Introduction to the Ensembl REST API

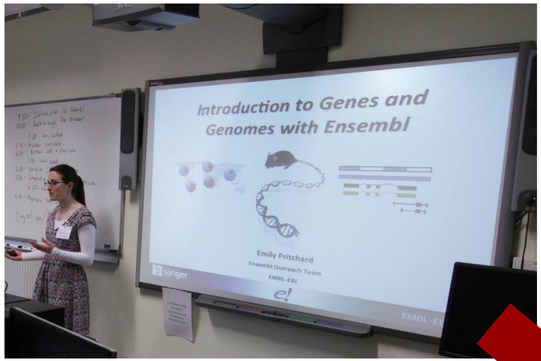
EMBL-EBI

e!Ensembl

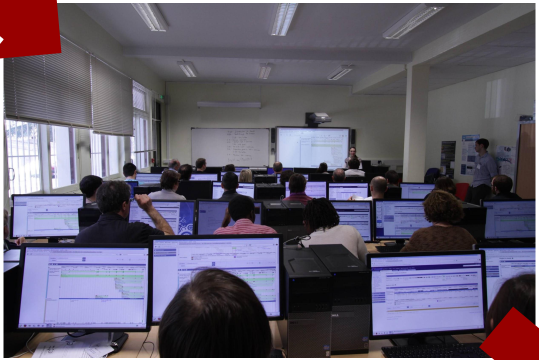
This webinar course

Date	Webinar topic	Instructor
4th Sept	Introduction to Ensembl Ensembl genes	Astrid Gall Emily Perry
6th Sept	Variation data in Ensembl and the Ensembl VEP Comparing genes and genomes with Ensembl Compara	Erin Haskell Astrid Gall
11th Sept	Finding features that regulate genes – the Ensembl Regulatory Build Data export with BioMart	Emily Perry Erin Haskell
13th Sept	Uploading your data to Ensembl Introduction to the Ensembl REST APIs	Astrid Gall Emily Perry

Structure



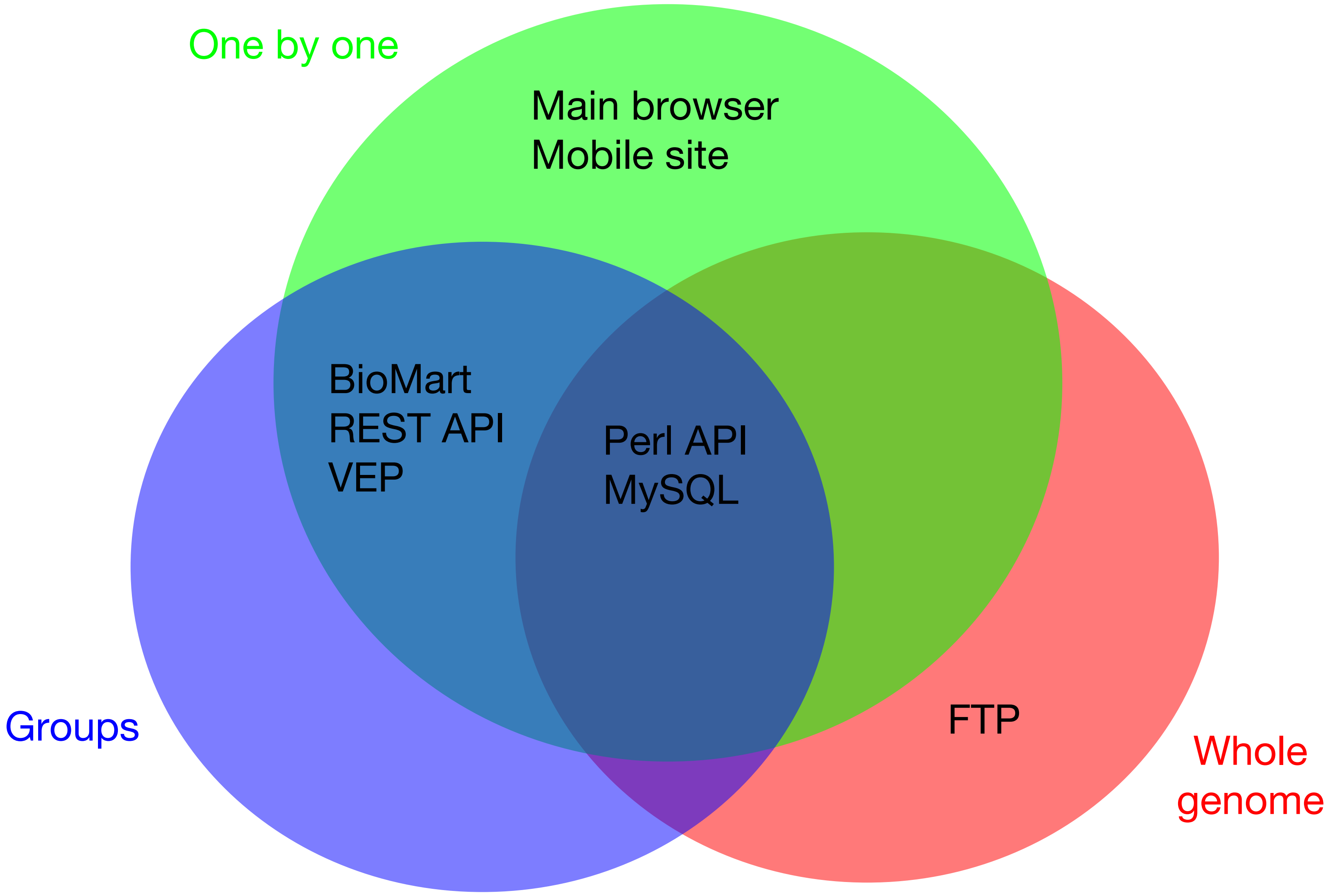
Presentation:
What a REST API is and how it works



Demo:
Trying out some endpoints

Take our online REST API course, if you like.

