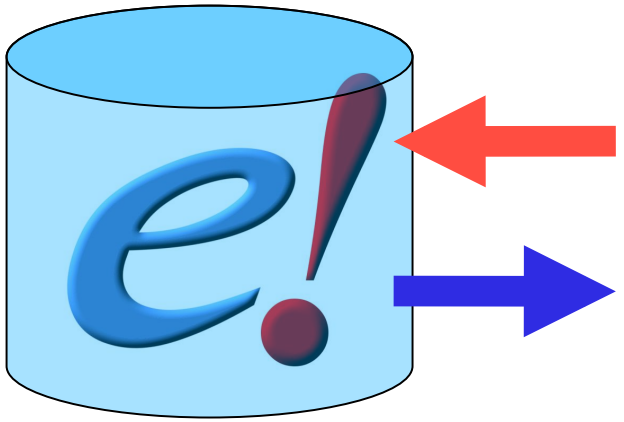
Ensembl Core API



EMBL-EBI

wellcome trust sanger institute

EMBL – European Bioinformatics Institute
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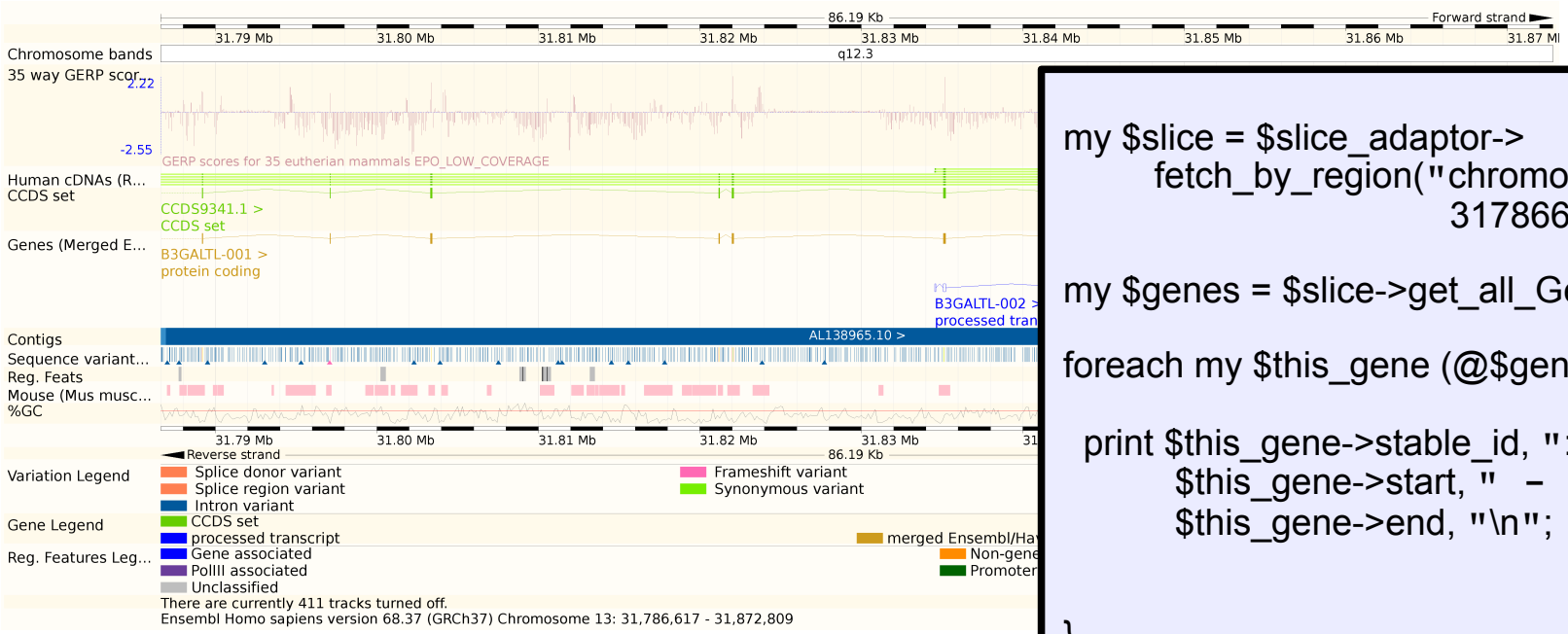
Outline

a. Introduction
b. Data objects & object adaptors
c. Ensembl documentation
d. The Registry & Ensembl API script design
e. Coordinate systems & slices
f. Features
g. Genes, transcripts, exons & translations
h. External references

Ensembl API

- Written in Object-Oriented Perl.
- Used to retrieve data from and to store data in Ensembl databases.
- Foundation for the Ensembl Pipeline and Ensembl Web interface.



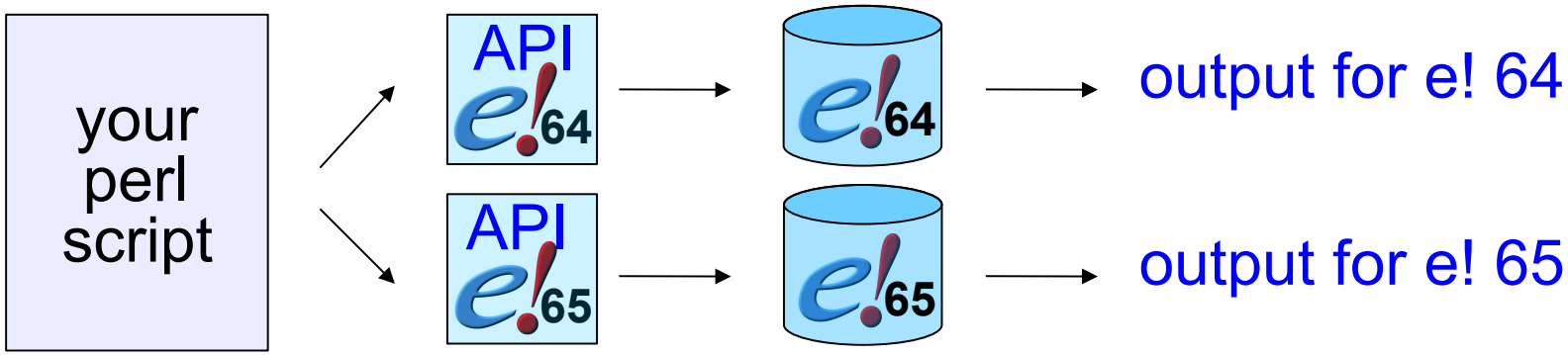

```
my $slice = $slice_adaptor->
        fetch_by_region("chromosome", "13",
                                31786617, 31872809);

my $genes = $slice->get_all_Genes();

foreach my $this_gene (@$genes) {

  print $this_gene->stable_id, ": ",
          $this_gene->start, "  -  ",
          $this_gene->end, "\n";


}
```

Why use an API?

- Uniform method of access to the data.
- Avoid writing the same thing twice: reusable in different systems.
- Reliable: lots of hard work, testing and optimisation already done.
- Insulates developers from underlying changes at a lower level (i.e. the database).

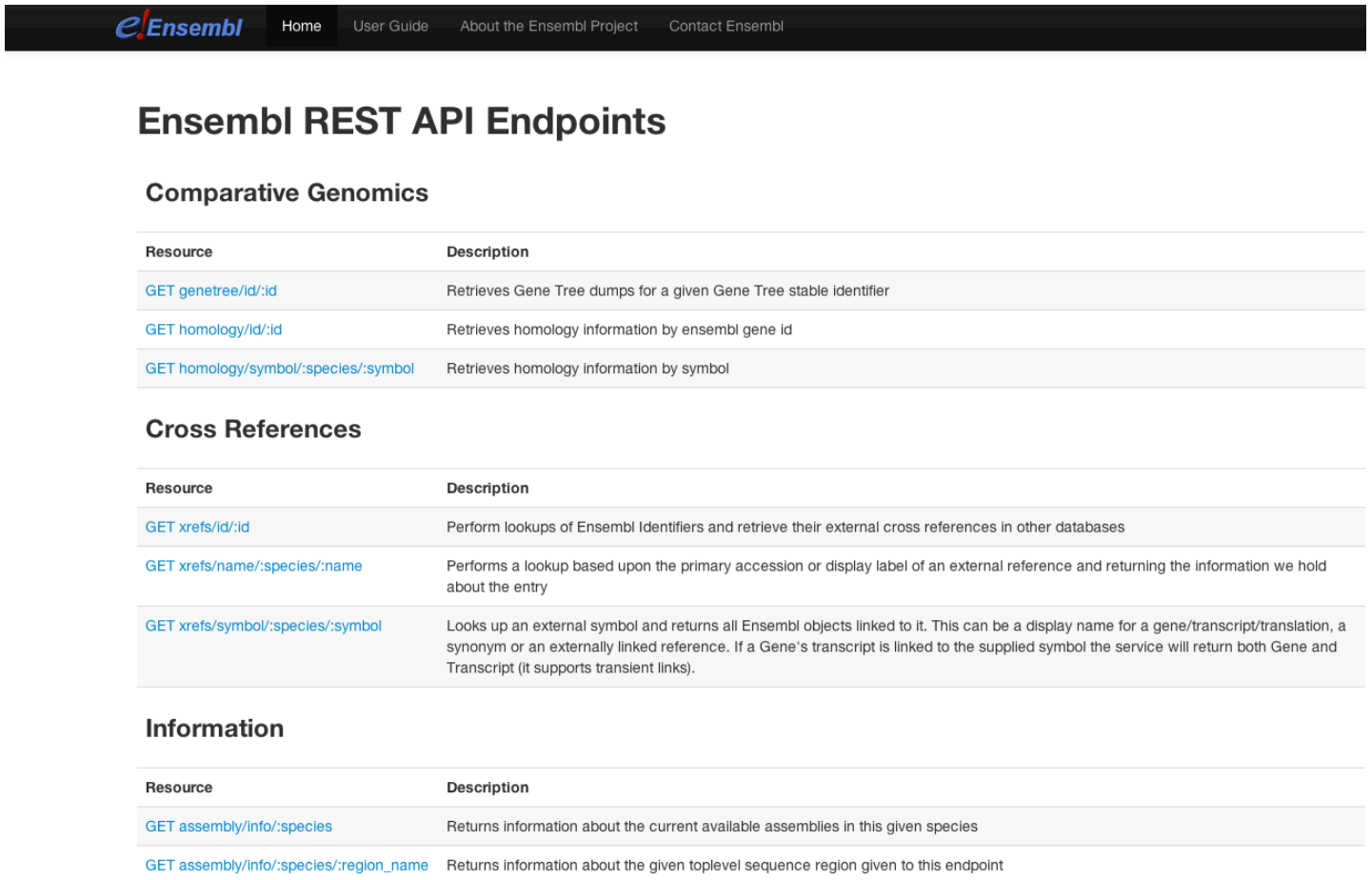
Using the correct API version

API version **must** match database version. Old scripts using the API *should* continue working with a newer API.



Run script ensembl/misc-scripts/ping_ensembl.pl to test if you can contact the Ensembl database server. The script will help you resolve issues with your setup.

