

Package ‘melbstreambiota’

May 30, 2017

Type Package

Title Habitat Suitability Models for Stream Biota and Macroinvertebrate Indices For The Melbourne Region

Version 0.1.0

Description Outputs of habitat suitability models (aka species distribution models) of 59 families of stream macroinvertebrates, 23 species of fish, and female and total platypus in the Melbourne (SE Australia) region. Predict fish species, platypus, and macroinvertebrate family occurrence and macroinvertebrate indices (LUMaR, SIGNAL2, number of sensitive families) for any reach in the region. Calculate the indices based on imported data and compare to predicted values. Diagnostic tools for interpreting results.

Depends R (>= 3.1.0)

Imports lubridate, gbm, RColorBrewer, classInt, rgdal, sp, vegan, dplyr, readxl, betareg, graphics, stats, utils

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.0.0

Suggests knitr, rmarkdown

VignetteBuilder knitr

R topics documented:

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bray.2halves	<i>Bray-Curtis similarity of two concatenated vectors</i>
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Description

A function to calculate Bray-Curtis dissimilarity index of two vectors that can be used in apply to return a vector of BCs for each row (used to calculate simOE in oestats)

Usage

```
bray.2halves(x)
```

Arguments

x a vector composed of the two vectors concatenated together.

Value

Bray-Curtis similarity of the two concatenated vectors

See Also

[vegdist](#)

Examples

```
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
                                                    package="melbstreambiota", mustWork = TRUE),
                                                    sheet = 3))
#Bray-Curtis similarity of first 2 sampprs
ab <- unlist(c(bugData[1,-1],bugData[2,-1]))
bray.2halves(ab)
```

bugfams	<i>"bestModelsBugfams" SIGNAL and other index grades for 174 macroinvertebrate families</i>
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Description

A data frame listing macroinvertebrate families and their grades for various SIGNAL variants and Rheophily index

Usage

bugfams

Format

a data frame of 174 rows and 9 columns

fam bugcode, consistent with EPA Victoria and AUSRIVAS conventions

family family name

SIGNAL2 SIGNAL grade from Chessman 2003

SIGNALWoV2001

SIGNALWoV2003

SIGNALWesPt2003

SIGNALYarra2003

Rheophily index from Bond et al 2012

Comment

note

bugModPred1	<i>Predict occurrence of a macroinvertebrate family in a set of sample-pairs</i>
-------------	--

Description

Predict occurrence of a macroinvertebrate family in a set of sample-pairs

Usage

bugModPred1(bugcode, sampprPreds)

Arguments

bugcode a 4-character code representing a macroinvertebrate family: one of the 59 `taxon.classes$fams`

sampprPreds a data.frame of sample-pair codes (samppr) each with associated environmental predictors.

Details

The `sampprPreds` table must contain the 10 predictor variables used in the models: `nspring`, `nriff`, `processN`, `AttImp_L9`, `AttForest_L35W1000`, `CatchmentArea_km2_InclDams`, `meanAnnQ_mm`, `mnAnnAirTm_deg`, `CatIgneous`, and `SRI_48mth_weighted`. The function `collateBugSampr` can be used to compile such a table

Value

A list of two vectors with length = number of rows in `sampprPred`, with each row corresponding to the equivalent row in `sampprPred`.

pred1 predicted probabilities of occurrence under conditions specified in `sampprPred`

pred1NHI predicted probabilities of occurrence under no human impact (`AttImp_L9` set to zero, `AttForest_L35W1000` set to 1)

See Also

[collateBugSampr](#), [taxon.classes](#)

Examples

```
qt25MWstreamsCurrent <- bugModPred1("QT25",melbstreambiota::mwstreams)
plotMWstreamsByVar(qt25MWstreamsCurrent$pred1,
  style = "fixed", fixedBreaks = seq(0,1,0.2),
  varName =
  paste(melbstreambiota::taxon.classes$family[melbstreambiota::taxon.classes$fam == "QT25"],
    "prob of occurrence"), legend.cex = 0.75)
```

bugModPred59

Compile predictions of occurrence for all 59 macroinvertebrate families and resulting indices in a set of sample-pairs

Description

Compile predictions of occurrence for all 59 macroinvertebrate families and resulting indices in a set of sample-pairs

Usage

```
bugModPred59(sampprPreds)
```

Arguments

`sampprPreds` a data.frame of sample-pair codes (`samppr`) each with associated environmental predictors. If there is no field called `samppr`, then the field `subc` if used.

Details

The `samprPreds` table must contain the 10 predictor variables used in the models: `nspring`, `nriff`, `processN`, `AttImp_L9`, `AttForest_L35W1000`, `CatchmentArea_km2_InclDams`, `meanAnnQ_mm`, `mnAnnAirTm_deg`, `CatIgneous`, and `SRI_48mth_weighted`. The function `collateBugSampr` can be used to compile such a table. Use `bugModPred1` to make equivalent predictions for a single family. Note that the LUMaR and number of sensitive families produced by this function are PREDICTED values given the environmental variables supplied in `samprPreds`. These values are likely to differ from observed values that can be calculated using the `lumar` function from your own appropriately processed macroinvertebrate data (see the `melbstreambiota` vignette for instructions). to the `obs.table` argument in the `lumar` function.

