Using Databases in R

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Relational Databases

Relational database basics

- Data stored in *tables*
- Tables related through *keys*
- Relational model called a *schema*
- Tables designed to avoid redundancy

Beneficial uses by R packages

- Out-of-memory data storage
- Fast access to data subsets
- Databases accessible by other software

Uses of Relational Databases in Bioconductor

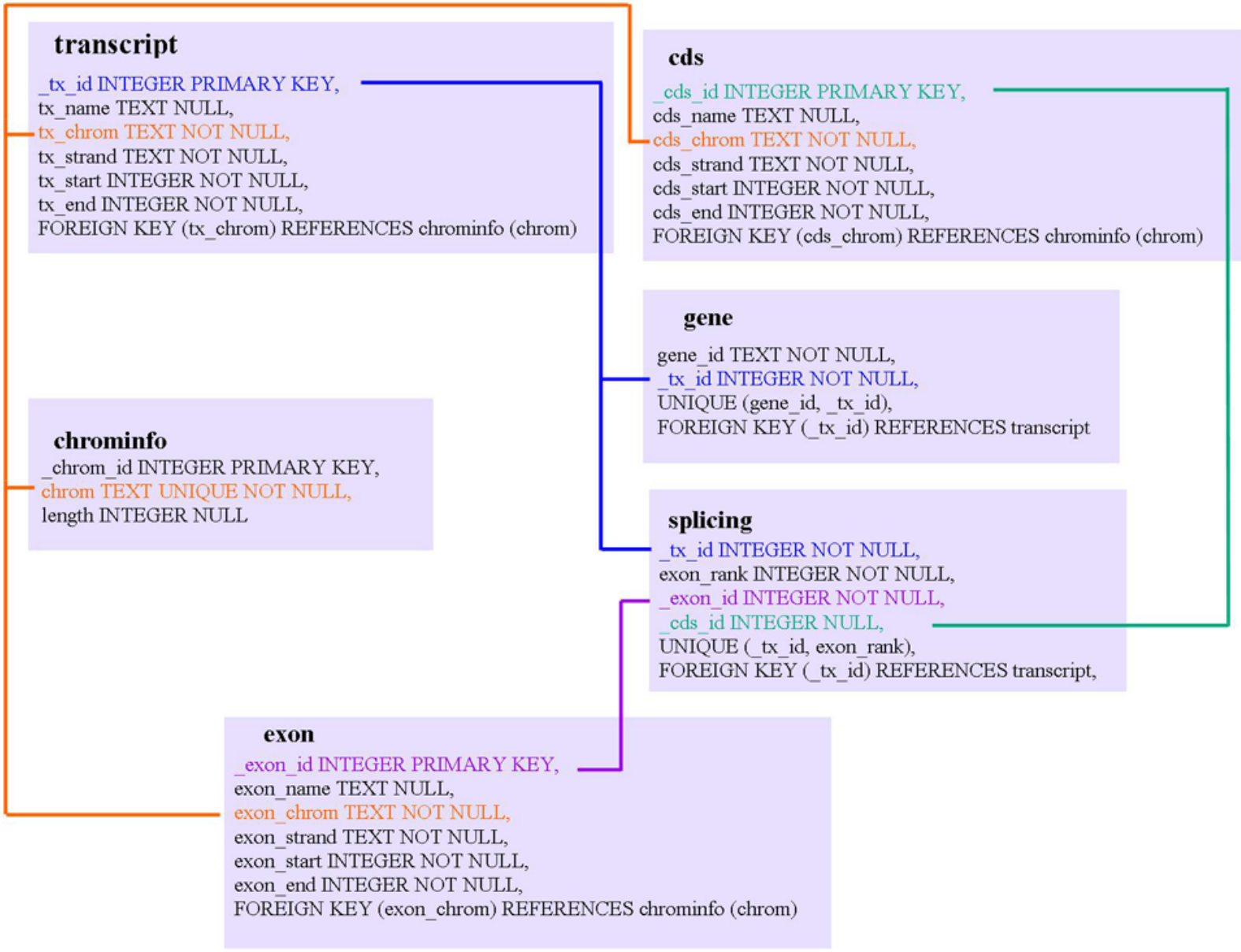
Annotation packages

- Organism, genome (e.g. *org.Hs.eg.db*)
- Microarray platforms (e.g. *hgu95av2.db*)
- Homology (e.g. *hom.Hs.inp.db*)

Software packages

- Transcript annotations (e.g. *GenomicFeatures*)
- NGS experiments (e.g. *Genominator*)
- Annotation infrastructure (e.g. *AnnotationDbi*)

What do I mean by relational?



SQL in 3 slides

Structured Query Language (SQL) is the most common language for interacting with relational databases.

