Package ‘patPRO’

February 2, 2016

Type Package

Title Visualizing Temporal Microbiome Data

Version 1.1.0

Date 2016-02-01

Author Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA

Maintainer Geoffrey D Hannigan `<ghanni@upenn.edu>`

Imports reshape2, ggplot2, grid, gridExtra, plyr, RColorBrewer

Description Quickly and easily visualize longitudinal microbiome profiles using standard output from the QIIME microbiome analysis toolkit (see <http://qiime.org> for more information).

License GPL-3

LazyLoad yes

NeedsCompilation no

Repository CRAN

Date/Publication 2016-02-02 17:25:52

R topics documented:

`patPRO-package` *Longitudinal Profiler of Microbiome Data*

Description

patPRO (short for Patient Profiler) is a package for formatting Qiime microbiome analysis output files for downstream analyses and generating powerful graphics for visualizing longitudinal datasets per patient or averages of patient cohorts.

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

An overview of how to use the package, including the most important functions, is included in the supplemental R notebook patPROExampleWorkflow.html.

Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. [Submitted] Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA. Bioinformatics.

`mergeMapMetaData` *Merge Mapping and Data Files*

Description

This function merges mapping file metadate (mapping file information formatted according to Qiime specifications) with dataset output from Qiime, including alpha diversity, bacterial relative abundance, and bacterial load (this must be aquired outside of standard Qiime sequencing methods). Merge the necessary mapping file columns (subject ID and time point which could be days, etc) into the datasets for alpha diversity, bacterial load, and taxa relative abundance.

Usage

```
mergeMapMetaData(map.file,
merging.file,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
merge.smpl.id,
sample.id.col="SampleID",
subject.id.col="SubjectID",
tmpt.id.col="Time_point")
```

Arguments

`map.file`	The mapping file `data.frame` used for upfront Qiime analyses and formatted according to Qiime specifications.
`merging.file`	The `data.frame` containing the alpha diversity, bacterial load, or relative abundance information that will be merged with the mapping file metadata.
`map.sub.id`	Name of the subject ID column found in the Qiime mapping file. Default is "SubjectID".
`map.tmpt`	Name of the time point column found in the Qiime mapping file. Default is "Time_point".
`map.smpl.id`	Name os the sample ID column found in the Qiime mapping file. Default is "SampleID".
`sample.id.col`	Desired name of the Sample ID column for the final merged `data.frame`. Default is "SampleID".
`subject.id.col`	Desired name of the Subject ID column for the final merged `data.frame`. Default is "SubjectID".
`tmpt.id.col`	Desired name of the Time Point column for the final merged `data.frame`. Default is "Time_point".
`merge.smpl.id`	Desired name of the sample ID column in the file to be merged with. This has no default.

Details

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Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
library("patPRO")
data("PatProOTU",package="patPRO")
data("PatProMap",package="patPRO")
transTestRelAbund <- transposeRelAbund(PatProOTU)
mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
merging.file=transTestRelAbund,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
```

`normalizeAlphaDiv` *Normalize Alpha Diversity Values for Plotting.*

Description

This function normalizes the alpha diversity values of a single patient's time course to the initial time point. The initial time point is used as 100 percent. This allows for plotting of multiple alpha diversity metrics on a single plot, despite differences in value magnitude.

Usage

```
normalizeAlphaDiv(alpha.div.input,
alpha.div.metric,
subject.id.range,
subject.id.col="SubjectID",
tmpt.id.col="Time_point")
```

Arguments

`alpha.div.input`	The `data.frame` from Qiime containing the alpha diversity information for the dataset. This should also include subject ID and time point information.
`alpha.div.metric`	The name(s) of the columns containing the alpha diversity metric information to be used for normalization.

`subject.id.range`	
`subject.id.col`	Name of the subject ID column found in alpha.div.input. Default is "SubjectID".
`tmpt.id.col`	Name of the time point column found in alpha.div.input. Default is "Time_point".

Details

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Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
data("PatProAlphaDiv",package="patPRO")
data("PatProMap",package="patPRO")
mergedMapAlpha <- mergeMapMetaData(map.file=PatProMap,
merging.file=PatProAlphaDiv,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
testNormAlphaDiv <- normalizeAlphaDiv(mergedMapAlpha, c("chao1","shannon"), 1)
```

`patientMean` *Calculate Mean Patient Values.*

Description

This function is used to create a data frame of the mean microbiome values from data frames for the top taxonomic relative abundance, normalized alpha diversity, and bacterial load. The resulting data frame is easy to use in downstream plotting applications. The means are calculated for each sampling time point.