An Alternative - REST



http://beta.rest.ensembl.org

Installing the Perl API from FTP

```
# cd to a location to install Ensembl to
mkdir src
cd src

# Get the latest API from FTP (always the live version) and BioPerl 1.2.3
wget ftp://ftp.ensembl.org/pub/ensembl-api.tar.gz
wget http://bioperl.org/DIST/old_releases/bioperl-1.2.3.tar.gz

# untar both
tar zxvf ensembl-api.tar.gz
tar zxvf bioperl-1.2.3.tar.gz

# open up .bashrc or .profile and add the following
PERL5LIB=${PERL5LIB}:${HOME}/src/bioperl-1.2.3
PERL5LIB=${PERL5LIB}:${HOME}/src/ensembl/modules
PERL5LIB=${PERL5LIB}:${HOME}/src/ensembl-compara/modules
PERL5LIB=${PERL5LIB}:${HOME}/src/ensembl-variation/modules
PERL5LIB=${PERL5LIB}:${HOME}/src/ensembl-functgenomics/modules
export PERL5LIB

# Checking your installation
perl $HOME/src/ensembl/misc-scripts/ping_ensembl.pl
```

Alternative Methods of Installation

- Ensembl tarball from http://cvs.sanger.ac.uk
  - Watch out for **&** character in Linux shells
- CVS checkout from cvs.sanger.ac.uk
- Ensembl Virtual Machine
  - ftp://ftp.ensembl.org/pub/current_virtual_machine
  - 64bit only in OVA format

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Ensembl API – Object Types

We have two main object types in Ensembl API:

1. Data Objects

   Talk to a particular row in a data table, such as the BRCA2 gene to get (or set) information related to this gene only.

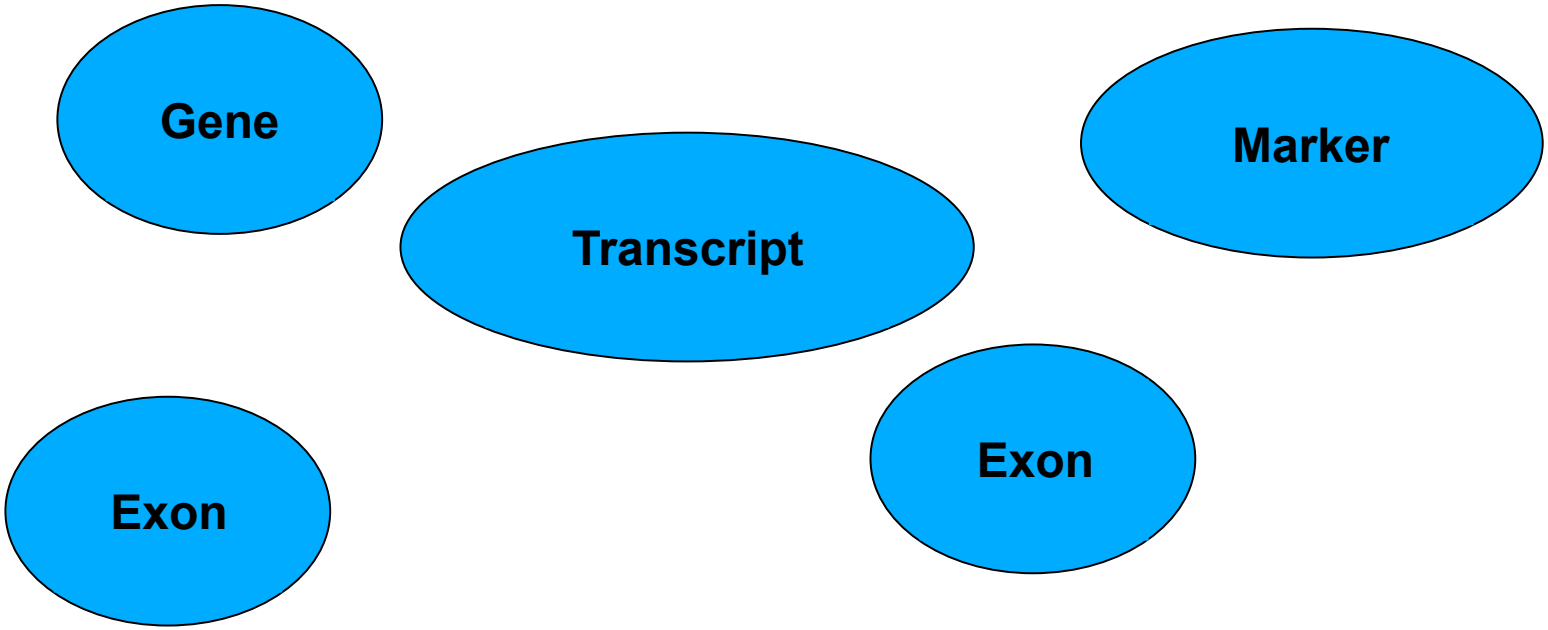
2. Object Adaptors

   Talk to a particular data table, such as the gene table to retrieve or store genes in the gene table.

Data Objects

Data objects model biological entities, e.g. genes, transcripts, exons…

A *Data Object* represents a piece of data that is (or can be) stored in the database.



Object Adaptors

Data Objects are retrieved from and stored in the database using ***Object Adaptors*.**

Each *Object Adaptor* is responsible for creating objects of only one particular type. For instance:

- The **Gene**Adaptor is used to fetch **Gene** objects
- The **Exon**Adaptor is used to fetch **Exon** objects

Object Adaptor *fetch*, *store*, and *remove* methods are used to retrieve, save, and delete information in the database.

Two types of methods:

- **fetch_by_....** returns 1 object (or undef)
- **fetch_all_by_...** returns a ref. to an array of objects (or ref. to an empty array)

Object methods in Ensembl API

An Object has attributes and methods.

We avoid accessing object attributes directly, we use methods instead.

Methods are called using the “arrow” (->) operator:

```
my $exons = $gene->get_all_Exons();
```

Many methods can be used to either get or set an attribute value:

GET (no arg.):

```
my $gene_id = $gene->stable_id( );
```

SET (new value):

```
$gene->stable_id(“ENSG00000000123152”);
```

Data Objects & Object Adaptors

```
# fetch a gene by its stable identifier using a gene
  adaptor

my $gene =
  $gene_adaptor->fetch_by_stable_id('ENSG00000139618');

# print out the name of a gene and its stable identifier

print $gene->external_name(), "\n";
print $gene->stable_id, "\n";
```

Ensembl Core modules

Name space for the modules:

- Object modules start with **Bio::EnsEMBL**
  - Bio::EnsEMBL::Gene for gene objects
  - Bio::EnsEMBL::Exon for exon objects
- ObjectAdaptors start with **Bio::EnsEMBL::DBSQL**
  - the GeneAdaptor is a Bio::EnsEMBL::DBSQL::GeneAdaptor
  - The ExonAdaptor is a Bio::EnsEMBL::DBSQL::ExonAdaptor

Naming conventions for the methods:

- For retrieving objects from the ObjectAdaptors:
  - fetch_by_ and fetch_all_by_
- For retrieving Objects attributes:
  - get_Object and get_all_Objects

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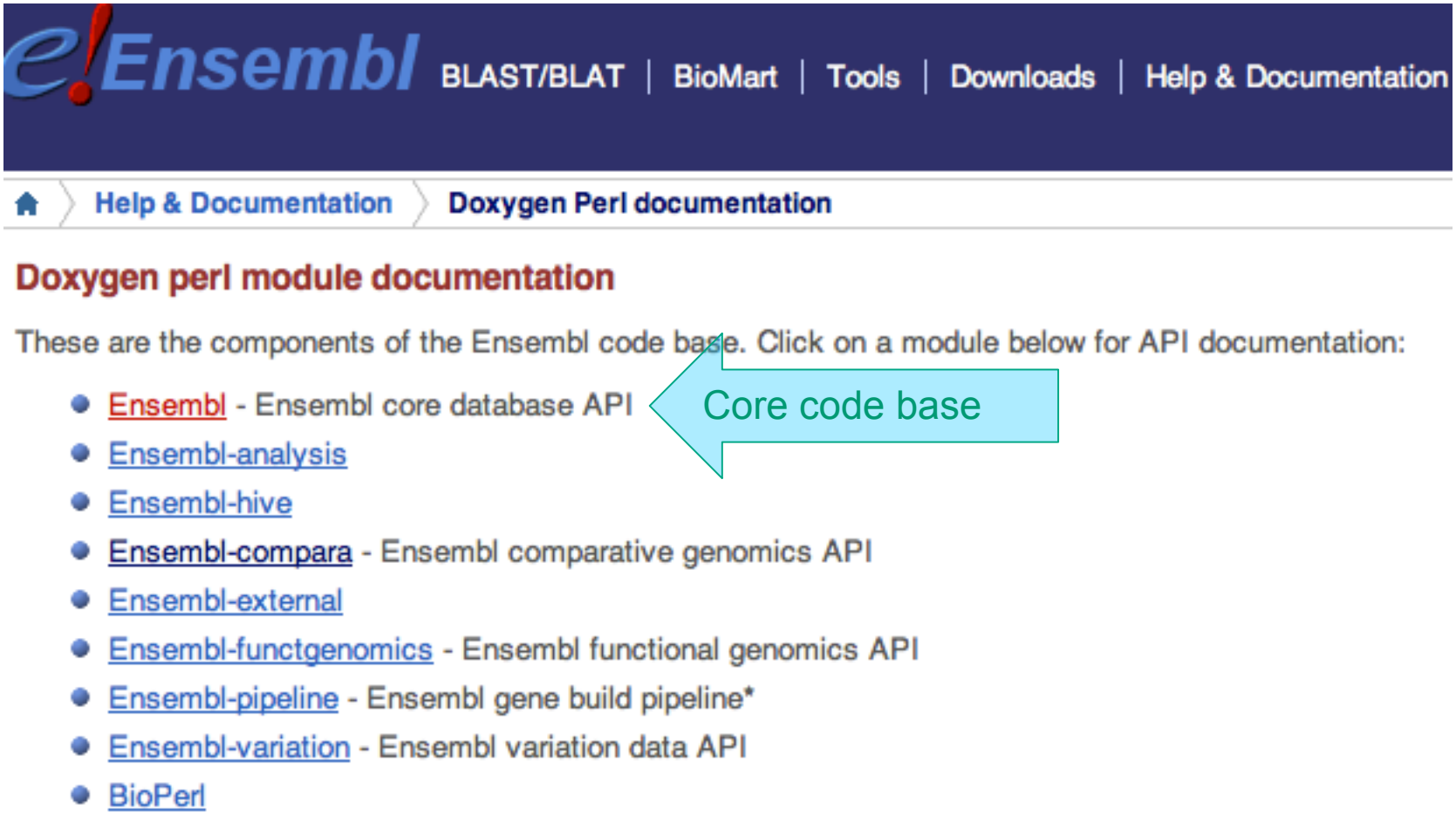
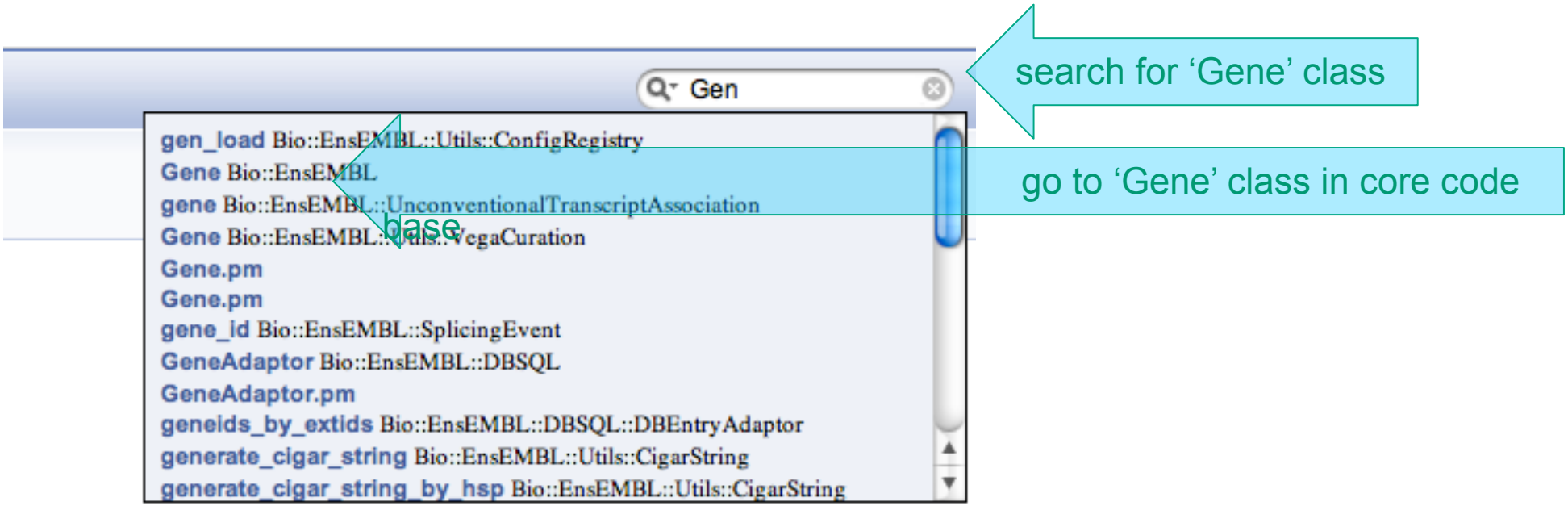
Ensembl API Documentation (1)

