

# Using the **SRADB** Package to Query the Sequence Read Archive

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## 1 Introduction

High throughput sequencing technologies have very rapidly become standard tools in biology. The data that these machines generate are large, extremely rich. As such, the Sequence Read Archives (SRA) have been set up at NCBI in the United States, EMBL in Europe, and DDBJ in Japan to capture these data in public repositories in much the same spirit as MIAME-compliant microarray databases like NCBI GEO and EBI ArrayExpress.

Accessing data in SRA requires finding it first. This R package provides a convenient and powerful framework to do just that. In addition, **SRADB** features functionality to determine availability of sequence files and to download files of interest.

SRA currently store aligned reads or other processed data that relies on alignment to a reference genome. Please refer to the SRA handbook (<http://www.ncbi.nlm.nih.gov/books/NBK47537/>) for details. NCBI GEO also often contain aligned reads for sequencing experiments and the **SRADB** package can help to provide links to these data as well. In combination with the **GEOmetadb** and **GEOquery** packages, these data are also, then, accessible.

## 2 Getting Started

Since SRA is a continuously growing repository, the **SRADB** SQLite file is updated regularly. The first step, then, is to get the **SRADB** SQLite file from the online location. The download and uncompress steps are done automatically with a single command, `getSRADBFile`.

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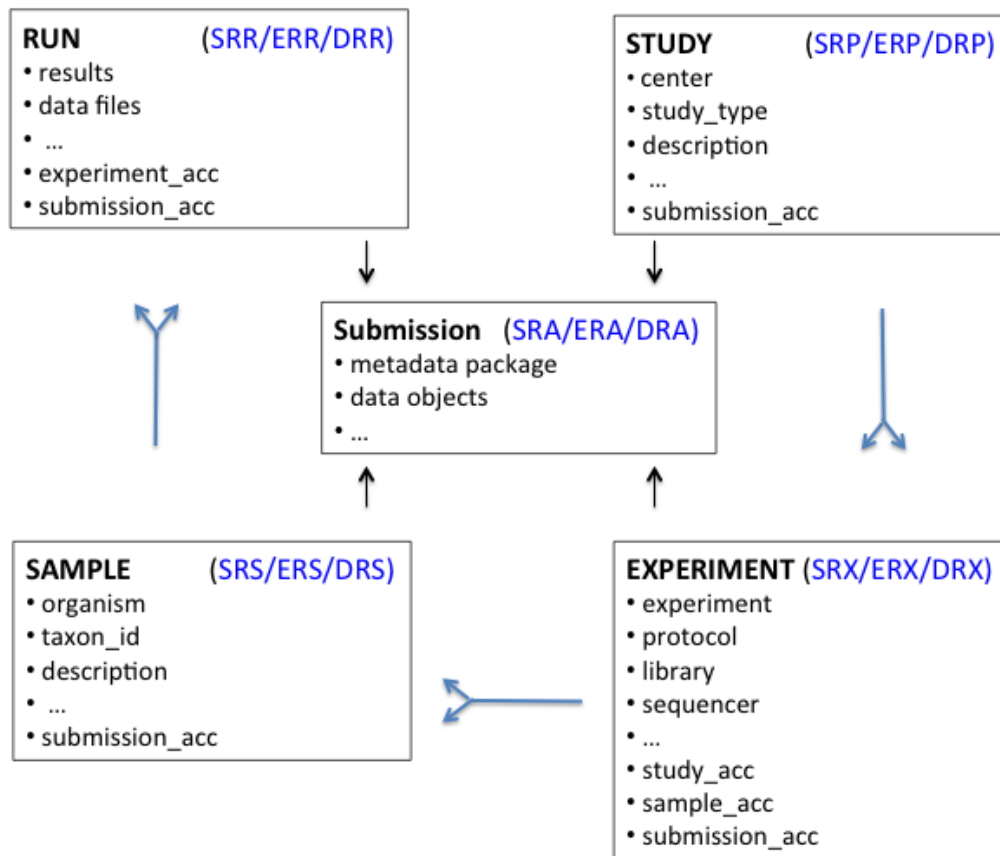


