

# Package ‘SNAGEEdata’

January 22, 2026

**Version** 1.47.0

**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** devel

**git\_last\_commit** 95d529e

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

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| SNAGEEdata-package | <i>SNAGEE - data</i> |
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**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:      | <a href="http://fleming.ulb.ac.be/SNAGEE">http://fleming.ulb.ac.be/SNAGEE</a> |

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|-------|------------------------------------------|
| getCC | Gene-gene correlations and list of genes |
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**Author(s)**

David Venet <davenet@ulb.ac.be>

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

**Examples**

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

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|       |                               |
|-------|-------------------------------|
| getCC | <i>Gene-gene correlations</i> |
|-------|-------------------------------|

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**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;
```

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