# BITAH05 - Databanktechnologie

Jasper Anckaert

# Lecture 2 – Database schema, normalization and MySQL Workbench

# Previously

- Database
  - Collection of data that needs to be stored
  - Structured
  - Used everywhere
- Database system
  - Hardware – data – software – users
  - Storage space – quick – little redundancy – secure – clear structure
- Database Management System (DBMS)
  - Software application that interacts with the user, other applications, and the database itself to capture and analyse data
  - Storage – Retrieval – Manipulation – Authentication & authorization
- Relational databases – Relational Database Management System (RDBMS)
  - Enforce data integrity
  - Enforce referential intigrety
  - Rules of E. Codd

# Previously

- MySQL
  - Install, connect to and secure server
  - User – host – database – table
  - Privileges
  - Options file

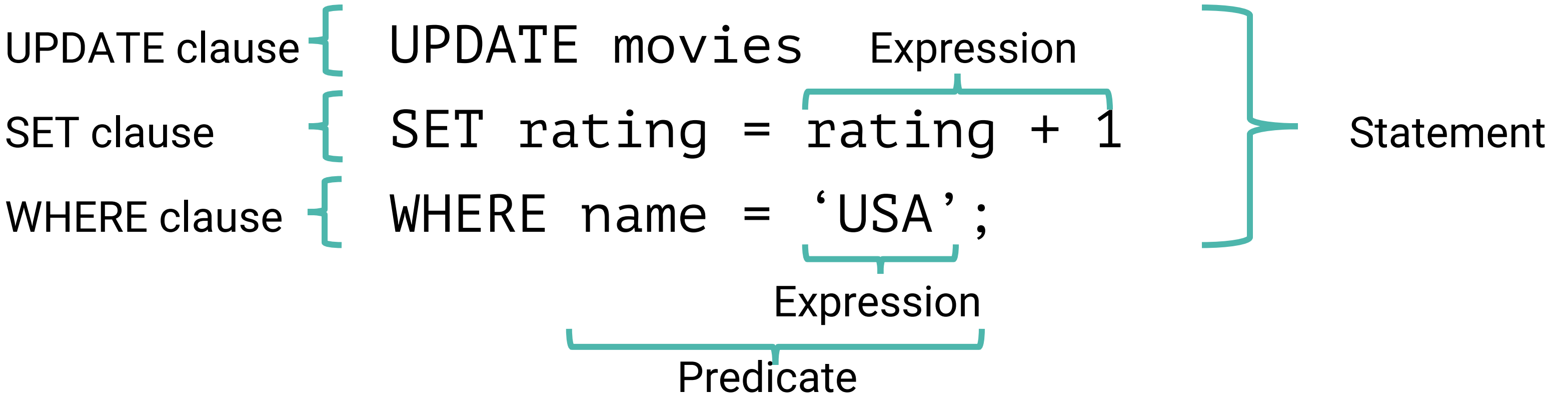
  - Create database
  - Grant privileges
  - Show databases, tables columns, create statement

# Previously

- `SQL`
  - Data definition language
    - Statements to design database
    - `CREATE`, `ALTER`, `DROP`, …
  - Data manipulation language
    - Statements to manage data
    - CRUD
    - `SELECT`, `INSERT`, `UPDATE`, `DELETE`
  - Data control language
    - Statements to manage database rights
    - `GRANT`, `REVOKE`

# Previously

SQL: Structured Query Language



```
UPDATE movies
SET rating = rating + 1
WHERE name = ‘USA’;
```

# Previously

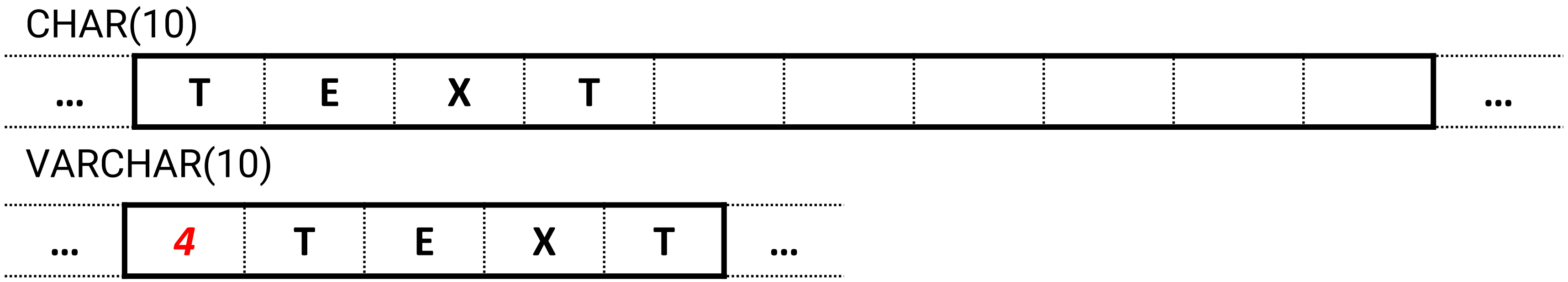
Column types

- INT
  - Integer
  - SIGNED: -2 147 483 648 tot 2 147 483 647
  - UNSIGNED: 0 tot 4 294 967 295
  - TINYINT, BIGINT, SMALLINT
- FLOAT & DOUBLE
  - Numbers with decimal point
  - FLOAT: 7 digits after decimal point, DOUBLE: 15 digits after decimal point
- DATE
  - YYYY-MM-DD
  - DATETIME
    - YYYY-MM-DD HH:MM:SS
    - ! TIMESTAMP ! No dates < 1970 and > 2038

# Previously

## Column types

- VARCHAR & CHAR
  - String with a certain number of characters
  - Define max number of characters e.g. VARCHAR(200)
  - VARCHAR: up to 65 535 characters
  - CHAR: up to 255 characters, spaces are added to reach required length



CHAR(10)

| … | T | E | X | T |  |  |  |  |  |  | … |
|---|---|---|---|---|---|---|---|---|---|---|---|

VARCHAR(10)

| … | 4 | T | E | X | T | … |
|---|---|---|---|---|---|---|

  - VARCHAR is more efficient in storage, CHAR is faster for reading data
  - Similar for INT vs BIGINT vs …

# Previously

## Column types

- TEXT & BLOB
  - Used for texts that are not queried often or do not have to be searchable
  - BLOB for binary data (images, …)
- ENUM
  - List of permitted values
    - E.g. Set of colours: ’red’, ‘green’, ‘blue’
  - Very efficient

# Previously

## Constraints

On top of column types, there are some additional requirements per column

- Primary key
    - Only 1 PK per table, all values must be unique
- UNIQUE
    - All values (or combinations) must be unique
- NOT NULL
    - Field can not be empty when adding data (empty = null)
- Default
    - Default value for a field
- Foreign key
    - Same constraints as referenced column
    - Security when adjusting linked data possible

# Previously

- INSERT

  `INSERT INTO` *`tbl`* `(`*`col1`*`,` *`col2`*`) VALUES (`*`val1`*`,` *`val2`*`);`

- SELECT

  `SELECT` *`columns`* `FROM` *`tbl;`*

- ORDER BY

  `SELECT` *`columns`* `FROM` *`tbl`* `ORDER BY` *`col1`* `[`*`asc|desc`*`] [,` *`col2`* `[`*`asc|desc`*`]...]`*`;`*

- Calculated rows
  - Built in functions for numbers, strings, dates
- Column aliases
  - Can be used in the `ORDER BY` clause
- WHERE

  `SELECT` *`columns`* `FROM` *`tbl`* `WHERE` *`condition(s)`* `[ORDER BY` *`sortcol`*`]`*`;`*

- NULL values

  `SELECT … WHERE` *`col`* `IS [NOT] NULL;`

  `SELECT ifnull(`*`col`*`,` *`value`*`) …`

# Previously

- AND, OR, NOT, XOR
  - Boolean logic
- DISTINCT

  SELECT DISTINCT(*cols*) FROM …
- LIMIT, OFFSET

  SELECT … LIMIT *n* [OFFSET *r*];
- Aggregation
  - Built in functions e.g. count(), sum(), min(), max(), …
- GROUP BY

  SELECT [*col*,] *aggregatefunctions* FROM *src* [WHERE *cond*] GROUP BY *col* [ORDER BY …];
- HAVING

  SELECT [*col*, ] *aggregatefunctions* FROM *src* [WHERE *cond1*] GROUP BY *col* HAVING *cond2* [ORDER BY …];

# Previously

Execution order

1. Input columns are determined
2. `WHERE` – input columns are filtered
3. `GROUP BY` – sorting & grouping of filtered input
4. Aggregation functions are calculated
5. `HAVING` – aggregation functions are filtered
6. `ORDER BY` – output is sorted
7. `LIMIT`/`OFFSET` – output is chopped

# Previously

- JOIN

  ```
  SELECT * FROM tbl1 JOIN tbl2 ON tbl1.col1 = tbl2.col2;
  ```

- INNER, LEFT, RIGHT, OUTER
- Foreign key
  - Primary key of other table
  - Index
- Relations between tables
  - 1:n one-to-many relationship
  - n:m many-to-many relationship (xref-table)
- Views

  ```
  CREATE VIEW viewname as SELECT …
  ```

- Index
  - 1 per query

# Previously

- Allow redundancy

| SNOWFLAKE | STAR |
|---|---|
| No redundancy | Redundant data |
| Easy to maintain and change | Less easy to maintain/change |
| Complex queries | Lower query complexity |
| Slower (more JOINs) | Faster |
| Uses less space | Uses more space (data is stored twice or more) |
| Bottom up | Top down |

- DUMP
  - Create database backup

# Relational databases with MySQL - JOINs

## Exercises (bioinf db)

- Give the accession number for the 3 longest human genes in the database
- How many genes are in the database for species with a genome size of at least 3000
- For the gene with accession number *NM_008220*, give
  - The length of the gene
  - The total genome size
- Retrieve all genes comming from a genome that was published in the first half of the year
- Retrieve all unique class names for model organisms with al least 10 chromosomes

# MySQL Workbench

## Database schema

- MySQL monitor to execute DDL commands
  - Servers
  - Advanced users
- GUI
  - HeidiSQL
  - MySQL Workbench

