BIT05 - Databanktechnologie

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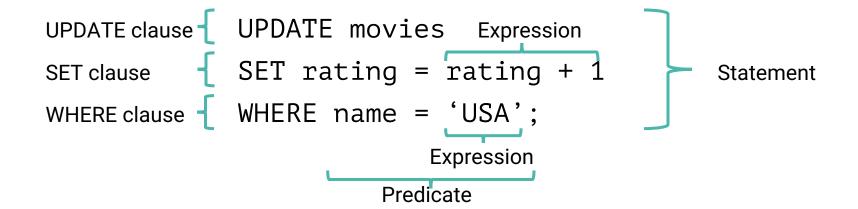
Lecture 2 – Relational databases 2

- 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

- MySQL
 - Install, connect to and secure server
 - User host database table
 - Privileges
 - Options file
 - Create database
 - Grant privileges
 - Show databases, tables columns, create statement

- 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

SQL: Structured Query Language

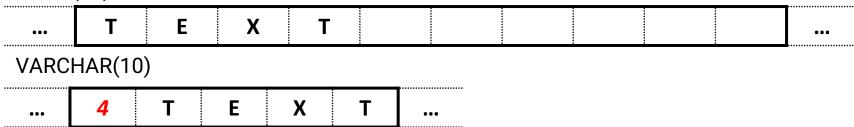


Column types

- 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

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)



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

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

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

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) ...
```

- 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 ...];
```

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

Exercises

- Return a list of the 3 biotypes with the most genes. Which biotype is a close fourth?
- Return a list of the number of genes per status
- Combining the 2 previous results, which biotype is most known?
- Select only those biotypes that cover at least 3% of the human genome (hint: 'size' in previous exercise, human genome is approx. 3 billion bp) and return this percentage.

Database upgrade

- Download 2.sql
- Create a new database bioinf
 mysql> CREATE database bioinf;
- Create the tables and insert the data
 \$ mysql bioinf < 2.sql

Joins

- Relation databases model entities and their relationships
- Different entities: different tables
- Allow you to combine information across different tables

Joins

What if we want to expand our database with a trajectory and course info

Student_number	Name	Last_name	Birthdate	Trajectory	Course
0293826	John	Doe	1991-10-02	FBT	Databases
0293749	Mel	Trotter	1991-04-11	MLT	Databases
0328273	Bill	Schuette	1990-12-01	MLT	Databases
0293826	John	Doe	1991-10-02	FBT	Scripting
0293826	John	Doe	1991-10-02	FBT	Linux

- Problem: redundant information
 - Waste of space
 - Error prone

Joins

Solution: relational databases with a foreign key

Students

Student_number	Name	Last_name	Birthdate	Trajectory_ID	Course
0293826	John	Doe	1991-10-02	1	Databases
0293749	Mel	Trotter	1991-04-11	2	Databases
0328273	Bill	Schuette	1990-12-01	2	Databases
0293826	John	Doe	1991-10-02	1	Scripting
0293826	John	Doe	1991-10-02	1	Linux

 Important: Data types of linked columns have to be equal! Foreign key is typically primary key of other table

Trajectories

	ID	Trajectory
	1	FBT
1	2	MLT

Joins

Students

Student_number	Name	Last_name	Birthdate	Trajectory_ID
0293826	John	Doe	1991-10-02	1
0293749	Mel	Trotter	1991-04-11	2
0328273	Bill	Schuette	1990-12-01	2

