

Week 2-2

# SQL and Query Processing



## Big Data

Prof. Hwanjo Yu  
POSTECH

# Interpreting complicated SQL

```
SELECT binid,  
       round(avg(cast(Fluo as float)),3) as Fluo,  
       round(avg(cast(Oxygen as float)),3) as Oxygen,  
       round(avg(cast(Nitrate_uM as float)),3) as Nitrate_uM,  
       round(avg(cast(longitude as float)),3) as longitude,  
       round(avg(cast(latitude as float)),3) as latitude  
FROM (  
  SELECT *,  
         cast(floor(ts) + floor((ts - floor(ts))*24*60/binsize) * binsize / (24*60) as datetime) as binid  
  FROM (  
    SELECT *,  
           cast(timestamp as float) as ts,  
           5.0 as binsize  
    FROM Tokyo_4_merged_data_time  
  ) x  
) bins  
GROUP BY binid  
ORDER BY binid ASC
```

# Interpreting complicated SQL

```
SELECT binid,  
       round(avg(cast(Fluo as float)),3) as Fluo,  
       round(avg(cast(Oxygen as float)),3) as Oxygen,  
       round(avg(cast(Nitrate_uM as float)),3) as Nitrate_uM,  
       round(avg(cast(longitude as float)),3) as longitude,  
       round(avg(cast(latitude as float)),3) as latitude  
FROM (  
  SELECT *,  
         cast(floor(ts) + floor((ts - floor(ts))*24*60/binsize) * binsize / (24*60) as datetime) as binid  
  FROM (  
    SELECT *,  
           cast(timestamp as float) as ts,  
           5.0 as binsize  
    FROM Tokyo_4_merged_data_time  
  ) x  
) bins  
GROUP BY binid  
ORDER BY binid ASC
```

# Interpreting complicated SQL

```
SELECT x.strain, x.chr, x.region as snp_region, x.start_bp as snp_start_bp, x.end_bp as snp_end_bp,
       w.start_bp as nc_start_bp, w.end_bp as nc_end_bp, w.category as nc_category,
       CASE WHEN (x.start_bp >= w.start_bp AND x.end_bp <= w.end_bp)
            THEN x.end_bp - x.start_bp + 1
            WHEN (x.start_bp <= w.start_bp AND w.start_bp <= x.end_bp)
            THEN x.end_bp - w.start_bp + 1
            WHEN (x.start_bp <= w.end_bp AND w.end_bp <= x.end_bp)
            THEN w.end_bp - x.start_bp + 1
       END AS len_overlap
FROM hotspots_deserts x JOIN table_noncoding_positions w ON x.chr = w.chr
WHERE (x.start_bp >= w.start_bp AND x.end_bp <= w.end_bp)
      OR (x.start_bp <= w.start_bp AND w.start_bp <= x.end_bp)
      OR (x.start_bp <= w.end_bp AND w.end_bp <= x.end_bp)
ORDER BY x.strain, x.chr ASC, x.start_bp ASC
```

# Interpreting complicated SQL

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SELECT x.strain, x.chr, x.region as snp_region, x.start_bp as snp_start_bp, x.end_bp as snp_end_bp,  
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             THEN x.end_bp - x.start_bp + 1  
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             THEN x.end_bp - w.start_bp + 1  
             WHEN (x.start_bp <= w.end_bp AND w.end_bp <= x.end_bp)  
             THEN w.end_bp - x.start_bp + 1  
       END AS len_overlap  
FROM hotspots_deserts x JOIN table_noncoding_positions w ON x.chr = w.chr  
WHERE (x.start_bp >= w.start_bp AND x.end_bp <= w.end_bp)  
      OR (x.start_bp <= w.start_bp AND w.start_bp <= x.end_bp)  
      OR (x.start_bp <= w.end_bp AND w.end_bp <= x.end_bp)  
ORDER BY x.strain, x.chr ASC, x.start_bp ASC
```

# Interpreting complicated SQL

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SELECT x.strain, x.chr, x.region as snp_region, x.start_bp as snp_start_bp, x.end_bp as snp_end_bp,  
       w.start_bp as nc_start_bp, w.end_bp as nc_end_bp, w.category as nc_category,  
       len_overlap(x.start_bp, x.end_bp, w.start_bp, w.end_bp)  
FROM hotspots_deserts x JOIN table_noncoding_positions w ON x.chr = w.chr  
WHERE (x.start_bp >= w.start_bp AND x.end_bp <= w.end_bp)  
      OR (x.start_bp <= w.start_bp AND w.start_bp <= x.end_bp)  
      OR (x.start_bp <= w.end_bp AND w.end_bp <= x.end_bp)  
ORDER BY x.strain, x.chr ASC, x.start_bp ASC
```

