Package ‘aqp’

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Description The Algorithms for Quantitative Pedology (AQP) project was started in 2009 to organize a loosely-related set of concepts and source code on the topic of soil profile visualization, aggregation, and classification into this package (aqp). Over the past 8 years, the project has grown into a suite of related R packages that enhance and simplify the quantitative analysis of soil profile data. Central to the AQP project is a new vocabulary of specialized functions and data structures that can accommodate the inherent complexity of soil profile information; freeing the scientist to focus on ideas rather than boilerplate data processing tasks <doi:10.1016/j.cageo.2012.10.020>. These functions and data structures have been extensively tested and documented, applied to projects involving hundreds of thousands of soil profiles, and deeply integrated into widely used tools such as SoilWeb <https://casoilresource.lawr.ucdavis.edu/soilweb-apps/>. Components of the AQP project (aqp, soilDB, sharpshootR, soilReports packages) serve an important role in routine data analysis within the USDA-NRCS Soil Science Division. The AQP suite of R packages offer a convenient platform for bridging the gap between pedometric theory and practice.
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Description

The aqp (Algorithms for Quantitative Pedology) package for R was developed to address some of the difficulties associated with processing soils information, specifically related to visualization, aggregation, and classification of soil profile data. This package is based on a mix of S3/S4 functions and classes, and most functions use basic dataframes as input, where rows represent soil horizons and columns define properties of those horizons. Common to most functions are the requirements that horizon boundaries are defined as depth from 0, and that profiles are uniquely defined by an id column. The aqp package defines an S4 class, "SoilProfileCollection", for storage of profile-level metadata, as well as summary, print, and plotting methods that have been customized for common tasks related to soils data.

Demos: demo(aqp)

demo(slope_effect_hz_thickness)

Project homepage.

Author(s)

Dylan E. Beaudette <debeaudette@ucdavis.edu> and Pierre Roudier

See Also

cal630, sp1, sp2, sp3, sp4, sp5
addBracket  

Description

Add depth-wise brackets to an existing plot of a SoilProfileCollection object.

Usage

```r
addBracket(x, label.cex=0.75, 
  tick.length = 0.05, arrow.length = 0.05, offset = -0.3, 
  missing.bottom.depth = NULL, 
  ...)  
```

Arguments

- `x` data.frame containing ID, ‘top’, ‘bottom’, and optionally ‘label’ columns
- `label.cex` scaling factor for label font
- `tick.length` length of bracket “tick” mark
- `arrow.length` length of arrowhead
- `offset` numeric, length of left-hand offset from each profile
- `missing.bottom.depth` distance (in depth units) to extend brackets that are missing a lower depth (defaults to max depth of collection)
- `...` further arguments passed on to segments or arrows

Details

Additional examples can be found in this tutorial.

Note

This is a ‘low-level’ plotting function: you must first plot a SoilProfileCollection object before using this function.

Author(s)

D.E. Beaudette

See Also

plotSPC
addVolumeFraction

Symbolize Volume Fraction on a Soil Profile Collection Plot

Description

Symbolize volume fraction on an existing soil profile collection plot.
addVolumeFraction

Usage

addVolumeFraction(x, colname, res = 10, cex.min = 0.1, cex.max = 0.5, pch = 1, col = "black")

Arguments

x a SoilProfileCollection object
colname character vector of length 1, naming the column containing volume fraction data (horizon-level attribute)
res integer, resolution of the grid used to symbolize volume fraction
cex.min minimum symbol size
cex.max maximum symbol size
pch plotting character
col color of the symbol

Details

This function can only be called after plotting a SoilProfileCollection object.

Note

Details associated with a call to plot.SoilProfileCollection are automatically accounted for within this function: e.g. plot.order, width, etc.

Author(s)

D.E. Beaudette

See Also

plotSPC

Examples

# sample data
data(loafercreek, package='soilDB')

# subset first 10 profiles
s <- loafercreek[1:10, ]

# replace 0% frags with NA
s$total_frags_pct[which(s$total_frags_pct == 0)] <- NA

# plot in random order, note that annotations follow
par(mar=c(0, 0, 3, 0))
plot(s, color='total_frags_pct', plot.order=sample(1:length(s)))
addVolumeFraction(s, 'total_frags_pct', pch=1)

par(mar=c(0, 0, 0, 0))
**aggregateColor**

```
plot(s, max.depth=100, name='total_frags_pct', cex.name=1, axis.line.offset=-4.25)
addVolumeFraction(s, 'total_frags_pct', pch=1)
```

---

**aggregateColor**  
*Summarize Soil Colors*

### Description
Summarize soil color data, weighted by occurrence and horizon thickness.

### Usage
```
aggregateColor(x, groups = "genhz", col = "soil_color")
```

### Arguments
- `x`  
a `SoilProfileCollection` object
- `groups`  
the name of a horizon or site attribute used to group horizons, see examples
- `col`  
the name of a horizon-level attribute with soil color specified in hexadecimal (i.e. "#rrggbb")

### Details
Weights are computed by:  
\[ w_i = \sqrt{\text{sum}(\text{thickness}_i)} \times n_i \]  
where \( w_i \) is the weight associated with color \( i \), \( \text{thickness}_i \) is the total thickness of all horizons associated with the color \( i \), and \( n_i \) is the number of horizons associated with color \( i \). Weights are computed within groups specified by `groups`.

### Value
A list with the following components:
- `scaled.data`  
a list of colors and associated weights, one item for each generalized horizon label with at least one color specified in the source data
- `aggregate.data`  
a `data.frame` of weighted-mean colors, one row for each generalized horizon label with at least one color specified in the source data

### Author(s)
D.E. Beaudette

### See Also
`generalize.hz`
Examples

# load some example data
data(spl, package='aqp')

# upgrade to SoilProfileCollection and convert Munsell colors
spl$soil_color <- with(spl, munsell2rgb(hue, value, chroma))
depths(spl) <- id ~ top + bottom
site(spl) <- ~ group

# generalize horizon names
n <- c('O', 'A', 'B', 'C')
p <- c('O', 'A', 'B', 'C')
spl$genhz <- generalize.hz(spl$name, n, p)

# aggregate colors over horizon-level attribute: 'genhz'
a <- aggregateColorColor(spl, 'genhz')

# aggregate colors over site-level attribute: 'group'
a <- aggregateColorColor(spl, 'group')

# aggregate colors over depth-slices
s <- slice(spl, c(5, 10, 15, 25, 50, 100, 150) ~ soil_color)
s$slice <- paste0(s$top, ' cm')
a <- aggregateColorColor(s, 'slice')

# Not run:
# optionally plot with helper function
if(require(sharpshootR))
  aggregateColorPlot(a)

# End(Not run)

# a more interesting example
# Not run:
data(loafercreek, package = 'soilDB')

# generalize horizon names using REGEX rules
n <- c('O1', 'A', 'BA', 'Bt1', 'Bt2', 'Bt3', 'Cr', 'R')
p <- c('O', 'A$|Ap|AB', 'BA$|Bw', 'Bt1$|B$|Bt2$|Bt3$|Bt4$|CBt$|Bct$|2Bt|2CB$|C$|Cr', 'R')
loafercreek$genhz <- generalize.hz(loafercreek$hzname, n, p)

# remove non-matching generalized horizon names
loafercreek$genhz[loafercreek$genhz == 'not-used'] <- NA
loafercreek$genhz <- factor(loafercreek$genhz)
a <- aggregateColorColor(loafercreek, 'genhz')

# plot results with helper function
par(mar=c(1,4,4,1))
aggregateColorPlot(a, print.n.hz = TRUE)
aggregateSoilDepth

# inspect aggregate data
a$aggregate.data

## End(Not run)

---

**aggregateSoilDepth**  
*Probabalisct Estimation of Soil Depth*

**Description**

Estimate the most-likely depth to contact within a collection of soil profiles.

**Usage**

```r
aggregateSoilDepth(x, groups, crit.prob = 0.9, name = "hzname", p = "Cr|R|Cd", ...)
```

**Arguments**

- `x`  
  a `SoilProfileCollection` object
- `groups`  
  the name of a site-level attribute that defines groups of profiles within a collection
- `crit.prob`  
  probability cutoff used to determine where the most likely depth to contact will be, e.g. 0.9 translates to 90% of profiles are shallower than this depth
- `name`  
  horizon-level attribute where horizon designation is stored
- `p`  
  a REGEX pattern that matches non-soil genetic horizons
- `...`  
  additional arguments to `slab`

**Details**

This function computes a probability-based estimate of soil depth by group. If no grouping variable exists, a dummy value can be used to compute a single estimate. The `crit.prob` argument sets the critical probability (e.g. 0.9) at which soil depth within a group of profiles is determined. For example, a `crit.prob` of 0.95 might result in an estimated soil depth (e.g. 120cm) where 95% of the profiles (by group) had depths that were less than or equal to 120cm.

**Value**

A `data.frame` is returned, with as many rows as there are unique group labels, as specified in `groups`.

**Author(s)**

D.E. Beaudette

**See Also**

`estimateSoilDepth, slab`
Examples

```r
data(sp1)
depths(sp1) <- id ~ top + bottom
site(sp1) <- ~ group
aggregateSoilDepth(sp1, 'group', crit.prob = 0.9)
```

**Amarillo Soils**

**Description**

This sample dataset contains laboratory and published soil survey (i.e. generalized) data on the Amarillo soil series.