Value

A list containing: two dataframes with number of rows = that of `samprPreds`, (each row corresponding to the equivalent row in `samprPred`) and 59 columns, corresponding to the 59 families listed in `taxon.classes`

samprPredsLumar data frame with 4 columns, `sampr`, `LUMaR`, `SIGNAL2`, and number of sensitive families (`nSensFams`) resulting from the predicted probabilities of occurrence. Number of rows = that of `samprPred`, (each row corresponding to the equivalent row in `samprPred`)

pred59 data frame containing predicted probabilities of occurrence under conditions specified in `samprPred`, with number of rows = that of `samprPred`, (each row corresponding to the equivalent row in `samprPred`) and 59 columns, corresponding to the 59 families listed in `taxon.classes`

See Also

[collateBugSampr](#), [bugModPred1](#), [taxon.classes](#)

Examples

```
mwstreamsCurrent <- bugModPred59(melbstreambiota::mwstreams)
plotMWstreamsByVar(mwstreamsCurrent$samprPredsLumar$lumar, nbreaks = 6,
  style = "fixed", fixedBreaks = c(-1,-0.25,0,0.25,0.5,0.75,1),
  varName = "LUMaR", legend.cex = 0.75)
```

bugModPredSIGNAL

Predict SIGNAL and SIGNAL2 scores for a set of sample-pairs

Description

Predict SIGNAL and SIGNAL2 scores for a set of sample-pairs

Usage

```
bugModPredSIGNAL(samprPreds)
```

Arguments

`samprPreds` a data.frame of sample-pair codes (`sampr`) each with associated environmental predictors. If there is no field called `sampr`, then the field `subc` if used.

Details

The `sampprPreds` table must contain the 10 predictor variables used in the macroinvertebrate models: `nspring`, `nriff`, `processN`, `AttImp_L9`, `AttForest_L35W1000`, `CatchmentArea_km2_InclDams`, `meanAnnQ_mm`, `mnAnnAirTm_deg`, `CatIgneous`, and `SRI_48mth_weighted`. The function `collateBugSamppr` can be used to compile such a table. The model uses two boosted regression trees that were developed from the observed SIGNAL and SIGNAL2 scores in the same 1724 samples used to calculate the 59 macroinvertebrate family models. SIGNAL scores are calculated from the full set of collected taxa not just the 59 modelled families. The predicted SIGNAL values are likely to differ from observed values, which can be calculated from supplied macroinvertebrate data using the `calcSIGNAL` function..

Value

A data frame with 5 columns, `samppr`, `SIGNAL` (under 2006 conditions), `SIGNALnhi` (under no human impact), `SIGNAL2` (under 2006 conditions), and `SIGNAL2nhi` (under no human impact) Number of rows = that of `sampprPred`, (each row corresponding to the equivalent row in `sampprPred`)

See Also

[collateObsTable](#), [bugModPred1](#), [taxon.classes](#)

Examples

```
mwstreamsCurrent <- bugModPred59(melbstreambiota::mwstreams)
plotMWstreamsByVar(mwstreamsCurrent$sampprPredsLumar$lumar, nbreaks = 6,
  style = "fixed", fixedBreaks = c(-1,-0.25,0,0.25,0.5,0.75,1),
  varName = "LUMaR", legend.cex = 0.75)
```

calcSIGNAL

Calculate SIGNAL and SIGNAL2 scores from macroinvertebrate data

Description

Collates macroinvertebrate data (in two possible formats) and returns SIGNAL and SIGNAL2 scores for each sample.

Usage

```
calcSIGNAL(bugData)
```

Arguments

`bugData` Table with either A) 2 columns (`samppr`, `bugcode`), or A) one row per `samppr`, with the first column `samppr` and the remaining column headings `bugcodes`

Details

While all other functions in this package require sample-pairs of rapid bioassessment samples, this function makes no assumption. SIGNAL scores can be calculated for any sample method. All bugcodes should be consistent with `taxon.classes`. See http://www.mdfrc.org.au/bugguide/resources/AUSRIVAS_Taxacodes.pdf for a full list including taxa other than those in `taxon.classes`. Note that the convention used in this package is to omit the trailing '9999' from each code. If bugcodes in `bugData` include trailing 4 digits, these are removed (this effectively combines any lower-taxonomic-level taxa to family-level.) SIGNAL is calculated using all taxa listed in `bugData` assigned a score in EPA Victoria (2003) Rapid bioassessment methodology for rivers and streams. Report 604.1. Environment Protection Authority Victoria, Melbourne. SIGNAL2 uses the scores listed by Chessman, B.C. (2003) New sensitivity grades for Australian river macroinvertebrates. Marine and Freshwater Research, 54, 95–103.

Value

A data.frame with 3 columns: `samppr`, matching `sampprs$samppr`; `SIGNAL` and `SIGNAL2`.

Examples

```
#Data in Form A
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
                                                    package="melbstreambiota", mustWork = TRUE),
                                                    sheet = 2))

#When importing data, replace the system.file() statement with "path/excelFile.xls"
signalScores1 <- calcSIGNAL(bugData)

#Data in Form B
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
                                                    package = "melbstreambiota", mustWork = TRUE),
                                                    sheet = 3))

signalScores2 <- calcSIGNAL(bugData)
#Check that data imported in both forms are equal
sum(signalScores1[-1] - signalScores2[-1]) # = 0
```

<code>collateBugSamppr</code>	<i>Collate and format sample-pair data for applying macroinvertebrate model predictions</i>
-------------------------------	---

Description

Collate and format sample-pair data for applying macroinvertebrate model predictions

Usage

```
collateBugSamppr(sampprTable, AttImp_L9 = "current (2006)",
  AttForest_L35W1000 = "current (2006)", meanAnnQ_mm = "current (2006)",
  mnAnnAirTm_deg = "long-term", SRI_48mth_weighted = "sample date")
```

Arguments

<code>sampprTable</code>	Table containing at least the fields <code>subc</code> , <code>nspring</code> , <code>nriff</code> , and either <code>process</code> or <code>processN</code> . If the table also contains a <code>samppr</code> identification column, it should be called 'samppr'
--------------------------	--

AttImp_L9	either the default value or a vector of new values for all subcs, or a single value if all sampprs are to have the same value
AttForest_L35W1000	either the default value or a vector of new values for all subcs, or a single value if all sampprs are to have the same value
meanAnnQ_mm	either the default value or a vector of new values for all subcs
mnAnnAirTm_deg	either the default values, or a single number, added to mwstreams\$mnAnnAirTm_deg (e.g. 1 = 1 degrees warmer)
SRI_48mth_weighted	if default, a "date" field must be supplied, or if a vector of length dim(sampprTable)[1], then those values are used

Details

If arguments AttImp_L9, AttForest_L35W1000, meanAnnQ_mm, mnAnnAirTm_deg, are default values, then 2006 values are drawn from the mwstreams table, matched by subc. If SRI_48mth_weighted is the default, values are drawn from sri48moW, matched by subc and date. Alternatively, for these arguments, vectors of length dim(sampprTable)[1] can be supplied to represent scenarios other than 2006 conditions. If supplying such data, care should be taken not to set values outside the experience of the model (see Walsh and Webb 2014). For instance, the maximum air temperature value in the experience of the models is 15.3, and setting mnAnnAirTm_deg to 2 (i.e. adding 2 degrees to the long-term average) raises the mean air temperature to >15.3 for many lowland reaches.

