

How to Use pkgDepTools

Seth Falcon

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1 Introduction

The `pkgDepTools` package provides tools for computing and analyzing dependency relationships among R packages. With it, you can build a graph-based representation of the dependencies among all packages in a list of CRAN-style package repositories. There are utilities for computing installation order of a given package and, if the `RCurl` package is available, estimating the download size required to install a given package and its dependencies.

This vignette demonstrates the basic features of the package.

2 Graph Basics

A graph consists of a set of nodes and a set of edges representing relationships between pairs of nodes. The relationships among the nodes of a graph are binary; either there is an edge between a pair of nodes or there is not. To model package dependencies using a graph, let the set of packages be the nodes of the graph with directed edges originating from a given package to each of its dependencies. Figure 1 shows a part of the Bioconductor dependency graph for the `Category` package. Since circular dependencies are not allowed, the resulting dependency graph will be a directed acyclic graph (DAG).

3 Building a Dependency Graph

```
> library("pkgDepTools")  
> library("Biobase")
```

```
> library("Rgraphviz")
```

The `makeDepGraph` function retrieves the meta data for all packages of a specified type (source, win.binary, or mac.binary) from each repository in a list of repository URLs and builds a *graphNEL*¹ instance representing the packages and their dependency relationships.

The function takes four arguments: 1) `repList` a character vector of CRAN-style package repository URLs; 2) `suggests.only` a logical value indicating whether the resulting graph should represent relations from the `Depends` field (`FALSE`, default) or the `Suggests` field (`TRUE`); 3) `type` a string indicating the type of packages to search for, the default is `getOption("pkgType")`; 4) `keep.builtin` which will keep packages that come with a standard R install in the dependency graph (the default is `FALSE`).

Here we use `makeDepGraph` to build dependency graphs of the BioC and CRAN packages. Each dependency graph is a *graphNEL* instance. The out-edges of a given node list its direct dependencies (as shown for package `annotate`). The node attribute “size” gives the size of the package in megabytes when the `dosize` argument is `TRUE` (this is the default). Obtaining the size of packages requires the `RCurl` package and can be time consuming for large repositories since a separate HTTP request must be made for each package. In the examples below, we set `dosize=FALSE` to speed the computations.

```
> library(BiocInstaller)
> biocUrl <- biocinstallRepos()["BioCsoft"]
> biocDeps <- makeDepGraph(biocUrl, type="source", dosize=FALSE)
> biocDeps
```

A *graphNEL* graph with directed edges

Number of Nodes = 2286

Number of Edges = 9639

```
> edges(biocDeps)["annotate"]
$annotate
[1] "AnnotationDbi" "XML"          "Biobase"      "DBI"
[5] "xtable"        "BiocGenerics" "RCurl"
> ## if dosize=TRUE, size in MB is stored
> ## as a node attribute:
> ## nodeData(biocDeps, n="annotate", attr="size")
```

¹See `help("graphNEL-class")`

4 Using the Dependency Graph

The dependencies of a given package can be visualized using the graph generated by `makeDepGraph` and the `Rgraphviz` package. The graph shown in Figure 1 was produced using the code shown below. The `acc` method from the `graph` package returns a vector of all nodes that are accessible from the given node. Here, it has been used to obtain the complete list of `Category`'s dependencies.

```
> categoryNodes <- c("Category",
+                   names(acc(biocDeps, "Category")[[1]]))
> categoryGraph <- subGraph(categoryNodes, biocDeps)
> nn <- makeNodeAttrs(categoryGraph, shape="ellipse")
> plot(categoryGraph, nodeAttrs=nn)
```

In R, there is no easy way to preview a given package's dependencies and estimate the amount of data that needs to be downloaded even though the `install.packages` function will search for and install package dependencies if you ask it to by specifying `dependencies=TRUE`. The `getInstallOrder` function provides such a "preview".

For computing installation order, it is useful to have a single graph representing the relationships among all packages in all available repositories. Below, we create such a graph combining all CRAN and Bioconductor packages.

```
> allDeps <- makeDepGraph(biocinstallRepos(), type="source",
+                       keep.builtin=TRUE, dosize=FALSE)
>
```

Calling `getInstallOrder` for package `GOstats`, we see a listing of only those packages that need to be installed. Your results will be different based upon your installed packages.

```
> getInstallOrder("GOstats", allDeps)
```

```
$packages
character(0)
```

```
$total.size
numeric(0)
```