# Interpreting complicated SQL

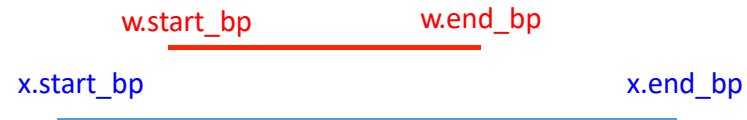
```
SELECT x.strain, x.chr, x.region as snp_region, x.start_bp as snp_start_bp, x.end_bp as snp_end_bp,  
       w.start_bp as nc_start_bp, w.end_bp as nc_end_bp, w.category as nc_category,  
       len_overlap(x.start_bp, x.end_bp, w.start_bp, w.end_bp)  
FROM hotspots_deserts x JOIN table_noncoding_positions w ON x.chr = w.chr  
WHERE (x.start_bp >= w.start_bp AND x.end_bp <= w.end_bp)  
      OR (x.start_bp <= w.start_bp AND w.start_bp <= x.end_bp)  
      OR (x.start_bp <= w.end_bp AND w.end_bp <= x.end_bp)  
ORDER BY x.strain, x.chr ASC, x.start_bp ASC
```

# Interpreting complicated SQL

$(x.start\_bp \geq w.start\_bp \text{ AND } x.end\_bp \leq w.end\_bp)$



OR  $(x.start\_bp \leq w.start\_bp \text{ AND } w.start\_bp \leq x.end\_bp)$



OR  $(x.start\_bp \leq w.end\_bp \text{ AND } w.end\_bp \leq x.end\_bp)$





# Interpreting complicated SQL

```
SELECT x.strain, x.chr, x.region as snp_region, x.start_bp as snp_start_bp, x.end_bp as snp_end_bp,  
       w.start_bp as nc_start_bp, w.end_bp as nc_end_bp, w.category as nc_category,  
       len_overlap(x.start_bp, x.end_bp, w.start_bp, w.end_bp)  
FROM hotspots_deserts x JOIN table_noncoding_positions w ON x.chr = w.chr  
WHERE overlaps(x.start_bp, x.end_bp, w.start_bp, w.end_bp)  
ORDER BY x.strain, x.chr ASC, x.start_bp ASC
```

# Interpreting complicated SQL

```
SELECT x.strain, x.chr, x.region as snp_region, x.start_bp as snp_start_bp, x.end_bp as snp_end_bp,  
       w.start_bp as nc_start_bp, w.end_bp as nc_end_bp, w.category as nc_category,  
       len_overlap(x.start_bp, x.end_bp, w.start_bp, w.end_bp)  
FROM hotspots_deserts x JOIN table_noncoding_positions w ON x.chr = w.chr  
WHERE overlaps(x.start_bp, x.end_bp, w.start_bp, w.end_bp)  
ORDER BY x.strain, x.chr ASC, x.start_bp ASC
```



```
SELECT x.strain, x.chr, x.region as snp_region, x.start_bp as snp_start_bp, x.end_bp as snp_end_bp,  
       w.start_bp as nc_start_bp, w.end_bp as nc_end_bp, w.category as nc_category,  
       len_overlap(x.start_bp, x.end_bp, w.start_bp, w.end_bp)  
FROM hotspots_deserts x, table_noncoding_positions w  
WHERE x.chr = w.chr AND overlaps(x.start_bp, x.end_bp, w.start_bp, w.end_bp)  
ORDER BY x.strain, x.chr ASC, x.start_bp ASC
```