**Usage**

data(amarillo)

**Format**

The format is: List of 2 data.frame': 323 obs. of 40 variables:

- `ID`: int [1:323] 1 2 3 4 5 6 7 8 9 10 ...
- `user_pedon_id`: chr [1:323] "53TX305059" "53TX305059" "53TX305059" "53TX305059" ...
- `user_site_id`: chr [1:323] "53TX305059" "53TX305059" "53TX305059" "53TX305059" ...
- `horizontal_datum_name`: chr [1:323] "" "" "" "" ...
- `latitude_direction`: chr [1:323] "north" "north" "north" "north" ...
- `latitude_degrees`: int [1:323] 33 33 33 33 33 33 33 33 33 33 ...
- `latitude_minutes`: int [1:323] 10 10 10 10 10 10 11 11 11 11 ...
- `latitude_seconds`: num [1:323] 30.0 30.0 30.0 30.0 30.0 30.0 5.5 5.5 5.5 5.5 ...
- `longitude_direction`: chr [1:323] "west" "west" "west" "west" ...
- `longitude_degrees`: int [1:323] 101 101 101 101 101 101 101 101 101 101 ...
- `longitude_minutes`: int [1:323] 47 47 47 47 47 47 46 46 46 46 ...
- `longitude_seconds`: num [1:323] 40.0 40.0 40.0 40.0 40.0 40.0 40.0 40.0 40.0 40.0 ...
- `latitude_std_decimal_degrees`: num [1:323] 33.2 33.2 33.2 33.2 33.2 33.2 33.2 33.2 33.2 33.2 ...
- `taxon_name`: chr [1:323] "Amarillo" "Amarillo" "Amarillo" "Amarillo" ...
- `class_type`: chr [1:323] "correlated" "correlated" "correlated" "correlated" ...
- `natural_key`: chr [1:323] "40A34174" "40A34175" "40A34176" "40A34177" ...
- `hzn_desgn`: chr [1:323] "Ap" "B1" "Bt1" "Bt2" ...
- `hzn_top`: int [1:323] 0 18 51 86 137 190 0 20 51 76 ...
- `hzn_bot`: int [1:323] 18 51 86 137 190 236 20 51 76 102 ...
- `CEC`: logi [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `EC`: logi [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `ph_h2o`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `ph_cacl2`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `caco3`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `c_gyp`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `EC`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `SAR`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `Total.Clay`: num [1:323] 17.9 19.5 25.2 29.2 32.6 32.6 32.6 32.6 32.6 32.6 ...
- `Total.Silt`: num [1:323] 9.4 9.4 14.7 18.7 26.8 25.5 10.5 13.6 16.6 15.3 ...
- `Total.Sand`: num [1:323] 72.7 71.1 60.5 51.0 35.4 41.9 78.7 59.6 57.9 53.9 ...
- `dB.33.bar`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `dB.15.bar`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `LE`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `Water.Ret..2mm.33.bar`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `Water.Ret..2mm.33.bar`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
- `Water.Ret..2mm.33.bar`: num [1:323] NA NA NA NA NA NA NA NA NA NA ...
| ID  | State | Database | Area.Symbol | Area.Name                     | mukey  | Mapunit.Symbol | Component.Name | SIR obsolete | cokey    | RV     | Local.Phase | chkey | Designation | top  | bott  | CECL | CECR | S | CECH | ECM | SARL | SARH | SARM | CLAYL | CLAYR | CLAYH | CLAYM | SILL | SILR | SILH | SILM | SANL | SANR | SANH | SANM | SKATL |
|-----|-------|----------|-------------|---------------|--------|----------------|----------------|--------------|-----------|---------|---------|----------|-------|-------------|------|------|------|------|---|------|-----|------|------|------|------|------|------|------|------|------|-----|------|-----|------|-----|------|------|
| 8177 | NM   | SSURGO   | NM021        | Harding County, New Mexico | 8178   | AM             | Amarillo       | NA           | NA        | NA      | NA      | NA      | NA     | NA            | 85   | 85   | 8.3 | 7.2 | 18 | 20   | 5   | 1   | 13  | 10   | 37.5 | 37.1 | 50.5 | 42.5 | 1  | 1.35 | 1.47 | 1.47 | 1.47 | 0.5 |
| 8179 | NM   | SSURGO   | NM021        | Harding County, New Mexico | 8180   | AM             | Amarillo       | NA           | NA        | NA      | NA      | NA      | NA     | NA            | 85   | 85   | 8.3 | 7.2 | 18 | 20   | 5   | 1   | 13  | 10   | 37.5 | 37.1 | 50.5 | 42.5 | 1  | 1.35 | 1.47 | 1.47 | 1.47 | 0.5 |
| 8181 | NM   | SSURGO   | NM021        | Harding County, New Mexico | 8182   | AM             | Amarillo       | NA           | NA        | NA      | NA      | NA      | NA     | NA            | 85   | 85   | 8.3 | 7.2 | 18 | 20   | 5   | 1   | 13  | 10   | 37.5 | 37.1 | 50.5 | 42.5 | 1  | 1.35 | 1.47 | 1.47 | 1.47 | 0.5 |
| 8183 | NM   | SSURGO   | NM021        | Harding County, New Mexico | 8184   | AM             | Amarillo       | NA           | NA        | NA      | NA      | NA      | NA     | NA            | 85   | 85   | 8.3 | 7.2 | 18 | 20   | 5   | 1   | 13  | 10   | 37.5 | 37.1 | 50.5 | 42.5 | 1  | 1.35 | 1.47 | 1.47 | 1.47 | 0.5 |
Multinominal Brier score

Compute the multinominal Brier score

Usage

brierScore(x, classLabels, actual = "actual")

Arguments

x  
data.frame, rows are predictions/observations, columns contain classes

classLabels  
vector of predicted class labels (probabilities), corresponding to column names in x

actual  
name of column containing the observed class

Value

A single numeric value.
Author(s)
D.E. Beaudette

References

Soil Data from the Central Sierra Nevada Region of California

Description
Site and laboratory data from soils sampled in the central Sierra Nevada Region of California.

Usage
data(ca630)

Format
List containing:
$site : A data frame containing site information.
  user_site_id national user site id
  mlra the MLRA
  county the county
  ssa soil survey area
  lon longitude, WGS84
  lat latitude, WGS84
  pedon_key national soil profile id
  user_pedon_id local soil profile id
  cntrl_depth_to_top control section top depth (cm)
  cntrl_depth_to_bot control section bottom depth (cm)
  sampled_taxon_name soil series name
$lab : A data frame containing horizon information.
  pedon_key national soil profile id
  layer_key national horizon id
  layer_sequence horizon sequence number
  hzn_top horizon top (cm)
  hzn_bot horizon bottom (cm)
hzn_desgn  horizon name
texture_description  USDA soil texture
nh4_sum_bases  sum of bases extracted by ammonium acetate (pH 7)
ex_acid  exchangeable acidity [method ?]
CEC8.2  cation exchange capacity by sum of cations method (pH 8.2)
CEC7  cation exchange capacity by ammonium acetate (pH 7)
bs_8.2  base saturation by sum of cations method (pH 8.2)
bs_7  base saturation by ammonium acetate (pH 7)

Details
These data were extracted from the NSSL database. ‘ca630’ is a list composed of site and lab data, each stored as dataframes. These data are modeled by a 1:many (site:lab) relation, with the ‘pedon_id’ acting as the primary key in the ‘site’ table and as the foreign key in the ‘lab’ table.

Note
These data are out of date. Pending some new data + documentation. Use with caution

Source
https://ncsslabdatamart.sc.egov.usda.gov/

Examples
```r
# Not run:
library(plyr)
library(lattice)
library(Hmisc)
library(maps)
library(sp)

# check the data out:
data(ca630)
str(ca630)

# note that pedon_key is the link between the two tables

# make a copy of the horizon data
c <- ca630$lab

# promote to a SoilProfileCollection class object
depths(ca) <- pedon_key ~ hzn_top + hzn_bot

# add site data, based on pedon_key
site(ca) <- ca630$site

# ID data missing coordinates: '|' is a logical OR
(missing.coords.idx <- which(is.na(ca$lat) | is.na(ca$lon)))
```
# remove missing coordinates by safely subsetting
if(length(missing.coords.idx) > 0)
ca <- ca[-missing.coords.idx, ]

# register spatial data
coordinates(ca) <- ~ lon + lat

# assign a coordinate reference system
proj4string(ca) <- '+proj=longlat +datum=NAD83'

# check the result
print(ca)

# map the data (several ways to do this, here is a simple way)
map(database='county', region='california')
points(coordinates(ca), col='red', cex=0.5)

# aggregate %BS 7 for all profiles into 1 cm slices
a <- slab(ca, fm= ~ bs_7)

# plot median & IQR by 1 cm slice
xyplot(
  top ~ p.q50, data=a, lower=a$p.q25, upper=a$p.q75,
  ylim=c(160,-5), alpha=0.5, scales=list(alternating=1, y=list(tick.num=7)),
  panel=panel.depth_function, prepanel=prepanel.depth_function,
  ylab='Depth (cm)', xlab='Base Saturation at pH 7',
  par.settings=list(superpose.line=list(col='black', lwd=2))
)

# aggregate %BS at pH 8.2 for all profiles by MLRA, along 1 cm slices
# note that mlra is stored in @site
a <- slab(ca, mlra ~ bs_8.2)

# keep only MLRA 18 and 22
a <- subset(a, subset=mlra %in% c('18', '22'))

# plot median & IQR by 1 cm slice, using different colors for each MLRA
xyplot(
  top ~ p.q50, groups=mlra , data=a, lower=a$p.q25, upper=a$p.q75,
  ylim=c(160,-5), alpha=0.5, scales=list(y=list(tick.num=7, alternating=3), x=list(alternating=1)),
  panel=panel.depth_function, prepanel=prepanel.depth_function,
  ylab='Depth (cm)', xlab='Base Saturation at pH 8.2',
  par.settings=list(superpose.line=list(col=c('black','blue'), lty=c(1,2), lwd=2)),
  auto.key=list(columns=2, title='MLRA', points=FALSE, lines=TRUE)
)

# safely compute hz-thickness weighted mean CEC (pH 7)
# using data.frame objects
head(lab.agg.cec_7 <- ddply(ca630$lab, .(pedon_key),
  .fun=summarise, CEC_7=wtd.mean(bs_7, weights=hzn_bot-hzn_top)))
# extract a SPDF with horizon data along a slice at 25 cm
s.25 <- slice(ca, fm=25 ~ bs_7 + CEC7 + ex_acid)
spplot(s.25, zcol=c('bs_7', 'CEC7', 'ex_acid'))

# note that the ordering is preserved:
all.equal(s.25$pedon_key, profile_id(ca))

# extract a data.frame with horizon data at 10, 20, and 50 cm
s.multiple <- slice(ca, fm=c(10,20,50) ~ bs_7 + CEC7 + ex_acid)

# Extract the 2nd horizon from all profiles as SPDF
ca.2 <- ca[, 2]

# subset profiles 1 through 10
ca.1.to.10 <- ca[1:10, ]

# basic plot method: profile plot
plot(ca.1.to.10, name='hzn_desgn')

## End(Not run)

---

confusionIndex  

### Confusion Index

**Description**

Calculate the confusion index of Burrough et al., 1997.

**Usage**

confusionIndex(x)

**Arguments**

- **x**: vector of probabilities [0,1], should not contain NA

**Value**

A single numeric value.

