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

Archive

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October 14, 2015

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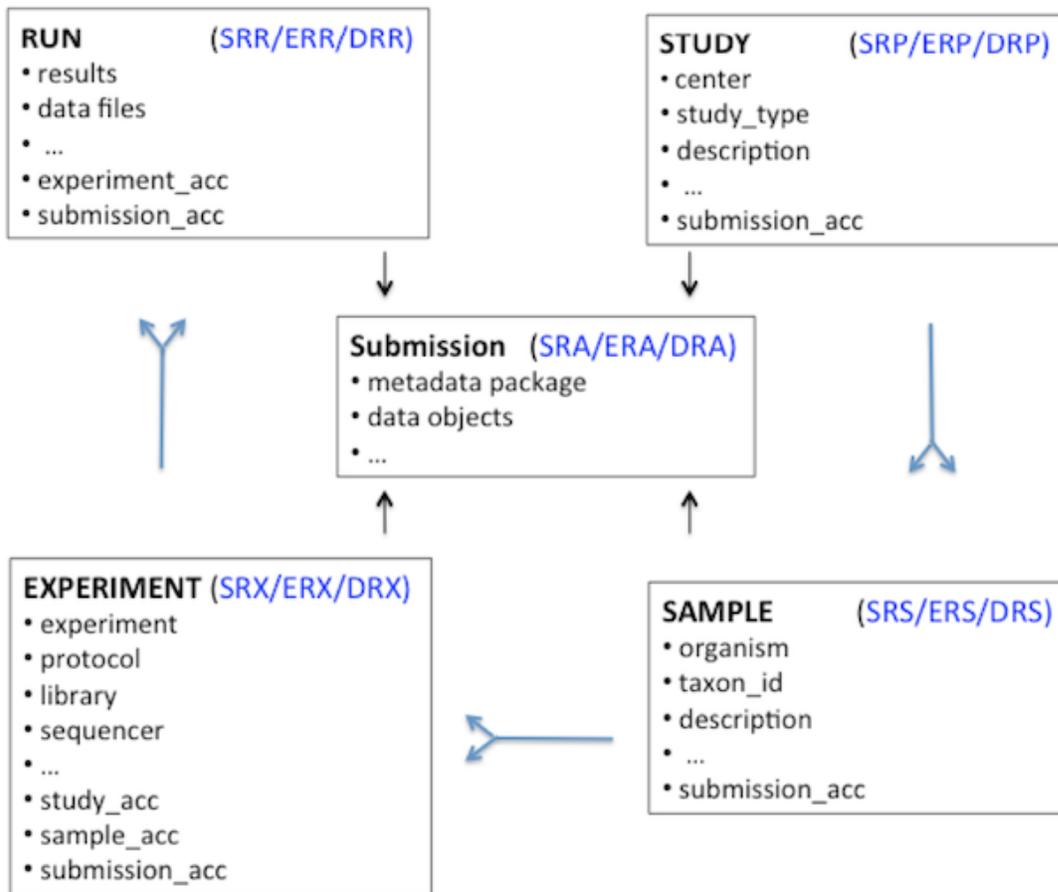
Figure 1: A graphical representation (sometimes called an *Entity-Relationship Diagram*) of the relationships between the main tables in the SRAdb package.

```
> 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 fews moments due to file size, depdending 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 13433397248 FALSE  644
                                mtime
SRAmetadb.sqlite 2015-10-14 21:30:23
                                ctime
SRAmetadb.sqlite 2015-10-14 21:30:23
                                atime uid gid
SRAmetadb.sqlite 2015-10-14 21:30:23 501  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 presenc
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       1306646
metaInfo               2
run              1695522
sra_ft_segments   395083
study              59141
```