Usage

```
patientMean(x,
sub.range,
subject.id.col="SubjectID",
tmpt.id.col="Time_point",
metric.col="Bacteria",
abundance.val="Abundance")
```

Arguments

`x`	The desired `data.frame` (top taxonomy, alpha diversity, or bacterial load) containing the values with which the means will be calculated.
`sub.range`	The numeric range of subject IDs for which the mean values are to be calcualted.
`subject.id.col`	The Sunject ID column name from data frame x. Default is "SubjectID".
`tmpt.id.col`	The time point ID column name from data frame x. Default is "Time_point".
`metric.col`	The metric ID column name from data frame x. This column includes the taxonomic IDs or alpha diversity metric categories. Default is "Bacteria".
`abundance.val`	The abundance column name from data frame x. This column includes the values which will be used to calcualte means across the categories and time points. Default is "Abundance".

Details

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References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
# Relative Abundance Mean
data("PatProOTU",package="patPRO")
```

```
data("PatProMap",package="patPRO")
transTestRelAbund <- transposeRelAbund(PatProOTU)
mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
  merging.file=transTestRelAbund,
  map.sub.id="SubjectID",
  map.tmpt="Time_point",
  map.smpl.id="SampleID",
  sample.id.col="SampleID")
top5RelAbund <- topRelAbundDataFrame(x=mergedMapTransRA, top.taxa.num=5)
topTaxaMean <- patientMean(x=top5RelAbund,
  sub.range=c(1:5),
  metric.col="Bacteria")
# Alpha Diversity Mean
data("PatProAlphaDiv",package="patPRO")
data("PatProMap",package="patPRO")
mergedMapAlpha <- mergeMapMetaData(map.file=PatProMap,
  merging.file=PatProAlphaDiv,
  map.sub.id="SubjectID",
  map.tmpt="Time_point",
  map.smpl.id="SampleID",
  sample.id.col="SampleID")
testNormAlphaDivForMean <- normalizeAlphaDiv(mergedMapAlpha, c("chao1","shannon"), 1:5)
AlphaDivMean <- patientMean(x=testNormAlphaDivForMean,
  sub.range=c(1:5),
  metric.col="variable",
  abundance.val="value")
# Bacterial Load Mean
data("PatProBacLoad",package="patPRO")
data("PatProMap",package="patPRO")
mergedMapBacLoad <- mergeMapMetaData(map.file=PatProMap,
  merging.file=PatProBacLoad,
  map.sub.id="SubjectID",
  map.tmpt="Time_point",
  map.smpl.id="SampleID",
  sample.id.col="SampleID")
BacMean <- patientMean(x=mergedMapBacLoad,
  sub.range=c(1:5),
  metric.col="",
  abundance.val="Num_Bacteria")
```

`PatProAlphaDiv` *Test Alpha Diversity Data Used as an Example for patPRO.*

Description

This is the test alpha diversity data used as an example for patPRO. The data is from Hannigan et al. 2014. "Culture-independent pilot study of microbiota colonizing open fractures and association with severity, mechanism, location, and complication from presentation to early outpatient follow-up". DOI: 10.1002/jor.22578

Usage

```
data(PatProAlphaDiv)
```

Format

data frame

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

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Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

Source

DOI: 10.1002/jor.22578

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

`PatProBacLoad` *Test Bacterial Load Data Used as an Example for patPRO.*

Description

This is the test bacterial load data used as an example for patPRO. The data is from Hannigan et al. 2014. "Culture-independent pilot study of microbiota colonizing open fractures and association with severity, mechanism, location, and complication from presentation to early outpatient follow-up". DOI: 10.1002/jor.22578

Usage

```
data(PatProBacLoad)
```

Format

data frame

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

An overview of how to use the package, including the most important functions, is included in the supplemental R notebook patPROExampleWorkflow.html.

Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

Source

DOI: 10.1002/jor.22578

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

`PatProMap` *Test Mapping File Data Used as an Example for patPRO.*

Description

This is the test mapping file data used as an example for patPRO. The data is from Hannigan et al. 2014. "Culture-independent pilot study of microbiota colonizing open fractures and association with severity, mechanism, location, and complication from presentation to early outpatient follow-up". DOI: 10.1002/jor.22578

Usage

