Package 'DDMarker'

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Type Package

Title Diagnose and Detect Markers in Extracellular Circulating

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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.

License GPL (>= 2)

LazyData TRUE

Depends R (>= 3.0.3), Rcpp (>= 0.12.0)

Imports Rcpp, GOstats, pathview, seqinr

LinkingTo Rcpp, GOstats, pathview, seqinr

R topics documented:

DDMarker-package *DDMarker*

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.
The main function of the package are `ddmarker()` and `DDMarkerMMC()`. The more details you can find in `DDMarker-method` and `MMC-method`

Details

Package:	DDMarker
Type:	Package
Version:	1.0
Date:	2015-05-27
Depends:	R (>= 3.0.3), Rcpp (>= 0.11.3)
LinkingTo:	Rcpp
License:	GPL (>= 2)
LazyLoad:	yes
LazyData:	true

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References

citation("DDMarker");
[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

DDMarker-method MMC-method EC demo

`data0` *DEMO*

Description

A demo for ddmarker and MMC.

Usage

```
data(data0)
```

Format

The format is: Large list [10 elements] ... - attr(*, "dimnames")=List of 10 ..$demo.pm : "numeric" ... ..$demo.ddm : "character" ... ..$demo.pro : "character" ... ..$demo.gen : "character" ... ..$demo.iso : "character" ... ..$demo.ent : "character" ... ..$demo.mir : "character" ... ..$demo.seq : "character" ... ..$MI : "numeric" ... ..$MP : "numeric" ...

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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] 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

DDMarker-package

Examples

```
data(data0);
\code{\LinkA{DDMarker-method}{DDMarker.Rdash.method}} \code{\LinkA{MMC-method}{MMC.Rdash.method}}
```

DDMarker *Diagnose and Detect Markers*

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.

results = ddmarker(data, . . .);

Arguments

data	Data vector.
pre	-pre should be ("gene", "protein", "MiRNA", "entrez", "isoform", "mix"), is a data type variable, telling DDMarker under which constraint DDMarker will do the diagnose and detect. If -pre is "mix", DDMarker will do the diagnose and detect on all constraints. default: "mix"

`file`	-file should be a filename to output the results if want to save, or use "FALSE" to ignore. default: "FALSE"
`type`	-type should be ("both", "blood", "urine", "all"), is a predict type variable, telling DDMarker which extracellular circulating DDMarker will do the diagnose and detect. If -pre is "all", DDMarker will do the diagnose and detect on all extracellular circulatings. default: "all"
`Seq`	-Seq should be ("T", "F"). If -Seq is True, the DDMarker will predic the sequence first, then doing DDMarker under the results of that. The sequence can come from the genes, the proteins, the micro RNAs, and the isoforms, and the data vector must be the sequence vector. default: "F"
`Path`	-Path should be ("T", "F"). If -Path is True, The DDMarker will do Minimal Metabolize Circulation, write the images into the files under the results of the diagnose and detect in ddmarker. default: "F"
`PV`	-PV should be a double number from 0.00 to 1.00. It is a variable of -Path, telling which metabolize circulation should be written out. If -PV is 0.05, the DDMarker will only write the statistical significant results. Else if -PV is 1.00, the DDMarker will write all the metabolize circulations. default: 0.05
`out`	-out should be a integer number greater than 0, a variable of -Path, DDMarker writting the minimal quantity between -out and the minimal metabolize circulation, or use "FALSE" to ignore. default: "F"
`pvalue`	-pvalue should be a vector, is a vector of path. If -pvalue is not "False", DDMarker not only writes the minimal metabolize circulation, but also entails the degree of the markers. default: "F"

Details

data(data0); results = ddmarker(data = data0$demo.ddm, pre = "Mix", file = "FALSE", type = "All", Seq = "F", Path = "FALSE", PV = 0.05, out = "FALSE", pvalue = "FALSE");