Get some high-level statistics could be to helpful to get overall idea about what data are availble 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  26930
2                     Other  15485
3    Transcriptome Analysis   7737
4              Metagenomics   4591
5                      <NA>   2615
6                Epigenetics    824
7        Population Genomics    692
8           Exome Sequencing    148
9            Cancer Genomics     76
10  Pooled Clone Sequencing     31
11        Synthetic Genomics      9
12                   RNASeq      3
```

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                                   <NA>
5             Illumina Genome Analyzer II
6                    Illumina HiSeq 2500
7            Illumina Genome Analyzer IIx
8                            unspecified
9                             454 GS FLX
10              Illumina Genome Analyzer
11                         454 GS Junior
12                     AB SOLiD 4 System
13                       Ion Torrent PGM
14                   Illumina HiSeq 1000
15                          PacBio RS II
16                           454 GS FLX+
17                             PacBio RS
18                     Helicos HeliScope
19                                454 GS
20                     Complete Genomics
21                   AB SOLiD System 3.0
22             AB 5500xl Genetic Analyzer
23                   Illumina HiSeq 1500
24              AB 5500 Genetic Analyzer
25                           NextSeq 500
26                    Illumina HiScanSQ
27                             454 GS 20
28                    Ion Torrent Proton
29                   AB SOLiD System 2.0
30                        AB SOLiD System
31             AB 3730xL Genetic Analyzer
32                            HiSeq X Ten
33               AB SOLiD 3 Plus System
34                     AB SOLiD 4hq System
35 AB 5500xl-W Genetic Analysis System
36                                 MinION
37             AB 3130xL Genetic Analyzer
38                  Illumina NextSeq 500
39                  Illumina HiSeq 4000
40                             454 GS FLX
41             AB 3500xL Genetic Analyzer
42                  Illumina HiSeq 3000
43               AB 3730 Genetic Analyzer
```

```
44                      AB SOLiD PI System
45              AB 310 Genetic Analyzer
46             AB 3500 Genetic Analyzer
47                          NextSeq 550
   Experiments
1      685640
2      112310
3       87614
4       81220
5       76208
6       64127
7       45770
8       32976
9       27511
10      17020
11      12335
12       9923
13       7024
14       6449
15       6049
16       5289
17       4029
18       3813
19       3225
20       3059
21       2429
22       2279
23       2091
24       1754
25       1657
26       1319
27        900
28        695
29        464
30        413
31        282
32        194
33        179
34        158
35         93
36         55
37         27
```

```
38          22
39          12
40          10
41           6
42           6
43           5
44           2
45           1
46           1
47           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  423860
2                 AMPLICON  214389
3                  RNA-Seq  179277
4                      WXS  172744
5                    OTHER   90225
6                     <NA>   81220
7                POOLCLONE   44307
8                  ChIP-Seq  40949
9                    SELEX   14875
10            Bisulfite-Seq   7884
11                     WGA    6450
12                miRNA-Seq   6399
13                   CLONE    6179
14                     EST    3341
15               VALIDATION   3272
16 DNase-Hypersensitivity    1361
17                MeDIP-Seq   1336
18                 FL-cDNA    1329
19                MNase-Seq   1060
20                ncRNA-Seq   1050
21                   Tn-Seq   1010
22                  MRE-Seq    948
23                  RAD-Seq    912
24                  MBD-Seq    743
25                  RIP-Seq    633
```

```
26                    WCS    386
27                    CTS    154
28            FAIRE-seq    127
29      Targeted-Capture    121
30            CLONEEND     52
31            ChIA-PET     26
32            FINISHING     20
33    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 SRS003462  SRX006133
2 SRP000931  SRA009053 SRS003458  SRX006127
3 SRP000931  SRA009053 SRS003453  SRX006130
       run
1 SRR018267
2 SRR018261
3 SRR018264
```

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

```
[13] "SRS004650"


$experiment
 [1] "SRX006133" "SRX006127" "SRX006130"
 [4] "SRX006123" "SRX006131" "SRX006132"
 [7] "SRX006126" "SRX006128" "SRX006134"
[10] "SRX006122" "SRX006124" "SRX006125"
[13] "SRX006135" "SRX006129" "SRX007396"


$run
 [1] "SRR018267" "SRR018261" "SRR018264"
 [4] "SRR018257" "SRR018265" "SRR018266"
 [7] "SRR018260" "SRR018262" "SRR018268"
[10] "SRR018256" "SRR018258" "SRR018259"
[13] "SRR018269" "SRR018263" "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] 12425    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
       12425           8630
```

```
     study_type          platform
              9                 6
instrument_model
             24
```

```
>
```

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] 10691    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] 2260    10
```

Find all submissions by GEO:

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