# MySQL Workbench

## Installation

- Available as for download (several operationg systems)
  - http://dev.mysql.com/downloads/workbench/

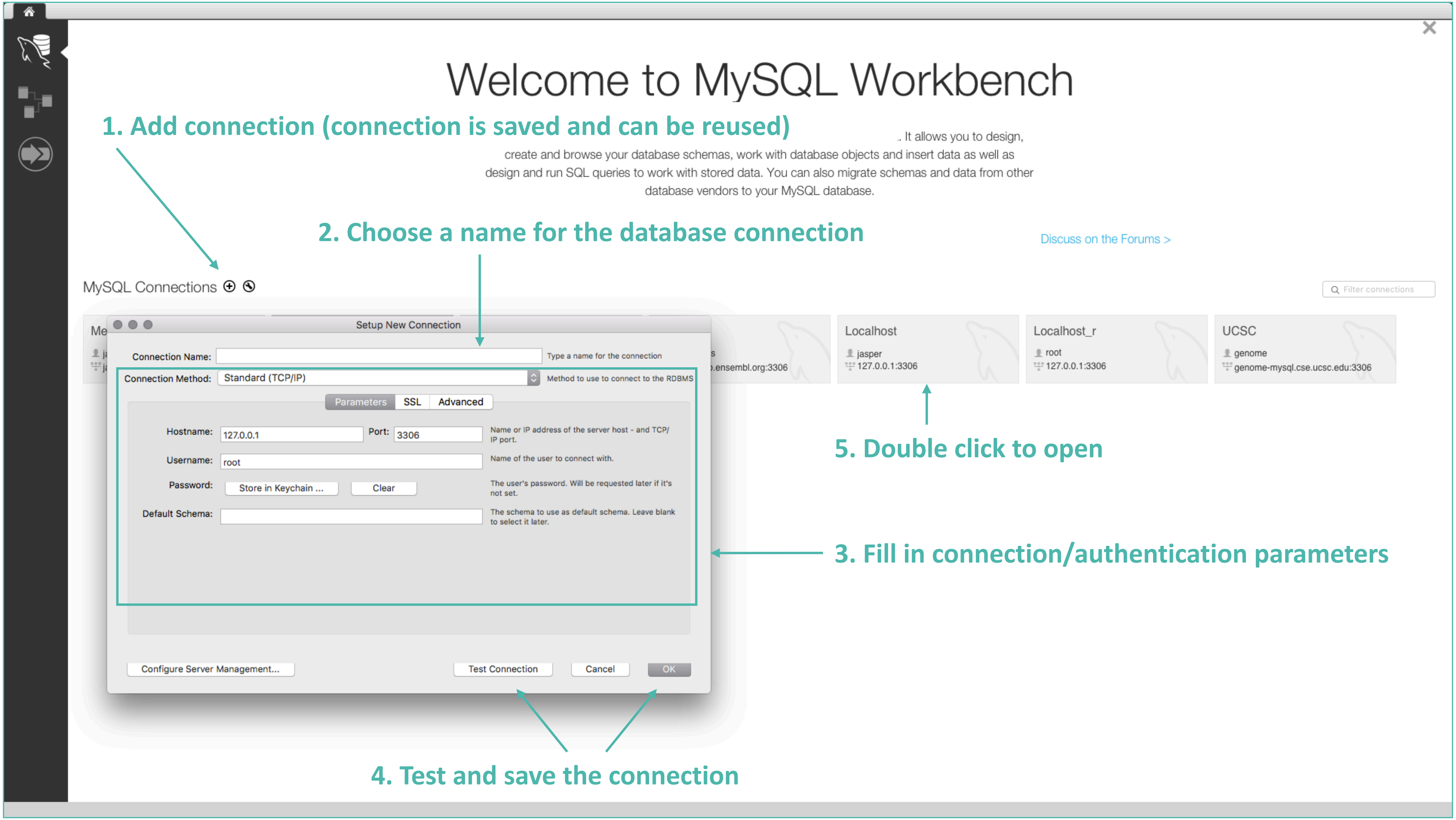
- To install DEB package

```
# dpkg -i package.deb
```

- To install RPM package

```
# rpm -Uvh package.rpm
```

- To install on Windows/Mac
  - Double click `package.msi` or `package.dmg`


Welcome to MySQL Workbench
. It allows you to design, create and browse your database schemas, work with database objects and insert data as well as design and run SQL queries to work with stored data. You can also migrate schemas and data from other database vendors to your MySQL database.
Discuss on the Forums >
MySQL Connections ⊕ ⊗
Filter connections
Localhost
jasper
127.0.0.1:3306
Localhost_r
root
127.0.0.1:3306
UCSC
genome
genome-mysql.cse.ucsc.edu:3306
.ensembl.org:3306
Setup New Connection
Parameters
SSL
Advanced
Store in Keychain ...
Clear
Configure Server Management...
Test Connection
Cancel
OK

1. Add connection (connection is saved and can be reused)

2. Choose a name for the database connection

Connection Name: Type a name for the connection

Connection Method: Standard (TCP/IP) Method to use to connect to the RDBMS

Hostname: 127.0.0.1 Port: 3306 Name or IP address of the server host - and TCP/IP port.

Username: root Name of the user to connect with.

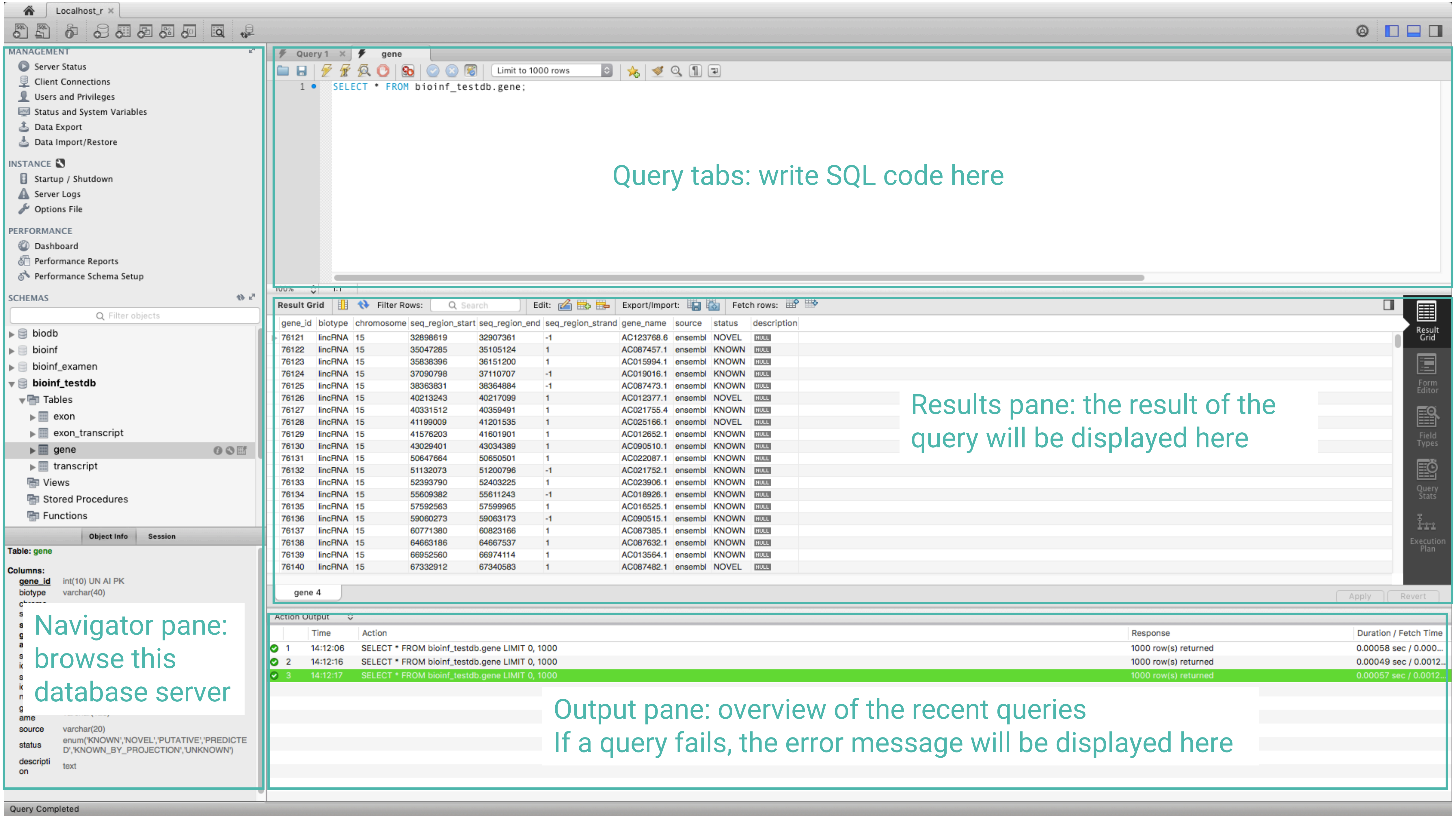
Password: The user's password. Will be requested later if it's not set.

Default Schema: The schema to use as default schema. Leave blank to select it later.

