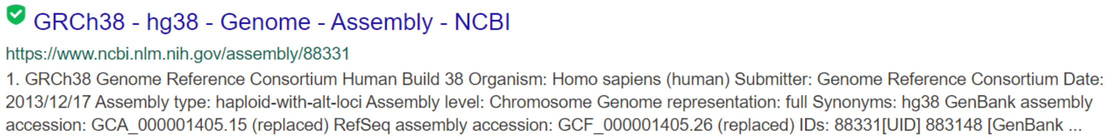
end of SM note 2

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/

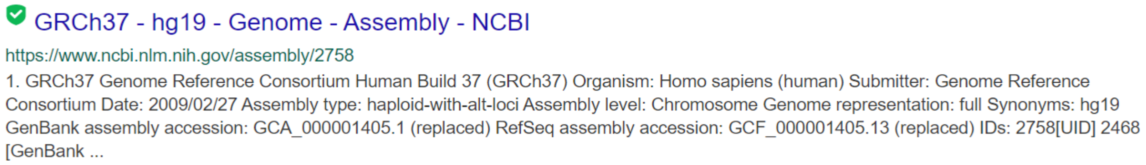
For this exercise, we use the latest Ensembl release, 104.

SM note 3: This question is about conversion of gene coordinates between two assemblies.
https://www.ncbi.nlm.nih.gov/assembly/88331



GRCh38 - hg38 - Genome - Assembly - NCBI
https://www.ncbi.nlm.nih.gov/assembly/88331
1. GRCh38 Genome Reference Consortium Human Build 38 Organism: Homo sapiens (human) Submitter: Genome Reference Consortium Date: 2013/12/17 Assembly type: haploid-with-alt-loci Assembly level: Chromosome Genome representation: full Synonyms: hg38 GenBank assembly accession: GCA_000001405.15 (replaced) RefSeq assembly accession: GCF_000001405.26 (replaced) IDs: 88331[UID] 883148 [GenBank ...

https://www.ncbi.nlm.nih.gov/assembly/2758/



GRCh37 - hg19 - Genome - Assembly - NCBI
https://www.ncbi.nlm.nih.gov/assembly/2758
1. GRCh37 Genome Reference Consortium Human Build 37 (GRCh37) Organism: Homo sapiens (human) Submitter: Genome Reference Consortium Date: 2009/02/27 Assembly type: haploid-with-alt-loci Assembly level: Chromosome Genome representation: full Synonyms: hg19 GenBank assembly accession: GCA_000001405.1 (replaced) RefSeq assembly accession: GCF_000001405.13 (replaced) IDs: 2758[UID] 2468 [GenBank ...

end of SM note 3

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

SM note 4: Setup and installation for Exercise. Ensembl Perl API tutorial (with video) http://uswest.ensembl.org/info/docs/api/api_installation.html was very helpful.
Presently, I did not make the additional installations for 'Variation genotype and frequency data'.

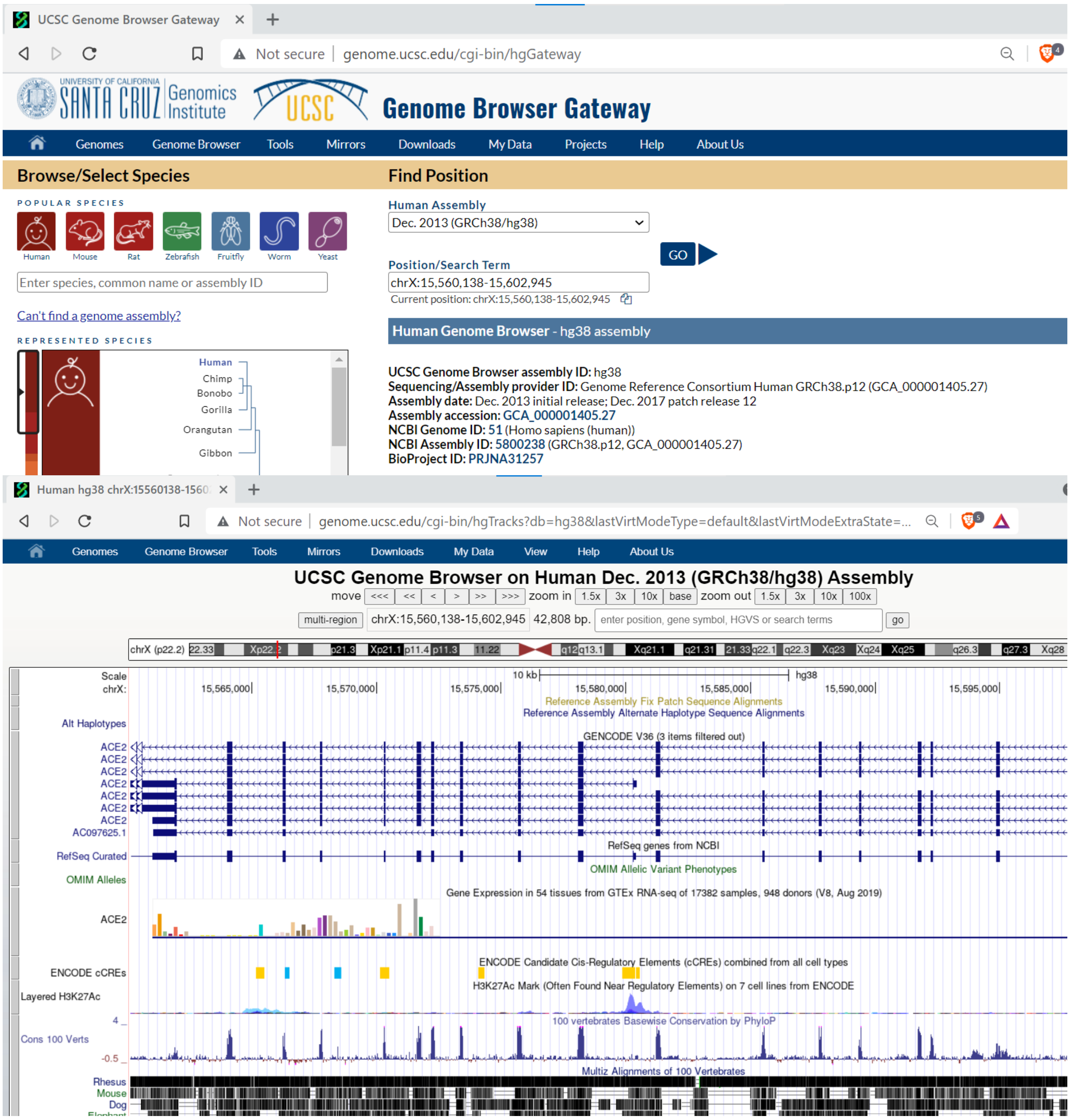
I used Ubuntu Release 20.04. Typing command 'lsb_release -a' on Terminal displays this information. *Please, note that a) text after '#' is for human not computer, b) text I greyed out is the command that needs to be typed on or copied to Terminal or Atom as the case maybe and c) after typing or copying the command hit Return/Enter key for it to execute.*
lsb_release -a #Displays version of Ubuntu d) Clicking on Terminal window and pressing Ctrl+C or Cmd+C ends any code running on Terminal.