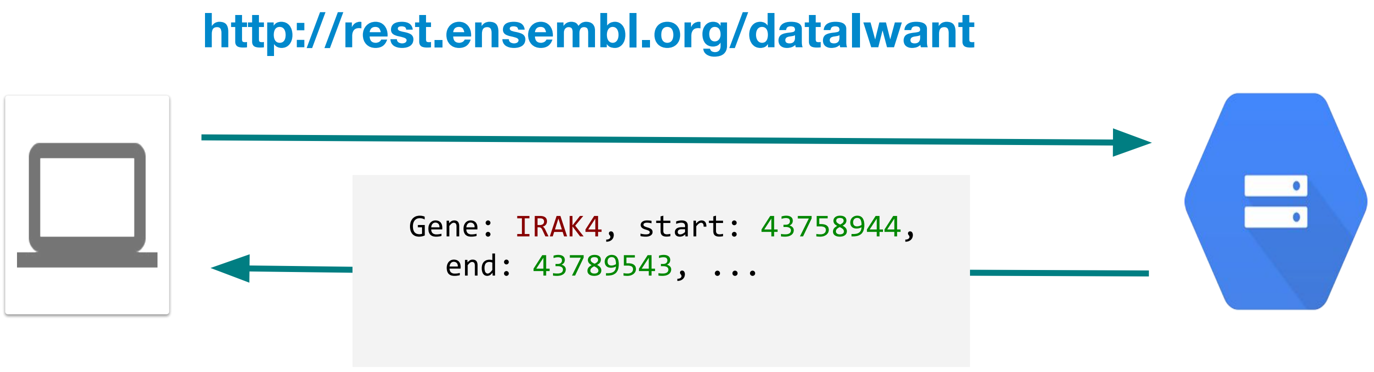
Access scales



What is a REST API?

REpresentational State Transfer. It describes how one system can communicate state with another.

Typically over HTTP(S), providing a machine readable, language agnostic method to access remote data or services.

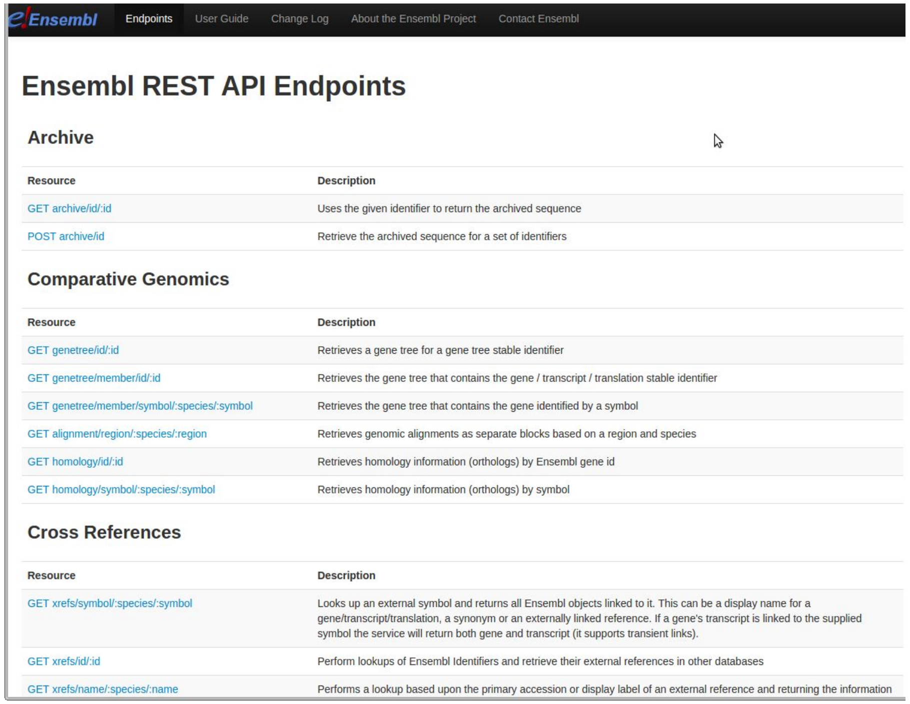


```
Gene: IRAK4, start: 43758944,
  end: 43789543, ...
```

Ensembl REST

- Language agnostic access to Ensembl datasets
- Only a fraction of the functionality of the Perl API is exposed

http://rest.ensembl.org



Ensembl REST API Endpoints

Archive

Resource	Description
GET archive/id/:id	Uses the given identifier to return the archived sequence
POST archive/id	Retrieve the archived sequence for a set of identifiers

Comparative Genomics

Resource	Description
GET genetree/id/:id	Retrieves a gene tree for a gene tree stable identifier
GET genetree/member/id/:id	Retrieves the gene tree that contains the gene / transcript / translation stable identifier
GET genetree/member/symbol/:species/:symbol	Retrieves the gene tree that contains the gene identified by a symbol
GET alignment/region/:species/:region	Retrieves genomic alignments as separate blocks based on a region and species
GET homology/id/:id	Retrieves homology information (orthologs) by Ensembl gene id
GET homology/symbol/:species/:symbol	Retrieves homology information (orthologs) by symbol

Cross References

Resource	Description
GET xrefs/symbol/:species/:symbol	Looks up an external symbol and returns all Ensembl objects linked to it. This can be a display name for a gene/transcript/translation, a synonym or an externally linked reference. If a gene's transcript is linked to the supplied symbol the service will return both gene and transcript (it supports transient links).
GET xrefs/id/:id	Perform lookups of Ensembl Identifiers and retrieve their external references in other databases
GET xrefs/name/:species/:name	Performs a lookup based upon the primary accession or display label of an external reference and returning the information

What Ensembl REST is and is not

- HTTP access to Ensembl data
- Stable service
- Limited by network latency
- Read only
- Versioned with archives

- Not HATEOAS[†], or fully RESTful*
- No mirrors
- Not an efficient data mining solution
- Incomplete coverage

[†] Hypermedia As The Engine Of Application State
* See lengthy debates about Roy Fielding's conception of REST

What is an endpoint?