Go to http://www.ensembl.org/info/docs/Doxygen/index.html



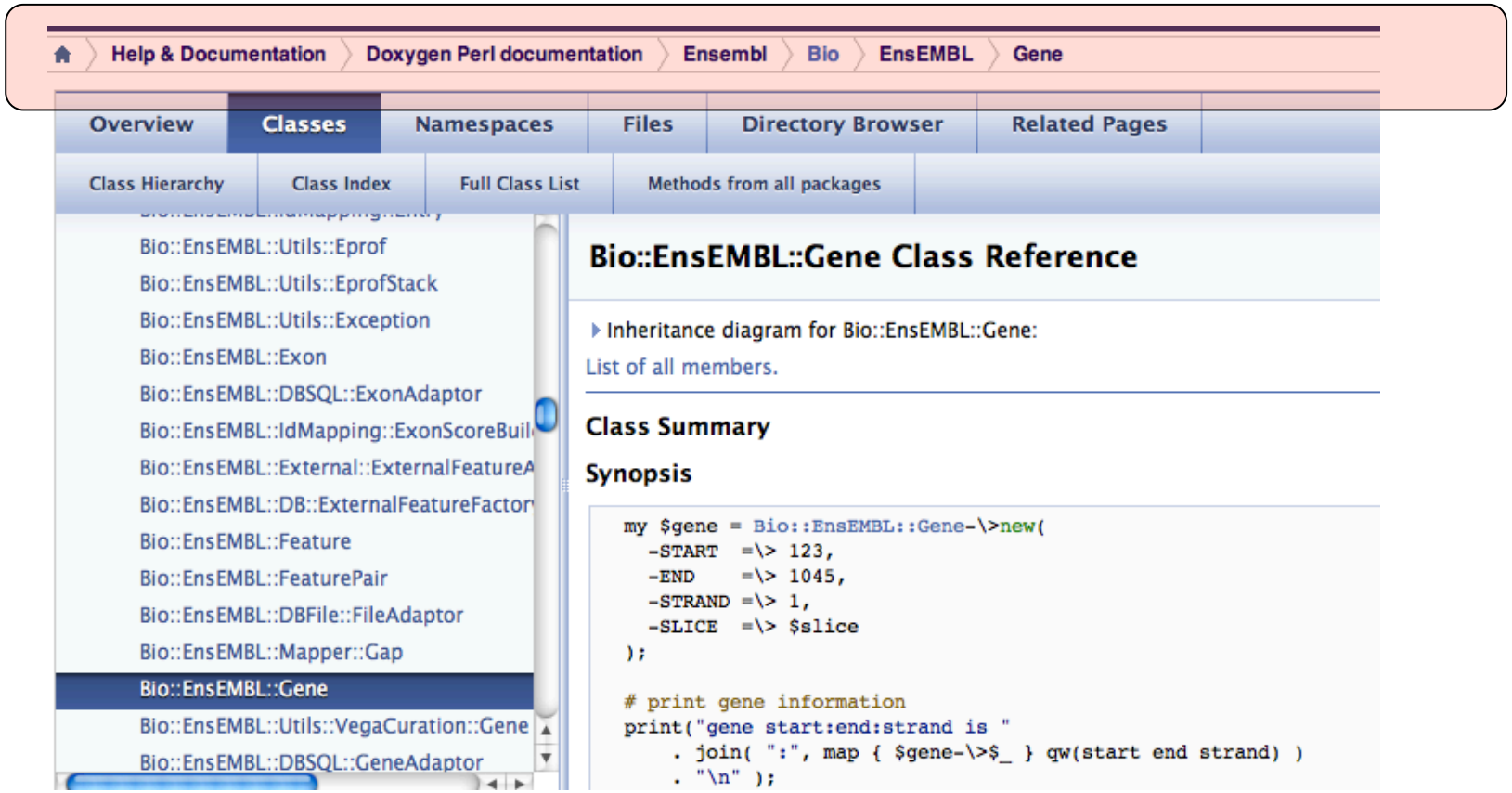
Ensembl API Documentation (2)

Search for classes or methods



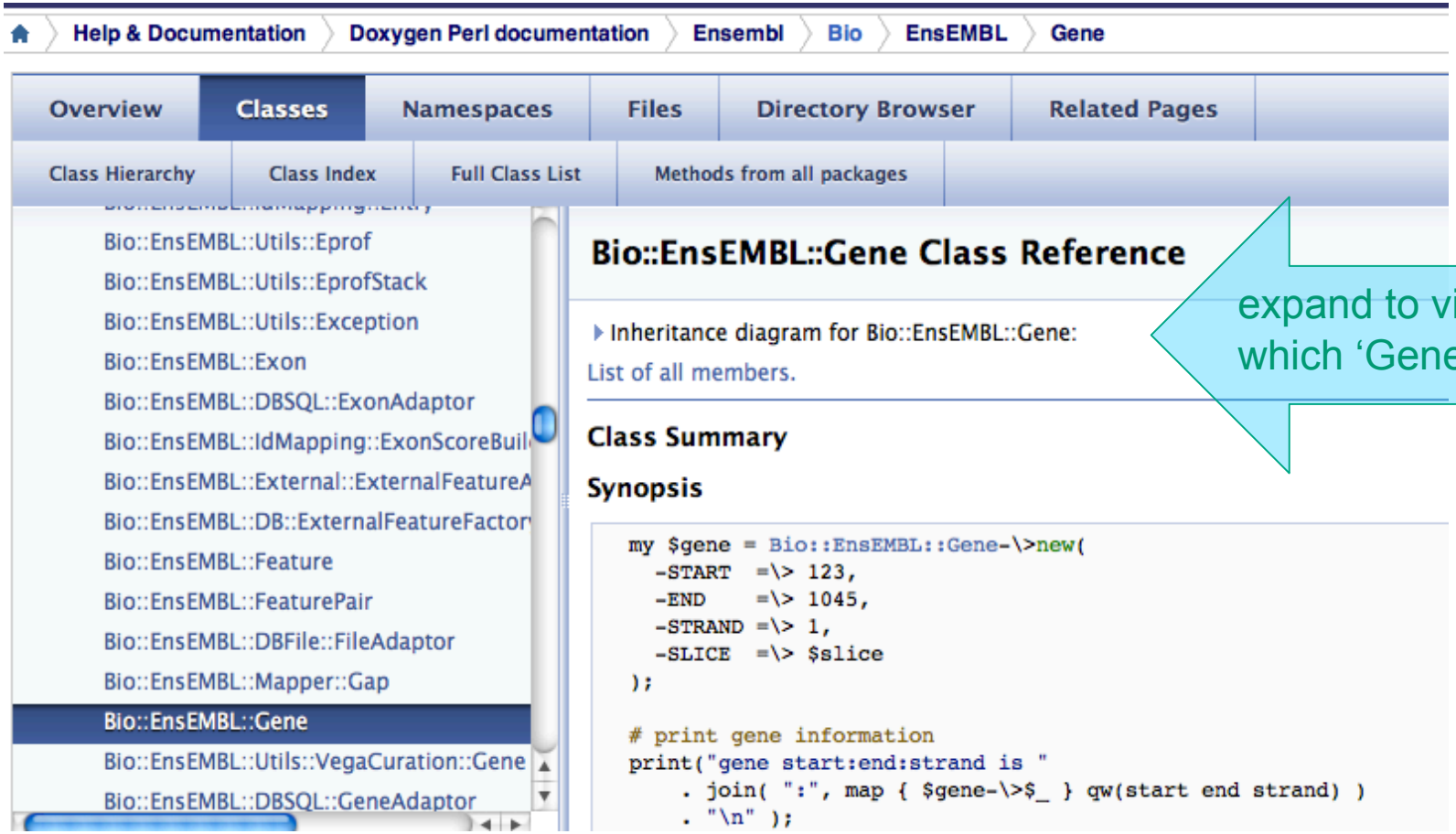
Ensembl API Documentation (3)

Breadcrumbs at the top of the page help you keep track of which code base you're in.



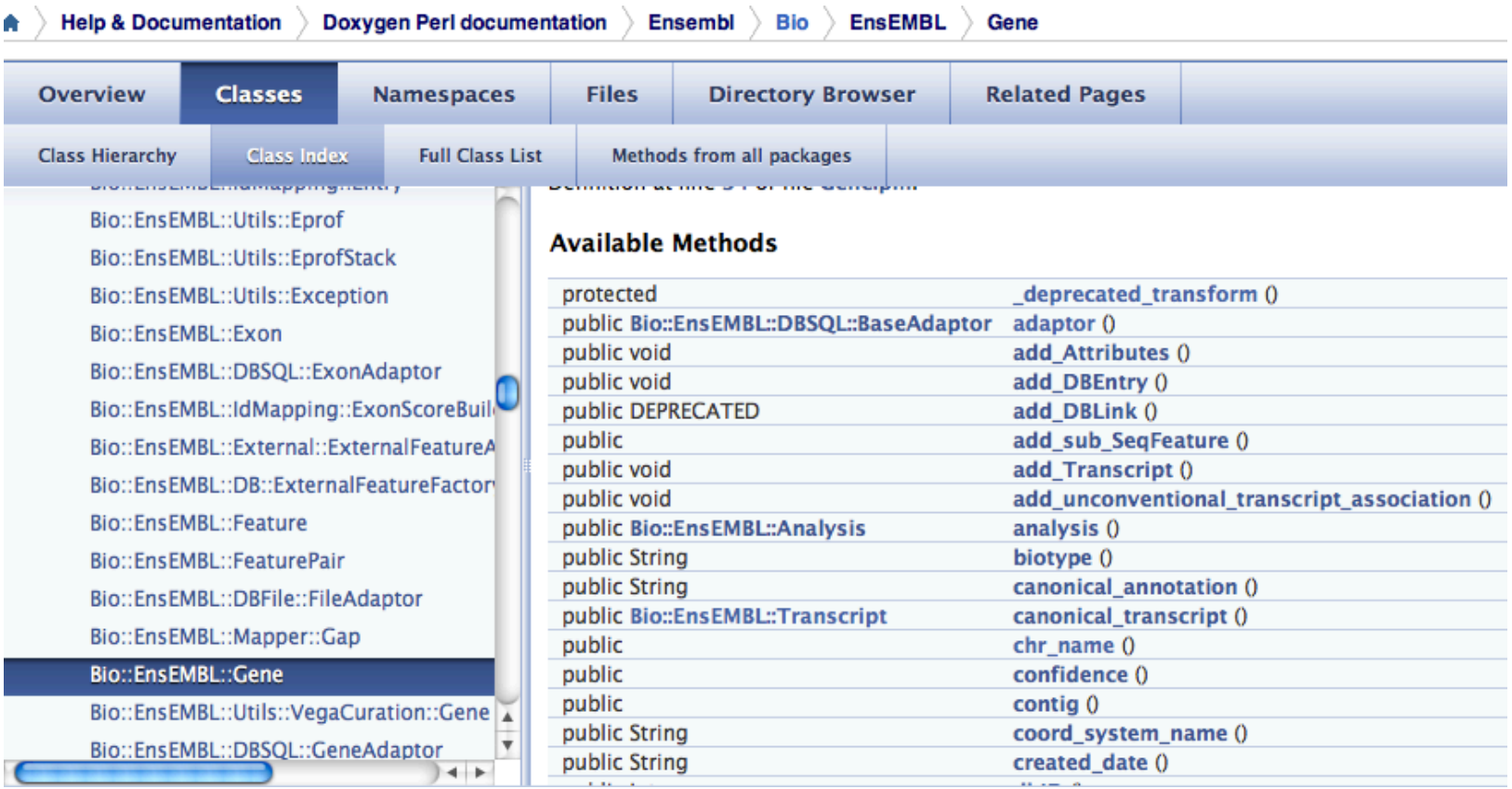
Ensembl API Documentation (4)

Classes can *inherit* attributes and methods from other classes. For instance a Gene is also a Feature as it can be located on a region of DNA so it inherits from the **Bio::EnsEMBL::Feature** object.