Figure 1: A graphical representation (sometimes called an *Entity-Relationship Diagram*) of the relationships between the main tables in the SRAdB package.

```
> library(SRAdb)
> sqlfile <- 'SRAmetadb.sqlite'
> if(!file.exists('SRAmetadb.sqlite')) sqlfile <- getSRADBFile()
```

The default storage location is in the current working directory and the default filename is “SRAmetadb.sqlite”; it is best to leave the name unchanged unless there is a pressing reason to change it. Note: the above downloading and uncompressing steps could take quite a few moments due to file size, depending on your network bandwidth. If interested, it can be timed using the following commands:

```
> timeStart <- proc.time()
> sqlfile <- getSRADBFile()
> proc.time() - timeStart
```

Since this SQLite file is of key importance in SRAdb, it is perhaps of some interest to know some details about the file itself.

```
> file.info('SRAmetadb.sqlite')

              size isdir mode
SRAmetadb.sqlite 11710134272 FALSE  644
              mtime
SRAmetadb.sqlite 2015-03-23 19:00:01
              ctime
SRAmetadb.sqlite 2015-03-23 19:00:01
              atime uid gid
SRAmetadb.sqlite 2015-03-23 19:00:01 501  20
              uname grname
SRAmetadb.sqlite biocbuild  staff
```

Then, create a connection for later queries. The standard DBI functionality as implemented in RSQLite function `dbConnect` makes the connection to the database. The `dbDisconnect` function disconnects the connection.

```
> sra_con <- dbConnect(SQLite(),sqlfile)
```

For further details, at this time see `help('SRAdb-package')`.

## 3 Using the SRAdb package

### 3.1 Interacting with the database

The functionality covered in this section is covered in much more detail in the DBI and RSQLite package documentation. We cover enough here only to be useful. The `dbListTables` function lists all the tables in the SQLite database handled by the connection object `sra_con` created in the previous section. A simplified illustration of the relationship between the SRA main data types is shown in the Figure 1.

```
> sra_tables <- dbListTables(sra_con)
> sra_tables

[1] "col_desc"          "experiment"
[3] "fastq"             "metaInfo"
[5] "run"               "sample"
[7] "sra"               "sra_ft"
[9] "sra_ft_content"    "sra_ft_segdir"
[11] "sra_ft_segments"   "study"
[13] "submission"
```

There is also the `dbListFields` function that can list database fields associated with a table.

```
> dbListFields(sra_con, "study")

[1] "study_ID"           "study_alias"
[3] "study_accession"    "study_title"
[5] "study_type"         "study_abstract"
[7] "broker_name"        "center_name"
[9] "center_project_name" "study_description"
[11] "related_studies"    "primary_study"
[13] "sra_link"           "study_url_link"
[15] "xref_link"          "study_entrez_link"
[17] "ddbj_link"          "ena_link"
[19] "study_attribute"    "submission_accession"
[21] "sradb_updated"
```

Sometimes it is useful to get the actual SQL schema associated with a table. Here, we get the table schema for the *study* table:

```
> dbGetQuery(sra_con, 'PRAGMA TABLE_INFO(study)')
```

	cid	name	type	notnull
1	0	study_ID	REAL	0
2	1	study_alias	TEXT	0
3	2	study_accession	TEXT	0
4	3	study_title	TEXT	0
5	4	study_type	TEXT	0
6	5	study_abstract	TEXT	0
7	6	broker_name	TEXT	0
8	7	center_name	TEXT	0
9	8	center_project_name	TEXT	0
10	9	study_description	TEXT	0

