

# 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*<sup>1</sup> 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 = 974
Number of Edges = 2571
```

```
> edges(biocDeps)["annotate"]
```

```
$annotate
[1] "AnnotationDbi" "Biobase"      "DBI"          "xtable"
[5] "XML"           "BiocGenerics"
```

---

<sup>1</sup>See `help("graphNEL-class")`

```

> ## if dosize=TRUE, size in MB is stored
> ## as a node attribute:
> ## nodeData(biocDeps, n="annotate", attr="size")

```

## 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"           "graphics"           "stats"
 [4] "parallel"          "BiocGenerics"       "utils"
 [7] "Biobase"           "DBI"                 "RSQLite"
[10] "stats4"            "IRanges"            "AnnotationDbi"
[13] "tools"             "graph"              "RBGL"
[16] "xtable"            "XML"                "annotate"
[19] "GSEABase"          "splines"            "survival"
[22] "genefilter"        "Category"           "GO.db"
[25] "org.Hs.eg.db"      "AnnotationForge"    "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] 3092
```

```
> table(usesMethods)
```

```
usesMethods
```

```
  0    1    2    3    4    5  
  1 1474 1403  190  23    2
```

```
>
```

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

- R version 3.0.0 (2013-04-03), x86\_64-unknown-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=C, LC\_NAME=C, LC\_ADDRESS=C,  
LC\_TELEPHONE=C, LC\_MEASUREMENT=en\_US.UTF-8,  
LC\_IDENTIFICATION=C
- Base packages: base, datasets, grDevices, graphics, grid, methods,  
parallel, stats, utils
- Other packages: Biobase 2.20.0, BiocGenerics 0.6.0,  
BiocInstaller 1.10.0, RBGL 1.36.0, RCurl 1.95-4.1, Rgraphviz 2.4.0,  
bitops 1.0-5, graph 1.38.0, pkgDepTools 1.26.0
- Loaded via a namespace (and not attached): stats4 3.0.0, tools 3.0.0

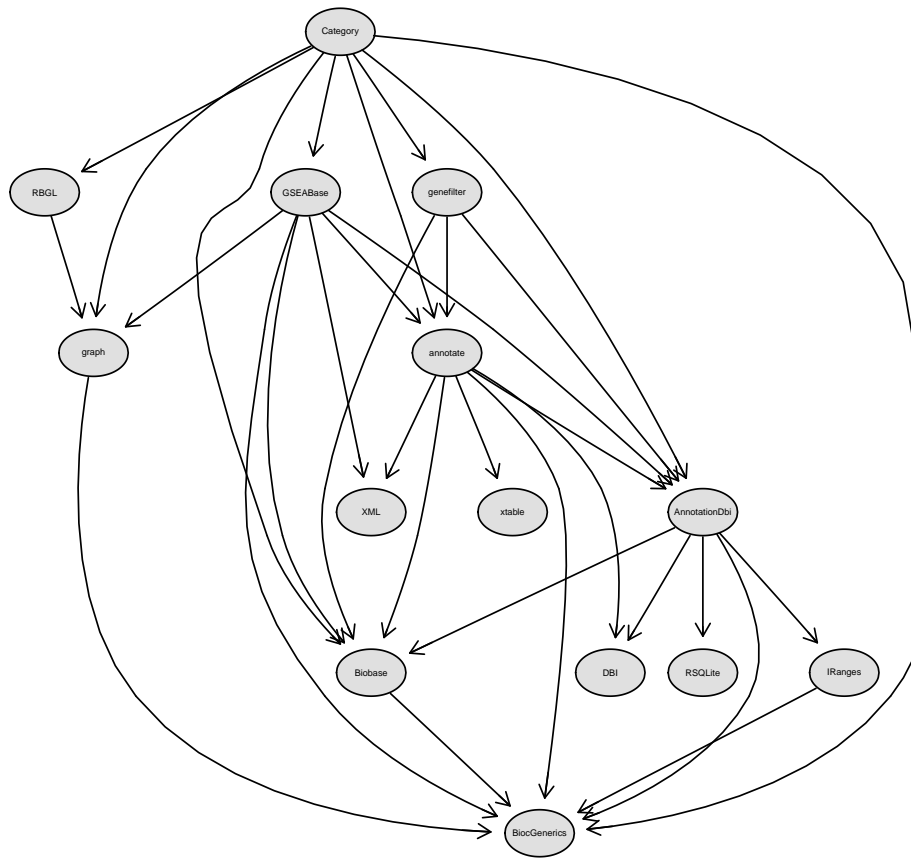


Figure 1: The dependency graph for the `Category` package.