

# Package ‘SNAGEEdata’

May 21, 2024

**Version** 1.40.0

**Date** 2012-01-26

**Title** SNAGEE data

**Author** David Venet <davenet@ulb.ac.be>

**Maintainer** David Venet <davenet@ulb.ac.be>

**Depends** R (>= 2.6.0)

**Suggests** ALL, hgu95av2.db, SNAGEE

**Description** SNAGEE data - gene list and correlation matrix

**License** Artistic-2.0

**biocViews** MicroarrayData

**URL** <http://fleming.ulb.ac.be/SNAGEE>

**git\_url** <https://git.bioconductor.org/packages/SNAGEEdata>

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 9ad4a3c

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-05-21

## Contents

SNAGEEdata-package . . . . .	2
getCC . . . . .	2
<b>Index</b>	<b>4</b>

---

SNAGEEdata-package      *SNAGEE - data*

---

### Description

Signal-to-Noise applied to Gene Expression Experiments - database of gene correlations.

### Details

Package: SNAGEEdata  
Version: 0.99.0  
Date: 2012-01-26  
Depends: R (>= 2.6.0)  
Suggests: SNAGEE  
License: Artistic-2.0  
URL: <http://fleming.ulb.ac.be/SNAGEE>

### Index:

getCC                      Gene-gene correlations and list of genes

### Author(s)

David Venet <davenet@ulb.ac.be>

Maintainer: David Venet <davenet@ulb.ac.be>

### Examples

```
# the gene-gene correlations
cc = getCC();
```

---

getCC                      *Gene-gene correlations*

---

### Description

Get the gene-gene correlations and the list of genes.

### Usage

```
getCC(mode="complete")
```

**Arguments**

mode                    Which correlations should be recovered. complete: calculated with all platforms; woAffy: calculated without the Affymetrix platforms.

**Value**

A list with two elements: g is the list of gene IDs, cc is the upper triangular part of the correlation matrix.

**Examples**

```
# Get the list of genes
geneList = getCC()$g;
```

# Index

`getCC`, [2](#)

`SNAGEEdata (SNAGEEdata-package)`, [2](#)

`SNAGEEdata-package`, [2](#)