Value

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

BLOOD	An object of `list`, having `Gene`, `Entrez`, `Isoform` and `Protein`.
URINE	An object of `list`, having `Gene`, `Entrez`, `Isoform` and `Protein`.
MIRNA	An object of `list`, having `RNA_name`, `RNA_class`, `RNA_type` and `Journal`.
Gene	An entailment, entails the symbol of the genes which can be diagnosed and detected in `Extracellular Ci`
Entrez	A entailment, entails the symbol of the entrez which can be diagnosed and detected in `Extracellular Cir`
Isoform	A entailment, entails the symbol of the isoform which can be diagnosed and detected in `Extracellular C`
Protein	A entailment, entails the the symbol of the protein which can be diagnosed and detected in `Extracellular`
RNA_name	A entailment, entails the symbol of the micro RNAs which can be diagnosed and detected in `Extracellula`
RNA_class	A entailment, entails the class of the micro RNAs.
RNA_type	A entailment, entails the type of the micro RNAs, simply which EC part it can be diagnosed and detected.
Journal	A entailment, if existed, entails in which scientific research, it being studied.

The R function, ddmarker will write the results in a file named by -file, IFF -file is not FALSE by default. The file will be in the Working Directory .
The R function, ddmarker will write the minimal metabolize circulation results in the files named by the MMC names, IFF -Path is not FALSE by default. The file will be in the Working Directory .

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References

citation("DDMarker");
[1] Yan Wang, et al. (2009) *DMarker: A Bio-Marker Inference System for Human Diseases based on Microarray Gene Expression Data* 2009
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[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

DDMarker-package MMC-method EC demo

Examples

```
data(data0);
# load the demo of DDMarker

results = ddmarker(data0$demo.ddm);
# run dmarker with default parameters
# results is a variable of list with,
#   $BLOOD,
#   $BLOOD[,"Gene"], entails the symbol of the genes which can be diagnosed and detected in BLOOD,
#   $BLOOD[,"Entrez"],entails the symbol of the entrez which can be diagnosed and detected in BLOOD,
#   $BLOOD[,"Isoform"], entails the symbol of the isoform which can be diagnosed and detected in BLOOD,
```

```
#   $BLOOD[,"Protein"], entails the the symbol of the protein which can be diagnosed and detected in BLOOD,
#    $URINE,
#   $URINE[,"Gene"], entails the symbol of the genes which can be diagnosed and detected in URINE,
#   $URINE[,"Entrez"], entails the symbol of the entrez which can be diagnosed and detected in URINE,
#   $URINE[,"Isoform"], entails the symbol of the isoform which can be diagnosed and detected in URINE,
#   $URINE[,"Protein"], entails the the symbol of the protein which can be diagnosed and detected in URINE,
#    $MIRNA,
#   $MIRNA[,"RNA_name"], entails the symbol of the micro RNAs which can be diagnosed and detected in extracell
#    $MIRNA[,"RNA_class"], entails the class of the micro RNAs,
#   $MIRNA[,"RNA_type"], entails the type of the micro RNAs, simply which EC part it can be diagnosed and detec
#   $MIRNA[,"Journal"], if existed, entails in which scientific research, it being studied,
# or results = ddmarker(data = data0$demo.ddm, pre = "Mix", file = "FALSE", type = "All", Seq = "F", Path = "FA

results = ddmarker(data0$demo.ddm, file = "DDMarkerResults.txt");
# Saving the results both in R variable results and the file, named DMarkerResults.txt by -file.

results = ddmarker(data0$demo.seq, Seq = "TRUE");
# Diagnose and detect the sequences of markers in extracellular circulating.

results = ddmarker(data0$demo.path, path = "TRUE", pvalue = data0$demo.pm);
# Doing both DDMarker and minimal metabolize circulation with the degree of the markers.

results = ddmarker(data = data0$demo.pro, pre = "protein", type = "blood");
# Proteins are diagnosed and detected whether in blood.

results = ddmarker(data = data0$demo.gen, pre = "gene", type = "urine");
# Genes are diagnosed and detected whether in urine.

results = ddmarker(data = data0$demo.iso, pre = "isoform", type = "both");
# Isoforms are diagnosed and detected whether in blood or urine

results = ddmarker(data = data0$demo.ent, pre = "entrez", type = "all");
# Entrezs are diagnosed and detected whether in extracellular circulating.

results = ddmarker(data = data0$demo.mir, pre = "MiRNA");
# Micro RNAs are diagnosed and detected whether in extracellular circulating.
```

EC *A Homo Sapiens Annotation Database for Diagnose and Detect Markers in Extracellular Circulating*

Description

A database is called HSAD, IFF, it entails the symbols among the genes, the proteins, the micro RNAs, the isoforms and their sequences by a deductive system.

