Contents

Chapter 1 What is Miqualat Database

With Miqualat Notebooks you have access to an easy-to-use Jupyter Notebook interface.
Miqualat Notebook allows you to save data from publications, genes, variants, tecnique and other and associate them with descriptions and tags.
A control system has been implemented to maintain flexibility and freedom to import data while maintaining control over them.
You can get this data from different databases as pubmed, ensembl, kegg and make automatically links.
This relational database allows you to link and export information from different tables.

Chapter 2 Setting Up the Working Environment

2.1 Install Jupyter Notebook

Update and upgrade your system (recommended).
$ sudo apt update && sudo apt upgrade

Install python3-pip.
$ sudo apt install python3-pip

Install jupyter notebook.
$ sudo apt install jupyter-notebook

If you need to configure the configuration file is located in
/root/.jupyter/jupyter_notebook_config.py
$ sudo jupyter-notebook --generate-config

To access Jupyter Notebook you may need to set up a password.
$ sudo jupyter-notebook password

Run jupyter notebook (on port 8888 by default).
$ sudo jupyter-notebook

2.2 Install Mysql Server

Install apache2 and mysql-server.
$ sudo apt install apache2
$ sudo apt install mysql-server

If you use raspberry or a similar system.
$ sudo apt install mariadb-server-10.0

Create user and set password for database (this user can be used to access in phpmyadmin, keep your credentials).
$ sudo mysql -u root
$ CREATE USER 'user'@'localhost' IDENTIFIED BY 'password';

Grant privileges on all databases.
$ GRANT ALL PRIVILEGES ON * . * TO 'user'@'localhost';

Grant privileges on one databases (safer).
$ GRANT ALL PRIVILEGES ON DATABASE. * TO 'user'@'localhost';
$ FLUSH PRIVILEGES;

!! IMPORTANT (pay attention before continuing with the command below), when you install phpmyadmin (command below) after select apache2 (with TAB) and press SPACE, after leave all

empty (press ENTER) !!
$ sudo apt install phpmyadmin
$ sudo systemctl restart apache2

Connect phpmyadmin using your browser (on port 80: /phpmyadmin).
http://192.168.0.(continue_your_ip).../phpmyadmin

Show your IP.
$ hostname -I

http://localhost/phpmyadmin (work only on local computer not for remote server)

2.3 Install Mysqlclient

Install mysqlclient (connect database remotely using python).
Get more information at: https://pypi.org/project/mysqlclient/
$ sudo apt-get install python3-dev default-libmysqlclient-dev build-essential
$ pip3 install mysqlclient

Update and upgrade your system (recommended).
$ sudo apt update && sudo apt upgrade

2.4 Install Required Python Libraries

The following libraries are required for use miqualat notebooks.
$ sudo pip3 install biopython
$ sudo pip3 install ensembl-rest
$ sudo pip3 install mygene

Chapter 3 Folder and Content Description

3.1 Description of the FUNCTIONS Folder

The functions in FUNCTIONS folder, contain python code that is recalled in the notebooks.

1. ensembl_search.py
   Use the ensembl-rest library to get information about genes from the Ensembl database.

2. ensembl_to_kegg_id.py
   Convert Ensembl gene id to the Kegg id of the gene and related pathways, using mygene and Bio.KEGG.REST (in biopython library).

3. MIQUALAT_data_import_and_check.py
   Import and check the csv files processed with previous notebooks, using MySQLdb (in mysqlclient library).

4. pubmed_search.py
   Carry out searches within the pubmed database using biopython.

5. python_parser_biomart_gene_csv.py
   Convert the biomart file (which contains all biomart genes) into the right format for the GENE table.

3.2 Description of the OUTPUT Folder

In the OUTPUT folder are saved all the files processed by the notebook, to be imported into the miqualat database.

3.3 Description of the DATABASE Folder

In the OUTPUT folder are saved all the files processed by the notebook, to be imported into the miqualat database

Chapter 4 Miqualat Notebooks Description and Usage

To use notebooks select the code cell and click on run, below will describe the notebooks and their functions.
Five notebooks have been built, that allow you to search, import and check into the miqualat database.

