# Week 07 Lectures

# Signature-based Selection

## Indexing with Signatures



Signature-based indexing:

- designed for *pmr* queries (conjunction of equalities)
- does not try to achieve better than *O(n)* performance
- attempts to provide an "efficient" linear scan

Each tuple is associated with a *signature*

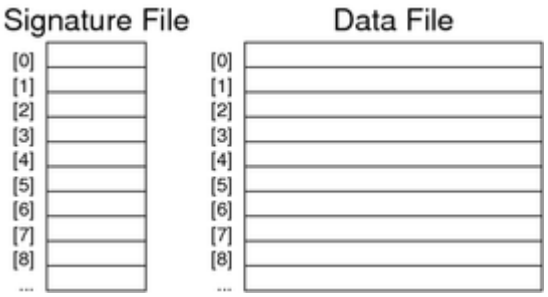
- a compact (lossy) descriptor for the tuple
- formed by combining information from multiple attributes
- stored in a signature file, parallel to data file

Instead of scanning/testing tuples, do pre-filtering via signatures.

### ... Indexing with Signatures



File organisation for signature indexing (two files)




One signature slot per tuple slot; unused signature slots are zeroed.

Record placement is independent of signatures ⇒ can use with other indexing.

## Signatures



A *signature* "summarises" the data in one tuple

A tuple consists of *N* attribute values $A_1$ .. $A_n$

A *codeword* $cw(A_i)$ is

- a bit-string, *m* bits long, where *k* bits are set to 1 ($k \ll m$)
- derived from the value of a single attribute $A_i$

A *tuple descriptor* (signature) is built by combining $cw(A_i)$, $i=1..n$

- could combine by overlaying or concatenating codewords
- aim to have roughly half of the bits set to 1

## Generating Codewords



Generating a *k-in-m* codeword for attribute $A_i$

```
bits codeword(char *attr_value, int m, int k)
{
```

```
   int  nbits = 0;    // count of set bits
   bits cword = 0;    // assuming m <= 32 bits
   srandom(hash(attr_value));
   while (nbits < k) {
      int i = random() % m;
      if (((1 << i) & cword) == 0) {
         cword |= (1 << i);
         nbits++;
      }
   }
   return cword;  // m-bits with k 1-bits and m-k 0-bits
}
```

---

## Superimposed Codewords (SIMC)



In a superimposed codewords (simc) indexing scheme

- a tuple descriptor is formed by overlaying attribute codewords

A tuple descriptor *desc(r)* is

- a bit-string, *m* bits long, where $j \leq nk$ bits are set to 1
- $desc(r) = cw(A_1)$ OR $cw(A_2)$ OR ... OR $cw(A_n)$

Method (assuming all *n* attributes are used in descriptor):

```
bits desc = 0
for (i = 1; i <= n; i++) {
   bits cw = codeword(A[i])
   desc = desc | cw
}
```

---

## SIMC Example



Consider the following tuple (from bank deposit database)

| Branch | AcctNo | Name | Amount |
|---|---|---|---|
| Perryridge | 102 | Hayes | 400 |

It has the following codewords/descriptor (for $m = 12$, $k = 2$)

| $A_i$ | $cw(A_i)$ |
|---|---|
| Perryridge | 010000000001 |
| 102 | 000000000011 |
| Hayes | 000001000100 |
| 400 | 000010000100 |
| *desc(r)* | 010011000111 |

---

## SIMC Queries



To answer query *q* in SIMC

- first generate a *query descriptor desc(q)*
- then use the query descriptor to search the signature file

*desc(q)* is formed by OR of codewords for known attributes.

E.g. consider the query `(Perryridge, ?, ?, ?)`.

| $A_i$ | $cw(A_i)$ |
|---|---|
| Perryridge | 010000000001 |
| ? | 000000000000 |
| ? | 000000000000 |
| ? | 000000000000 |
| *desc(q)* | 010000000001 |

---

### ... SIMC Queries



Once we have a query descriptor, we search the signature file:

```
pagesToCheck = {}
for each descriptor D[i] in signature file {
    if (matches(D[i],desc(q))) {
        pid = pageOf(tupleID(i))
        pagesToCheck = pagesToCheck U pid
    }
}
for each P in pagesToCheck {
    Buf = getPage(f,P)
    check tuples in Buf for answers
}
// where ...
#define matches(rdesc,qdesc)
              ((rdesc & qdesc) == qdesc)
```

---

## Example SIMC Query



Consider the query and the example database:

| Signature | Deposit Record |
|---|---|
| 010000000001 | (Perryridge,?,?,?) |
| 100101001001 | (Brighton,217,Green,750) |
| 010011000111 | (Perryridge,102,Hayes,400) |
| 101001001001 | (Downtown,101,Johnshon,512) |
| 101100000011 | (Mianus,215,Smith,700) |
| 010101010101 | (Clearview,117,Throggs,295) |
| 100101010011 | (Redwood,222,Lindsay,695) |

Gives two matches: one true match, one *false match*.

---

## SIMC Parameters



*False match probablity* $p_F$ = likelihood of a false match

How to reduce likelihood of false matches?

- use different hash function for each attribute ($h_i$ for $A_i$)
- increase descriptor size ($m$)
- choose $k$ so that $\cong$ half of bits are set

Larger $m$ means reading more descriptor data.

Having $k$ too high $\Rightarrow$ increased overlapping.
Having $k$ too low $\Rightarrow$ increased hash collisions.

---



How to determine "optimal" $m$ and $k$?

1. start by choosing acceptable $p_F$
   (e.g. $p_F \leq 10^{-5}$ i.e. one false match in 10,000)
2. then choose $m$ and $k$ to achieve no more than this $p_F$.

Formulae to derive $m$ and $k$ given $p_F$ and $n$:

$$k = 1/\log_e 2 \,.\, \log_e ( 1/p_F )$$

$$m = ( 1/\log_e 2 )^2 \,.\, n \,.\, \log_e ( 1/p_F )$$

---

## Query Cost for SIMC



Cost to answer *pmr* query: $Cost_{pmr} = b_D + b_q$

- read $r$ descriptors on $b_D$ descriptor pages
- then read $b_q$ data pages and check for matches

$b_D = ceil( r/c_D )$ and $c_D = floor(B/ceil(m/8))$

E.g. $m=64$, $B=8192$, $r=10^4$ $\Rightarrow$ $c_D = 1024$, $b_D=10$

$b_q$ includes pages with $r_q$ matching tuples and $r_F$ false matches

Expected false matches = $r_F = (r - r_q).p_F \cong r.p_F$ if $r_q \ll r$

E.g. Worst $b_q = r_q+r_F$, Best $b_q = 1$, Avg $b_q = ceil(b(r_q+r_F)/r)$

---

## Exercise 1: SIMC Query Cost



Consider a SIMC-indexed database with the following properties

- all pages are $B = 8192$ bytes
- tuple descriptors have $m = 64$ bits ( = 8 bytes)
- total records $r = 102{,}400$, records/page $c = 100$
- false match probability $p_F = 1/1000$
- answer set has 1000 tuples from 100 pages
- 90% of false matches occur on data pages with true match
- 10% of false matches are distributed 1 per page

Calculate the total number of pages read in answering the query.

