# Package ‘SNAGEEdata’

February 1, 2017

**Version**: 1.10.0  
**Date**: 2012-01-26  
**Title**: SNAGEE data  
**Author**: David Venet <davenet@ulb.ac.be>  
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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](http://fleming.ulb.ac.be/SNAGEE)  
**NeedsCompilation**: no

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## Description

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

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getCC

getCC

Gene-gene correlations and list of genes

Author(s)

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

Examples

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

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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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