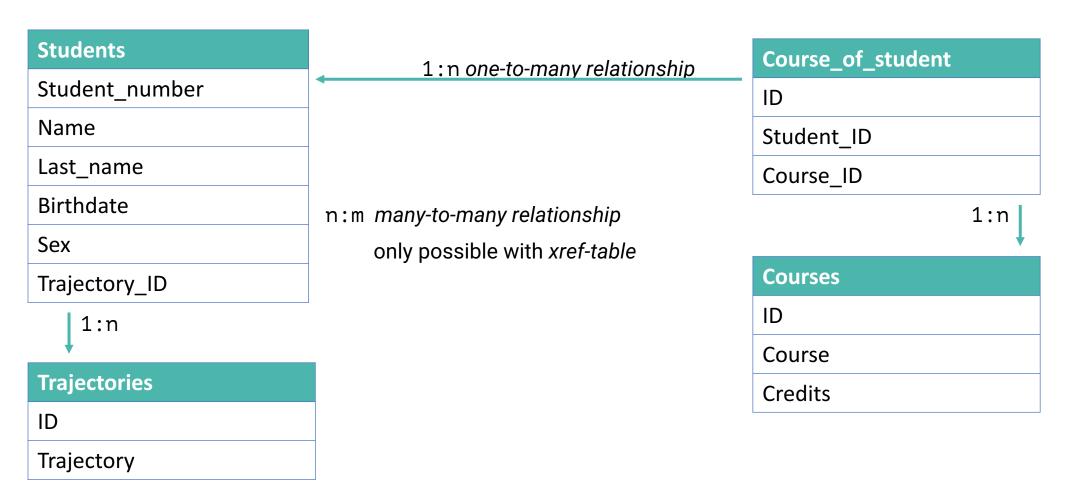
Course_of_student

Courses

Student_id	Course_ID
0293826	1
0293826	2
0293826	3
0293749	1
0328273	1

ID	Course
1	Databases
2	Scripting
3	Linux

Joins



Database model= Entity Relationship Diagram (ERD)

Joins – Information is spread across multiple tables

- Create script that retrieves tables separately
- JOIN tables with query

Students		Stud
Student_number		0293
Name		0293
Last_name		0328
Birthdate		0293
Sex		0293
Trajectory_ID		
Trajectories)ata
ID	t	he d
Traiectory		

Student_number	Name	Last_name	Birthdate	Course
0293826	John	Doe	1991-10-02	Databases
0293749	Mel	Trotter	1991-04-11	Databases
0328273	Bill	Schuette	1990-12-01	Databases
0293826	John	Doe	1991-10-02	Scripting
0293826	John	Doe	1991-10-02	Linux

Data representation does not have to be equal to the way the data is stored

Joins

Retrieve linked rows from different tables with JOIN

```
mysql> SELECT * FROM Students

JOIN Trajectories ON Students.Trajectory_ID = Trajectories.ID;
```

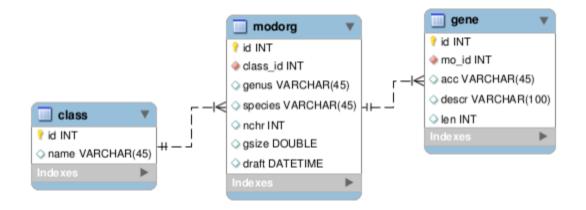
Students

Student_number	Name	Last_name	Birthdate	Trajectory_ID
0293826	John	Doe	1991-10-02	1
0293749	Mel	Trotter	1991-04-11	2
0328273	Bill	Schuette	1990-12-01	2
0324312	Penelope	Tracy	1989-07-24	NULL

ID	Trajectory
1	FBT
2	MLT
3	TI

Joins – back to our database

- modorg.class_id is a foreign key that references class.id
- gene.mo_id is a foreign key that references modorg.id



Joins – Cartesian product

- Multiple tables in a query → database server generates all possible combinations
 = Cartesian product
 - table class has 6 rows
 table modorg has 10 rows
 query SELECT * FROM modorg, class has 60 rows

Joins

Filtered Cartesian product
 SELECT * FROM modorg, class WHERE modorg.class_id = class.id;
 SELECT * FROM modorg [INNER] JOIN class ON modorg.class_id = class.id;

Joins

Avoid ambiguity

```
mysql> SELECT id, name, genus, species FROM modorg, class WHERE
modorg.class_id = class.id;
```

```
ERROR 1052 (23000): Column 'id' in field list is ambiguous
```

Ambiguous columns must be qualified. And additionally you can choose an alias:
 mysql> SELECT modorg.id as mo_id, name, genus, species FROM modorg, class WHERE modorg.class_id = class.id;

Joins – data source alias

- Join table with itself or select data from subquery
 - Use alias for data source

```
mysql> SELECT a.col, b.col FROM src1 [as] a, src2 [as] b WHERE ...
```

Joins – data source alias

 For each class, give the class name, organism name and date of the organism that was sequenced first

```
mysql> SELECT class_id, min(draft) as dr FROM modorg GROUP BY
class_id;
```