---

## Page-level SIMC



SIMC has one descriptor per tuple ... potentially inefficient.

Alternative approach: one descriptor for each data page.

Every attribute of every tuple in page contributes to descriptor.

Size of page descriptor (PD) (clearly larger than tuple descriptor):

- use above formulae but with $c.n$ "attributes"

E.g. $n = 4$, $c = 128$, $p_F = 10^{-3}$ $\Rightarrow$ $m \cong 7000bits \cong 900bytes$

Typically, pages are 1..8KB ⇒ 8..64 PD/page ($N_{PD}$).

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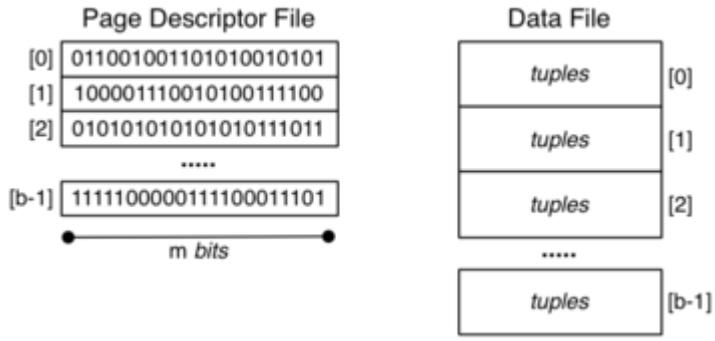
## Page-Level SIMC Files



File organisation for page-level superimposed codeword index

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## Exercise 2: Page-level SIMC Query Cost



Consider a SIMC-indexed database with the following properties

- all pages are $B = 8192$ bytes
- page descriptors have $m = 4096$ bits ( = 512 bytes)
- total records $r = 102{,}400$, records/page $c = 100$
- false match probability $p_F = 1/1000$
- answer set has 1000 tuples from 100 pages
- 90% of false matches occur on data pages with true match
- 10% of false matches are distributed 1 per page

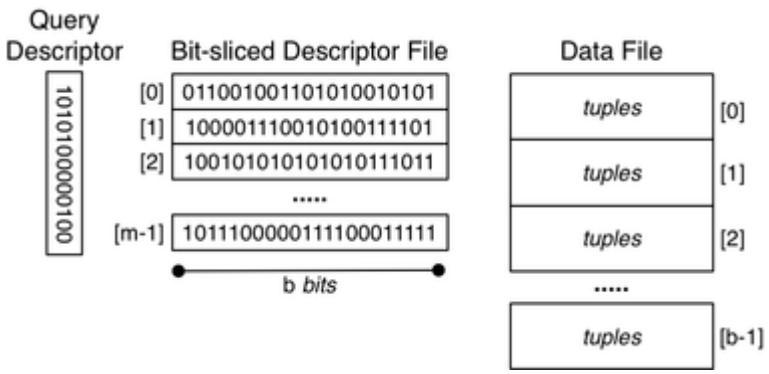
Calculate the total number of pages read in answering the query.

---

### ... Page-Level SIMC Files



Improvement: store $b$ $m$-bit page descriptors as $m$ $b$-bit "bit-slices"




---

### ... Page-Level SIMC Files



At query time

```
matches = ~0  //all ones
for each bit i set to 1 in desc(q) {
   slice = fetch bit-slice i
   matches = matches & slice
}
for each bit i set to 1 in matches {
   fetch page i
```

```
   scan page for matching records
}
```

Effective because *desc(q)* typically has less than half bits set to 1

---

## Exercise 3: Bit-sliced SIMC Query Cost



Consider a SIMC-indexed database with the following properties

- all pages are $B = 8192$ bytes
- $r = 102{,}400$, $c = 100$, $b = 1024$
- page descriptors have $m = 4096$ bits ( = 512 bytes)
- bit-slices have $b = 1024$ bits ( = 128 bytes)
- false match probability $p_F = 1/1000$
- query descriptor has $k = 10$ bits set to 1
- answer set has 1000 tuples from 100 pages
- 90% of false matches occur on data pages with true match
- 10% of false matches are distributed 1 per page

Calculate the total number of pages read in answering the query.

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# Similarity Retrieval

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## Similarity Selection



*Relational selection* is based on a boolean condition *C*

- evaluate *C* for each tuple *t*
- if *C(t)* is true, add *t* to result set
- if *C(t)* is false, *t* is not part of solution
- result is a set of tuples $\{ t_1, t_2, ..., t_n \}$ all of which satisfy *C*

Uses for relational selection:

- precise matching on structured data
- using individual attributes with known, exact values

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### ... Similarity Selection



*Similarity selection* is used in contexts where

- cannot define a precise matching condition
- *can* define a measure *d* of "distance" between tuples
- *d=0* is an exact match, *d>0* is less accurate match
- result is a list of pairs $[ (t_1,d_1), (t_2,d_2), ..., (t_n,d_n) ]$ (ordered by $d_i$)

Uses for similarity matching:

- text or multimedia (image/music) retrieval
- ranked queries in conventional databases

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## Similarity-based Retrieval



Similarity-based retrieval typically works as follows:

- query is given as a *query object q* (e.g. sample image)
- system finds objects that are *like q* (i.e. small distance)

The system can measure distance between any object and *q* ...

How to restrict solution set to only the "most similar" objects:

- *threshold* $d_{max}$ (only objects *t* such that $dist(t,q) \leq d_{max}$)
- *count k* (*k* closest objects (*k* nearest neighbours))

---

## ... Similarity-based Retrieval



Tuple structure for storing such data typically contains

- `id` to uniquely identify object (e.g. PostgreSQL `oid`)
- metadata (e.g. artist, title, genre, date taken, ...)
- `value` of object itself (e.g. PostgreSQL BLOB or `bytea`)

Properties of typical distance functions (on objects *x,y,z*)

- $dist(x,y) \geq 0$, $dist(x,x) = 0$, $dist(x,y) = dist(y,x)$
- $dist(x,z) < dist(x,y) + dist(y,z)$ (triangle inequality)

Distance calculation often requires substantial computational effort

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## ... Similarity-based Retrieval



Naive approach to similarity-based retrieval

```
q = ...    // query object
dmax = ... // dmax > 0  =>  using threshold
knn = ...  // knn > 0   =>  using nearest-neighbours
Dists = [] // empty list
foreach tuple t in R {
    d = dist(t.val, q)
    insert (t.oid,d) into Dists  // sorted on d
}
n = 0;  Results = []
foreach (i,d) in Dists {
    if (dmax > 0 && d > dmax) break;
    if (knn > 0 && ++n > knn) break;
    insert (i,d) into Results  // sorted on d
}
return Results;
```

Cost = read all *r* feature vectors + compute *distance()* for each

---

## ... Similarity-based Retrieval



For some applications, *Cost(dist(x,y))* is comparable to $T_r$

⇒ computing `dist(t.val,q)` for every tuple `t` is infeasible.

To improve this aspect:

- compute *feature vector* which captures "critical" object properties
- store feature vectors "in parallel" with objects (cf. signatures)
- compute distance using feature vectors (not objects)

i.e. replace $dist(t,t_q)$ by $dist'(vec(t),vec(t_q))$ in previous algorithm.

