Outline

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b. Data objects & object adaptors
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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

Gene Adaptor
Marker Adaptor
Exon Adaptor
Variation Adaptor
Genotype Adaptor

Core DB Adaptor
Variation DB Adaptor

Human Core DB
Mouse Core DB
Human Variation DB
Mouse Variation DB

Ensembl Registry
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');
#!/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');
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).*