11	10	related_studies	TEXT	0
12	11	primary_study	TEXT	0
13	12	sra_link	TEXT	0
14	13	study_url_link	TEXT	0
15	14	xref_link	TEXT	0
16	15	study_entrez_link	TEXT	0
17	16	ddbj_link	TEXT	0
18	17	ena_link	TEXT	0
19	18	study_attribute	TEXT	0
20	19	submission_accession	TEXT	0
21	20	sradb_updated	TEXT	0
		dflt_value	pk	
1		<NA>	0	
2		<NA>	0	
3		<NA>	0	
4		<NA>	0	
5		<NA>	0	
6		<NA>	0	
7		<NA>	0	
8		<NA>	0	
9		<NA>	0	
10		<NA>	0	
11		<NA>	0	
12		<NA>	0	
13		<NA>	0	
14		<NA>	0	
15		<NA>	0	
16		<NA>	0	
17		<NA>	0	
18		<NA>	0	
19		<NA>	0	
20		<NA>	0	
21		<NA>	0	

The table "col\_desc" contains information of filed name, type, descritption and default values:

```
> colDesc <- colDescriptions(sra_con=sra_con)[1:5,]
> colDesc[, 1:4]
```

	col_desc_ID	table_name	field_name
1	1	submission	ID
2	2	submission	accession
3	3	submission	alias

```

4          4 submission submission_comment
5          5 submission                files
      type
1      int
2 varchar
3 varchar
4      text
5      text

```

## 3.2 Writing SQL queries and getting results

Select 3 records from the *study* table and show the first 5 columns:

```

> rs <- dbGetQuery(sra_con,"select * from study limit 3")
> rs[, 1:3]

```

```

      study_ID study_alias study_accession
1           1   DRP000001      DRP000001
2           2   DRP000002      DRP000002
3           3   DRP000003      DRP000003

```

Get the SRA study accessions and titles from SRA study that study\_type contains “Transcriptome”. The “%” sign is used in combination with the “like” operator to do a “wildcard” search for the term “Transcriptome” with any number of characters after it.

```

> rs <- dbGetQuery(sra_con, paste( "select study_accession,
+      study_title from study where",
+      "study_description like 'Transcriptome%'",sep=" "))
> rs[1:3,]

```

```

      study_accession
1      ERP000233
2      ERP000350
3      ERP000527

```

```

1 Identification of the expression profile of Staphylococcus aureus grown in the presence of
2
3

```

Transcriptome Analysis of the

Of course, we can combine programming and data access. A simple `sapply` example shows how to query each of the tables for number of records.

```

> getTableCounts <- function(tableName,conn) {
+   sql <- sprintf("select count(*) from %s",tableName)

```

```
+ return(dbGetQuery(conn,sql)[1,1])
+ }
> do.call(rbind,sapply(sra_tables[c(2,4,5,11,12)],
+                       getTableCounts, sra_con, simplify=FALSE))
```

```
      [,1]
experiment 1044035
metaInfo    2
run         1411313
sra_ft_segments 368432
study       51680
```

Get some high-level statistics could be to helpful to get overall idea about what data are available in the SRA database. List all study types and number of studies contained for each of the type:

```
> rs <- dbGetQuery(sra_con, paste( "SELECT study_type AS StudyType,
+ count( * ) AS Number FROM `study` GROUP BY study_type order
+ by Number DESC ", sep=""))
> rs
```

	StudyType	Number
1	Whole Genome Sequencing	26121
2	Other	11282
3	Transcriptome Analysis	6622
4	Metagenomics	4144
5	Epigenetics	2064
6	Population Genomics	680
7	<NA>	510
8	Exome Sequencing	135
9	Cancer Genomics	73
10	Pooled Clone Sequencing	32
11	Synthetic Genomics	9
12	RNASeq	8

List all Instrument Models and number of experiments for each of the Instrument Models:

```
> rs <- dbGetQuery(sra_con, paste( "SELECT instrument_model AS
+ 'Instrument Model', count( * ) AS Experiments FROM `experiment`
+ GROUP BY instrument_model order by Experiments DESC", sep=""))
> rs
```