**Author(s)**

D.E. Beaudette

**References**

**estimateSoilDepth**

**Examples**

```r
# a very simple example
p <- c(0.25, 0.25, 0.4, 0.05, 0.05)
confusionIndex(p)
```

**Description**

Estimate the soil depth of a single profile within a SoilProfileCollection object. This function would typically be called by `profileApply`.

**Usage**

```r
estimateSoilDepth(f, name = "hznname", top = "hzdept", bottom = "hzdepb", p = 'Cr|R|Cd', no.contact.depth = NULL, no.contact.assigned = NULL)
```

**Arguments**

- `f` A SoilProfileCollection object of length 1, e.g. a single profile
- `name` the name of the column that contains horizon designations
- `top` the name of the column that contains horizon top depths
- `bottom` the name of the column that contains horizon bottom depths
- `p` a REGEX pattern for determining contact with bedrock
- `no.contact.depth` in the absence of contact with bedrock, a depth at which we can assume a standard depth
- `no.contact.assigned` assumed standard depth

**Value**

a single integer, the soil depth

**Author(s)**

D.E. Beaudette and J.M. Skovlin

**See Also**

`getSoilDepthClass`, `profileApply`
Examples

data(spl)
depths(spl) <- id ~ top + bottom

# apply to each profile in a collection, and save as site-level attribute
spl$depth <- profileApply(spl, estimateSoilDepth, name='name', top='top', bottom='bottom')

# this function can be used to "find" depth to any feature
# that can be defined via REGEX pattern matching on the horizon name
# for example, locate the depth to the top "Bt" horizon
# returning NA when there is no match
spl$top_Bt <- profileApply(spl, estimateSoilDepth, name='name', top='top',
  bottom='bottom', p='Bt', no.contact.depth=0, no.contact.assigned=NA)

# reduced margins
par(mar=c(1,1,1,2))
# adjust default y-offset and depth scaling for following examples
plot(spl, y.offset=10, scaling.factor=0.5)

# get plotting parameters for profile widths and depth scaling factors
lsp <- get("last_spc_plot", envir = aqp.env)

# positions on x-axis, same for both depth and top "Bt" horizon
x.positions <- (1:length(spl)) - lsp$width

# annotate contact with unicode right-arrow
# y-position is adjusted based on plot y-offset and scaling factor
y.positions <- lsp$y.offset + (spl$depth * lsp$scaling.factor)
text(x.positions, y.positions, '\u2192', col='red', adj=1, cex=1.25, lwd=2)

# annotate top "Bt" depth with unicode right-arrow
# y-position is adjusted based on plot y-offset and scaling factor
y.positions <- lsp$y.offset + (spl$top_Bt * lsp$scaling.factor)
text(x.positions, y.positions, '\u2192', col='blue', adj=1, cex=1.25, lwd=2)

## Not run:
# sample data
data(gopheridge, package='soilDB')

# run on a single profile
estimateSoilDepth(gopheridge[1, ])

# apply to an entire collection
profileApply(gopheridge, estimateSoilDepth)

## End(Not run)
Description

Data-driven evaluation of generalized horizon labels using nMDS and silhouette width.

Usage

evalGenHZ(obj, genhz, vars, non.matching.code = "not-used", stand = TRUE, trace = FALSE, metric = "euclidean")

Arguments

obj a SoilProfileCollection object
genhz name of horizon-level attribute containing generalized horizon labels
vars character vector of horizon-level attributes to include in the evaluation
non.matching.code code used to represent horizons not assigned a generalized horizon label
stand standardize variables before computing distance matrix (default = TRUE), passed to daisy
trace verbose output from passed to isoMDS, (default = FALSE)
metric distance metric, passed to daisy

Details

Non-metric multidimensional scaling is performed via isoMDS. The input distance matrix is generated by daisy using (complete cases of) horizon-level attributes from obj as named in vars.

Silhouette widths are computed via silhouette. The input distance matrix is generated by daisy using (complete cases of) horizon-level attributes from obj as named in vars. Note that observations with genhz labels specified in non.matching.code are removed filtered before calculation of the distance matrix.

Value

a list is returned containing:

horizons c(‘mds.1’, ‘mds.2’, ‘sil.width’, ‘neighbor’)
stats mean and standard deviation of vars, computed by generalized horizon label
dist the distance matrix as passed to isoMDS

Author(s)

D.E. Beaudette

See Also

get.ml.hz
**evalMissingData**

*Evaluate Missing Data*

**Description**
Evaluate missing data in a SoilProfileCollection object

**Usage**
```
evalMissingData(x, vars, name = "hzname", p = "Cr|R|Cd")
```

**Arguments**
- `x`: a SoilProfileCollection object
- `vars`: a character vector naming horizon-level attributes in `x`
- `name`: the name of a horizon-level attribute where horizon designations are stored
- `p`: REGEX pattern used to match non-soil horizons

**Details**
Data completeness is evaluated by profile, based on the thickness of horizons with complete horizon-level attribute values (specified in `vars`) divided by the total thickness. The default REGEX pattern, `p`, should catch most non-soil horizons which are excluded from the evaluation. Elements of `vars` that do not exist in `horizonNames(x)` are ignored.

**Value**
A vector values ranging from 0 to 1, representing the percentage of non-NA data (as specified in `vars`) for each profile.

**Author(s)**
D.E. Beaudette

**Examples**
```
# example data
data(sp2)
# init SPC object
depths(sp2) <- id ~ top + bottom
# compute data completeness
sp2$data.complete <- evalMissingData(sp2, vars = c('r', 'g', 'b'), name = 'name')
# rank
new.order <- order(sp2$data.complete)
# plot along data completeness ranking
plot(sp2, plot.order=new.order)
# add axis, note re-ordering of axis labels
axis(side=1, at=1:length(sp2), labels = round(sp2$data.complete[new.order], 2),
line=-2, cex.axis=0.75)
```
Example Objective Function for Full-Pattern Matching

Description

Basic objective function that can be used as a starting point for developing XRD full-pattern matching strategies. [details pending...]

Usage

f.noise(inits, pure.patterns, sample.pattern, eps.total = 0.05)

Arguments

- inits: vector of initial guesses for mineral fractions, last item is a noise component
- pure.patterns: a matrix of XRD patterns of pure samples, resampled to the same twotheta resolution and rescaled according to an external standard
- sample.pattern: the unknown or composite pattern, aligned to the same twotheta axis as the pure patterns and rescaled to an external standard
- eps.total: precision of comparisons; currently not used

Details

This is similar to the work of Chipera and Bish (2002), using the methods described in (Bish, 1994). If the flexibility of a custom objective function is not required, the linear model framework should be sufficient for pattern fitting. GLS should be used if realistic standard errors are needed.

Value

the sum of absolute differences between the unknown pattern and combination of pure patterns for the current set of mixture proportions

Author(s)

Dylan E. Beaudette

References


See Also

resample.twtheta
Examples

```r
# sample data
data(rruff.sample)

# get number of measurements
n <- nrow(rruff.sample)

# number of components
n.components <- 6

# mineral fractions, normally we don't know these
w <- c(0.346, 0.232, 0.153, 0.096, 0.049, 0.065)

# make synthetic combined pattern
# scale the pure substances by the known proportions
rruff.sample$synthetic_pat <- apply(sweep(rruff.sample[,2:7], 2, w, '*'), 1, sum)

# add 1 more substance that will be unknown to the fitting process
rruff.sample$synthetic_pat <- rruff.sample$synthetic_pat + (1 - sum(w)) * rruff.sample[,8]

# try adding some nasty noise
# rruff.sample$synthetic_pat <- apply(sweep(rruff.sample[,2:7], 2, w, '*'), 1, sum) +
# runif(n, min=0, max=100)

# look at components and combined pattern
par(mfcol=c(7,1), mar=c(0,0,0,0))
plot(1:n, rruff.sample$synthetic_pat, type='l', axes=FALSE)
legend('topright', bty='n', legend='combined pattern', cex=2)
for(i in 2:7)
{
  plot(1:n, rruff.sample[, i], type='l', axes=FALSE)
  legend('topright', bty='n',
         legend=paste(names(rruff.sample)[i], ', ', w[i-1], ', ', sep=''), cex=2)
}

## fit pattern mixtures with a linear model
l <- lm(synthetic_pat ~ nontronite + montmorillonite + clinohlore
+ antigorite + chamosite + hematite, data=rruff.sample)

summary(l)

par(mfcol=c(2,1), mar=c(0.3,0,0,0))
plot(1:n, rruff.sample$synthetic_pat, type='l', lwd=2, lty=2, axes=FALSE,
     xlab=' ', ylab=' ')
lines(1:n, predict(l), col=2)
axis(2, cex.axis=0.75, las=2)
```
legend('topright', legend=c('original', 'fitted'), col=c(1,2), lty=c(2,1), lwd=c(2,1), bty='n', cex=1.25)

plot(1:n, resid(l), type='l', axes=FALSE, xlab='', ylab='', col='blue')
abline(h=0, col=grey(0.5), lty=2)
axis(2, cex.axis=0.75, las=2)
legend('topright', legend=c('residuals'), bty='n', cex=1.25)

## fitting by minimizing an objective function (not run)

# SANN is a slower algorithm, sometimes gives strange results
# default Nelder-Mead is most robust
# CG is fastest --> 2.5 minutes max
# component proportions (fractions), and noise component (intensity units)
# initial guesses may affect the stability / time of the fit

## this takes a while to run
## synthetic pattern
# o <- optim(par=c(0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1), f.noise, method='CG', pure.patterns=rruff.sample[,2:7],
# sample.pattern=rruff.sample$synthetic_pat)
#
## estimated mixture proportions
# o$par
#
## compare with starting proportions
# rbind(o$par[1:n.components], w)
#
## if we had an unkown pattern we were trying to match, compare fitted here
## compute R value 0.1 - 0.2 considered good
## sum(D^2) / sum(s)
## o$value / sum(rruff.sample$sample)
#
## plot estimated mixture vs sample
## combine pure substances
# pure.mixture <- apply(sweep(rruff.sample[,2:7], 2, o$par[1:n.components], 'x'), 1, sum)
#
## add in noise
# noise.component <- o$par[n.components+1]
# est.pattern <- pure.mixture + noise.component
#
## plot results
# par(mfcol=c(2,1), mar=c(0,3,0,0))
# plot(1:n, rruff.sample$synthetic_pat, type='l', lwd=2, lty=2, axes=FALSE,
# xlab='', ylab='')
# lines(1:n, est.pattern, col=2)
# lines(1:n, rep(noise.component, n), col=3)
generalize.hz

Description
Generalize a vector of horizon names, based on new classes, and REGEX patterns.