Please see guide "2.4_Install_Perl_PerlModules_BioPerl_EnsemblPerlAPI.pdf" for detailed Perl, Perl modules, BioPerl and Ensembl Perl API installation steps (with screenshots and/or video descriptions where available).

end of SM note 4

SM note 5

Used tutorials http://uswest.ensembl.org/info/docs/api/core/core_tutorial.html and http://uswest.ensembl.org/info/docs/api/general_instructions.html to get an idea of lines of code that need to be written to access and use Ensembl Perl API. I used Atom to write the 'convert_chr_region_hu.pl' script and executed the script from Ubuntu Terminal above where my .bashrc has PERL5LIB in its path. At this time, I don't know how to get Atom to run 'convert_chr_region_hu.pl' script using the installation libraries PERL5LIB. Using UCSC genome browser can view the region of the genome format "chr1:213941196-213942363"



UCSC Genome Browser Gateway
Not secure | genome.ucsc.edu/cgi-bin/hgGateway
UNIVERSITY OF CALIFORNIA SANTA CRUZ Genomics Institute
UCSC Genome Browser Gateway
Genomes
Genome Browser
Tools
Mirrors
Downloads
My Data
Projects
Help
About Us
Browse/Select Species
Find Position
POPULAR SPECIES
Human
Mouse
Rat
Zebrafish
Fruitfly
Worm
Yeast
Enter species, common name or assembly ID
Can't find a genome assembly?
REPRESENTED SPECIES
Human
Chimp
Bonobo
Gorilla
Orangutan
Gibbon
GO

Human Assembly: Dec. 2013 (GRCh38/hg38)

Position/Search Term: chrX:15,560,138-15,602,945

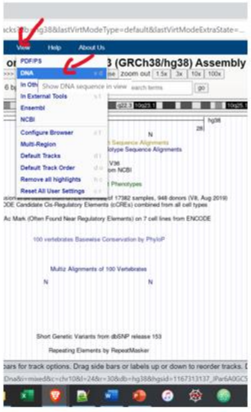
Current position: chrX:15,560,138-15,602,945

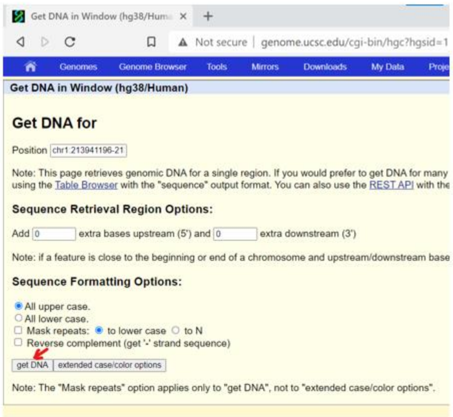
Human Genome Browser - hg38 assembly

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p12 (GCA_000001405.27)
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 12
Assembly accession: GCA_000001405.27
NCBI Genome ID: 51 (Homo sapiens (human))
NCBI Assembly ID: 5800238 (GRCh38.p12, GCA_000001405.27)
BioProject ID: PRJNA31257

