

# Package ‘LungCancerACvsSCCGEO’

February 20, 2024

**Version** 1.38.0

**Date** 2013-7-13

**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>

**git\_branch** RELEASE\_3\_18

**git\_last\_commit** 1b11989

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.18

**Date/Publication** 2024-02-20

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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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