# User-defined functions

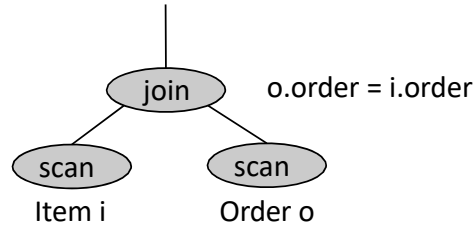
- As a user, you can write a function, register it in the database, call it from SQL, set permissions on it
- Scalar functions  
`SELECT myfunc(r.a, r.b)...`  
`WHERE yourfunc(r.c, r.d) < 5`
- Aggregate functions  
`SELECT x, concat(r.s) ...`  
`GROUP BY x`
- Table functions  
`SELECT ... FROM tablefunc(a,b)`

# User-defined function support

- PostgreSQL (and Greenplum)
  - SQL, PL/pgSQL, Python, C/C++, R,
- Microsoft SQL Server
  - SQL, T-SQL, C# or any CLR language
- Oracle
  - SQL, PL-SQL, Java, C/C++, Python, others
- SQLite
  - NONE!! (sorry)

# Same logical expression, different physical algorithms

```
SELECT *  
FROM   Order o, Item i  
WHERE  o.order = i.order
```



Option 1: Nested loop join

```
for each record i in Item:  
  for each record o in Order:  
    if o.order = i.order:  
      return matching pair
```

*Which is faster?*

Option 2: Hash join

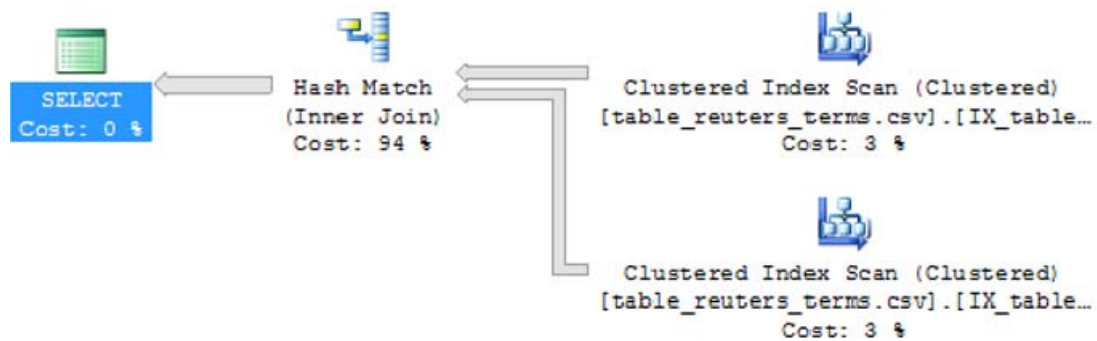
```
for each record i in Item:  
  insert into hashtable  
  
for each record o in Order:  
  lookup corresponding records in hashtable  
  return matching pairs
```

# Exposing the algebra: Microsoft SQL server

“Find pairs of terms that co-occur in documents”

```
1 select a.term_id, b.term_id
2 from [billhowe].[reuters] a, [billhowe].[reuters] b
3 where a.doc_id = b.doc_id
4      and a.term_id != b.term_id
```

*EXPLAIN*

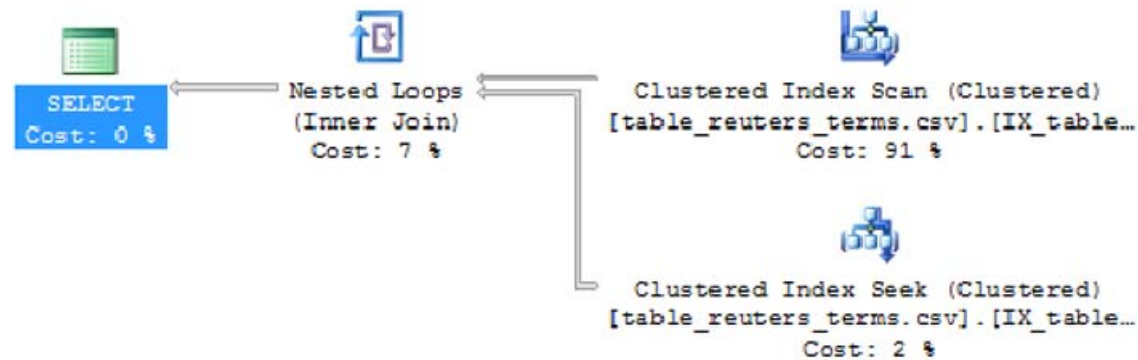


# Exposing the algebra: Microsoft SQL server

“Find pairs of terms that co-occur ‘parliament’ in documents”