Value

The original sampprTable with additional columns required for model predictions

Examples

```
sampprs <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package="melbstreambiota", mustWork = TRUE),
  sheet = 1))
#When importing data, replace the system.file() statement with "path/excelFile.xls"
sampprs1 <- collateBugSampr(sampprs)
```

collateObsTable	<i>Collate and format observed table for LUMaR calculation from macroinvertebrate data</i>
-----------------	--

Description

Collates macroinvertebrate data (in two possible formats) into an observed family-by-sample-pair matrix for calculation of LUMaR (and other indices). The function also compares the macroinvertebrate data to the sample-pair table to ensure consistency.

Usage

```
collateObsTable(bugData, sampprTable)
```


Arguments

bugData	Table with either A) 2 columns (samppr, bugcode), or B) one row per sample pair, with the first column samppr and the remaining column headings bugcodes
sampprTable	Table containing at least the fields subc, nspring, nriff, and either process or processN (see collateBugSamppr)

Details

The vector of unique sampprs in bugData must completely match sampprTable\$samppr. If bugData is in form A, it is assumed that any listed family is present in the sample-pair (i.e. there are no taxa listed with abundance = 0). If there are duplicate entries of a family in a sample-pair, it is recorded as a single presence. If bugData is in form B, any family other than the 59 `taxon.classes$fams` are removed, and any of the 59 that are missing are inserted with abundance zero. All bugcodes should be consistent with `taxon.classes`. See http://www.mdfrc.org.au/bugguide/resources/AUSRIVAS_Taxacodes.pdf for a full list including taxa other than those in `taxon.classes`. Note that the convention used in this package is to omit the trailing 9999 from each code. If bugcodes in bugData include trailing 4 digits, these are removed (this effectively combines any lower-taxonomic-level taxa to family-level.) Taxonomic conventions used in the models are standard family-level with the following exceptions: Chironomidae are identified to sub-family. The tribes of sub-family Chironominae ("QDAG", "QDAH", "QDAI") are combined to "QDAJ", 'Old' odonate taxonomy is used: new families split from Corduliidae ("QO23", "QO26", "QO28", "QO27", "QO30") are consolidated to "QO16", and two families formerly considered Aeshnidae ("QO21", "QO12") are combined as "QO12". If bugData contains any of these family, this function converts them as above.

Value

A data.frame with 56 columns, the first samppr, matching `sampprs$samppr`, and the rest with names equal to `taxon.classes$fam`. Presence are recorded as 1s and absences as 0s.

Examples

```
#Data in Form A
sampprTable <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package="melbstreambiota", mustWork = TRUE),
  sheet = 1))
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package="melbstreambiota", mustWork = TRUE),
  sheet = 2))
#When importing data, replace the system.file() statement with "path/excelFile.xls"
obsTable1 <- collateObsTable(bugData, sampprTable)
#Data in Form B
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 3))
obsTable2 <- collateObsTable(bugData, sampprTable)
#Check that data imported in both forms are equal
sum(obsTable1[-1] - obsTable2[-1]) # = 0
```

collateSampleFP	<i>Collate and format sample data for applying fish or platypus model predictions</i>
-----------------	---

Description

Collate and format sample data for applying fish or platypus model predictions

Usage

```
collateSampleFP(sampleTable, FishOrPlatypus = "fish",
  AttImp_L9 = "current (2006)", AttForest_L35W1000 = "current (2006)",
  meanAnnQ_mm = "current (2006)", mnAnnAirTm_deg = "long-term",
  SRI_48mth_weighted = "sample date", barriersFromYear = TRUE,
  PartBarriersDS = NA, FullBarriersDS = NA)
```

Arguments

sampleTable	Table containing at least the field subc
FishOrPlatypus	Predictor variables to be assembled for "fish" (the default) or "platypus"
AttImp_L9	either the default value or a vector of new values for all subcs, or a single value if all sampprs are to have the same value. If FishOrPlatypus = "platypus", AttImpMin4k_L9 is substituted, and the field AttImpMin4k_L9.
AttForest_L35W1000	either the default value or a vector of new values for all subcs, or a single value if all sampprs are to have the same value
meanAnnQ_mm	either the default value or a vector of new values for all subcs
mnAnnAirTm_deg	either the default values, or a single number, added to mwstreams\$mnAnnAirTm_deg (e.g. 1 = 1 degrees warmer)
SRI_48mth_weighted	if default, a "date" field must be supplied, or if a vector of length dim(sampleTable)[1], then those values are used
barriersFromYear,	if TRUE and FishOrPlatypus = "fish", a "date" field must be supplied, if FALSE values must be provided for nPartBarriersDS, nFullBarriersDS
PartBarriersDS	Only use if barriersFromYear is FALSE and FishOrPlatypus = "fish". Must be a single numeric value (i.e. a number of barriers) to be applied ot all samples, or a vector of values of length(SampleTable\$subc) to be applied to each sample.
FullBarriersDS	As for nPartBarriersDS

Details

If arguments AttImp_L9, AttForest_L35W1000, meanAnnQ_mm, mnAnnAirTm_deg, are default values, then 2006 values are drawn from the mwstreams table, matched by subc. If SRI_48mth_weighted is the default, values are drawn from sri48moW, matched by subc anddate. If barriers is the default, then "nPartBarriersDS" and "nFullBarriersDS" are drawn from the barriers fields in mwstreams that match the year in which each sample was collected (as determined by date. Alternatively, for these arguments, vectors of length dim(sampleTable)[1] can be supplied to represent

scenarios other than 2006 conditions. If supplying such data, care should be taken not to set values outside the experience of the model (see Walsh and Webb 2014). For instance, the maximum air temperature value in the experience of the models is 15.3, and setting mnAnnAirTm_deg to 2 (i.e. adding 2 degrees to the long-term average) raises the mean air temperature to >15.3 for many lowland reaches.

