

# Package ‘SNAGEEdata’

November 29, 2022

**Version** 1.34.0

**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\_16

**git\_last\_commit** e763a13

**git\_last\_commit\_date** 2022-11-01

**Date/Publication** 2022-11-29

## R topics documented:

SNAGEEdata-package . . . . .	2
getCC . . . . .	3

<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`, [3](#)

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

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