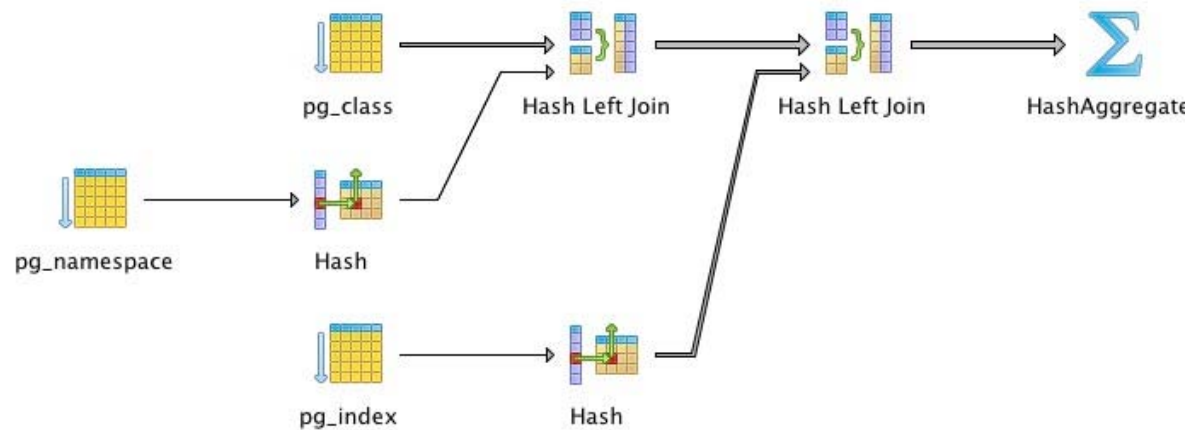
```
1 select a.term_id, b.term_id
2 from [billhowe].[reuters] a, [billhowe].[reuters] b
3 where a.doc_id = b.doc_id
4      and a.term_id != b.term_id
5      and a.term_id = 'parliament'
```

