Data management with MySQL

Msc Modelization

Outline

- Data types and data values
- Introduction to relational algebra
- SQL queries: SELECT
- Joining multiple sources of data to query data relationships

Installing MySQL

```
login into system
• sudo apt-get install mysql-server
```

• sudo apt-get install mysql-workbench

(Remember to set root password)

Using MySQL

```
login into system
open a terminal
Open mysql database session:
• mysql -u root -p
   (enter your root password)
mysql>
```

Also, use Mysql workbench tool, connect to mysql (localhost connection)

• mysql-workbench

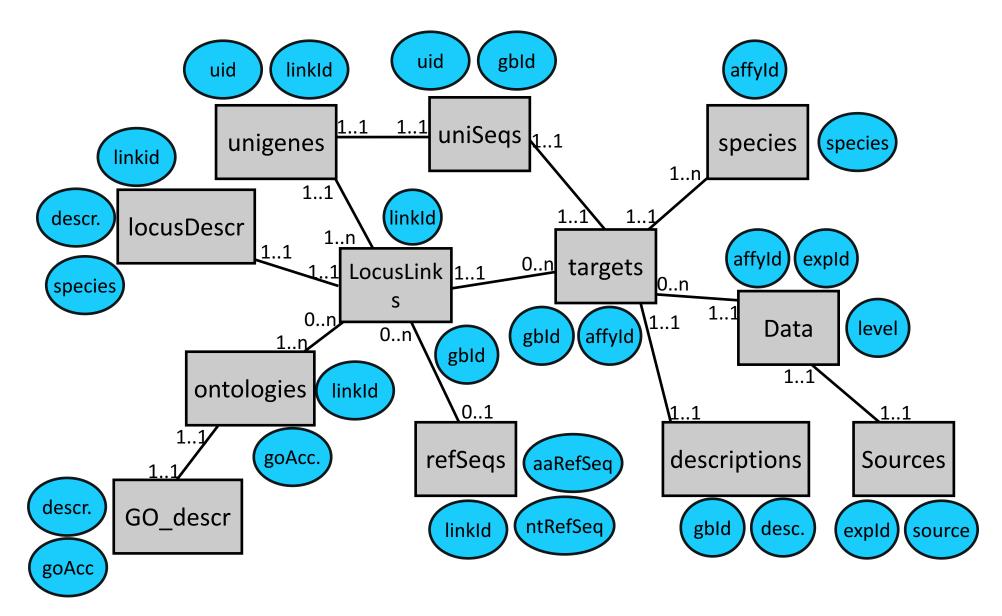
Importing data into MySQL

```
Download experiments.sql file
cd Downloads
Open mysql database session:
• mysql -u root -p
  (enter your root password)
mysql>create database experiments;
Mysql>show databases;
Mysql>quit;
Now, import the dataset into the database
mysql -u root -p experiments < experiments.sql
```

Importing data to MySQL

```
Open mysql database session:
• mysql -u root -p
   (enter your root password)
mysql>show databases;
Mmysql>use experiments;
Mmysql>describe data;
```

Experiments database



MySQL data types: numeric

- Integer (INT)
 - Signed -2147483648 to 2147483647
 - Unsigned 1844674407370551615
- Real (FLOAT/DOUBLE)
 - Decimal values, 1.234, 1.47564839E+5
- dates (DATE/DATETIME)
 - 'YYYY-MM-DD HH:MM:SS'
- TIMESTAMP
 - YYYYMMDDHHMMSS

MySQL datatypes: alphanumeric

- VARCHAR(string length)
 - Stores a string of characters smaller than 255

- TEXT
 - Stores a string smaller than 65535

Getting info on databases

mysql>show databases;

| Database | test | large | la

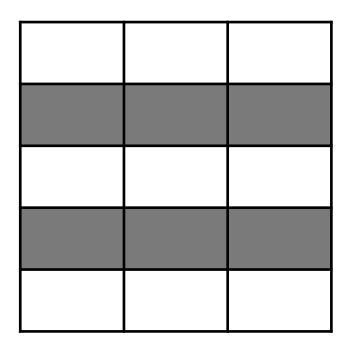
mysql>show tables from experiments;

Getting info on tables

- mysql>use experiments;
- mysql>describe Data;

