

Package: lpcover (via r-universe)

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Title LPCover: Functionality for integer programming methods for covering

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Description Integer programming functionality for different 'covering' optimizations as presented in Ke et al, ``Efficient Representations of Tumor Diversity with Paired DNA-RNA Anomalies".

Depends R (>= 3.6), lpSolve

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

biocViews Software, StatisticalMethod

Suggests knitr, rmarkdown

VignetteBuilder knitr

Repository <https://marchionnilab.r-universe.dev>

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RemoteUrl <https://github.com/marchionniLab/lpcover>

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```
computeMinimalCovering
```

Cover a proportion of a given binary set with the smallest number of features

Usage

```
computeMinimalCovering(mat, alpha = 0.05, maxsol = 100, J = 1, solver = "")
```

Arguments

mat	A binary data matrix with each column corresponding to a sample and each row corresponding to a feature.
alpha	A value in the $0 \leq \alpha < 1$ range indicating what proportion of samples to be considered as outlier. By default $\alpha = 0.05$, indicating 95
	\itemmaxsolThe number of optimal solutions to be returned. Default is 100.
	\itemJThe number of times each sample is to be covered. By default $J=1$, indicating that each sample is to be covered with at least one feature.
	\itemsolverA character string indicating whether to use gurobi or lpSolve.

A list with items "obj": the objective returned by the optimization (as a vector), "sol": a character matrix of solutions(each column a solution), "r": a list where each element contains vectors of results obtained for x and lambda vectors, and "result": the direct output returned by the optimization (by either gurobi or lpSolve).

Function for computing the minimal covering for a given binary data matrix given a minimum proportion of samples to cover

```
optim.out = computeMinimalCovering(mat=mat, alpha=0.05, maxsol=1, J=1, solver="lpSolve")
```

```
cover, optimize
```

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