Value

The original sampleTable with additional columns required for model predictions

Examples

```
# A sample table that would be used for fish samples taken on the same day as the example
# macroinvertebrate samples
samprsr <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
                                                    package="melbstreambiota", mustWork = TRUE),
                                                    sheet = 1))

#When importing data, replace the system.file() statement with "path/excelFile.xls"
samprsr1 <- collateSampleFP(samprsr)
#A hypothetical sample from a subc in the mwstreams table (average antecedent
#flow, all fish barriers removed)
exampleFishSamp <- collateSampleFP(sampleTable = mwstreams[1,],
                                   FishOrPlatypus = "fish",
                                   SRI_48mth_weighted = 1,
                                   barriersFromYear = FALSE,
                                   PartBarriersDS = 0, FullBarriersDS = 0)

exampleFishSamp
```

famCovariateEffects	<i>Find the relative contribution of families to differences in LUMaR associated with a covariate</i>
---------------------	---

Description

Find the relative contribution of families to differences in LUMaR associated with a covariate

Usage

```
famCovariateEffects(obs.table, exp.table, covariate)
```

Arguments

obs.table	a data.frame with first column samprsr (or row.names = samprsr), and 59 columns with names = taxon.classes\$fam. Data for each samprsr are 1s for observed presences and 0 for absences
exp.table	a data.frame with the same structure as obs.table, but filled with probabilities of occurrence as predicted by the 59 distribution models described by Walsh (in prep) under no human impact
covariate	a vector of covariate values corresponding to samprsr used as a contrast in LUMaR scores

Value

A data frame with rows corresponding to the families found or expected in the sampprs (≤ 59) and 6 columns:

fam the bugcodes matched by `taxon.classes$fam`

unexp 0 = families whose presence contributed to differences in LUMaR by their sensitivity grade;
1 = families whose presence contributed by their unexpected grade.

coef the coefficient of a beta regression of the weighted occurrences of each families against the covariate

lwr the 10th percentile confidence interval of coef

upr the 90th percentile confidence interval of coef

sig 'significance': TRUE if the range between lwr and upr includes zero

See Also

[collateBugSamppr](#), [predCurrNHI59](#), [collateObsTable](#)

Examples

```
sampprs <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
                                                    package = "melbstreambiota", mustWork = TRUE),
                                                    sheet = 1))
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
                                                    package = "melbstreambiota", mustWork = TRUE),
                                                    sheet = 2))

sampprs <- collateBugSamppr(sampprs)
expTable <- predCurrNHI59(sampprs)$predNHI
obsTable <- collateObsTable(bugData, sampprs)
sampprs$stream <- substr(sampprs$samppr, 3, 5)
famCovariateEffects(obsTable, expTable, sampprs$stream)
```

lumar

Calculate LUMaR index and associated statistics from observed and expected tables

Description

Calculate LUMaR index and associated statistics from observed and expected tables formatted to include the 59 families in the same order as `taxon.classes$fam`

Usage

```
lumar(obs.table, exp.table)
```

Arguments

obs.table a data.frame with first column `samppr` (or `row.names = samppr`), and 59 columns with names = `taxon.classes$fam`. Data for each `samppr` are 1s for observed presences and 0 for absences

exp.table a data.frame with the same structure as `obs.table`, but filled with probabilities of occurrence as predicted by the 59 distribution models described by Walsh (in prep) under no human impact

Value

A data frame with the same number of rows as the input tables and 14 columns: the LUMaR index and its components #'

samppr samppr as in input tables

lumar LUMaR index

nSensFams Number of sensitive families (as defined by Walsh 2017) in each sample

obs.wt.sens

obs.wt.unexp

obs.wt.A

obs.wt.B

obs.wt.C

obs.wt.D

obs.wt.weedy

unexp.wt.B

unexp.wt.D

unexp.wt.weedy

unexp.wt.invas

exp.wt

See Also

[collateBugSamppr](#), [predCurrNHI59](#), [collateObsTable](#)

Examples

```
sampprs <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 1))
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 2))
sampprs <- collateBugSamppr(sampprs)
expTable <- predCurrNHI59(sampprs)$predNHI
obsTable <- collateObsTable(bugData, sampprs)
lumar(obsTable, expTable)
```

mwCoastMap

Map of the Melbourne region coastline

Description

A SpatialLinesDataDataFrame of the coastline

Usage

```
mwCoastMap
```

Format

A SpatialLinesDataDataFrame of 37 rows (polylines) and 1 columns

ID unique ID

Source

<http://land.vic.gov.au>

mwstreams	<i>Environmental predictor variables for 8246 stream reaches (subcs) across the Melbourne region</i>
-----------	--

Description

A data frame data listing environmental predictor variables for all subc values in mwStreamsMap.

