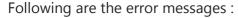# Bayesian Network with R

Asked 6 years, 10 months ago   Modified 2 years ago   Viewed 8k times

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I am trying to build a Bayesian network model. However I am unable to install a suitable package. Tried `gRain`, `bnlearn` and `Rgraphviz` for plotting. I have tried in R 2.15 and 3.2

Following are the error messages :

```
library(gRain)
Loading required package: gRbase
Loading required package: graph
Error: package 'graph' could not be loaded
In addition: Warning message:
In library(pkg, character.only = TRUE, logical.return = TRUE, lib.loc = lib.loc) :
  there is no package called 'graph'

> install.packages("graph")
Warning message:
package 'graph' is not available (for R version 2.15.3)
```

Same for R 3.2.1

```
> install.packages("graph")
(as 'lib' is unspecified)
Warning message:
package 'graph' is not available (for R version 3.2.1)


> install.packages("Rgraphviz")
(as 'lib' is unspecified)
--- Please select a CRAN mirror for use in this session ---
Warning messages:
1: In open.connection(con, "r") : unable to resolve 'cran.r-project.org'
2: package 'Rgraphviz' is not available (for R version 3.2.1)

> install.packages("Rgraphviz")
(as 'lib' is unspecified)
Warning message:
package 'Rgraphviz' is not available (for R version 2.15.3)
```

Other info for the model

1) No of variables - 17 2) Type of variables - discrete/continuous

`r`   `bayesian-networks`

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edited Jul 6, 2015 at 19:23

🧑 rcs
64.7k ● 22 ● 167 ● 149

asked Jul 6, 2015 at 17:31

🧑 Learner
157 ● 3 ● 14

2 Answers

答えが見つからない？日本語で聞いてみましょう。 ✕

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The packages `graph` , `RBGL` and `Rgraphviz` are not on CRAN but on [bioconductor](#).

To install these packages, execute

```r
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(c("graph", "RBGL", "Rgraphviz"))
```

Then install the packages from CRAN in the usual way:

```r
install.packages("gRain", dependencies=TRUE)
```

See also the `gRain` [installation instructions](#).

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edited May 6, 2020 at 19:10

user20650
23.3k ● 5 ● 52 ● 85

answered Jul 6, 2015 at 19:20

rcs
64.7k ● 22 ● 167 ● 149

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For R version 3.5 or greater, you can install *Bioconductor* packages using *BiocManager*. Please see: https://bioconductor.org/install.

I installed them using the following code:

```r
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(version = "3.10")
BiocManager::install(c("gRbase", "RBGL", "Rgraphviz", "gRain"))
```

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edited Mar 25, 2020 at 8:13

סטנלי גרונן
2,849 ● 23 ● 46 ● 65

answered Mar 25, 2020 at 7:45

Binh T Nguyen
41 ● 1