

# Package ‘mineCitrus’

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**Type** Package

**Title** Extract and Analyze Median Molecule Intensity from 'citrus'  
Output

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**Description** Citrus is a computational technique developed for the analysis of high dimensional cytometry data sets. This package extracts, statistically analyzes, and visualizes marker expression from 'citrus' data. This code was used to generate data for Figures 3 and 4 in the forthcoming manuscript: Throm et al. “Identification of Enhanced Interferon-Gamma Signaling in Polyarticular Juvenile Idiopathic Arthritis with Mass Cytometry”, JCI-Insight. For more information on Citrus, please see: Bruggner et al. (2014) <doi:10.1073/pnas.1408792111>. To download the 'citrus' package, please see <<https://github.com/nolanlab/citrus>>.

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**Imports** ggplot2

**Depends** R (>= 2.10)

**Suggests**

**RoxygenNote** 6.0.1

**NeedsCompilation** no

**Repository** CRAN

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allmeds	<i>Gets matrices of medians for each individual sample for all measured parameters for all clusters</i>
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## Description

Gets matrices of medians for each individual sample for all measured parameters for all clusters

## Usage

```
allmeds(citrus.combinedFCSSet, citrus.foldClustering, citrus.foldFeatureSet)
```

## Arguments

citrus.combinedFCSSet  
loaded from citrusClustering.RData file generated by Citrus run

citrus.foldClustering  
loaded from citrusClustering.RData file generated by Citrus run

citrus.foldFeatureSet  
computed from first two variables using citrus.calculateFoldFeatureSet function from citrus package

## Value

Returns a list with each element corresponding to a matrix (rows as samples, columns as measured parameters) for a different cluster (for the minimum threshold specified)

## Examples

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
```

---

`citrus.combinedFCSSet` *Cytometry data set for example of Citrus data set from nolanlab/citrus*

---

## Description

A dataset containing the a simple example of cytometry data

## Usage

```
citrus.combinedFCSSet
```

## Format

A large citrus.combinedFCSSet object with 5 elements:

**data** Toy data set for cytometry

**fileChannelNames** Names of channels for measured parameters included in toy cytometry data set

**fileIds** ID numbers for each file included in toy cytometry data set

**fileNames** Names of files included in toy cytometry data set

**fileReagentNames** Names of measured channels in toy cytometry data set ...

## Source

<https://github.com/nolanlab/citrus>

---

`citrus.foldClustering` *Clustering data for example of Citrus data set from nolanlab/citrus*

---

### Description

A dataset containing the clustering of different cell groups

### Usage

```
citrus.foldClustering
```

### Format

A large `citrus.foldClustering` object with 5 elements:

**allClustering** A list describing which events belong to which clusters

**foldClustering** A list describing which events belong to which clusters for each fold

**foldMappingAssignments** A list describing assignments with fold clustering

**folds** Descriptions of each data clustering

**nFolds** The number of times data is clustered ...

### Source

<https://github.com/nolanlab/citrus>

---

`citrus.foldFeatureSet` *Correlation data for example of Citrus data set from nolanlab/citrus*

---

### Description

A dataset containing the association of red and blue in clusters with different sample groups

### Usage

```
citrus.foldFeatureSet
```

### Format

A list with 8 elements:

**allFeatures** Data set for each sample for all markers and clusters

**allLargeEnoughClusters** Vector of clusters meeting size threshold

**foldFeatures** Data for each fold clustering

**foldLargeEnoughClusters** Clusters meeting size threshold for each fold clustering

- fold** Descriptions of each data clustering
- leftoutFeatures** Data omitted from analyses
- minimumClusterSizePercent** Minimum size threshold to retain clusters in analysis
- nFolds** The number of times data is clustered ...

### Source

<https://github.com/nolanlab/citrus>

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classclustermeds	<i>Gets matrices of medians for each individual sample for all measured parameters for all clusters</i>
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---

### Description

Gets matrices of medians for each individual sample for all measured parameters for all clusters

### Usage

```
classclustermeds(citrus.foldFeatureSet, citrus.foldClustering,
  citrus.combinedFCSSet, groupsizes, meds)
```

### Arguments

- citrus.foldFeatureSet  
computed from first two variables using citrus.calculateFoldFeatureSet function from citrus package
- citrus.foldClustering  
loaded from citrusClustering.RData file generated by Citrus run
- citrus.combinedFCSSet  
loaded from citrusClustering.RData file generated by Citrus run
- groupsizes  
list of sizes of the groups run in Citrus, in order of the selection for citrus run
- meds  
The names of the columns from citrus.combinedFCSSet\$data of interest to extract medians for

### Value

Returns a list of matrices with columns corresponding to selected features and rows corresponding to sample groups; each list element corresponds to data for a different cluster

**Examples**