“In REST, the resource typically refers to some object or set of objects that are exposed at an API endpoint. /api/users/johnny. An endpoint by itself is just a reference to a uri that accepts web requests that may or may not be RESTful. /services/service.asmx.”

An endpoint is a particular output that you can get given a particular input.

It is a function that interacts with our database.

Endpoint documentation

Full documentation of all the endpoints is found at:

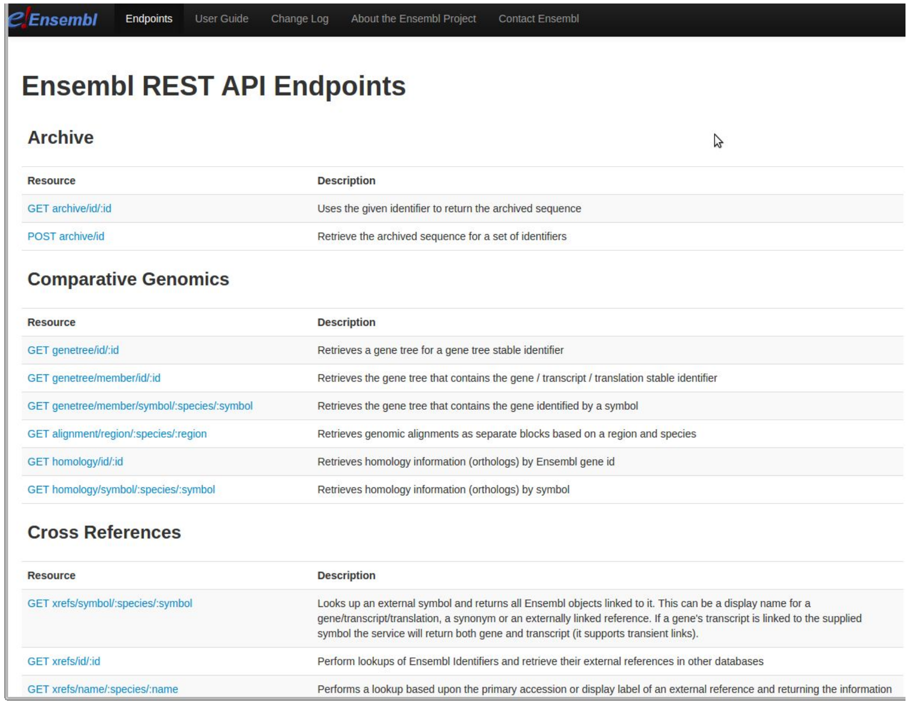
http://rest.ensembl.org

The documentation lists:

- All the endpoints grouped by function
- The required parameters for each endpoint
- Optional parameters
- Example code for using the endpoints

Functional groupings

- Archive
- Comparative Genomics
- Cross References
- Information
- Lookup
- Mapping
- Ontology & Taxonomy
- Sequence
- Variation, etc...



Ensembl | Endpoints | User Guide | Change Log | About the Ensembl Project | Contact Ensembl

Ensembl REST API Endpoints

Archive

Resource	Description
GET archive/id/:id	Uses the given identifier to return the archived sequence
POST archive/id	Retrieve the archived sequence for a set of identifiers