```
data(PatProMap)
```

Format

data frame

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

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Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

Source

DOI: 10.1002/jor.22578

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

`PatProOTU` *Test Relative Abundance Data Used as an Example for patPRO.*

Description

This is the test relative abundance data used as an example for patPRO. The data is from Hannigan et al. 2014. "Culture-independent pilot study of microbiota colonizing open fractures and association with severity, mechanism, location, and complication from presentation to early outpatient follow-up". DOI: 10.1002/jor.22578

Usage

```
data(PatProOTU)
```

Format

data frame

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
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Author(s)

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Source

DOI: 10.1002/jor.22578

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

`patproPlotThree` *Generate Patient Profile of Three Plots.*

Description

Use this function to generate a patient profile containing three figures. The figures included are the alpha diversity, bacterial load, and top taxa plots over time. This should be used when bacterial load information is available, and the normalized relative abundance plot is not desired.

Usage

```
patproPlotThree(alpha.div.plot,
bac.load.plot,
top.taxa.plot,
patpro.plot.title,
legend.one.h=0.77,
legend.two.h=0.25)
```

Arguments

`alpha.div.plot`	The alpha diversity plot to be used in the patient profile.
`bac.load.plot`	The bacterial load plot to be used in the patient profile.
`patpro.plot.title`	The desired plot title.
`legend.one.h`	Allows the user to manually set the height of the first figure legend (decimal digit between 0 and 1). Very important if adjusting legend text size. Defalut is 0.77.
`legend.two.h`	Allows the user to manually set the height of the second figure legend (decimal digit between 0 and 1). Very important if adjusting legend text size. Defalut is 0.25.
`top.taxa.plot`	The relative abundance plot to be used in the patient profile.

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

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References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
# Plot individual patient
data("PatProAlphaDiv",package="patPRO")
data("PatProMap",package="patPRO")
data("PatProOTU",package="patPRO")
data("PatProBacLoad",package="patPRO")
# Alpha Diversity
mergedMapAlpha <- mergeMapMetaData(map.file=PatProMap,
  merging.file=PatProAlphaDiv,
  map.sub.id="SubjectID",
  map.tmpt="Time_point",
```

```
    map.smpl.id="SampleID",
    sample.id.col="SampleID")
  testNormAlphaDiv <- normalizeAlphaDiv(mergedMapAlpha, c("chao1","shannon"), 1)
  alphaDivPlot <- plotNormalizedAlphaDiv(testNormAlphaDiv,
    c("chao1","shannon"),
    plot.title="Subject One Diversity",
    color.brewer.set="Set2",
    legend.text.size = 12)
  # Bacterial Load
  mergedMapBacLoad <- mergeMapMetaData(map.file=PatProMap,
    merging.file=PatProBacLoad,
    map.sub.id="SubjectID",
    map.tmpt="Time_point",
    map.smpl.id="SampleID",
    sample.id.col="SampleID")
  bacLoad <- plotBacterialLoad(mergedMapBacLoad,
    1,
    bac.load.col="Num_Bacteria",
    plot.title="Subject One Bacterial Load")
  # Taxa Relative Abundance
  transTestRelAbund <- transposeRelAbund(PatProOTU)
  mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
    merging.file=transTestRelAbund,
    map.sub.id="SubjectID",
    map.tmpt="Time_point",
    map.smpl.id="SampleID",
    sample.id.col="SampleID")
  top5RelAbund <- topRelAbundDataFrame(x=mergedMapTransRA, top.taxa.num=5)
  topTaxa <- plotTopTaxa(top5RelAbund,
    1,
    plot.title="Subject One Taxonomy",
    color.brewer.set="Set2",
    mark.events=TRUE,
    mark.times=c(2,6),
    mark.text="Surgery",
    legend.text.size=8)
  # Plot three
  patproPlotThree(alphaDivPlot, bacLoad, topTaxa, "Subject One Profile")
```

`patproPlotTwo` *Generate Patient Profile of Two Plots.*

Description

Use this function to generate a patient profile containing two figures. The figures included are the alpha diversity and top taxa plots over time. This should be used when there is no bacterial load data, or when the normalized top taxa plot is used.