Usage
generalize.hz(x, new, pat, non.matching.code, hzdepm)

Arguments
x      a character vector of horizon names
new    a character vector of new horizon classes
pat    a character vector of REGEX, same length as x
non.matching.code text used to describe any horizon not matching any item in pat
hzdepm a numeric vector of horizon mid-points, must not contain NA, same length as x

Value
factor of the same length as x

Author(s)
Dylan E. Beaudette

References
http://casoilresource.lawr.ucdavis.edu/
get.ml.hz

Examples

```r
data(spl)

# check original distribution of hz designations
table(spl$name)

# generalize
spl$genhz <- generalize.hz(spl$name,
  new=c('0','A','B','C','R'),
  pat=c('0', '^A','^B','C','R'))

# see how we did / what we missed
table(spl$genhz, spl$name)
```

---

determine ml horizon boundaries

Description

This function accepts input from slab() along with a vector of horizon names, and returns a data.frame of the most likely horizon boundaries.

Usage

```r
get.ml.hz(x, o.names)
```

Arguments

- `x` output from slab
- `o.names` an optional character vector of horizon designations that will be used in the final table

Details

This function expects that `x` is a data.frame generated by slab. If `x` was not generated by slab, then `o.names` is required.

Value

A dataframe with the following columns:

- `hz` horizon names
- `top` top boundary
- `bottom` bottom boundary
- `confidence` integrated probability over thickness of each ML horizon, rounded to the nearest integer
pseudo.brier  A "pseudo" Brier Score for a multi-class prediction, where the most-likely horizon label is treated as the "correct" outcome. Details on the calculation for traditional Brier Scores here: [http://en.wikipedia.org/wiki/Brier_score#Original_definition_by_Brier](http://en.wikipedia.org/wiki/Brier_score#Original_definition_by_Brier). Lower values suggest better agreement between ML horizon label and class-wise probabilities.

mean.H  mean Shannon entropy (bits), derived from probabilities within each most-likely horizon. Larger values suggest more confusion within each ML.

**Author(s)**

D.E. Beaudette

**See Also**

slab

**Examples**

```r
data(sp1)
depths(sp1) <- id ~ top + bottom

# normalize horizon names: result is a factor
sp1$name <- generalize.hz(sp1$name,
                  new=c('0','A','B','C'),
                  pat=c('0','^A','^B','C'))

# compute slice-wise probability so that it sums to contributing fraction, from 0-150
a <- slab(sp1, f=-. name, cpms=1, slab.structure=0:150)

# generate table of ML horizonation
get.ml.hz(a)
```

---

**getSoilDepthClass  Generate Soil Depth Class Matrix**

**Description**

Generate a boolean matrix of soil depth classes from a SoilProfileCollection object.

**Usage**

`getSoilDepthClass(f, depth.classes = c(very.shallow = 25, shallow = 50, mod.deep = 100, deep = 150, very.deep = 1000), ...)`

**Arguments**

- `f`  a SoilProfileCollection object
- `depthclasses`  a named vector of classes and depth breaks
- `...`  arguments passed to `estimateSoilDepth`
groupedProfilePlot

Value

A data.frame containing soil depth and depth class for each profile, see examples.

Author(s)

D.E. Beaudette and J.M. Skovlin

See Also

estimateSoilDepth

Examples

data(sp1)
depths(sp1) <- id ~ top + bottom

# generate depth-class matrix
sdc <- getSoilDepthClass(sp1, name='name', top='top', bottom='bottom')

# inspect
head(sdc)

# join back into sp1 as site-level data
site(sp1) <- sdc

## Not run:
## sample data
data(gopheridge, package='soilDB')

getSoilDepthClass(gopheridge)

## End(Not run)

---

groupedProfilePlot  Grouped Soil Profile Plot

Description

Plot a collection of soil profiles, sorted and labeled by group.

Usage

groupedProfilePlot(x, groups, group.name.offset = -5,
group.name.cex = 0.75, group.line.col = "RoyalBlue",
group.line.lwd = 2, group.line.lty = 2, break.style='line',
arrow.offset=group.name.offset + 5, arrow.length=0.1, ...)
groupedProfilePlot

Arguments

x
a SoilProfileCollection object

groups
the name of a site-level attribute that defines groups, factor levels will influence plotting order

group.name.offset
vertical offset for group names, single numeric value or vector of offsets

group.name.cex
font size for group names

group.line.col
color for line that splits groups

group.line.lwd
width of line that splits groups

group.line.lty
style of line that splits groups

break.style
style of group boundaries: "line", "arrow", "both"

arrow.offset
vertical offset for "arrow" style boundaries, single numeric value or vector of offsets

arrow.length
value passed to arrows to define arrow head size

... further arguments to plotSPC

Details

The ordering of groups can be adjusted by converting the site-level attribute used for grouping into a factor and explicitly setting the levels.

Author(s)

D.E. Beaudette

See Also

plotSPC

Examples

# sample data
data(sp1)
# convert colors from Munsell to hex-encoded RGB
sp1$soil_color <- with(sp1, munsell2rgb(hue, value, chroma))

# promote to SoilProfileCollection
depths(sp1) <- id ~ top + bottom
site(sp1) <- ~ group

# plot profiles, sorted and annotated by 'group'
par(mar=c(1,1,1,1))
groupedProfilePlot(sp1, groups='group', max.depth=150, group.name.offset = -12, id.style='side')

# make fake site-level attribute and adjust levels
sp1$new.group <- sample(letters[1:3], size=length(sp1), replace=TRUE)

**guessGenHzLevels**

**Guess Appropriate Ordering for Generalized Horizon Labels**

**Description**

This function makes an (educated) guess at an appropriate set of levels for generalized horizon labels using the median of horizon depth mid-points.
Usage

guessGenHzLevels(x, hz = "genhz")

Arguments

x       a SoilProfileCollection object
hz      name of horizon-level attribute containing generalized horizon labels, see details

Details

This function is useful when groups of horizons have been generalized via some method other than generalize.hz. For example, it may be useful to generalize horizons using labels derived from slice depths. The default sorting of these labels will not follow a logical depth-wise sorting when converted to a factor. guessGenHzLevels does a good job of "guessing" the proper ordering of these labels based on median horizon depth mid-point.

Value

a list:

levels  a vector of levels sorted by median horizon depth mid-point
median.depths  a vector of median horizon mid-points

Author(s)

D.E. Beaudette

See Also

generalize.hz

Examples

# load some example data
data(sp1, package='aqp')

# upgrade to SoilProfileCollection
depths(sp1) <- id - top + bottom

# generalize horizon names
n <- c('O', 'A', 'B', 'C')
p <- c('O', 'A', 'B', 'C')
sp1$genhz <- generalize.hz(sp1$name, n, p)

# note: levels are in the order in which originally defined:
levels(sp1$genhz)

# generalize horizons by depth slice
s <- slice(sp1, c(5, 10, 15, 25, 50, 100, 150) - .)
s$slice <- paste0(s$top, ' cm')
hzDistinctnessCodeToOffset

Convert Horizon Distinctness Codes

Description
This function accepts a vector of horizon distinctness codes, a look-up vector of codes, and a corresponding vector of vertical offsets. The defaults are based on USDA-NCSS field methods.

Usage
hzDistinctnessCodeToOffset(x, codes = c("A", "C", "G", "D"), offset = c(0.5, 1.5, 5, 10))

Arguments
x vector of distinctness codes to be converted to offsets
codes vector of unique distinctness codes
offset vector of offsets associated with distinctness codes

Details
Missing data (NA) or codes that are not defined in the 'codes' argument are returned as 0 offsets.

Value
a vector of vertical offsets, with the same length as the number of distinctness codes passed to the function

Author(s)
D.E. Beaudette

References
http://www.nrcs.usda.gov/wps/portal/nrcs/detail/soils/ref/?cid=nrcs142p2_054184
See Also

plotSPC

Examples

data(spl)
hzDistinctnessCodeToOffset(spl$bound_distinct)

hzTransitionProbabilities

*Horizon Transition Probabilities*

Description

Functions for creating and working with horizon (sequence) transition probability matrices.

Usage

hzTransitionProbabilities(x, name, loopTerminalStates = FALSE)

genhzTableToAdjMat(tab)

mostLikelyHzSequence(mc, t0, maxIterations=10)

Arguments

x
A SoilProfileCollection object.

name
A horizon level attribute in x that names horizons.

loopTerminalStates
should terminal states loop back to themselves? This is useful when the transition probability matrix will be used to initialize a markovchain object. See examples below.

tab
A cross-tabulation relating original horizon designations to new, generalized horizon designations.

mc
A markovchain object, initialized from a horizon sequence transition probability matrix with looped terminal states.

t0
Time-zero: a label describing an initial state within a markovchain object.

maxIterations
the maximum number of iterations when search for the most-likely horizon sequence

Details

Details and related tutorial pending...
hzTransitionProbabilities

Value

The function hzTransitionProbabilities returns a square matrix of transition probabilities. See examples.

The function genhzTableToAdjMat returns a square adjacency matrix. See examples.

The function mostLikelyHzSequence returns the most likely sequence of horizons, given a markovchain object initialized from horizon transition probabilities and an initial state, t0. See examples.

Note

These functions are still experimental and subject to change.

Author(s)

D.E. Beaudette

See Also

generalize.hz

Examples

data(sp4)
depths(sp4) <- id ~ top + bottom

# horizon transition probabilities: row -> col transitions
(tp <- hzTransitionProbabilities(sp4, 'name'))

## Not run:
## plot TP matrix with functions from sharpshootR package
library(sharpshootR)
par(mar=c(0,0,0,0), mfcol=c(1,2))
plot(sp4)
plotSoilRelationGraph(tp, graph.mode = 'directed', edge.arrow.size=0.5)

## demonstrate genhzTableToAdjMat usage
data(loafercreek, package='soilDB')

# convert contingency table -> adj matrix / TP matrix
tab <- table(loafercreek$hzname, loafercreek$genhz)
m <- genhzTableToAdjMat(tab)

# plot
par(mar=c(0,0,0,0), mfcol=c(1,1))
plotSoilRelationGraph(m, graph.mode = 'directed', edge.arrow.size=0.5)

## demonstrate markovchain integration
library(markovchain)
.tp.loops <- hzTransitionProbabilities(sp4, 'name', loopTerminalStates = TRUE)
# init new markovchain from TP matrix
mc <- new("markovchain", states=dimnames(tp.loops)[[1]], transitionMatrix = tp.loops)

# simple plot
plot(mc, edge.arrow.size=0.5)

# check absorbing states
absorbingStates(mc)

# steady-state:
steadyStates(mc)

## End(Not run)

---

#### missingDataGrid

**Missing Data Grid**

**Description**

Generate a levelplot of missing data from a SoilProfileCollection object.