Further optimisation: dimension-reduction to make vectors smaller

---

## ... Similarity-based Retrieval



Content of feature vectors depends on application ...

- image ... colour histogram (e.g. 100's of values/dimensions)
- music ... loudness/pitch/tone (e.g. 100's of values/dimensions)
- text ... term frequencies (e.g. 1000's of values/dimensions)

Typically use multiple features, concatenated into single vector.

Feature vectors represent points in a *very* high-dimensional space.

Query: feature vector representing one point in vh-dim space.

Answer: list of objects "near to" query object in this space.

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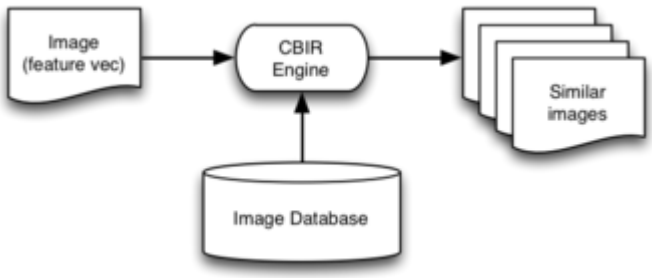
## Example: Content-based Image Retrieval



User supplies a description or sample of desired image (features).

System returns a ranked list of "matching" images from database.

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### ... Example: Content-based Image Retrieval



At the SQL level, this might appear as ...

```
// relational matching
create view Sunset as
select image from MyPhotos
where  title = 'Pittwater Sunset'
       and taken = '2012-01-01';
// similarity matching with threshold
create view SimilarSunsets as
select title, image
from   MyPhotos
where  (image ~~ (select * from Sunset)) < 0.05
order  by (image ~~ (select * from Sunset));
```

where the (imaginary) ~~ operator measures distance between images.

---

### ... Example: Content-based Image Retrieval



Implementing content-based retrieval requires ...

- a collection of "pertinent" image features
  - e.g. colour, texture, shape, keywords, ...
- some way of describing/representing image features
  - typically via a vector of numeric values
- a distance/similarity measure based on features
  - e.g. Euclidean distance between two vectors

$$dist(x,y) = \sqrt{(x_1-y_1)^2 + (x_2-y_2)^2 + \ldots (x_n-y_n)^2}$$

---

### ... Example: Content-based Image Retrieval



**Inputs** to content-based similarity-retrieval:

- a database of $r$ objects $(obj_1, obj_2, \ldots, obj_r)$ plus associated ...
- $r \times n$-dimensional feature vectors $(v_{obj_1}, v_{obj_2}, \ldots, v_{obj_r})$
- a query image $q$ with associated $n$-dimensional vector $(v_q)$
- a distance measure $D(v_i,v_j) : [0..1)$ $(D=0 \rightarrow v_i=v_j)$

**Outputs** from content-based similarity-retrieval:

- a list of the *k* nearest objects in the database $[a_1, a_2, \ldots a_k]$
- ordered by distance $D(v_{a_1},v_q) \leq D(v_{a_2},v_q) \leq \ldots \leq D(v_{a_k},v_q)$

---

## Approaches to *k*NN Retrieval



Partition-based

- use auxiliary data structure to identify candidates
- space/data-partitioning methods: e.g. k-d-B-tree, R-tree, ...
- unfortunately, such methods "fail" when #dims > 10..20
- absolute upper bound on *d* before linear scan is best *d = 610*

Approximation-based

- use approximating data structure to identify candidates
- signatures: VA-files
- projections: iDistance, LSH, MedRank, CurveIX, Pyramid

---

### ... Approaches to *k*NN Retrieval



Above approaches mostly try to reduce number of objects considered.

Other optimisations to make *k*NN retrieval faster

- reduce I/O by reducing size of vectors (compression, *d*-reduction)
- reduce I/O by placing "similar" records together (clustering)
- reduce I/O by remembering previous pages (caching)
- reduce cpu by making distance computation faster

---

## Similarity Retrieval in PostgreSQL



PostgreSQL has always supported simple "similarity" on strings

```
select * from Students where name like '%oo%';
select * from Students where name ~ '[Ss]mit';
```

Also provides support for ranked similarity on `text` values

- using `tsvector` data type (stemmed, stopped feature vector for `text`)
- using `tsquery` data type (stemmed, stopped feature vector for strings)
- using `@@` similarity operator

---

### ... Similarity Retrieval in PostgreSQL



Example of PostgreSQL text retrieval:

```
create table Docs
   ( id integer, title text, body text );
// add column to hold document feature vectors
alter table Docs add column features tsvector;
update Docs set features =
   to_tsvector('english', title||' '||body);
// ask query and get results in ranked order
select title, ts_rank(d.features, query) as rank
from   Docs d,
       to_tsquery('potter|(roger&rabbit)') as query
where  query @@ d.features
order  by rank desc
limit 10;
```

For more details, see PostgreSQL documentation, Chapter 12.

---

# Implementing Join

## Join



DBMSs are engines to *store*, *combine* and *filter* information.

*Join* (⋈) is the primary means of *combining* information.

*Join* is important and potentially expensive

Most common join condition: equijoin, e.g. `(R.pk = S.fk)`

Join varieties (natural, inner, outer, semi, anti) all behave similarly.

We consider three strategies for implementing join

- *nested loop* ... simple, widely applicable, inefficient without buffering
- *sort-merge* ... works best if tables are soted on join attributes
- *hash-based* ... requires good hash function and sufficient buffering

## Join Example



Consider a university database with the schema:

```
create table Student(
   id     integer primary key,
   name   text,  ...
);
create table Enrolled(
   stude  integer references Student(id),
   subj   text references Subject(code),  ...
);
create table Subject(
   code   text primary key,
   title  text,  ...
);
```

### ... Join Example



*List names of students in all subjects, arranged by subject.*

SQL query to provide this information:

```
select E.subj, S.name
from   Student S, Enrolled E
where  S.id = E.stude
order  by E.subj, S.name;
```

And its relational algebra equivalent:

*Sort*[subj] ( *Project*[subj,name] ( *Join*[id=stude](*Student*,*Enrolled*) ) )

To simplify formulae, we denote `Student` by *S* and `Enrolled` by *E*

### ... Join Example



Some database statistics:

| Sym | Meaning | Value |
|---|---|---|
| $r_S$ | # student records | 20,000 |
| $r_E$ | # enrollment records | 80,000 |

| | | |
|---|---|---|
| $c_S$ | `Student` records/page | 20 |
| $c_E$ | `Enrolled` records/page | 40 |
| $b_S$ | # data pages in `Student` | 1,000 |
| $b_E$ | # data pages in `Enrolled` | 2,000 |

Also, in cost analyses below, $N$ = number of memory buffers.