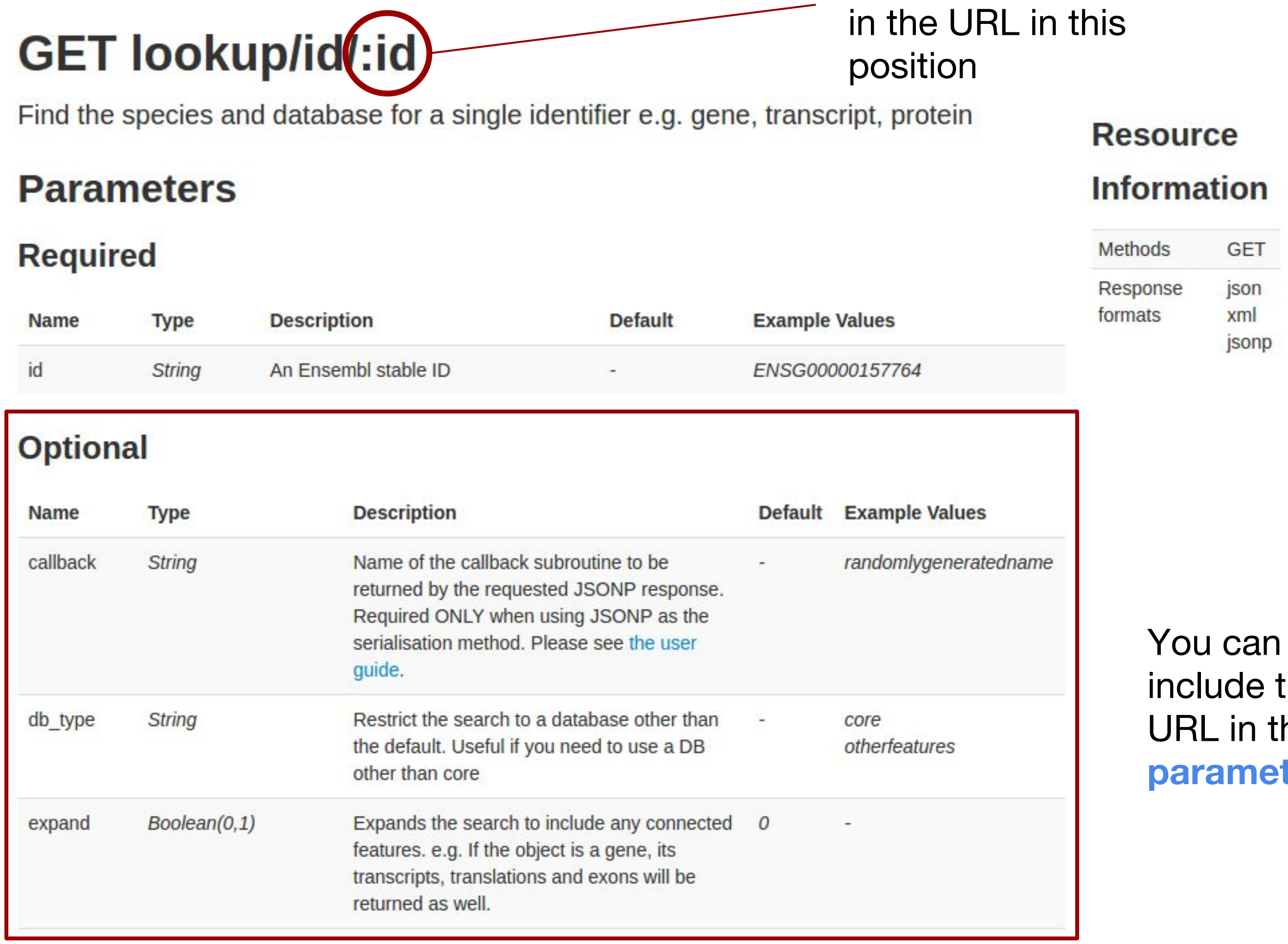
Comparative Genomics

Resource	Description
GET genetree/id/:id	Retrieves a gene tree for a gene tree stable identifier
GET genetree/member/id/:id	Retrieves the gene tree that contains the gene / transcript / translation stable identifier
GET genetree/member/symbol/:species/:symbol	Retrieves the gene tree that contains the gene identified by a symbol
GET alignment/region/:species/:region	Retrieves genomic alignments as separate blocks based on a region and species
GET homology/id/:id	Retrieves homology information (orthologs) by Ensembl gene id
GET homology/symbol/:species/:symbol	Retrieves homology information (orthologs) by symbol

Cross References

Resource	Description
GET xrefs/symbol/:species/:symbol	Looks up an external symbol and returns all Ensembl objects linked to it. This can be a display name for a gene/transcript/translation, a synonym or an externally linked reference. If a gene's transcript is linked to the supplied symbol the service will return both gene and transcript (it supports transient links).
GET xrefs/id/:id	Perform lookups of Ensembl Identifiers and retrieve their external references in other databases
GET xrefs/name/:species/:name	Performs a lookup based upon the primary accession or display label of an external reference and returning the information

Endpoint Documentation



GET lookup/id/:id

Find the species and database for a single identifier e.g. gene, transcript, protein

Parameters

Required

Name	Type	Description	Default	Example Values
id	*String*	An Ensembl stable ID	-	*ENSG00000157764*

Optional

Name	Type	Description	Default	Example Values
callback	*String*	Name of the callback subroutine to be returned by the requested JSONP response. Required ONLY when using JSONP as the serialisation method. Please see the user guide.	-	*randomlygeneratedname*
db_type	*String*	Restrict the search to a database other than the default. Useful if you need to use a DB other than core	-	*core* *otherfeatures*
expand	*Boolean(0,1)*	Expands the search to include any connected features. e.g. If the object is a gene, its transcripts, translations and exons will be returned as well.	*0*	-