	Instrument Model
1	Illumina HiSeq 2000

2                   Illumina MiSeq  
 3                   454 GS FLX Titanium  
 4       Illumina Genome Analyzer II  
 5       Illumina Genome Analyzer IIx  
 6                   Illumina HiSeq 2500  
 7                   unspecified  
 8                   454 GS FLX  
 9       Illumina Genome Analyzer  
 10                   <NA>  
 11                   454 GS Junior  
 12                   AB SOLiD 4 System  
 13                   PacBio RS II  
 14                   Ion Torrent PGM  
 15                   Illumina HiSeq 1000  
 16                   454 GS FLX+  
 17                   Helicos HeliScope  
 18                   Complete Genomics  
 19                   PacBio RS  
 20                   AB SOLiD System 3.0  
 21       AB 5500xl Genetic Analyzer  
 22       AB 5500 Genetic Analyzer  
 23                   Illumina HiScanSQ  
 24                   454 GS 20  
 25                   Illumina HiSeq 1500  
 26                   454 GS  
 27                   AB SOLiD System 2.0  
 28                   AB SOLiD System  
 29                   Ion Torrent Proton  
 30       AB 3730xL Genetic Analyzer  
 31                   HiSeq X Ten  
 32                   AB SOLiD 4hq System  
 33                   AB SOLiD 3 Plus System  
 34                   NextSeq 500  
 35                   MinION  
 36   AB 5500xl-W Genetic Analysis System  
 37                   454 GS FLX  
 38       AB 3500xL Genetic Analyzer  
 39       AB 3730 Genetic Analyzer  
 40                   Illumina NextSeq 500  
 41       AB 3130xL Genetic Analyzer  
 42                   AB SOLiD PI System  
 43       AB 310 Genetic Analyzer



44 AB 3500 Genetic Analyzer  
45 Illumina HiSeq 4000

Experiments

1	576428
2	81112
3	79416
4	74743
5	42277
6	40181
7	31765
8	25955
9	16617
10	14054
11	11120
12	9464
13	5616
14	5469
15	5060
16	3806
17	3777
18	3056
19	2934
20	2377
21	1804
22	1622
23	1142
24	891
25	840
26	503
27	464
28	378
29	270
30	199
31	179
32	158
33	138
34	126
35	39
36	22
37	10
38	6
39	5

40	4
41	3
42	2
43	1
44	1
45	1

List all types of library strategies and number of runs for each of them:

```
> rs <- dbGetQuery(sra_con, paste( "SELECT library_strategy AS
+      'Library Strategy', count( * ) AS Runs FROM `experiment`
+      GROUP BY library_strategy order by Runs DESC", sep=""))
> rs
```

	Library Strategy	Runs
1	WGS	375890
2	AMPLICON	176811
3	WXS	167794
4	RNA-Seq	148720
5	OTHER	79598
6	ChIP-Seq	36579
7	<NA>	14054
8	POOLCLONE	8240
9	Bisulfite-Seq	6635
10	WGA	5320
11	CLONE	4636
12	miRNA-Seq	4437
13	EST	3328
14	VALIDATION	3266
15	FL-cDNA	1303
16	MeDIP-Seq	1255
17	DNase-Hypersensitivity	1218
18	MNase-Seq	861
19	Tn-Seq	792
20	MBD-Seq	712
21	MRE-Seq	565
22	RAD-Seq	539
23	ncRNA-Seq	482
24	RIP-Seq	354
25	WCS	328
26	CTS	104
27	FAIRE-seq	94
28	CLONEEND	51
29	SELEX	32

30	FINISHING	20
31	ChIA-PET	10
32	Synthetic-Long-Read	7

### 3.3 Conversion of SRA entity types

Large-scale consumers of SRA data might want to convert SRA entity type from one to others, e.g. finding all experiment accessions (SRX, ERX or DRX) and run accessions (SRR, ERR or DRR) associated with "SRP001007" and "SRP000931". Function `sraConvert` does the conversion with a very fast mapping between entity types.