Usage

```
data(EC)
```

Format

The format is: Large list [5 elements, 18.1 Mb] ... - attr(*, "dimnames")=List of 5 ..$Mi : "character" ... ..$G : "numeric" ... ..$P : "numeric" ... ..$HSAD : "list" ... ..$V : "numeric" ...

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References

citation("DDMarker");
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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
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[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/
[6] Francesco Russo, et al. (2012) *miRandola: Extracellular Circulating MicroRNAs Database* PLoS ONE 2012, 7(10): e47786, 2012
[7] Francesco Russo, et al. (2014) *A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs* BMC Genomics 2014, 15(Suppl 3):S4, 2014

See Also

DDMarker-package

Examples

```
data(EC);
```

LOG *LOG*

Description

The logs of Diagnose and Detect Markers in Extracellular Circulating

logs();

Details

logs();

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References

citation("DDMarker");

See Also

DDMarker-package DDMarker-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 datebase;
# 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; st
# 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;
# DDMarker 2.1.1, 07/26/2016 more illustrates are uploaded as the draft;
# DDMarker 2.1.2, 07/27/2016 Push a poster.
```

MMC *Minimal Metabolize Circulation*

Description

Minimal Metabolize Circulation for Diagnose and Detect Markers in Extracellular Circulating

results = DDMarkerMMC(gene, . . .);

Arguments

gene	Data vector.
IDType	-IDType shoulde be ("Entrez", "GENE", "TCGA"), "Entrez" denotes the entrez IDs, "GENE" denotes the gene IDs, "TCGA" denotes the TCGA IDs. default: "Entrez"
PV	-PV should be a double number from 0.00 to 1.00. Telling which metabolize circulation should be written out. If -PV is 0.05, the DDMarkerMMC will only write the statistical significant results. Else if -PV is 1.00, the DDMarkerMMC will write all the metabolize circulations. default: 0.05
out	-out should be a integer number greater than 0, a variable of -Path, DDMarker-MMC writting the minimal quantity between -out and the minimal metabolize circulation, or use "FALSE" to ignore. default: "F"
mirna	-mirna shoulde be ("T", "F"). If -mirna is "TRUE", the DDMarkerMMC will not only do MMC function, but also write out the regulating relationship among Micro RNAs, no matter how less the statistical significant is. default: "F"
pvalue	-pvalue should be a vector, only working significant when DDMarker is called by DDMarker. default: "F"

Details

results = DDMarkerMMC(gene = c(), IDType = "Entrez", PV = 0.05, out = FALSE, mirna = FALSE, pvalue = FALSE);

Value

The R function, DDMarkerMMC returns an object of list, comes from the packages pathview:

plot.data.gene	data.frame returned by node.map function for rendering mapped gene nodes, including node name, type, p
plot.data.cpd	same as plot.data.gene function, except for mapped compound node data. d plot.data.cpd=NULL. Default

The R function, DDMarkerMMC will write the result images in files named by the minimal metabolize circulations. The images will be in the Working Directory .

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References

citation("DDMarker");

See Also

DDMarker-package DDMarker-method EC MMC demo

Examples

```
data(data0);
# load the demo of DDMarker

results = DDMarkerMMC();
# run MMC with default parameters
# use a demo data named MMC.rda comes from the packages DDMarkerMMC

results = DDMarkerMMC(data0$demo.pm, mirna = "TRUE");
# run MMC uses a demo MiRNA data

results = DDMarkerMMC(data0$MI, mirna = "TRUE");
# run MMC uses another demo MiRNA data

# results is a variable of list comes from the packages pathview,
#   $plot.data.gene, data.frame returned by node.map function for rendering mapped gene nodes, including node
#   $plot.data.cpd, same as plot.data.gene function, except for mapped compound node data. d plot.data.cpd=NU
# The results returned by keggview.native and codekeggview.graph are both a list of graph plotting parameters
```

NAR *NAR*

Description

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

nar();

Details

nar();

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References

citation("DDMarker");
[1] Juan Cui, et al. (2011) *An integrated transcriptomic and computational analysis for biomarker identification in gastric cancer* Nucleic Acids Research, 39: 1197-1207
[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/DMarker/

See Also

DDMarker-package DDMarker-method LOG

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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