Human hg38 chrX:15560138-1560
Not secure | genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=default&lastVirtModeExtraState=...
Genomes
Genome Browser
Tools
Mirrors
Downloads
My Data
View
Help
About Us
UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x
multi-region
chrX:15,560,138-15,602,945 42,808 bp.
enter position, gene symbol, HGVS or search terms
go
chrX (p22.2)
Scale
chrX:
10 kb
hg38
15,565,000|
15,570,000|
15,575,000|
15,580,000|
15,585,000|
15,590,000|
15,595,000|
Reference Assembly Fix Patch Sequence Alignments
Reference Assembly Alternate Haplotype Sequence Alignments
Alt Haplotypes
GENCODE V36 (3 items filtered out)
ACE2
ACE2
ACE2
ACE2
ACE2
ACE2
ACE2
AC097625.1
RefSeq genes from NCBI
RefSeq Curated
OMIM Allelic Variant Phenotypes
OMIM Alleles
Gene Expression in 54 tissues from GTEx RNA-seq of 17382 samples, 948 donors (V8, Aug 2019)
ACE2
ENCODE Candidate Cis-Regulatory Elements (cCREs) combined from all cell types
ENCODE cCREs
H3K27Ac Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE
Layered H3K27Ac
100 vertebrates Basewise Conservation by PhyloP
4 _
Cons 100 Verts
-0.5 _
Multiz Alignments of 100 Vertebrates
Rhesus
Mouse
Dog
Elephant

Can also obtain sequence of DNA for the region by clicking > View > DNA




Get DNA in Window (hg38/Huma
Not secure | genome.ucsc.edu/cgi-bin/hgc?hgsid=1
Genomes
Genome Browser
Tools
Mirrors
Downloads
My Data
Proje

Get DNA in Window (hg38/Human)

Get DNA for

Position chr1:213941196-21

Note: This page retrieves genomic DNA for a single region. If you would prefer to get DNA for many using the Table Browser with the "sequence" output format. You can also use the REST API with the

Sequence Retrieval Region Options:

Add 0 extra bases upstream (5') and 0 extra downstream (3')

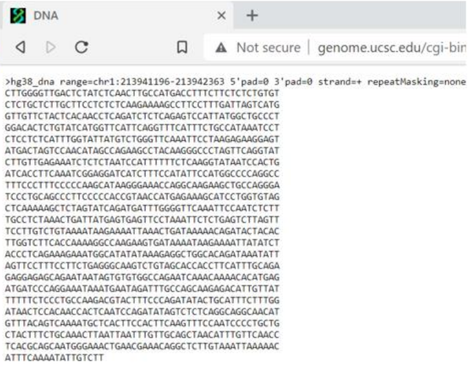
Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream base

Sequence Formatting Options:

● All upper case.
○ All lower case.
□ Mask repeats: ● to lower case ○ to N
□ Reverse complement (get '-' strand sequence)

get DNA | extended case/color options

Note: The "Mask repeats" option applies only to "get DNA", not to "extended case/color options".



```
>hg38_dna range=chr1:213941196-213942363 5'pad=0 3'pad=0 strand=+ repeatMasking=none
CTTGGGGTTGACTCTATCTCAACTTGCCATGACCTTTCTTCTCTCTGTGT
CTCTGCTCTTGCTTCCTCTCTCAAGAAAAGCCTTCCTTTGATTAGTCATG
GTTGTTCTACTCACAACCTCAGATCTCTCAGAGTCCATTATGGCTGCCCT
GGACACTCTGTATCATGGTTCATTCAGGTTTCATTTCTGCCATAAATCCT
CTCCTCTCATTTGGTATTATGTCTGGGTTCAAATTCCTAAGAGAAGGAGT
ATGACTAGTCCAACATAGCCAGAAGCCTACAAGGGCCCTAGTTCAGGTAT
CTTGTTGAGAAATCTCTCTAATCCATTTTTTCTCAAGGTATAATCCACTG
ATCACCTTCAAATCGGAGGATCATCTTTCCATATTCCATGGCCCCAGGCC
TTTCCCTTTCCCCCAAGCATAAGGGAAACCAGGCAAGAAGCTGCCAGGGA
TCCCTGCAGCCCTTCCCCCACCGTAACCATGAGAAAGCATCCTGGTGTAG
CTCAAAAAGCTCTAGTATCAGATGATTTGGGGTTCAAATTCCAATCTCTT
TGCCTCTAAACTGATTATGAGTGAGTTCCTAAATTCTCTGAGTCTTAGTT
TCCTTGTCTGTAAAATAAGAAAATTAAACTGATAAAAACAGATACTACAC
TTGGTCTTCACCAAAAGGCCAAGAAGTGATAAAATAAGAAAATTATATCT
ACCCTCAGAAAGAAATGGCATATATAAAGAGGCTGGCACAGATAAATATT
AGTTCCTTTCCTTCTGAGGGCAAGTCTGTAGCACCACCTTCATTTGCAGA
GAGGAGAGCAGAATAATAGTGTGTGGCCAGAATCAAACAAAACACATGAG
ATGATCCCAGGAAATAAATGAATAGATTTGCCAGCAAGAGACATTGTTAT
TTTTTCTCCCTGCCAAGACGTACTTTCCCAGATATACTGCATTTCTTTGG
ATAACTCCACAACCACTCAATCCAGATATAGTCTCTCAGGCAGGCAACAT
GTTTACAGTCAAAATGCTCACTTCCACTTCAAGTTTCCAATCCCCTGCTG
CTACTTTCTGCAAACTTAATTAATTTGTTGCAGCTAACATTTGTTCAACC
TCACGCAGCAATGGGAAACTGAACGAAACAGGCTCTTGTAAATTAAAAAC
ATTTCAAAATATTGTCTT
```