Ensembl API Documentation (5)

Scroll down to see a list of available methods in the ‘Gene’ class. Can you find a method to retrieve all transcripts for a gene? What variable type does this method return?



Ensembl API Documentation (6)

Clicking on a method takes you to a description with associated arguments, return types and exceptions.

public Bio::EnsEMBL::Slice Bio::EnsEMBL::Feature::slice ( )

```
Arg [1]     : (optional) Bio::EnsEMBL::Slice $slice
Example     :

  $seqname = $feature->slice()->name();

Description: Getter/Setter for the Slice that is associated with this
             feature.  The slice represents the underlying sequence that this
             feature is on.  Note that this method call is analagous to the
             old SeqFeature methods contig(), entire_seq(), attach_seq(),
             etc.
Returntype : Bio::EnsEMBL::Slice
Exceptions : thrown if an invalid argument is passed
Caller     : general
Status     : Stable
```

Code:
click to view
Reimplemented in Bio::EnsEMBL::Exon, and Bio::EnsEMBL::Map::DitagFeature.

Ensembl API Documentation (7)

Clicking on **Code:** shows the method's implementation

Code:

```
sub  slice  {
  my ( $self, $slice ) = @_;

  if ( defined($slice) ) {
    if (    !check_ref( $slice, 'Bio::EnsEMBL::Slice' )
         && !check_ref( $slice, 'Bio::EnsEMBL::LRGSlice' ) )
    {
      throw('slice argument must be a Bio::EnsEMBL::Slice');
    }

    $self->{'slice'} = $slice;
  } elsif ( @_ > 1 ) {
    delete($self->{'slice'});
  }

  return $self->{'slice'};
}
```

Reimplemented in Bio::EnsEMBL::Exon, and Bio::EnsEMBL::Map::DitagFeature.

Ensembl Core DB Documentation (1)

Go to http://www.ensembl.org/info/docs/api/core/core_schema.html

Ensembl Core - Schema documentation

This document gives a high-level description of the tables that make up the EnsEMBL core schema. Tables are grouped into logical groups, and the purpose of each table is explained. It is intended to allow people to familiarise themselves with the schema when encountering it for the first time, or when they need to use some tables that they've not used before.

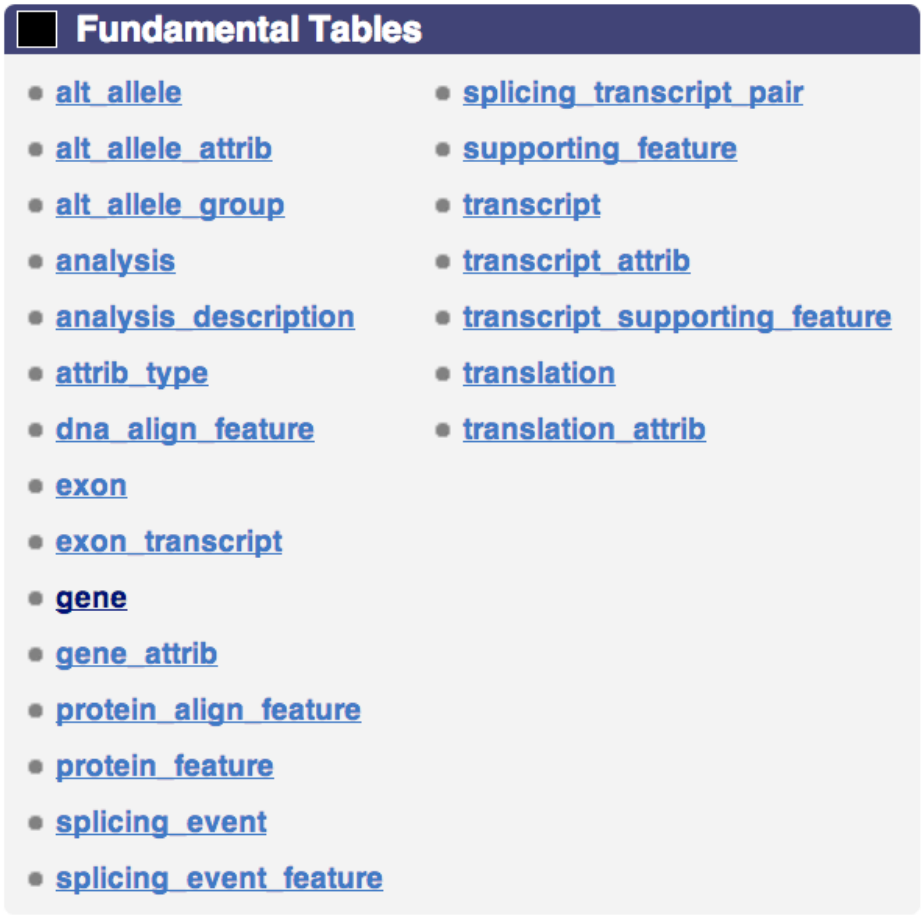
This document refers to version **73** of the EnsEMBL core schema.

The core database schema is available in several diagrams (PDF format) here:

List of the tables:

Ensembl Core DB Documentation (2)

Scroll down to the list of Fundamental Tables and click on the gene table.



Ensembl Core DB Documentation (3)

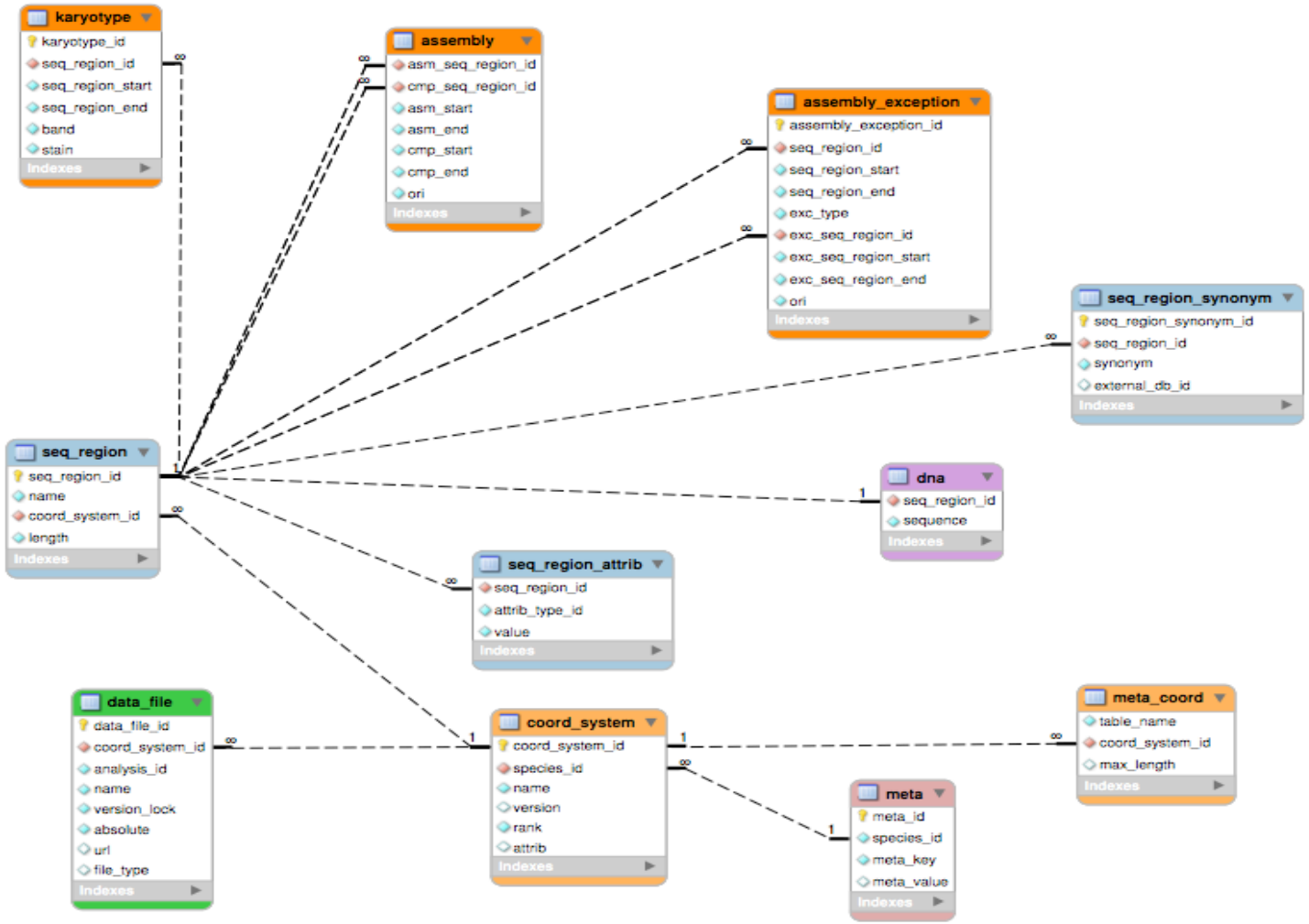
Click on the ‘show columns’ link to the right to expand a list of gene table columns, their types, descriptions and indices over the columns.

gene — Hide columns | [Back to top]

Allows transcripts to be related to genes.

Column	Type	Default value	Description
gene_id	INT(10)		Primary key, internal identifier.
biotype	VARCHAR(40)		Biotype, e.g. protein_coding.
analysis_id	SMALLINT		Foreign key references to the analysis table.
seq_region_id	INT(10)		Foreign key references to the seq_region table.
seq_region_start	INT(10)		Sequence start position.
seq_region_end	INT(10)		Sequence end position.
seq_region_strand	TINYINT(2)		Sequence region strand: 1 - forward; -1 - reverse.
display_xref_id	INT(10)		External reference for EnsEMBL web site. Foreign key re
source	VARCHAR(20)		e.g ensembl, havana etc.
status	ENUM('KNOWN', 'NOVEL', 'PUTATIVE', 'PREDICTED', 'KNOWN_BY_PROJECTION', 'UNKNOWN', 'ANNOTATED')		Status, e.g.'KNOWN', 'NOVEL', 'PUTATIVE', 'PREDICTED 'KNOWN_BY_PROJECTION', 'UNKNOWN'.
description	TEXT		Gene description

Ensembl Core DB Documentation (4)



Exercise 1

a) Find documentation for the Exon class in the Ensembl core code base. Which method would you use to retrieve the DNA sequence for an exon? What is the return type for this method?

b) Can you find a table which stores stable ids for transcripts? Which table stores DNA sequence? How many columns does this table have?

