

# Package ‘SNAGEEdata’

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**Version** 1.43.0

**Date** 2012-01-26

**Title** SNAGEE data

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**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>

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## Contents

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

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SNAGEEdata-package      *SNAGEE - data*

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

### Index:

getCC                      Gene-gene correlations and list of genes

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### Examples

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

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getCC                      *Gene-gene correlations*

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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;
```

# Index

`getCC`, [2](#)

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

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