---

### ... Join Example



`Out` = *Student* ⋈ *Enrolled* relation statistics:

| Sym | Meaning | Value |
|---|---|---|
| $r_{Out}$ | # tuples in result | 80,000 |
| $C_{Out}$ | result records/page | 80 |
| $b_{Out}$ | # data pages in result | 1,000 |

Notes:

- $r_{Out}$ ... one result tuple for each `Enrolled` tuple
- $C_{Out}$ ... result tuples have only `subj` and `name`
- in analyses, ignore cost of writing result ... same in all methods

---

# Nested Loop Join

---

## Nested Loop Join



Basic strategy (R.a ⋈ S.b):

```
Result = {}
for each page i in R {
   pageR = getPage(R,i)
   for each page j in S {
      pageS = getPage(S,j)
      for each pair of tuples tR,tS
                        from pageR,pageS {
         if (tR.a == tS.b)
            Result = Result U (tR:tS)
}  }  }
```

Needs input buffers for R and S, output buffer for "joined" tuples

Terminology: R is outer relation, S is inner relation

Cost = $b_R$ . $b_S$ ... ouch!

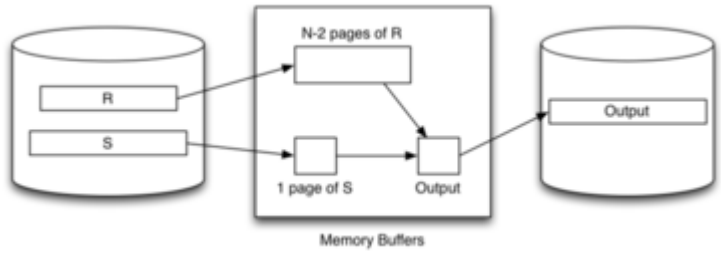
---

## Block Nested Loop Join



Method (for $N$ memory buffers):

- read $N$-2-page chunk of $R$ into memory buffers
- for each $S$ page
  check join condition on all $(t_R,t_S)$ pairs in buffers
- repeat for all $N$-2-page chunks of $R$




---

### ... Block Nested Loop Join



Best-case scenario: $b_R \leq N\text{-}2$

- read $b_R$ pages of relation $R$ into buffers
- while $R$ is buffered, read $b_S$ pages of $S$

Cost = $b_R + b_S$

Typical-case scenario: $b_R > N\text{-}2$

- read $ceil(b_R/N\text{-}2)$ chunks of pages from $R$
- for each chunk, read $b_S$ pages of $S$

Cost = $b_R + b_S \,.\, ceil(b_R/N\text{-}2)$

Note: always requires $r_R.r_S$ checks of the join condition

---

## Exercise 4: Nested Loop Join Cost



Compute the cost (# pages fetched) of $(S \bowtie E)$

| Sym | Meaning | Value |
|---|---|---|
| $r_S$ | # student records | 20,000 |
| $r_E$ | # enrollment records | 80,000 |
| $c_S$ | `Student` records/page | 20 |
| $c_E$ | `Enrolled` records/page | 40 |
| $b_S$ | # data pages in `Student` | 1,000 |
| $b_E$ | # data pages in `Enrolled` | 2,000 |

for $N = 22, 202, 2002$ and different inner/outer combinations

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## Exercise 5: Nested Loop Join Cost (cont)



If the query in the above example was:

```
select j.code, j.title, s.name
from   Student s
       join Enrolled e on (s.id=e.student)
       join Subject j on (e.subj=j.code)
```

how would this change the previous analysis?

What join combinations are there?

Assume 2000 subjects, with $c_J = 10$

How large would the intermediate tuples be? What assumptions?

Compute the cost (# pages fetched, # pages written) for $N = 22$

---

### ... Block Nested Loop Join



Why block nested loop join is actually useful in practice ...

Many queries have the form

```
select * from R,S where r.i=s.j and r.x=k
```

This would typically be evaluated as

*Join [i=j] ((Sel[r.x=k](R)), S)*

If *|Sel[r.x=k](R)|* is small ⇒ may fit in memory (in small #buffers)

---

## Index Nested Loop Join



A problem with nested-loop join:

- needs repeated scans of *entire* inner relation *S*

If there is an index on *S*, we can avoid such repeated scanning.

Consider *Join[R.i=S.j](R,S)*:

```
for each tuple r in relation R {
    use index to select tuples
        from S where s.j = r.i
    for each selected tuple s from S {
        add (r,s) to result
}   }
```

---

### ... Index Nested Loop Join



This method requires:

- one scan of *R* relation ($b_R$)
  - only one buffer needed, since we use *R* tuple-at-a-time
- for each *tuple* in *R* ($r_R$), one index lookup on *S*
  - cost depends on type of index and number of results
  - best case is when each *R.i* matches few *S* tuples

Cost = $b_R + r_R.Sel_S$ ($Sel_S$ is the cost of performing a select on *S*).

Typical $Sel_S$ = 1-2 (hashing) .. $b_q$ (unclustered index)

Trade-off: $r_R.Sel_S$ vs $b_R.b_S$, where $b_R \ll r_R$ and $Sel_S \ll b_S$

---

## Exercise 6: Index Nested Loop Join Cost



Consider executing *Join[i=j](S,T)* with the following parameters:

- $r_S = 1000$, $b_S = 50$, $r_T = 3000$, $b_T = 600$
- *S.i* is primary key, and *T* has index on *T.j*
- *T* is sorted on *T.j*, each *S* tuple joins with 2 *T* tuples
- DBMS has $N = 12$ buffers available for the join

Calculate the costs for evaluating the above join

- using block nested loop join
- using index nested loop join

$Cost_r$ = # pages read and $Cost_j$ = # join-condition checks

---

# Sort-Merge Join

## Sort-Merge Join



Basic approach:

- sort both relations on join attribute (reminder: *Join[R.i=S.j](R,S)*)
- scan together using *merge* to form result `(r,s)` tuples

Advantages:

- no need to deal with "entire" *S* relation for each *r* tuple
- deal with runs of matching *R* and *S* tuples

Disadvantages:

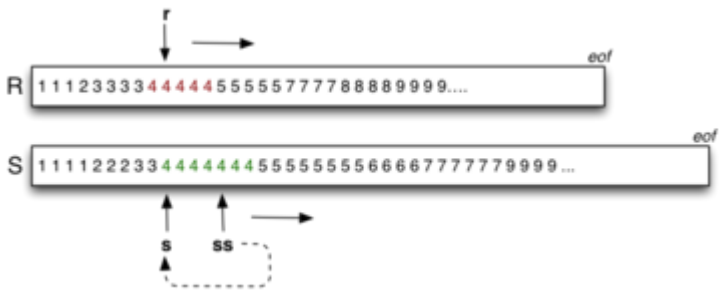
- cost of sorting both relations (already sorted on join key?)
- some rescanning required when long runs of *S* tuples

### ... Sort-Merge Join



Method requires several cursors to scan sorted relations:

- `r` = current record in *R* relation
- `s` = start of current run in *S* relation
- `ss` = current record in current run in *S* relation




### ... Sort-Merge Join



Algorithm using query iterators/scanners:

```
Query ri, si;  Tuple r,s;

ri = startScan("SortedR");
si = startScan("SortedS");
while ((r = nextTuple(ri)) != NULL
       && (s = nextTuple(si)) != NULL) {
    // align cursors to start of next common run
    while (r != NULL && r.i < s.j)
           r = nextTuple(ri);
    if (r == NULL) break;
    while (s != NULL && r.i > s.j)
           s = nextTuple(si);
    if (s == NULL) break;
    // must have (r.i == s.j) here
...
```

### ... Sort-Merge Join



```
...
    // remember start of current run in S
    TupleID startRun = scanCurrent(si)
```

```
    // scan common run, generating result tuples
    while (r != NULL && r.i == s.j) {
        while (s != NULL and s.j == r.i) {
            addTuple(outbuf, combine(r,s));
            if (isFull(outbuf)) {
                writePage(outf, outp++, outbuf);
                clearBuf(outbuf);
            }
            s = nextTuple(si);
        }
        r = nextTuple(ri);
        setScan(si, startRun);
    }
}
```

---

### ... Sort-Merge Join



Buffer requirements:

- for sort phase:
  - as many as possible (remembering that cost is $O(log_N)$ )
  - if insufficient buffers, sorting cost can dominate
- for merge phase:
  - one output buffer for result
  - one input buffer for relation *R*
  - (preferably) enough buffers for longest run in *S*

---

### ... Sort-Merge Join



Cost of sort-merge join.

