Exercise 5 : Run genscan in the pipeline

Let's now try to set up an analysis for Genscan into our mouse37_mini_ref and add rules and input_ids to the database, like we did with the RepeatMask analysis.

An example of an analysis set-up file is:

```
[Genscan]
db=HumanIso.smat
db_file=HumanIso.smat
program_file=genscan
module=Genscan
input_id_type=500kSLICE
```

Make sure you don't include any empty spaces at the end of the line (you can check with

```
cat -vet <filename>
```

Note: We usually run genscan on 500,000 bp (500k) sequences. In this exercise we will run it on CONTIGS to save us from needing to set up another submission (dummy) analysis.

Instructions

- Use the analysis_setup.pl script to add the analysis to your database
- Check that the analysis has been added to your database
- Using the RuleHandler.pl script from Exercise 3, add rules for the genscan analysis into your database. The submission analysis is SubmitContig and the goal is ... genscan !
- Also add an entry for the Genscan.pm analysis in the BatchQueue.pm file : ensembl-pipeline/modules/Bio/EnsEMBL/Pipeline/Config/BatchQueue.pm

- Now, run a test_runnable on one contig :

```
perl $HOME/ensembl-src/ensembl-analysis/scripts/test_RunnableDB\
 -logic_name Genscan \
-input_id contig:NCBIM37:AC087062.25:1:224451:1 \
-dbhost localhost -dbuser ens-training -dbport 3306 \
-dbname mouse37_mini_ref -dbpass workshop -verbose
```

- If the test_runnable is successful, run the whole analysis in the rule manager :

```
perl  $HOME/ensembl-src/ensembl-pipeline/scripts/rulemanager.pl\
-logic_name Genscan \
-dbhost localhost -dbuser ens-training -dbport 3306 \
-dbname mouse37_mini_ref -dbpass workshop
```

* * * End of Exercise * * *