Usage

mwstreams

Format

a data frame of 8246 rows and 61 columns

subc unique subcatchment ID corresponding to subcs in mwStreamsMap

segmentno geofabric segmentno (BoM, 2011)

AttImp_L9 Attenuated imperviousness in 2006 as calculated by Walsh and Webb 2014 (exponential weighting to nearest stormwater drain or stream with a half-decay distance of 9.4 m). Variously also called dai9 (as it is in the subcs table), AI (in Walsh and Kunapo, 2009; Walsh and Webb 2013, 2014, 2016), and DCI (in various MW publications)

CatchmentArea_km2_InclDams catchment area calculated from the DCI subcatchment layer, and for sites downstream of large dams that rarely spill, includes the catchment upstream of the dam. (note that these areas were excluded in the determination of AttImp_L9)

Elevation_m Elevation above sea-level in m (derived from 10 m DEM). [used in early macroinvertebrate models of Walsh and Webb (2014, 2016), but not subsequently]

meanAnnQ_mm An estimate of mean annual runoff depth in mm, derived from the gridded monthly runoff data from The Australian Water Availability Project (AWAP; Raupach et al. 2009)

SolarRadiation STRANRAD from geofabric (BoM, 2011)

mnAnnAirTm_deg mean annual air temperature in Degrees Celsius at the centroid of each subc (derived from 5-km grid from BOM).

AFb10L1000 Attenuated forest cover, calculated as the unweighted (laterally) forest cover less than or equal to 10m from the stream, and exponentially weighted upstream with a half-decay distance of 1000 m. [used in the temperature model]

NHImnAnnStreamTm Predicted stream temperature in the absence of human impacts (full forest cover, no attenuated imperviousness), as predicted by the mean annual stream temperature model [originally planned to be used in the biological models, but as it is a function of mnAnnAirTm_deg, meanAnnQ_mm and CatchmentArea_km2_InclDams, mnAnnAirTm_deg is used instead]

AttForest_L35W1000 Attenuated forest cover with HDD overland to nearest stream of 35 m, and upstream 1 km (Walsh and Webb, 2014)

CatIgneous Percentage of catchment with igneous geology: CATIGN from Geofabric (BoM, 2011)

CVMonthlyQ RUNMTHCOFV (Monthly coefficient of variation in discharge from Geofabric (BoM, 2011)

AttImpMin4k_L9 Minimum AttImp_L9 within 4 km downstream of a reach (Martin et al 2014)

LWDBank Number of large woody debris pieces per area of bank, calculated only for large streams surveyed for the Index of Stream Condition

vegBank Proportion of bank along reach covered by vegetation, calculated only for large streams surveyed for the Index of Stream Condition

vegBed Proportion of bed along reach covered by vegetation, calculated only for large streams surveyed for the Index of Stream Condition

Att.Forest_10mBuffer AttForest_L35W1000, but assuming a 10-m buffer along all streams of the region

Att.Forest_20mBuffer AttForest_L35W1000, but assuming a 20-m buffer along all streams of the region

Att.Forest_40mBuffer AttForest_L35W1000, but assuming a 40-m buffer along all streams of the region

Att.Forest_100mBuffer AttForest_L35W1000, but assuming a 100-m buffer along all streams of the region

strLen_m total length of stream in each subc

strLenNat_m total length of natural stream in each subc

strLenCha_m total length of channel in each subc

strLenPip_m total length of piped stream in each subc

nPartBarriersDS_pre1997 Number of partial barriers downstream before 1997

nPartBarriersDS_1997 Number of partial barriers downstream in 1997

nPartBarriersDS_1999 Number of partial barriers downstream in 1999

nPartBarriersDS_2000 Number of partial barriers downstream in 2000

nPartBarriersDS_2002 Number of partial barriers downstream in 2002

nPartBarriersDS_2004 Number of partial barriers downstream in 2004

nPartBarriersDS_2005 Number of partial barriers downstream in 2005

nPartBarriersDS_2006 Number of partial barriers downstream in 2006

nPartBarriersDS_2007 Number of partial barriers downstream in 2007

nPartBarriersDS_2008 Number of partial barriers downstream in 2008

nPartBarriersDS_2009 Number of partial barriers downstream in 2009

nPartBarriersDS_2010 Number of partial barriers downstream in 2010

nPartBarriersDS_2016 Number of partial barriers downstream in 2016

nFullBarriersDS_pre2007 Number of full barriers downstream before 2007

nFullBarriersDS_2007 Number of full barriers downstream in 2007

nFullBarriersDS_2008 Number of full barriers downstream in 2008

nFullBarriersDS_2009 Number of full barriers downstream in 2009

nFullBarriersDS_2012 Number of full barriers downstream in 2012

- nFullBarriersDS_2014** Number of full barriers downstream in 2014
- MU_ID** Melbourne Water Management Unit
- SYS_ID** Melbourne Water System (broadly catchments)
- AttImp_L9_2014** AttImp_L9 updated to 2014 accounting for new development
- AttImp_L9_Ultimate** AttImp_L9 updated to a likely ~2050 future assuming infill development of areas zoned for urban development in the urban growth boundary
- AttImpMin4k_L9_2014** AttImpMin4k_L9 updated to 2014 accounting for new development
- AttImpMin4k_L9_Ultimate** AttImpMin4k_L9 updated to a likely ~2050 future assuming infill development of areas zoned for urban development in the urban growth boundary
- AttForest_L35W1000_1996** AttForest_L35W1000 calculated from 1996 imagery: MW data in progress: as of this version this field has only been calculated for "MARI" subcs: all other values in this field = AttForest_L35W1000 (2006)
- AttForest_L35W1000_2016** AttForest_L35W1000 calculated from 2016 imagery: MW data in progress: as of this version this field has only been calculated for "MARI" subcs: all other values in this field = AttForest_L35W1000 (2006)
- nspring** Number of Spring samples: specific to samples, but set to 0 (i.e. 2 autumn samples) for running scenarios
- nriff** Number of riffle samples: specific to samples, but set to 1 (i.e. a riffle-edge pair) for running scenarios
- processN** Process: 0 = lab-sort, 1 = field-sort, set to for running scenarios
- SRI_48mth_weighted** specific to samples but set to 1 (i.e. the 48-month linearly-weighted antecedent discharge was equivalent to the long-term mean discharge: 0.5 = half the long-term mean, 2 = twice the long-term mean)