1. MIQUALAT_PUBLICATION_data_assess.ipynb
   Carry out searches within the pubmed database, automatize data collection for PUBLICAITON table.
   Creates PUBLICATION.csv file and move all searches (PUBMED_SEARCH_DATA_Y-m-d_H-M-S.txt format) in the OUTPUT folder.

2. MIQUALAT_KEGG_data_assess.ipynb
   Download genes and pathways from kegg database (from kegg code), automatize data collection for KEGG table.
   Creates ALL_KEGG_GENE.csv (all kegg genes from kegg code) in the OUTPUT folder.
   Creates ALL_KEGG_PATH.csv (all kegg pathways from kegg code) in the OUTPUT folder.

3. MIQUALAT_GENE_data_assess.ipynb
   Allows you to download genes from ensembl database, automatize data collection for GENE table.
   Option 1) get information from specific genes (ensembl gene id required).
   Option 2) convert all genes downloaded from biomart (GENE.csv required).
   In any case creates GENE.csv and move it in the OUTPUT folder.

4. MIQUALAT_GEN_KEGG_data_assess.ipynb
   Correlates the ensembl gene id to the kegg id (if possible) of the gene and related pathway, automatize data collection for GEN_KEGG table.
   Option 1) correlates the ensembl gene id to the kegg id of the gene and related pathways for specific gene (ensembl gene id required), for specific gene.
   Option 2) processes the entire GENE.csv file.
   Creates ENS_GENE_ID.csv (Ensembl gene id to Kegg gene id) in the OUTPUT folder.
   Creates ENS_PATH_ID.csv (Ensembl gene id to Kegg pathways id) in the OUTPUT folder.

5. MIQUALAT_data_import_and_check.ipynb
   Allows the import of files processed with previous notebooks, once checked.
   An error control system prevents the import of incorrect information.

Chapter 5 Create Biomart File

Go to https://www.ensembl.org/biomart/martview/afe982e758c87b06e672bc93a42a4f30.

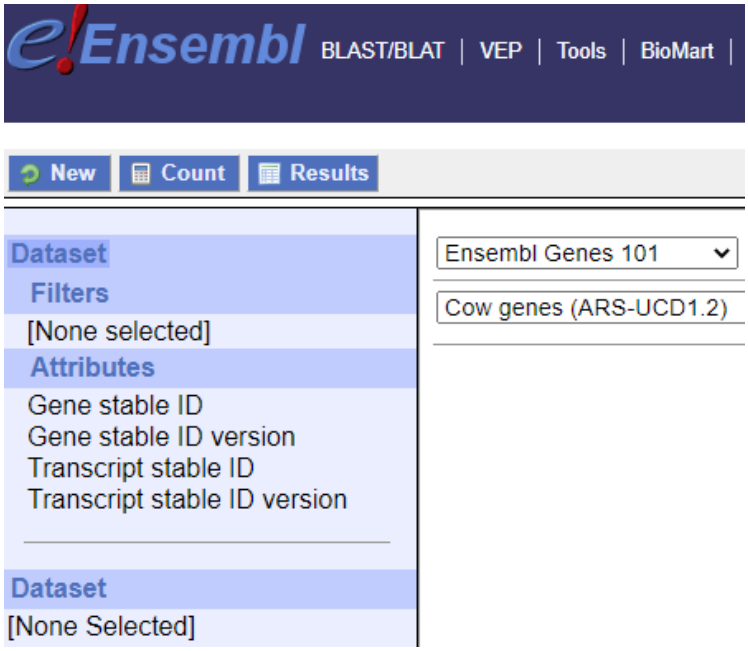
Export all results to File CSV.