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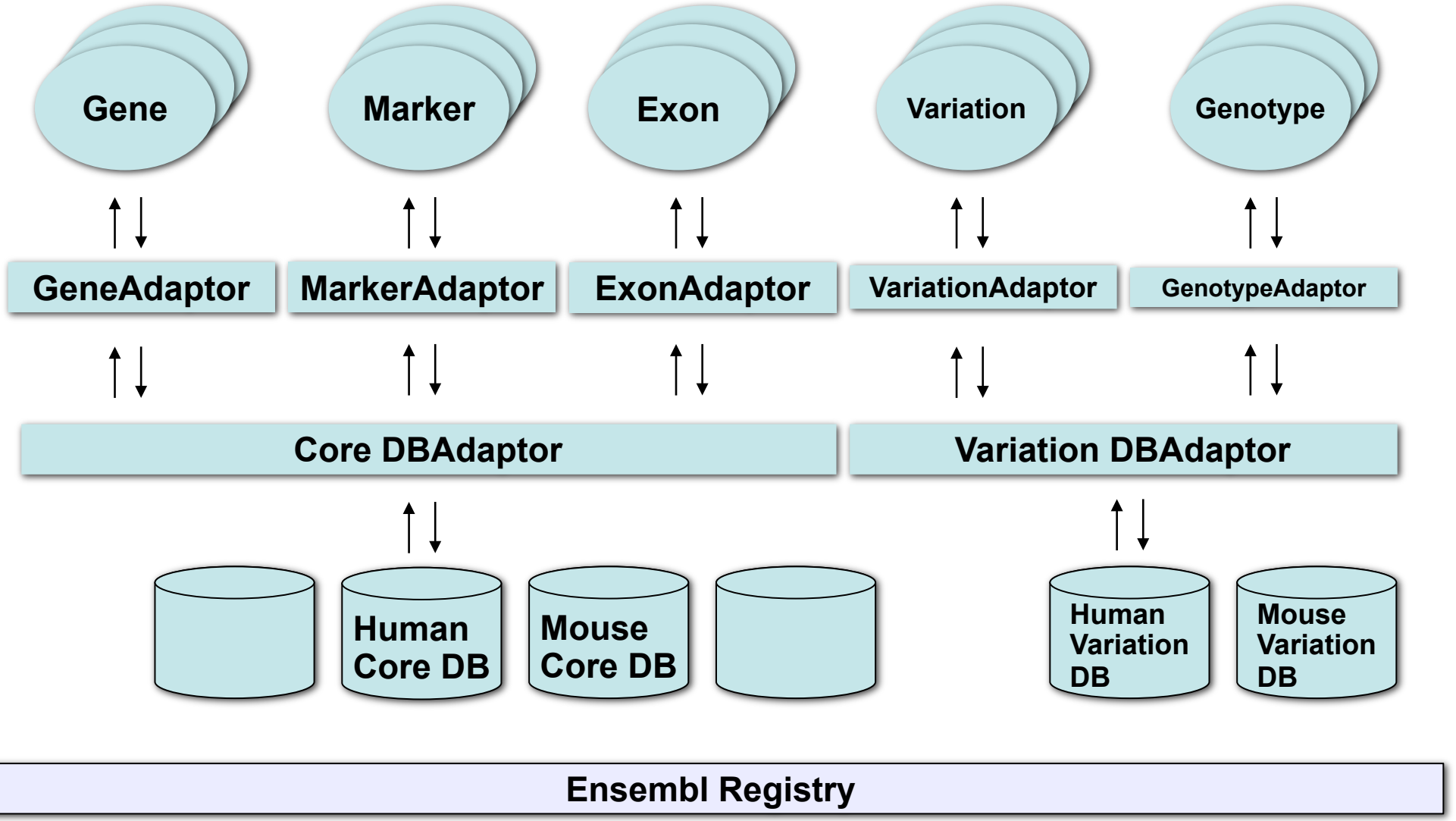
The Registry

We know how to use Data Objects and Object Adaptors.
How do we make sure we get those from the right database?
This is what we use the Registry for.

The Registry:

- loads all databases of the same version as the API
- lazy loads so no connections are made until requested

Ensembl API Architecture



The beginning of each script

```
#!/usr/bin/env perl

use strict;
use warnings;
use Bio::EnsEMBL::Registry;

my $registry = 'Bio::EnsEMBL::Registry';

$registry->load_registry_from_db(
    -host => 'ensembldb.ensembl.org',
    -user => 'anonymous'
);

my $gene_adaptor = $registry->get_adaptor('Human','Core','Gene');
```

Use ‘strict’ and ‘warnings’

species database object type

Connecting to Ensembl Genomes

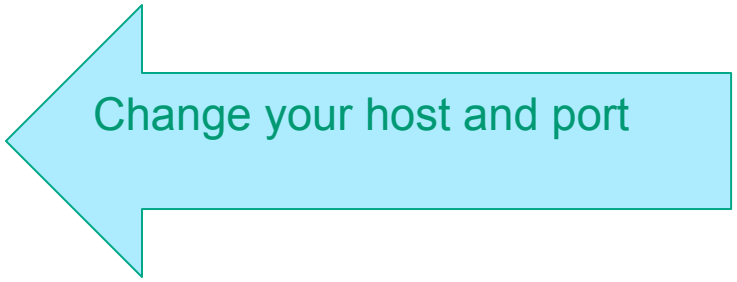
```
#!/usr/bin/env perl

use strict;
use warnings;
use Bio::EnsEMBL::Registry;

my $registry = 'Bio::EnsEMBL::Registry';

$registry->load_registry_from_db(
    -host => 'mysql.ebi.ac.uk',
    -port => 4157,
    -user => 'anonymous'
);

my $gene_adaptor = $registry->get_adaptor('silkmoth','Core', 'Gene');
```



species database object type

Exercise 2

Create a script which uses the method load_registry_from_db to load all databases into the Registry and prints the names of the databases loaded.

Hint: Have a look at the Doxygen documentation for the Registry object and method load_registry_from_db (http://www.ensembl.org/info/docs/Doxygen/index.html).

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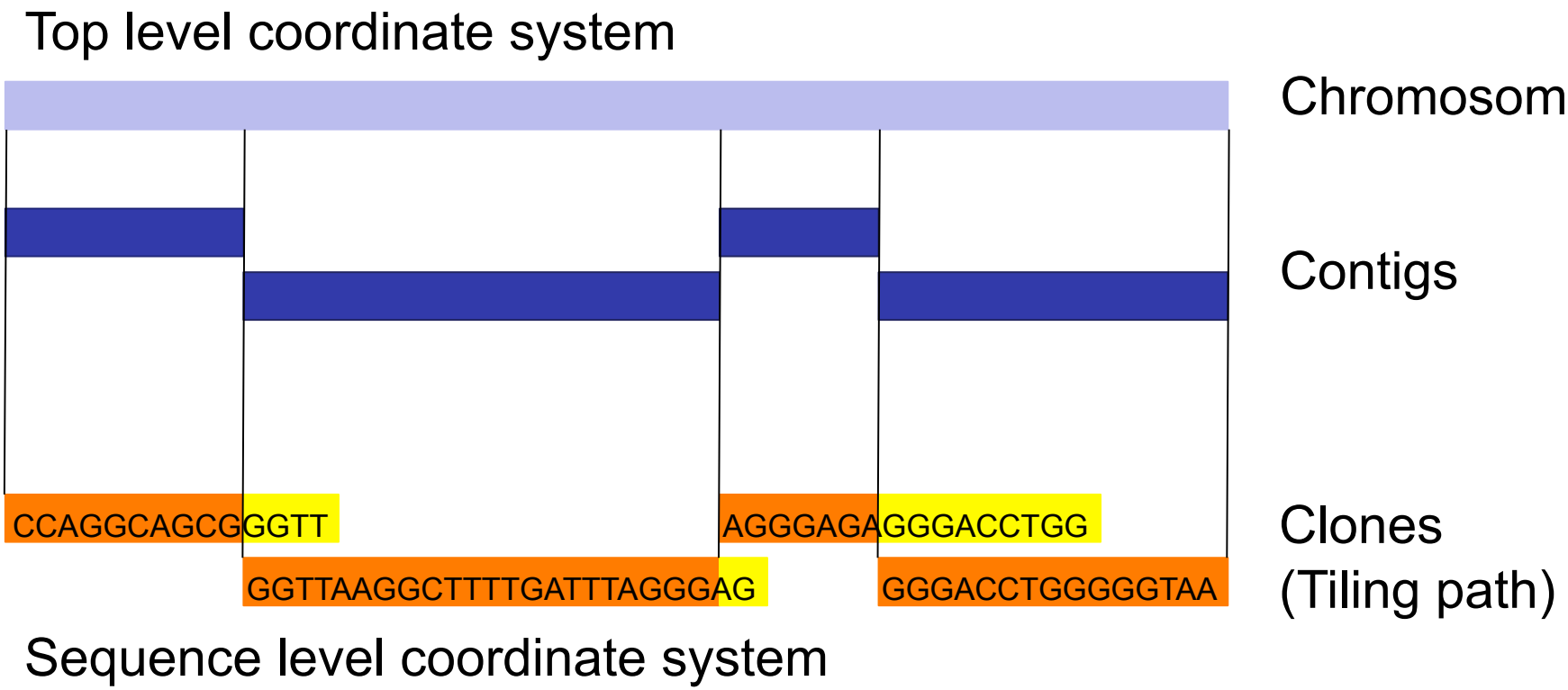
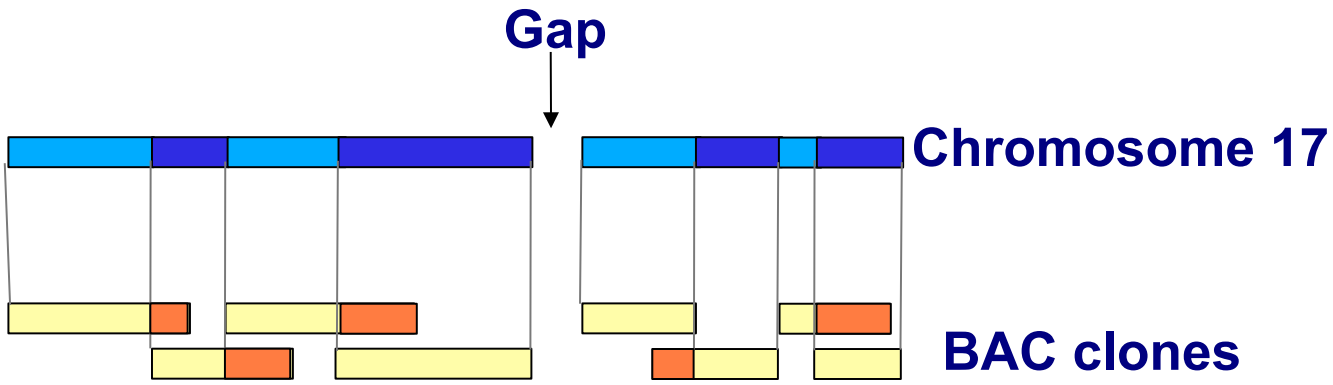
Coordinate Systems (1)

Ensembl stores features and DNA sequence in a number of coordinate systems.



Coordinate Systems (2)

Regions in one coordinate system may be constructed from a tiling path of regions from another coordinate system.