Source

- BoM (2011) Australian hydrological geospatial fabric (geofabric) product guide. Version 2.0 – November 2011. Australian Government, Bureau of Meteorology, Canberra.
- Martin, E.H., Walsh, C.J., Serena, M. & Webb, J.A. (2014) Urban stormwater runoff limits distribution of platypus. *Austral Ecology*, 39, 337–345.
- Raupach, M.R., Briggs, P.R., Haverd, V., King, E.A., Paget, M. & Trudinger, C.M. (2009) Australian Water Availability Project (AWAP): CSIRO Marine and Atmospheric Research Component: Final Report for Phase 3. The Centre for Australian Weather and Climate Research, Canberra, Australia.
- Walsh, C. J. (in preparation) LUMaR: a sensitive macroinvertebrate index of stream condition combining observed:expected ratios and sensitivity weightings.
- Walsh, C.J. & Kunapo, J. (2009) The importance of upland flow paths in determining urban effects on stream ecosystems *Journal of the North American Benthological Society*, 28, 977–990.
- Walsh, C.J. & Webb, J.A. (2013) Predicting stream macroinvertebrate assemblage composition as a function of land use, physiography and climate: a guide for strategic planning for river and water management in the Melbourne Water region. Department of Resource Management and Geography, The University of Melbourne, Melbourne.
- Walsh, C.J. & Webb, J.A. (2014) Spatial weighting of land use and temporal weighting of antecedent discharge improves prediction of stream condition. *Landscape Ecology*, 29, 1171–1185.
- Walsh, C.J. & Webb, J.A. (2016) Interactive effects of urban stormwater drainage, land clearance, and flow regime on stream macroinvertebrate assemblages across a large metropolitan region. *Freshwater Science*, 35, 324–339.

mwStreamsMap	<i>Map of streams of the Melbourne region</i>
--------------	---

Description

A SpatialLinesDataDataFrame of all modelled reaches in the region

Usage

```
mwStreamsMap
```

Format

A SpatialLinesDataDataFrame of 25945 rows (polylines) and 4 columns

subc reach ID as in mwstreams

streamName Name of stream

source Original source of the mapped stream line

length_m length of each polyline in m (note there may be multiple polylines per subc and they are summed in mwstreams\$strLen_m)

Source

Melbourne Water: a combination of their Natural Waterway and channel layers. This stream network is an augmented and corrected version of the DCI stream layer used by Walsh and Webb 2013.

oestats8	<i>All index variants considered by Walsh (in prep)</i>
----------	---

Description

Calculate all OE indices, and others, compared to LUMaR by Walsh (in prep). Note that SIGNAL indices n need to be calculated using the full list of families collected in samples, not just the 59 families used in this function

Usage

```
oestats8(obs.table, exp.table, general.threshold = NA)
```

Arguments

obs.table a data.frame with first column samppr (or row.names = samppr), and 59 columns with names = taxon.classes\$fam. Data for each samppr are 1s for observed presences and 0 for absences

exp.table a data.frame with the same structure as obs.table, but filled with probabilities of occurrence as predicted by the 59 distribution models described by Walsh (in prep) under no human impact

general.threshold
if not NA, a single proportion signifying the presence-absence threshold to be applied to all families

Value

A data frame with the same number of rows as the input tables and 28 columns #'

samppr samppr as in input tables

OE50

wOE50

OE25

wOE25

OE.prev

wOE.prev

OE.pa.prev

wOE.pa.prev

wOE

wOE.signal

wOE.signal1

wOE.signal.prev

OE.signal.pa.prev

simOE

simOE.prev

wOE.sensif

wOE.sensif1

wOE.sensif.prev

OE.sensif.pa.prev

wOE.sensif.minweed.prev

wOE.sensif.minweed.prevA

wOE.sensif.minweed.prevB

wOE.sentif.minweed.prev1

wOE.sentif.minweed.prev1A

wOE.sentif.minweed.prev1B

wOE.signal.minweed.prev

wOE.signal.minweed.prev1

See Also

[collateBugSamppr](#), [predCurrNHI59](#), [collateObsTable](#)

Examples

```
sampprs <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package="melbstreambiota", mustWork = TRUE),
  sheet = 1))
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package="melbstreambiota", mustWork = TRUE),
  sheet = 2))

sampprs <- collateBugSamppr(sampprs)
expTable <- predCurrNHI59(sampprs)$predNHI
obsTable <-collateObsTable(bugData, sampprs)
oestats(obsTable, expTable)
```

plotMWstreams1col *Plot a map of Melbourne's streams (or a subset) by a single colour*

Description

Plot a map of Melbourne's streams (or a subset) by a single colour

Usage

```
plotMWstreams1col(col, subcSubset = NA, ...)
```

Arguments

col	a single colour
subcSubset	if NA the whole stream network is mapped. If a vector of subcs (a subset of mwstreams\$subc) is provided, only that subset will be mapped.
...	other arguments to be passed to classInt::classIntervals or sp::plot

Details

A more flexible option for plotMWstreamsByVar, when var is a single value

Value

A plot of the streams of Melbourne

plotMWstreamsByVar *Plot a map of Melbourne's streams colour-coded by a variable*

Description

Plot a map of Melbourne's streams colour-coded by a variable

Usage

```
plotMWstreamsByVar(var, nbreaks = 5, style = "quantile",
  varName = "Variable", palette = "Spectral", rev = FALSE,
  legend = TRUE, legend.cex = 1.5, fixedBreaks = NA, subcSubset = NA,
  ...)
```

Arguments

var	A vector (length 8246) of variable values for each subc in mwstreams (the function assumes that the vector is in the same order as mwstreams)
nbreaks	number of classes to be plotted: equals n argument in classInt
style	chosen style as in classIntervals: one of "fixed", "sd", "equal", "pretty", "quantile", "kmeans", "hclust", "bclust", "fisher", or "jenks
varName	character string for legend title

palette	an RcolorBrewer palette (see RColorBrewer::brewer.pal)
rev	inverts palette if TRUE
legend	plots legend if TRUE
legend.cex	character expansion factor for legend
fixedBreaks	NA unless style = "fixed", and then must equal a vector of breaks with length nbreaks + 1
subcSubset	if NA the whole stream network is mapped. If a vector of subcs (a subset of mwstreams\$subc) is provided, only that subset will be mapped.
...	other arguments to be passed to classInt::classIntervals or sp::plot

Details

The "fixed" style permits a classIntervals object to be specified with given breaks, set in the fixedBreaks argument; the length of fixedBreaks should be nbreaks+1; this style can be used to insert rounded break values. The "jenks" style is not implemented.