3. Fill in connection/authentication parameters

4. Test and save the connection

5. Double click to open



```
SELECT * FROM bioinf_testdb.gene;
```

Query tabs: write SQL code here

Table: gene

Columns:

| | |
|---|---|
| gene_id | int(10) UN AI PK |
| biotype | varchar(40) |
| source | varchar(20) |
| status | enum('KNOWN','NOVEL','PUTATIVE','PREDICTED','KNOWN_BY_PROJECTION','UNKNOWN') |
| description | text |

Navigator pane: browse this database server

| gene_id | biotype | chromosome | seq_region_start | seq_region_end | seq_region_strand | gene_name | source | status | description |
|---|---|---|---|---|---|---|---|---|---|
| 76121 | lincRNA | 15 | 32898619 | 32907361 | -1 | AC123768.6 | ensembl | NOVEL | NULL |
| 76122 | lincRNA | 15 | 35047285 | 35105124 | 1 | AC087457.1 | ensembl | KNOWN | NULL |
| 76123 | lincRNA | 15 | 35838396 | 36151200 | 1 | AC015994.1 | ensembl | KNOWN | NULL |
| 76124 | lincRNA | 15 | 37090798 | 37110707 | -1 | AC019016.1 | ensembl | KNOWN | NULL |
| 76125 | lincRNA | 15 | 38363831 | 38364884 | -1 | AC087473.1 | ensembl | KNOWN | NULL |
| 76126 | lincRNA | 15 | 40213243 | 40217099 | 1 | AC012377.1 | ensembl | NOVEL | NULL |
| 76127 | lincRNA | 15 | 40331512 | 40359491 | 1 | AC021755.4 | ensembl | KNOWN | NULL |
| 76128 | lincRNA | 15 | 41199009 | 41201535 | 1 | AC025166.1 | ensembl | NOVEL | NULL |
| 76129 | lincRNA | 15 | 41576203 | 41601901 | 1 | AC012652.1 | ensembl | KNOWN | NULL |
| 76130 | lincRNA | 15 | 43029401 | 43034389 | 1 | AC090510.1 | ensembl | KNOWN | NULL |
| 76131 | lincRNA | 15 | 50647664 | 50650501 | 1 | AC022087.1 | ensembl | KNOWN | NULL |
| 76132 | lincRNA | 15 | 51132073 | 51200796 | -1 | AC021752.1 | ensembl | KNOWN | NULL |
| 76133 | lincRNA | 15 | 52393790 | 52403225 | 1 | AC023906.1 | ensembl | KNOWN | NULL |
| 76134 | lincRNA | 15 | 55609382 | 55611243 | -1 | AC018926.1 | ensembl | KNOWN | NULL |
| 76135 | lincRNA | 15 | 57592563 | 57599965 | 1 | AC016525.1 | ensembl | KNOWN | NULL |
| 76136 | lincRNA | 15 | 59060273 | 59063173 | -1 | AC090515.1 | ensembl | KNOWN | NULL |
| 76137 | lincRNA | 15 | 60771380 | 60823166 | 1 | AC087385.1 | ensembl | KNOWN | NULL |
| 76138 | lincRNA | 15 | 64663186 | 64667537 | 1 | AC087632.1 | ensembl | KNOWN | NULL |
| 76139 | lincRNA | 15 | 66952560 | 66974114 | 1 | AC013564.1 | ensembl | KNOWN | NULL |
| 76140 | lincRNA | 15 | 67332912 | 67340583 | 1 | AC087482.1 | ensembl | NOVEL | NULL |

Results pane: the result of the query will be displayed here

| | Time | Action | Response | Duration / Fetch Time |
|---|---|---|---|---|
| ✓ 1 | 14:12:06 | SELECT * FROM bioinf_testdb.gene LIMIT 0, 1000 | 1000 row(s) returned | 0.00058 sec / 0.000... |
| ✓ 2 | 14:12:16 | SELECT * FROM bioinf_testdb.gene LIMIT 0, 1000 | 1000 row(s) returned | 0.00049 sec / 0.0012... |
| ✓ 3 | 14:12:17 | SELECT * FROM bioinf_testdb.gene LIMIT 0, 1000 | 1000 row(s) returned | 0.00057 sec / 0.0012... |

Output pane: overview of the recent queries
If a query fails, the error message will be displayed here

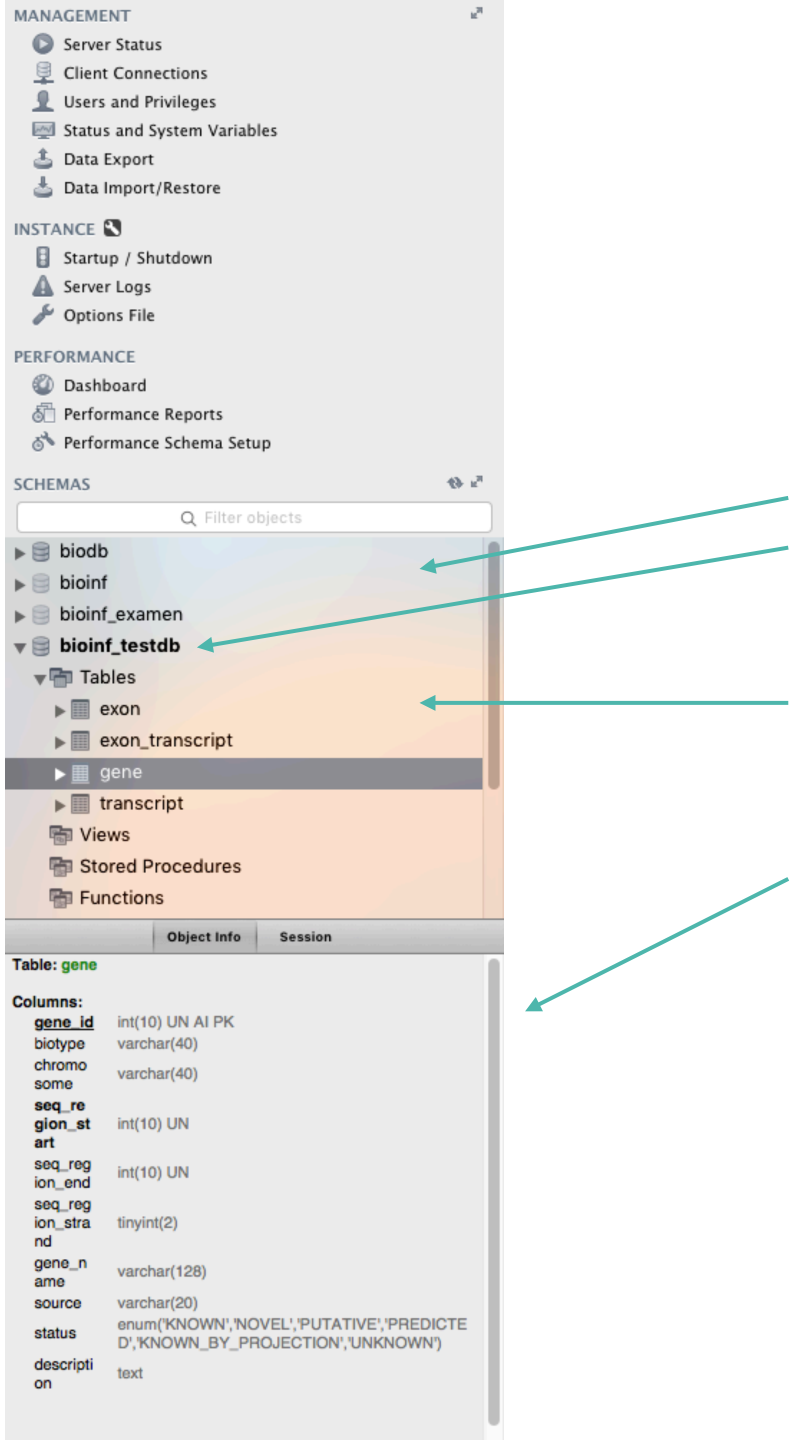


**Table:** gene

**Columns:**

| | |
|---|---|
| **gene_id** | int(10) UN AI PK |
| biotype | varchar(40) |
| chromosome | varchar(40) |
| **seq_region_start** | int(10) UN |
| seq_region_end | int(10) UN |
| seq_region_strand | tinyint(2) |
| gene_name | varchar(128) |
| source | varchar(20) |
| status | enum('KNOWN','NOVEL','PUTATIVE','PREDICTED','KNOWN_BY_PROJECTION','UNKNOWN') |
| description | text |

Different databases on this server

**BOLD** = currently active database, all queries will be executed in this db, double click to change

Browse tables in the db here

More information on the currently selected item

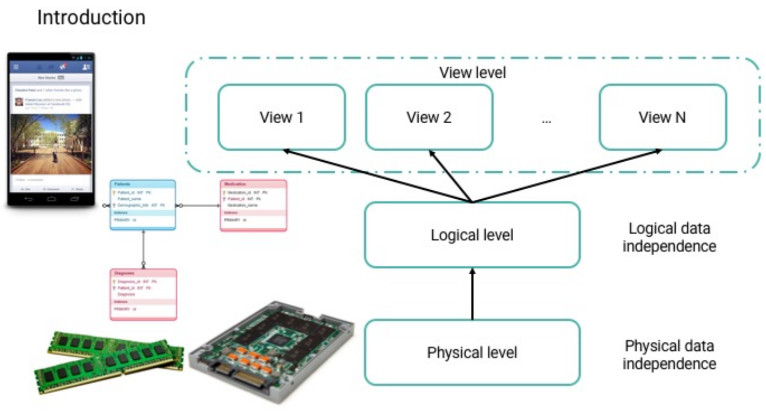
# MySQL Workbench

## Exercices

- Connect to the MySQL database server
- Explore the server
  - How many databases are available to you?
  - How many tables does each database have?
  - What are the column types of the gene table (bioinf_testdb)?

# MySQL Workbench

## Data model



- Determines the structure of data
  - Conceptual data model
    - Structure of and relations between entities
    - Entity Relationship Diagram
  - Logical data model
    - Structure of and references between tables
    - Relations → foreign key constraints
    - Data Structure Diagram
  - Physical data model
    - Physical means by which data are stored (partitions, CPUs, tablespaces, …)

# MySQL Workbench

## Database models

- Flat model
    - Single two-dimensional array of data elements
    - E.g. spreadsheet
- Hierarchical model
    - Data is organized into a tree-like structure
    - Records are connected through links
- Network model
    - Each record can have multiple parents and child records

# MySQL Workbench

Database models

- Relational model
  - Tables are relations
  - Links between tables are not explicitely defined → use keys
  - What we've been using so far but with deviations
- Object-relational model
  - Relational model with object-oriented features
  - PostgreSQL
- Object oriented model
  - Data is represented in the form of objects
  - Use same model of representation as in programming language

# MySQL Workbench

Creating a database - Normalisation

- Organizing columns and tables
  - Reduce redundancy
  - Improve integrity

- Remember E. Codd?