Usage

```
patproPlotTwo(alpha.div.plot,
norm.top.taxa.plot,
patpro.plot.title,
legend.one.h=0.70,
legend.two.h=0.30)
```

Arguments

`alpha.div.plot`	The alpha diversity plot to be used in the patient profile.
`norm.top.taxa.plot`	The normalized or non-normalized taxonomic relative abundance plot to be included in the patient profile.
`patpro.plot.title`	The desired plot title.
`legend.one.h`	Allows the user to manually set the height of the first figure legend (decimal digit between 0 and 1). Very important if adjusting legend text size. Defalut is 0.70.
`legend.two.h`	Allows the user to manually set the height of the second figure legend (decimal digit between 0 and 1). Very important if adjusting legend text size. Defalut is 0.30.

Details

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References

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Examples

```
# Plot individual patient
```

```
data("PatProAlphaDiv",package="patPRO")
data("PatProMap",package="patPRO")
data("PatProOTU",package="patPRO")
data("PatProBacLoad",package="patPRO")
# Alpha Diversity
mergedMapAlpha <- mergeMapMetaData(map.file=PatProMap,
merging.file=PatProAlphaDiv,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
testNormAlphaDiv <- normalizeAlphaDiv(mergedMapAlpha, c("chao1","shannon"), 1)
alphaDivPlot <- plotNormalizedAlphaDiv(testNormAlphaDiv,
c("chao1","shannon"),
plot.title="Subject One Diversity",
color.brewer.set="Set2",
legend.text.size = 12)
# Absolute Abundance Estimation
transTestRelAbund <- transposeRelAbund(PatProOTU)
mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
merging.file=transTestRelAbund,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
top5RelAbund <- topRelAbundDataFrame(x=mergedMapTransRA, top.taxa.num=5)
mergedMapBacLoad <- mergeMapMetaData(map.file=PatProMap,
merging.file=PatProBacLoad,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
absAbundOutDf <- topAbsAbundDataFrame(top5RelAbund, mergedMapBacLoad, bac.load.id="Num_Bacteria")
normTopTaxa <- topAbsAbundPlot(absAbundOutDf,
1,
bac.load.col="Num_Bacteria",
plot.title="Subject One Normalized Taxonomy",
color.brewer.set="Set2",
mark.events=TRUE,
mark.times=c(2,6),
mark.text="Surgery",
legend.text.size = 8)
patproPlotTwo(alphaDivPlot, normTopTaxa, "Subject One Profile")
```

`plotBacterialLoad` *Plot Supplemental Bacterial Load Information.*

Description

Plot the supplemental bacterial load data, which would have been obtained by qPCR for the 16S rRNA gene. Because this data is straightforward relative to the other data types, it will not require much formatting before plotting.

Usage

```
plotBacterialLoad(input.bac.load,
subject.id,
subject.id.col="SubjectID",
bac.load.col="bac_load",
tmpt.id.col="Time_point",
y.lab="Bacterial Load",
x.lab="Time Point",
plot.title,
mean.mark=FALSE)
```

Arguments

`input.bac.load`	The `data.frame` containing the bacterial load information, as well as the subject IDs and time points associated with those load data points.
`subject.id`	The subject identification that will be plotted. If this value is specified as blank (ie ""), then the function will assume the input data frame is of mean values, and will not attempt to select a specific subject to plot.
`subject.id.col`	Name of the subject ID column. Default is "SubjectID".
`bac.load.col`	Name of the bacterial load value column. Default is "bac_load".
`tmpt.id.col`	Name of the time point column. Default is "Time_point".
`y.lab`	Name of the y axis label to be used in the plot. Default is "Absolute Abundance".
`x.lab`	Name of the x axis label to be used in the plot. Default is "Time Point".
`plot.title`	The desired plot title.
`mean.mark`	Allows the user to define whether this is used to plot mean values (including standard error; set to TRUE) or if this is for a single subject. Default is FALSE.