EXPLAIN



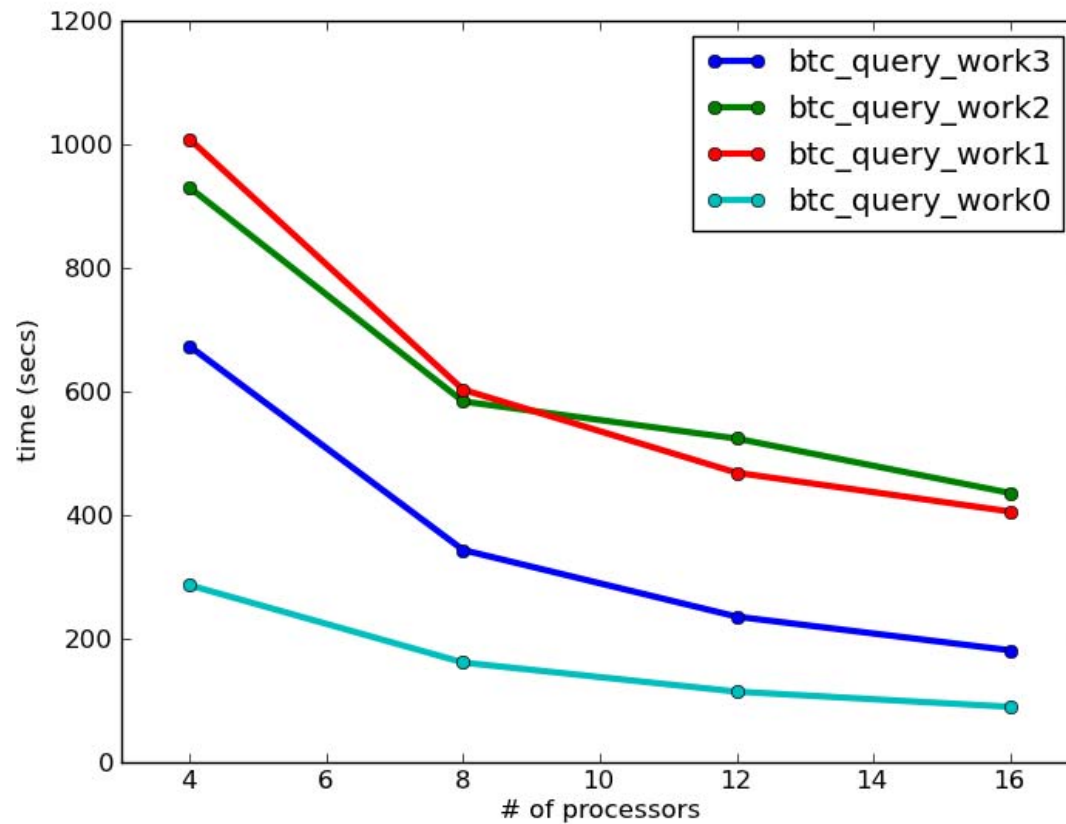
# Exposing the algebra: PostgreSQL

EXPLAIN SELECT ....





# Algebraic optimization matters



*BTC 2010 Dataset*

*3B quads  
623 GB processed*

# Equivalent logical expressions; different costs

$$\sigma_{p=\text{knows}}(R) \bowtie_{o=s} (\sigma_{p=\text{holdsAccount}}(R) \bowtie_{o=s} \sigma_{p=\text{accountHompag}}(R))$$

right associative

$$(\sigma_{p=\text{knows}}(R) \bowtie_{o=s} \sigma_{p=\text{holdsAccount}}(R)) \bowtie_{o=s} \sigma_{p=\text{accountHompag}}(R)$$

left associative

$$\sigma_{p1=\text{knows} \ \& \ p2=\text{holdsAccount} \ \& \ p3=\text{accountHompag}}(R \times R \times R)$$

cross product

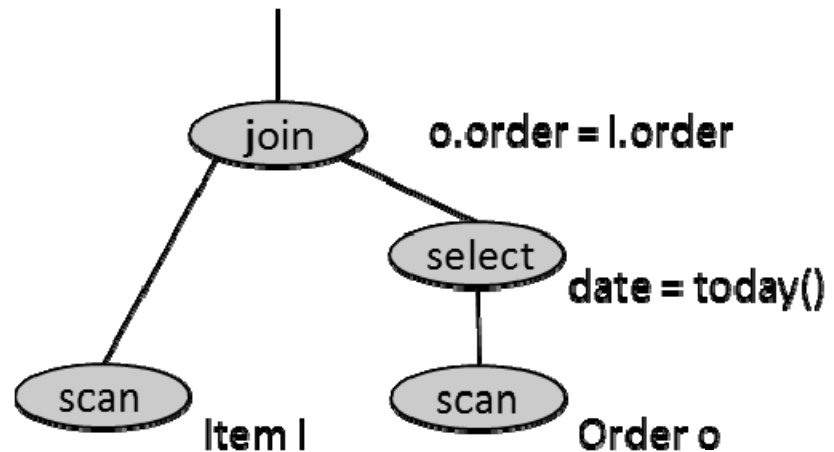
# Key idea: Declarative languages

Order(order, date, account)

Item(order, part)

*Find all orders from today, along with the items ordered*

```
SELECT *  
FROM Order o, Item i  
WHERE o.order = i.order  
AND o.date = today()
```



# SQL is the “WHAT” not the “HOW”

Product(pid, name, price)

