

```
> library(graph)
```

```
Loading required package: cluster
```

```
Loading required package: Ruuid
```

```
Creating a new generic function for "print" in "Ruuid"
```

```
Loading required package: Biobase
```

```
Welcome to Bioconductor
```

```
  Vignettes contain introductory material.  To view,  
  simply type: openVignette()
```

```
  For details on reading vignettes, see  
  the openVignette help page.
```

```
> library(RbcBook1)
```

```
> cache("bigran", randomGraph(paste("a", 1:50), 1:30,  
+   0.4))
```

```
A graph with undirected edges
```

```
Number of Nodes = 50
```

```
Number of Edges = 1214
```