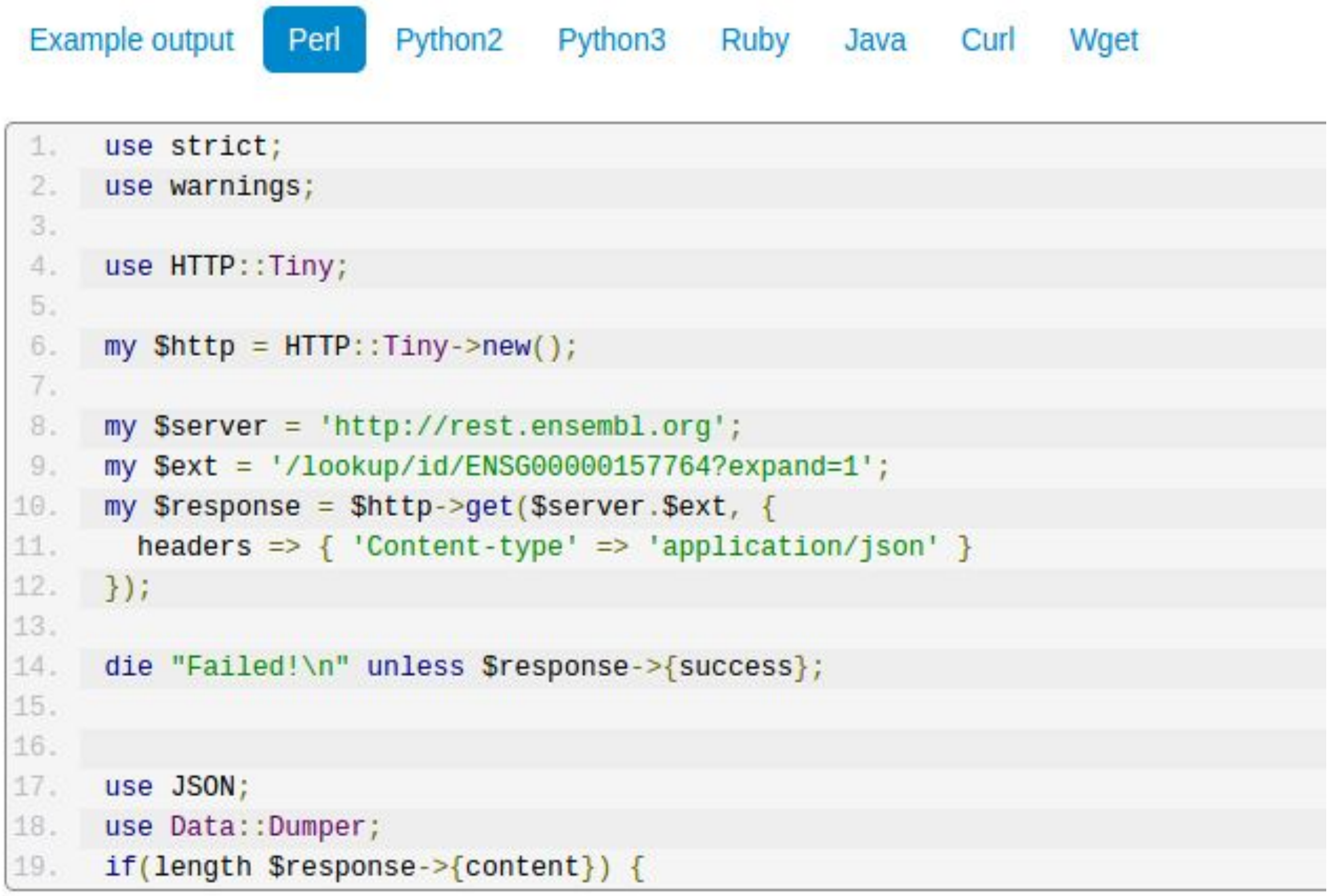
Resource Information

Methods	GET
Response formats	json xml jsonp

You must include the id in the URL in this position

You can choose to include these in the URL in the format: **parameter=option**

Sample Code



```
use strict;
use warnings;

use HTTP::Tiny;

my $http = HTTP::Tiny->new();

my $server = 'http://rest.ensembl.org';
my $ext = '/lookup/id/ENSG00000157764?expand=1';
my $response = $http->get($server.$ext, {
  headers => { 'Content-type' => 'application/json' }
});

die "Failed!\n" unless $response->{success};


use JSON;
use Data::Dumper;
if(length $response->{content}) {
```

Making a REST call in the browser

- The easiest way to make REST calls is to put URLs into the browser
- This can be used as a quick look-up
- This can help you to test the URLs in your scripts to see:
    - If they work
    - If you've included the correct parameters
    - What the output looks like

Pinging the database

Ping confirms that you have a connection to the database

http://rest.ensembl.org/info/ping?content-type=application/json

```
{
  ping: 1
}
```

Requesting a gene by ID

http://rest.ensembl.org/lookup/id/ENSG00000157764?content-type=application/json

```
{
  "source": "ensembl_havana",
  "object_type": "Gene",
  "logic_name": "ensembl_havana_gene",
  "version": 12,
  "species": "homo_sapiens",
  "description": "B-Raf proto-oncogene, serine/threonine kinase [Source:HGNC
Symbol;Acc:HGNC:1097]",
  "display_name": "BRAF",
  "assembly_name": "GRCh38",
  "biotype": "protein_coding",
  "end": 140924764,
  "seq_region_name": "7",
  "db_type": "core",
  "strand": -1,
  "id": "ENSG00000157764",
  "start": 140719327
}
```

Scripting around REST API calls

Scripting around calls allows you to:

- Extract specific bits of data from your REST call.
- Output in your preferred format.
- Link together calls for more complicated queries.
- Integrate your queries into a larger pipeline.

Language agnostic access

- REST APIs are designed to be accessed using any programming language.
- Calls can be made and decoded within any script.
- We have examples in Python, Perl and R.

Requesting a gene by ID – Python

```python
import requests, sys, json
from pprint import pprint

def fetch_endpoint(server, request, content_type):

    r = requests.get(server+request, headers={ "Content-Type" : content_type})

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

    if content_type == 'application/json':
        return r.json()
    else:
        return r.text


server = "http://rest.ensembl.org/"
ext = "lookup/id/ENSG00000157764?"
con = "application/json"
get_gene = fetch_endpoint(server, ext, con)

pprint (get_gene)
```

Requesting a gene by ID – Perl

```perl
use strict;
use warnings;

use Data::Dumper;
use HTTP::Tiny;
use JSON;

# Fetch an endpoint from the server, allow overriding of the default content type
sub fetch_endpoint {
    my $http = HTTP::Tiny->new();
    my ($server, $extension, $content_type) = @_;
    $content_type ||= 'application/json';
    my $response = $http->get($server.$extension, { headers => { 'Accept' => $content_type }
});
    die "Error: ", $response->{status}, "\n" unless $response->{success};
    if($content_type eq 'application/json') {
        return decode_json($response->{content});
    } else {
        return $response->{content};
    }
}

my $server = "http://rest.ensembl.org/";
my $ext = "lookup/id/ENSG00000157764?";
my $con = "application/json";
my $get_gene = fetch_endpoint($server, $ext, $con);

print Dumper $get_gene;
```

