

Ensembl REST API Workshop

Tuesday, 17th to Thursday, 19th October 2023

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:

- Access main data types in Ensembl: genomes, genes, genetic variation, regulatory features and comparative genomics.
- 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.

Workshop recording

- [Day 1](#)
- [Day 2](#)
- [Day 3](#)

Course Overview

Agenda

Tuesday, 17th October 2023, 09:00 - 12:00 (BST)

- Introduction to the Ensembl REST API
- Accessing GET queries via a browser
- Scripting around REST API calls
- Decoding JSON responses

Wednesday, 18th October 2023, 09:00 - 12:00 (BST)

- Using results: fetching specific data points
- Chaining REST API queries

Thursday, 19th October 2023, 09:00 - 12:00 (BST)

- Accessing POST queries: bulk REST API calls
- Other content types
- Rate limits
- Closing remarks

Trainers

[Louisse Paola Mirabueno](#)

Demo, exercises and slides available to download

https://training.ensembl.org/events/2023/2023-10-17-Open_API

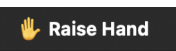
Feedback survey

<https://forms.gle/efxLx1NA5F4trP3M7>

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  button 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.

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. **Q:** For me, the code seems to work even without the `str()` function (Martti Tolvanen)

```
# Enter script here if applicable
for variant in decoded:
    print(variant["Variation"], "\t",
          variant["attributes"].get("p_value"), "\t",
          variant["attributes"].get("external_reference"), "\t",
          variant["attributes"].get("risk_allele"), "\t",
          variant["attributes"].get("associated_gene")
    )
```

rs62444550	6.00e-6	PMID:31217584	None	None
rs671	4.00e-153	PMID:31959922	None	ALDH2
rs10127720	7.00e-12	PMID:31046077	C	LOC102723661
rs10275488	1.00e-9	PMID:31217584	None	None
rs56113850	8.00e-16	PMID:31046077	C	CYP2A6
rs2106727	2.00e-11	PMID:31217584	None	None
rs9275576	6.00e-9	PMID:31837886	T	HLA-DQA2
rs10683220	1.00e-7	PMID:31217584	None	None

A: Hi Martti, thanks for sharing your script! Yours is definitely a more efficient script, so I wonder if it simply has something to do with printing the values as you are cycling through the JSON with your `for` loop. In the case of our example answer, we cycled through the JSON first, saved the individual values into variables *and then* printed the entire table. If you did it “our way”, you would get an error if you didn’t include the `str()` function. But “your way” allows you to print keys that do not exist. Could you provide your output please? Just curious to see how it looks (just the first 10ish lines suffice).

A: Thanks for sharing! Yep, that’s definitely a better way to write the script 😊 I might update our example to yours!

2. **Q:** Another alternative code version, for 3.3. I just built the expression for `mouse_dict` one level at the time to see what I got, then copied for `human_dict`

and changed 'target' to 'source'. This would not work in a result of multiple species, though, as the for-loop construction would

```
# Enter script here if applicable
# Exercise 3.3

import requests, sys
from pprint import pprint

server = "https://rest.ensembl.org"
ext = "/homology/symbol/human/BRCA2?target_species=mouse"

r = requests.get(server+ext, headers={ "Content-Type" :
"application/json"})

if not r.ok:
    r.raise_for_status()
    sys.exit()

decoded = r.json()

mouse_dict = decoded["data"][0]['homologies'][0]['target']
human_dict = decoded["data"][0]['homologies'][0]['source']

print("Human ", human_dict['id'])
print(human_dict['align_seq'])
print("Mouse ", mouse_dict['id'])
print(mouse_dict['align_seq'])
```

A: Brilliant, thanks so much! I really like seeing how other people write their scripts as it helps me understand what we can improve in our examples 😊

3. **Q:**

```
# Enter script here if applicable
```

A:

```
# Enter script here if applicable
```

4. **Q:**

Enter script here if applicable

A:

Enter script here if applicable

5. **Q:**

Enter script here if applicable

A:

Enter script here if applicable

6. **Q:**

Enter script here if applicable

A:

Enter script here if applicable

7. **Q:**

Enter script here if applicable

A:

Enter script here if applicable

8. **Q:**

Enter script here if applicable

A:

Enter script here if applicable

9. **Q:**

Enter script here if applicable

A:

Enter script here if applicable

10. Q:

Enter script here if applicable

A:

Enter script here if applicable

11. Q:

Enter script here if applicable

A:

Enter script here if applicable

12. Q:

Enter script here if applicable

A:

Enter script here if applicable

13. Q:

Enter script here if applicable

A:

Enter script here if applicable

14. Q:

Enter script here if applicable

A:

Enter script here if applicable

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.

Helpful websites

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 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 runs 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](#).