Using Databases in R

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Outline

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)

Outline

The GenomicFeatures package

What is does

- Builds databases on the fly as needed.
- Supported sources: UCSC tracks, biomaRt, or custom.
- Has accessor methods to make it easy to use this data.

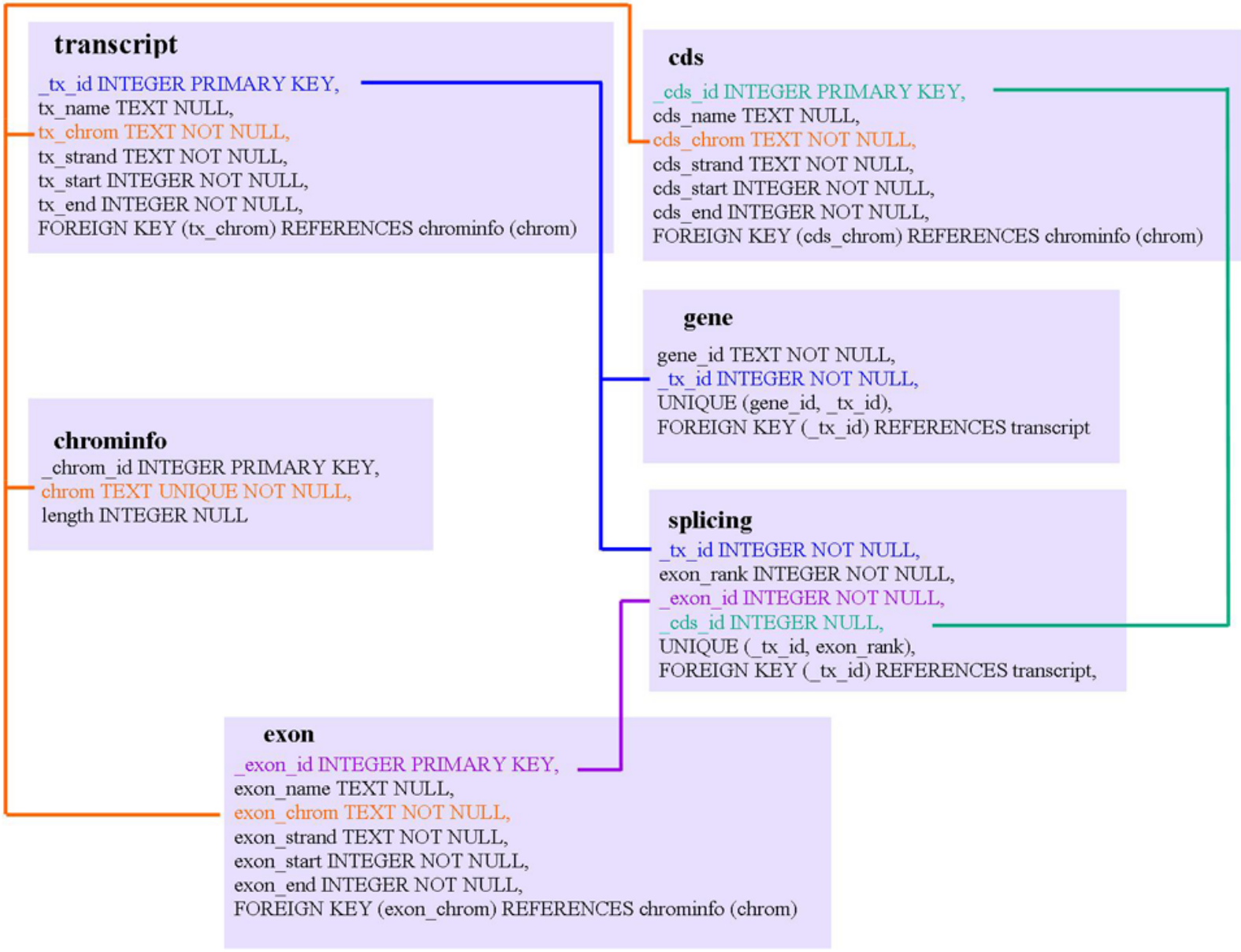
Why it was built

- Needed a generic way to support access to multiple resources
- Users needed reproducible data for research
- Data needed to be formatted in a convenient way

Why it uses a database

- Annotation data is highly relational
- Other annnotation data is also stored in SQLite databases
- Allows access from disc (which can free up memory)

What do I mean by relational?



TranscriptDb Basics

Making a TranscriptDb object

```
> library(GenomicFeatures)
> mm9KG <-
+   makeTranscriptDbFromUCSC(genome = "mm9",
+                            tablename = "knownGene")
```

Saving and Loading

```
> saveFeatures(mm9KG, file="mm9KG.sqlite")
> mm9KG <-
+   loadFeatures(system.file("extdata", "mm9KG.sqlite",
+                            package = "AdvancedR"))
```

Accessing the TranscriptDb

```
> head(transcripts(mm9KG), 3)
```

```
GRanges with 3 ranges and 2 elementMetadata values
    seqnames              ranges strand |     tx_id
       <Rle>           <IRanges>  <Rle> | <integer>
[1]     chr9 [3215314, 3215339]      + |     24312
[2]     chr9 [3335231, 3385846]      + |     24315
[3]     chr9 [3335473, 3343608]      + |     24313
        tx_name
    <character>
[1]  uc009oas.1
[2]  uc009oat.1
[3]  uc009oau.1

seqlengths
         chr1          chr2 ...  chrX_random  chrY_random
    197195432     181748087 ...      1785075     58682461
```

What actually happens when we do this?

