

Package ‘ebimetagenomics’

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Title EBI Metagenomics Portal

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Description Functions for querying the EBI Metagenomics Portal (<https://www.ebi.ac.uk/metagenomics/>). The current main focus is on taxa abundance data, but the intention is that this package should evolve into a general purpose package for working with EBI Metagenomics data using R.

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convertOtuTad	<i>Converts an OTU count data frame to a TAD data frame</i>
---------------	---

Description

This function takes as input a data frame representing OTU counts, such as returned by `getRunOtu`, and tabulates it in the form of a taxa abundance distribution (TAD).

Usage

```
convertOtuTad(otu)
```

Arguments

otu	An OTU data frame.
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Value

An R data frame representing a taxa abundance distribution (TAD). The first column is species abundance and the second column represents the number of species with that level of abundance in the sample.

See Also

[getSampleOtu](#), [getRunOtu](#), [mergeOtu](#)

Examples

```
ps=getProjectSummary("SRP047083")
samp=projectSamples(ps)
runs=runsBySample(ps,samp[2])
otu=getRunOtu(ps,runs[1])
tad=convertOtuTad(otu)
head(tad)
```

getProjectsList	<i>Download the EMG projects list into a data frame</i>
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Description

This downloads an EMG projects list (detailed info) into an R data frame for subsequent analysis.

Usage

```
getProjectsList()
```

Value

An R data frame containing a list of all public EMG projects, one row per project.

See Also

[getProjectSummary](#), [projectSamples](#)

Examples

```
p1 = getProjectsList()
str(p1)

# Find big projects
biggies = p1$Study.ID[p1$Number.Of.Samples >= 100]
ps = getProjectSummary(biggies[3])

# Find some 16S projects
p1$Study.ID[agrep("16S",p1$Project.Name)]
```

getProjectSummary	<i>Download an EMG project summary into a data frame</i>
-------------------	--

Description

This downloads an EMG project summary file into an R data frame for subsequent analysis.

Usage

```
getProjectSummary(projectID)
```

Arguments

projectID A character string representing an EMG project ID (eg. SRP047083).

Value

An R data frame containing a list of all samples and runs associated with the project, one row per run. The projectID is associated with the data frame via the attribute `project.id`.

See Also

[getProjectsList](#), [projectSamples](#), [projectRuns](#), [runsBySample](#)

Examples

```
ps=getProjectSummary("SRP047083")
# Tabulate number of runs per by sample
table(ps$Sample.ID)
```

getRunOtu

Downloads OTU count data associated with a EMG run

Description

This function downloads an OTU count data file associated with a particular run from the EMG portal. The OTU data is returned as a data frame.

Usage

```
getRunOtu(summ, runID, verb=FALSE, plot.preston=FALSE)
```

Arguments

summ	An EMG project summary file, as returned by <code>getProjectSummary</code> .
runID	A string representing a valid EMG run ID within the project summ.
verb	If true, outputs runID to console.
plot.preston	If true, produces a Preston plot for the taxa abundance distribution of the run.

Value

An R data frame containing OTU count data. The first column is the OTU ID, the second is the count, and the third contains a taxonomic classification.

See Also

[getSampleOtu](#), [mergeOtu](#), [projectRuns](#)

Examples

```
ps=getProjectSummary("SRP047083")
samp=projectSamples(ps)
runs=runsBySample(ps,samp[2])
getRunOtu(ps,runs[1])
```

getSampleOtu

Downloads and merges all of the OTU count data associated with a EMG sample

Description

This function downloads the OTU count data files from all runs associated with a particular sample from the EMG portal, and merges it using `mergeOtu`. The merged OTU data is returned as a data frame.

Usage

```
getSampleOtu(summ, sampleID, verb=TRUE, plot.preston=FALSE)
```

Arguments

summ	An EMG project summary file, as returned by <code>getProjectSummary</code> .
sampleID	A string representing a valid EMG sample ID within the project summ.
verb	If true, outputs each runID to console.
plot.preston	If true, produces a Preston plot for the taxa abundance distribution of each run as it is downloaded.