Requesting a gene by ID – R

```r
library(httr)
library(jsonlite)

fetch_endpoint <- function(server, request, content_type){

    r <- GET(paste(server, request, sep = ""), accept(content_type))

    stop_for_status(r)

    if (content_type == 'application/json'){
        return (fromJSON(content(r, "text")))
    } else {
        return (content(r, "text"))
    }
}

server <- "http://rest.ensembl.org/"
ext <- "lookup/id/ENSG00000157764?"
con <- "application/json"
get_gene <- fetch_endpoint(server, ext, con)

prettify(toJSON(get_gene))
```

Requesting a gene by ID

http://rest.ensembl.org/lookup/id/ENSG00000157764?content-type=application/json

```
{
  "source": "ensembl_havana",
  "object_type": "Gene",
  "logic_name": "ensembl_havana_gene",
  "version": 12,
  "species": "homo_sapiens",
  "description": "B-Raf proto-oncogene, serine/threonine kinase [Source:HGNC
Symbol;Acc:HGNC:1097]",
  "display_name": "BRAF",
  "assembly_name": "GRCh38",
  "biotype": "protein_coding",
  "end": 140924764,
  "seq_region_name": "7",
  "db_type": "core",
  "strand": -1,
  "id": "ENSG00000157764",
  "start": 140719327
}
```

Decoding JSON

- Most of the time you'll get results in JSON format
- JSON is essentially a massive dictionary/hash/dataframe with keys and values.
- Sometimes a key may then contain another nested dictionary or list
  - Which may contain another
    - And another
      - And another
- Look at the json to work out what keys you need
- You can cycle through all keys in a dictionary with for loops

Using results

Since JSON is a dictionary, you can pull out a single datapoint using the key.

```
{
  "source": "ensembl_havana",
  "object_type": "Gene",
  "logic_name": "ensembl_havana_gene",
  "version": 12,
  "species": "homo_sapiens",
  "description": "B-Raf proto-oncogene, serine/threonine kinase [Source:HGNC
Symbol;Acc:HGNC:1097]",
  "display_name": "BRAF",
  "assembly_name": "GRCh38",
  "biotype": "protein_coding",
  "end": 140924764,
  "seq_region_name": "7",
  "db_type": "core",
  "strand": -1,
  "id": "ENSG00000157764",
  "start": 140719327
}
```

Linking endpoints together

- If you can pull a datapoint from the JSON, you can use it as input for another endpoint.
- You’ll need to link objects and extensions together.

Sequence from a gene name – Python

```python
import requests, sys, json
from pprint import pprint

def fetch_endpoint(server, request, content_type):

    r = requests.get(server+request, headers={ "Content-Type" : content_type})

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

    if content_type == 'application/json':
        return r.json()
    else:
        return r.text

gene_name = "IRAK4"

server = "http://rest.ensembl.org/"
ext = "lookup//symbol/homo_sapiens/" + gene_name + "?"
con = "application/json"

# submit the query
get_lookup = fetch_endpoint(server, ext_get_lookup, con)

# define the REST query to get the sequence from the gene
ext_get_seq = "/sequence/id/" + get_lookup['id'] + "?"
get_seq = fetch_endpoint(server, ext_get_seq, "text/x-fasta")

# print the gene name, ID and sequence
print (">", gene_name, "\n" + get_seq)
```

Sequence from a gene name – Perl

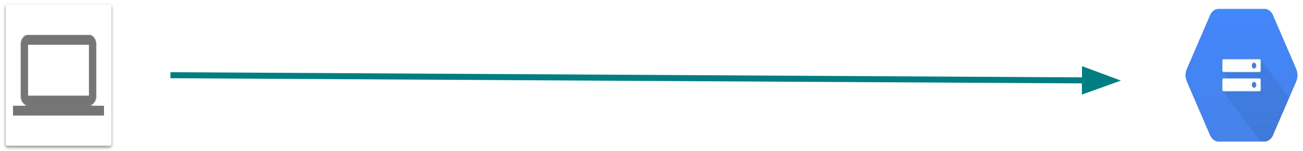
```perl
use strict;
use warnings;

use Data::Dumper;
use HTTP::Tiny;
use JSON;

# Fetch an endpoint from the server, allow overriding of the default content type
sub fetch_endpoint {
    my $http = HTTP::Tiny->new();
    my ($server, $extension, $content_type) = @_;
    $content_type ||= 'application/json';
    my $response = $http->get($server.$extension, { headers => { 'Accept' => $content_type } });
    die "Error: ", $response->{status}, "\n" unless $response->{success};
    if($content_type eq 'application/json') {
        return decode_json($response->{content});
    } else {
        return $response->{content};
    }
}

my $gene_name = "IRAK4";

my $server = "http://rest.ensembl.org/";
my $ext = join("", "lookup/id/ENSG00000157764", $gene_name, "?");
my $json = "application/json";
my $get_gene = fetch_endpoint($server, $ext_get_lookup, $json);

# define the REST query to get the sequence from the gene
my $ext_get_seq = join("", "/sequence/id/", $get_lookup->{id}, "?");
my $fasta = "text/x-fasta";
my $get_seq = fetch_endpoint($server, $ext_get_seq, $fasta);

# print the gene name, ID and sequence
print "> ", $gene_name, "/n", $get_seq;
```