# MySQL Workbench

## Normalisation

- UNF
  - Unnormalized form
  - Group all data in one entity
- 1NF
  - Eliminate repeating (and calculated) groups in individual tables
  - Create separate table for each set of related data
  - Identify each set of related data with a primary key
- 2NF
  - Every non-prime attribute of the table is dependent on the whole key of every candidate key
- 3NF
  - Every non-prime attribute is non-transitively dependent on every key

# MySQL Workbench

## Normalisation

- BCNF
  - Any attribute on which some other attribute is fully functionally dependent = determinant
  - Every determinant is a candidate key

- 4NF – ETNF – 5NF – 6NF – DKNF

# MySQL Workbench

## Normalisation – example

| Patient_no | Patient_name | Appointment_id | Time | Doctor |
|---|---|---|---|---|
| 1 | John | 0 | 09:00 | Zorro |
| 2 | Kerr | 0 | 09:00 | Killer |
| 3 | Adam | 1 | 10:00 | Zorro |
| 4 | Robert | 0 | 13:00 | Killer |
| 5 | Zane | 1 | 14:00 | Zorro |

UNF DB(Patno,PatName,appNo,time,doctor)

1NF DB(Patno,PatName,appNo,time,doctor)

2NF DB(Patno,appNo,time,doctor)
R1(Patno,PatName)

3NF 2NF

BCNF DB(Patno,time,doctor)
R1(Patno,PatName)
R2(time,appNo)

# MySQL Workbench

## Normalisation – example

- Why is this table not in 1NF?
- Normalize up to 3NF
- Identify all keys in your 3NF relations

| branchNo | branchAddress | telNos |
|---|---|---|
| B001 | 8 Jefferson Way, Portland, OR 97201 | 503-555-3618, 503-555-2727, 503-555-6534 |
| B002 | City Center Plaza, Seattle, WA 98122 | 206-555-6756, 206-555-8836 |
| B003 | 14 – 8th Avenue, New York, NY 10012 | 212-371-3000 |
| B004 | 16 – 14th Avenue, Seattle, WA 98128 | 206-555-3131, 206-555-4112 |

# MySQL Workbench

## Exercises

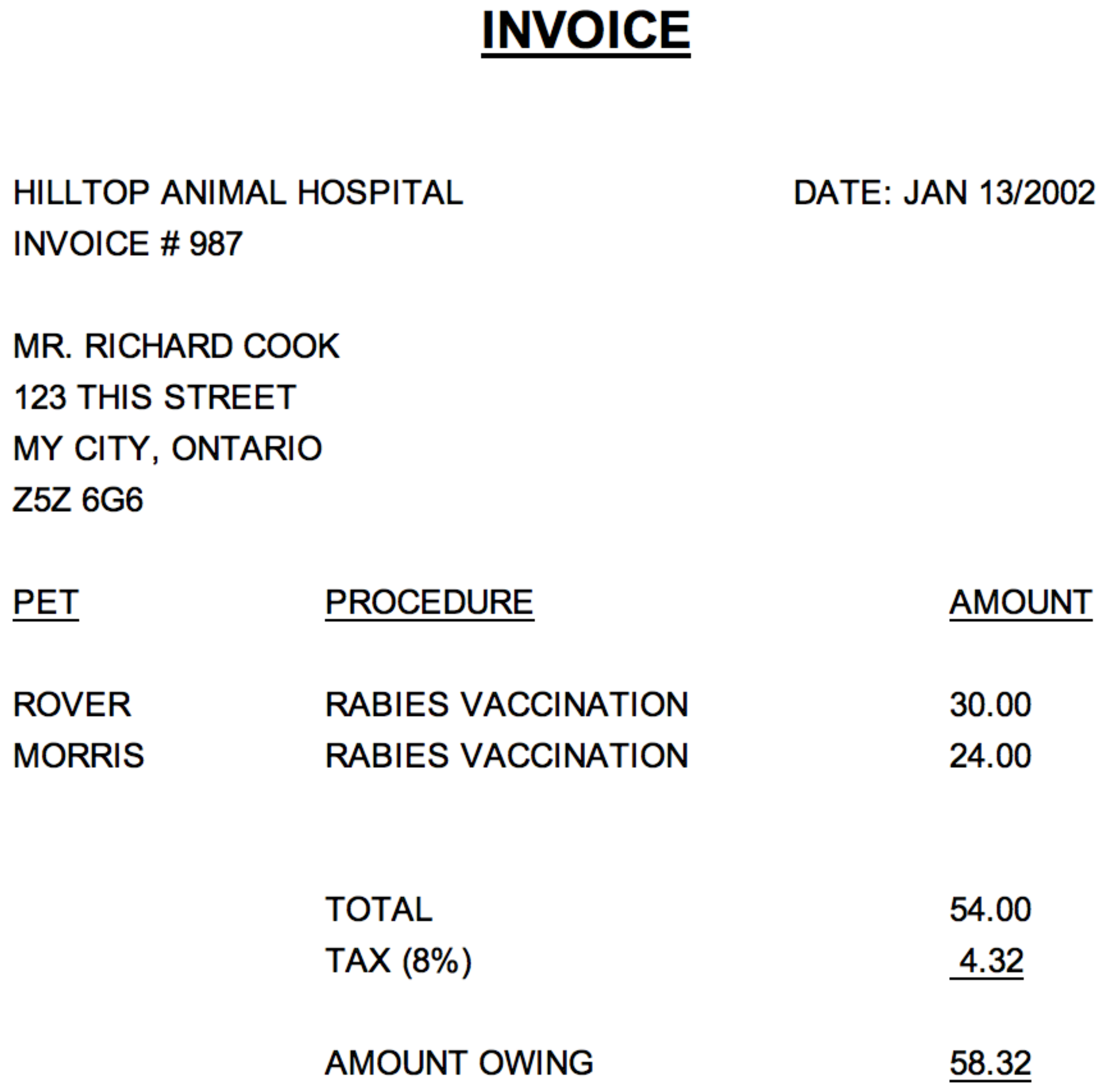
- Normalise up to 3NF (note: a procedure may occur on multiple dates)

| Pet_id | Pet_name | Pet_type | Pet_age | owner | Visit_date | procedure |
|---|---|---|---|---|---|---|
| 246 | Rover | dog | 12 | Sam Coock | 2002-01-13 | 01 – Rabies vaccination |
| | | | | | 2005-03-27 | 10 - Examination |
| | | | | | 2003-04-02 | 05 – Heart worm test |
| 296 | Spot | dog | 2 | Terry Kim | 2002-01-21 | 08 – Tetanus vaccination |
| | | | | | 200-03-10 | 05 – Heart worm test |
| 341 | Morris | cat | 4 | Sam Coock | 2001-01-23 | 01– Rabies vaccination |
| | | | | | 2002-01-13 | 01 – Rabies vaccination |
| 519 | Tweedy | bird | 2 | Terry Kim | 2002-04-30 | 20 – Check up |
| | | | | | 2002-04-30 | 12 – Eye wash |

# MySQL Workbench

## Exercises

- Normalise up to 3NF



**INVOICE**

HILLTOP ANIMAL HOSPITAL DATE: JAN 13/2002
INVOICE # 987

MR. RICHARD COOK
123 THIS STREET
MY CITY, ONTARIO
Z5Z 6G6

| PET | PROCEDURE | AMOUNT |
|---|---|---|
| ROVER | RABIES VACCINATION | 30.00 |
| MORRIS | RABIES VACCINATION | 24.00 |
| | TOTAL | 54.00 |
| | TAX (8%) | 4.32 |
| | AMOUNT OWING | 58.32 |

# MySQL Workbench

## Exercises

- Normalise up to BCNF
  - Grade_report(StudNo,StudName,(Major,Adviser,(CourseNo,Ctitle,InstrucName,InstructLocn,Grade)))
  - Functional dependencies
    - StudNo -> StudName
      CourseNo -> Ctitle,InstrucName
      InstrucName -> InstrucLocn
      StudNo,CourseNo,Major -> Grade
      StudNo,Major -> Advisor
      Advisor -> Major

# MySQL Workbench

## Exercises

video(title,director,serial)
customer(name,addr,memberno)
hire(memberno,serial,date)

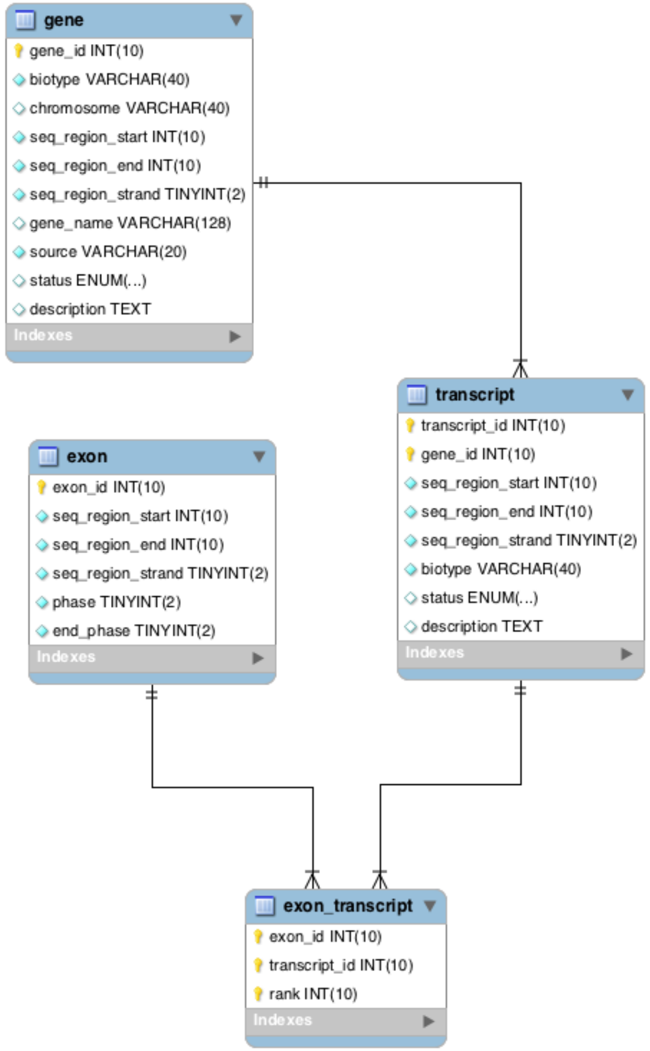
title->director,serial
serial->title serial->director
name,addr -> memberno
memberno -> name,addr
serial,date -> memberno