```

library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
medians<-classclustermeds(citrus.foldFeatureSet,citrus.foldClustering,
                          citrus.combinedFCSSet,group sizes=c(10,10),meds=meds)

```

---

clustermeds	<i>Gets matrix of medians for desired measured features for all clusters meeting threshold requirements specified in Citrus</i>
-------------	---

---

**Description**

Gets matrix of medians for desired measured features for all clusters meeting threshold requirements specified in Citrus

**Usage**

```

clustermeds(citrus.foldFeatureSet, citrus.foldClustering, medsofinterest,
            citrus.combinedFCSSet)

```

**Arguments**

citrus.foldFeatureSet  
     computed from first two variables using citrus.calculateFoldFeatureSet function from citrus package

citrus.foldClustering  
     loaded from citrusClustering.RData file generated by Citrus run

medsofinterest The names of the columns from citrus.combinedFCSSet\$data of interest to extract medians for

citrus.combinedFCSSet  
     loaded from citrusClustering.RData file generated by Citrus run

**Value**

Returns a matrix with columns corresponding to selected features and rows corresponding to samples

**Examples**

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
medians<-clustermeds(citrus.foldFeatureSet=citrus.foldFeatureSet,
                     citrus.foldClustering=citrus.foldClustering,
                     medsofinterest=c("Red","Blue"),
                     citrus.combinedFCSSet=citrus.combinedFCSSet)
```

---

difMarkerPlots	<i>Plot dot plots of features where both clusters are significantly different from the reference cluster without processing data before hand</i>
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---

**Description**

Plot dot plots of features where both clusters are significantly different from the reference cluster without processing data before hand

**Usage**

```
difMarkerPlots(data, clusters, markers, diffclust, strat)
```

**Arguments**

data	output from call to allmeds function
clusters	clusterIDs of the desired clusters to compare and plot
markers	indices of the columns of the data matrix for features to be analyse
diffclust	clusterID of for cluster to statisticaly compare others to
strat	clusterIDs for stratifying clusters as indicated by Citrus results

**Value**

Dot plots for all features where both clusters are significantly different from the reference cluster

**Examples**

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
graphs<-difMarkerPlots(data=meds,clusters=c(19999,19972,19988),
                       markers=c(2,3),diffclust=19999,strat=19999)
```

---

difMarkerPlots2	<i>Plot dot plots of features where one cluster is significantly different from the reference cluster without processing data before hand</i>
-----------------	---

---

## Description

Plot dot plots of features where one cluster is significantly different from the reference cluster without processing data before hand

## Usage

```
difMarkerPlots2(data, clusters, markers, diffclust, strat)
```

## Arguments

data	output from call to allmeds function
clusters	clusterIDs of the desired clusters to compare and plot
markers	indices of the columns of the data matrix for features to be analyse
diffclust	clusterID of for cluster to statisticaly compare others to
strat	clusterIDs for stratifying clusters as indicated by Citrus results

## Value

Dot plots for all features where one cluster is significantly different from the reference cluster

## Examples

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
graphs<-difMarkerPlots2(data=meds,clusters=c(19999,19972,19988),markers=c(2,3),
                       diffclust=19999,strat=19999)
```



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filterMarker	<i>Filters list of data matrices with columns corresponding to the measured parameters of interest</i>
--------------	--

---

**Description**

Filters list of data matrices with columns corresponding to the measured parameters of interest

**Usage**

```
filterMarker(clustdat, markers)
```

**Arguments**

clustdat	a list of data matrices with list elements corresponding to clusters and matrices of intensities of measured parameters
markers	Indices of the columns of parameters to keep

**Value**

A list of data matrices with columns of data matrices only corresponding to measured parameters of interest

**Examples**

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
meds2<-filterMarker(clustdat=meds,markers=c(2,3))
```

---

findclust	<i>Filters list to contain only desired clusters</i>
-----------	--

---

**Description**

Filters list to contain only desired clusters

**Usage**

```
findclust(data, clusters)
```

**Arguments**

`data` a list of data matrices with list elements corresponding to clusters and matrices of intensities of measured parameters

`clusters` indices of the clusters to retain

**Value**

A list of data matrices for the desired clusters

**Examples**

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
filteredmeds<-findclust(data=meds,clusters=c(19999,19972,19988))
```

