

Package ‘DMarker’

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Title DMarker

Description Biomarker discovery is a medical term describing the process by which biomarkers are discovered. Many commonly used blood tests in medicine are biomarkers. There is interest in biomarker discovery on the part of the pharmaceutical industry; blood-test or other biomarkers could serve as intermediate markers of disease in clinical trials, and as possible drug targets. DMarker is a package to predict whether the protein or gene can be detected in blood and urine.

Depends R (>= 3.0.3), Rcpp (>= 0.11.3)

Type Package

License GPL (>= 2)

LinkingTo Rcpp

LazyLoad yes

LazyData true

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DMarker-package

*DMarker***Description**

Biomarker discovery is a medical term describing the process by which biomarkers are discovered. Many commonly used blood tests in medicine are biomarkers. There is interest in biomarker discovery on the part of the pharmaceutical industry; blood-test or other biomarkers could serve as intermediate markers of disease in clinical trials, and as possible drug targets. DMarker is a package to predict whether the protein or gene can be detected in blood and urine.

The main function of the package is `dmarker()`, and the more details you can find in [DMarker-method](#)

Details

Package:	DMarker
Type:	Package
Version:	1.0
Date:	2015-05-27
Depends:	R ($\geq 3.0.3$), Rcpp ($\geq 0.11.3$)
LinkingTo:	Rcpp
License:	GPL (≥ 2)
LazyLoad:	yes
LazyData:	true

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References

- [1] Yan Wang, et al. (2009) *DMarker: A Bio-Marker Inference System for Human Diseases based on Microarray Gene Expression Data* 2009
- [2] Juan Cui, et al. (2008) *Computational prediction of human proteins that can be secreted into the bloodstream* BIOINFORMATICS, Vol.24 no. 20 2008 pages 2370-2375
- [3] Jiaxin Wang, et al. (2013) *Computational Prediction of Human Salivary Proteins from Blood Circulation and Application to Diagnostic Biomarker Identification* PLoS ONE, DOI: 10.1371/journal.pone.0080211, 2013
- [4] S Hong, et al. (2011) *A Computational Method for Prediction of Excretory Proteins and Application to Identification of cancer markers in urine and application to gastric cancer* PLoS ONE,6(2):e16875, 2011

[5] <http://bioinfosrv1.bmb.uga.edu/DMarker/>

See Also

[DMarker-method](#) [DMarker uniprot](#)

DMarker	<i>DMarker main function</i>
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Description

DMarker is a package to predict whether the protein or gene can be detected in blood and urine.

The function `dmarker` is the main function of the package. It predicts the biomarker in a data vector, and helps to know whether the protein or gene can be detected in blood and urine.

```
results = dmarker(data, ...);
```

Arguments

<code>data</code>	Data vector.
<code>pre</code>	-pre should be ("gene", "protein"), is a data type variable, telling DMarker gene or protein you are using. default: "GENE"
<code>file</code>	-file should be a filename to output the results if want to save that, or use "FALSE" to ignore. default: "FALSE"
<code>type</code>	-type should be ("both", "blood", "urine"), is a predict type variable, telling DMarker where the data can be detected in blood, urine or both. default: "both"
<code>Seq</code>	-Seq should be ("T", "F"). If Seq is True, the DMarker would predict the sequence whether can be detected in blood or urine, and the data vector must be the sequence vector. default: "F"

Details

```
results = dmarker(data, pre = "Gene", file = "FALSE", type = "both");
```

Value

The R function, `dmarker` returns an object of `list`:

BLOOD	An object of <code>list</code> , having GENE and PROTEIN.
URINE	An object of <code>list</code> , having GENE and PROTEIN.
GENE	A result vector, containing the gene names which can be detected in BLOOD or URINE.
PROTEIN	A result vector, containing the protein names which can be detected in BLOOD or URINE.

The R function, `dmarker` will write the results in a file named by `-file`, if `-file` is not `FALSE` by default. The file will be in the Working Directory .

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See Also

[DMarker-package](#) [DMarker-method](#) [uniprot](#)

Examples

```
data(data);
# load the example vector

results = dmarker(data);
# run dmarker with default parameters
# results is a variable of list with,
#   $BLOOD,
#   $BLOOD$GENE, which genes can be detected in BLOOD,
#   $BLOOD$PROTEIN, which proteins can be detected in BLOOD,
#   $URINE,
#   $URINE$GENE, which genes can be detected in BLOOD,
#   $URINE$PROTEIN, which proteins can be detected in URINE,
# or results = dmarker(data, pre = "Gene", file = "FALSE", type = "both");

results = dmarker(data, pre = "Gene", file = "DMarkerResults.txt", type = "both", Seq = "F");
# Saving the results both in R variable results and the file named DMarkerResults.txt by -file.
```

uniprot

Database from DMarker

Description

Database from DMarker

Usage

```
data(uniprot)
```

Format

The format is: num [1:43462, 1:5] ... - attr(*, "dimnames")=List of 2 ..\$: chr [1:43462] "1" "2" "3" "4"\$: chr [1:5] "Protein" "Gene" "blood" "urine" ...

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See Also

[DMarker-package](#) [DMarker-method](#)

Examples

```
data(uniprot);
```

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