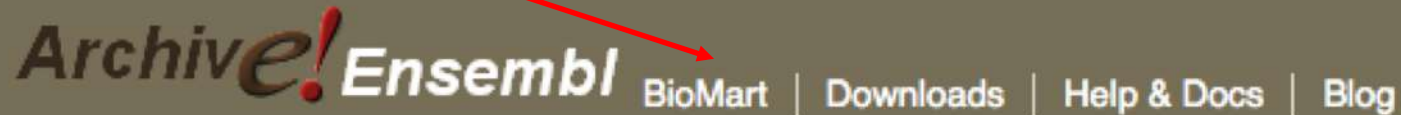


# Data mining with Ensembl Biomart (answers to questions)

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# Start using Ensembl/BioMart

- Go to Ensembl website  
<http://jan2019.archive.ensembl.org/index.html>
- Click on BioMart in the top menu



- CHOOSE DATABASE : select “Ensembl Genes 95”
- CHOOSE DATASET : select “Human genes (GRCh38.p12)”



# Exercise 1: get annotations of a gene

- 1.
  - Click on Filters (left panel),
  - Expand the “GENE” section
  - Select “Input external references ID list”, select “Gene Name(s) in the drop down list and enter IDH1.
  - Click on Count in the top left panel  . You should get **Dataset 1 / 64914 Genes**
  - Click on Attributes (left menu)
  - Select “Features” (selected by default)
  - Select Gene stable ID, Transcript stable ID and Gene Name
  - Click on Results (top left menu) 



Gene stable ID	Transcript stable ID	Gene name
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000345146</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000446179</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000415913</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000484575</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000415282</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000462386</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000417583</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000451391</a>	<a href="#">IDH1</a>
<a href="#">ENSG00000138413</a>	<a href="#">ENST00000481557</a>	<a href="#">IDH1</a>

- 9 transcripts are found




# Exercise 1: get annotations of a gene

- 2.
  - You can leave the Dataset and Filters the same, and go directly to the Attributes section
  - Click on Attributes (left panel)
  - Select “Sequences”
  - Expand the SEQUENCES section
  - Select Exon sequences
  - Expand “Header Information”
  - Unselect “Gene stable ID” (Gene Information)
  - Select Gene name (Gene Information), transcript stable IDs (Transcript Information) and Exon stable IDs (Exon Information).
  - Click on Results 
- 3.
  - You can leave the Dataset and Filters the same, and go directly to the Attributes section
  - Click on Attributes (left panel)
  - In the SEQUENCES section
  - select Coding sequence
  - “Header Information”: unselect Gene name (Gene Information) and select transcript stable ID (Transcript Information) and Exon stable IDs (Exon Information).
  - Click on Results 



# Exercise 1: get annotations of a gene

- 4.
  - You can leave the Dataset and Filters the same, and go directly to the Attributes section
  - Click on Attributes (left panel)
  - Select “Features” (selected by default)
  - In the GENE section: Gene stable ID, Transcript stable ID and Gene Name should be selected
  - Expand the EXTERNAL section
  - Select GO Term Name, GO domain and GO Term Accession
  - Click on Results 
- 5.
  - You can leave the Dataset and Filters the same, and go directly to the Attributes section
  - Click on Attributes (left panel)
  - Select “Variant (Germline)”
  - In the GENE section: Gene stable ID, Transcript stable ID and Gene Name should be selected
  - Expand the GERMLINE VARIANT INFORMATION section
  - Select Variant Name, Variant Alleles, Minor allele frequency, Chromosome/scaffold name, Chromosome /scaffold position start (bp), Chromosome/scaffold position end (bp), Variant Consequence
  - Click on Results 