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References

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Examples

```
data("PatProBacLoad",package="patPRO")
data("PatProMap",package="patPRO")
mergedMapBacLoad <- mergeMapMetaData(map.file=PatProMap,
merging.file=PatProBacLoad,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
# Plot individual subject
bacLoad <- plotBacterialLoad(mergedMapBacLoad,
1,
bac.load.col="Num_Bacteria",
plot.title="Subject One Bacterial Load")
# Plot subject means
BacMean <- patientMean(x=mergedMapBacLoad,
sub.range=c(1:5),
metric.col="",
abundance.val="Num_Bacteria")
bacLoadMean <- plotBacterialLoad(BacMean,
"",
bac.load.col="Num_Bacteria",
plot.title="Mean Bacterial Load For Subjects 1-5",
mean.mark=TRUE)
```

`plotNormalizedAlphaDiv` *Plot Normalized Alpha Diversity.*

Description

Plot the normalized alpha diversity data, over time, of the desired patient or patient group means. The patient patient.mean function must be used to calculate and format the normalized data for this plotting function. If only a single patient plot is desired, please use the patient mean function with only a single patient. This subroutine takes in the data frame output from normalize.alpha.div.

Usage

```
plotNormalizedAlphaDiv(input.df,
alpha.div.metrics,
tmpt.id.col="Time_point",
y.lab="Normalized Alpha Diversity Value",
x.lab="Time Point",
```

```
plot.title,
color.brewer.set="",
color.manual.set="",
mean.mark=FALSE,
legend.text.size = 7)
```

Arguments

`input.df`	The `data.frame` output from the diversity normalization subroutine normalize.alpha.div containing the alpha diversity information for the dataset. This will be the data frame used for plotting.
`alpha.div.metrics`	The name(s) of the alpha diversity metrics to be plotted.
`tmpt.id.col`	Name of the time point column found in alpha.div.input. Default is "Time_point".
`y.lab`	Name of the y axis label to be used in the plot. Default is "Normalized Alpha Diversity Value".
`x.lab`	Name of the x axis label to be used in the plot. Default is "Time Point".
`plot.title`	The desired plot title.
`color.brewer.set`	Name of the color brewer palet to use for plot coloring. Default value uses default colors.
`color.manual.set`	Name of the manually specified color palet to use for plot coloring. Default value uses default colors.
`mean.mark`	Allows the user to define whether this is used to plot mean values (including standard error; set to TRUE) or if this is for a single subject. Default is FALSE.
`legend.text.size`	Allows the user to manually set the figure legend text size digit. Default is size 7.

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References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
# Plot individual patient
data("PatProAlphaDiv",package="patPRO")
data("PatProMap",package="patPRO")
mergedMapAlpha <- mergeMapMetaData(map.file=PatProMap,
merging.file=PatProAlphaDiv,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
testNormAlphaDiv <- normalizeAlphaDiv(mergedMapAlpha, c("chao1","shannon"), 1)
alphaDivPlot <- plotNormalizedAlphaDiv(testNormAlphaDiv,
c("chao1","shannon"),
plot.title="Subject One Diversity",
color.brewer.set="Set2",
legend.text.size = 12)
# Plot patient average
data("PatProAlphaDiv",package="patPRO")
data("PatProMap",package="patPRO")
mergedMapAlpha <- mergeMapMetaData(map.file=PatProMap,
  merging.file=PatProAlphaDiv,
  map.sub.id="SubjectID",
  map.tmpt="Time_point",
  map.smpl.id="SampleID",
  sample.id.col="SampleID")
testNormAlphaDivForMean <- normalizeAlphaDiv(mergedMapAlpha, c("chao1","shannon"), 1:5)
AlphaDivMean <- patientMean(x=testNormAlphaDivForMean,
  sub.range=c(1:5),
  metric.col="variable",
  abundance.val="value")
alphaDivPlotMean <- plotNormalizedAlphaDiv(AlphaDivMean,
c("chao1","shannon"),
plot.title="Mean Diversity For Subjects 1-5",
color.brewer.set="Set2",
mean.mark=TRUE,
legend.text.size = 12)
```

`plotTopTaxa` *Plot a Specific Patient Relative Abundance of Top Taxa.*

Description

Uses the results from the top.rel.abund.data.frame function for graphing relative abundance of the top taxonomy.

Usage