Value

A plot of Melbourne's streams.

See Also

[classIntervals](#), [brewer.pal](#)

Examples

```
plotMWstreamsByVar(melbstreambiota::mwstreams$AttForest_L35W1000, style = "fixed",
  fixedBreaks = seq(0,1,0.2), varName = "Attenuated Forest Cover",
  legend.cex = 0.75)
```

plotSensFamDiagnostics

Which families drive differences in LUMaR between groups of sample-pairs?

Description

Diagnostic plots to identify the most influential families influencing differences between groups of sample pairs, a trend among sample-pairs explained by a covariate

Usage

```
plotSensFamDiagnostics(lumarObject, covariate, covariateName = "Covariate",
  sensLinEffects, famLinEffects)
```

Arguments

lumarObject a data.frame produced by the function lumar
 covariate a vector length = number of rows in lumarObject (that explains some of the variation in LUMaR scores)
 covariateName a character vector for labelling the output plot
 sensLinEffects ...
 famLinEffects ...

Value

A plot identifying variation of observed LUMaR score from predicted values under 2006 conditions and under no human impact, as well as the most influential families driving any differences. If returnTable = TRUE a list of 2 data.frames is also returned:

InfluencesFromRef ...

InfluencesFromPred ...

Examples

```
sampprs <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 1))
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 2))
sampprs <- collateBugSamppr(sampprs)
expTables <- predCurrNHI59(sampprs)
obsTable <- collateObsTable(bugData, sampprs)
exampleLumar <- lumar(obsTable, expTables$predNHI)[,1:8]
stream <- substr(exampleLumar$samppr, 1, 3)
# What families explain differences in LUMaR between the two streams (BRS and OLN)
famStreamEffects <- famCovariateEffects(obsTable, expTables$predNHI, stream)
sensStreamEffects <- sensGpCovariateEffects(exampleLumar, stream)
plotSensFamDiagnostics(exampleLumar, stream, covariateName = "stream",
  sensLinEffects = sensStreamEffects,
  famLinEffects = famStreamEffects)
```

predCurrNHI59

Compile predictions of occurrence for all 59 macroinvertebrate families in a set of sample-pairs

Description

Compile predictions of occurrence for all 59 macroinvertebrate families in a set of sample-pairs

Usage

```
predCurrNHI59(sampprPreds)
```

Arguments

`sampprPreds` a data.frame of sample-pair codes (`samppr`) each with associated environmental predictors. If there is no field called `samppr`, then the field `subc` is used as `samppr`.

Details

The `sampprPreds` table must contain the 10 predictor variables used in the models: `nspring`, `nriff`, `processN`, `AttImp_L9`, `AttForest_L35W1000`, `CatchmentArea_km2_InclDams`, `meanAnnQ_mm`, `mnAnnAirTm_deg`, `CatIgneous`, and `SRI_48mth_weighted`. The function `collateBugSamppr` can be used to compile such a table. Use `bugModPred1` to make equivalent predictions for a single taxon.

Value

A list of two dataframes with number of rows = that of `sampprPred`, (each row corresponding to the equivalent row in `sampprPred`) and 59 columns, corresponding to the 59 families listed in `taxon.classes`

predCurr predicted probabilities of occurrence under conditions specified in `sampprPred`

predNHI predicted probabilities of occurrence under no human impact (`AttImp_L9` set to zero, `AttForest_L35W1000` set to 1)

See Also

[collateBugSamppr](#), [bugModPred1](#), [taxon.classes](#)

<code>prob59ToPA</code>	<i>Convert a data frame of probabilities of occurrence of 59 families to presence-absence</i>
-------------------------	---

Description

Convert a data frame of probabilities of occurrence of 59 families to presence-absence

Usage

```
prob59ToPA(prob59)
```

Arguments

`prob59` a data.frame with first column `samppr` (or `row.names = samppr`), and 59 columns with names = `taxon.classes$fam`. Data for each `samppr` are 1s for observed presences and 0 for absences

Details

Presence is inferred if the probability of occurrence (rounded to 3 decimal places) is greater than or equal to the `pa.threshold` for each family as listed in `taxon.classes`

Value

A data.frame the same structure as `prob59`, but with probabilities of occurrence converted to presences (1) or absences (0)

Examples

```
test59preds <- predCurrNHI59(melbstreambiota::mwstreams[1:4,])
prob59ToPA(test59preds$predCurr)
```

sampprDiagnostic *Interpretation of an observed LUMaR score at an individual site*

Description

Interpretation of an observed LUMaR score at an individual site

Usage

```
sampprDiagnostic(samppri, obsTable, currentPredTable, NHIPredTable,
  returnTable = FALSE)
```

Arguments

samppri	a data.frame with a single row, with fields samppr, and subc (a subc value drawn from mwstreams).
obsTable	a data.frame with first column samppr (or row.names = samppri) (the data can contain multiple rows, but one row must contain the value of samppri\$samppr) and 59 columns with names matching taxon.classes\$fam. Values = 1 for presences and 0 for absences. under no human impact
currentPredTable	A data.frame the same structure as obs.table, but filled with probabilities of occurrence under current conditions as predicted by the 59 distribution models described by Walsh (2017).
NHIPredTable	A data.frame the same structure as obs.table, but filled with probabilities of occurrence under no human impact as predicted by the 59 distribution models described by Walsh (2017)
returnTable	logical, if TRUE, returns 2 tables in addition to plotting results

Value

A plot identifying variation of observed LUMaR score from predicted values under 2006 conditions and under no human impact, as well as the most influential families driving any differences. If returnTable - TRUE a list of 2 data.frames is also returned:

InfluencesFromRef ...

