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# An example script demonstrating the use of BioMart API.
# This perl API representation is only available for
configuration versions >= 0.5
use strict;
use BioMart::Initializer;
use BioMart::Query;
use BioMart::QueryRunner;

my $confFile = "PATH TO YOUR REGISTRY FILE UNDER biomart-perl/
conf/. For Biomart Central Registry navigate to
                                http://www.biomart.org/biomart/
martservice?type=registry";
#
# NB: change action to 'clean' if you wish to start a fresh
configuration
# and to 'cached' if you want to skip configuration step on
subsequent runs from the same registry
#

my $action='cached';
my $initializer = BioMart::Initializer->new('registryFile'=>
$confFile, 'action'=>$action);
my $registry = $initializer->getRegistry;

my $query = BioMart::Query->new('registry'=>
$registry,'virtualSchemaName'=>'default');

    $query->setDataset("hsapiens_gene_ensembl");
    $query->addAttribute("ensembl_gene_id");
    $query->addAttribute("ensembl_transcript_id");
    $query->addAttribute("description");
    $query->addAttribute("external_gene_name");
    $query->addAttribute("hgnc_symbol");
    $query->addAttribute("hgnc_transcript_name");
    $query->addAttribute("uniprot_genename");
    $query->addAttribute("family_description");
    $query->addAttribute("family");

$query->formatter("TSV");

my $query_runner = BioMart::QueryRunner->new();
##### GET COUNT
#####
# $query->count(1);
# $query_runner->execute($query);
# print $query_runner->getCount();

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#####  
#####
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##### GET RESULTS
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#####
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# to obtain unique rows only
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# $query_runner->uniqueRowsOnly(1);
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```
$query_runner->execute($query);
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$query_runner->printHeader();
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$query_runner->printResults();
```

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$query_runner->printFooter();
```

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#####
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#####
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