## Exercise 2: get annotations for a set of genes

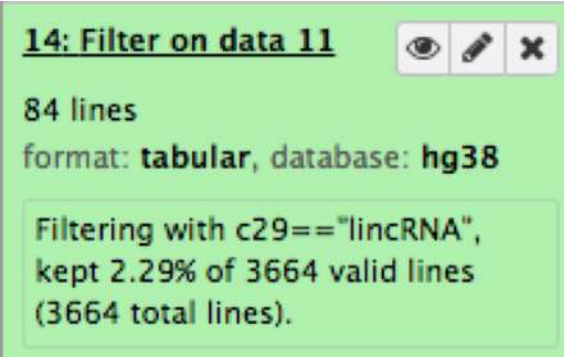
- 1.
  - In Ensembl/BioMart, create a new request (see slide 2.)
  - Click on Filters (left panel)
  - Expand the GENE section
  - Select “Input external references ID list” and select “Gene stable ID(s)” in the drop down list
  - Click on “Browse” and select the file siMitfvssiLuc.up.txt
  - Click on “Count” (top left button) . You should have the number of genes you have in your file generated by SARTools: 3663
  - Click on Attributes (left panel)
  - Select “Features” (selected by default), Expand the GENE section, select Gene stable ID, Chromosome/scaffold name, Gene Start (bp), Gene End (bp), Strand, Gene Name and Gene type.
  - Click on Results 
  - Select Compressed file (.gz) in the drop down menu. Click on Go  to download the resulting file.




## Exercise 2: get annotations for a set of genes

- 2.
  - Go to GalaxEast (<http://use.galaxeast.fr>)
  - Open the upload utility: click on  in top of the tool panel and drag and drop your files (siMitfvssiLuc.up.txt and mart\_export.txt.gz) into the opened window
  - Click on Start
- 3.
  - Run the tool “Join Two Datasets”
    - Join: siMitfvssiLuc.up.txt
    - Using column: Column: 1
    - With: mart\_export.txt
    - And column: Column: 1
    - Keep lines of first input that do not join with second input: No
    - Keep lines of first input that are incomplete: No
    - Fill empty columns: No
    - Click on Execute 

## Exercise 2: get annotations for a set of genes

- 4.
  - Click on the button  of the dataset you've just generated "join two datasets on (...)"
  - In the "Attributes" tab, enter siMitfvssiLuc.up.annot.txt in the text box "Name".
  - Click on Save
- 5.
  - Run the tool "**Filter** data on any column using simple expressions" with the following parameters
    - Filter: siMitfvssiLuc.up.annot.txt
    - With following condition: c29=="lincRNA"
    - Number of header lines to skip: 1
    - Click on Execute 



**14: Filter on data 11**   

84 lines  
format: **tabular**, database: **hg38**

Filtering with c29=="lincRNA",  
kept 2.29% of 3664 valid lines  
(3664 total lines).



## Exercise 2: get annotations for a set of genes

- 6.
  - Don't change Dataset and Filters – simply click on Attributes.
  - Click on Attributes (left panel)
  - Select “Sequences”
  - Expand the SEQUENCES section
  - Select Flank (Transcript) and enter 2000 in the Upstream flank text box
  - Expand the Header information section
  - Select, in addition to the default selected attributes, Gene description and Gene Name
  - Note: Flank (Transcript) will give the flanks for all transcripts of a gene with multiple transcripts. Flank (Gene) will give the flanks for one possible transcript in a gene (the most 5' coordinates for upstream flanking)

## Exercise 3: get annotations in the genome

- 1.
  - In Ensembl/BioMart, create a new request (see slide 2.)
  - Click on Filters (left panel)
  - Expand the REGION section
  - Select “Multiple regions” and enter 2:208226227:208276270 in the text box
  - Click on count. **4 genes are found.**
- 2.
  - In Ensembl/BioMart, create a new request (see slide 2.)
  - Click on Filters (left panel)
  - Expand the REGION section
  - Select “Chromosome/scaffold” and multiple select 1 -> MT (click and drag). This corresponds to 58676 / 64914 Genes
  - Click on Attributes (left panel)
  - Select “Features” (selected by default)
  - In GENE, select Gene stable ID, Chromosome/scaffold name, Gene Start (bp), Gene End (bp), strand and Gene Name
  - Click on Results 