**Usage**

```r
missingDataGrid(s, max_depth, vars, filter.column = NULL,
                filter.regex = NULL, cols = NULL, ...)
```

**Arguments**

- `s` a SoilProfileCollection object
- `max_depth` integer specifying the max depth of analysis
- `vars` character vector of column names over which to evaluate missing data
- `filter.column` a character string naming the column to apply the filter REGEX to
- `filter.regex` a character string with a regular expression used to filter horizon data OUT of the analysis
- `cols` a vector of colors
- `...` additional arguments passed on to levelplot

**Details**

This function evaluates a ‘missing data fraction’ based on slice-wise evaluation of named variables in a SoilProfileCollection object.

**Value**

A data.frame describing the percentage of missing data by variable.
Note

A lattice graphic is printed to the active output device.

Author(s)

D.E. Beaudette

See Also

slice

Examples

```r
## visualizing missing data
# 10 random profiles
require(plyr)
s <- ldply(1:10, random_profile)

# randomly sprinkle some missing data
s[sample(nrow(s), 5), 'p1'] <- NA
s[sample(nrow(s), 5), 'p2'] <- NA
s[sample(nrow(s), 5), 'p3'] <- NA

# set all p4 and p5 attributes of 'soil 1' to NA
s[which(s$id == '1'), 'p4'] <- NA
s[which(s$id == '1'), 'p5'] <- NA

# upgrade to SPC
depths(s) <- id ~ top + bottom

# plot missing data via slicing + levelplot
missingDataGrid(s, max_depth=100, vars=c('p1', 'p2', 'p3', 'p4', 'p5'),
    main='Missing Data Fraction')
```

Description

A lookup table of interpolated Munsell color chips for common soil colors.

Usage

```r
data(munsell)
```
Format

A data frame with 8825 rows.

- hue  Munsell Hue, upper case
- value  Munsell Value
- chroma  Munsell Chroma
- r  sRGB "red" value (0-1)
- g  sRGB "green" value (0-1)
- b  sRGB "blue" value (0-1)
- L  CIE LAB "L" coordinate
- A  CIE LAB "A" coordinate
- B  CIE LAB "B" coordinate

Details

See munsell2rgb for conversion examples. Note that this table does not currently have entries for values of 2.5—common in most soil color books. These chips should be added in the next major release of aqp. Values are referenced to the D65 standard illuminant.

Source

Color chip XYZ values: http://www.rit.edu/cos/colorscience/rc_munsell_renotation.php

References

http://dx.doi.org/10.1016/j.cageo.2012.10.020  Methods used to generate this table

Examples

data(munsell)

munsell2rgb  Convert Munsell Notation to and from sRGB color coordinates

Description

Color conversion based on a look-up table of common soil colors.

Usage

munsell2rgb(the_hue, the_value, the_chroma, alpha=1,
maxColorValue=1, return_triplets=FALSE)
rgb2munsell(color, colorSpace='LAB', nClosest=1)
parseMunsell(munsellColor, convertColors=TRUE, ...)
getClosestMunsellChip(munsellColor, convertColors=TRUE, ...)
Arguments

the_hue a vector of one or more hues, upper-case
the_value a vector of one or more values
the_chroma a vector of one or more chromas, may be NA for neutral hues
alpha alpha channel value (for transparency effects)
maxColorValue maximum sRGB color value (see rgb)
return_triplets should the function return raw sRGB triplets instead of an R color
color a data.frame or matrix object containing color-space coordinates: [R, G, B]
colorSpace the colorspace to use for finding the closest chip, LAB is the most accurate, sRGB is another possibility
nClosest number of closest Munsell colors to return
munsellColor character vector of strings containing Munsell colors, e.g. '10YR 4/3'
convertColors logical, should parsed Munsell colors be converted into sRGB values
... further arguments to munsell2rgb

Details

These functions generalize to vectorized usage, as long as the length of each argument is the same. Both functions will pad output with NA if there are any NA present in the inputs.

Neutral hues are approximated by greyscale shades ranging from 20% (darker) to 80% (lighter). No chroma is required for neutral hues.

Gley soil colors that are missing a chroma will not be correctly interpreted. Consider using a chroma of 1.

Values of "2.5" (common in soil color descriptions) are silently truncated to "2".

Non-standard Munsell colors (e.g. '7.9YR 2.7/2.0') can be matched (nearest-neighbor, no interpolation) to the closest color within the 'munsell' sRGB look-up table via getClosestMunsellChip(). See examples below.

Value

For Munsell to sRGB conversion, a vector of R colors is returned that is the same length as the input data. If return_triplets is TRUE, then a dataframe (of sample length as input) of r,g,b values is returned.

For sRGB to Munsell conversion, a dataframe (NA-padded) of hue, value, chroma, and Euclidean distance to nearest matching color is returned.

Note

Care should be taken when using the resulting sRGB values; they are close to their Munsell counterparts, but will vary based on your monitor and ambient lighting conditions. Also, the value used for maxColorValue will affect the brightness of the colors. The default value (1) will usually give acceptable results, but can be adjusted to force the colors closer to what the user thinks they should look like.
Author(s)

D.E. Beaudette

References


Examples

# Munsell to sRGB triplets:
# function is vectorized as long as arguments are the same length
color <- munsell2rgb(the_hue=c('10YR', '2.5YR'), the_value=c(3, 5),
the_chroma=c(5, 6), return_triplets=TRUE)

# RGB triplets to closest Munsell color (in sRGB space)
# function is vectorized
rgb2munsell(color)

# neutral hues (N) map to approximate greyscale colors
# chroma may be any number or NA
g <- expand.grid(hue='N', value=2:8, chroma=NA, stringsAsFactors=FALSE)
munsell2rgb(g$hue, g$value, g$chroma)

# basic example: no factors!
d <- expand.grid(hue='10YR', value=2:8, chroma=1:8, stringsAsFactors=FALSE)
d$color <- with(d, munsell2rgb(hue, value, chroma))

# similar to the 10YR color book page
plot(value ~ chroma, data=d, col=d$color, pch=15, cex=3)

# multiple pages of hue:
hues <- c('2.5YR','5YR','7.5YR','10YR')
d <- expand.grid(hue=hues, value=2:8, chroma=seq(2,8,by=2), stringsAsFactors=FALSE)
d$color <- with(d, munsell2rgb(hue, value, chroma))

# plot: note that we are setting panel order from red--->yellow
library(lattice)
xyplot(value ~ factor(chroma) | factor(hue, levels=hues),
main="Common Soil Colors", layout=c(4,1), scales=list(alternating=1),
strip=strip.custom(bg=grey(0.85)),
data=d, as.table=TRUE, subscripts=TRUE, xlab='Chroma', ylab='Value',
panel=function(x, y, subscripts, ...){
  panel.xyplot(x, y, pch=15, cex=4, col=d$color[subscripts])
}
)
# try again, this time annotate with LAB coordinates:
if(require(colorspace)) {
  d.rgb <- with(d, munsell2rgb(hue, value, chroma, return_triplets=TRUE))
d.lab <- as(with(d.rgb, sRGB(r,g,b)), 'LAB')
d <- data.frame(d, d.lab@coords)

xyplot(value ~ factor(chroma) | factor(hue, levels=hues),
        main="Common Soil Colors - Annotated with LAB Coordinates", layout=c(4,1),
        scales=list(alternating=1), strip=strip.custom(bg=grey(0.85)),
        data=d, as.table=TRUE, subscripts=TRUE, xlab='Chroma', ylab='Value',
        panel=function(x, y, subscripts, ...) {
          panel.xyplot(x, y, pch=15, cex=7, col=d$subscripts[color])
          lab.text <- with(d[subscripts, ], paste(round(L), round(A), round(B), sep='\n'))
          panel.text(x, y, labels=lab.text, cex=0.75, col='white', font=2)}
}

# also demonstrate A ~ hue for each slice of chroma
xyplot(A ~ factor(hue, levels=hues) | factor(value), groups=chroma, data=d,
        scales=list(alternating=1), strip=strip.custom(bg=grey(0.85)),
        main="A-coordinate vs. Munsell Hue", sub='panels are Munsell value, colors are Munsell chroma',
        xlab='Munsell Hue', ylab='A-coordinate', pch=16,
        type='b', as.table=TRUE, auto.key=list(lines=TRUE, points=FALSE, columns=4))

# soils example
data(sp1)

# convert colors
sp1$soil_color <- with(sp1, munsell2rgb(hue, value, chroma))

# simple plot, may need to tweak gamma-correction...
image(matrix(1:nrow(sp1)), axes=FALSE, col=sp1$soil_color, main='Soil Colors')

# convert into a more useful color space
# you will need the colorspace package for this to work
if(require(colorspace)) {
  # keep RGB triplets from conversion
  sp1.rgb <- with(sp1, munsell2rgb(hue, value, chroma, return_triplets=TRUE))

  # convert into LAB color space
  sp1.lab <- as(with(sp1.rgb, sRGB(r,g,b)), 'LAB')
  plot(sp1.lab)
}

# convert a non-standard color to closest "chip" in `munsell` look-up table
getClosestMunsellChip(7.9YR 2.7/2.0, convertColors = FALSE)

# convert directly to R color
getClosestMunsellChip(7.9YR 2.7/2.0)
panel.depth_function  Lattice Panel Function for Soil Profiles

Description

Panel function for plotting grouped soil property data, along with upper and lower estimates of uncertainty.