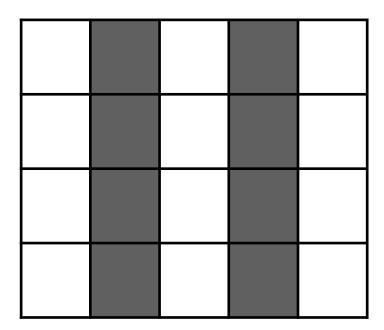
Relational algebra basic operations

• Restrict: eliminate tuples that do not fulfill a specific criteria



Relational algebra basic operations

• Project: eliminate attributes that are not required



Example: Restrict

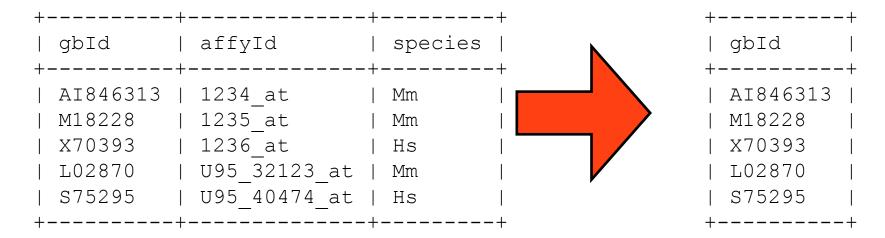
SELECT * from targets;

SELECT * from targets where species="Mm";

+	- +		+.		+
gbId		affyId		species	
AI846313 M18228	İ	 1235_at		Mm Mm	+
L02870 +	 -+	U95_32123_at 	+	Mm 	+

Project example

SELECT gbld from targets;



Typical query structure: SELECT

SELECT whatever we need to get

FROM table or tables

WHERE conditions that must be TRUE

Simple query translation

```
SELECT gbId
FROM targets
WHERE species="Mm";
```

- Get all Gene Bank id's
- from table "targets"
- where genes belong to "Mus musculus" species

Simple query exercise

- 1. Get all data from Locus Descriptions
- 2. Get all data from Locus Descriptions where locus belongs to Human species (Hs)
- 3. Get all LocusLinks id's from table "LocusDescriptions" where locus belong to Human species

Using aggregate values on queries

- AVG: Average of attribute values
 - AVG(level)
- COUNT: Count of attribute values
 - COUNT(affyId)
- MAX: Maximum value of attributes
 - MAX(level)
- MIN: Minimum value of attributes
 - MIN(species)
- SUM: Total sum of attribute values
 - SUM(level)

Work!

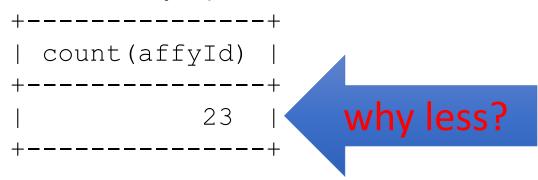
- 1. Get all rows from table Data
- 2. Get level values from table Data
- 3. Get average, maximum, minimum expression level from Data

Use of DISTINCT in attributes

SELECT count(affyld) from data

```
+----+
| count(affyId) |
+----+
| 37 |
+-----
```

SELECT count(DISTINCT affyld) from data



Using arithmetic expressions

- Get measured expression level and doubled value in the same query
- First: get all experimental data: SELECT * from data

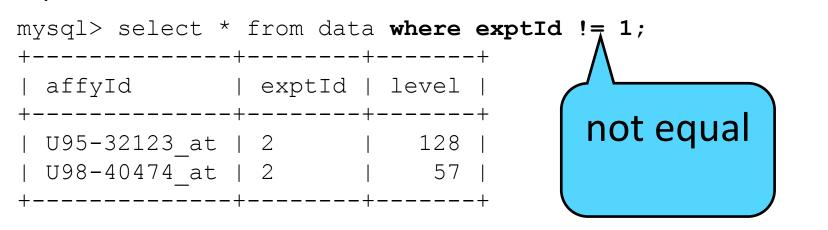
• Then, create your needed columns: SELECT level, level*2 FROM data

+		+		+
-	level		level*2	
+		+		+
	128		256	
	128		256	
	57		114	
	57		114	
+		+		+

Specifying conditions at where

Expressions must be TRUE

Use comparisons of text or numeric values



Work: specify conditions

- 1. Get all expression data on Affymetrix Bio Probes: "AFFX-BioB-3_at"
- 2. Get all expression data on Affymetrix Bio Probes: "AFFX-BioB-3_at" AND "AFFX-BioB-5_at"
- 3. Get all expression data on Affymetrix Bio Probes: "AFFX-BioB-3_at" AND "AFFX-BioB-5 at" AND "AFFX-BioB-M at"