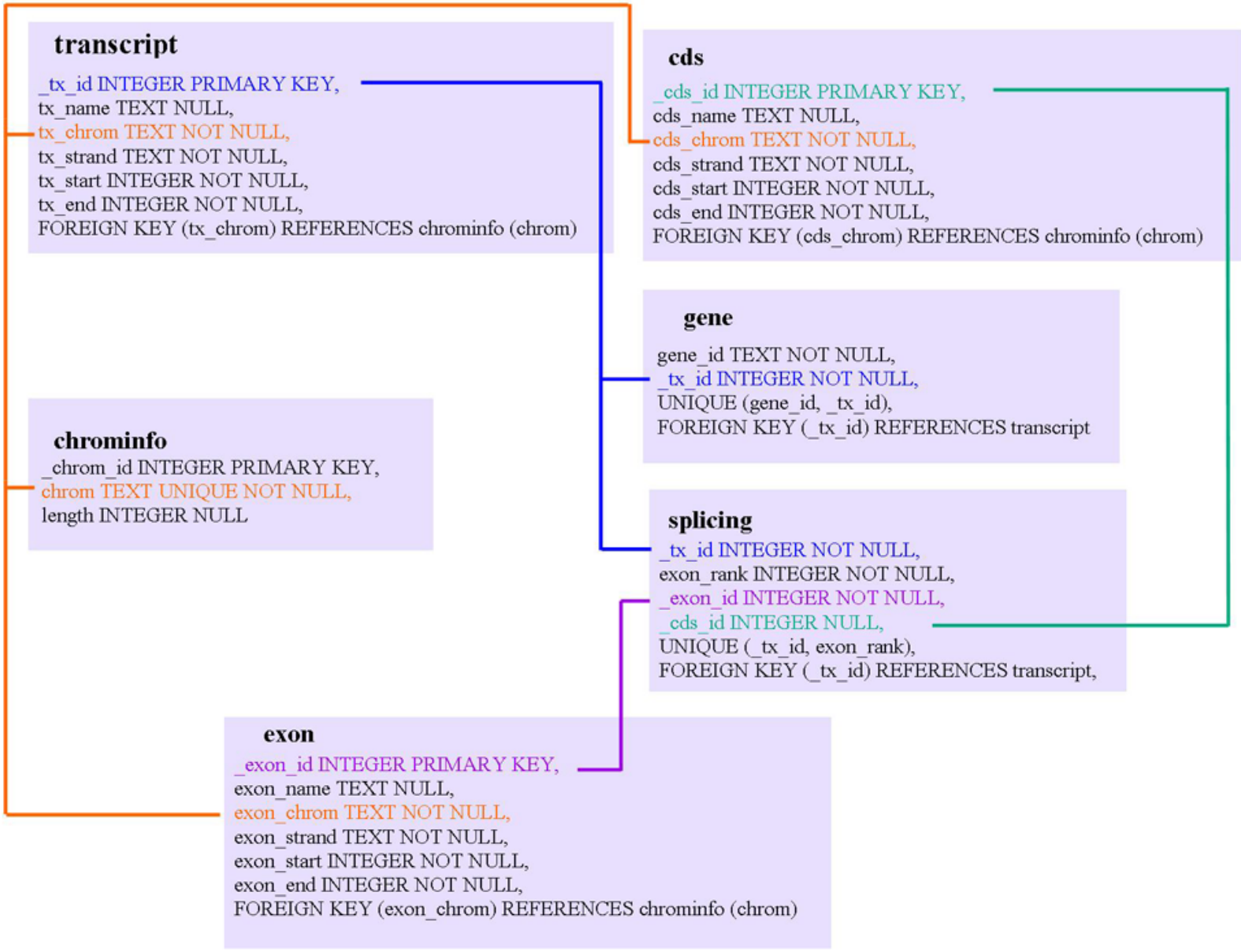
```
> options(verbose=TRUE)
> txs <- transcripts(mm9KG)

SQL QUERY: SELECT tx_chrom, tx_start, tx_end, tx_strand,
transcript._tx_id AS tx_id , tx_name FROM transcript
ORDER BY tx_chrom, tx_strand, tx_start, tx_end
```

Notice how the database query is pretty simple?

- DB joins promote flexible access
- BUT: there is a cost if using A LOT of joins
- Therefore (in this case) a hybrid approach: Retrieve relevant records and subset in R

Our database schema



Outline

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);
```

Outline

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 <- dbDriver("SQLite")
> con <- dbConnect(drv, dbname=system.file("extdata",
+                     "mm9KG.sqlite", package="AdvancedR"))
> dbListTables(con)
[1] "cds"        "chrominfo"  "exon"       "gene"
[5] "metadata"   "splicing"   "transcript"

> dbListFields(con,"transcript")
[1] "_tx_id"    "tx_name"   "tx_chrom"  "tx_strand"
[5] "tx_start"  "tx_end"
```

The dbGetQuery approach

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

```
> dbClearResult(res)
```

```
[1] TRUE
```

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

Your turn

Select the exons from the minus strand of chromosome 9.

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 <- dbDriver("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
```

Your turn again

Create a database and then put a table in it called genePheno to store the genes mutated and a phenotypes associated with each. Plan for genePheno to hold the following gene IDs and phenotypes (as a toy example):

```
data = data.frame(id=c(69773,20586,258822,18315),
                  string=c("Dead",
                           "Alive",
                           "Dead",
                           "Alive"),
                  stringsAsFactors=FALSE)
```

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

Your turn part 3

Now take a moment to insert that data into your database.

in SQLite, you can ATTACH Dbs

The SQL what 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="AdvancedR")
> 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

Your turn part 4

Now create a cross join to your database and extract the _tx_id 's from the gene table there using your gene IDs as a foreign key.

Your turn part 5

Now conect your cross join to the transcript table in the database and extract the fields from that table while still using your gene IDs as a foreign key.