InfluencesFromPred ...

Examples

```
sampprs <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 1))
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 2))
sampprs <- collateBugSamppr(sampprs)
```

```
expTable <- predCurrNHI59(samprsr)
obsTable <- collateObsTable(bugData, samprsr)
samprDiagnostic(samprri = samprsr[8,],
                obsTable = obsTable, currentPredTable = expTable$predCurr,
                NHIPredTable = expTable$predNHI)
```

sensGpCovariateEffects

Find the relative contribution of taxon-sensitivity groups to differences in LUMaR associated with a covariate

Description

Find the relative contribution of taxon-sensitivity groups to differences in LUMaR associated with a covariate

Usage

```
sensGpCovariateEffects(lumarObject, covariate)
```

Arguments

<code>lumarObject</code>	a data.frame as produced by the <code>lumar</code> function
<code>covariate</code>	a vector of covariate values corresponding to <code>sampr</code> used as a contrast in LUMaR scores

Value

A data frame with rows corresponding to the families found or expected in the `samprsr` (≤ 59) and 6 columns:

fam the bugcodes matched by `taxon.classes$fam`

unexp 0 = families whose presence contributed to differences in LUMaR by their sensitivity grade;
1 = families whose presence contributed by their unexpected grade.

coef the coefficient of a beta regression of the weighted occurrences of each families against the covariate

lwr the 10th percentile confidence interval of `coef`

upr the 90th percentile confidence interval of `coef`

sig 'significance': TRUE if the range between `lwr` and `upr` includes zero

See Also

[collateBugSampr](#), [predCurrNHI59](#), [collateObsTable](#)

Examples

```
samprsr <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 1))
bugData <- as.data.frame(readxl::read_excel(system.file("extdata", "exampleData.xlsx",
  package = "melbstreambiota", mustWork = TRUE),
  sheet = 2))
samprsr <- collateBugSamprsr(samprsr)
expTables <- predCurrNHI59(samprsr)
obsTable <- collateObsTable(bugData, samprsr)
exampleLumar <- lumar(obsTable, expTables$predNHI)
stream <- substr(exampleLumar$samprsr, 3, 5)
#What families explain differences in LUMaR between the two streams (BRS and OLN)
sensGpCovariateEffects(exampleLumar, stream)
```

sri48moW

*Monthly 48-month linearly-weighted antecedent discharge since 1986
for all mwstream subcs*

Description

A data frame data of subcs each with monthly 48-month linearly-weighted antecedent discharge since (1986-2014 [some to 2016]) for all mwstream subcs, calculated as described by Walsh and Webb (2014, 2016)

Usage

```
sri48moW
```

Format

a data frame of 2806548 rows and 3 columns

date POSIXct date, time zone "UTC"

subc subcatchment ID equivalent to mwstreams\$subc

SRI_48mth_weighted 48-month linearly-weighted antecedent discharge as a proportion of mean annual discharge

@details The general method for SRI_48mth_weighted was described by Walsh and Webb 2014. These data are the variant, calculated from the Australian Water Availability Project data (AWAP; Raupach et al. 2009) as described in Walsh (in preparation). The date field equals the first of each month from Jan 1986 to Feb 2014 for most subcs, and to July 2016 for some (Main Creek, French Island, Bass, Lang Lang, Yallock, and Bunyip catchments).

Source

Walsh, C. J. (in preparation) LUMaR: a sensitive macroinvertebrate index of stream condition combining observed:expected ratios and sensitivity weightings.

streamsubcs.allus2017 *A list of subcatchments each with a list of all upstream subcatchments that contain stream reaches in mwstreams*

Description

A list of subcatchments each with a list of all upstream subcatchments that contain stream reaches in mwstreams

Usage

streamsubcs.allus2017

Format

a list of length 8257

taxon.classes *Details of the 59 modelled families*

Description

A data frame listing the 59 families that are modelled in bestModelsBugfams, with relevant statistics

Usage

taxon.classes

Format

a data frame of 59 rows and 10 columns

fam bugcode, consistent with EPA Victoria and AUSRIVAS conventions

family family name

devexp proportion explained deviance explained by the model

pa.threshold presence-absence threshold used in the LUMaR index

sens.gp sensitivity group used in the LUMaR index

SIGNAL SIGNAL grade (Chessman 1995)

SIGNAL2 SIGNAL2 grade (Chessman 2003)

unexp.grade sensitivity grade used in the LUMaR index

sens.grade unexpected grade used in the LUMaR index

Source

Walsh, C. J. (in preparation) LUMaR: a sensitive macroinvertebrate index of stream condition combining observed:expected ratios and sensitivity weightings.

vertPred	<i>Predict occurrence of a fish species or platypus (total or female) in a set of subcatchments</i>
----------	---

Description

Predict occurrence of a fish species or platypus (total or female) in a set of subcatchments

Usage

```
vertPred(code, vertSamps)
```

Arguments

code	an 8-character code as listed in vertSpp
vertSamps	a data.frame of subcatchments (from mwstreams) each with associated environmental predictors.

Details

The vertSamps table must contain the 9 predictor variables used in the models. The function collateSampleFP can be used to compile such a table. (Note platypus and fish species have different predictors)

Value

A vector with length = number of rows in vertSamps, with each row corresponding to the equivalent row in vertSamps.

predicted probabilities of occurrence under conditions specified in sampprPred

See Also

[collateSampleFP](#), [vertSpp](#)

vertSpp	<i>Fish species and platypus groups modelled</i>
---------	--

Description

A data frame listing 23 fish species and associated codes (and two platypus groups) used in models

Usage

```
vertSpp
```

Format

a data frame of 25 rows and 4 columns

vertcode the code used to identify models in the package

species

authority

Common name

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