

How to Use pkgDepTools

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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(BiocManager)
> biocUrl <- repositories()["BioCsoft"]
> biocDeps <- makeDepGraph(biocUrl, type="source", dosize=FALSE)
> biocDeps
```

A *graphNEL* graph with directed edges

Number of Nodes = 2920

Number of Edges = 14563

```
> 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(repositories(), 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"            "ellipsis"
[16] "digest"           "glue"             "vctrs"
[19] "blob"             "memoise"          "pkgconfig"
[22] "Rcpp"             "BH"               "plogr"
[25] "RSQLite"          "AnnotationDbi"    "grid"
[28] "grDevices"        "lattice"          "Matrix"
[31] "graph"            "RBGL"             "XML"
[34] "xtable"           "bitops"           "RCurl"
[37] "annotate"         "GSEABase"         "splines"
[40] "survival"         "genefilter"       "Category"
[43] "GO.db"            "AnnotationForge"  "Rgraphviz"
[46] "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] 14468

> table(usesMethods)
```

```
usesMethods
```

```
  0    1    2    3    4    5    6  
  1 4583 8799 1050   33    2    1
```

```
>
```

```
> toLatex(sessionInfo())
```

- R version 4.0.0 (2020-04-24), x86_64-w64-mingw32
- Locale: LC_COLLATE=C, LC_CTYPE=English_United States.1252, LC_MONETARY=English_United States.1252, LC_NUMERIC=C, LC_TIME=English_United States.1252
- Running under: Windows Server 2012 R2 x64 (build 9600)
- Matrix products: default
- Base packages: base, datasets, grDevices, graphics, grid, methods, parallel, stats, utils
- Other packages: Biobase 2.48.0, BiocGenerics 0.34.0, BiocManager 1.30.10, RBGL 1.64.0, RCurl 1.98-1.2, Rgraphviz 2.32.0, graph 1.66.0, pkgDepTools 1.54.0
- Loaded via a namespace (and not attached): bitops 1.0-6, compiler 4.0.0, stats4 4.0.0, tools 4.0.0

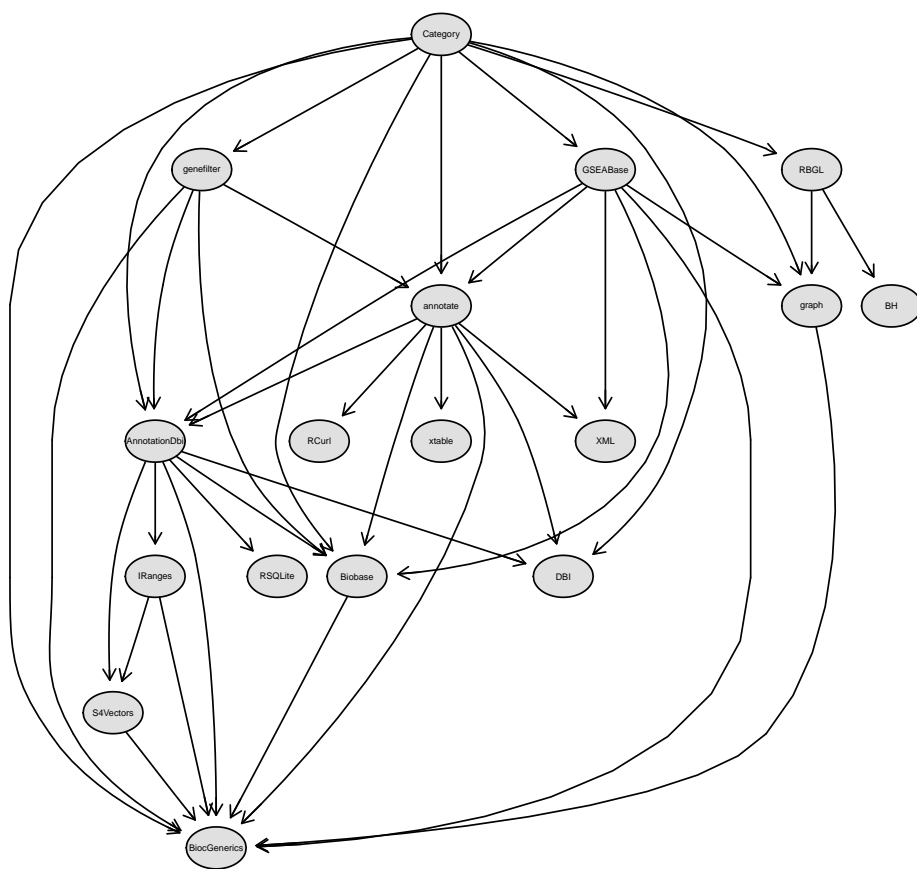


Figure 1: The dependency graph for the **Category** package.