Coordinate Systems - Code Example

```
#   Obtain all coordinate systems for human

use Bio::EnsEMBL::Registry;
my $registry = 'Bio::EnsEMBL::Registry';

$registry->load_registry_from_db(
    -host => 'ensembldb.ensembl.org',
    -user => 'anonymous'
);
my $coordsystem_adaptor = $reg->get_adaptor( 'Human', 'Core', 'CoordSystem' );

my $coordsystems = $coordsystem_adaptor->fetch_all;

while ( my $coordsystem = shift @{$coordsystems} ){
    print $coordsystem->name, "\t",
          $coordsystem->version, "\t",
          $coordsystem->rank ,"\n";
}
```

Note use of ‘while’ and ‘shift’ instead of ‘foreach’ – more memory efficient way for large datasets

Coordinate Systems – Code Output

```
OUTPUT:
name                 version      rank

chromosome       GRCh37           1
supercontig      GRCh37           2
clone                             3

contig                            4

chromosome       NCBI36           5
chromosome       NCBI35           6
chromosome       NCBI34           7

lrg                               8
```

Latest assembly, top level

Latest assembly, sequence level

Old assemblies, used for mapping features between assembly versions.

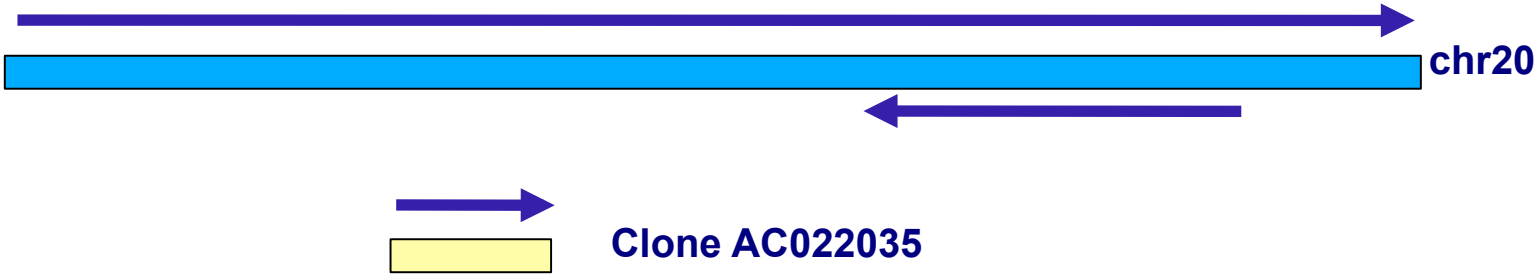
Locus-Reference Genes, used in clinical tests

Slices

A *Slice* Data Object represents an arbitrary region of a genome, a slice of a Sequence Region.

Slices are not directly stored in the database.

A *Slice* is used to request sequence or features from a specific region in a specific coordinate system.



Slices - Code Example (1)

```
# get a slice covering the entire human Y chromosome

my $slice_adaptor = $registry->get_adaptor( 'Human', 'Core', 'Slice' );
my $slice = $slice_adaptor->fetch_by_region( 'chromosome', 'Y' );
print  "Coord system:\t", $slice->coord_system_name, "\n",
           "Seq region:\t", $slice->seq_region_name, "\n",
           "Start:\t\t", $slice->start,"\n",
           "End:\t\t", $slice->end,"\n",
        "Strand:\t\t", $slice->strand,"\n",
        "Slice:\t\t", $slice->name, "\n";
```

OUTPUT:

```
Coord system:   chromosome
Seq region:     Y
Start:          1
End:                59373566
Strand:         1
Slice:          chromosome:GRCh37:Y:1:59373566:1
```

Slices - Code Example (2)

```
# get the slice adaptor
$slice_adaptor = $reg->get_adaptor('human', 'core', 'slice');

# fetch a slice on a region of chromosome 12
$slice = $slice_adaptor->fetch_by_region('chromosome', '12',
                                         1e6, 2e6);


# print out the sequence from this region
print $slice->seq, "\n";

# get all clones in the database and print out their names
@slices = @{ $slice_adaptor->fetch_all('clone') };
foreach $slice (@slices) {
  print $slice->seq_region_name, "\n";
}
```

Exercise 3

(a) Fetch all chromosomes for human. Determine their number and print the name and length for each of them. *The number of chromosomes is probably not what you would expect! Why is this?*

(b) Use the gene stable id 'ENSG00000101266' to fetch a slice surrounding this gene with 2kb of flanking sequence.

(a)hint: use the Ensembl API documentation to find an appropriate method in SliceAdaptor class which retrieves a slice given a gene stable id (pay attention to the method's arguments)

(c) Fetch the sequence of the first 10MB of chromosome 20 and write it to a file in FASTA format. Print the number of genes in this region.

- ✓ hint: Slice objects inherit from Bio::Seq so can be written to file easily using Bio::SeqIO, e.g.:

```
my $output = Bio::SeqIO->new( -file=>'>filename.fasta',
   -format=>'Fasta');
$output->write_seq($slice);
```

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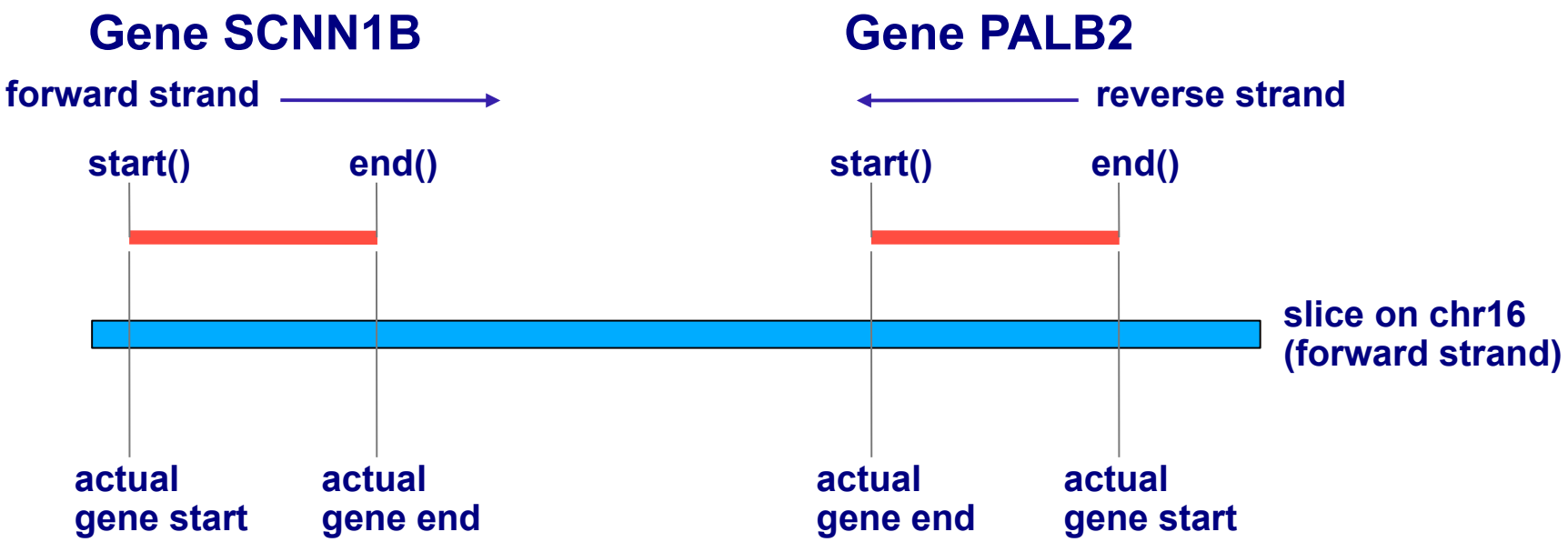
Features (1)

Features have a defined location on the genome and are stored in a single coordinate system

All *Features* have a *start*, *end*, *strand* and *slice*

Start and *end* are plotted onto the forward strand: start < end

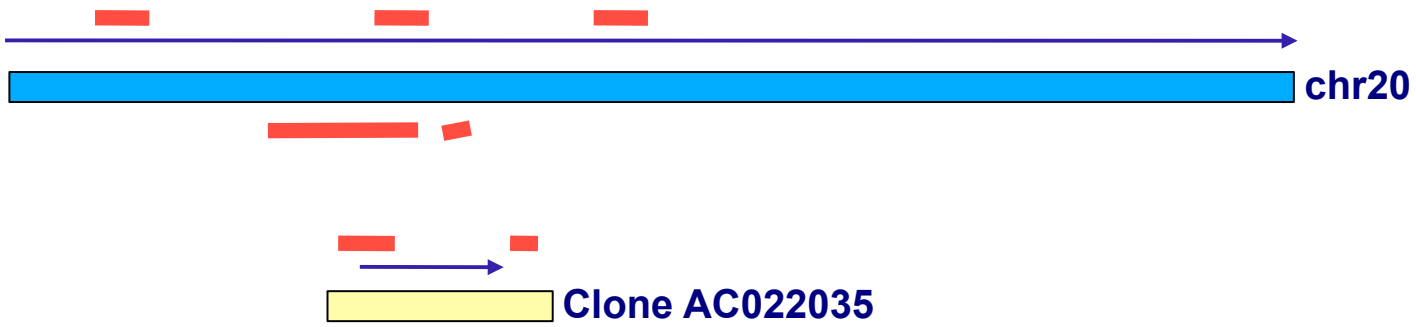


Features (2)

slice method returns the Slice object with which the *Feature* is associated

feature_Slice method returns the *Slice* object which covers the *Feature*

Features are retrieved from Object Adaptors using identifiers or regions (slices).



Features Objects – Biological Correspondence

Object	Biological entity
Gene, Transcript, Exon	**Ensembl gene models**
PredictionTranscript, PredictionExon	Genscan gene models
DNAAlignFeature, ProteinAlignFeature	cDNAs, proteins
RepeatFeature	**repeats**
MarkerFeature	markers
OligoFeature	microarray probes
KaryotypeBandFeature	cytogenetic bands
SimpleFeature	results of cpg, Eponine, FirstEF and tRNAscan
MiscFeature	clones, ENCODE regions
ProteinFeature	protein domains

Exercise 4

(a) Get all the repeat features from chromosome 20:1-500k. Print out the name and position of each on the chromosome and the total number.

- hint: create a slice, retrieve repeat features on this slice

(b) Find which genomic region the RefSeq dna entry NM_000059.3 was mapped to. Print the name of the region and coordinates of the alignment on the genome as well as the name of the region and coordinates of the alignment on the RefSeq dna entry. Print the score and percentage identity for the alignment.

