

Package ‘DDMarkerFAST’

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Type Package

Title Diagnose and Detect Markers in Extracellular Circulating Feature Selection Method

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Author

Yu Shang, Qiong Yu, Huansheng Cao, Guoqing Liu, Xiufeng Liu, Hao Wu, Yan Wang, Ying Xu

Maintainer Yu Shang <yushang@uga.edu>

Correspond Qiong Yu <yuqiong@uga.edu>, Ying Xu <xyn@bmb.uga.edu>

Description Diagnose and Detect Markers in Extracellular Circulating is a homo sapiens deductive system solving the markers in extracellular circulating. It entails the symbols of markers, like the genes, the proteins, the micro RNAs, and the isoforms, whether can be diagnose and detect in extracellular circulating, especially the blood serum and the urine for the biological and medicine significance. With the help of a homo sapiens annotation database in DDMarkerData package, DDMarker can even diagnose and detect the sequence among the genes, the proteins, the micro RNAs, and the isoforms. There are two main function in this package, the ddmarker, and the MMC, short for Minimal Metabolize Circulation. MMC entails the markers among the minimal metabolize circulation. FAST is the feature selection method of DDMarker. It shows a way to predict your own data not only like DDMarker and cui's nucleic acids research did, but also can do it in 4 new ways: Support vector machines, the most stable method in biomarkers diagnosis; Adaboost, also known as the the most efficiency and accuracy method; Naive bayes cluster; Recursive partitioning and regression trees; Decision trees.

License GPL (>= 2)

LazyData TRUE

Depends R (>= 3.0.3), e1071, adabag, rpart, C50

Imports e1071, adabag, rpart, C50

LinkingTo e1071, adabag, rpart, C50

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DDMarkerFAST-package *DDMarkerFAST*

Description

Diagnose and Detect Markers in Extracellular Circulating is a homo sapiens deductive system solving the markers in extracellular circulating. It entails the symbols of markers, like the genes, the proteins, the micro RNAs, and the isoforms, whether can be diagnose and detect in extracellular circulating, especially the blood serum and the urine for the biological and medicine significance. With the help of a homo sapiens annotation database in DDMarkerData package, DDMarker can even diagnose and detect the sequence among the genes, the proteins, the micro RNAs, and the isoforms. There are two main function in this package, the `ddmarker`, and the `DDMarkerMMC`, short for Minimal Metabolize Circulation. `DDMarkerMMC` entails the markers among the minimal metabolize circulation.

FAST package is the FeAture SelecTion method of DDMarker, the main function is `DDMarkerFAST()` and `DDMarkerP()`. The more details you can find in [DDMarkerFAST-method](#) and [DDMarkerP-method](#)

Details

Package:	DDMarkerFAST
Type:	Package
Version:	1.0
Date:	2016-07-12
Depends:	R (>= 3.0.3), e1071, adabag, rpart, C50
License:	GPL (>= 2)
LazyLoad:	yes
LazyData:	true

Author(s)

Yu Shang (JLU & UGA) <yushang@uga.edu>
 Qiong Yu (JLU & UGA) <yuqiong@uga.edu> <yujoan_2001@163.com>
 Huansheng Cao (UGA) <hshcao@uga.edu>
 Guoqing Liu (IMUST & UGA) <gqliu@uga.edu> <gqliu1010@163.com>
 Xiufeng Liu (GZUCM & UGA) <xfliu@uga.edu> <liu_xf@gzucm.edu.cn>
 Hao Wu (BIT & UGA) <wuhao@uga.edu> <wuhao@bit.edu.cn>
 Yan Wang (JLU & UGA) <wy6868@hotmail.com>
 Ying Xu (JLU & UGA) <xyn@uga.edu> <xyn@bmb.uga.edu>

Maintainer: Yu Shang (JLU & UGA) <yushang@uga.edu>

References

- citation("DDMarkerFAST");
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 - [3] <http://bioinfosrv1.bmb.uga.edu/DDMarker/>
 - [4] Breiman L. (1999) *Prediction games and arcing classifiers*. Neural Comput 11(7):1493:1517
 - [5] Breiman L, et al. (1984) *Classification and regression trees*. Wadsworth, Belmont
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 - [7] Dietterich TG. (1997) *Machine learning: Four current directions*. AI Mag 18(4):97:136
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 - [9] Domingos P, et al. (1997) *On the optimality of the simple Bayesian classifier under zero-one loss*. Mach Learn 29:103:130
 - [10] Fix E, et al. (1951) *Discriminatory analysis, nonparametric discrimination*. USAF School of Aviation Medicine, Randolph Field, Tex., Project 21-49-004, Rept. 4, Contract AF41(128)-31, February 1951
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 - [17] Herbrich R, et al. (2000) *Rank boundaries for ordinal regression*. Adv Mar Classif pp 115:132
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See Also