end of SM note 5

Exercise

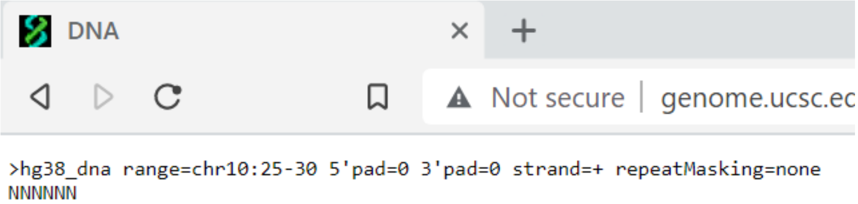
Using the Perl API on the latest human data for Ensembl release 104, convert coordinates on chromosome 10, from 25.000 to 30.000 to the same region in GRCh37.

SM Answer Exercise

Git Link: https://github.com/smukher2/EMBL_git_ensembl_perl_API_Ex1.git

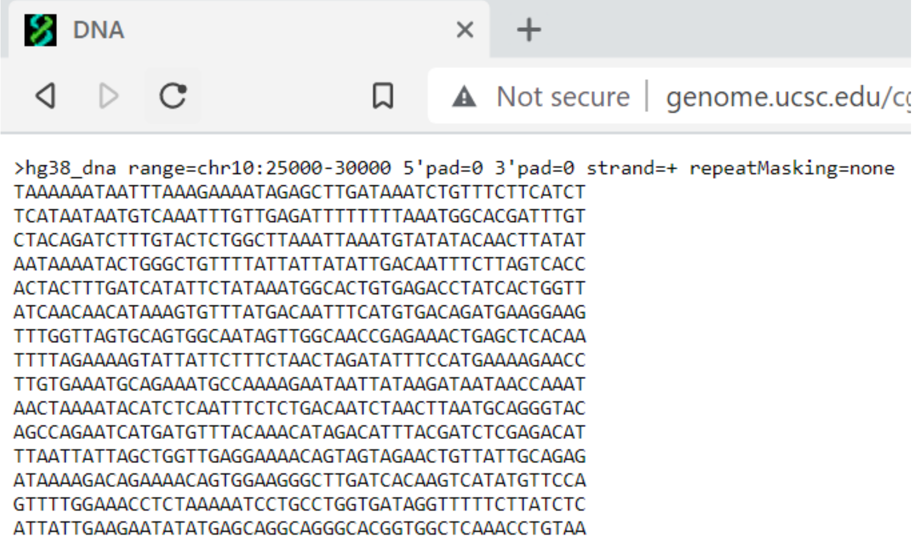
Point 1 of 4: Changed Input or Query Coordinates As Original One Provided In The Question Has No Sequence "No Data" or Gap region:

Upon checking UCSC genome browser for region GRCh38 chromosome 10, from 25.000 to 30.000, I found that this region does not exist.



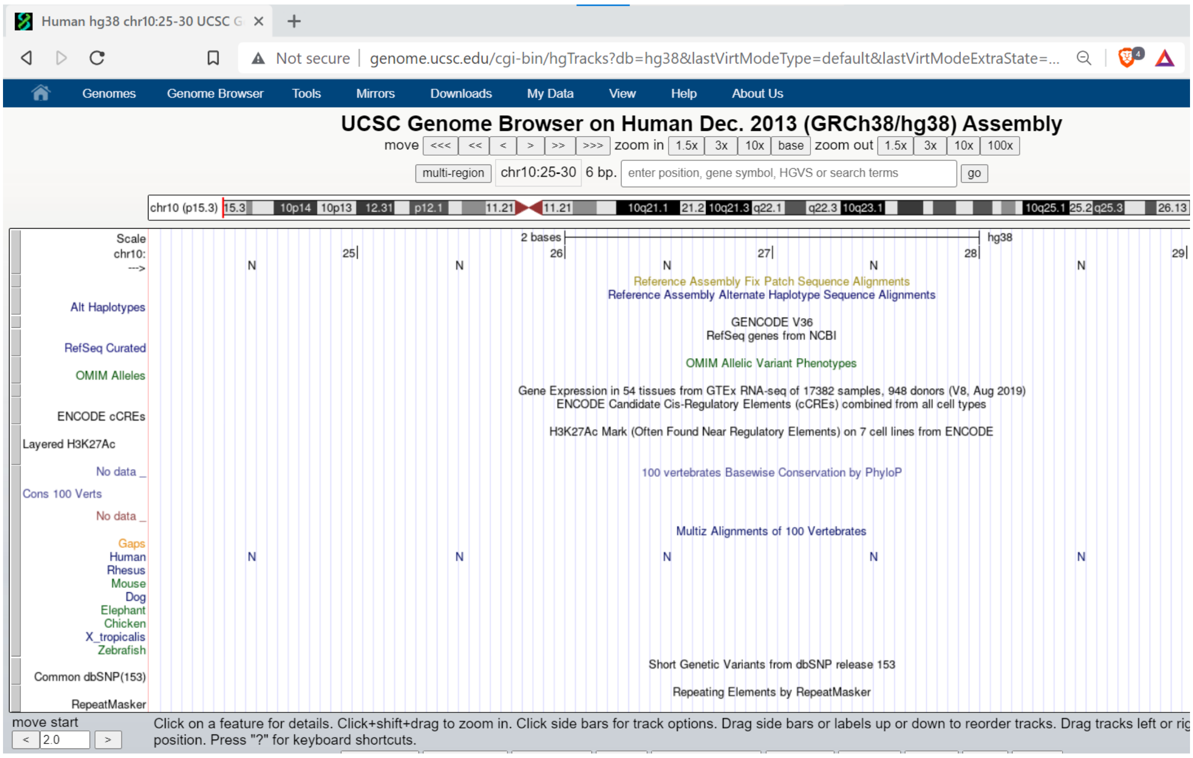
```
>hg38_dna range=chr10:25-30 5'pad=0 3'pad=0 strand=+ repeatMasking=none
NNNNNN
```