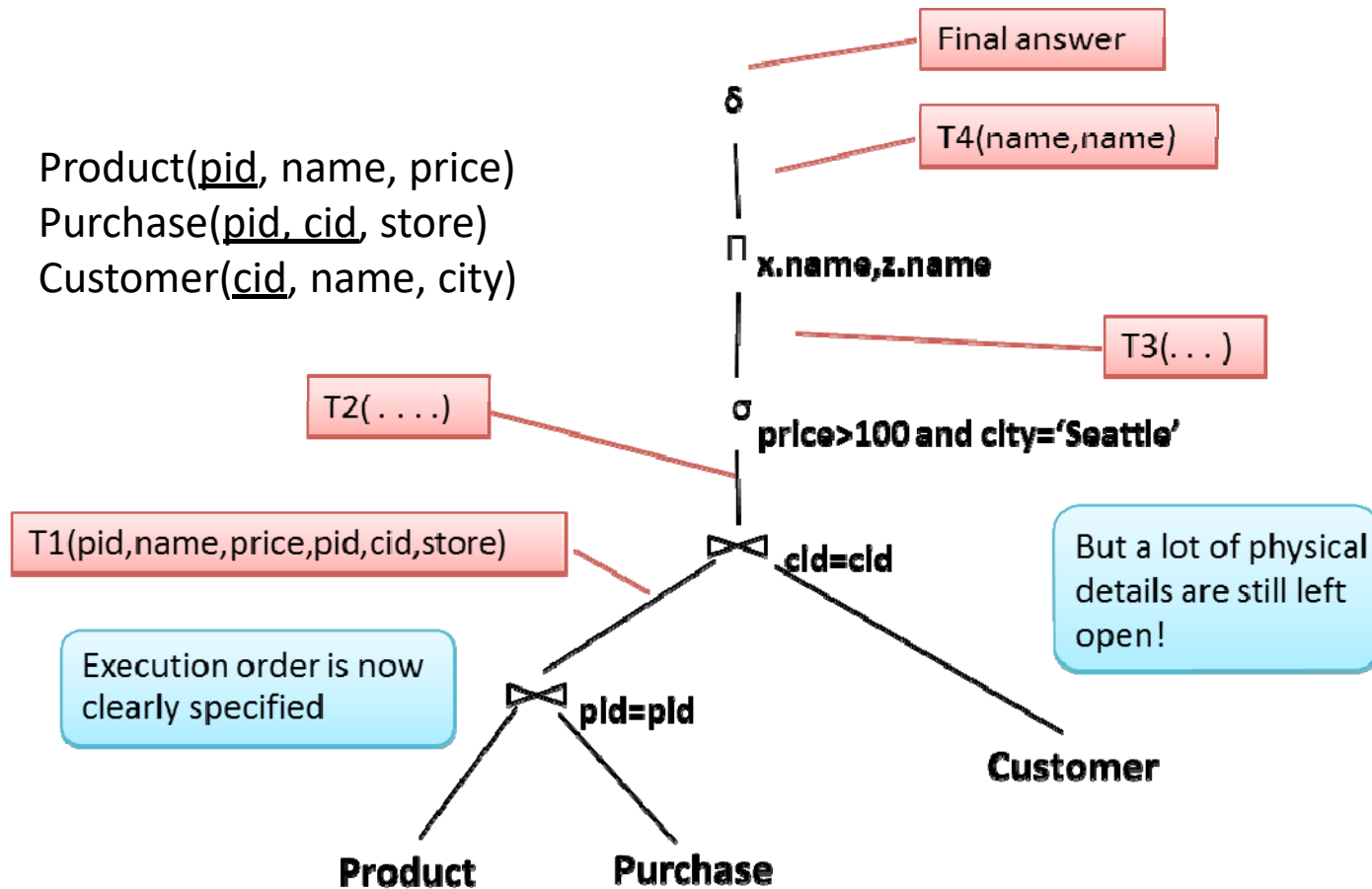
Purchase(pid, cid, store)

Customer(cid, name, city)

```
SELECT DISTINCT x.name, z.name  
FROM Product x, Purchase y, Customer z  
WHERE x.pid = y.pid and y.cid = z.cid and  
       x.price > 100 and z.city = 'Seattle'
```