Covert "SRP001007" and "SRP000931" to other possible types in the `SRAmetadb.sqlite`:

```
> conversion <- sraConvert( c('SRP001007','SRP000931'), sra_con = sra_con )
> conversion[1:3,]
```

	study	submission	sample	experiment
1	SRP000931	SRA009053	SRS003457	SRX006126
2	SRP000931	SRA009053	SRS003456	SRX006125
3	SRP000931	SRA009053	SRS003455	SRX006124

	run
1	SRR018260
2	SRR018259
3	SRR018258

Check what SRA types and how many entities for each type:

```
> apply(conversion, 2, unique)
```

```
$study
```

```
[1] "SRP000931" "SRP001007"
```

```
$submission
```

```
[1] "SRA009053" "SRA009276"
```

```
$sample
```

```
[1] "SRS003457" "SRS003456" "SRS003455"
[4] "SRS003453" "SRS003458" "SRS003461"
[7] "SRS003462" "SRS003454" "SRS003460"
[10] "SRS003463" "SRS003459" "SRS003464"
[13] "SRS004650"
```

```
$experiment
```

```
[1] "SRX006126" "SRX006125" "SRX006124"
[4] "SRX006130" "SRX006129" "SRX006122"
```

```
[7] "SRX006127" "SRX006132" "SRX006133"
[10] "SRX006123" "SRX006131" "SRX006134"
[13] "SRX006128" "SRX006135" "SRX007396"
```

```
$run
```

```
[1] "SRR018260" "SRR018259" "SRR018258"
[4] "SRR018264" "SRR018263" "SRR018256"
[7] "SRR018261" "SRR018266" "SRR018267"
[10] "SRR018257" "SRR018265" "SRR018268"
[13] "SRR018262" "SRR018269" "SRR020740"
[16] "SRR020739"
```

### 3.4 Full text search

Searching by regular table and field specific SQL commands can be very powerful and if you are familiar with SQL language and the table structure. If not, SQLite has a very handy module called Full text search (fts3), which allow users to do Google like search with terms and operators. The function `getSRA` does Full text search against all fields in a fts3 table with terms constructed with the Standard Query Syntax and Enhanced Query Syntax. Please see <http://www.sqlite.org/fts3.html> for detail.

Find all run and study combined records in which any given fields has "breast" and "cancer" words, including "breast" and "cancer" are not next to each other:

```
> rs <- getSRA( search_terms = "breast cancer",
+               out_types = c('run','study'), sra_con )
> dim(rs)

[1] 10269    23

> rs <- getSRA( search_terms = "breast cancer",
+               out_types = c("submission", "study", "sample",
+                             "experiment", "run"), sra_con )
> # get counts for some information interested
> apply( rs[, c('run','sample','study_type','platform',
+               'instrument_model')], 2, function(x)
+       {length(unique(x))} )

      run      sample
10269      7269
study_type platform
9         6
instrument_model
23
```

```
>
```

If you only want SRA records containing exact phrase of "breast cancer", in which "breast" and "cancer" do not have other characters between other than a space:

```
> rs <- getSRA (search_terms = '"breast cancer"',
+             out_types=c('run','study'), sra_con)
> dim(rs)

[1] 9021  23
```

Find all sample records containing words of either "MCF7" or "MCF-7":

```
> rs <- getSRA( search_terms = 'MCF7 OR "MCF-7"',
+             out_types = c('sample'), sra_con )
> dim(rs)

[1] 1796  10
```

Find all submissions by GEO:

```
> rs <- getSRA( search_terms = 'submission_center: GEO',
+             out_types = c('submission'), sra_con )
> dim(rs)

[1] 7371   6
```

Find study records containing a word beginning with 'Carcino':

```
> rs <- getSRA( search_terms = 'Carcino*',
+             out_types = c('study'), sra_con=sra_con )
> dim(rs)

[1] 423  12
```

### 3.5 Download SRA data files

List ftp addresses of the fastq files associated with "SRX000122":

```
> rs = listSRAfile( c("SRX000122"), sra_con, fileType = 'sra' )
```

