

# Package ‘CDS’

March 17, 2016

**Type** Package

**Title** Concomitant identification of distinctness and similarity in gene expression analysis.

**Date** 2012-05-23

**Version** 1.0.0

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**Description** The Concomitant evaluation of Distinctness and Similarity (CDS) is a fold-change-based statistical test that allows to detect differentially and similarly expressed genes. Given two sets of gene measurements in different biological conditions, probabilities of making type I and type II errors in stating that a gene is differentially or similarly expressed from one condition to the other can be calculated. Furthermore, a confidence interval for the fold-change can be delineated.

**License** GPL-3

**Depends** R (>= 3.1),

**Imports** rJava

**biocViews** StatisticalMethod, Microarray, GeneExpression

**VignetteBuilder** knitr

**Suggests** knitr,rmarkdown

**RoxygenNote** 5.0.1

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compQ0	xxx
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**Description**

xxx

**Usage**

compQ0(m1, s1, m2, s2, TAN\_ALPHA\_0)

**Arguments**

m1	xxx
s1	xxx
m2	xxx
TAN_ALPHA_0	xxx
m2	xxx

**Value**

xxx

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compQA	xxx
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**Description**

xxx

**Usage**

compQA(m1, s1, m2, s2, TAN\_ALPHA\_A)

**Arguments**

m1	xxx
s1	xxx
m2	xxx
TAN_ALPHA_A	xxx
m2	xxx

**Value**

xxx

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compR	xxx
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**Description**

xxx

**Usage**

compR(m1, s1, m2, s2, ESPILON)

**Arguments**

m1	xxx
s1	xxx
m2	xxx
ESPILON	xxx
m2	xxx

**Value**

xxx

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