Pattern matching with LIKE

Sorting results with ORDER BY

```
mysql> SELECT * FROM refseqs
    -> where linkId like "105%"
    -> ORDER BY linkId DESC;
+-----+
| linkId | ntRefSeq | aaRefSeq |
+-----+
| 105910 | NM_134094 | NP_598855 |
| 105892 | NM_128276 | XP_128276 |
| 105887 | NM_127943 | XP_127943 |
| 105870 | XM_128254 | XP_128254 |
```

Sorting results with ORDER BY

```
mysql> SELECT *
   -> FROM refseqs
   -> WHERE linkId LIKE "105%"
   -> ORDER BY aaRefSeq ASC;
  ----+
 linkId | ntRefSeq | aaRefSeq
   1057 | NR 001275 |
   1053 | NM 001805 | NP 001796
   1054 | NM 001806 | NP 001797 |
   1056 | NM 001807 | NP 001798 |
   1058 | NM 001809 | NP 001800
```

Work: ORDER BY

1. Get all values of table Data of experiment '3' sorted by expression level

Asking for more WHERE conditions

```
mysql> SELECT affyId, level
    -> FROM data
    -> WHERE level BETWEEN 80 AND 100
    -> LIMIT 5;
  affyId
                           level
  31324 at
                              91
  31356 at
                              91
 AFFX-BioB-3 at
                              97
 AFFX-HSAC07/X00351 M at | 86
 AFFX-HUMTFFR/M11507 at | 90
```

Asking for more WHERE conditions

```
mysql> SELECT *
   -> FROM uniseqs
   -> WHERE gbid NOT LIKE "NM_%"
   -> LIMIT 5;
  -----+
| uId | gbId
 _____+
| Hs.2 | D90042
Hs.11 | D90278
Hs.11 | L00693
Hs1640 | L02870
Hs.21 | M16652
 ----+
```

Querying expression levels with WHERE

```
mysql> SELECT * FROM data
   -> WHERE level BETWEEN 80 AND 100 OR level < 21
   -> LIMIT 5;
 affyId
        | exptId | level
 31324 at
                       91
 31356 at
                          91
 AFFX-BioB-3 at | 3 |
 AFFX-BioB-5 at | 3 | 20
                    1 20
 AFFX-BioB-M at | 3
```

Querying expression levels with WHERE

```
mysql> SELECT affyId, level
    -> FROM data
    -> WHERE exptId != "hs-cer-1"
      AND level BETWEEN 250 AND 300
    -> LIMIT 5;
  affyId
                             level
 31315 at
                             250
  31362 at
                               260
 31510 s at
                            257 I
 AFFX-HUMBAPDH/M33197 3 st | 277 |
                      | 271 |
 AFFX-M27830 3 at
```

Joining data from two tables

 Get the result from two matching tables and then look for tuples that match a specific condition

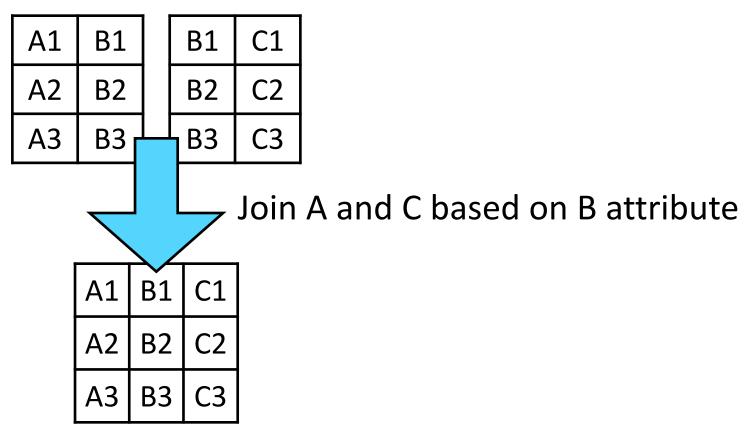


Table Joins

How to get gene ontology descriptions for linkID=4017?