The above function does not check file availability, size and date of the sra data files on the server, but the function getSRAinfo does this, which is good to know if you are preparing to download them:

```
> rs = getSRAinfo ( c("SRX000122"), sra_con, sraType = "sra" )
> rs[1:3,]
```

```

1 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX000/SRX000122/
2 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX000/SRX000122/
3 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX000/SRX000122/
  experiment      study      sample      run
1  SRX000122 SRP000098 SRS000290 SRR000648
2  SRX000122 SRP000098 SRS000290 SRR000649
3  SRX000122 SRP000098 SRS000290 SRR000650
  size(KB)      date
1      281 Jan 19 2012
2    130940 Jan 19 2012
3      844 Jan 19 2012

```

Next you might want to download sra data files from the ftp site. The `getSRAfile` function will download all available sra data files associated with "SRR000648" and "SRR000657" from the NCBI SRA ftp site to the current directory:

```

> getSRAfile( c("SRR000648","SRR000657"), sra_con, fileType = 'sra' )

      run      study      sample experiment
1 SRR000648 SRP000098 SRS000290  SRX000122
2 SRR000657 SRP000098 SRS000290  SRX000122

1 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX000/SRX000122/
2 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX000/SRX000122/

```

Then downloaded sra data files can be easily converted into fastq files using `fastq-dump` in SRA Toolkit ( <http://trace.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?view=software> ):

```

> ## system ("fastq-dump SRR000648.lite.sra")

```

Or directly download fastq files from EBI using ftp protocol:

```

> getFASTQinfo( c("SRR000648","SRR000657"), srcType = 'ftp' )
> getSRAfile( c("SRR000648","SRR000657"), sra_con, fileType = 'fastq' )

```

### 3.6 Download SRA data files using fasp protocol

Currently both NCBI and EBI supports fasp protocol for downloading SRA data files, which has several advantages over ftp protocol, including high-speed transferring large files over long distance. Please check EBI or NCBI web site or Aspera (<http://www.asperasoft.com/>) for details. SRADB has included two wrapper functions for using ascp command line program (fasp protocol) to download SRA data files from either the NCBI or EBI, which is included in Aspera Connect software. But, due to complexity of installation of the software and options within it, the functions developed here ask users to supply main ascp commands.

Download fastq files from EBI ftp site using fasp protocol:

```

> ## List fasp addresses for associated fastq files:
> listSRAfile( c("SRX000122"), sra_con, fileType = 'fastq', srcType='fasp')
> ## get fasp addresses for associated fastq files:
> getFASTQinfo( c("SRX000122"), srcType = 'fasp' )
> ## download fastq files using fasp protocol:
> # the following ascpCMD needs to be constructed according custom
> # system configuration
> # common ascp installation in a Linux system:
> ascpCMD <- 'ascp -QT -l 300m -i
+ /usr/local/aspera/connect/etc/asperaweb_id_dsa.putty'
> ## common ascpCMD for a Mac OS X system:
> # ascpCMD <- "'/Applications/Aspera Connect.app/Contents/
> # Resources/ascp' -QT -l 300m -i '/Applications/
> # Aspera Connect.app/Contents/Resources/asperaweb_id_dsa.putty'"
>
> getSRAfile( c("SRX000122"), sra_con, fileType = 'fastq',
+           srcType = 'fasp', ascpCMD = ascpCMD )

```

Download sra files from NCBI using fasp protocol:

```

> ## List fasp addresses of sra files associated with "SRX000122"
> listSRAfile( c("SRX000122"), sra_con, fileType = 'sra', srcType='fasp')
> ## download sra files using fasp protocol
> getSRAfile( c("SRX000122"), sra_con, fileType = 'sra',
+ srcType = 'fasp', ascpCMD = ascpCMD )

```

The downloading message will show significant faster downloading speed than the ftp protocol:

```

' SRR000658.sra 100Completed: 159492K bytes transferred in 5 seconds (249247K bits/sec),
in 1 file. ... '

```

## 4 Interactive views of sequence data

Working with sequence data is often best done interactively in a genome browser, a task not easily done from R itself. We have found the Integrative Genomics Viewer (IGV) a high-performance visualization tool for interactive exploration of large, integrated datasets, increasing usefully for visualizing sequence alignments. In `SRADB`, functions `startIGV`, `load2IGV` and `load2newIGV` provide convenient functionality for R to interact with IGV. Note that for some OS, these functions might not work or work well.