Database Retrieval

Single table selections

```
SELECT * FROM gene;
SELECT gene_id, gene._tx_id FROM gene;

SELECT * FROM gene WHERE _tx_id=49245;
SELECT * FROM transcript WHERE tx_name LIKE '%oap.1';
```

Inner joins

```
SELECT gene.gene_id,transcript._tx_id
  FROM gene, transcript
  WHERE gene._tx_id=transcript._tx_id;

SELECT g.gene_id,t._tx_id
  FROM gene AS g, transcript AS t
  WHERE g._tx_id=t._tx_id
  AND t._tx_id > 10;
```

Database Modifications

CREATE TABLE

```
CREATE TABLE foo (
  id INTEGER,
  string TEXT
);
```

INSERT

```
INSERT INTO foo (id, string) VALUES (1,"bar");
```

CREATE INDEX

```
CREATE INDEX fooInd1 ON foo(id);
```

Some extra tricks

You can use AS to rename parts of a query

```
SELECT * FROM gene AS g;
```

You can use ORDER BY to ensure that things are sorted

```
SELECT * FROM gene ORDER BY gene_id;
```

You can use () to indicate sub-queries. This can be useful when you have more complex queries to express or if you need to combine different kinds of joins into a single query.

```
SELECT * FROM transcript as t, (SELECT * FROM gene) AS g
 WHERE g._tx_id = t._tx_id;
```

It's sometimes a good idea to use a stand-alone client

- SQLite3 demo

The *DBI* package

- Provides a nice generic access to databases in R
- Many of the functions are convenient and simple to use

Some popular DBI functions

```
> library(RSQLite) #loads DBI too, (but we need both)
> drv <- SQLite()
> con <- dbConnect(drv, dbname=system.file("extdata",
+                  "mm9KG.sqlite", package="AdvancedR2011")
> dbListTables(con)
```

```
[1] "cds"        "chrominfo"
[3] "exon"       "gene"
[5] "metadata"   "splicing"
[7] "transcript"
```

```
> dbListFields(con,"transcript")
```

```
[1] "_tx_id"    "tx_name"   "tx_chrom"
[4] "tx_strand" "tx_start"  "tx_end"
```

The dbGetQuery approach

```
> dbGetQuery(con, "SELECT * FROM transcript LIMIT 3")
  _tx_id    tx_name tx_chrom tx_strand
1  24308 uc009oap.1     chr9         -
2  24309 uc009oao.1     chr9         -
3  24310 uc009oaq.1     chr9         -
  tx_start  tx_end
1  3186316 3186344
2  3133847 3199799
3  3190269 3199799
```

The dbSendQuery approach

If you use result sets, you also need to put them away

```
> res <- dbSendQuery(con, "SELECT * FROM transcript")
> fetch(res, n= 3)
```

```
  _tx_id    tx_name tx_chrom tx_strand
1  24308 uc009oap.1     chr9         -
2  24309 uc009oao.1     chr9         -
3  24310 uc009oaq.1     chr9         -
  tx_start  tx_end
1  3186316 3186344
2  3133847 3199799
3  3190269 3199799
```

```
> dbClearResult(res)
```

```
[1] TRUE
```

Calling fetch again will get the next three results. This allows for simple iteration.

Setting up a new DB

First, lets close the connection to our other DB:

```
>    dbDisconnect(con)
```

```
[1] TRUE
```

Then lets make a new database. Notice that we specify the database name with "dbname" This allows it to be written to disc instead of just memory.

```
> drv <- SQLite()
> con <- dbConnect(drv, dbname="myNewDb.sqlite")
```

Once you have this, you may want to make a new table

```
> dbGetQuery(con, "CREATE Table foo (id INTEGER, string TEXT)")
```

```
NULL
```

The *RSQLite* package

- Provides SQLite access for R
- Much better support for complex inserts

Prepared queries

```
> data <- data.frame(c(226089,66745),
+                    c("C030046E11Rik","Trpd52l3"),
+                    stringsAsFactors=FALSE)
> names(data) <- c("id","string")
> sql <- "INSERT INTO foo VALUES ($id, $string)"
> dbBeginTransaction(con)
```

```
[1] TRUE
```

```
> dbGetPreparedQuery(con, sql, bind.data = data)
```

```
NULL
```

```
> dbCommit(con)
```

```
[1] TRUE
```

Notice that we want strings instead of factors in our data.frame

in SQLite, you can ATTACH Dbs

The (SQLite specific) SQL that we want looks quite simple:

```
ATTACH "mm9KG.sqlite" AS db;
```

So we just need to do something like this:

```
> db <- system.file("extdata", "mm9KG.sqlite",
+                   package="AdvancedR2011")
> dbGetQuery(con, sprintf("ATTACH '%s' AS db",db))
NULL
```

You can join across attached Dbs

The SQL this looks like:

```
SELECT * FROM db.gene AS dbg, foo AS f
WHERE dbg.gene_id=f.id;
```

Then in R:

```
>   sql <- "SELECT * FROM db.gene AS dbg,
+            foo AS f WHERE dbg.gene_id=f.id"
>   res <- dbGetQuery(con, sql)
>   res
```

	gene_id	_tx_id	id	string
1	226089	48508	226089	C030046E11Rik
2	226089	48509	226089	C030046E11Rik
3	226089	48511	226089	C030046E11Rik
4	226089	48510	226089	C030046E11Rik
5	66745	48522	66745	Trpd52l3

The End.

```
[1] TRUE
```