Ensembl REST API workshop

24th-27th May 2022

helpdesk@ensemblgenomes.org

Welcome to the ‘Living Document’ for this Ensembl REST API 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!

By the end of the course you will be able to:

- Describe the data types accessible through the Ensembl REST API
- Describe the methods in the Ensembl REST API
- Navigate the Ensembl REST API documentation to find available methods
- Write scripts to access data via the Ensembl REST API

Course Overview

1. Overview of the Ensembl REST API and GET endpoints, browser calls
2. Making REST API requests programmatically
3. Fetching specific data points from REST responses
4. Other media types
5. Chaining REST queries together
6. Bulk REST API queries with POST
7. Rate limiting

Trainers:

Aleena Mushtaq

Webinar, Slides and Demo available to download:
https://training.ensembl.org/events/2022/2022-05-23-NextGenHelper_REST_May_106

We would really appreciate it if you could share your thoughts with us regarding
Feedback survey:
https://forms.gle/DraKR1mL9noRNgBf8
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 Raise Hand so that the 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><Question>How genome is assembled?**
   <Louisse> Genomes are assembled by the researchers who submit their genomes to the databases we retrieve genome assemblies from (e.g. International Nucleotide Sequence Database Collaboration; INSDC). Ensembl does not perform the genome assembly. Here are some useful sites that will introduce you to genome assembly:
   - **https://training.galaxyproject.org/training-material/topics/assembly/tutorials/general-introduction/tutorial.html**
   - **https://www.cd-genomics.com/an-overview-of-genome-assembly.html**
   - **https://bioinformaticsworkbook.org/dataAnalysis/GenomeAssembly/Intro_GenomeAssembly.html#gsc.tab=0**

2. **<Name><Question>What is end point documentation?**
   <Louisse> The endpoint documentation are the individual pages that you land in when you click the links in the Ensembl REST API page: https://rest.ensembl.org/.

3. **<Name><Question>What is role of REST API?**
   <Louisse> The Ensembl REST API is a language agnostic way to access the Ensembl database. You can:
   - ***Access Ensembl's gene, variation, comparative genomics and regulation data using a programming language of your choice.***

- ***Analyse variation data through the Linkage Disequilibrium (LD), Transcript Haplotypes and Variant Effect Predictor (VEP) endpoints.***
- ***Convert co-ordinates from one assembly to another.***

Here is a general summary of what REST API is if you are unfamiliar with it: https://www.techtarget.com/searchapparchitecture/definition/RESTful-API. Often, one would use REST API to access biological data as part of an analysis pipeline.

4. **<Name><Question>Why gene ids so long?**
   <Louisse> Gene IDs are auto-generated when they are first annotated in Ensembl. They are often quite long to make sure that every gene has its own unique ID.

5. **<Name> QuestionWhat is use of accessing ensemble gene, variation, comparative genomics?With what purpose we should access it?**
   <Louisse> This really depends on your research questions. For example, you might be interested in a particular gene and would like to find out the different variants within that gene. You might be interested in the evolutionary history of a gene and want to view its gene tree. You might want to look at the different regulatory regions of a sequence. Some researchers may use Ensembl to download sequence files only. There are a lot of different ways to use Ensembl and it really depends on what you are working on.

   If you are interested in bioinformatics in general and don't really know where to start, please see these useful courses on the EMBL-EBI training site:
   - **A guide to…: Introducing concepts and resources in bioinformatics: https://www.ebi.ac.uk/training/online/courses/a-guide-to/**
   - **Bioinformatics for the terrified: An introduction to the science of bioinformatics: https://www.ebi.ac.uk/training/online/courses/bioinformatics-terrified/**

   Once you understand the concepts behind bioinformatics, it will be much easier for you to come up with research questions.

6. **<Name><Question>Can we use ensembl as tool also or it is browser only?**
   <Tutor><You can use the tools provided in Ensembl, such as VEP, BioMart to retrieve the Ensembl data. You can also retrieve Ensembl data programmatically via REST API, FTP site and Mysql.

7. **<Name><Question>I am having interest in doing research activity in it but how could i start not getting way to enter in it. So pls tell me how should i proceed? I do not know how to design a problem?**
   <Louisse> I'm afraid we cannot comment on how you should perform your research. We can refer you to some very useful courses that address bioinformatics resources and concepts. For example on the EMBL-EBI training site (https://www.ebi.ac.uk/training/online/courses/) you will be able to find very useful bioinformatics introductory courses:
   - **A guide to…: Introducing concepts and resources in bioinformatics: https://www.ebi.ac.uk/training/online/courses/a-guide-to/**
   - **Bioinformatics for the terrified: An introduction to the science of bioinformatics: https://www.ebi.ac.uk/training/online/courses/bioinformatics-terrified/**

   There are many other courses on the EMBL-EBI training page, not just introductory courses.

   Finally, you can do some research online regarding bioinformatics project ideas. Please see the following site for some bioinformatics FAQs: https://omicstutorials.com/frequently-asked-questions-about-bioinformatics/.

8. **<Name><Question>Today i am not getting access to meeting.**
9. **<Louisse> Hi, here is a link to the WebEx meeting: https://nextgenhelper-2.webex.com/nextgenhelper-2-en/j.php?MTID=mb6f39997c83fcf4d3edf93d73a947bcd**

10. **<Name><Question>It's showing that the cohost or host has restricted the access of joining this meeting.**
    <Louisse> Apologies about this! Please email Mamta at support@nextgenhelper.com regarding this.

11. **<Name><Question> why showing restricted?**
    <Louisse> Hi, I'm sorry, I do not know why the meeting is showing as restricted for you. The WebEx meeting was created by Nextgenhelper, so please contact them about this.

12. **<Name><Question>**
    <Tutor><Answer>

13. **<Name><Question>**
    <Tutor><Answer>

14. <Name><Question>
    <Tutor><Answer>

15. <Name><Question>
    <Tutor><Answer>

16. <Name><Question>
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17. <Name><Question>
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28. <Name><Question>
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29. <Name><Question>

<Tutor><Answer>

30. <Name><Question>
<Tutor><Answer>

31. <Name><Question>
<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.