Sequence from a gene name – R

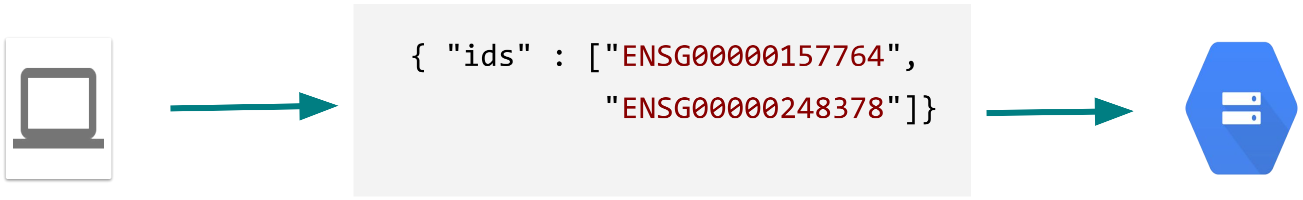
```
library(httr)
library(jsonlite)

fetch_endpoint <- function(server, request, content_type){

    r <- GET(paste(server, request, sep = ""), accept(content_type))

    stop_for_status(r)

    if (content_type == 'application/json'){
        return (fromJSON(content(r, "text")))
    } else {
        return (content(r, "text"))
    }
}

gene_name <- "IRAK4"

server <- "http://rest.ensembl.org/"
con <- "application/json"
ext_get_lookup <- paste("lookup/symbol/homo_sapiens/", gene_name, "?", sep ="")

get_lookup <- fetch_endpoint(server, ext_get_lookup, con)

stable_id <- get_lookup$id

# define the REST query to get the sequence from the gene
ext_get_seq <- paste("sequence/id/", get_lookup$id, "?", sep = "")
get_seq <- fetch_endpoint(server, ext_get_seq, 'text/x-fasta')

# print the gene name, ID and sequence
paste(">", gene_name, sep = "")
get_seq
```

HTTP Methods - GET vs POST

GET http://rest.ensembl.org/lookup/ENSG00000157764



POST http://rest.ensembl.org/lookup/



```
{ "ids" : ["ENSG00000157764",
           "ENSG00000248378"]}
```

Rate limiting

Requests are rate limited to prevent a single user from monopolising the resources.

```
X-RateLimit-Limit: 55000
X-RateLimit-Reset: 892
X-RateLimit-Period: 3600
X-RateLimit-Remaining: 54999
```

Response headers show we are allowed 55000 requests over an hour (3600 seconds)

An average 15 requests per second

1 request used and 892 sec (~15 minutes) from reset

Rate limiting

Requests are rate limited to prevent a single user from monopolising the resources.

```
Retry-After: 40.0
X-RateLimit-Limit: 55000
X-RateLimit-Reset: 892
X-RateLimit-Period: 3600
X-RateLimit-Remaining: 54999
```

Wait 40 seconds before sending another request or...

429

Full course

- If you’re keen on working with the REST API, we have a full course online
- The course uses Jupyter notebooks to run code accessing our REST API
- You can do the course in:
    - Python
    - Perl
    - R
- https://notebooks.azure.com/ensembl-training