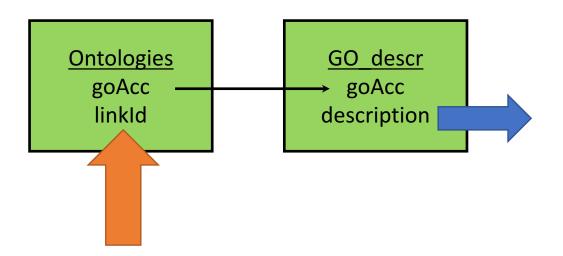
1. Get accession number for my link id=4017 -->ontology table

```
mysql> select goAcc
    -> from ontologies
    -> where ontologies.linkId=4017;
```

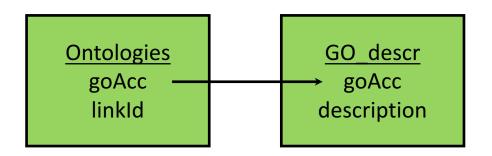
2. Get gene ontology terms for found accesion numbers --> GO_descr table

```
mysql> select description
   -> from GO_descr
   -> where GO_descr.goAcc= ?;
```

Get GO descriptions for linkIds



Joining ontologies and go_descr

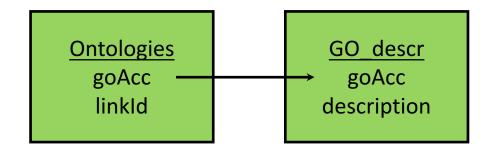


Query all linklds for GO descriptions

mysql> select go_descr.description, ontologies.linkId

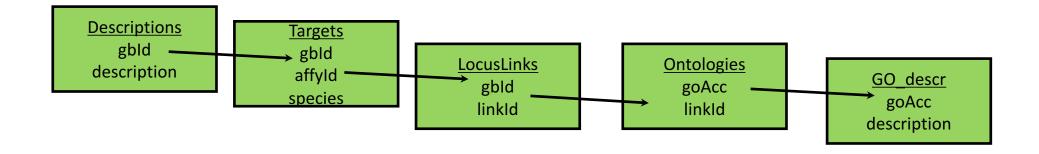
- -> from go descr, ontologies
- -> where ontologies.goAcc=go_descr.goAcc;

+	
description	linkId
Serine Prot. Glucan Enz fructose-2, 6-biophosphatase 2-phosphatase regulation of mitosis protein kinase protein kinase extracellular space	1294 2632 4015 4016 4017 4018 4019
† ⁻	r



Work:

Translate this schema to a mysql query:



Join example

```
mysql> SELECT descriptions.description AS gene description,
              go descr.description AS GO description
              FROM descriptions, go descr, locuslinks, ontologies, targets
              WHERE descriptions.gbId=targets.gbId AND
              targets.gbId=locuslinks.gbId AND
              locuslinks.linkId=ontologies.linkId AND
              ontologies.goAcc=go descr.goAcc
              LIMIT 5;
            ______
 gene description
                                         | GO description
 HSLFBPS7 Human fructose-1, 6-biphosphatase | fructose-2, 6-biophosphatase 2-phosphatase
 HSU30872 Human mitosin mRNA
                                            | regulation of mitosis
 HSU33052 Human lipid-activated protein kinase | protein kinase
 HSU33053 Human lipid-activated protein kinase | protein kinase
 Human clone lambda 5 semaphorin mRNA
                                             | extracellular space
   Descriptions
                       Targets
      gbld
                       gbld
                                       LocusLinks
                                                           Ontologies
   description
                       affyld
                                                                               GO descr
                                         gbld
                                                             goAcc
                       species
                                                                                 goAcc
                                         linkld
                                                             linkId
```

description

Natural joins to get data from tables

- Take profit from tables relationships by traversing the database schema
- SELECT and JOIN refer to more than one table
- WHERE uses common attributes to define expressions that must be true

Work!

- Join locus descriptions and locus links using linkId
 - show: descriptions, locuslinks

GROUP BY

- GROUP BY is good for retrieving information about a group of data
- GROUP BY is useful when you have many similar things
- For example, if you have a number of elements of the same type, and you want to find out some statistical information like the minimum, maximum, or other top-level info

GROUP BY example

- Apply group by on data table
- We want information on the expression values of the experiments:
 - aggregate by experiment
 - get information on expression value

GROUP BY aggregations

```
SELECT exptId, MIN(level)
FROM data
GROUP BY exptId;
```

+-		+	+
1	exptId		MIN(level)
+-		+	+
	1		57
	2		57
	3		8
	4		51
	5		8
	6		4
	7		20
	8		40
Ì	9	1	20
+-		+	+

GROUP BY rules

- The column that you GROUP BY must also be in your SELECT statement.
- Remember to group by the column you want information about and not the one you are applying the aggregate function on.
- In our above example we wanted information on the level and the aggregate function was applied to the experiment ID attribute.