- What normal form is this?
- Convert to BCNF

# MySQL Workbench

## Creating tables

- Use the ”model” interface in MySQL Workbench
    - DDL statements will be auto-generated
- Tables can be placed anywhere and dragged around
- Foreign keys will be displayed as lines and arrows

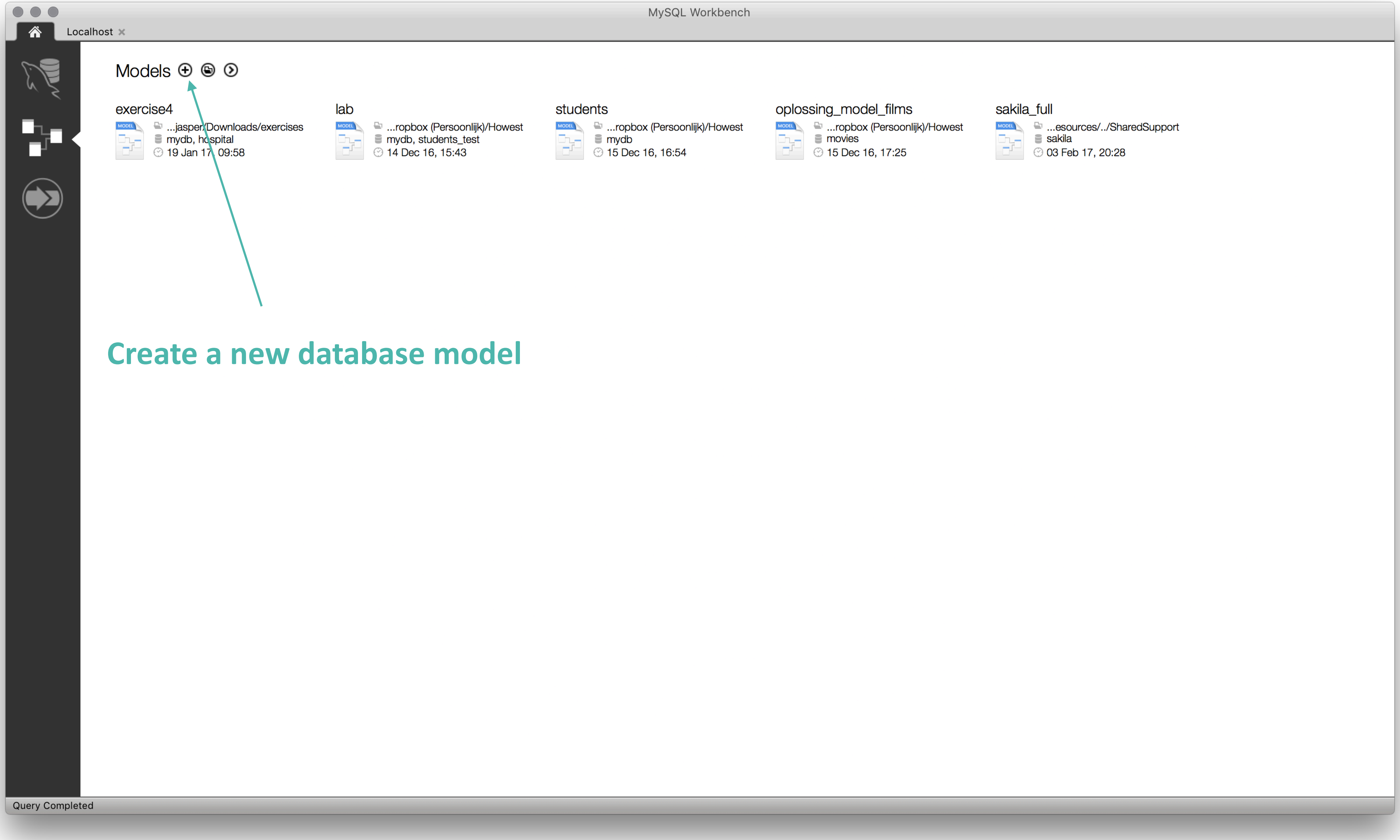


gene
gene_id INT(10)
biotype VARCHAR(40)
chromosome VARCHAR(40)
seq_region_start INT(10)
seq_region_end INT(10)
seq_region_strand TINYINT(2)
gene_name VARCHAR(128)
source VARCHAR(20)
status ENUM(...)
description TEXT
Indexes

transcript
transcript_id INT(10)
gene_id INT(10)
seq_region_start INT(10)
seq_region_end INT(10)
seq_region_strand TINYINT(2)
biotype VARCHAR(40)
status ENUM(...)
description TEXT
Indexes

exon
exon_id INT(10)
seq_region_start INT(10)
seq_region_end INT(10)
seq_region_strand TINYINT(2)
phase TINYINT(2)
end_phase TINYINT(2)
Indexes

exon_transcript
exon_id INT(10)
transcript_id INT(10)
rank INT(10)
Indexes



MySQL Workbench

Localhost

Models

exercise4
...jasper/Downloads/exercises
mydb, hospital
19 Jan 17, 09:58

lab
...ropbox (Persoonlijk)/Howest
mydb, students_test
14 Dec 16, 15:43

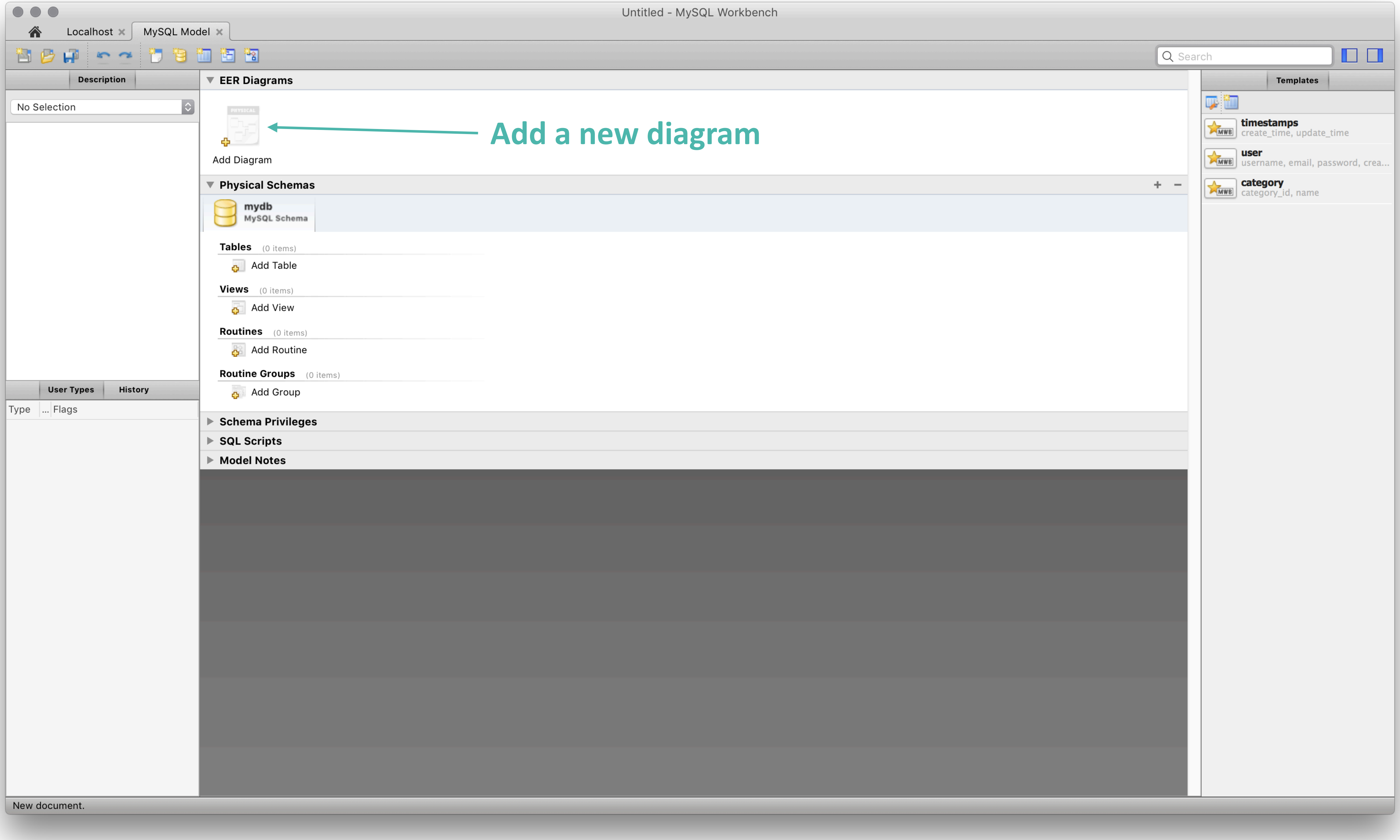
students
...ropbox (Persoonlijk)/Howest
mydb
15 Dec 16, 16:54