[DDMarkerFAST-method](#) [DDMarkerP-method](#) [DDMarker NAR](#)

DDMarkerFAST

*DDMarker FeAture SelecTion***Description**

The Feature Selection Method of Diagnose and Detect Markers in Extracellular Circulating

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

Arguments

data	Data matrix, the first column must contain the feature types, eg. BLOOD, URINE, ... , and the following ones should be the features just like the references [1] and [2] did.
method	-method should be ("svm", "adaboost", "bayes", "cart", "c5"), "svm" denotes Support Vector Machines, the most stable method in biomarkers diagnosis, "adaboost" denotes AdaBoost, also known as the the most efficiency and accuracy method, "bayes" denotes Naive Bayes Cluster, "cart" denotes Recursive Partitioning and "c5" denotes Decision Trees. default: "svm"

Details

```
models = DDMarkerFAST(data = data, method = "svm");
```

Value

The R function, DDMarkerFAST returns an object of list:

class	shows the method used.
names	shows the model attributes, which can be used in the prediction method, the more details will be found in references.
vardep.summary, xlevels, ylevels	adaboost and cart will return the elements, the more details will be found in references.

Author(s)

Yu Shang (JLU & UGA) <yushang@uga.edu>
 Qiong Yu (JLU & UGA) <yuqiong@uga.edu> <yujoan_2001@163.com>
 Huansheng Cao (UGA) <hshcao@uga.edu>
 Guoqing Liu (IMUST & UGA) <gqliu@uga.edu> <gqliu1010@163.com>
 Xiufeng Liu (GZUCM & UGA) <xfliu@uga.edu> <liu_xf@gzucm.edu.cn>
 Hao Wu (BIT & UGA) <wuhao@uga.edu> <wuhao@bit.edu.cn>
 Yan Wang (JLU & UGA) <wy6868@hotmail.com>
 Ying Xu (JLU & UGA) <xyn@uga.edu> <xyn@bmb.uga.edu>

Maintainer: Yu Shang (JLU & UGA) <yushang@uga.edu>

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See Also

[DDMarkerFAST-package](#) [DDMarkerP-method](#) [DDMarker](#) [NAR](#)

Examples

```
models = DDMarkerFAST();
```

DDMarkerP

DDMarker Prediction

Description

The Prediction Method of Diagnose and Detect Markers in Extracellular Circulating

```
results = DDMarkerP(model, ...);
```

Arguments

model	FAST class, should be the result computing by DDMarkerFAST()
data	Data matrix, which will be entailed whether can be diagnosed and detected in extracellular circulating, just like the references did

Details

```
results = DDMarkerP(model = model, data = data);
```

Value

The R function, DDMarkerP returns an object of vector, and entails the results.

Author(s)

Yu Shang (JLU & UGA) <yushang@uga.edu>
 Qiong Yu (JLU & UGA) <yuqiong@uga.edu> <yujoan_2001@163.com>
 Huansheng Cao (UGA) <hshcao@uga.edu>
 Guoqing Liu (IMUST & UGA) <gqliu@uga.edu> <gqliu1010@163.com>
 Xiufeng Liu (GZUCM & UGA) <xfliu@uga.edu> <liu_xf@gzucm.edu.cn>
 Hao Wu (BIT & UGA) <wuhao@uga.edu> <wuhao@bit.edu.cn>
 Yan Wang (JLU & UGA) <wy6868@hotmail.com>
 Ying Xu (JLU & UGA) <xyn@uga.edu> <xyn@bmb.uga.edu>

Maintainer: Yu Shang (JLU & UGA) <yushang@uga.edu>

References

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- [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] <http://bioinfosrv1.bmb.uga.edu/DDMarker/>

See Also

[DDMarkerFAST-package](#) [DDMarkerFAST-method](#) [DDMarker](#) [NAR](#)

Examples

```
models = DDMarkerFAST();  
results = DDMarkerP(models);
```

LOG

LOG

Description

The logs of Diagnose and Detect Markers in Extracellular Circulating

logs();