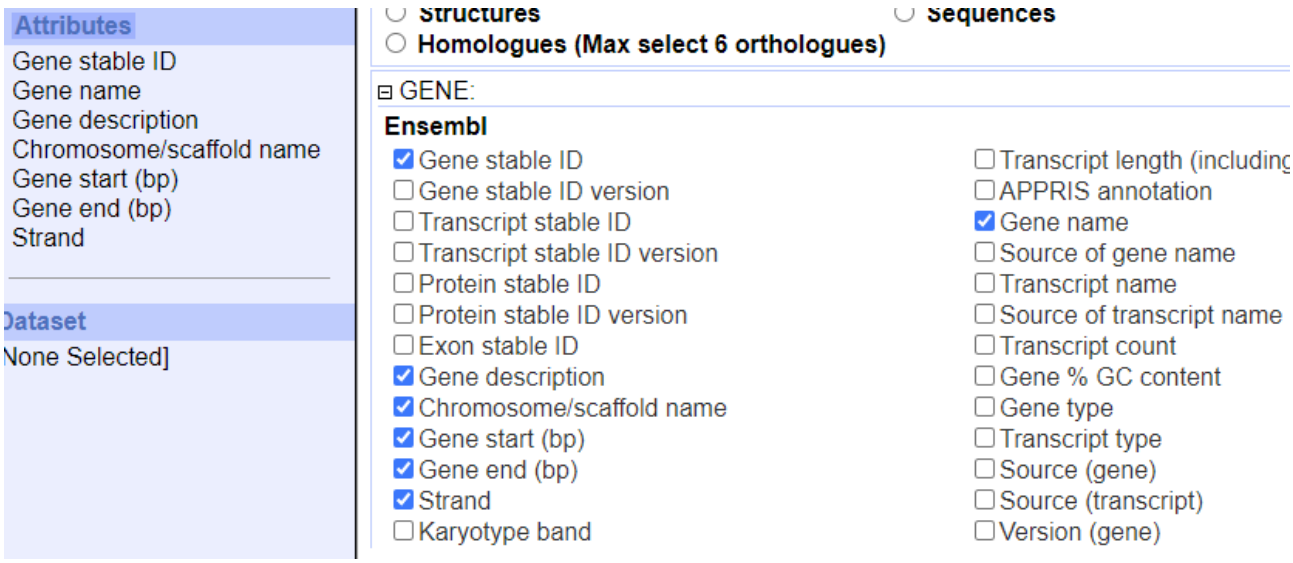
Select dataset Ensembl Gene 101.

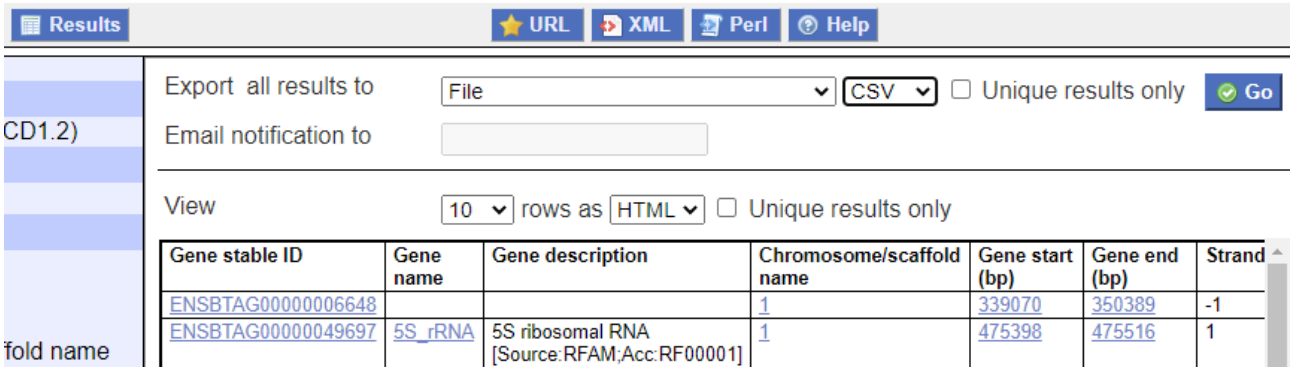
Select Species (refseq) (ex Cow genes (ARS-UCD1.2)).

Go to Attributes, Gene and create the biomart file following this header (select in the right order).