When `needed.only=FALSE`, the complete dependency list is returned regardless of what packages are currently installed.

```
> getInstallOrder("GOstats", allDeps, needed.only=FALSE)
```

```
$packages
```

```
[1] "methods"      "utils"        "graphics"
[4] "stats"        "parallel"     "BiocGenerics"
[7] "Biobase"      "stats4"       "S4Vectors"
[10] "IRanges"      "DBI"          "bit"
[13] "bit64"        "rlang"        "Rcpp"
[16] "tibble"       "blob"         "digest"
[19] "memoise"      "pkgconfig"    "RSQLite"
[22] "AnnotationDbi" "grid"         "grDevices"
[25] "lattice"      "Matrix"       "graph"
[28] "RBGL"         "XML"          "xtable"
[31] "bitops"       "RCurl"        "annotate"
[34] "GSEABase"     "splines"      "survival"
[37] "genefilter"   "Category"     "GO.db"
[40] "AnnotationForge" "Rgraphviz"   "GOstats"
```

```
$total.size
```

```
[1] NA
```

The edge directions of the dependency graph can be reversed and the resulting graph used to determine the set of packages that make use of (even indirectly) a given package. For example, one might like to know which packages make use of the `methods` package. Here is one way to do that:

```
> allDepsOnMe <- reverseEdgeDirections(allDeps)
> usesMethods <- dijkstra.sp(allDepsOnMe, start="methods")$distance
> usesMethods <- usesMethods[is.finite(usesMethods)]
> length(usesMethods) - 1 ## don't count methods itself
```

```
[1] 10522
```

```
> table(usesMethods)
```

```
usesMethods
```

```
  0   1   2   3   4   5
  1 3538 6100 830  52   2
```

>

> `toLatex(sessionInfo())`

- R version 3.4.2 (2017-09-28), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 16.04.3 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.6-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.6-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, grid, methods, parallel, stats, utils
- Other packages: Biobase 2.38.0, BiocGenerics 0.24.0, BiocInstaller 1.28.0, RBGL 1.54.0, RCurl 1.95-4.8, Rgraphviz 2.22.0, bitops 1.0-6, graph 1.56.0, pkgDepTools 1.44.0
- Loaded via a namespace (and not attached): compiler 3.4.2, stats4 3.4.2, tools 3.4.2

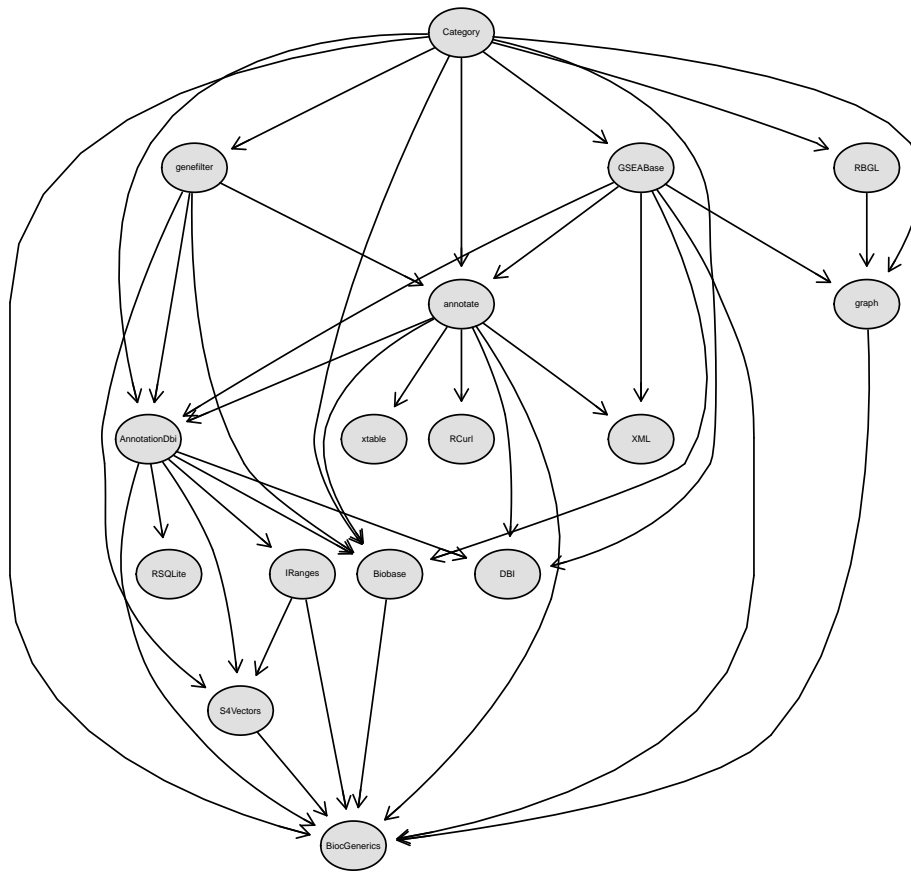


Figure 1: The dependency graph for the `Category` package.