It's clear WHAT we want, unclear HOW to get it

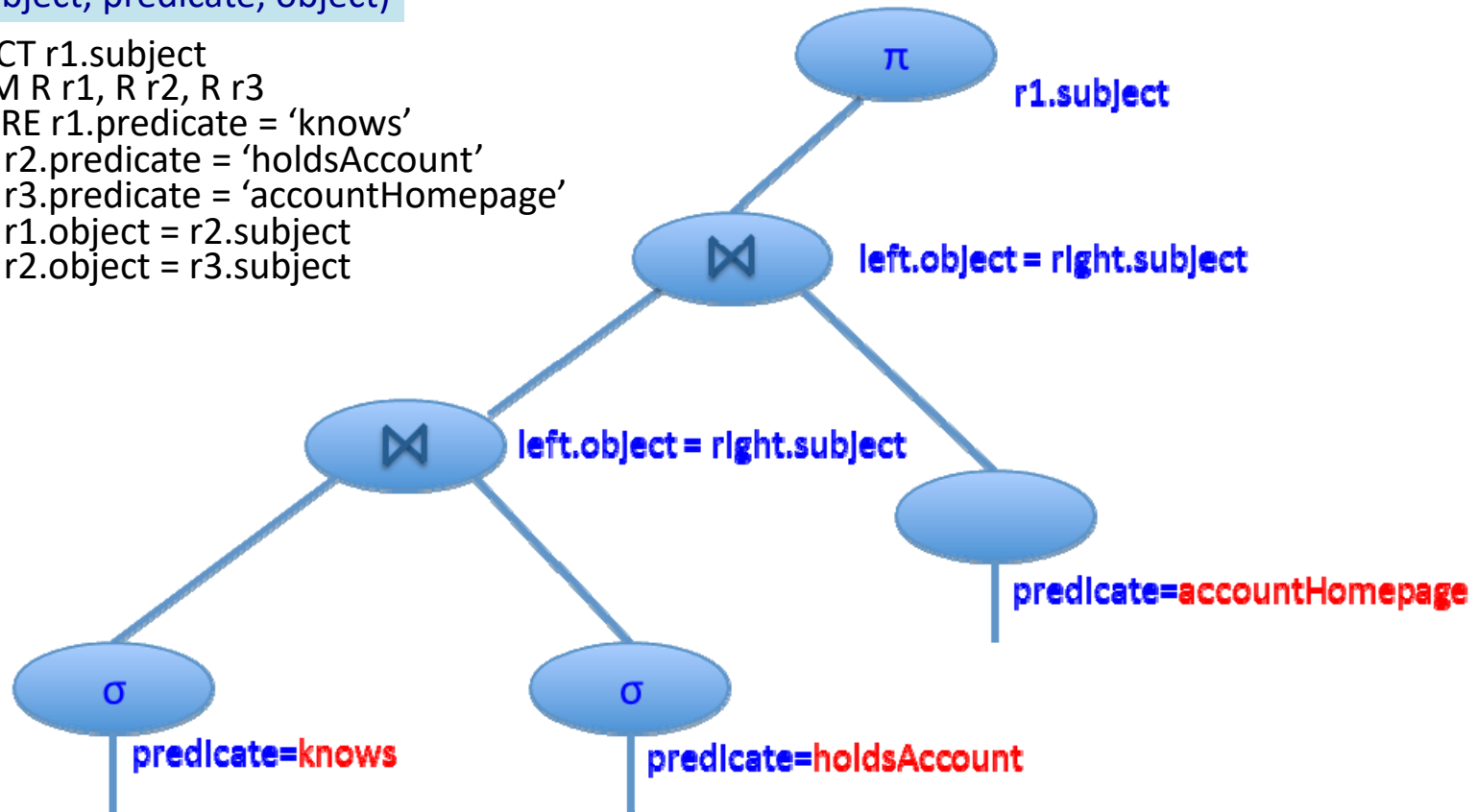
# Relational algebra



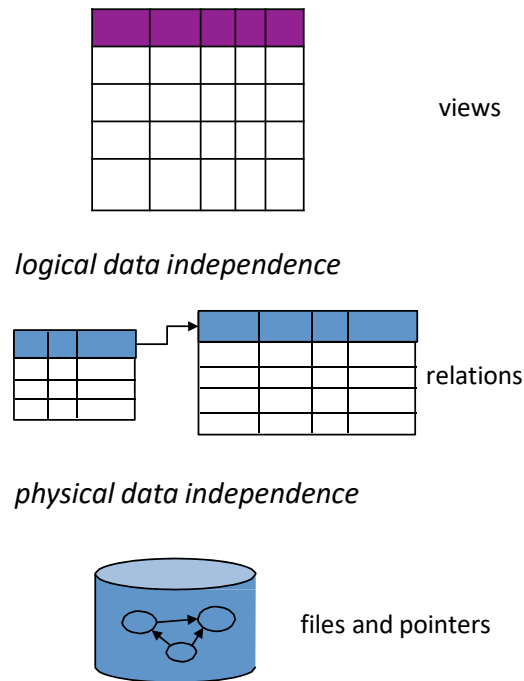
## Another example

R(subject, predicate, object)

```
SELECT r1.subject  
FROM R r1, R r2, R r3  
WHERE r1.predicate = 'knows'  
AND r2.predicate = 'holdsAccount'  
AND r3.predicate = 'accountHomepage'  
AND r1.object = r2.subject  
AND r2.object = r3.subject
```



# Key idea: “Logical data independence”



```
SELECT *  
FROM my_sequences
```

```
SELECT seq  
FROM ncbi_sequences  
WHERE seq = 'GATTACGATATTA';
```

```
f = fopen ('table_file');  
fseek (10030440);  
while (True) {  
    fread (&buf, 1, 8192, f);  
    if (buf == GATTACGATATTA) {  
        ...  
    }}
```

# What are views?

- A **view** is just a query with a name
- We can use the view just like a real table

Why can we do this?

