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## **ENSEMBL BROWSER AND API WORKSHOP (5-6 SEPTEMBER 2013)**

### **INSTRUCTOR:**

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### **VENUE:**

South African National Bioinformatics Institute, University of the Western  
Cape

**APPLICATION:** please complete the online application form at:

<http://www.sanbi.ac.za/training-2/short-courses-and-lectures/ensembl-browser-and-api-workshop/>

**COST: 50 rands.**

## **DAY 1 ENSEMBL BROWSER WORKSHOP**

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The Ensembl project (<http://www.ensembl.org>) provides a comprehensive and integrated source of annotation of, mainly vertebrate, genome sequences.

The workshop on day 1 offers participants the possibility of gaining hands-on experience in the use of the Ensembl genome browser, which can be extended to invertebrate metazoa, plants, fungi, protists, and bacteria at [www.ensemblgenomes.org](http://www.ensemblgenomes.org).

### **For whom?**

The workshop is primarily targeted at wetlab researchers.

### **Programme Outline:**

**MORNING:** The following modules will be covered:

- Introduction to Ensembl: origin, goals and organization of the Ensembl project
- Worked example: guided tour of the most important pages of the Ensembl website
- Data retrieval with BioMart: retrieving complex / large datasets using the data retrieval tool BioMart

**AFTERNOON:** two or three of the following modules will be covered, depending on the interests of the participants. To decide which modules will

be covered, a pre-workshop survey will be sent out to the participants prior to the workshop.

- **Comparative genomics:** orthologues and paralogues, protein families, whole genome alignments and syntenic regions
- **Variation:** sequence variants, structural variants, Variant Effect Predictor
- **Regulation:** “best guess” set of regulatory elements, segmentation tracks, ENCODE
- **Custom annotation:** uploading / attaching your own data (BED, GFF/GTF, BAM, VCF files) to Ensembl
- **Advanced access:** other ways to access Ensembl data (MySQL, Perl API, REST API)

Most modules consist of a presentation and demo, followed by ample opportunity to do exercises.

Participants are encouraged to bring problems/questions about their research to try to tackle these during the workshop using Ensembl.

### **Prerequisites**

The prerequisite for this workshop is a general knowledge of molecular biology / genetics and a familiarity with web browsers

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## **DAY-2 ENSEMBL API WORKSHOP**

Ensembl data are accessible through an interactive web site, flat files, the data mining tool BioMart, direct database querying and a set of Perl APIs.

Day-2 covers the basics of the Ensembl Perl APIs and offers participants the possibility of gaining hands-on experience in the use of the Perl core API. In addition, an introduction to the recently developed REST API will be given.

### **For whom?**

The workshop is primarily targeted at bioinformaticians as well as wet-lab researchers who are interested in programmatically retrieving data from Ensembl.

### **Programme**

After a general introduction to the Ensembl Perl APIs, most of the workshop will be focused on the core databases, that store genome sequences and most of the annotation information, and the Perl core API.

The database schema and the API design as well as its most important objects and their methods will be presented. This will be followed by practical

sessions in which the participants can put the learned into practice by writing their own Perl scripts to retrieve data from the core databases.

In addition, an introduction will be given to the REST API, which recently has been developed to supplement the current Perl API to improve access to Ensembl data from other languages.

### **Prerequisites**

The prerequisite for this workshop is a working knowledge of Perl and molecular biology / genetics. A basic knowledge of Ensembl is advantageous, but not absolutely necessary. Participants without any knowledge of Ensembl are encouraged to attend the Ensembl Browser workshop.