Launch IGV with 2 GB maximum usable memory support:

```

> startIGV("mm")

```

IGV offers a remort control port that allows R to communicate with IGV. The current command set is fairly limited, but it does allow for some IGV operations to be performed in the R console. To utilize this functionality, be sure that IGV is set to allow communication via the “enable port” option in IGV preferences. To load BAM files to IGV and then manipulate the window:

```
> exampleBams = file.path(system.file('extdata',package='SRADB'),
+   dir(system.file('extdata',package='SRADB'),pattern='bam$'))
> sock <- IGVsocket()
> IGVgenome(sock, 'hg18')
> IGVload(sock, exampleBams)
> IGVgoto(sock, 'chr1:1-1000')
> IGVsnapshot(sock)
```

## 5 Graphic view of SRA entities

Due to the nature of SRA data and its design, sometimes it is hard to get a whole picture of the relationship between a set of SRA entities. Functions of `entityGraph` and `sraGraph` in this package generate graphNEL objects with `edgemode='directed'` from input `data.frame` or directly from search terms, and then the `plot` function can easily draw a diagram.

Create a graphNEL object directly from full text search results of terms 'primary thyroid cell line'

```
> library(SRADb)
> library(Rgraphviz)
> g <- sraGraph('primary thyroid cell line', sra_con)
> attrs <- getDefaultAttrs(list(node=list(
+   fillcolor='lightblue', shape='ellipse'))))
> plot(g, attrs=attrs)
> ## similiar search as the above, returned much larger data.frame and graph is too cl
> g <- sraGraph('Ewing Sarcoma', sra_con)
> plot(g)
>
```

Please see the Figure 2 for an example diagram.

It's considered good practise to explicitly disconnect from the database once we are done with it:

```
> dbDisconnect(sra_con)
```

```
[1] TRUE
```