Therefore, for conversion to GRCh37, I used most likely region GRCh38 chromosome 10, from 25000 to 30000 to continue with this exercise.



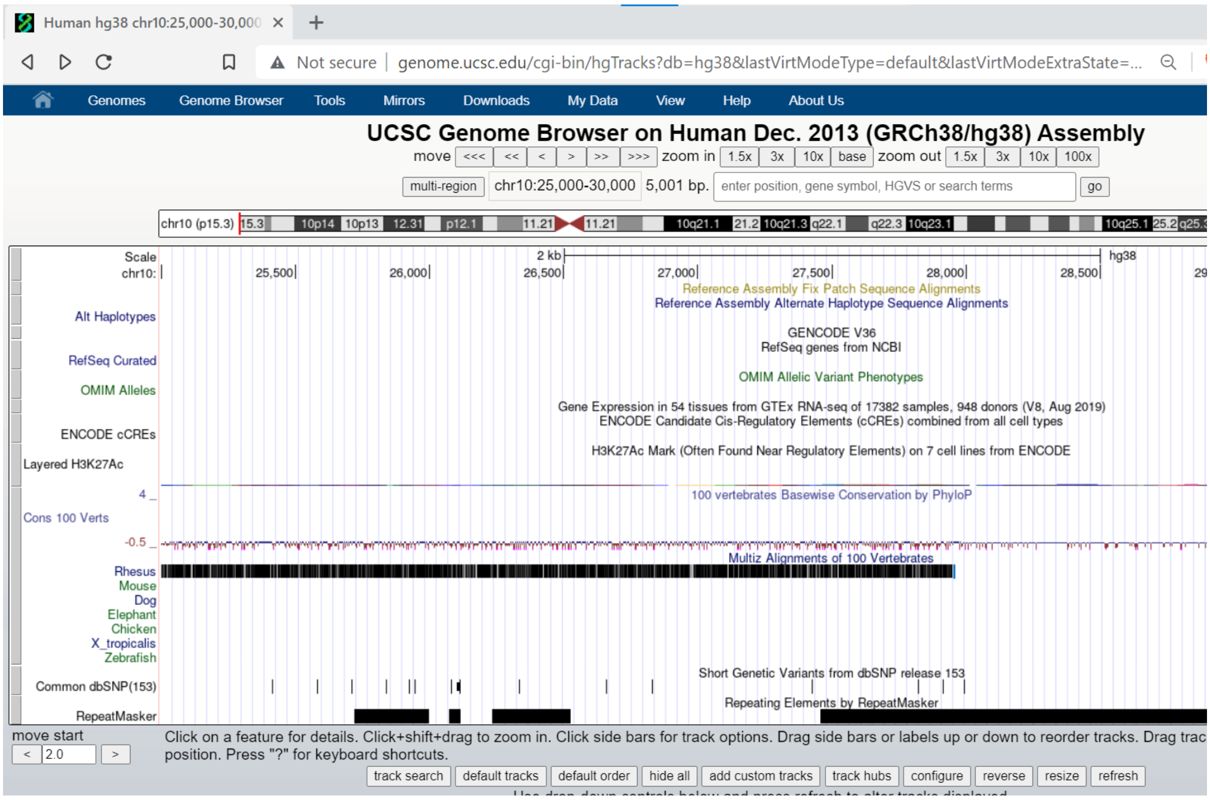
```
>hg38_dna range=chr10:25000-30000 5'pad=0 3'pad=0 strand=+ repeatMasking=none
TAAAAAATAATTTAAAGAAAATAGAGCTTGATAAATCTGTTTCTTCATCT
TCATAATAATGTCAAATTTGTTGAGATTTTTTTTAAATGGCACGATTTGT
CTACAGATCTTTGTACTCTGGCTTAAATTAAATGTATATACAACTTATAT
AATAAAATACTGGGCTGTTTTATTATTATATTGACAATTTCTTAGTCACC
ACTACTTTGATCATATTCTATAAATGGCACTGTGAGACCTATCACTGGTT
ATCAACAACATAAAGTGTTTATGACAATTTCATGTGACAGATGAAGGAAG
TTTGGTTAGTGCAGTGGCAATAGTTGGCAACCGAGAAACTGAGCTCACAA
TTTTAGAAAAGTATTATTCTTTCTAACTAGATATTTCCATGAAAAGAACC
TTGTGAAATGCAGAAATGCCAAAAGAATAATTATAAGATAATAACCAAAT
AACTAAAATACATCTCAATTTCTCTGACAATCTAACTTAATGCAGGGTAC
AGCCAGAATCATGATGTTTACAAACATAGACATTTACGATCTCGAGACAT
TTAATTATTAGCTGGTTGAGGAAAACAGTAGTAGAACTGTTATTGCAGAG
ATAAAAGACAGAAAACAGTGGAAGGGCTTGATCACAAGTCATATGTTCCA
GTTTTGGAAACCTCTAAAAATCCTGCCTGGTGATAGGTTTTTCTTATCTC
ATTATTGAAGAATATATGAGCAGGCAGGGCACGGTGGCTCAAACCTGTAA
```