- add class name: join with table class
- add organism name: join with table modorg

Joins - data source alias

Add class name

```
mysql> SELECT name, dr FROM
    (SELECT class_id, min(draft) as dr FROM modorg GROUP BY
    class_id) as s, class WHERE s.class_id=class_id;
```

add organism name: join with table modorg

```
mysql> SELECT name, concat(genus," ",species) as org_name, dr
   FROM (SELECT class_id, min(draft) as dr FROM modorg GROUP BY
   class_id) as s, class, modorg WHERE s.class_id=class.id AND
   s.dr=draft;
```

Exercises

- For all rows in table gene, show
 - Organism name
 - Class name
 - Accession
 - Length
 - Description of the gene

Joins – 4 types

- INNER JOIN
 - Only rows present in both tables
- LEFT JOIN
 - All rows from left table, even without linked data in right table
- RIGHT JOIN
 - All rows from right table, even without linked data in left table
- OUTER JOIN
 - All rows from both tables
 - Doesn't exist in MySQL

Joins - INNER JOIN

Students

Student_number	Name	Last_name	Birthdate	Trajectory_ID
0293826	John	Doe	1991-10-02	1
0293749	Mel	Trotter	1991-04-11	2
0328273	Bill	Schuette	1990-12-01	2
0324312	Penelope	Tracy	1989-07-24	NULL

ID	Trajectory
1	FBT
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3	Ti



Student_number	Name	Last_name	Birthdate	Trajectory
0293826	John	Doe	1991-10-02	FBT
0293749	Mel	Trotter	1991-04-11	MLT
0328273	Bill	Schuette	1990-12-01	MLT

Joins - LEFT JOIN

Students

Student_number	Name	Last_name	Birthdate	Trajectory_ID
0293826	John	Doe	1991-10-02	1
0293749	Mel	Trotter	1991-04-11	2
0328273	Bill	Schuette	1990-12-01	2
0324312	Penelope	Tracy	1989-07-24	NULL

ID	Trajectory		
1	FBT		
2	MLT		
3	Ti		



Student_number	Name	Last_name	Birthdate	Trajectory
0293826	John	Doe	1991-10-02	FBT
0293749	Mel	Trotter	1991-04-11	MLT
0328273	Bill	Schuette	1990-12-01	MLT
0324312	Penelope	Tracy	1989-07-24	NULL

Joins - RIGHT JOIN

Students

Student_number	Name	Last_name	Birthdate	Trajectory_ID
0293826	John	Doe	1991-10-02	1
0293749	Mel	Trotter	1991-04-11	2
0328273	Bill	Schuette	1990-12-01	2
0324312	Penelope	Tracy	1989-07-24	NULL

ID	Trajectory
1	FBT
2	MLT
3	TI



Student_number	Name	Last_name	Birthdate	Trajectory
0293826	John	Doe	1991-10-02	FBT
0293749	Mel	Trotter	1991-04-11	MLT
0328273	Bill	Schuette	1990-12-01	MLT
NULL	NULL	NULL	NULL	TI

Joins - OUTER JOIN

Students

Student_number	Name	Last_name	Birthdate	Trajectory_ID
0293826	John	Doe	1991-10-02	1
0293749	Mel	Trotter	1991-04-11	2
0328273	Bill	Schuette	1990-12-01	2
0324312	Penelope	Tracy	1989-07-24	NULL

ID	Trajectory
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Student_number	Name	Last_name	Birthdate	Trajectory
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0328273	Bill	Schuette	1990-12-01	MLT
0324312	Penelope	Tracy	1989-07-24	NULL
NULL	NULL	NULL	NULL	TI

Joins – characteristics

- * is used to select all columns from all tables
- Use tbl.col to specify column
- Very inefficient
 - A lot of memory, a lot of time
- Use ON to specify linked columns

Execution order

- 1. Input columns are determined
 - a. JOIN clause
- 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

Excercises

- Switch back to the bioinf_testdb database
 - Experiment with the 3 types of JOIN on your own tables
 - Examine the gene, transcript and exon table, how are they connected?
 - How many transcript does the MALAT1 gene have?
 - Return the position of the exons of transcript 237999
 - Return the transcripts of the TP53 gene
 - Return their exons as well
 - Find the longest spliced transcript of *TP53* (taking into account the intron-exon structure)
 - How many exons does each transcript have?