Usage

```r
panel.depth_function(x, y, id = NULL, upper = NULL, lower = NULL,
                      subscripts = NULL, groups = NULL, sync.colors = FALSE,
                      cf = NULL, cf.col = NA, cf.interval = 20, ...)
```

Arguments

- **x**: x values (generated by calling lattice function)
- **y**: y values (generated by calling lattice function)
- **id**: vector of id labels, same length as x and y—only required when plotting segments (see Details section)
- **upper**: vector of upper confidence envelope values
- **lower**: vector of lower confidence envelope values
- **subscripts**: paneling indices (generated by calling lattice function)
- **groups**: grouping data (generated by calling lattice function)
- **sync.colors**: optionally sync the fill color within the region bounded by (lower–upper) with the line colors
- **cf**: optionally annotate contributing fraction data at regular depth intervals see `slab`
- **cf.col**: optionally color for contributing fraction values, typically used to override the line color
- **cf.interval**: number of depth units to space printed contributing fraction values
- **...**: further arguments to lower-level lattice plotting functions, see below

Details

This function can be used to replace `panel.superpose` when plotting depth function data. When requested, contributing fraction data are printed using colors the same color as corresponding depth function lines unless a single color value is given via `cf.col`.

Author(s)

Dylan E. Beaudette

References

http://casoilresource.lawr.ucdavis.edu/
plotMultipleSPC

Description

Combine multiple SoilProfileCollection objects into a single profile sketch, with annotated groups.

Usage

plotMultipleSPC(spc.list, group.labels, 
    args = rep(list(NA), times=length(spc.list)), 
    arrow.offset = 2, bracket.base.depth = 95, 
    ...)

Arguments

- `spc.list`: a list of SoilProfileCollection objects
- `group.labels`: a vector of group labels, one for each SoilProfileCollection object
- `args`: a list of arguments passed to plotSPC, one for each SoilProfileCollection object

See Also

- `sp1`, `slice`, `slab`

Examples

```r
library(lattice)
data(sp1)

# 1. plotting mechanism for step-functions derived from soil profile data
xyplot(cbind(top, bottom) ~ prop, data=sp1, id=sp1$id, 
    panel=panel.depth.function, ylim=c(250, -10), 
    scales=list(y=list(tick.number=10)), xlab='Property', 
    ylab='Depth (cm)', main='panel.depth.function() demo'
)

# 1.1 include groups argument to leverage lattice styling framework
sp1$group <- factor(sp1$group, labels=c('Group 1', 'Group2'))

xyplot(cbind(top, bottom) ~ prop, groups=group, data=sp1, id=sp1$id, 
    panel=panel.depth.function, ylim=c(250, -10), 
    scales=list(y=list(tick.number=10)), xlab='Property', 
    ylab='Depth (cm)', main='panel.depth.function() demo', 
    auto.key=list(columns=2, points=FALSE, lines=TRUE), 
    par.settings=list(superpose.line=list(col=c('Orange', 'RoyalBlue')))
)
```
arrow.offset  vertical offset in depth from base of start / end profiles and group bracket arrows
bracket.base.depth
    baseline depth used for group brackets
...
    additional arguments to the first call to plotSPC

Details
See examples below for usage.

Note
Multiple color legends for thematic profile sketches are not currently supported, use with caution.

Author(s)
D.E. Beaudette and Ben Marshall

See Also
profileGroupLabels

Examples
# load sample data
data(sp3)
data(sp4)

# convert soil colors
sp3$h <- NA; sp3$s <- NA; sp3$v <- NA
sp3.rgb <- with(sp3, munsell2rgb(hue, value, chroma, return_triplets=TRUE))
sp3[, c('h','s','v')] <- t(with(sp3.rgb, rgb2hsv(r, g, b, maxColorValue=1)))

# promote to SoilProfileCollection
depths(sp3) <- id ~ top + bottom
depths(sp4) <- id ~ top + bottom

# combine into a list
spc.list <- list(sp3, sp4)

# plot multiple SPC objects, with list of named arguments for each call to plotSPC
par(mar=c(1,1,3,3))
plotMultipleSPC(spc.list, group.labels=c('Collection 1', 'Collection 2'),
args=list(list(name='name', id.style='top'),
list(name='name', id.style='side')), bracket.base.depth=120)
plot_distance_graph

**Between Individual Distance Plot**

**Description**
Plot pair-wise distances between individuals as line segments.

**Usage**
```
plot_distance_graph(D, idx = 1:dim(as.matrix(D))[1])
```

**Arguments**
- `D` distance matrix, should be of class 'dist' or compatible class
- `idx` an integer sequence defining which individuals should be compared

**Details**
By default all individuals are plotting on the same axis. When there are more than about 10 individuals, the plot can become quite messy. See examples below for ideas.

**Value**
No value is returned.

**Author(s)**
Dylan E Beaudette

**References**
http://casoilresource.lawr.ucdavis.edu/

**See Also**
- `sp2`, `profile_compare`

**Examples**
```
data(sp2)

d <- profile_compare(sp2, vars=c('prop','field_ph','hue','value'),
  max_d=100, k=0.01, sample_interval=5)

par(mfcol=c(3,1), mar=c(2.5,4.5,1,1))
plot_distance_graph(d, idx=1:6)
plot_distance_graph(d, idx=7:12)
plot_distance_graph(d, idx=12:18)
```
profileApply-methods  Apply a function to soil profiles within a SoilProfileCollection object.

Description

Apply a function to soil profiles within a SoilProfileCollection object, each iteration has access to a SoilProfileCollection object.

Usage

# method for SoilProfileCollection objects
profileApply(object, FUN, simplify=TRUE, ...)

Arguments

- **object**: a SoilProfileCollection
- **FUN**: a function to be applied to each profile within the collection
- **simplify**: logical, should the result be simplified to a vector? see examples
- **...**: further arguments passed to FUN

Value

When simplify is TRUE, a vector of length nrow(object) (horizon data) or of length length(object) (site data). When simplify is FALSE, a list is returned.

Methods

signature(object = "SoilProfileCollection")

See Also

slab, estimateSoilDepth

Examples

data(sp1)
depths(sp1) <- id ~ top + bottom

# estimate soil depth using horizon designations
profileApply(sp1, estimateSoilDepth, name='name', top='top', bottom='bottom')

# scale properties within each profile
# scaled = (x - mean(x)) / sd(x)
sp1$d <- profileApply(sp1, FUN=function(x) round(scale(x$prop), 2))
plot(sp1, name='d')

# compute depth-wise differencing by profile
# note that our function expects that the column 'prop' exists
f <- function(x) ( c(x$prop[1], diff(x$prop)) )
sp1$d <- profileApply(sp1, FUN=f)
plot(sp1, name='d')

# compute depth-wise cumulative sum by profile
# note the use of an anonymous function
sp1$d <- profileApply(sp1, FUN=function(x) cumsum(x$prop))
plot(sp1, name='d')

# compute profile-means, and save to @site
# there must be some data in @site for this to work
site(sp1) <- ~ group
sp1$mean_prop <- profileApply(sp1, FUN=function(x) mean(x$prop, na.rm=TRUE))

# re-plot using ranks defined by computed summaries (in @site)
plot(sp1, plot.order=rank(sp1$mean_prop))

## iterate over profiles, subsetting horizon data

# example data
data(sp1)

# promote to SoilProfileCollection
depths(sp1) <- id ~ top + bottom
site(sp1) <- ~ group

# make some fake site data related to a depth of some importance
sp1$dep <- profileApply(sp1, function(i) (round(rnorm(n=1, mean=mean(i$top)))))

# custom function for subsetting horizon data, by profile
# keep horizons with lower boundary < site-level attribute 'dep'
fun <- function(i) {
  # extract horizons
  h <- horizons(i)
  # make an expression to subset horizons
  exp <- paste('bottom < ', i$dep, sep='')
  # subset horizons, and write-back into current SPC
  horizons(i) <- subset(h, subset=eval(parse(text=exp)))
  # return modified SPC
  return(i)
}

# list of modified SoilProfileCollection objects
l <- profileApply(sp1, fun, simplify=FALSE)

# re-combine list of SoilProfileCollection objects into a single SoilProfileCollection
sp1.sub <- do.call(rbind, l)

# graphically check
par(mfrow=c(2,1), mar=c(0,0,1,0))
plot(spl)
points(1:length(spl), spl$dep, col='red', pch=7)
plot(spl$sub)

## Not run:
##
## helper functions: these must be modified to suit your own data
##
# compute the weighted-mean of some property within a given diagnostic horizon
# note that this requires conditional eval of data that may contain NA
# see ?slab for details on the syntax
# note that function expects certain columns within 'x'
f.diag.wt.prop <- function(x, d_hz, prop) {
  # extract diagnostic horizon data
d <- diagnostic_hz(x)
  # subset to the requested diagnostic hz
d <- d[d$diag_kind == d_hz, ]
  # if missing return NA
if(nrow(d) == 0)
  return(NA)
  # extract depths and check for missing
sv <- c(d$featdepb, d$featdept)
if(any(is.na(sv)))
  return(NA)
  # create formula from named property
fm <- as.formula(paste('~', prop))
  # return just the (weighted) mean, accessed from @horizons
s <- slab(x, fm, slab.structure=sv, slab.fun=mean)$value
return(s)
}

# conditional eval of thickness of some diagnostic feature or horizon
# will return a vector of length(x), you can save to @site
f.diag.thickness <- function(x, d_hz) {
  # extract diagnostic horizon data
d <- diagnostic_hz(x)
  # subset to the requested diagnostic hz
d <- d[d$diag_kind == d_hz, ]
  # if missing return NA
if(nrow(d) == 0)
  return(NA)
  # compute thickness
thick <- d$featdepb - d$featdept
return(thick)
profileGroupLabels

Description

Labels groups of soil profiles within soil profile sketches.

Usage

profileGroupLabels(x0, x1, labels, y0 = 100, y1 = 98, label.offset = 2, label.cex = 0.75)

Arguments

x0 integer indices to the first profile within each group
x1 integer indices to the last profile within each group
labels vector of group labels
y0 baseline depth used for group brackets
profileGroupLabels

y1  depth used for start and end markers for group brackets (see examples)
label.offset  vertical offset of group labels from baseline
label.cex  label size

Details

See examples below for ideas.

Note

This function is typically called by some other convenience function such as plotMultipleSPC.