Please see below screenshots of these genomic regions.
GRCh38 chromosome 10, from 25.000 to 30.000 does not exist.


Human hg38 chr10:25-30 UCSC G
Not secure | genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=default&lastVirtModeExtraState=...
Genomes
Genome Browser
Tools
Mirrors
Downloads
My Data
View
Help
About Us
UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x
multi-region chr10:25-30 6 bp. enter position, gene symbol, HGVS or search terms go
chr10 (p15.3) 15.3 10p14 10p13 12.31 p12.1 11.21 11.21 10q21.1 21.2 10q21.3 q22.1 q22.3 10q23.1 10q25.1 25.2 q25.3 26.13
Scale
chr10:
2 bases
hg38
25|
26|
27|
28|
29|
N
Alt Haplotypes
RefSeq Curated
OMIM Alleles
ENCODE cCREs
Layered H3K27Ac
No data _
Cons 100 Verts
No data _
Gaps
Human
Rhesus
Mouse
Dog
Elephant
Chicken
X_tropicalis
Zebrafish
Common dbSNP(153)
RepeatMasker
Reference Assembly Fix Patch Sequence Alignments
Reference Assembly Alternate Haplotype Sequence Alignments
GENCODE V36
RefSeq genes from NCBI
OMIM Allelic Variant Phenotypes
Gene Expression in 54 tissues from GTEx RNA-seq of 17382 samples, 948 donors (V8, Aug 2019)
ENCODE Candidate Cis-Regulatory Elements (cCREs) combined from all cell types
H3K27Ac Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE
100 vertebrates Basewise Conservation by PhyloP
Multiz Alignments of 100 Vertebrates
Short Genetic Variants from dbSNP release 153
Repeating Elements by RepeatMasker
move start
< 2.0 >

Click on a feature for details. Click+shift+drag to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or rig position. Press "?" for keyboard shortcuts.

GRCh38 chromosome 10, from 25000 to 30000 does exist, and was used for this exercise.


Human hg38 chr10:25,000-30,000
Not secure | genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=default&lastVirtModeExtraState=...
Genomes
Genome Browser
Tools
Mirrors
Downloads
My Data
View
Help
About Us
UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x
multi-region chr10:25,000-30,000 5,001 bp. enter position, gene symbol, HGVS or search terms go
chr10 (p15.3) 15.3 10p14 10p13 12.31 p12.1 11.21 11.21 10q21.1 21.2 10q21.3 q22.1 q22.3 10q23.1 10q25.1 25.2 q25.3
Scale
chr10:
2 kb
hg38
25,500|
26,000|
26,500|
27,000|
27,500|
28,000|
28,500|
29
Alt Haplotypes
RefSeq Curated
OMIM Alleles
ENCODE cCREs
Layered H3K27Ac
4 _
Cons 100 Verts
-0.5 _
Rhesus
Mouse
Dog
Elephant
Chicken
X_tropicalis
Zebrafish
Common dbSNP(153)
RepeatMasker
Reference Assembly Fix Patch Sequence Alignments
Reference Assembly Alternate Haplotype Sequence Alignments
GENCODE V36
RefSeq genes from NCBI
OMIM Allelic Variant Phenotypes
Gene Expression in 54 tissues from GTEx RNA-seq of 17382 samples, 948 donors (V8, Aug 2019)
ENCODE Candidate Cis-Regulatory Elements (cCREs) combined from all cell types
H3K27Ac Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE
100 vertebrates Basewise Conservation by PhyloP
Multiz Alignments of 100 Vertebrates
Short Genetic Variants from dbSNP release 153
Repeating Elements by RepeatMasker
move start
< 2.0 >
track search
default tracks
default order
hide all
add custom tracks
track hubs
configure
reverse
resize
refresh

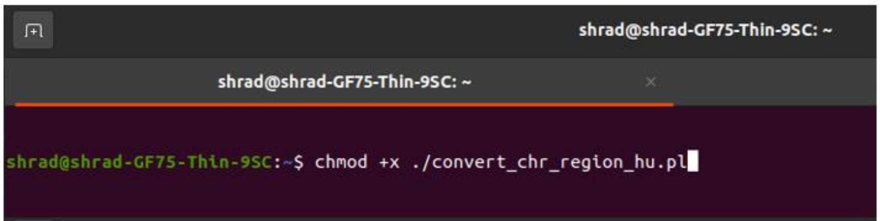
Click on a feature for details. Click+shift+drag to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag trac position. Press "?" for keyboard shortcuts.