Step 1: sort each relation (if not already sorted):

- Cost = $2.b_R\ (1 + log_{N-1}(b_R/N))\ +\ 2.b_S\ (1 + log_{N-1}(b_S/N))$
  (where $N$ = number of memory buffers)

Step 2: merge sorted relations:

- if every run of values in *S* fits completely in buffers,
  merge requires single scan, Cost = $b_R + b_S$
- if some runs in of values in *S* are larger than buffers,
  need to re-scan run for each corresponding value from *R*

---

## Sort-Merge Join on Example



Case 1: *Join[id=stude](Student,Enrolled)*

- relations are not sorted on *id#*
- memory buffers *N=32*; all runs are of length *< 30*

Cost = $sort(S) + sort(E) + b_S + b_E$

= $2b_S(1+log_{31}(b_S/32)) + 2b_E(1+log_{31}(b_E/32)) + b_S + b_E$

= $2\times1000\times(1+2) + 2\times2000\times(1+2) + 1000 + 2000$

= $6000 + 12000 + 1000 + 2000$

= $21,000$

---

### ... Sort-Merge Join on Example



Case 2: *Join[id=stude](Student,Enrolled)*

- *Student* and *Enrolled* already sorted on *id#*
- memory buffers *N=4* (*S* input, 2 × *E* input, output)
- 5% of the "runs" in *E* span two pages
- there are no "runs" in *S*, since *id#* is a primary key

For the above, no re-scans of *E* runs are ever needed

*Cost = 2,000 + 1,000 = 3,000* (regardless of which relation is outer)

---

## Exercise 7: Sort-merge Join Cost



Consider executing *Join[i=j](S,T)* with the following parameters:

- $r_S = 1000$, $b_S = 50$, $r_T = 3000$, $b_T = 150$
- *S.i* is primary key, and *T* has index on *T.j*
- *T* is sorted on *T.j*, each *S* tuple joins with 2 *T* tuples
- DBMS has *N = 42* buffers available for the join

Calculate the cost for evaluating the above join

- using sort-merge join
- compute #pages read/written
- compute #join-condition checks performed

---

# Hash Join

---

## Hash Join



Basic idea:

- use hashing as a technique to partition relations
- to avoid having to consider all pairs of tuples

Requires sufficent memory buffers

- to hold substantial portions of partitions
- (preferably) to hold largest partition of outer relation

Other issues:

- works only for equijoin `R.i=S.j` (but this is a common case)
- susceptible to data skew (or poor hash function)

Variations: *simple*, *grace*, *hybrid*.

---

## Simple Hash Join



Basic approach:

- hash part of outer relation *R* into memory buffers (build)
- scan inner relation *S*, using hash to search (probe)
  - if R.i=S.j, then h(R.i)=h(S.j) (hash to same buffer)
  - only need to check one memory buffer for each *S* tuple
- repeat until whole of *R* has been processed

No overflows allowed in in-memory hash table

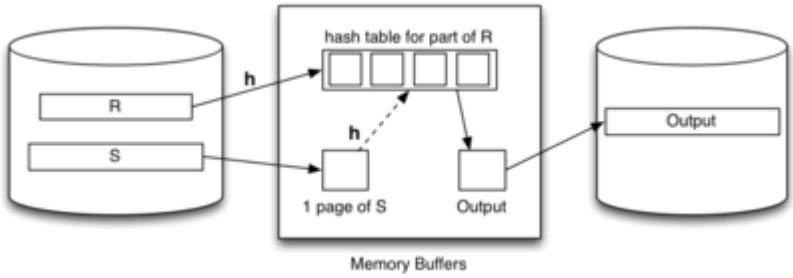
- works best with uniform hash function
- can be adversely affected by data/hash skew

---

### ... Simple Hash Join



Data flow:




---

### ... Simple Hash Join



Algorithm for simple hash join *Join[R.i=S.j](R,S)*:

```
for each tuple r in relation R {
   if (buffer[h(R.i)] is full) {
      for each tuple s in relation S {
         for each tuple rr in buffer[h(S.j)] {
            if ((rr,s) satisfies join condition) {
               add (rr,s) to result
      }  }  }
      clear all hash table buffers
   }
   insert r into buffer[h(R.i)]
}
```

# join tests $\leq r_S.c_R$ (cf. nested-loop $r_S.r_R$)

# page reads depends on #buffers *N* and properties of data/hash.

---

## Exercise 8: Simple Hash Join Cost



Consider executing *Join[i=j](R,S)* with the following parameters:

- $r_R = 1000$, $b_R = 50$, $r_S = 3000$, $b_S = 150$, $c_{Res} = 30$
- *R.i* is primary key, each *R* tuple joins with 2 *S* tuples
- DBMS has $N = 42$ buffers available for the join
- data + hash have uniform distribution

Calculate the cost for evaluating the above join

- using simple hash join
- compute #pages read/written
- compute #join-condition checks performed
- assume that hash table has *L=0.75* for each partition

---

## Grace Hash Join



Basic approach (for $R \bowtie S$ ):

- partition both relations on join attribute using hashing (*h1*)
- load each partition of *R* into N-buffer hash table (*h2*)
- scan through corresponding partition of *S* to form results
- repeat until all partitions exhausted

For best-case cost ($O(b_R + b_S)$ ):

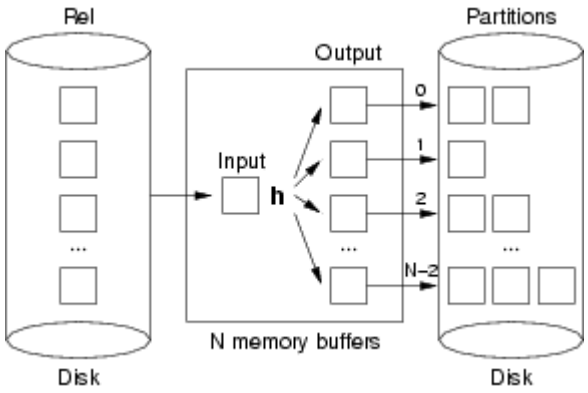
- need $\geq \sqrt{b_R}$ buffers to hold largest partition of outer relation