Author(s)

D.E. Beaudette

See Also

plotMultipleSPC

Examples

# load sample data
data(sp3)
data(sp4)

# convert soil colors
sp3$h <- NA; sp3$s <- NA; sp3$v <- NA
sp3$rgb <- with(sp3, munsell2rgb(hue, value, chroma, return_triplets=TRUE))
sp3[, c('h','s','v')] <- t(with(sp3$rgb, rgb2hsv(r, g, b, maxColorValue=1)))

# promote to SoilProfileCollection
depths(sp3) <- id ~ top + bottom
depths(sp4) <- id ~ top + bottom

# combine into a list
spc.list <- list(sp3, sp4)

# compute group lengths and start/stop locations
n.groups <- length(spc.list)
spc.lengths <- sapply(spc.list, length)
n.pedons <- sum(spc.lengths)
group.starts <- c(1, 1 + cumsum(spc.lengths[-n.groups]))
group.ends <- cumsum(spc.lengths)

# determine depths of first / last profile in each group
yy <- unlist(sapply(spc.list, function(i) profileApply(i, max)))
tick.heights <- yy[c(group.starts, group.ends)] + 2

# plot 2 SoilProfileCollection objects on the same axis
par(mar=c(1,1,1,1))
profile_compare-methods

Numerical Soil Profile Comparison

Description

Performs a numerical comparison of soil profiles using named properties, based on a weighted, summed, depth-segment-aligned dissimilarity calculation. If \( s \) is a \texttt{SoilProfileCollection}, site-level variables (2 or more) can also be used. The site-level and horizon-level dissimilarity matrices are then re-scaled and averaged.

Usage

```r
pc(s, vars, max_d, k, filter=NULL, sample_interval=NA,
replace_na=TRUE, add_soil_flag=TRUE,
return_depth_distances=FALSE, strict_hz_eval=FALSE,
progress='none', plot.depth.matrix=FALSE, rescale.result=FALSE,
verbose=FALSE)
```

Arguments

- **s**: a dataframe with at least 2 columns of soil properties, and an 'id' column for each profile. horizon depths must be integers and self-consistent.
- **vars**: A vector with named properties that will be used in the comparison. These are typically column names describing horizon-level attributes (2 or more), but can also contain site-level attributes (2 or more) if \( s \) is a \texttt{SoilProfileCollection}.
- **max_d**: depth-slices up to this depth are considered in the comparison.
- **k**: a depth-weighting coefficient, use '0' for no depth-weighting (see examples below).
- **filter**: an index used to determine which horizons (rows) are included in the analysis.
- **sample_interval**: use every n-th depth slice instead of every depth slice, useful for working with > 1000 profiles at a time.
- **replace_na**: if TRUE, missing data are replaced by maximum dissimilarity (TRUE).
- **add_soil_flag**: The algorithm will generate a 'soil'/non-soil' matrix for use when comparing soil profiles with large differences in depth (TRUE). See details section below.
- **return_depth_distances**: return intermediate, depth-wise dissimilarity results (FALSE).
- **strict_hz_eval**: should horizons be strictly checked for internal self-consistency? (FALSE)
progress 'none' (default): argument passed to `dplyr` and related functions, see `create_progress_bar` for all possible options; 'text' is usually fine.

plot.depth.matrix should a plot of the 'soil'/non-soil' matrix be returned (FALSE)

rescale.result should the result be rescaled by dividing by max(D) (FALSE)

verbose extra debug output (FALSE)

Details

Variability in soil depth can interfere significantly with the calculation of between-profile dissimilarity—what is the numerical “distance” (or dissimilarity) between a slice of soil from profile A and the corresponding, but missing, slice from a shallower profile B? Gower’s distance metric would yield a NULL distance, despite the fact that intuition suggests otherwise: shallower soils should be more dissimilar from deeper soils. For example, when a 25 cm deep profile is compared with a 50 cm deep profile, numerical distances are only accumulated for the first 25 cm of soil (distances from 26 - 50 cm are NULL). When summed, the total distance between these profiles will generally be less than the distance between two profiles of equal depth. Our algorithm has an option (setting `replace_na=TRUE`) to replace NULL distances with the maximum distance between any pair of profiles for the current depth slice. In this way, the numerical distance between a slice of soil and a corresponding slice of non-soil reflects the fact that these two materials should be treated very differently (i.e. maximum dissimilarity).

This alternative calculation of dissimilarities between soil and non-soil slices solves the problem of comparing shallow profiles with deeper profiles. However, it can result in a new problem: distances calculated between two shallow profiles will be erroneously inflated beyond the extent of either profile’s depth. Our algorithm has an additional option (setting `add_soil_flag=TRUE`) that will preserve NULL distances between slices when both slices represent non-soil material. With this option enabled, shallow profiles will only accumulate mutual dissimilarity to the depth of the deeper profile.

Note that when the `add_soil_flag` option is enabled (default), slices are classified as 'soil' down to the maximum depth to which at least one of variables used in the dissimilarity calculation is not NA. This will cause problems when profiles within a collection contain all NAs within the columns used to determine dissimilarity. An approach for identifying and removing these kind of profiles is presented in the examples section below.

A notice is issued if there are any NA values within the matrix used for distance calculations, as these values are optionally replaced by the max dissimilarity.

Our approach builds on the work of (Moore, 1972) and the previously mentioned depth-slicing algorithm.

Value

A dissimilarity matrix object of class 'dissimilarity, dist', optionally scaled by max(D).

Methods

- data = "SoilProfileCollection" see `SoilProfileCollection`
- data = "data.frame" see `profile_compare`
profile_compare-methods

Author(s)

Dylan E. Beaudette

References


See Also

slice, daisy

Examples

```r
## 1. check out the influence depth-weight coef:
require(lattice)
z <- rep(1:100,4)
k <- rep(c(0,0.1,0.05,0.01), each=100)
w <- 100*exp(-k*z)

xyplot(z ~ w, groups=k, ylim=c(105,-5), xlim=c(-5,105), type='l',
ylab='Depth', xlab='Weighting Factor',
auto.key=list(columns=4, lines=TRUE, points=FALSE, title="k", cex=0.8, size=3),
panel=function(...) { 
  panel.grid(h=-1,v=-1)
  panel.superpose(...)
})

## 2. basic implementation, requires at least two properties
# implementation for a data.frame class object
data(spi)
d <- profile_compare(spi1, vars=c('prop','group'), max_d=100, k=0.01, plot.depth.matrix=TRUE)

# upgrade to SoilProfileCollection
depths(spi1) <- id ~ top + bottom
op <- par(mfrow=c(1,2))
# perform comparison on SoilProfileCollection object
# compare soil/non-soil matrix plot
d <- profile_compare(spi1, vars=c('prop','group'), max_d=100, k=0.01, plot.depth.matrix=TRUE)

# plot profile collection
plot(spi1)
# annotate max depth of profile comparison
abline(h=100, col='red', lty=2)
par(op)
```
# more soil properties
data(sp2)
d.1 <- profile_compare(sp2, vars=c('prop','field_ph','hue','value'),
                      max_d=100, k=0.01, plot.depth.matrix=TRUE)

# add some missing data:
sp2$prop[1:2] <- NA
d.2 <- profile_compare(sp2, vars=c('prop','field_ph','hue','value'),
                      max_d=100, k=0.01, plot.depth.matrix=TRUE)

# note small changes in d:
cor(d.1, d.2)

## 3. identify profiles within a collection that contain all NAs
require(plyr)
s <- ldply(1:10, random_profile)
depths(s) <- id ~ top + bottom

# replace first profile's data with NA
na.required <- nrow(s[1, ])
s$p[1:na.required] <- NA
s$p2[1:na.required] <- NA

# attempt profile comparison: this won't work, throws an error
# d <- profile_compare(s, vars=c('p1','p2'), max_d=100, k=0)

# check for soils that are missing all clay / total RF data
f.check.NA <- function(i) length(which(is.na(s$p1) | is.na(s$p2))) / nrow(i) == 1
missing.too.much.data.idx <- which(profileApply(s, f.check.NA))

# remove bad profiles and try again: works
s.no.na <- profile_compare(s[-missing.too.much.data.idx, ], vars=c('p1','p2'),
                           max_d=100, k=0, plot.depth.matrix=TRUE)

## 4. better plotting of dendrograms with ape package:
if(require(ape) & require(cluster) & require(MASS)) {
  h <- diana(d)
p <- as.phylo(as.hclust(h))
plot(ladderize(p), cex=0.75, label.offset=1)
tiplot(col=1, pch=15)
}

## 5. other uses of the dissimilarity matrix
# Sammon Mapping: doesn't like '0' values in dissimilarity matrix
d.sam <- sammon(d)

# simple plot
dev.off(); dev.new()
plot(d.sam$points, type = "n", xlim=range(d.sam$points[,1] * 1.5))
text(d.sam$points, labels=row.names(as.data.frame(d.sam$points)),
cex=0.75, col=1)
## random_profile

**Description**

Generate a random soil profile according to set criteria, with correlated depth trends.

**Usage**

```r
random_profile(id, n = c(3, 4, 5, 6), min_thick = 5, max_thick = 30, n_prop = 5, exact = FALSE, method = 'random_walk', HzDistinctSim=FALSE, ...)
```

**Arguments**

- **id** a character or numeric id used for this profile
- **n** vector of possible number of horizons, or the exact number of horizons (see below)
- **min_thick** minimum thickness criteria for a simulated horizon
- **max_thick** maximum thickness criteria for a simulated horizon
- **n_prop** number of simulated soil properties (columns in the returned dataframe)
- **exact** should the exact number of requested horizons be generated? (defaults to FALSE)
- **method** named method used to synthesize depth function ('random_walk' or 'LPP'), see details
- **HzDistinctSim** optionally simulate horizon boundary distinctness codes
- **...** additional parameters passed-in to the LPP (.lpp) function
Details

The random walk method produces profiles with considerable variation between horizons and is based on values from the normal distribution seeded with means and standard deviations drawn from the uniform distribution of [0, 10].

The logistic power peak (LPP) function can be used to generate random soil property depth functions that are sharply peaked. LPP parameters can be hard-coded using the optional arguments: "lpp.a", "lpp.b", "lpp.u", "lpp.d", "lpp.e". Amplitude of the peak is controlled by ("lpp.a + "lpp.b"), depth of the peak by "lpp.u", and abruptness by "lpp.d" and "lpp.e". Further description of the method is outlined in (Brenton et al, 2011). Simulated horizon distinctness codes are based on the USDA-NCSS field description methods (http://www.nrcs.usda.gov/wps/portal/nrcs/detail/?cid=nrcs142p2_054184). Simulated distinctness codes are constrained according to horizon thickness, i.e. a gradual boundary (+/- 5cm) will not be simulated for horizons that are thinner than 3x this vertical distance.

Value

A dataframe with the simulated profile.

Note

See examples for ideas on simulating several profiles at once.