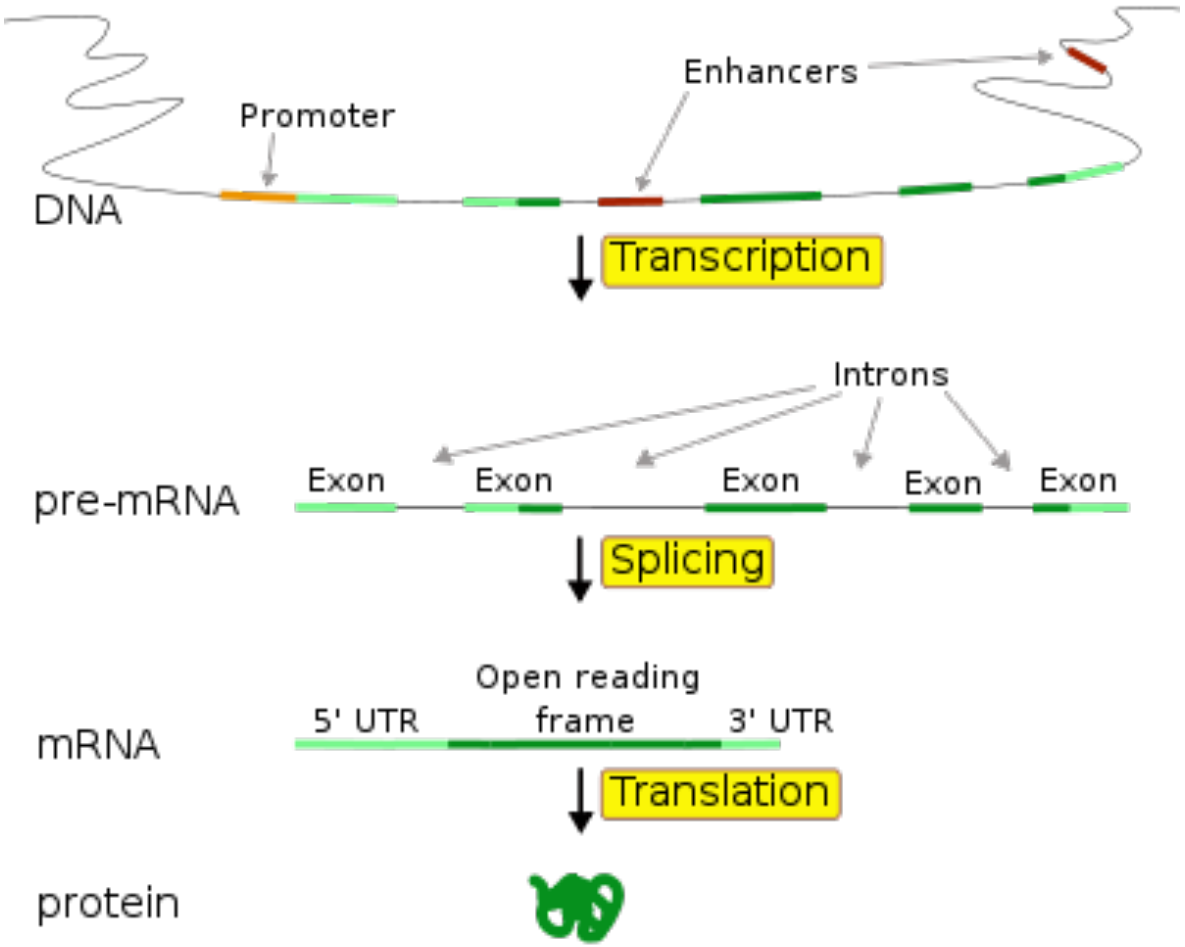
- ✓ hint: use DnaAlignFeatureAdaptor; use the core schema documentation as a guide to appropriate methods which correspond to columns in dna_align_feature table

A list of useful Feature methods is in the Appendix at the end of the presentation slides

Outline

a. Introduction
b. Data objects & object adaptors
c. Ensembl documentation
d. The Registry & Ensembl API script design
e. Coordinate systems & slices
f. Features
g. Genes, transcripts, exons & translations
h. External references

Genes, transcripts, exons & translations



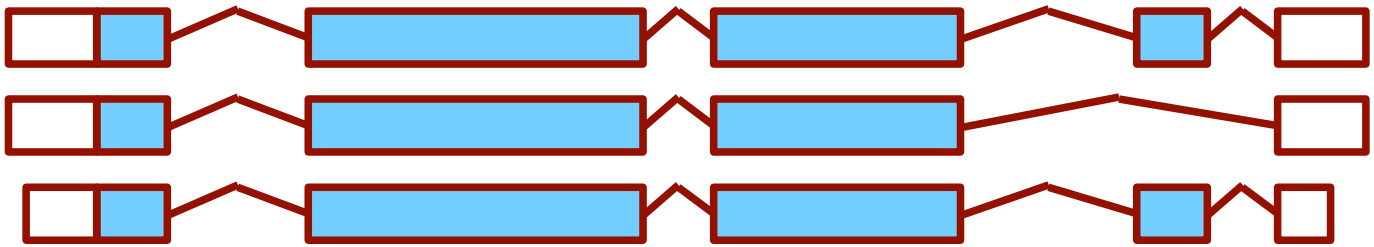
Genes, Transcripts and Exons

Genes, Transcript and Exons are objects that can be used just like any other Feature object

A Gene is a set of alternatively spliced Transcripts

A Transcript is a set of Exons

Introns are not explicitly defined in the database



Genes, Transcripts, Exons – Code Output

```
# helper function: returns location and stable_id string for a feature
sub get_string {
  my $feature = shift;
  my $stable_id  = $feature->stable_id;
  my $seq_region = $feature->slice->seq_region_name;
  my $start = $feature->start;
  my $end = $feature->end;
  my $strand = $feature->strand;
  return "$stable_id  $seq_region:$start-$end($strand)";
}
# fetch a gene by its stable identifier
my $gene = $gene_adaptor->fetch_by_stable_id('ENSG00000123427');

# print out the gene, its transcripts, and its exons
print "Gene: ", get_string($gene), "\n";
foreach my $transcript (@{ $gene->get_all_Transcripts }) {
  print "  Transcript: ", get_string($transcript), "\n";
  foreach my $exon (@{ $transcript->get_all_Exons }) {
    print "    Exon: ", get_string($exon), "\n";
  }
}
```

Genes, Transcripts, Exons – Code Output

OUTPUT:

```
Gene: ENSG00000123427  12:58165275-58176324(1)
  Transcript: ENST00000548256  12:58165275-58174213(1)
    Exon: ENSE00002360002  12:58165275-58165408(1)
    Exon: ENSE00003090890  12:58166800-58166911(1)
    Exon: ENSE00003030714  12:58168412-58168550(1)
    Exon: ENSE00002406112  12:58174038-58174213(1)
  Transcript: ENST00000551420  12:58165983-58174563(1)
    Exon: ENSE00002355737  12:58165983-58166180(1)
    Exon: ENSE00003223131  12:58166800-58166911(1)
    Exon: ENSE00002376752  12:58174038-58174563(1)
  Transcript: ENST00000300209  12:58166383-58176186(1)
    Exon: ENSE00002301479  12:58166383-58166684(1)
    Exon: ENSE00003090890  12:58166800-58166911(1)
    Exon: ENSE00002393444  12:58174038-58176186(1)
                                                    etc.
```

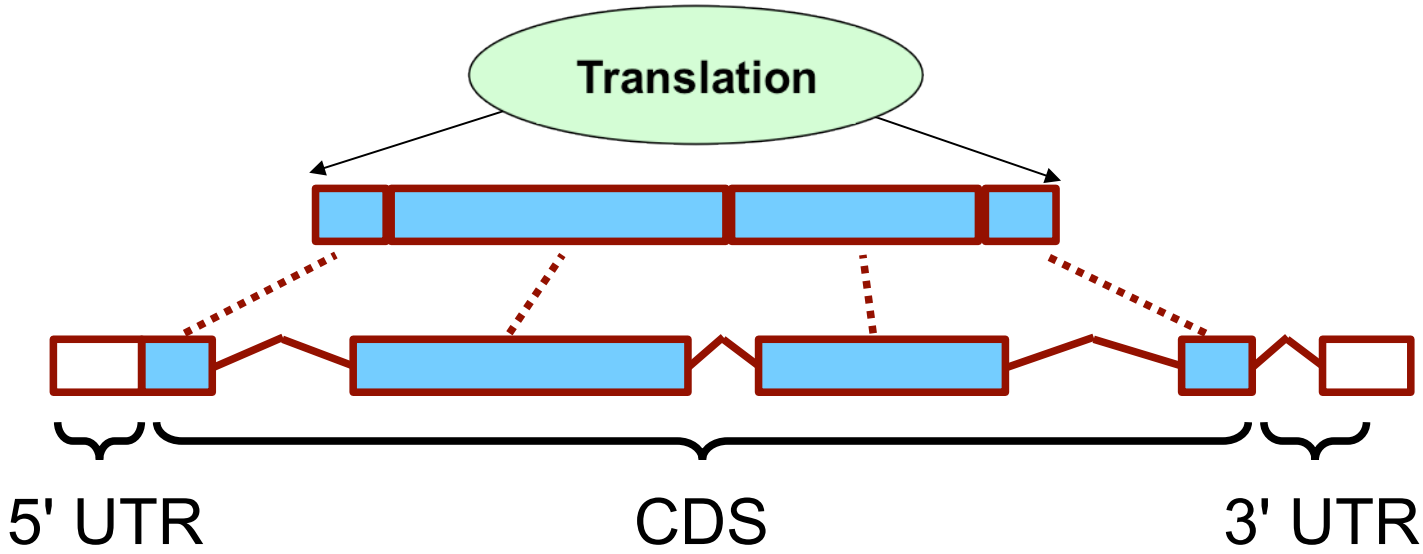
Translations

Translations are not Features.

A Translation object defines the UTR and CDS of a Transcript.

Peptides are not stored in the database, they are computed on the fly using Transcript objects.

Not all transcripts have a translation (e.g. ncRNAs)



Translations – Code Example

```
my $transcript_adaptor = $registry->get_adaptor( 'Homo sapiens', 'Core',
    'Transcript' );
# fetch a transcript from the database
my $transcript =
  $transcript_adaptor->fetch_by_stable_id('ENST00000333012');

# obtain the translation of the transcript
my $translation = $transcript->translation;

# print out the translation info
print "Translation: ", $translation->stable_id, "\n";
print "Start Exon: ",$translation->start_Exon->stable_id,"\n";
print "End Exon:   ", $translation->end_Exon->stable_id, "\n";

# cDNA start and end (spliced sequence with UTR)
print "Start : ", $translation->cdna_start, "\n";
print "End   : ", $translation->cdna_end, "\n";

# print the peptide which is the product of the translation
print "Peptide : ", $transcript->translate->seq, "\n";
```

Translations – Code Output

OUTPUT:

```
Translation: ENSP00000327425
Start Exon: ENSE00002340145
End Exon:   ENSE00002428887
Start : 48
End   : 497
Peptide :
   MADPGPDPESESESVFPREVGLFADSYSEKSQFCFCGHVLTITQNFGSRLGVAARVWDAALSLCNYFESQNVDFR
   GKKVIELGAGTGIVGILAALQGAYGLVRETEDDVIEQELWRGMRGACGHALSMSTMTPWESIKGSSVRGGCYHH
```

Exercise 5

(a) Fetch gene ‘CSNK2A1’and print the number of its transcripts and exons.

- ✓ hint: use GeneAdaptor method fetch_by_display_label; remember that not all transcripts have a translation

Gene: CSNK2A1 ENSG00000101266

Description	casein kinase 2, alpha 1 polypeptide [Source:HGNC Symbol;Acc:2457]
Location	Chromosome 20: 459,116-524,482 reverse strand.
Transcripts ⊟	This gene has 5 transcripts

Show/hide columns Filter

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
CSNK2A1-001	ENST00000349736	4299	ENSP00000339247	391	Protein coding	CCDS13003
CSNK2A1-002	ENST00000217244	4416	ENSP00000217244	391	Protein coding	CCDS13003
CSNK2A1-201	ENST00000400217	2507	ENSP00000383076	255	Protein coding	CCDS13004
CSNK2A1-202	ENST00000400227	1483	ENSP00000383086	385	Protein coding	-
CSNK2A1-003	ENST00000460062	768	No protein product	-	Processed transcript	-

(b) For the above gene, get all the transcripts and list the number of exons in each and the translations.

(c) Why do the exon numbers not match?