If $< \sqrt{b_R}$ buffers or poor hash distribution

- need to scan some partitions of *S* multiple times

---

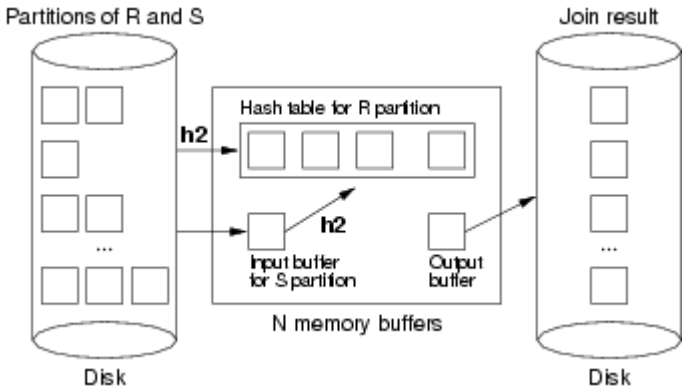
Partition phase (applied to both *R* and *S*):




---



Probe/join phase:




The second hash function (`h2`) simply speeds up the matching process.
Without it, would need to scan entire *R* partition for each record in *S* partition.

---



Cost of grace hash join:

- #pages in all partition files of *Rel* $\cong b_{Rel}$ (maybe slightly more)
- partition relation *R* ... Cost = $b_R.T_r + b_R.T_w = 2b_R$
- partition relation *S* ... Cost = $b_S.T_r + b_S.T_w = 2b_S$
- probe/join requires one scan of each (partitioned) relation
  Cost = $b_R + b_S$
- all hashing and comparison occurs in memory $\Rightarrow$ $\cong 0$ cost

Total Cost = $2b_R + 2b_S + b_R + b_S = 3\,(b_R + b_S)$

---

## Exercise 9: Grace Hash Join Cost



Consider executing *Join[i=j](R,S)* with the following parameters:

- $r_R = 1000$, $b_R = 50$, $r_S = 3000$, $b_S = 150$, $c_{Res} = 30$
- *R.i* is primary key, each *R* tuple joins with 2 *S* tuples
- DBMS has $N = 43$ buffers available for the join
- data + hash have reasonably uniform distribution

Calculate the cost for evaluating the above join

- using Grace hash join
- compute #pages read/written
- compute #join-condition checks performed

- assume that no *R* partition is larger than 40 pages

---

## Exercise 10: Grace Hash Join Cost



Consider executing *Join[i=j](R,S)* with the following parameters:

- $r_R = 1000$, $b_R = 50$, $r_S = 3000$, $b_S = 150$, $c_{Res} = 30$
- *R.i* is primary key, each *R* tuple joins with 2 *S* tuples
- DBMS has $N = 42$ buffers available for the join
- data + hash have reasonably uniform distribution

Calculate the cost for evaluating the above join

- using Grace hash join
- compute #pages read/written
- compute #join-condition checks performed
- assume that one *R* partition has 50 pages, others < 40 pages
- assume that the corresponding *S* partition has 30 pages

---

## Hybrid Hash Join



A variant of grace join if we have $\sqrt{b_R} < N < b_R+2$

- create $k \ll N$ partitions, $m$ in memory, $k-m$ on disk
- buffers: 1 input, $k-m$ output, $p = N-(k-m)-1$ for in-memory partitions

When we come to scan and partition *S* relation

- any tuple with hash in range $0..m-1$ can be resolved
- other tuples are written to one of $k$ partition files for *S*

Final phase is same as grace join, but with only $k$ partitions.

Comparison:

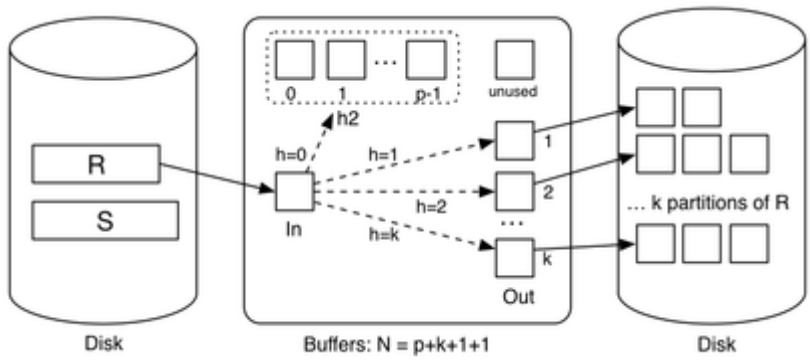
- grace hash join creates $N-1$ partitions on disk
- hybrid hash join creates $m$ (memory) + $k$ (disk) partitions

---

### ... Hybrid Hash Join



First phase of hybrid hash join with $m=1$ (partitioning *R*):

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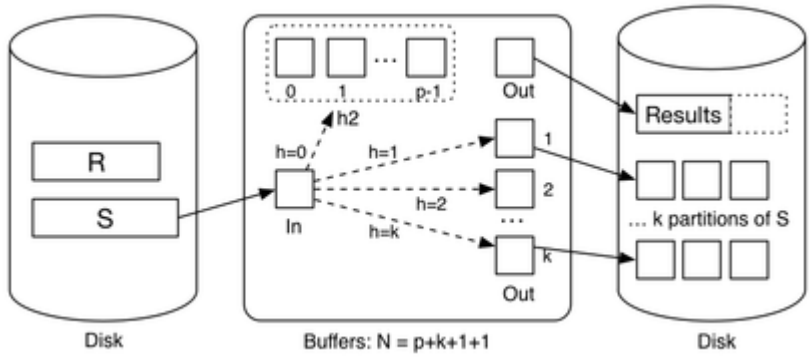
### ... Hybrid Hash Join



Next phase of hybrid hash join with $m=1$ (partitioning *S*):

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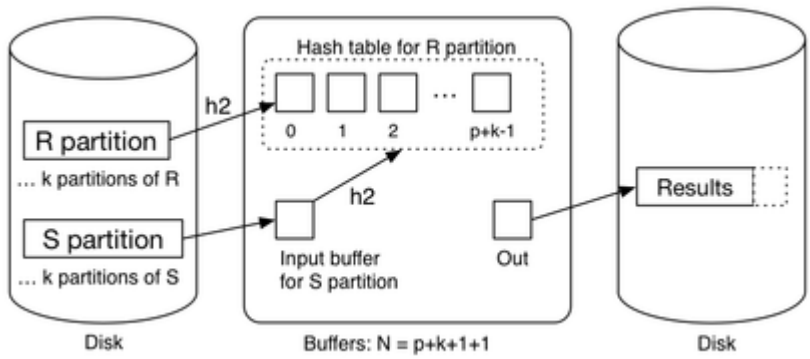
### ... Hybrid Hash Join



Final phase of hybrid hash join with *m=1* (finishing join):

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### ... Hybrid Hash Join



Some observations:

- with $k$ partitions, each partition has expected size $b_R/k$
- holding $m$ partitions in memory needs $\lceil mb_R/k \rceil$ buffers
- trade-off between in-memory partition space and #partitions

Best-cost scenario:

- $m = 1$, $k \simeq \lceil b_R/N \rceil$ (satisfying above constraint)

Other notes:

- if $N = b_R+2$, using block nested loop join is simpler
- cost depends on $N$ (but less than grace hash join)

---

## Exercise 11: Hybrid Hash Join Cost



Consider executing *Join[i=j](R,S)* with the following parameters:

- $r_R = 1000$, $b_R = 50$, $r_S = 3000$, $b_S = 150$, $c_{Res} = 30$
- *R.i* is primary key, each *R* tuple joins with 2 *S* tuples
- DBMS has $N = 42$ buffers available for the join
- data + hash have reasonably uniform distribution

Calculate the cost for evaluating the above join

- using hybrid hash join with *m=1, p=40*
- compute #pages read/written
- compute #join-condition checks performed
- assume that no *R* partition is larger than 40 pages

---

## Join Summary



No single join algorithm is superior in some overall sense.