GROUP BY work!

• Find maximum expression value from data table for each experiment

Counting aggregated values

- The COUNT function is an aggregate function that simply counts all the items that are in a group
- One use of COUNT might be to find out how many items of each type there are in the table

How many probes for each experiment?

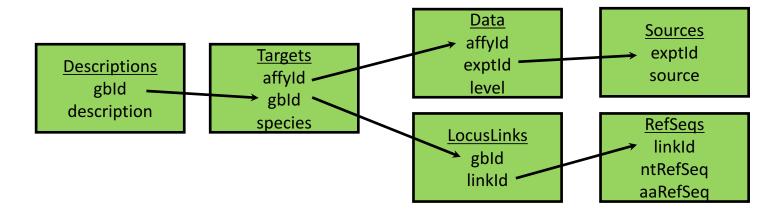
SELECT exptId, COUNT(affyId)

```
FROM
       data
GROUP BY exptId;
  exptId | COUNT(affyId)
                       16
  6
```

Count Work!

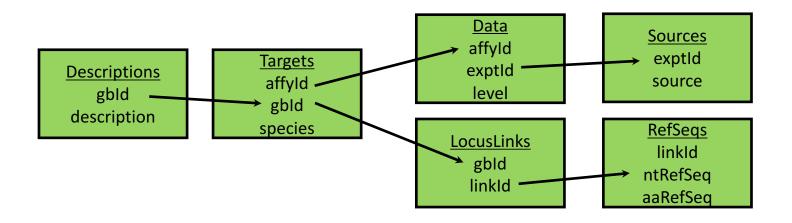
 Count the number of elements of table targets for each individual species

Mega table join



Mega table join

```
SELECT descriptions.description, sources.source, refseqs.ntrefseq
FROM descriptions, sources, refseqs, targets, locuslinks, data
WHERE descriptions.gbId=targets.gbId and
Targets.gbid = locuslinks.gbId
locuslinks.linkId=refseqs.linkId and
targets.affyId=data.affyId and
data.exptId=sources.exptId
```



Mega table join

description

```
mysql> select descriptions.description, sources.source, refseqs.ntrefseq
          FROM descriptions, sources, refseqs, targets, locuslinks, data
          WHERE descriptions.gbId=targets.gbId and
          Targets.gbid = locuslinks.gbId
          locuslinks.linkId=refseqs.linkId and
          targets.affyId=data.affyId and
          data.exptId=sources.exptId
  description
                                                                 source
                                                                               ntrefsea
  Homo sapiens immunoglobulin lambda locus DNA, clone 288A10 | Human Liver |
                                                                               NG 000002
  Human rearranged immunoglobulin lambda light chain mRNA
                                                               | Human Liver
                                                                               NG 000002
  Homo sapiens immunoglobulin lambda locus DNA, clone 31F3
                                                                Human Liver
                                                                               NG 000002
  Homo sapiens immunoglobulin lambda locus DNA, clone 288A10 |
                                                                 Human Liver
                                                                               NG 000002
  Human rearranged immunoglobulin lambda light chain mRNA
                                                                Human Liver
                                                                               NG 000002
                                                      Data
                                                                         Sources
                                                      affyld
                                                                         exptld
                               Targets
                                                      exptld
           Descriptions
                                affyld -
                                                                         source
              gbld
                                                      level
                                 gbld
```

species

RefSeqs

linkId

ntRefSeq

aaRefSeq

LocusLinks

gbld

linkId

Self join

• Explore data relationships within a table

```
SELECT data1.affyId, data1.exptId AS exptId1, data2.exptId AS exptId2, data1.level AS level1, data2.level AS level2

FROM data data1, data data2

WHERE data1.affyId=data2.affyId AND data1.level>=data2.level*2;
```

+	exptId1	exptId2	level1	+ level2 +
31325_at 31325_at 31325_at 31325_at 31325_at	1 1 1 2 5	4 5 6 6	191 191 191 101 71	51 71 31 31 31