oplossing_model_films
...ropbox (Persoonlijk)/Howest
movies
15 Dec 16, 17:25

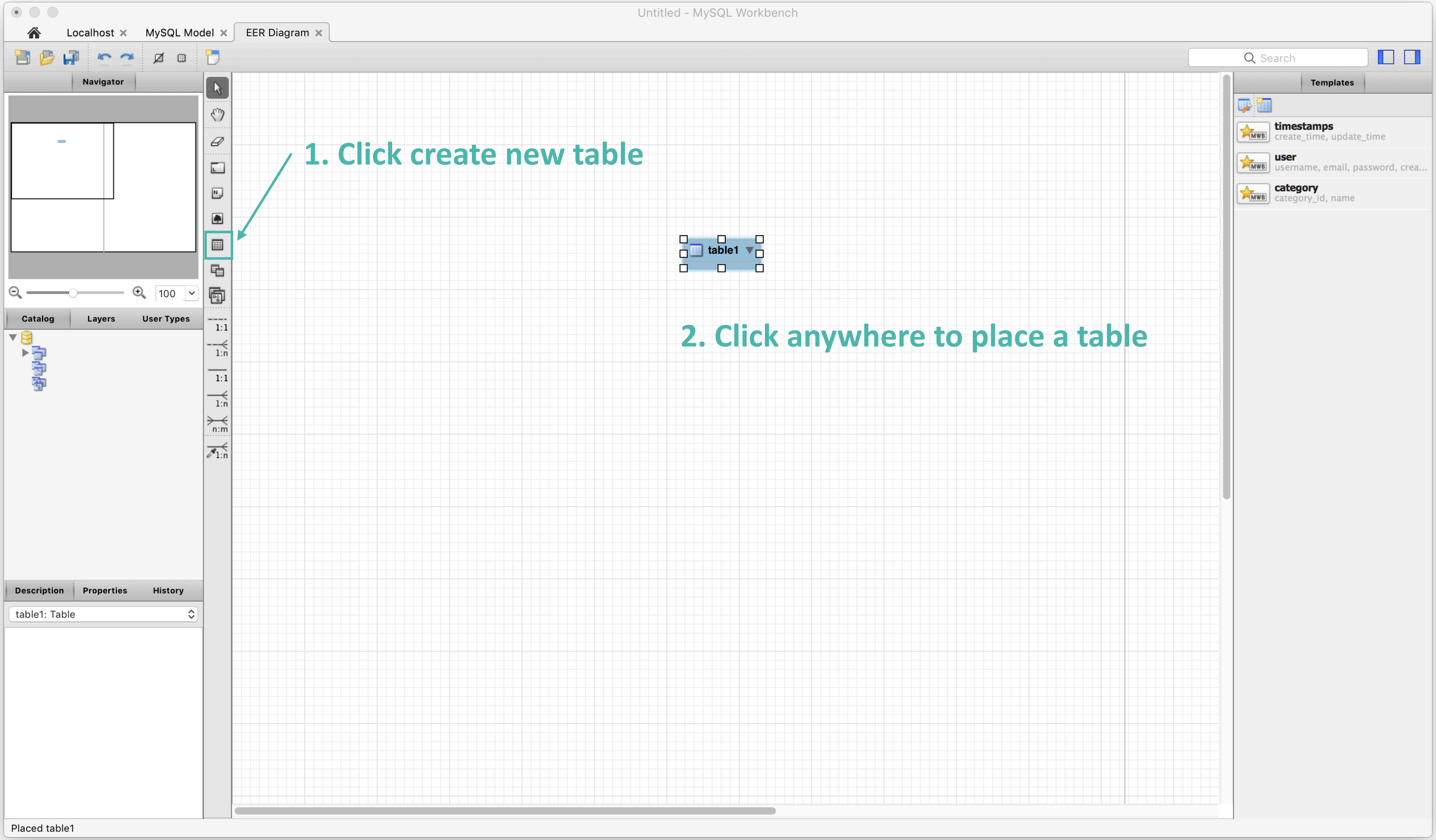
sakila_full
...esources/../SharedSupport
sakila
03 Feb 17, 20:28

Query Completed

Create a new database model



Add a new diagram



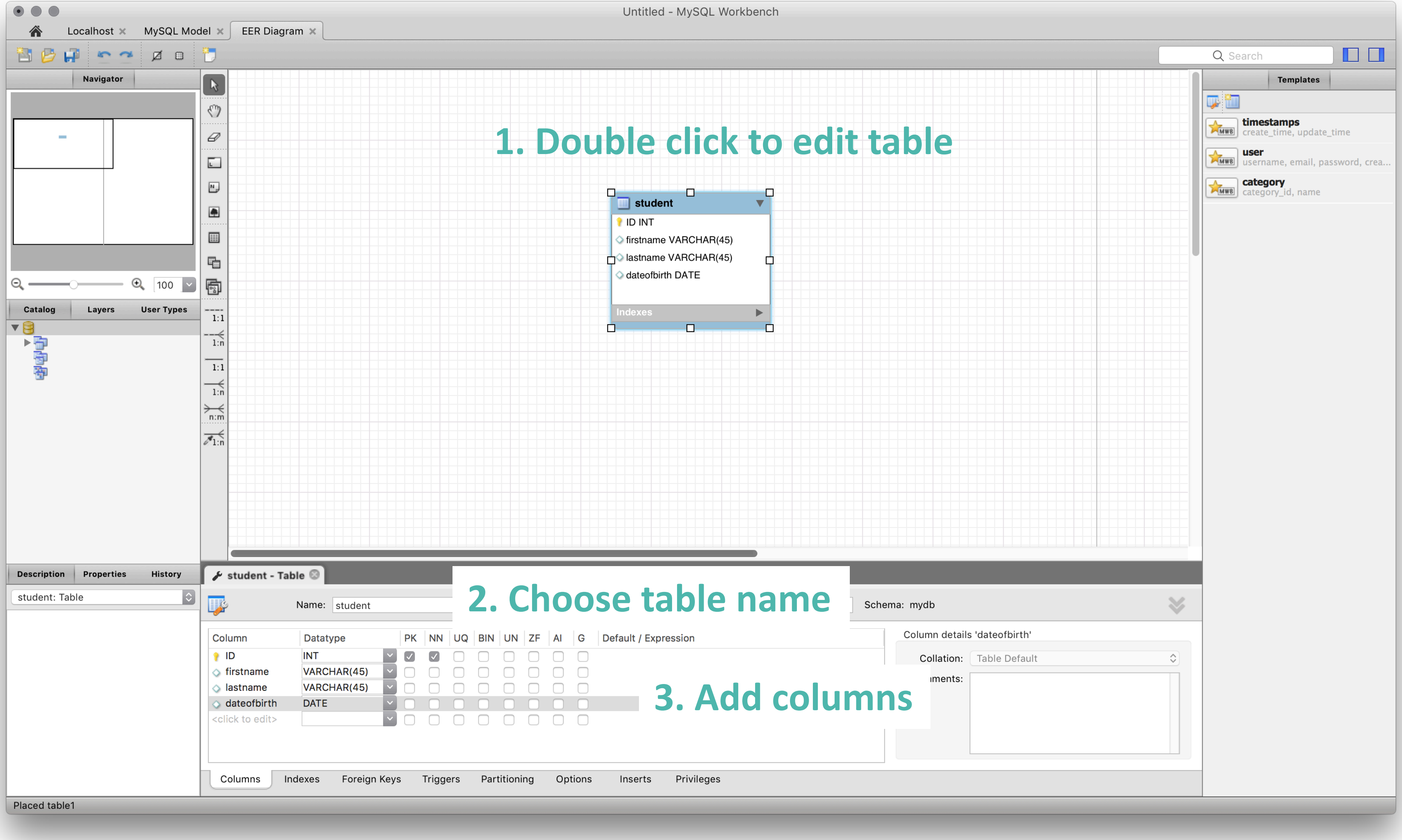
1. Click create new table

2. Click anywhere to place a table

Placed table1

# MySQL Workbench

## Creating tables



1. Double click to edit table

student
- ID INT
- firstname VARCHAR(45)
- lastname VARCHAR(45)
- dateofbirth DATE

Indexes

2. Choose table name

Name: student

Schema: mydb

3. Add columns

| Column | Datatype | PK | NN | UQ | BIN | UN | ZF | AI | G | Default / Expression |
|---|---|---|---|---|---|---|---|---|---|---|
| ID | INT | ☑ | ☑ | □ | □ | □ | □ | □ | □ | |
| firstname | VARCHAR(45) | □ | □ | □ | □ | □ | □ | □ | □ | |
| lastname | VARCHAR(45) | □ | □ | □ | □ | □ | □ | □ | □ | |
| dateofbirth | DATE | □ | □ | □ | □ | □ | □ | □ | □ | |
| <click to edit> | | □ | □ | □ | □ | □ | □ | □ | □ | |

Column details 'dateofbirth'

Collation: Table Default

ıments:

# MySQL Workbench

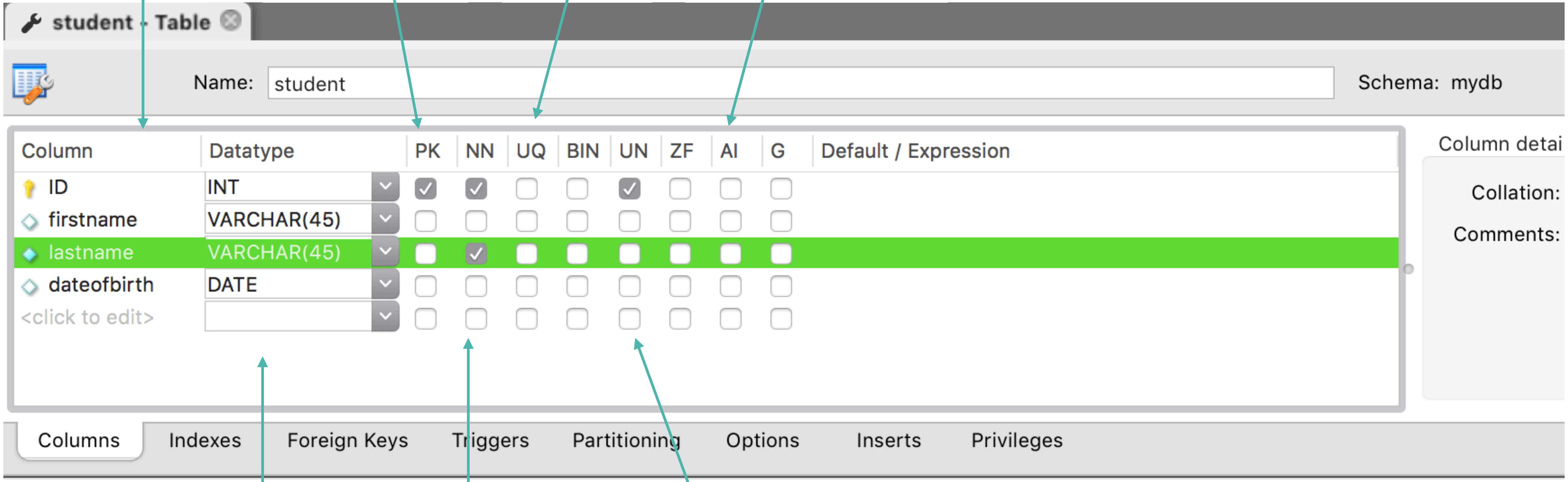
## Add columns to table

Column name

Primary key

UNIQUE

Auto increment



student - Table

Name: student

Schema: mydb

| Column | Datatype | PK | NN | UQ | BIN | UN | ZF | AI | G | Default / Expression |
|---|---|---|---|---|---|---|---|---|---|---|
| ID | INT | ☑ | ☑ | □ | □ | ☑ | □ | □ | □ | |
| firstname | VARCHAR(45) | □ | □ | □ | □ | □ | □ | □ | □ | |
| lastname | VARCHAR(45) | □ | ☑ | □ | □ | □ | □ | □ | □ | |
| dateofbirth | DATE | □ | □ | □ | □ | □ | □ | □ | □ | |
| <click to edit> | | □ | □ | □ | □ | □ | □ | □ | □ | |