Which algorithm is best for a given query depends on:

- sizes of relations being joined, size of buffer pool
- any indexing on relations, whether relations are sorted
- which attributes and operations are used in the query
- number of tuples in *S* matching each tuple in *R*
- distribution of data values (uniform, skew, ...)

Choosing the "best" join algorithm is critical because the cost difference between best and worst case can be very large.

E.g. *Join[id=stude](Student,Enrolled)*: 3,000 ... 2,000,000

---

## Join in PostgreSQL



Join implementations are under: **`src/backend/executor`**

PostgreSQL suports three kinds of join:

- nested loop join (**`nodeNestloop.c`**)
- sort-merge join (**`nodeMergejoin.c`**)
- hash join (**`nodeHashjoin.c`**) (hybrid hash join)

Query optimiser chooses appropriate join, by considering

- physical characteristics of tables being joined
- estimated selectivity (likely number of result tuples)

---

## Exercise 12: Outer Join?



Above discussion was all in terms of theta inner-join.

How would the algorithms above adapt to outer join?

Consider the following ...

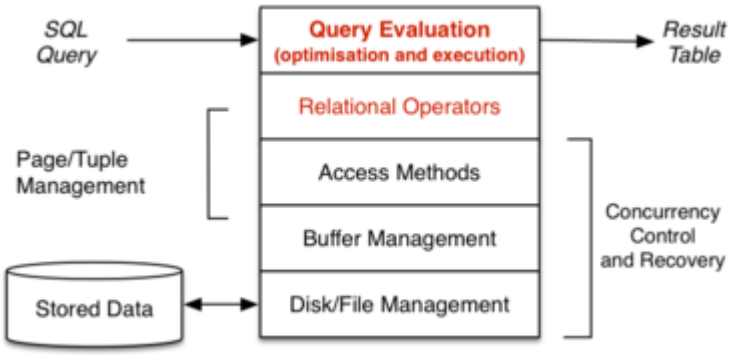
```
select *
from   R left outer join S on (R.i = S.j)

select *
from   R right outer join S on (R.i = S.j)

select *
from   R full outer join S on (R.i = S.j)
```

---

# Query Evaluation

---

## Query Evaluation

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## ... Query Evaluation



A *query* in SQL:

- states *what* kind of answers are required (declarative)
- does not say *how* they should be computed (procedural)

A *query evaluator/processor* :

- takes declarative description of query (in SQL)
- parses query to internal representation (relational algebra)
- determines plan for answering query (expressed as DBMS ops)
- executes method via DBMS engine (to produce result tuples)

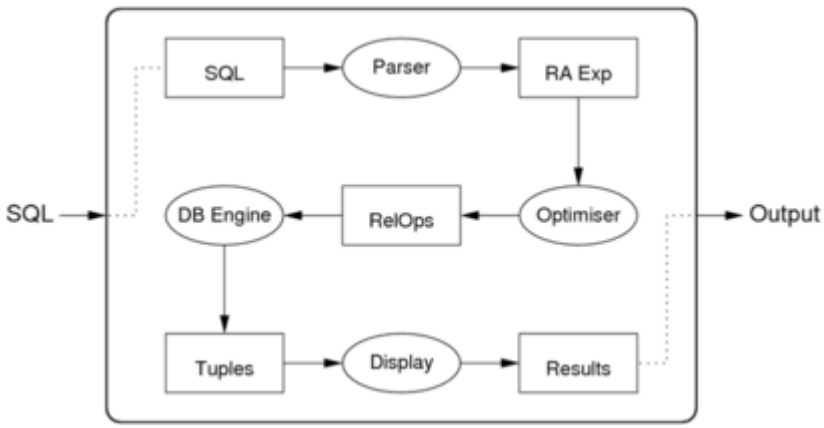
Some DBMSs can save query plans for later re-use.

---

## ... Query Evaluation



Internals of the query evaluation "black-box":

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## ... Query Evaluation



DBMSs provide several "flavours" of each RA operation.

For example:

- several "versions" of selection ($\sigma$) are available
- each version is effective for a particular kind of selection, e.g

```
select * from R where id = 100   -- hashing
select * from S                  -- Btree index
where age > 18 and age < 35
select * from T                  -- MALH file
where a = 1 and b = 'a' and c = 1.4
```

Similarly, $\pi$ and $\bowtie$ have versions to match specific query types.

---

We call these specialised version of RA operations *RelOps*.

One major task of the query processor:

- given a set of RA operations to be executed
- find a combination of RelOps to do this efficiently

Requires the query translator/optimiser to consider

- information about relations (e.g. sizes, primary keys, ...)
- information about operations (e.g. selection reduces size)

RelOps are realised at execution time

- as a collection of inter-communicating *nodes*
- communicating either via pipelines or temporary relations

---

## Terminology Variations



Relational algebra expression of SQL query

- intermediate query representation
- logical query plan

Execution plan as collection of RelOps

- query evaluation plan
- query execution plan
- physical query plan

Representation of RA operators and expressions

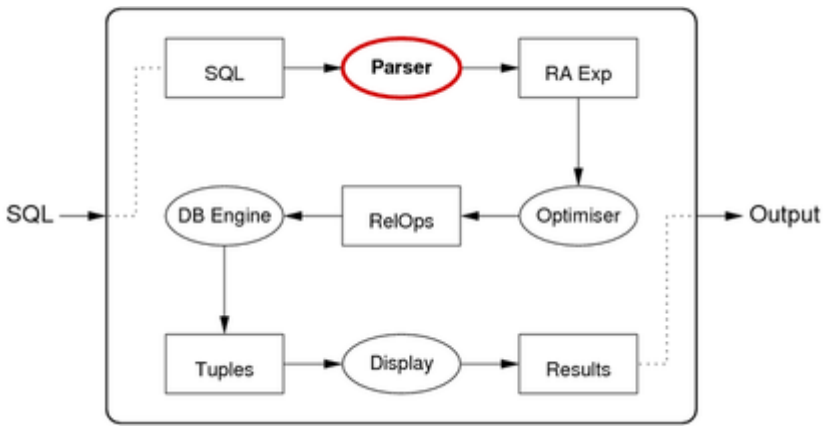
- $\sigma$ = *Select* = *Sel*, $\pi$ = *Project* = *Proj*
- $R \bowtie S$ = *R Join S* = *Join(R,S)*, $\wedge$ = &, $\vee$ = |

---

## Query Translation



Query translation: SQL statement text → RA expression




---

## Query Translation



Translation step: SQL text → RA expression

Example:

```
SQL: select name from Students where id=7654321;
-- is translated to
RA:  Proj[name](Sel[id=7654321]Students)
```

Processes: lexer/parser, mapping rules, rewriting rules.

