

# Package ‘LungCancerACvsSCCGEO’

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**Version** 1.41.0

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**Title** A lung cancer dataset that can be used with maPredictDSC package for developing outcome prediction models from Affymetrix CEL files.

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**Depends** R (>= 2.15.0)

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**Description** This package contains 30 Affymetrix CEL files for 7 Adenocarcinoma (AC) and 8 Squamous cell carcinoma (SCC) lung cancer samples taken at random from 3 GEO datasets (GSE10245, GSE18842 and GSE2109) and other 15 samples from a dataset produced by the organizers of the IMPROVER Diagnostic Signature Challenge available from GEO (GSE43580).

**License** GPL-2

**URL** <http://bioinformaticsprb.med.wayne.edu/>

**biocViews** CancerData, LungCancerData, MicroarrayData, GEO

**LazyLoad** yes

**git\_url** <https://git.bioconductor.org/packages/LungCancerACvsSCCGEO>

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LungCancerACvsSCCGEO *Annotation of a small set of training and test set samples (30 total) used by team 221 in the IMPROVER DSC for the lung cancer sub-challenge.*

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### Description

The LungCancerACvsSCCGEO dataset consists: i) a data frame `anoLC` giving the file names of the affy cel files used in the training phase and their corresponding phenotype (AC or SCC) and ii) `gsLC` the gold standard, i.e. the class membership of each test sample appearing in `anoLC`.

### Usage

`data(LC)`

### Source

GEO for the training data, while the test data comes from the citation below: Adi L. Tarca, Mario Lauria, Michael Unger, Erhan Bilal, Stephanie Boue, Kushal Kumar Dey, Julia Hoeng, Heinz Koepl, Florian Martin, Pablo Meyer, Preetam Nandy, Raquel Norel, Manuel Peitsch, Jeremy J Rice, Roberto Romero, Gustavo Stolovitzky, Marja Talikka, Yang Xiang, Christoph Zechner, and IMPROVER DSC Collaborators, Strengths and limitations of microarray-based phenotype prediction: Lessons learned from the IMPROVER Diagnostic Signature Challenge. Bioinformatics, submitted 2013.

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## \* **datasets**

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anoLC (LungCancerACvsSCCGEO), [2](#)

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