```
plotTopTaxa(top.taxa.data.frame,
pat.id,
subject.id.col="SubjectID",
tmpt.id.col="Time_point",
y.lab="Percent Relative Abundance",
x.lab="Time Point", plot.title,
mark.events=FALSE, mark.times,
mark.text="",
color.brewer.set="",
color.manual.set="",
legend.text.size = 7)
```

Arguments

`top.taxa.data.frame`	The `data.frame` from the top.rel.abund.data.frame function which will be used for plotting the top taxa.
`pat.id`	The patient identifier to specify the case which should be visualized.
`subject.id.col`	Name of the subject ID column found in x. Default is "SubjectID".
`tmpt.id.col`	Name of the time point column found in x. Default is "Time_point".
`y.lab`	Name of the y axis label to be used in the plot. Default is "Percent Relative Abundance".
`x.lab`	Name of the x axis label to be used in the plot. Default is "Time Point".
`plot.title`	The desired plot title.
`mark.events`	Specify whether arrows will be used to specify specific time events. Set as TRUE for using arrows. Default is FALSE.
`mark.times`	The time points to be marked with arrows when mark.events=TRUE. These numbers need to be set as a vector.
`mark.text`	The text to be used to annotate the arrow markers when mark.events=TRUE.
`color.brewer.set`	Name of the color brewer palet to use for plot coloring. Default value uses default colors.
`color.manual.set`	Name of the manually specified color palet to use for plot coloring. Default value uses default colors.
`legend.text.size`	Allows the user to manually set the figure legend text size digit. Default is size 7.

Details

Package:	patPRO
Type:	Package
Version:	1.0.0

Date:	2015-09-18
License:	GPLv3

An overview of how to use the package, including the most important functions, is included in the supplemental R notebook patPROExampleWorkflow.html.

Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
data("PatProOTU",package="patPRO")
data("PatProMap",package="patPRO")
transTestRelAbund <- transposeRelAbund(PatProOTU)
mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
merging.file=transTestRelAbund,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
top5RelAbund <- topRelAbundDataFrame(x=mergedMapTransRA, top.taxa.num=5)
topTaxa <- plotTopTaxa(top5RelAbund,
1,
plot.title="Subject One Taxonomy",
color.brewer.set="Set2",
mark.events=TRUE,
mark.times=c(2,6),
mark.text="Surgery",
legend.text.size=8)
```

`plotTopTaxaMean` *Plot the Mean Relative Abundance of Top Taxa.*

Description

Uses the results from the top.rel.abund.data.frame and the patient.mean function for graphing relative abundance of the top taxonomy. This is used seperate from the plotTopTaxaMean function because it uses mean values.

Usage

```
plotTopTaxaMean(top.taxa.data.frame,
tmpt.id.col="Time_point",
y.lab="Percent Relative Abundance",
x.lab="Time Point", plot.title,
mark.events=FALSE,
mark.times,
mark.text="",
color.brewer.set="",
color.manual.set="",
legend.text.size = 7)
```

Arguments

`top.taxa.data.frame`	The `data.frame` from the top.rel.abund.data.frame function which will be used for plotting the top taxa.
`tmpt.id.col`	Name of the time point column found in x. Default is "Time_point".
`y.lab`	Name of the y axis label to be used in the plot. Default is "Percent Relative Abundance".
`x.lab`	Name of the x axis label to be used in the plot. Default is "Time Point".
`plot.title`	The desired plot title.
`mark.events`	Specify whether arrows will be used to specify specific time events. Set as TRUE for using arrows. Default is FALSE.
`mark.times`	The time points to be marked with arrows when mark.events=TRUE. These numbers need to be set as a vector.
`mark.text`	The text to be used to annotate the arrow markers when mark.events=TRUE.
`color.brewer.set`	Name of the color brewer palet to use for plot coloring. Default value uses default colors.
`color.manual.set`	Name of the manually specified color palet to use for plot coloring. Default value uses default colors.
`legend.text.size`	Allows the user to manually set the figure legend text size digit. Default is size 7.

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

An overview of how to use the package, including the most important functions, is included in the supplemental R notebook patPROExampleWorkflow.html.

Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
data("PatProOTU",package="patPRO")
data("PatProMap",package="patPRO")
transTestRelAbund <- transposeRelAbund(PatProOTU)
mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
  merging.file=transTestRelAbund,
  map.sub.id="SubjectID",
  map.tmpt="Time_point",
  map.smpl.id="SampleID",
  sample.id.col="SampleID")
top5RelAbund <- topRelAbundDataFrame(x=mergedMapTransRA, top.taxa.num=5)
topTaxaMean <- patientMean(x=top5RelAbund, sub.range=c(1:5), metric.col="Bacteria")
topTaxaMeanPlot <- plotTopTaxaMean(topTaxaMean,
plot.title="Mean Taxonomy For Subjects 1-5",
color.brewer.set="Set2",
legend.text.size = 8)
```

`topAbsAbundDataFrame` *Format and Normalize Top Taxa and Bac Load for Plotting.*

Description

Calcualte the top taxa relative abundance normalized to the overall bacterial load. Prepare the data frame for graphing.

Usage

```
topAbsAbundDataFrame(rel.abund,
bac.load,
bac.load.id="bac_load",
abund.id.col="Abundance",
subject.id.col="SubjectID",
tmpt.id.col="Time_point",
bacteria.id.col="Bacteria")
```

Arguments

`rel.abund`	The transposed relative abundance `data.frame` to be used for graphing of microbial relative abundances.
`bac.load`	The `data.frame` containing the bacterial load information, as well as the subject IDs and time points associated with those load data points.
`bac.load.id`	Name of the bacterial load value column. Default is "bac_load".
`abund.id.col`	Name of the column containing the relative abundance values for the top taxa relative abundance. Default is "Abundance".
`subject.id.col`	Name of the subject ID column. Default is "SubjectID".
`tmpt.id.col`	Name of the time point column. Default is "Time_point".
`bacteria.id.col`	Name of the column to contain the bacterial load values. Default is "Bacteria".

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

An overview of how to use the package, including the most important functions, is included in the supplemental R notebook patPROExampleWorkflow.html.

Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
data("PatProOTU",package="patPRO")
data("PatProMap",package="patPRO")
data("PatProBacLoad",package="patPRO")
transTestRelAbund <- transposeRelAbund(PatProOTU)
mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
merging.file=transTestRelAbund,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
```

```
top5RelAbund <- topRelAbundDataFrame(x=mergedMapTransRA, top.taxa.num=5)
mergedMapBacLoad <- mergeMapMetaData(map.file=PatProMap,
merging.file=PatProBacLoad,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
absAbundOutDf <- topAbsAbundDataFrame(top5RelAbund, mergedMapBacLoad, bac.load.id="Num_Bacteria")
```

`topAbsAbundPlot` *Plot Top Taxa Abundance Normalized to Bacterial Load.*

Description

Uses the results from the top.abs.abund.data.frame function for graphing relative abundance of the top taxonomy normalized under the absolute bacterial load calculated from qPCR results.

Usage

```
topAbsAbundPlot(rel.abund.df,
patient.id,
subject.id.col="SubjectID",
tmpt.id.col="Time_point",
abs.abund.id.col="absolute_abund",
bac.id.col="Bacteria",
bac.load.col="bac_load",
y.lab="Relative Abundance of Bacterial Load",
x.lab="Time Point",
plot.title,
mark.events=FALSE,
mark.times,
mark.text="",
color.brewer.set="",
color.manual.set="",
legend.text.size = 7)
```

Arguments

`rel.abund.df`	The `data.frame` from the top.abs.abund.data.frame function which will be used for plotting the top taxa.
`patient.id`	The patient identifier to specify the case which should be visualized.
`subject.id.col`	Name of the subject ID column. Default is "SubjectID".
`tmpt.id.col`	Name of the time point column. Default is "Time_point".
`abs.abund.id.col`	Name of the column containing the normalized relative abundance information. Default is "absolute_abund".

`bac.id.col`	Name of the column containing the taxonomic identifiers for the dataset. Default is "Bacteria".
`bac.load.col`	Name of the column containing the bacterial load information. Default is "bac_load".
`y.lab`	Name of the y axis label to be used in the plot. Default is "Relative Abundance of Absolute Abundance".
`x.lab`	Name of the x axis label to be used in the plot. Default is "Time Point".
`plot.title`	The desired plot title.
`mark.events`	Specify whether arrows will be used to specify specific time events. Set as TRUE for using arrows. Default is FALSE.
`mark.times`	The time points to be marked with arrows when mark.events=TRUE. These numbers need to be set as a vector.
`mark.text`	The text to be used to annotate the arrow markers when mark.events=TRUE.
`color.brewer.set`	Name of the color brewer palet to use for plot coloring. Default value uses default colors.
`color.manual.set`	Name of the manually specified color palet to use for plot coloring. Default value uses default colors.
`legend.text.size`	Allows the user to manually set the figure legend text size digit. Default is size 7.