<u>Point 2 of 4: Conversion of Coordinates form GRCh38 to GRCh37:</u> I used Ensemble Perl API to convert GRCh38 human genome region chr10: 25000-30000 to corresponding GRCh37**.** I used 'Atom' Editor to write the 'convert_chr_region_hu.pl' script and executed the script from Ubuntu Terminal using command (Ref: file permission https://cets.seas.upenn.edu/answers/chmod.html and running perl script https://www.geeksforgeeks.org/hello-world-program-in-perl/). I found helpful tutorials at https://m.ensembl.org/info/website/tutorials/grch37.html and https://rest.ensembl.org/documentation/info/assembly_map.

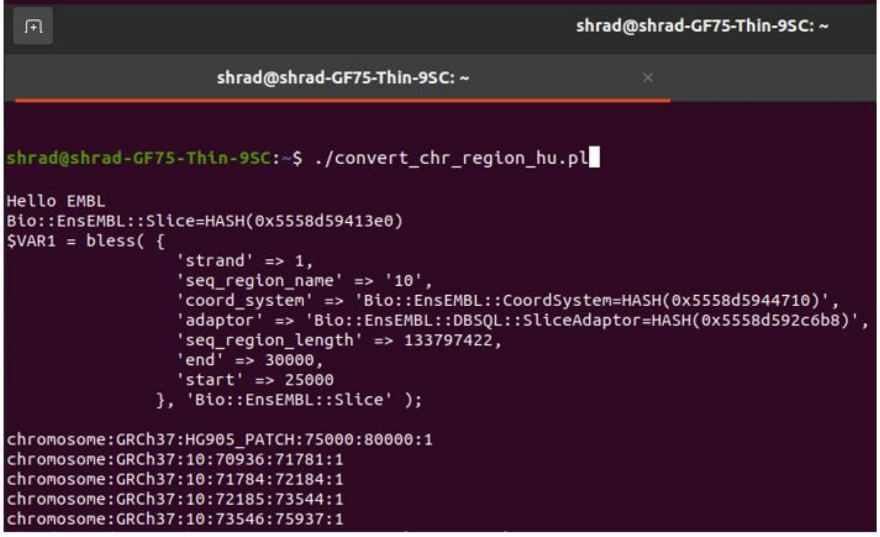
which perl #this gives location of perl used in first line of script for me its #!/usr/bin/perl

chmod +x ./convert_chr_region_hu.pl #gives file permission to make script executable for all users

./convert_chr_region_hu.pl #run the script



```
shrad@shrad-GF75-Thin-9SC:~$ chmod +x ./convert_chr_region_hu.pl
```



```
shrad@shrad-GF75-Thin-9SC:~$ ./convert_chr_region_hu.pl

Hello EMBL
Bio::EnsEMBL::Slice=HASH(0x5558d59413e0)
$VAR1 = bless( {
                 'strand' => 1,
                 'seq_region_name' => '10',
                 'coord_system' => 'Bio::EnsEMBL::CoordSystem=HASH(0x5558d5944710)',
                 'adaptor' => 'Bio::EnsEMBL::DBSQL::SliceAdaptor=HASH(0x5558d592c6b8)',
                 'seq_region_length' => 133797422,
                 'end' => 30000,
                 'start' => 25000
               }, 'Bio::EnsEMBL::Slice' );

chromosome:GRCh37:HG905_PATCH:75000:80000:1
chromosome:GRCh37:10:70936:71781:1
chromosome:GRCh37:10:71784:72184:1
chromosome:GRCh37:10:72185:73544:1
chromosome:GRCh37:10:73546:75937:1
```

<u>Point 3 of 4: Results From Exercise</u>: The results for this exercise, for conversion to GRCh37 is as follows,
chromosome:GRCh37:HG905_PATCH:75000:80000:1
chromosome:GRCh37:10:70936:71781:1
chromosome:GRCh37:10:71783:72184:1
chromosome:GRCh37:10:72184:73544:1
chromosome:GRCh37:10:73545:75937:1

<u>Point 4 of 4: Pre-requisites for this exercise:</u> I started with the assumption that anyone trying to run this exercise has internet connection and a computer (Mac, Windows or Linux), with no background in coding. Therefore, I uploaded detailed description of all setup/installation steps and a detailed tutorial in github repository **Git Link: https://github.com/smukher2/EMBL_git_ensembl_perl_API_Ex1.git.**

Installation instruction files are:
2.1_Install_Ubuntu_dual_boot_any_computer.pdf
2.2_Install_Ubuntu_different_software.pdf
2.3_Install_Atom_Its_More_Than_Just_Text_Editor.pdf
2.4_Install_Perl_PerlModules_BioPerl_EnsemblPerlAPI.pdf
Tutorial file is:
4.1_Tutorial_Complete_Guide_Ubuntu_To_EnsemblPerlAPI.pdf

end of SM Answer Exercise

Alternatives

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

SM Answer Alternatives
Git Link: https://github.com/smukher2/EMBL_git_ensembl_perl_API_Ex1.git

Point 1 of 5: Alternative Tool: As an alternative we can use a 'LiftOver' Ensembl tool http://uswest.ensembl.org/info/docs/tools/index.html that is web-browser based and does not require installation http://uswest.ensembl.org/Homo_sapiens/Tools/AssemblyConverter.