Column detai

Collation:

Comments:

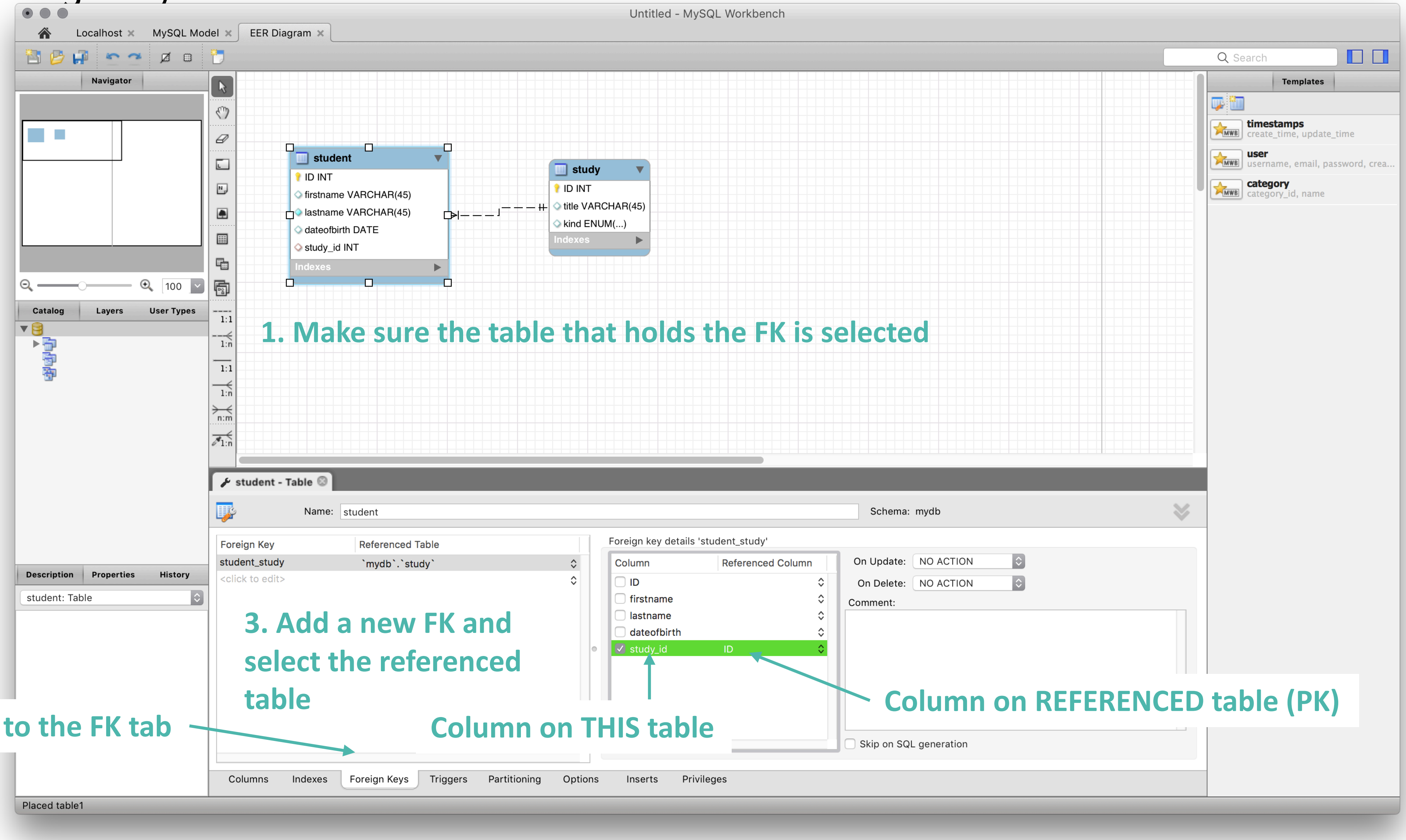
Column type

Not NULL

Unsigned (for numeric types e.g. INT)

# MySQL Workbench

## Add foreign keys to table



student
- ID INT
- firstname VARCHAR(45)
- lastname VARCHAR(45)
- dateofbirth DATE
- study_id INT
- Indexes

study
- ID INT
- title VARCHAR(45)
- kind ENUM(...)
- Indexes

timestamps
create_time, update_time

user
username, email, password, crea...

category
category_id, name

student: Table

student - Table

Name: student

Schema: mydb

| Foreign Key | Referenced Table |
|---|---|
| student_study | \`mydb\`.\`study\` |
| <click to edit> | |

Foreign key details 'student_study'

| Column | Referenced Column |
|---|---|
| ☐ ID | |
| ☐ firstname | |
| ☐ lastname | |
| ☐ dateofbirth | |
| ☑ study_id | ID |

On Update: NO ACTION

On Delete: NO ACTION

Comment:

☐ Skip on SQL generation

Placed table1

1. Make sure the table that holds the FK is selected

2. Switch to the FK tab

3. Add a new FK and select the referenced table

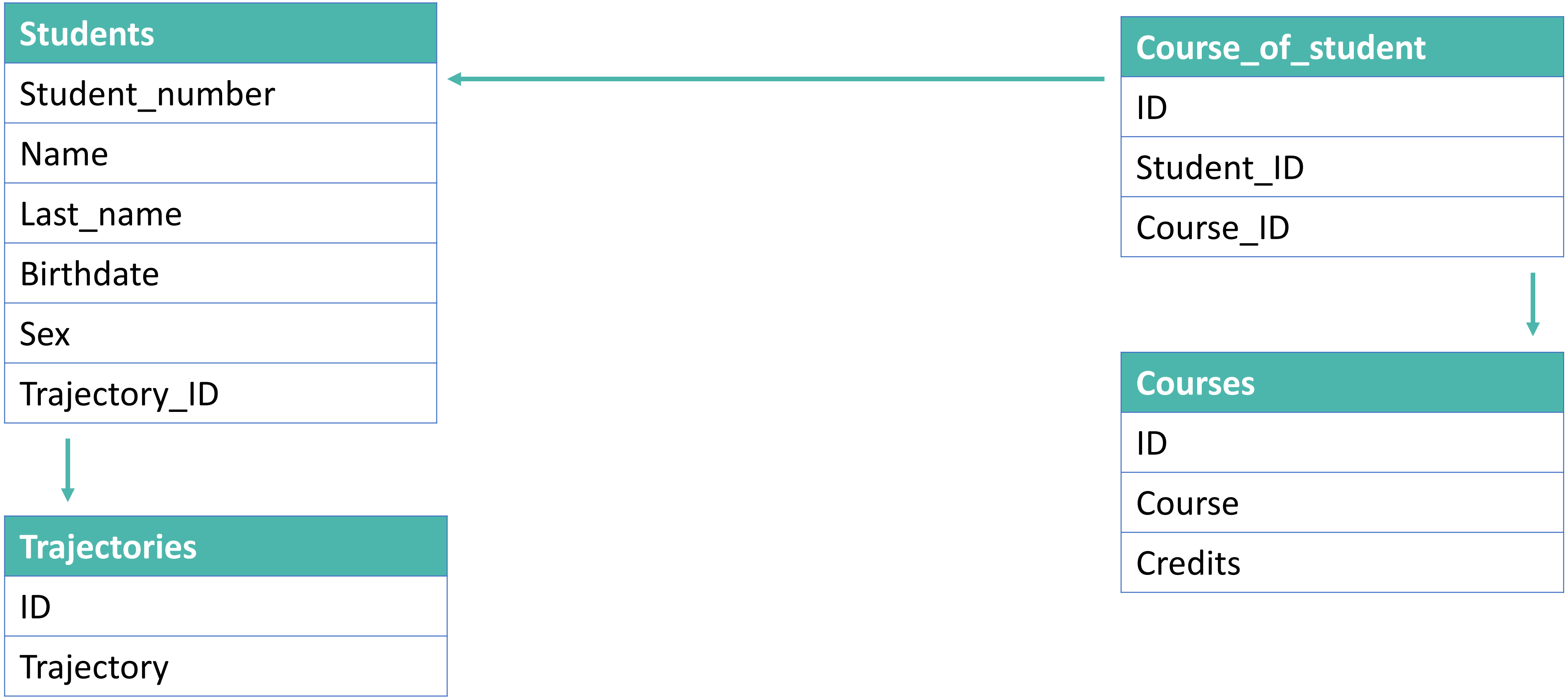
Column on THIS table

Column on REFERENCED table (PK)

# MySQL Workbench

## Exercises

- Create the following database schema



| Students |
|---|
| Student_number |
| Name |
| Last_name |
| Birthdate |
| Sex |
| Trajectory_ID |

| Trajectories |
|---|
| ID |
| Trajectory |

| Course_of_student |
|---|
| ID |
| Student_ID |
| Course_ID |

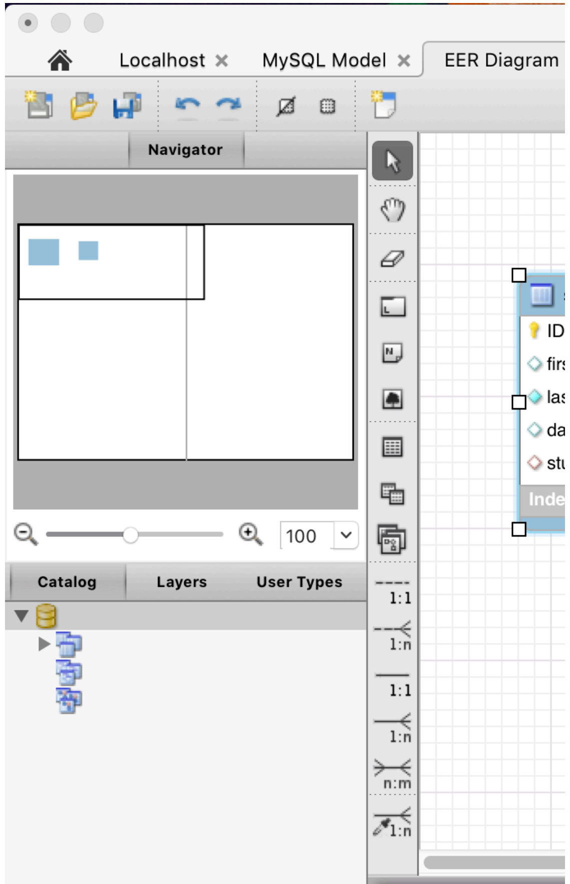
| Courses |
|---|
| ID |
| Course |
| Credits |