Gene stable ID,Gene name,Gene description,Chromosome/scaffold name,Gene start (bp),Gene end (bp),Strand






Results
URL
XML
Perl
Help
CD1.2)
fold name
Export all results to
File
CSV
Unique results only
Go
Email notification to
View
10
rows as
HTML
Unique results only
Gene stable ID
Gene name
Gene description
Chromosome/scaffold name
Gene start (bp)
Gene end (bp)
Strand
ENSBTAG00000006648
1
339070
350389
-1
ENSBTAG00000049697
5S_rRNA
5S ribosomal RNA [Source:RFAM;Acc:RF00001]
1
475398
475516
1

Chapter 6 Create Table File

To pass the check the csv must have the following headers.

!! Create the Table file following this headers (create the header as it is written, do not add quotes or anything else). !!

1. PUB_GEN_TEC_VAR_TAG TABLE

   integer_progressive_ID,pubmed_ID,ensembl_gene_ID,variant_name,tecnique,keyword_tags,relationship_note

2. PUBLICATION TABLE

   pubmed_ID,doi,article_title,article_authors,article_journal,publication_year

3. TECNIQUE TABLE

   tecnique,tecnique_short_description

4. TAG TABLE

   keyword_tags,tags_short_description

5. GENE TABLE

   ensembl_gene_ID,gene_name,gene_short_description,refseq,species,chromosome,start_coordinate,end_coordinate,strand