Point 2 of 5: Advantages Of Alternative Tool: The Ensembl "LiftOver" tool has the following advantaged:

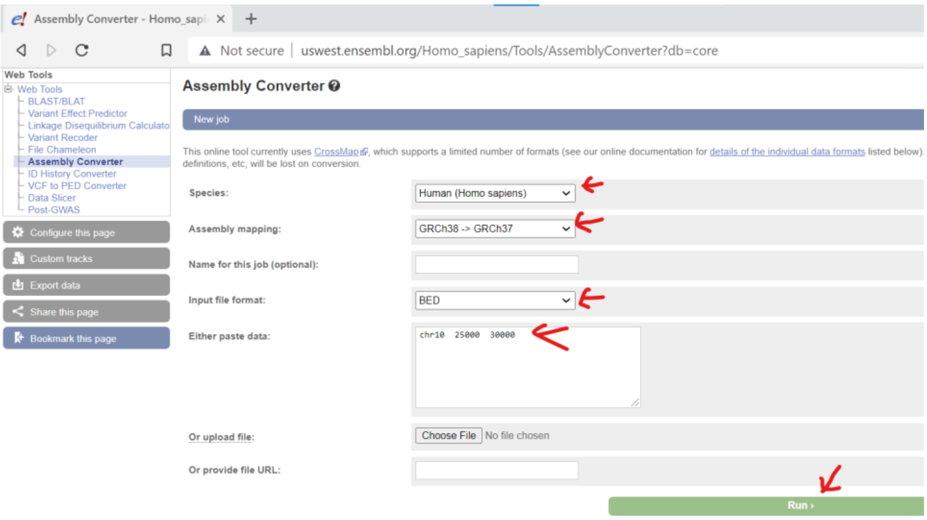
1. Web-based ready to use tool that does not require setup/installation.
2. Usage of tool does not require any coding experience.

Point 3 of 5: Disadvantage Of Alternative Tool: The Ensembl "LiftOver" tool has the following disadvantaged:

1. Web results are deleted after 10 days. So user needs to manually download results in 10 days. In the coding exercise results are automatically saved/downloaded to the computer.
2. Its tedious to use when user has multiple coordinate files to convert, such as from samples of different experimental and control groups, and replicates. For repetitive tasks coding exercise method is preferable.

Point 4 of 5: Usage Of Alternative Tool: The steps to do conversion of GRCh38 chromosome 10, from 25000 to 30000 to GRCh37.

1. Visit 'LiftOver' tool http://uswest.ensembl.org/Homo_sapiens/Tools/AssemblyConverter
2. Input coordinates GRCh38 in bed format and click 'Run' to execute conversion, as shown in screenshot https://m.ensembl.org/info/website/upload/bed.html.
   chr10 25000 30000



Assembly Converter

This online tool currently uses CrossMap, which supports a limited number of formats (see our online documentation for details of the individual data formats listed below). definitions, etc, will be lost on conversion.

Species: Human (Homo sapiens)

Assembly mapping: GRCh38 -> GRCh37

Name for this job (optional):

Input file format: BED

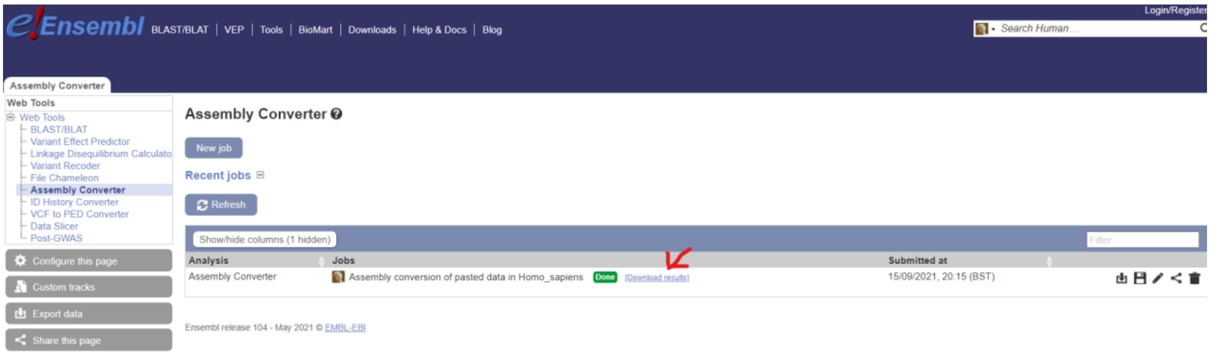
Either paste data:

```
chr10  25000  30000
```

Or upload file: No file chosen

Or provide file URL:

3. Click ‘Download’ to download GRCh37 converted results as shown in screenshot below.



Assembly Converter

Analysis	Jobs	Submitted at
Assembly Converter	Assembly conversion of pasted data in Homo_sapiens Done [Download results]	15/09/2021, 20:15 (BST)

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<u>Point 5 of 5: Results From Alternative Tool</u>: The results for this exercise, for conversion to GRCh37 is as follows,

```
HG905_PATCH     75000  80000
chr10   70936  71781
chr10   71783  72184
chr10   72184  73544
chr10   73545  75937
```

end of SM Answer Alternatives