



Browsing Genes and Genomes with Ensembl

Stella Maris College - 4th-6th August 2021

helpdesk@ensembl.org

Welcome to the 'Living Document' for this Ensembl Browser Workshop. Everyone who is registered for the course has access to edit this document. Please feel free to use this document to ask questions to the Ensembl team throughout the workshop. If you wish to ask questions privately, please do not hesitate to contact the [Ensembl Helpdesk](#).

The 'Living Document' is a great way of capturing the knowledge exchanged during the course and saving it for future use by yourselves and those who can't attend this course. Remember - you don't have to contribute, but any additions will be welcomed!

The course learning outcomes are:

- view genomic regions and manipulate the view to add features.
- explore information about genes and their sequences.
- analyse genomic variants and associated phenotypes and your own variation data using the VEP.
- view homologous genes and genomic regions.
- view functional elements involved in gene regulation and their activity in different cell types.
- export gene data in bulk using BioMart.

Course Overview

- 4th August: Introduction to Ensembl
Genes and Transcripts
- 5th August: Variation and the Variant Effect Predictor (VEP)
Comparative Genomics
- 6th August: Regulation
Data export with BioMart

Trainers:

[Michal Szpak](#)

Webinar, Slides and Demo available to download:

<http://training.ensembl.org/events/2021/2021-08-04-StellaMaris>

Feedback survey:

<https://forms.gle/UefeLxWttPymnqA18>

We would really appreciate it if you could share your thoughts with us regarding these sessions. We are interested in your opinions, how you feel the experience has benefited you and how it could be improved. If you could find a few minutes to complete a short survey at the end of the last session it would really help us in improving the training we can deliver.

The golden rules for efficient online training

We suggest everyone follows these few simple rules for the course to run as smoothly as possible:

- Mute all your microphones to reduce the background noise - only unmute when asking a question
- If you have questions during the course, either:
 - Unmute yourself and ask question out loud
 - Type your question in this shared reference document. Avoid typing in the Zoom chat as it is difficult to keep track there
- When you are ready to move on from a practical/exercises please click the



Raise Hand button so that the [Raise Hand](#) tutor knows you are ready and can proceed with the course. Please remember there are more exercises than we have time for. You are not expected to complete all of them, but rather pick and choose the ones most relevant to your work and you are welcome to finish them in your own time.

Resources:

www.ensembl.org - Ensembl genome browser (chordates)

grch37.ensembl.org - Ensembl archive for browsing data associated with the human GRCh37 genome assembly

www.ensemblgenomes.org - Ensembl Genomes genome browser (non-chordates)

www.ebi.ac.uk - EMBL-EBI website

www.ebi.ac.uk/services - EMBL-EBI databases and tools

[Train Online](#) - EMBL-EBI e-learning for our databases and tools

Questions

If you have any questions/problems that you would like to share and are applicable to the whole class please write them below. A tutor will answer your question.

Write your question after the last one you can see in this document and write your name.

1. **<Name>** Does ensembl provide gene ontology annotation services?
<Aleena> Ensembl associates gene ontology terms to genes via uniprot mappings. More information here
<http://m.ensembl.org/Help/View?id=285>
<Ben> Michal will cover exploring gene ontology annotations in the Genes and Transcripts module later today.
2. **<Name>**What is the difference between “Information and statistics” & “More information and statistics” pages? Both seem to be the same, is there any extra detail available in more information?
Information & statistics:
http://bacteria.ensembl.org/Mycobacterium_tuberculosis_h37ra_gca_000016145/Info/Annotation/#about
More information & Statistics:
http://bacteria.ensembl.org/Mycobacterium_tuberculosis_h37ra_gca_000016145/Info/Annotation/#assembly
<Michal><Would you mind sharing links to these pages so that I can have a look?
It seems to be a duplicated page. We'll look into it. I'm afraid there's no more details available for this particular genome assembly.>
3. **<><>**
<Tutor><Answer>
4. **<Name>**<Question>



<Tutor><Answer>

5. <Name><Question>

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<Tutor><Answer>



Other resources

This section of the Living Document provides additional resources that might be useful to you in developing skills and knowledge in the course topic area.

Train online

EMBL-EBI provides an e-learning platform called [Train online](#). Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to become a confident user of our data resources; we are not trying to train you to become a bioinformatician.

Tutorials of interest might include:

- [Ensembl: Quick Tour](#)
- [Ensembl: Browsing Genomes](#)
- [Ensembl Genomes \(non-chordates\): Quick Tour](#)
- [Ensembl REST API](#)

Webinar series

The EMBL-EBI training team also run regular [webinar series](#) featuring the EBI resources. See the [Training pages](#) for more information. You can also catch up on any webinars that you might have missed in [Train online](#) or on [Youtube](#).