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

An overview of how to use the package, including the most important functions, is included in the supplemental R notebook patPROExampleWorkflow.html.

Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
data("PatProOTU",package="patPRO")
data("PatProMap",package="patPRO")
data("PatProBacLoad",package="patPRO")
transTestRelAbund <- transposeRelAbund(PatProOTU)
mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
merging.file=transTestRelAbund,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
top5RelAbund <- topRelAbundDataFrame(x=mergedMapTransRA, top.taxa.num=5)
mergedMapBacLoad <- mergeMapMetaData(map.file=PatProMap,
merging.file=PatProBacLoad,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
absAbundOutDf <- topAbsAbundDataFrame(top5RelAbund, mergedMapBacLoad, bac.load.id="Num_Bacteria")
normTopTaxa <- topAbsAbundPlot(absAbundOutDf,
1,
bac.load.col="Num_Bacteria",
plot.title="Subject One Normalized Taxonomy",
color.brewer.set="Set2",
mark.events=TRUE,
mark.times=c(2,6),
mark.text="Surgery",
legend.text.size = 8)
```

`topRelAbundDataFrame` *Format Top Taxa Data Frame for Graphing.*

Description

Prepare the data frame for graphing of the relative abundances of the defined top taxa using the transposed output (originally from Qiime) using 'transposeRelAbund'.

Usage

```
topRelAbundDataFrame(x,
top.taxa.num,
subject.id.col="SubjectID",
sample.id.col="SampleID",
tmpt.id.col="Time_point")
```

Arguments

`x`	The transposed relative abundance `data.frame` to be used for graphing of microbial relative abundances.

`top.taxa.num`	The number of top taxa requested.
`subject.id.col`	Name of the subject ID column found in x. Default is "SubjectID".
`sample.id.col`	Name of the sample ID column found in x. Default is "SampleID".
`tmpt.id.col`	Name of the time point column found in x. Default is "Time_point".

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

An overview of how to use the package, including the most important functions, is included in the supplemental R notebook patPROExampleWorkflow.html.

Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
data("PatProOTU",package="patPRO")
data("PatProMap",package="patPRO")
transTestRelAbund <- transposeRelAbund(PatProOTU)
mergedMapTransRA <- mergeMapMetaData(map.file=PatProMap,
merging.file=transTestRelAbund,
map.sub.id="SubjectID",
map.tmpt="Time_point",
map.smpl.id="SampleID",
sample.id.col="SampleID")
top5_rel_abund <- topRelAbundDataFrame(x=mergedMapTransRA, top.taxa.num=5)
```

`transposeRelAbund` *Transpose a Data Frame.*

Description

This function will transpose a data frame, with the result maintained as a data frame (unlike other functions which work with matrices). Although this was written with relative abundance tables in mind, it may be applied to other data frame types.

Usage

```
transposeRelAbund(x,
sample.id.col="SampleID")
```

Arguments

`x`	The relative abundance `data.frame` (or other type of `data.frame`) to be transposed.
`sample.id.col`	The Sample ID column name from data frame x. Default is "SampleID".

Details

Package:	patPRO
Type:	Package
Version:	1.0.0
Date:	2015-09-18
License:	GPLv3

An overview of how to use the package, including the most important functions, is included in the supplemental R notebook patPROExampleWorkflow.html.

Author(s)

Geoffrey Hannigan <ghanni@upenn.edu>, Loesche MA, Hodkinson BP, Mehta S, Elizabeth Grice <egrice@upenn.edu>

References

patPRO: An R package for the visualization of longitudinal microbiome data. Hannigan GD, Loesche MA, Hodkinson BP, Mehta S, Grice EA.

Examples

```
data("PatProOTU",package="patPRO")
transTestRelAbund <- transposeRelAbund(PatProOTU)
```

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