Excercises

- What is the name of the gene associated with transcript 260392?
- A mutation was found on chromosome 20, position 44002590. Which gene(s) overlap(s) with this position?
 - Select only those genes that have exons that overlap with this mutation. Which genes are they?
- A biotype column can be found in both the gene and transcript table. Are there transcripts that have a different biotype from the gene they're part of? What are their names?
 - Does the same go for status?
- Which chromosome has the most genes and how many are there?
- Which exon is the largest in the genome and how many base pairs are there?
- Which transcript has the most exons and how many are there?

Efficiency and speed

- Complex queries tend to become
 - Large system load
 - Slow interface, user has to wait
- · Mind your choices of column types and included columns in the query
- Frequently used queries can be sped up
 - Views
 - Indices
 - Allow redundancy

Views

- Re-use same query
- Query can be saved as a special table-like object
- Usually read-only data source
- Speed gain depends on use case
- MySQL
 - Virtual table
 - Used to serve up data in an orderly fashion
- Oracle i.a.
 - Materialized view: result of a SELECT query is stored
 - Very efficient

Views

Create a new view
 mysql> CREATE VIEW viewname as SELECT ...

• Use a view as a table mysql> SELECT ... FROM viewname WHERE ... ORDER BY ...

Exercises

- Create a view (genevw) from the query in the previous exercise
- Select all genes containing hemoglobin in the description and sort the result set by gene length.

Next:

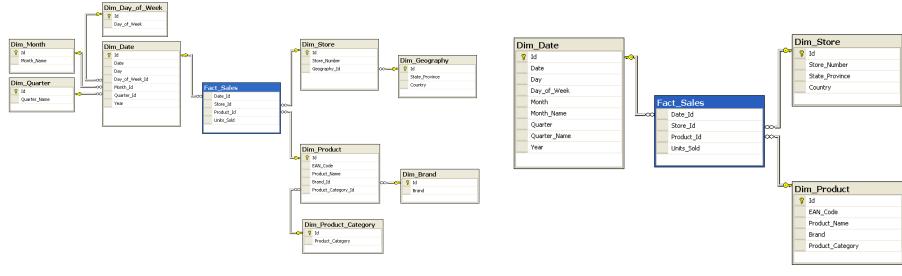
- What is the minimum and maximum gene length?
- What is the average gene length?
- And the standard deviation?
- Does the view show up when using mysql> show tables;

Index

- Quickly find certain rows
- Stored separately
- Golden rule: Use indices on columns you will use in your WHERE clause
- Only 1 index per query is used
 CREATE [UNIQUE|FULLTEXT|SPATIAL] INDEX index_name ON tbl (col);
- Foreign key
 - Index used to speed up JOIN queries
 - Not essential for JOIN queries

Allow redundancy

- Schema with least redundancy isn't always the quickest
- Allow redundancy to reduce number of JOINs
- E.g. Data warehouse with real-time reporting
 - High efficiency is required
- Snowflake vs Star schema



