

intcomp:
Pairwise integration of gene expression and copy
number data

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1 Introduction

A number of algorithms have been recently suggested for integrating gene expression and DNA copy number observations. This R package provides simulated example data and a comparison pipeline to evaluate the performance of the different approaches.

1.1 Comparison methods

The current version compares the following algorithms: DRI (3), edira (4), intCNGEan (5), SIM (2), pint (1), PMA (6).

2 Examples

This Section shows how to run the simulated data through the comparison pipeline, and to reproduce the results.

2.1 Simulated data

Use of the package is demonstrated with a simulated example data set containing paired observations of gene expression and copy number.

Example data set contains (i) gene expression matrix, (ii) gene copy number matrix, (iii) sample class labels (tumor/normal), and (iv) list of 'known' cancer genes.

2.2 Pollack et al. breast cancer data set

Read Pollack et al. (2002) data set (4719CopyNoGeneDataset.tsv¹) and a list of known breast cancer genes. Ground truth list of known breast cancer genes²

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¹<http://www.pnas.org/content/suppl/2002/09/23/162471999.DC1/4719CopyNoGeneDatasetLegend.html>
accessed June 2, 2010.

²<http://www.nature.com/onc/journal/v18/n56/abs/1203335a.html>

```
( 'tgdb_by_name.cgi.html' and 'tgdb.txt' 3)

> library(intcomp)

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> data(pollack)
> library("org.Hs.eg.db")
```

3 Methods

Acknowledgements

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References

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