---

findSig

*Assesses significance of ANOVA and t-test results*

---

**Description**

Assesses significance of ANOVA and t-test results

**Usage**

```
findSig(posHocRes)
```

**Arguments**

`posHocRes` results from a call to the posthoc function

**Value**

A dataframe indicating the significances of results

**Examples**

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
```

```
filteredmeds<-findclust(data=meds,clusters=c(19999,19972,19988))
meds2<-filterMarker(clustdat=filteredmeds,markers=c(2,3))
foranova<-processforanova(filtereddata=meds2)
ttests<-posthoc(processedDat=foranova,clustIDdif=19999)
sig<-findSig(posHocRes=ttests)
```

---

plotdif	<i>Plot dot plots of features where both clusters are significantly different from the reference cluster</i>
---------	--

---

### Description

Plot dot plots of features where both clusters are significantly different from the reference cluster

### Usage

```
plotdif(BJHdf, anovadata, strat)
```

### Arguments

BJHdf	results of a call to findsig
anovadata	results of call to processforanova
strat	clusterIDs for clusters that are stratifying

### Value

Dot plots for all features where both clusters are significantly different from the reference cluster

### Examples

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
filteredmeds<-findclust(data=meds,clusters=c(19999,19972,19988))
meds2<-filterMarker(clustdat=filteredmeds,markers=c(2,3))
foranova<-processforanova(filtereddata=meds2)
ttests<-posthoc(processedDat=foranova,clustIDdif=19999)
sig<-findSig(posHocRes=ttests)
graphs<-plotdif(BJHdf=sig,anovadata=foranova,strat=19999)
```

---

plotdif2	<i>Plot dot plots of features where one cluster is significantly different from the reference cluster</i>
----------	---

---

### Description

Plot dot plots of features where one cluster is significantly different from the reference cluster

### Usage

```
plotdif2(BJHdf, anovadata, strat)
```

### Arguments

BJHdf	results of a call to findsig
anovadata	results of call to processforanova
strat	clusterIDs for clusters that are stratifying

### Value

Dot plots for all features where one cluster is significantly different from the reference cluster

### Examples

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
filteredmeds<-findclust(data=meds,clusters=c(19999,19972,19988))
meds2<-filterMarker(clustdat=filteredmeds,markers=c(2,3))
foranova<-processforanova(filteredmeds)
ttests<-posthoc(processedDat=foranova,clustIDdif=19999)
sig<-findSig(posHocRes=ttests)
graphs<-plotdif2(BJHdf=sig,anovadata=foranova,strat=19999)
```

---

posthoc	<i>Runs ANOVA and t-tests comparing clusters and markers in clusters</i>
---------	--

---

### Description

Runs ANOVA and t-tests comparing clusters and markers in clusters

**Usage**

```
posthoc(processedDat, clustIDdif)
```

**Arguments**

processedDat    data that has been processed using the processforanova function  
 clustIDdif      ID number of the cluster to compare the others to

**Value**

A list of t-test results for each of the comparisons

**Examples**

```
library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
filteredmeds<-findclust(data=meds,clusters=c(19999,19972,19988))
meds2<-filterMarker(clustdat=filteredmeds,markers=c(2,3))
foranova<-processforanova(filteredmeds)
ttests<-posthoc(processedDat=foranova,clustIDdif=19999)
```

---

processforanova

*Processes cluster signaling data in form for statistical analysis*

---

**Description**

Processes cluster signaling data in form for statistical analysis

**Usage**

```
processforanova(filteredmeds)
```

**Arguments**

filteredmeds    a list with each element corresponding to a cluster of interest and matrices containing individual sample data for desired markers

**Value**

A dataframe sufficient for using the posthoc function to compute statistics

**Examples**

```

library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
meds<-allmeds(citrus.combinedFCSSet=citrus.combinedFCSSet,
              citrus.foldClustering=citrus.foldClustering,
              citrus.foldFeatureSet=citrus.foldFeatureSet)
filteredmeds<-findclust(data=meds,clusters=c(19999,19972,19988))
foranova<-processforanova(filteredmeds)

```

---

sortmat	<i>Reorders to rows (corresponding to different clusters) of a matrix of medians to a desired order</i>
---------	---

---

**Description**

Reorders to rows (corresponding to different clusters) of a matrix of medians to a desired order

**Usage**

```
sortmat(mat, desiredorder)
```

**Arguments**

mat	matrix of median data
desiredorder	row labels from matrix in desired order

**Value**

Returns a matrix with rows rearranged in desired order

**Examples**

```

library(mineCitrus)
data("citrus.combinedFCSSet")
data("citrus.foldClustering")
data("citrus.foldFeatureSet")
medians<-clustermeds(citrus.foldFeatureSet=citrus.foldFeatureSet,
                     citrus.foldClustering=citrus.foldClustering,
                     medsofinterest=c("Red", "Blue"),
                     citrus.combinedFCSSet=citrus.combinedFCSSet)
names<-rownames(medians)
names<-names[c(31,1:30)]
sortedmedians<-sortmat(mat=medians,desiredorder=names)

```

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