```
[1] 9232     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] 523  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"), sra_con, srcType = 'ftp' )
> getSRAfile( c("SRR000648","SRR000657"), sra_con, fileType = 'fastq' )
```

## 3.6 Download SRA data files using fasp protocol

Curretly both NCBI and EBI supports fasp protocol for downloading SRA data files, which has several advantages over ftp protocol, including high-speed transfering large files over long distance. Please check EBI or NCBI web site or Aspera (http://www.asperasoft.com/) for details. SRAdb has indcluded two wraper functions for using ascp command line program (fasp protocol) to download SRA data files frm either the NCBI or EBI, which is included in in Aspera Connect software. But, due to complexity of installaton of the software and options within it, the funcitons develpped here ask users to supply main ascp comands.

Download fastq files from EBI ftp siteusing 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"), sra_con, 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 messege will show signigicant 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)
>
```
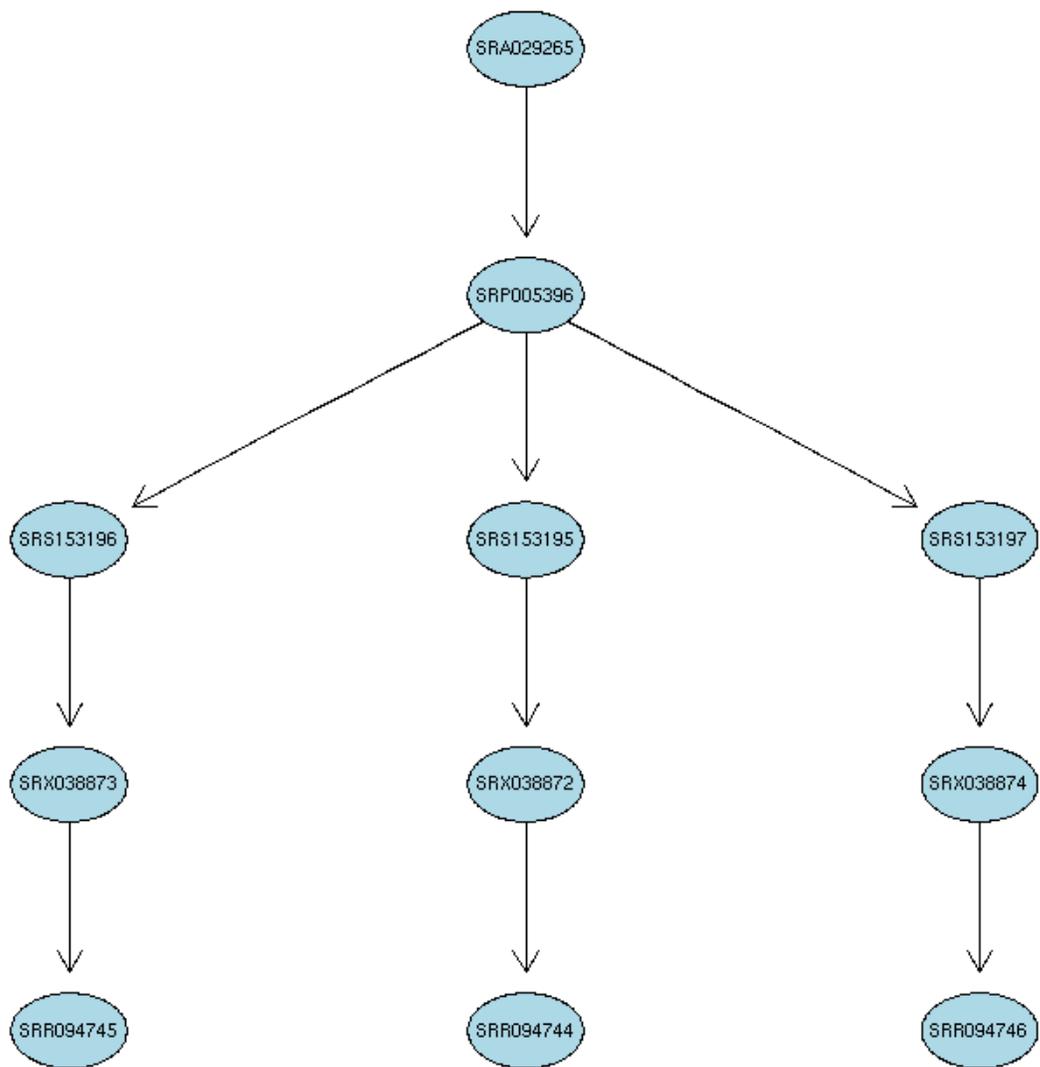
Figure 2: A graphical representation of the relationships between the SRA entities.

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
```

# 6   Example use case

This sesection 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 snapshoots programmtically 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 compeleted.

# 7  sessionInfo

- R version 3.2.2 Patched (2015-10-08 r69496), `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 1.48.0, RCurl 1.95-4.7, RSQLite 1.0.0, SRAdb 1.28.0

- Loaded via a namespace (and not attached): Biobase 2.30.0, BiocGenerics 0.16.0, GEOquery 2.36.0, parallel 3.2.2, stats4 3.2.2, tools 3.2.2, XML 3.98-1.3