Mapping from SQL to RA may include some optimisations, e.g.

```
select * from Students where id = 54321 and age > 50;
-- is translated to
Sel[age>50](Sel[id=54321]Students)
-- rather than ... because of index on id
Sel[id=54321&age>50](Students)
```

---

## Parsing SQL



Parsing task is similar to that for programming languages.

Language elements:

- keywords: `create`, `select`, `from`, `where`, ...
- identifiers: `Students`, `name`, `id`, `CourseCode`, ...
- operators: `+`, `-`, `=`, `<`, `>`, `AND`, `OR`, `NOT`, `IN`, ...
- constants: `'abc'`, `123`, `3.1`, `'01-jan-1970'`, ...

PostgreSQL parser ...

- implemented via lex/yacc (**`src/backend/parser`**)
- maps all identifiers to lower-case (A-Z → a-z)
- needs to handle user-extendable operator set
- makes extensive use of catalog (**`src/backend/catalog`**)

---

## Mapping SQL to Relational Algebra



A given SQL query typically has many translations to RA.

For example:

```
SELECT s.name, e.subj
FROM   Students s, Enrolments e
WHERE  s.id = e.sid AND e.mark < 50;
```

is equivalent to any of

- $\pi_{s.name,e.subj}( \sigma_{s.id=e.sid \wedge e.mark<50} ( Students \times Enrolments ) )$
- $\pi_{s.name,e.subj}( \sigma_{s.id=e.sid} ( \sigma_{e.mark<50} ( Students \times Enrolments ) ) )$
- $\pi_{s.name,e.subj}( \sigma_{e.mark<50} ( Students \bowtie_{s.id=e.sid} Enrolments ) ) )$
- $\pi_{s.name,e.subj}( Students \bowtie_{s.id=e.sid} ( \sigma_{e.mark<50} ( Enrolments ) ) )$

---

### ... Mapping SQL to Relational Algebra



More complex example:

```
select   distinct s.code
from     Course c, Subject s, Enrolment e
where    c.id = e.course and c.subject = s.id
group by s.id  having count(*) > 100;
```

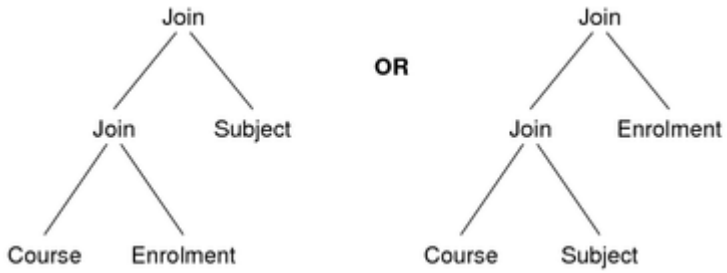
can be translated to the relational algebra expression

$$
\begin{array}{l}
Uniq(Proj_{[code]}( \\
\quad GroupSelect_{[groupSize>100]}( \\
\quad\quad GroupBy_{[s.id]} ( \\
\quad\quad\quad Enrolment \bowtie Course \bowtie Subjects \\
)))) 
\end{array}
$$

---

### ... Mapping SQL to Relational Algebra

The join operations could be done in two different ways:




Note: for a join on *n* tables, there are potentially *O(n!)* possible trees

The *query optimiser* aims to find version with lowest total cost.

---

## Mapping Rules



Mapping from SQL → RA expression requires:

- a collection of *templates*, ≥1 for each kind of query
- a process to match an SQL statement to a template
- mapping rules for translating matched query into RA

May need to apply >1 templates to map whole SQL statement.

After mapping, apply rewriting rules to "improve" RA expression

- convert to equivalent, simpler, more efficient expression

Note: PostgreSQL also has user-defined mapping rules (`CREATE RULE`)

---

### ... Mapping Rules



**Projection:**

`SELECT` *a+b* `AS` *x, c* `AS` *y* `FROM` *R ...*

⇒ $Proj_{[x \leftarrow a+b,\ y \leftarrow c]}(R)$

SQL projection extends RA projection with renaming and assignment

**Join:**

`SELECT` *...* `FROM` *... R, S ...* `WHERE` *... R.f op S.g ...* , or

`SELECT` *...* `FROM` *... R* `JOIN` *S* `ON` *(R.f op S.g) ...* `WHERE` *...*

⇒ $Join_{[R.f\ op\ S.g\ ]}(R,S)$

---

### ... Mapping Rules



**Selection:**

`SELECT` *...* `FROM` *... R ...* `WHERE` *... R.f op val ...*

⇒ $Select_{[R.f\ op\ val]}(R)$

`SELECT` *...* `FROM` *... R ...* `WHERE` *...* $Cond_{1,R}$ `AND` $Cond_{2,R}$ *...*

⇒ $Select_{[Cond_{1,R}\ \&\ Cond_{2,R}]}(R)$

or

⇒ $Select_{[Cond_{1,R}]}(Select_{[Cond_{2,R}]}(R))$

---

## Exercise 13: Mapping OR expressions



Possible mappings for `WHERE` expressions with `AND` are

*`SELECT` ... `FROM` ... R ... `WHERE` ... X `AND` Y ...*

⇒ $Select_{[X \& Y]}(R)$ or $Select_{[X]}(Select_{[Y]}(R))$

What are possible mappings for

*`SELECT` ... `FROM` ... R ... `WHERE` ... X `OR` Y ...*

Use these to translate:

```
select * from R where (a=1 or a=3) and b < c
```

---

## Mapping Rules



Aggregation operators (e.g. `MAX`, `SUM`, ...):

- add as new operators in extended RA
  e.g. `SELECT MAX(age) FROM ...` ⇒ $max(Proj_{[age]}(...))$

Sorting (`ORDER BY`):

- add *Sort* operator into extended RA (e.g. $Sort_{[+name,-age]}(...)$)

Duplicate elimination (`DISTINCT`):

- add *Uniq* operator into extended RA (e.g. *Uniq(Proj(...))*)

Grouping (`GROUP BY`, `HAVING`):

- add operators into extended RA (e.g. *GroupBy, GroupSelect* )

---

### ... Mapping Rules



*View* example: assuming *Employee(id,name,birthdate,salary)*

```
-- view definition
create view OldEmps as
select * from Employees
where  birthdate < '01-01-1960';
-- view usage
select name from OldEmps;
```

yields

- $OldEmps = Select_{[birthdate<'01-01-1960']}(Employees)$
- $Proj_{name}(OldEmps)$
  ⇒ $Proj_{name}(Select_{[birthdate<'01-01-1960']}(Employees))$

---

## Exercise 14: Mapping Views



Given the following definitions:

```
create table R(a integer, b integer, c integer);

create view RR(f,g,h) as
select * from R where a > 5 and b = c;
```

Show how the following might be mapped to RA:

```
select * from RR where f > 10;
```

---