6. KEGG TABLE

   kegg_ID,kegg_object_type,kegg_object_name

7. GEN_KEGG TABLE

   ensembl_gene_ID,kegg_ID

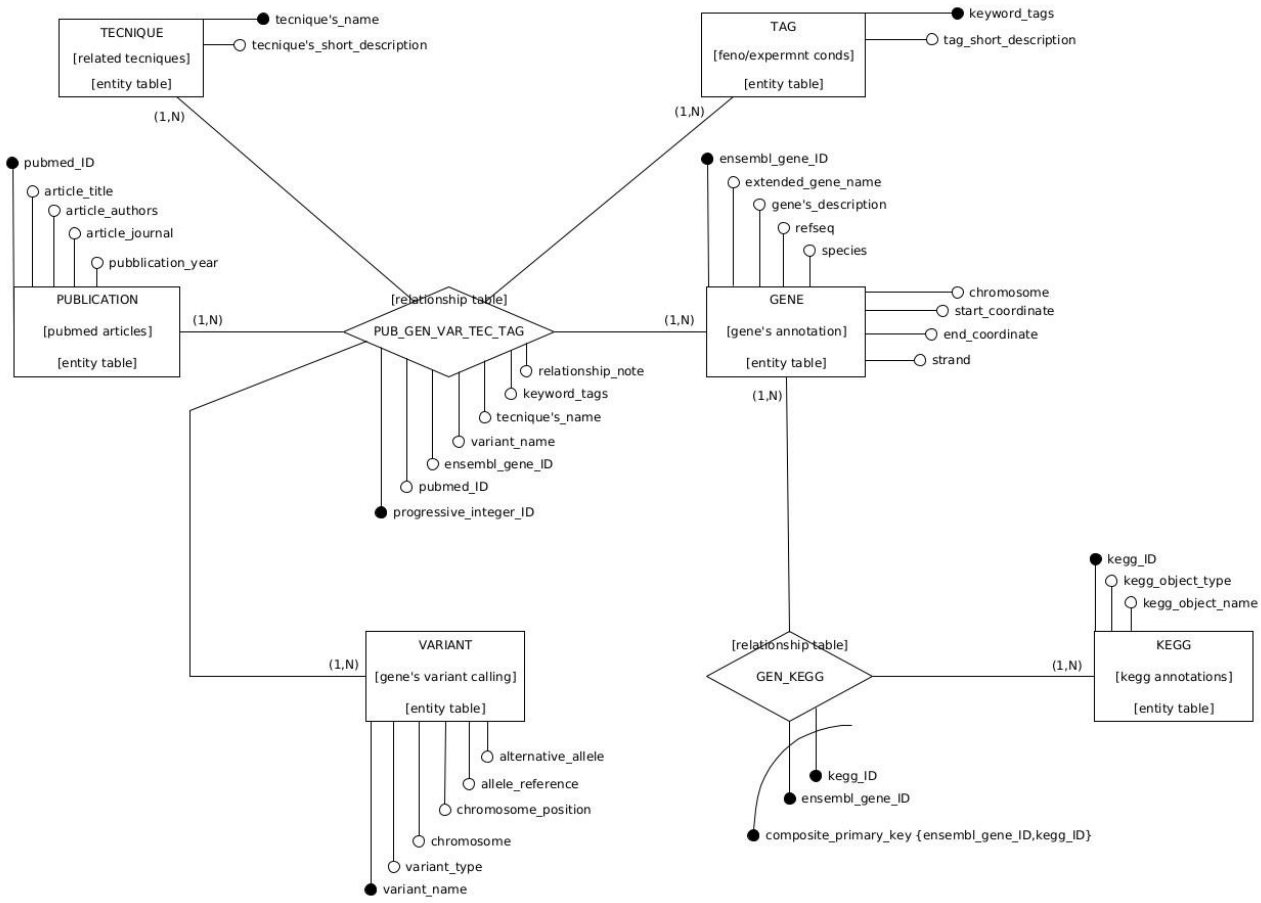
8. VARIANT TABLE

   variant_name,variant_type,chromosome,chromosome_position,allele_reference,alternative_allele_reference

Chapter 7 Database Description

7.1 Database Schema

Below the physical Entity-Relationship diagram (ERD) of the Miqualat database.