Value

An R data frame containing OTU count data. The first column is the OTU ID, the second is the count, and the third contains a taxonomic classification.

See Also

[getRunOtu](#), [mergeOtu](#), [projectSamples](#)

Examples

```
ps=getProjectSummary("SRP047083")
samp=projectSamples(ps)
runs=runsBySample(ps, samp[2])
getRunOtu(ps, runs[1])
```

mergeOtu	<i>Merges two OTU count data data frames to produce a combined OTU count data data frame</i>
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Description

This function merges two or more OTU count data data frames, such as returned by `getRunOtu`. The merged OTU data is returned as a data frame. The ordering of the two data frames to be merged should not be significant. The operation of merging should also be associative.

Usage

```
mergeOtu(...)
```

Arguments

...	A sequence of OTU data frames to be merged.
-----	---

Value

An R data frame containing OTU count data. The first column is the OTU ID, the second is the count, and the third contains a taxonomic classification.

See Also

[getSampleOtu](#), [getRunOtu](#), [projectRuns](#)

Examples

```
ps=getProjectSummary("SRP047083")
samp=projectSamples(ps)
runs=runsBySample(ps,samp[2])

# merge two:
otu1=getRunOtu(ps,runs[1])
otu2=getRunOtu(ps,runs[2])
mergeOtu(otu1,otu2)

# merge many:
otuList=lapply(as.list(runs[1:10]),function(rid){getRunOtu(ps,rid)})
Reduce(mergeOtu,otuList)
```

plotOtu

Plots OTU count data

Description

This function takes as input a data frame representing OTU counts, such as returned by `getRunOtu`, plots it on the graphics device.

Usage

```
plotOtu(otu)
```

Arguments

otu An OTU data frame.

Value

The function returns silently, and is called purely for its side-effect of rendering plots on the graphics device.

See Also

[getSampleOtu](#), [getRunOtu](#), [convertOtuTad](#)

Examples

```
ps=getProjectSummary("SRP047083")
samp=projectSamples(ps)
runs=runsBySample(ps,samp[2])
otu=getRunOtu(ps,runs[1])
tad=plotOtu(otu)
```

projectRuns	<i>Find runs associated with an EMG project</i>
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Description

This function queries an already-downloaded project summary file for vector of EMG run IDs associated with the project.

Usage

```
projectRuns(summ)
```

Arguments

summ	An EMG project summary file, as returned by <code>getProjectSummary</code> .
------	--

Value

An R vector containing a list of strings representing EMG run IDs.

See Also

[getProjectSummary](#), [projectSamples](#), [runsBySample](#)

Examples

```
ps=getProjectSummary("SRP047083")
projectRuns(ps)
```

projectSamples	<i>Find samples associated with an EMG project</i>
----------------	--

Description

This function queries an already-downloaded project summary file for vector of EMG sample IDs associated with the project.

Usage

```
projectSamples(summ)
```

Arguments

summ	An EMG project summary file, as returned by <code>getProjectSummary</code> .
------	--

Value

An R vector containing a list of strings representing EMG sample IDs.

See Also

[getProjectSummary](#), [projectRuns](#), [runsBySample](#)

Examples

```
ps=getProjectSummary("SRP047083")
projectSamples(ps)
```

runsBySample	<i>Find runs associated with a particular sample ID within an EMG project</i>
--------------	---

Description

This function queries an already-downloaded project summary file for vector of EMG run IDs associated with a particular sample ID within the project.

Usage

```
runsBySample(summ, sampleID)
```

Arguments

summ	An EMG project summary file, as returned by <code>getProjectSummary</code> .
sampleID	A string representing a valid EMG sample ID within the project summ.

Value

An R vector containing a list of strings representing EMG run IDs.

See Also

[getProjectSummary](#), [projectSamples](#), [projectRuns](#)

Examples

```
ps=getProjectSummary("SRP047083")  
samp=projectSamples(ps)  
runsBySample(ps,samp[2])
```

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