# MySQL Workbench

## Forward engineering

- Function in MySQL Workbench
  - Generates SQL code to create/modify a database based on your model
- Make sure the name of your database is correct!
  - Located under *Database* > *Forward engineer*
  - Check in the database browser (Refresh)

Double click to change



# MySQL Workbench

## Exercises

- Create a MySQL table to track the movies you have watched:
  - Movie title
  - Genre: action, comedy, drama, horror, science fiction
  - Date you watched to movie
  - Score: 0-10
  - Comments
- Create a table to store your favourite directors and link it with the movie table
- Create a table to store your favourite actors and link it with the movie table
- Forward engineer your tables to your database
- Add some rows to the table you have created

# MySQL Workbench

## Creating a database

- Important questions
  - Which data?
  - Constraints?
  - Application?
  - Relations between data?

⇨ Entity relationship diagram

# MySQL Workbench

## Exercises

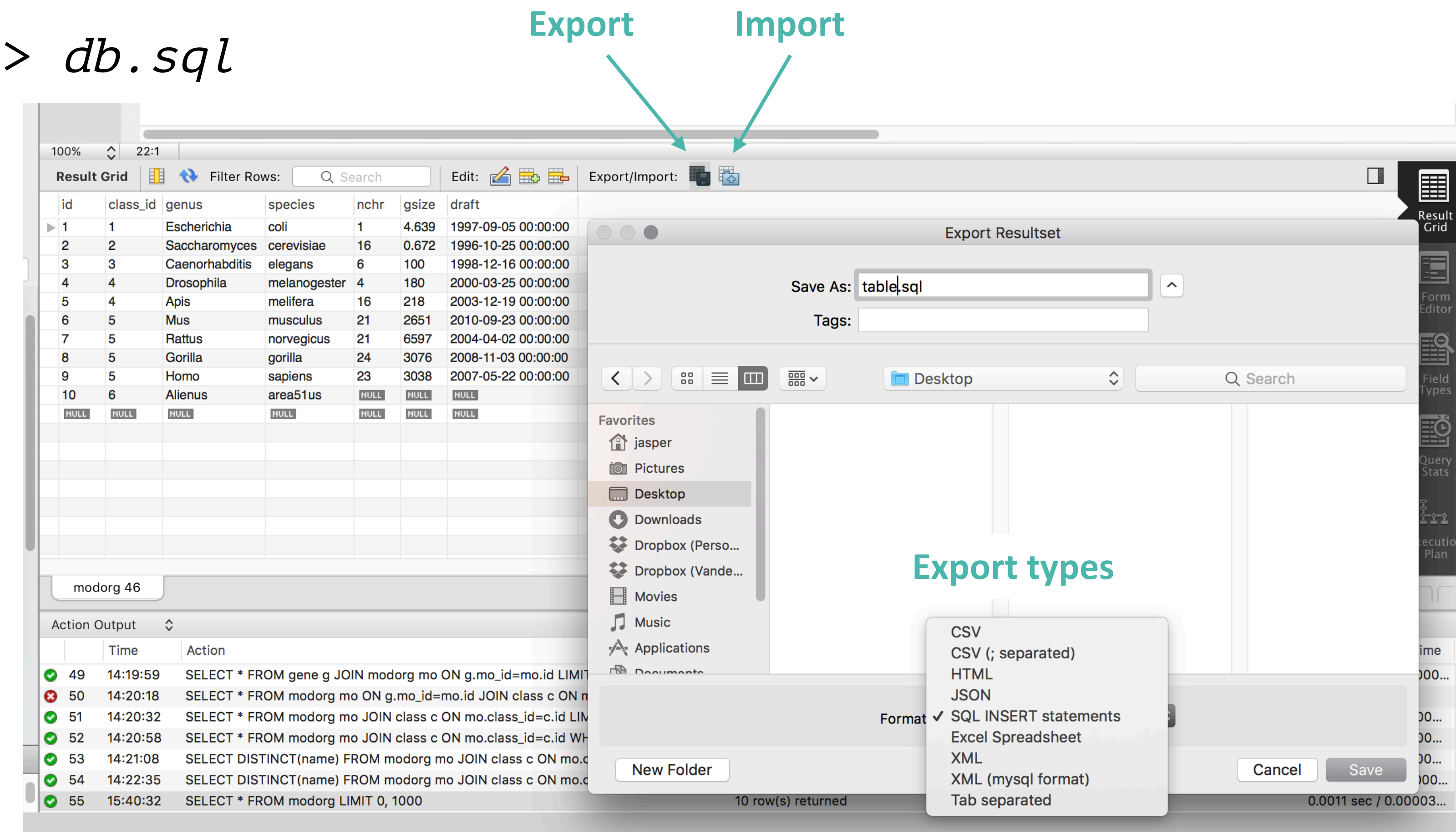
- Reverse engineer the model of the bioinf_testdb
  - Check out the relationships between the different tables
  - Give the names of all the keys used

# MySQL Workbench

## Exporting data

- Remember

  `$ mysqldump [opt] db > db.sql`
- Dump your database
  - Structure, data or both
  - Useful for backup
- Ability to export part of results (JSON, CSV, HTML, XML, …)



| id | class_id | genus | species | nchr | gsize | draft |
|---|---|---|---|---|---|---|
| 1 | 1 | Escherichia | coli | 1 | 4.639 | 1997-09-05 00:00:00 |
| 2 | 2 | Saccharomyces | cerevisiae | 16 | 0.672 | 1996-10-25 00:00:00 |
| 3 | 3 | Caenorhabditis | elegans | 6 | 100 | 1998-12-16 00:00:00 |
| 4 | 4 | Drosophila | melanogester | 4 | 180 | 2000-03-25 00:00:00 |
| 5 | 4 | Apis | melifera | 16 | 218 | 2003-12-19 00:00:00 |
| 6 | 5 | Mus | musculus | 21 | 2651 | 2010-09-23 00:00:00 |
| 7 | 5 | Rattus | norvegicus | 21 | 6597 | 2004-04-02 00:00:00 |
| 8 | 5 | Gorilla | gorilla | 24 | 3076 | 2008-11-03 00:00:00 |
| 9 | 5 | Homo | sapiens | 23 | 3038 | 2007-05-22 00:00:00 |
| 10 | 6 | Alienus | area51us | NULL | NULL | NULL |
| NULL | NULL | NULL | NULL | NULL | NULL | NULL |

Save As: table.sql

Tags:

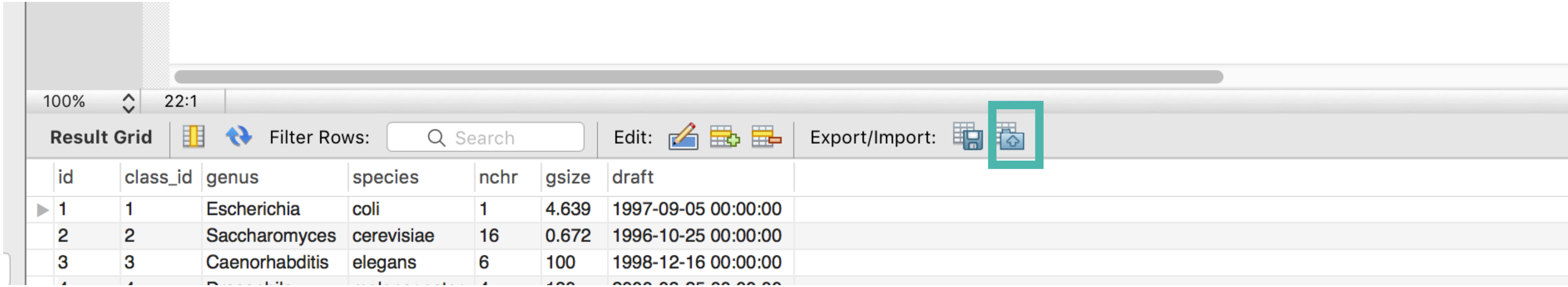
Format ✓ SQL INSERT statements

```
    Time      Action
✓ 49  14:19:59  SELECT * FROM gene g JOIN modorg mo ON g.mo_id=mo.id LIMIT
✗ 50  14:20:18  SELECT * FROM modorg mo ON g.mo_id=mo.id JOIN class c ON m
✓ 51  14:20:32  SELECT * FROM modorg mo JOIN class c ON mo.class_id=c.id LIM
✓ 52  14:20:58  SELECT * FROM modorg mo JOIN class c ON mo.class_id=c.id WH
✓ 53  14:21:08  SELECT DISTINCT(name) FROM modorg mo JOIN class c ON mo.c
✓ 54  14:22:35  SELECT DISTINCT(name) FROM modorg mo JOIN class c ON mo.c
✓ 55  15:40:32  SELECT * FROM modorg LIMIT 0, 1000          10 row(s) returned          0.0011 sec / 0.00003...
```

# MySQL Workbench

## Import data

- Import entire dump file
- Import data from file (CSV, existing table, SQL, JSON)



| id | class_id | genus | species | nchr | gsize | draft |
|---|---|---|---|---|---|---|
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# MySQL Workbench

## Excercises

- Export the data from the `modorg` table in your `biodb` database
- Empty your table (`TRUNCATE`)
- Import data into the `modorg` table using your export file