7.2 Database Description

```
##using the MIQUALAT database and displaying tables##
mysql> use MIQUALAT;
Database changed
mysql> SHOW TABLES;
+---------------------+
| Tables_in_MIQUALAT  |
+---------------------+
| GENE                |
| GEN_KEGG            |
| KEGG                |
| PUBLICATION         |
| PUB_GEN_VAR_TEC_TAG |
| TAG                 |
| TECNIQUE            |
| VARIANT             |
+---------------------+
8 rows in set (0.00 sec)

##description of the structure of the tables and the type of data
of the attributes of each entity and relation##
mysql> DESCRIBE GENE;
+------------------------+--------------+------+-----+---------+-------+
| Field                  | Type         | Null | Key | Default | Extra |
+------------------------+--------------+------+-----+---------+-------+
| ensembl_gene_ID        | varchar(20)  | NO   | PRI | NULL    |       |
| gene_name              | varchar(20)  | YES  |     | NULL    |       |
| gene_short_description | varchar(300) | YES  |     | NULL    |       |
| refseq                 | varchar(50)  | NO   |     | NULL    |       |
| species                | varchar(50)  | NO   |     | NULL    |       |
| chromosome             | tinyint      | NO   |     | NULL    |       |
| start_coordinate       | int unsigned | NO   |     | NULL    |       |
| end_coordinate         | int unsigned | NO   |     | NULL    |       |
| strand                 | tinyint      | NO   |     | NULL    |       |
+------------------------+--------------+------+-----+---------+-------+
9 rows in set (0.00 sec)

mysql> DESCRIBE GEN_KEGG;
+-----------------+-------------+------+-----+---------+-------+
| Field           | Type        | Null | Key | Default | Extra |
+-----------------+-------------+------+-----+---------+-------+
| ensembl_gene_ID | varchar(20) | NO   | PRI | NULL    |       |
| kegg_ID         | varchar(20) | NO   | PRI | NULL    |       |
+-----------------+-------------+------+-----+---------+-------+
2 rows in set (0.00 sec)

mysql> DESCRIBE KEGG;
+------------------+--------------+------+-----+---------+-------+
| Field            | Type         | Null | Key | Default | Extra |
+------------------+--------------+------+-----+---------+-------+
| kegg_ID          | varchar(20)  | NO   | PRI | NULL    |       |
| kegg_object_type | varchar(30)  | NO   |     | NULL    |       |
| kegg_object_name | varchar(300) | NO   |     | NULL    |       |
+------------------+--------------+------+-----+---------+-------+
3 rows in set (0.00 sec)
```

```
mysql> DESCRIBE PUBLICATION;
+------------------+--------------+------+-----+---------+-------+
| Field            | Type         | Null | Key | Default | Extra |
+------------------+--------------+------+-----+---------+-------+
| pubmed_ID        | int unsigned | NO   | PRI | NULL    |       |
| article_title    | varchar(300) | NO   |     | NULL    |       |
| article_authors  | varchar(300) | NO   |     | NULL    |       |
| article_journal  | varchar(100) | NO   |     | NULL    |       |
| publication_year | year         | NO   |     | NULL    |       |
+------------------+--------------+------+-----+---------+-------+
5 rows in set (0.01 sec)
```

```
mysql> DESCRIBE PUB_GEN_VAR_TEC_TAG;
+------------------------+--------------+------+-----+---------+----------------+
| Field                  | Type         | Null | Key | Default | Extra          |
+------------------------+--------------+------+-----+---------+----------------+
| integer_progressive_ID | int unsigned | NO   | PRI | NULL    | auto_increment |
| pubmed_ID              | int unsigned | NO   | MUL | NULL    |                |
| ensembl_gene_ID        | varchar(20)  | YES  | MUL | NULL    |                |
| variant_name           | varchar(30)  | YES  | MUL | NULL    |                |
| tecnique               | varchar(50)  | YES  | MUL | NULL    |                |
| keyword_tags           | varchar(50)  | YES  | MUL | NULL    |                |
| relationship_note      | varchar(200) | YES  |     | NULL    |                |
+------------------------+--------------+------+-----+---------+----------------+
7 rows in set (0.01 sec)
```

```
mysql> DESCRIBE TAG;
+------------------------+--------------+------+-----+---------+-------+
| Field                  | Type         | Null | Key | Default | Extra |
+------------------------+--------------+------+-----+---------+-------+
| keyword_tags           | varchar(50)  | NO   | PRI | NULL    |       |
| tags_short_description | varchar(200) | NO   |     | NULL    |       |
+------------------------+--------------+------+-----+---------+-------+
2 rows in set (0.01 sec)
```

```
mysql> DESCRIBE TECNIQUE;
+---------------------------+--------------+------+-----+---------+-------+
| Field                     | Type         | Null | Key | Default | Extra |
+---------------------------+--------------+------+-----+---------+-------+
| tecnique                  | varchar(50)  | NO   | PRI | NULL    |       |
| tecnique_short_description | varchar(300) | NO   |     | NULL    |       |
+---------------------------+--------------+------+-----+---------+-------+
2 rows in set (0.01 sec)
```

```
mysql> DESCRIBE VARIANT;
+-----------------------------+------------------+------+-----+---------+-------+
| Field                       | Type             | Null | Key | Default | Extra |
+-----------------------------+------------------+------+-----+---------+-------+
| variant_name                | varchar(30)      | NO   | PRI | NULL    |       |
| variant_type                | varchar(30)      | NO   |     | NULL    |       |
| chromosome                  | tinyint unsigned | NO   |     | NULL    |       |
| chromosome_position         | int unsigned     | NO   |     | NULL    |       |
| allele_reference            | varchar(50)      | NO   |     | NULL    |       |
| alternative_allele_reference | varchar(50)     | NO   |     | NULL    |       |
+-----------------------------+------------------+------+-----+---------+-------+
6 rows in set (0.00 sec)
```

##IT IS A RELATIONAL DATABASEIT IS A RELATIONAL DATABASE##
*WITH 6 ENTITY TABLES{
——————————————————————————————PUBLICATION,
——————————————————————————————GENE,
——————————————————————————————VARIANT,
——————————————————————————————TECNIQUE,
——————————————————————————————TAG,
——————————————————————————————KEGG
}

*AND 2 RELATIONAL TABLES{
——————————————————————————————PUB_GEN_VAR_TEC_TAG,
——————————————————————————————GEN_KEGG
}

7.3 Check Description

1) entries fields number

2) entry duplicates

3) entries already present in the database

4) entry fields of a whole numerical nature

5) existence of foreign_keys for relational tables

6) special check for table PUB_GEN_VAR_TEC_TAG

7) special check for table GEN_KEGG