Questions

- We’ve muted all the mics
- Ask questions in the Slack workspace

Astrid Gall

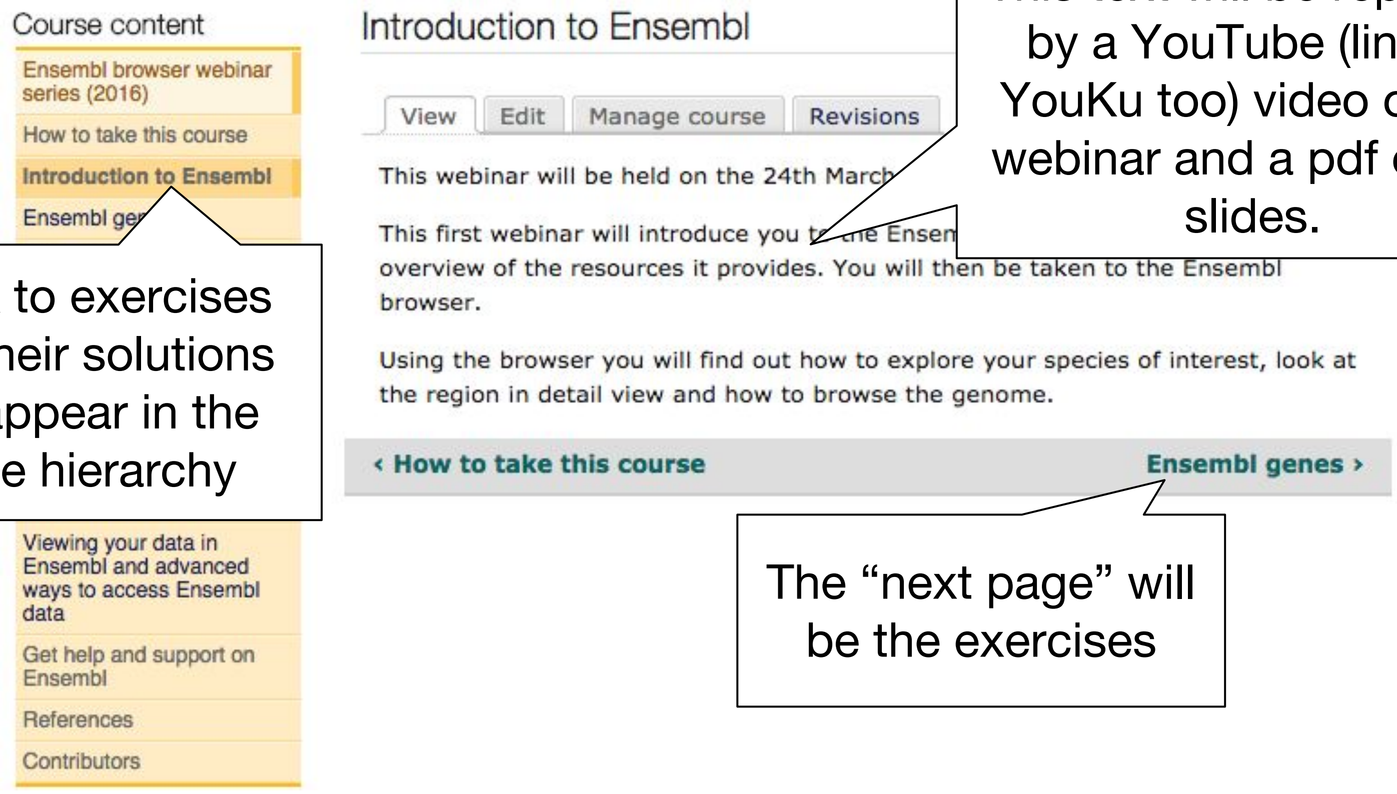
Erin Haskell

slack

EMBL-EBI

Course exercises

http://www.ebi.ac.uk/training/online/course/ensembl-browser-webinar-series-2016



Course content

- Ensembl browser webinar series (2016)
- How to take this course
- Introduction to Ensembl
- Ensembl ge
- Viewing your data in Ensembl and advanced ways to access Ensembl data
- Get help and support on Ensembl
- References
- Contributors

Introduction to Ensembl

This webinar will be held on the 24th March

This first webinar will introduce you to the Ensem overview of the resources it provides. You will then be taken to the Ensembl browser.

Using the browser you will find out how to explore your species of interest, look at the region in detail view and how to browse the genome.

This text will be replaced by a YouTube (link to YouKu too) video of the webinar and a pdf of the slides.

A link to exercises and their solutions will appear in the page hierarchy

The “next page” will be the exercises

Get help with the exercises

- Use the exercise solutions in the online course
- Join our Slack workspace and discuss the exercises with everybody in dedicated channels (register to get sent a link)
- Email us helpdesk@ensembl.org

This webinar course

Date	Webinar topic	Instructor
4th Sept	Introduction to Ensembl Ensembl genes	Astrid Gall Emily Perry
6th Sept	Variation data in Ensembl and the Ensembl VEP Comparing genes and genomes with Ensembl Compara	Erin Haskell Astrid Gall
11th Sept	Finding features that regulate genes – the Ensembl Regulatory Build Data export with BioMart	Emily Perry Erin Haskell
13th Sept	Uploading your data to Ensembl Introduction to the Ensembl REST APIs	Astrid Gall Emily Perry

Help and documentation

Courses online
http://www.ebi.ac.uk/training/online/subjects/11

Tutorials
www.ensembl.org/info/website/tutorials

Flash animations
www.youtube.com/user/EnsemblHelpdesk
http://u.youku.com/Ensemblhelpdesk

Email us helpdesk@ensembl.org

Ensembl public mailing lists dev@ensembl.org, announce@ensembl.org

Follow us

www.facebook.com/Ensembl.org

@Ensembl

www.ensembl.info

Publications

http://www.ensembl.org/info/about/publications.html

Ensembl 2018
Zerbino *et al*
http://europepmc.org/abstract/MED/29155950

Topic-specific publications mentioned throughout workshop

Ensembl 2018

Ensembl Acknowledgements

The Entire Ensembl Team

Daniel R. Zerbino[1], Premanand Achuthan[1], Wasiu Akanni[1], M. Ridwan Amode[1], Daniel Barrell[1,2], Jyothish Bhai[1], Konstantinos Billis[1], Carla Cummins[1], Astrid Gall[1], Carlos García Giroń[1], Laurent Gil[1], Leo Gordon[1], Leanne Haggerty[1], Erin Haskell[1], Thibaut Hourlier[1], Osagie G. Izuogu[1], Sophie H. Janacek[1], Thomas Juettemann[1], Jimmy Kiang To[1], Matthew R. Laird[1], Ilias Lavidas[1], Zhicheng Liu[1], Jane E. Loveland[1], Thomas Maurel[1], William McLaren[1], Benjamin Moore[1], Jonathan Mudge[1], Daniel N. Murphy[1], Victoria Newman[1], Michael Nuhn[1], Denye Ogeh[1], Chuang Kee Ong[1], Anne Parker[1], Mateus Patricio[1], Harpreet Singh Riat[1], Helen Schuilenburg[1], Dan Sheppard[1], Helen Sparrow[1], Kieron Taylor[1], Anja Thormann[1], Alessandro Vullo[1], Brandon Walts[1], Amonida Zadissa[1], Adam Frankish[1], Sarah E. Hunt[1], Myrto Kostadima[1], Nicholas Langridge[1], Fergal J. Martin[1], Matthieu Muffato[1], Emily Perry[1], Magali Ruffier[1], Dan M. Staines[1], Stephen J. Trevanion[1], Bronwen L. Aken[1], Fiona Cunningham[1], Andrew Yates[1] and Paul Flicek[1,3]

[1]European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SD, UK, [2]Eagle Genomics Ltd., Wellcome Genome Campus, Hinxton, Cambridge CB10 1DR, UK and [3]Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SA, UK

Funding

wellcome

EMBL

National Human Genome Research Institute

Open Targets

SAVE THE TASMANIAN DEVIL PROGRAM APPEAL

BBSRC bioscience for the future

TRANSFORMING GENETIC MEDICINE INITIATIVE

Co-funded by the European Union