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To install this package, start R and enter:

```
source("http://bioconductor.org/biocLite.R")
biocLite("Rgraphviz")
```

In most cases, you don't need to download the package archive at all.

# **Rgraphviz**



## Provides plotting capabilities for R graph objects

Bioconductor version: Release (3.1)

Interfaces R with the AT and T graphviz library for plotting R graph objects from the graph package.

Author: Kasper Daniel Hansen [cre, aut], Jeff Gentry [aut], Li Long [aut], Robert Gentleman [aut], Seth Falcon [aut], Florian Hahne [aut], Deepayan Sarkar [aut]

Maintainer: Kasper Daniel Hansen <kasperdanielhansen at gmail.com>

Citation (from within R, enter citation("Rgraphviz")):

Hansen KD, Gentry J, Long L, Gentleman R, Falcon S, Hahne F and Sarkar D. *Rgraphviz: Provides plotting capabilities for R graph objects*. R package version 2.12.0.

#### Installation

To install this package, start R and enter:

```
source("http://bioconductor.org/biocLite.R")
biocLite("Rgraphviz")
```

#### **Documentation**

To view documentation for the version of this package installed in your system, start R and enter:

```
browseVignettes("Rgraphviz")
```

PDF R Script A New Interface to Plot Graphs Using Rgraphviz

PDF R Script How To Plot A Graph Using Rgraphviz

PDF Reference Manual

Text NEWS

#### **Details**

since

biocViews GraphAndNetwork, Software, Visualization

Version 2.12.0

In Bioconductor

BioC 1.6 (R-2.1) or earlier (> 10 years)

License EPL

Depends  $R ( \ge 2.6.0)$ , methods, utils, graph, grid

Imports stats4, graphics, grDevices

LinkingTo

Suggests <u>RUnit</u>, <u>BiocGenerics</u>, <u>XML</u> SystemRequirements optionally Graphviz (>= 2.16)

Enhances

**URL** 

biocGraph, BioMVCClass, CellNOptR, flowCL, flowMerge, gaucho,

Depends On Me GOFunction, MineICA, mvGST, netresponse, paircompviz, pathRender,

ROntoTools, SplicingGraphs, TDARACNE, ToPASeq, TRONCO

apComplex, biocGraph, CompGO, DEGraph, EnrichmentBrowser, facopy,

Imports Me flowWorkspace, GOFunction, hyperdraw, nem, OncoSimulR, paircompviz,

pathview, apgraph, RchyOptimyx, SplicingGraphs

altcdfenys, annotate, BiocCaseStudies, Category, CNORfeeder, CNORfuzzy,

ddgraph, DEGraph, flowCore, GeneNetworkBuilder, geneplotter,

Suggests Me

GlobalAncova, globaltest, GOstats, GSEABase, KEGGgraph, MLP, NCIgraph,

NCIgraph, Classification of the College o

NCIgraphData, oneChannelGUI, pcaGoPromoter, pkgDepTools, RBGL, RBioinf, rBiopaxParser, RDAVIDWebService, RpsiXML, Rtreemix, safe,

SNAData, SPIA, SRAdb, Streamer, topGO, vtpnet

#### **Build Report**

### **Package Archives**

Follow <u>Installation</u> instructions to use this package in your R session.

Package Source Rgraphviz 2.12.0.tar.gz

Windows Binary Rgraphviz 2.12.0.zip (32- & 64-bit)

Mac OS X 10.6 (Snow Leopard) Rgraphviz 2.12.0.tgz
Mac OS X 10.9 (Mavericks) Rgraphviz 2.12.0.tgz

Subversion source (username/password: readonly)

Git source <a href="https://github.com/Bioconductor-mirror/Rgraphviz/tree/release-3.1">https://github.com/Bioconductor-mirror/Rgraphviz/tree/release-3.1</a>

Package Short Url http://bioconductor.org/packages/Rgraphviz/

Package Downloads Report Download Stats

Documentation »

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- Package <u>vignettes</u> and manuals.
- Workflows for learning and use.
- Course and conference material.
- Videos.
- Community <u>resources</u> and <u>tutorials</u>.

R / CRAN packages and documentation

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- Support site for questions about Bioconductor packages
- Bioc-devel mailing list for package developers



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