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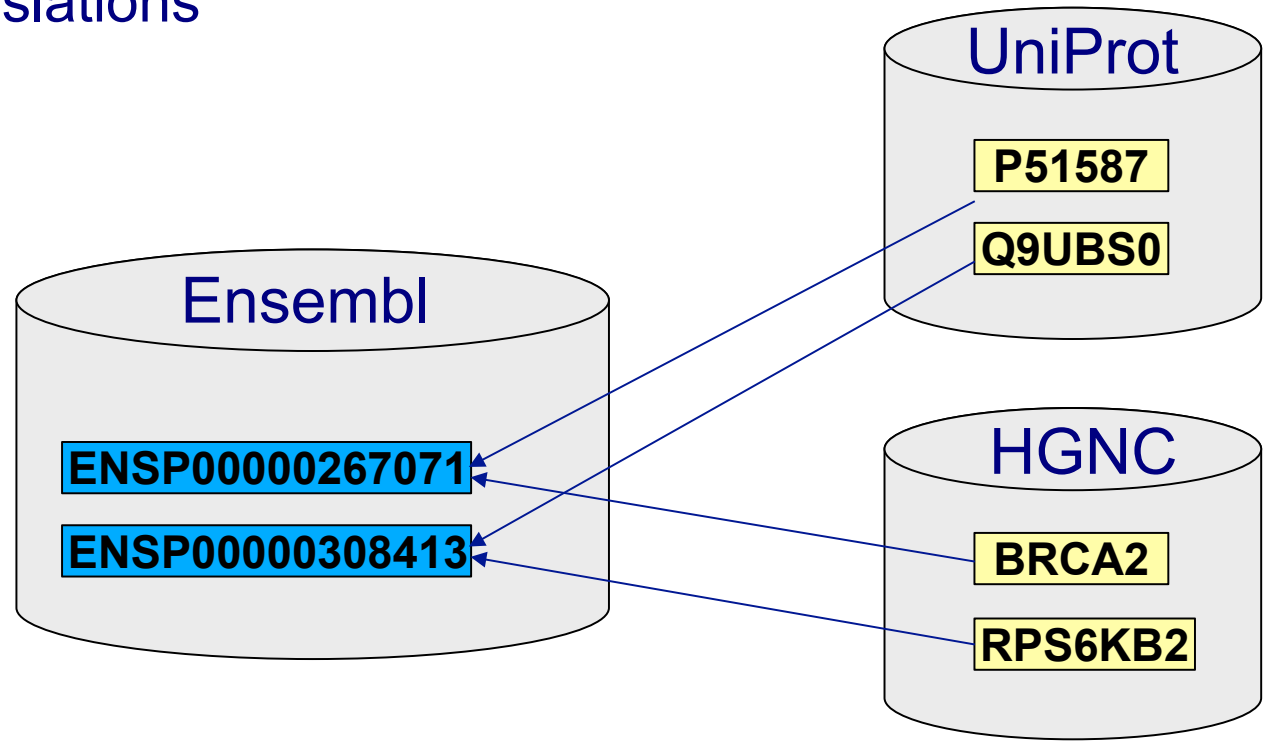
External References

Ensembl cross references its Gene models with identifiers from other databases, such as HGNC, WikiGenes, UniProtKB/Swiss-Prot, RefSeq, MIM etc.

External References (Xrefs) can be linked to genes, transcripts or translations



Xrefs - Code Example (1)

```
# Obtain external references for Ensembl gene ENSG00000139618

my $gene = $gene_adaptor->fetch_by_stable_id( 'ENSG00000139618' );

my $gene_xrefs = $gene->get_all_DBEntries;
print "Xrefs on gene level: \n\n";

foreach my $gene_xref( @{$gene_xrefs} ){
  print $gene_xref->dbname, ":", $gene_xref->display_id, "\n";
}

my $all_xrefs = $gene->get_all_DBLinks;

print "\nXrefs on gene, transcript and protein level: \n\n";
foreach my $all_xref( @{$all_xrefs} ){
  print $all_xref->dbname, ":", $all_xref->display_id, "\n";
}
```

this method will only return xrefs linked to the object it's called on (e.g. gene)

this method will return xrefs on all levels (gene, transcript and translation)

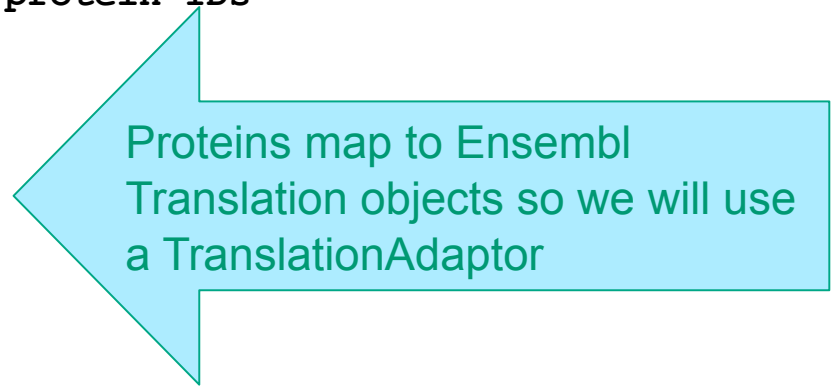
Xrefs – Code Output (1)

OUTPUT:

```
Xrefs on gene level:

OTTG:OTTHUMG00000017411
ArrayExpress:ENSG00000139618
EntrezGene:BRCA2
HGNC:BRCA2
MIM_MORBID: BREAST CANCER [#114480]
MIM_MORBID: FANCONI ANEMIA, COMPLEMENTATION GR [#227650]
MIM_MORBID: FANCONI ANEMIA, COMPLEMENTATION GR [#605724]
MIM_MORBID: BREAST-OVARIAN CANCER, FAMILIAL, S [#612555]
MIM_MORBID: GLIOMA SUSCEPTIBILITY 3 [#613029]
MIM_MORBID: PANCREATIC CANCER, SUSCEPTIBILITY  [#613347]]
MIM_GENE: BRCA2 GENE [*]
Orphanet:Hereditary breast and ovarian cancer syndrome
Orphanet:Familial prostate cancer
Orphanet:Fanconi anemia
Orphanet:Familial pancreatic carcinoma
UniGene:Hs.34012
Uniprot_genename:BRCA2
WikiGene:BRCA2
DBASS3:BRCA2
DBASS5:BRCA2

Xrefs on gene, transcript and translation level:
(same as on gene level + transcript and translation
    level)

CCDS:CCDS9344.1
Uniprot/SWISSPROT:BRCA2_HUMAN
RefSeq_peptide:NP_000050.2
RefSeq_mRNA:NM_000059.3
Vega_transcript:BRCA2-001
Vega_transcript:OTTHUMT00000046000
Uniprot/SPTREMBL:E9PIQ1_HUMAN
Uniprot/SPTREMBL:K4JTT2_HUMAN
Uniprot/SPTREMBL:K4JXT6_HUMAN
Uniprot/SPTREMBL:K4K7W0_HUMAN
Uniprot/SPTREMBL:Q8IU64_HUMAN
Uniprot/SPTREMBL:Q8IU77_HUMAN
Uniprot/SPTREMBL:Q8IU82_HUMAN
Uniprot/SPTREMBL:Q9H4L3_HUMAN
UCSC:uc001uub.
                                                etc.
```

Xrefs - Code Example (2)

```
# Retrieve Ensembl IDs for a list of UniProt protein IDs

my $translation_adaptor
  = $registry->get_adaptor(
    'Human','Core','Translation');


my @uniprot_ids = qw(P51587 P15056 B8A597 B8A595 B7ZW72);

foreach my $uniprot_id (@uniprot_ids){

  my @trans = @{
   $translation_adaptor->fetch_all_by_external_name($uniprot_id,'Uniprot%')
  };

  foreach my $translation (@trans){
    print $translation->stable_id."\t".$uniprot_id."\n";
  }
}
```



Xrefs – Code Output (2)

OUTPUT:

```
ENSP00000369497   P51587
ENSP00000439902   P51587
ENSP00000288602   P15056
ENSP00000387217   B8A597
ENSP00000386781   B8A595
ENSP00000442513   B7ZW72
ENSP00000307640   B7ZW72
```

Cross references can map to more than one Ensembl identifier

Exercise 6

Retrieve a list of GO term IDs and term names linked to the gene with stable id ‘ENSG00000139618’

- ✓ Use *get_all_DBLinks* with an external database name argument to restrict the number of xrefs returned
- ✓ Ontology term data such as term name and definition are stored outside of the core database. Create an OntologyTerm Adaptor with the help of the Registry method *get_adaptor* using arguments: ‘Multi’ (species), ‘Ontology’ (database type), ‘OntologyTerm’ (adaptor type)
- ✓ For all xrefs returned by *get_all_DBLinks* use the OntologyTerm Adaptor to fetch the relevant term and print its accession and name (xref display_id is the same as term accession)

Recap - Ensembl API script design

Always:

- Load the registry

Which features (genes, repeats, SNPs, etc.) are in my particular region of interest?

- Get the SliceAdaptor
- Fetch the Slice for you region of interest
- Get the features from your Slice

What do we know about a particular gene (or any other feature)?

- Get the GeneAdaptor
- Fetch your Gene of interest
- Get more details about the gene:
  - Gene structure (transcripts, exons, translations)
  - Annotations: GO xrefs, HGNC symbols, etc.
  - Features in the same region -> get the Slice for the Gene!

Documentation & Help

- Installation instructions, web-browsable version of the POD (Perldoc), database schema and tutorial:

  http://www.ensembl.org/info/docs/api/index.html

- Inline Perl POD (Plain Old Documentation)
- dev@ensembl.org mailing list:

  http://www.ensembl.org/info/about/contact/mailing.html

  searchable mailing list archive:
  http://blog.gmane.org/gmane.science.biology.ensembl.devel

- Ensembl helpdesk:

  helpdesk@ensembl.org

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SEVENTH FRAMEWORK PROGRAMME

Quantomics

From Sequence to Consequence : Tools for the Exploitation of Livestock Genomes

GEN2PHEN

BLUEPRINT epigenome

Appendix – CoordSystem Methods

Attribute	Example value(s)	Method(s)
name	`chromosome, scaffold, contig, clone`	`$coordsystem->name`
version	`GRCh37, NCBI36, NCBIM37`	`$coordsystem->version`

Appendix – Feature Methods

Attribute	Example value(s)	Method(s)
name	AluSp, D1S2217	$feature->display_id
coordinates		$feature->seq_region_name $feature->start } slice relative $feature->end $feature->seq_region_start $feature->seq_region_end } chromosome relative $feature->strand
sequence		$feature->seq
length	399	$feature->length
slice	returns Slice object with which feature is associated	$feature->slice
feature slice	returns Slice object that covers feature	$feature->feature_Slice

Appendix – Gene Methods

Attribute	Example value(s)	Method(s)
stable ID	ENSG00000139618	$gene->stable_id
name	BRCA2	$gene->external_name
description	breast cancer 2, early onset	$gene->description
biotype	protein_coding, miRNA	$gene->biotype
analysis	ensembl, havana, ensembl_havana_gene	$gene->analysis->logic_name
status	KNOWN, NOVEL	$gene->status
transcripts	returns listref of Transcript objects	$gene->get_all_Transcripts
exons	returns listref of Exon objects	$gene->get_all_Exons

Appendix - Transcript Methods

Attribute	Example value(s)	Method(s)
stable ID	`ENST00000380152`	`$transcript->stable_id`
name	`BRCA2-001`	`$transcript->external_name`
biotype	`protein_coding, nonsense_mediated_decay`	`$transcript->biotype`
analysis	`ensembl, havana, ensembl_havana_transcript`	`$transcript->analysis-> logic_name`
status	`KNOWN, NOVEL`	`$transcript->status`
CDS (spliced sequence, no UTR)	`ATGCCTATTGGATCCAAAGAGAGGC...`	`$transcript->translateable_seq`
UTRs	`returns Seq object`	`$transcript->five_prime_utr` `$transcript->three_prime_utr`
cDNA (spliced sequence + UTR)	`GGGCTTGTGGCGCGAGCTTCTGAAA...`	`$transcript->spliced_seq`
translation	`returns Translation object`	`$transcript->translation`
exons	`returns listref of Exon objects`	`$transcript->get_all_Exons`
introns	`returns listref of Intron objects`	`$transcript->get_all_Introns`

Appendix - Translation Methods

Attribute	Example value(s)	Method(s)
stable id	`ENSP00000369497`	`$translation->stable_id`
length	`3418`	`$translation->length`
sequence	`MPIGSKERPTFFEIFKTRCNKADLG...`	`$translation->seq`