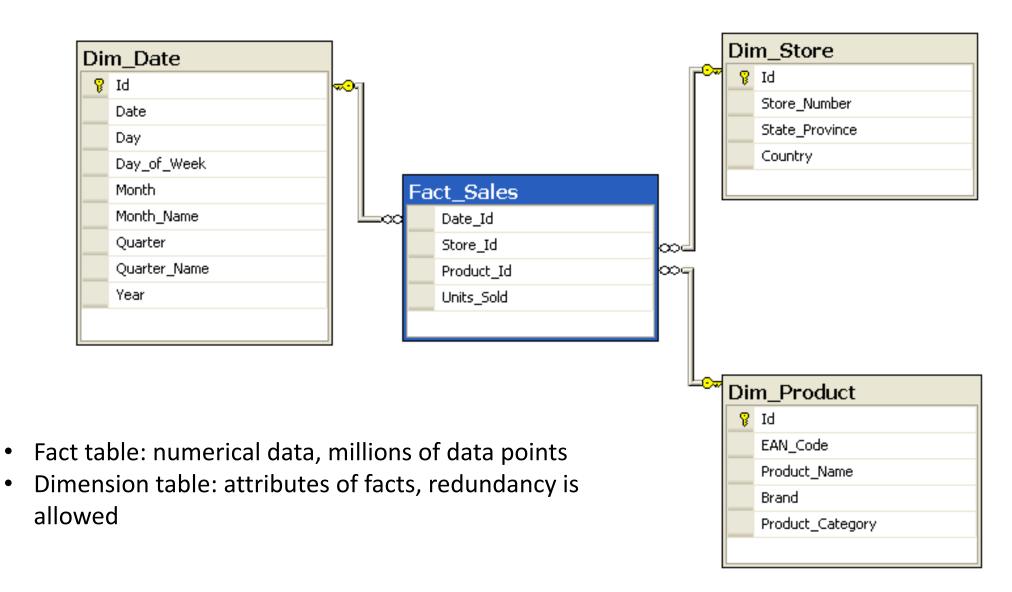
Snowflake Star

P.Product Category Id = C.Id

GROUP BY B.Brand, **G**.Country

WHERE D.Year = 1997 AND C.Product_Category = 'tv'

SNOWFLAKE STAR Redundant data No redundancy 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) Top down Bottom up **SELECT** B.Brand, SELECT P.Brand, G. Country, S. Country **AS** Countries, **SUM**(F.Units Sold) **SUM**(F.Units Sold) FROM Fact Sales F FROM Fact Sales F **INNER JOIN** Dim Date D **ON** F.Date Id = D.Id **INNER JOIN** Dim Date D **ON** (F.Date Id = D.Id) **INNER JOIN** Dim Store S **ON** F.Store Id = S.Id **INNER JOIN** Dim Store S **ON** (F.Store Id = S.Id) INNER JOIN Dim_Geography G ON S.Geography_Id = G.Id INNER JOIN Dim_Product P ON (F.Product_Id = P.Id) INNER JOIN Dim Product P ON F. Product Id = P.Id WHERE D.Year = 1997 AND P.Product_Category = 'tv' INNER JOIN Dim_Brand B ON P.Brand Id = B.Id **GROUP BY** P.Brand, S.Country INNER JOIN Dim_Product_Category C ON



Database backup

- Dump a complete database into a tekst file
 - \$ mysqldump [opt] db > db.sql
- Includes
 - Statements for creating the database if the option --databases is used
 - Statements for creating tables, views, ...
 - Statements for inserting data
- Restore the database (may need to create first)
 - \$ mysql db < db.sql

Exercises

- Create a separate dump file for each of your own databases
- Check the contents of each file
- For the bold ones
 - Drop your databases and recreate them using your dump files

Rehearsal exercises

- Create a new database for your lab and include following data
 - All trainings
 - Subject, duration
 - All lab members
 - Name, lastname, birth_date, training
 - All equipment
 - Name, manufacturer, purchase_date
 - All experiments
 - Name, performed_by, equipment_used, date
 - All results
 - Directory, experiment, status
- Fill with some data

```
CREATE TABLE Kit order (
          order number CHAR(16) NOT NULL,
          manufacturer VARCHAR(255),
          kit name VARCHAR(255),
          supplier VARCHAR(255),
          PRIMARY KEY (order number),
          FOREIGN KEY (manufacturer, kit name)
          REFERENCES Kit(manufacturer, name),
          FOREIGN KEY (supplier)
          REFERENCES Supplier(supplier name));
      CREATE TABLE Kit (
                manufacturer VARCHAR(255) NOT NULL,
                name VARCHAR(255) NOT NULL,
                kit cost DECIMAL(6,2),
                buffer VARCHAR(255),
                buffer conc FLOAT,
                enzyme VARCHAR(255),
                enzyme conc FLOAT,
                nucl mix VARCHAR(255),
                nucl conc FLOAT,
      PRIMARY KEY (manufacturer, name));
```

Rehearsal exercises (part 2)

- In your newly created database, search for
 - All experiment equipment purchased after 1st of January 1985
 - The number of experiments each lab member conducted
 - A list with all equipment used in a successful experiment
 - A list with all lab members that failed an experiment
 - Who followed wich trainings?
 - Number of participants per training