Because we know that every query returns a relation:  
We say that the language is “algebraically closed”



# View example

A view is a relation defined by a query

Purchase(customer, pid, store)  
Product(pid, price)

StorePrice(store, price)

```
CREATE VIEW StorePrice AS  
SELECT x.store, y.price  
FROM Purchase x, Product y  
WHERE x.pid = y.pid
```

This is like a new table  
StorePrice(store,price)

# View example

Customer(cid, name, city)  
Purchase(customer, product, store)  
Product(pname, price)

StorePrice(store, price)

## How to Use a View?

- A "high end" store is a store that sold some product over 1000. For each customer, find all the high end stores that they visit. Return a set of (customer- name, high-end-store) pairs.

```
SELECT DISTINCT z.name, u.store  
FROM Customer z, Purchase u, StorePrice v  
WHERE z.cid = u.customer  
AND u.store = v.store  
AND v.price > 1000
```

# Key idea: Indexes

- Databases are especially, but not exclusively, effective at “Needle in Haystack” problems:
  - Extracting small results from big datasets
  - Your query will finish, regardless of dataset size.
  - Indexes are easily built and automatically used when appropriate

```
CREATE      INDEX seq_idx ON  sequence(seq);
```

```
SELECT      seq  
FROM        sequence  
WHERE       seq='GATTACGATATTA';
```

# SQL exercise

- Install SQLite (Search Internet) in your favorite machine
- create table Documents(DocID int, Term text, Count int);
- .mode csv
- .import Documents.csv Documents (You need to make csv data files.)

# Documents.csv

1	data	4
1	base	3
1	system	5
1	fall	6
1	semester	2
2	data	1
2	base	2
2	structure	3
2	network	4
2	algorithm	5
3	ds	2
3	sd	3
3	final	4
3	mid	5
4	system	1
4	ds	4
4	sd	3
4	pl	5
4	data	2
5	base	2
5	structure	2
5	network	3
5	fall	4
6	data	2
6	base	4

# SQL exercise

Documents(DocID int, Term text, Count int);

1. Write a SQL query that is equivalent to the following relational algebra expression.
  - $\pi_{\text{Term}}(\sigma_{\text{Docid}=2}(\text{Documents})) \cup \pi_{\text{Term}}(\sigma_{\text{count}=3}(\text{Documents}))$
  - Try both union and union all to see the difference
  - Try “or” instead of “union” and compare results with using union
2. Write a SQL query to count the number of documents containing the word “data”.
3. Write a SQL query to find all documents that have more than 3 terms.
4. Write a SQL query to count the number of documents that contain both the word “data” and “base”.
5. Write a SQL query to compute the similarity of every pair of documents in Documents. The similarity here is computed by summing the same term counts of two documents. For example, the similarity of Doc1 <'a':2, 'b':1, 'c':3> and Doc2 <'b':2, 'c':1, 'd':4> is  $1*2$  ('b') +  $3*1$  ('c') = 5. (Hint: to avoid computing the similarity of both (Doc1, Doc2) and (Doc2, Doc1), add a condition of the form  $a.\text{DocID} < b.\text{DocID}$ .)

# We didn't cover...

- Design of Relational Databases
  - Drawing ER Diagram, e.g. 1-to-1, many-to-1, many-to-many
  - Relational Normalization, e.g. 1<sup>st</sup>, 2<sup>nd</sup>, 3<sup>rd</sup> normal forms
- Query Processing
  - Indexing methods, e.g. B+tree, Hash, R-tree, ...
  - Data organization in disk, e.g. directory, block, fragmentation
  - Disk-based sorting, e.g. multiway merge sort
- Query Optimization
  - Query rewriting, Query execution plan tree, ...
- Transaction management
  - ACID properties, two-phase locking, ...
- Recovery
  - Logging, WAL, ...



1 semester  
of course