Details

logs();

Author(s)

Yu Shang (JLU & UGA) <yushang@uga.edu>
Qiong Yu (JLU & UGA) <yuqiong@uga.edu> <yujoan_2001@163.com>
Huansheng Cao (UGA) <hshcao@uga.edu>
Guoqing Liu (IMUST & UGA) <gqliu@uga.edu> <gqliu1010@163.com>
Xiufeng Liu (GZUCM & UGA) <xfliu@uga.edu> <liu_xf@gzucm.edu.cn>
Hao Wu (BIT & UGA) <wuhao@uga.edu> <wuhao@bit.edu.cn>
Yan Wang (JLU & UGA) <wy6868@hotmail.com>
Ying Xu (JLU & UGA) <xyn@uga.edu> <xyn@bmb.uga.edu>

Maintainer: Yu Shang (JLU & UGA) <yushang@uga.edu>

References

citation("DDMarkerFAST");

See Also

[DDMarkerFAST-package](#) [DDMarkerFAST-method](#) [DDMarkerP-method](#) [NAR](#)

Examples

```
logs();
# print the logs of DDMarker

## LOG
# DDMarker 1.0, 05/27/2015, Recomputed the blood and urine predicted biomarkers from the latest database;
# DDMarker 1.1, 08/27/2015, DDMarker can entails the sequence of proteins;
# DDMarker 1.2, 12/28/2015, adds a visualization function of biomarkers; isoform proteins can be diagnosed; s
# DDMarker 1.3, 01/12/2016, more illustrates are upload as the draft;
# DDMarker 1.4, 03/12/2016, adds the medical guidance in the results;
# DDMarker 1.4.1, 04/01/2016, bug fixed;
# DDMarker 1.4.2, 05/02/2016, bug fixed;
# DDMarker 1.4.3, 05/23/2016, bug fixed;
# DDMarker 1.5, 05/27/2016, bug fixed;
# DDMarker 2.0, 07/07/2016, DDMarker2 published;
# DDMarker 2.1, 07/12/2016, adds 4 methods in DDMarker FAST method.
```

NAR	NAR
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Description

The famous features, which were used in nucleic acids research and centers for disease control and prevention

nar();

Details

nar();

Author(s)

Yu Shang (JLU & UGA) <yushang@uga.edu>
Qiong Yu (JLU & UGA) <yuqiong@uga.edu> <yujoan_2001@163.com>
Huansheng Cao (UGA) <hshcao@uga.edu>
Guoqing Liu (IMUST & UGA) <gqliu@uga.edu> <gqliu1010@163.com>
Xiufeng Liu (GZUCM & UGA) <xfliu@uga.edu> <liu_xf@gzucm.edu.cn>
Hao Wu (BIT & UGA) <wuhao@uga.edu> <wuhao@bit.edu.cn>
Yan Wang (JLU & UGA) <wy6868@hotmail.com>
Ying Xu (JLU & UGA) <xyn@uga.edu> <xyn@bmb.uga.edu>

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- [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] <http://bioinfosrv1.bmb.uga.edu/DDMarker/>

See Also

[DDMarkerFAST-package](#) [DDMarkerFAST-method](#) [DDMarkerP-method](#) [DDMarker](#)

Examples

```
nar();
# print the famous features, which were used in Nucleic Acids Research and Centers for Disease Control and Pre
# See the references

## Features used in DDMarker:
##
# http://bidd.cz3.nus.edu.sg/cgi-bin/prof/protein/profnew.cgi
# http://www.expasy.org/proteomics/protein_structure
# http://molbiol-tools.ca/Protein_secondary_structure.htm
# http://www.cbs.dtu.dk/services/
# http://coot.embl.de/cgi/sscp_serv.pl
# http://phobius.sbc.su.se/cgi-bin/predict.pl
# http://bip.weizmann.ac.il/fldbin/findex
# http://www.cbs.dtu.dk/services/TatP/
# http://bmbpcu36.leeds.ac.uk/~andy/betaBarrel/AACompPred/aaTMB_Hunt.cgi
# http://jing.cz3.nus.edu.sg/cgi-bin/prof/prof.cgi
# http://www.cbs.dtu.dk/services/NetNGlyc/
# http://www.cbs.dtu.dk/services/NetOGlyc/
# http://www.scfbio-iitd.res.in/software/proteomics/rg.jsp
# http://web.expasy.org/cgi-bin/compute_pi/pi_tool
```

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