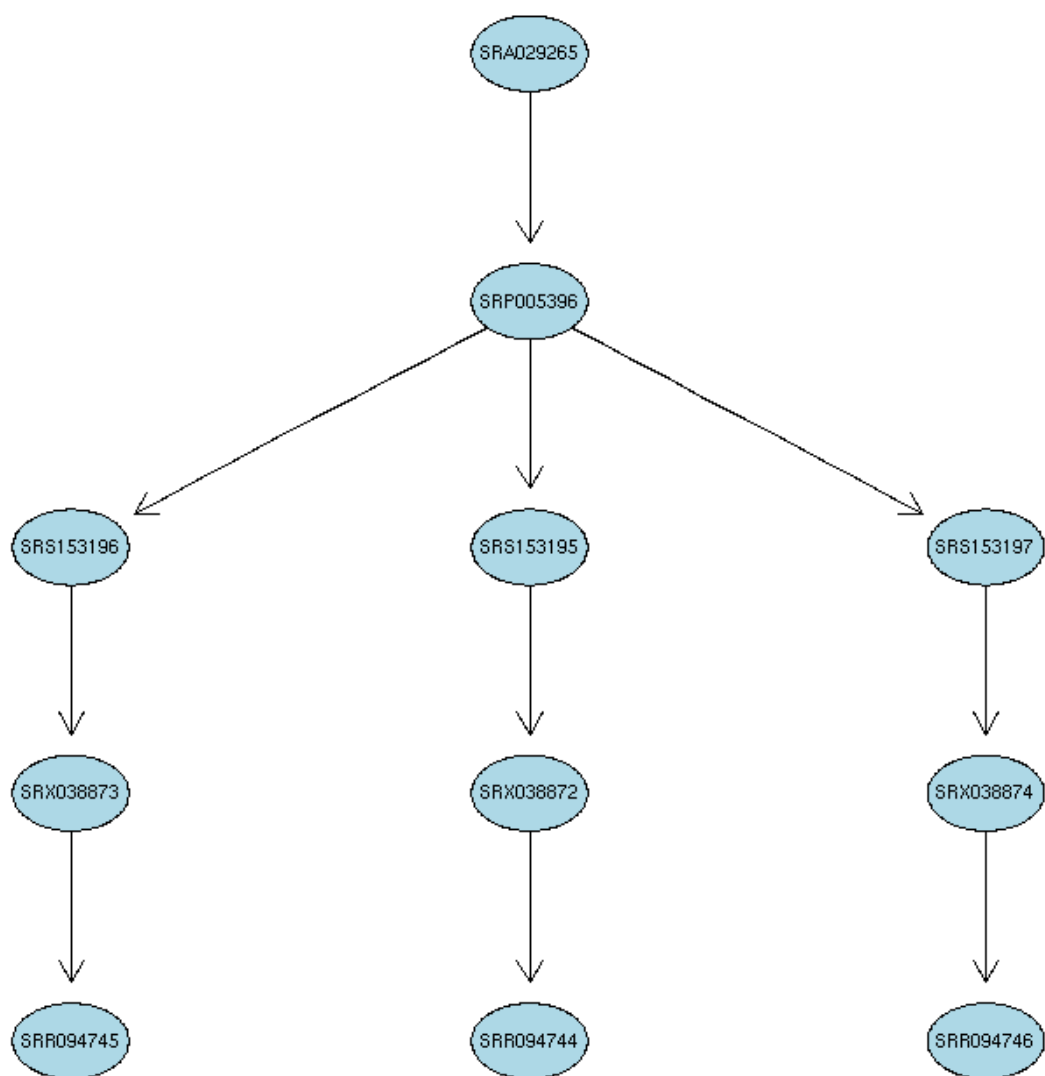


Figure 2: A graphical representation of the relationships between the SRA entities.

## 6 Example use case

This section will use the functionalities in the **SRADB** package to explore data from the 1000 genomes project. Mainly,

1. Get some statistics of meta data and data files from the 1000 genomes project using the **SRADB**
2. Download data files
3. Load bam files into the IGV from R
4. Create some snapshots programmatically from R

```
> library(SRADb)
> setwd('1000g')
> if( ! file.exists('SRAMetadb.sqlite') ) {
+     sqlfile <- getSRADBFile()
+ } else {
+     sqlfile <- 'SRAMetadb.sqlite'
+ }
> sra_con <- dbConnect(SQLite(),sqlfile)
> ## get all related accessions
> rs <- getSRA( search_terms = '"1000 Genomes Project"',
+     sra_con=sra_con, acc_only=TRUE)
> dim(rs)
> head(rs)
> ## get counts for each data types
> apply( rs, 2, function(x) {length(unique(x))} )
```

After you decided what data from the 1000 Genomes, you would like to download data files from the SRA. But, it might be helpful to know file size before downloading them:

```
> runs <- tail(rs$run)
> fs <- getSRAinfo( runs, sra_con, sraType = "sra" )
```

Now you can download the files through ftp protocol:

```
> getSRAfile( runs, sra_con, fileType='sra', srcType = "ftp" )
```

Or, you can download them through fasp protocol:

```
> ascpCMD <- "'/Applications/Aspera Connect.app/Contents/Resources/ascp' -QT -l 300m -"
> sra_files = getSRAfile( runs, sra_con, fileType='sra', srcType = "fasp", ascpCMD =
```

Next you might want to convert the downloaded sra files into fastq files:

```
> for( fq in basename(sra_files$fasp) ) {
+     system ("fastq-dump SRR000648.lite.sra")
+ }
```

... to be completed.

## 7 sessionInfo

- R version 3.1.3 (2015-03-09), x86\_64-apple-darwin10.8.0
- Locale: en\_US.UTF-8/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: bitops 1.0-6, DBI 0.3.1, graph 1.44.1, RCurl 1.95-4.5, RSQLite 1.0.0, SRADB 1.20.13
- Loaded via a namespace (and not attached): Biobase 2.26.0, BiocGenerics 0.12.1, GEOquery 2.32.0, parallel 3.1.3, stats4 3.1.3, tools 3.1.3, XML 3.98-1.1