Author(s)

Dylan E. Beaudette

References


See Also

profile_compare, hzDistinctnessCodeToOffset

Examples

# generate 10 random profiles with default settings:
require(plyr)
d <- ldply(1:10, random_profile)

# add a fake color
d$soil_color <- 'white'

# promote to SoilProfileCollection and plot
depths(d) <- id ~ top + bottom
plot(d)

# simulate horizon boundary distinctness codes:
d <- ldply(1:10, random_profile, HzDistinctSim=TRUE)
d$soil_color <- grey(0.85)
depths(d) <- id ~ top + bottom
d$HzD <- HzDistinctnessCodeToOffset(d$HzDistinctCode)
plot(d, Hz.distinctness.offset='HzD')

# depth functions are generated using the LPP function
opar <- par(mfrow=c(2,1), mar=c(0,0,3,0))
# generate data
d <- ldply(1:10, random_profile, n=c(6,7,8), n_prop=1, method='LPP')

# promote to SPC and plot
depths(d) <- id ~ top + bottom
plot(d, color='pl')

# do this again, this time set all of the LPP parameters
d <- ldply(1:10, random_profile, n=c(6,7,8), n_prop=1, method='LPP',
  lpp.a=5, lpp.b=10, lpp.d=5, lpp.e=5, lpp.u=25)
depths(d) <- id ~ top + bottom
plot(d, color='pl')

# reset plotting defaults
par(opar)

# try plotting the LPP-derived simulated data
# aggregated over all profiles
a <- slab(d, fm=-p1)
a$mid <- with(a, (top + bottom) / 2)

library(lattice)
(p1 <- xyplot(mid ~ p.q50, data=a,
  lower=a$p.q25, upper=a$p.q75, ylim=c(150,-5), alpha=0.5,
  panel=panel.depth_function, prepanel=prepanel.depth_function,
  cf=a$contributing_fraction, xlab='Simulated Data', ylab='Depth',
  main='LPP(a=5, b=10, d=5, e=5, u=25)',
  par.settings=list(superpose.line=list(col='black', lwd=2))
))

# optionally add original data as step-functions
if(require(latticeExtra)) {
  h <- horizons(d)
  p1 + as.layer(xyplot(top ~ p1, groups=id, data=h,
    horizontal=TRUE, type='S',
    par.settings=list(superpose.line=list(col='blue', lwd=1, lty=2)))
}

Resample an XRD Pattern

Description

Resample an XRD pattern along a user-defined twotheta resolution via local spline interpolation.

Usage

```
resample.twotheta(twotheta, x, tt.min = min(twotheta),
                 tt.max = max(twotheta), new.res = 0.02)
```

Arguments

- `twotheta`: a vector of twotheta value
- `x`: a vector of diffraction intensities corresponding with twotheta values
- `tt.min`: new minimum twotheta value, defaults to current minimum
- `tt.max`: new maximum twotheta value, defaults to current maximum
- `new.res`: new twotheta resolution, defaults to 0.02

Details

Sometimes XRD patterns are collected at different resolutions, or at a resolution that is too great for full pattern matching. This function can be used to resample patterns to a consistent twotheta resolution, or to decimate massive patterns.

Value

A dataframe with the following columns

- `twotheta`: new sequence of twotheta values
- `x`: resampled diffraction intensities

Author(s)

Dylan E Beaudette

References

http://casoilresource.lawr.ucdavis.edu/

See Also

`rruff.sample`
Examples

```r
data(rruff.sample)

# resample single pattern
nontronite.resamp <- with(rruff.sample,
    resample.twotheta(twotheta, nontronite, new.res=0.02) )

# plot original vs. resampled pattern
plot(nontronite ~ twotheta, data=rruff.sample, type='l', col='grey')
lines(nontronite.resamp, col='blue')
```

### rruff.sample

#### Sample XRD Patterns

### Description
Several sample XRD patterns from the RRUFF project site.

### Usage

data(rruff.sample)

### Format
A data frame with 3000 observations on the following 8 variables.

- `twotheta`: twotheta values
- `nontronite`: XRD pattern for nontronite
- `montmorillonite`: XRD pattern for montmorillonite
- `clinochlore`: XRD pattern for clinochlore
- `antigorite`: XRD pattern for antigorite
- `chamosite`: XRD pattern for chamosite
- `hematite`: XRD pattern for hematite
- `goethite`: XRD pattern for goethite

### Source

http://rruff.info/

### References

http://rruff.info/
Examples

data(rruff.sample)

# plot all patterns
matplot(rruff.sample, type='l', lty=1)

---

shannonEntropy  Shannon Entropy

Description

A very simple implementation of Shannon entropy.

Usage

shannonEntropy(x, b = 2)

Arguments

x    vector of probabilities [0,1], must sum to 1, should not contain NA
b    logarithm base

Details

0s are automatically removed by na.rm=TRUE, as (0 * log(0) = NaN)

Value

A single numeric value.

Note

The result is the normalized Shannon entropy when b = length(x) (Kempen et al, 2009).

References


Examples

# a very simple example
p <- c(0.25, 0.25, 0.4, 0.05, 0.05)

shannonEntropy(p)
Simulate Soil Profiles

Description

Simulate a collection of soil profiles based on the horizonation of a single soil profile.

Usage

sim(x, n=1, iterations=25, hz.sd=2, min.thick=2)

Arguments

- x: a SoilProfileCollection object containing a single profile from which to draw simulated data
- n: the number of requested simulations
- iterations: sampling iterations used to determine each horizon thickness
- hz.sd: standard deviation used to simulate horizon thickness, can be a vector but must divide evenly into the number of horizons found in x
- min.thick: minimum horizon thickness allowed in simulation results

Details

This function generates a collection of simulated soil profiles based on the horizon thickness data associated with a single "template" profile. Simulation is based on sampling from a family of gaussian distribution with means defined by the "template" profile and standard deviation defined by the user.

Value

A SoilProfileCollection object with n simulated profiles, each containing the same number of horizons and same data as x.

Author(s)

D. E. Beaudette

See Also

random_profile
Examples

# load sample data and convert into SoilProfileCollection
data(sp3)
depths(sp3) <- id ~ top + bottom

# select a profile to use as the basis for simulation
s <- sp3[3,]

# reset horizon names
s$name <- paste('H', seq_along(s$name), sep='')

# simulate 25 new profiles, using 's' and function defaults
sim.1 <- sim(s, n=25)

# simulate 25 new profiles using 's' and variable SD for each horizon
sim.2 <- sim(s, n=25, hz.sd=c(1, 2, 5, 5, 10, 2))

# plot
par(mfrow=c(2,1), mar=c(0, 0, 0, 0))
plot(sim.1)
mtext('SD = 2', side=2, line=-1.5, font=2, cex=0.75)
plot(sim.2)
mtext('SD = c(1, 2, 5, 5, 10, 2)', side=2, line=-1.5, font=2, cex=0.75)

# aggregate horizonation of simulated data
# note: set class_prob_mode=2 as profiles were not defined to a constant depth
sim.2$name <- factor(sim.2$name)
a <- slab(sim.2, ~ name, class_prob_mode=2)

# convert to long format for plotting simplicity
library(reshape)
a.long <- melt(a, id.vars=c('top','bottom'), measure.vars=levels(sim.2$name))

# plot horizon probabilities derived from simulated data
# dashed lines are the original horizon boundaries
library(lattice)
xyplot(top ~ value, groups=variable, data=a.long, subset=value > 0,
ylim=c(100, -5), type=c('l','g'), asp=1.5,
ylab='Depth (cm)', xlab='Probability',
auto.key=list(columns=4, lines=TRUE, points=FALSE),
panel=function(...) {
  panel.xyplot(...)
  panel.abline(h=s$top, lty=2, lwd=2)
})
Description

Aggregate soil properties along user-defined 'slabs', and optionally within groups.

Usage

# method for SoilProfileCollection objects
slab(object, fm, slab.structure=1, strict=FALSE,
slab.fun=.slab.fun.numeric.default, cpm=1, weights=NULL, ...)

Arguments

object  a SoilProfileCollection
fm      A formula: either 'groups ~ var1 + var2 + var3' where named variables are aggregated within 'groups' OR where named variables are aggregated across the entire collection ' ~ var1 + var2 + var3'. If 'groups' is a factor it must not contain NA.
slab.structure A user-defined slab thickness (defined by an integer), or user-defined structure (numeric vector). See details below.
strict    logical: should horizons be strictly checked for self-consistency?
slab.fun  Function used to process each 'slab' of data, ideally returning a vector with names attribute. Defaults to a wrapper function around hdquantile. See details.
cpm       Strategy for normalizing slice-wise probabilities, dividing by either: number of profiles with data at the current slice (cpm=1), or by the number of profiles in the collection (cpm=2). Mode 1 values will always sum to the contributing fraction, while mode 2 values will always sum to 1.
weights   Column name containing weights. NOT YET IMPLEMENTED
...      further arguments passed to slab.fun

Details

Multiple continuous variables OR a single categorical (factor) variable can be aggregated within a call to slab. Basic error checking is performed to make sure that top and bottom horizon boundaries make sense. User-defined aggregate functions (slab.fun) should return a named vector of results.
A new, named column will appear in the results of slab for every named element of a vector returned by slab.fun. See examples below for a simple example of a slab function that computes mean, mean-1SD and mean+1SD. The default slab function wraps hdquantile from the Hmisc package, which requires at least 2 observations per chunk. Note that if ‘group’ is a factor it must not contain NAs.
Execution time scales linearly (slower) with the total number of profiles in object, and exponentially (faster) as the number of profiles / group is increased. slab() and slice() are much faster and require less memory if input data are either numeric or character.
There are several possible ways to define slabs, using slab.structure:

a single integer  e.g. 10: data are aggregated over a regular sequence of 10-unit thickness slabs
a vector of 2 integers  e.g. c(50, 60): data are aggregated over depths spanning 50–60 units
a vector of 3 or more integers  e.g. c(0, 5, 10, 50, 100): data are aggregated over the depths spanning 0–5, 5–10, 10–50, 50–100 units
Value

Output is returned in long format, such that slice-wise aggregates are returned once for each combination of grouping level (optional), variable described in the `fn` argument, and depth-wise 'slab'.

Aggregation of numeric variables, using the default slab function:

- **variable** The names of variables included in the call to `slab`.
- **groupname** The name of the grouping variable when provided, otherwise a fake grouping variable named 'all.profiles'.
- **p.q5** The slice-wise 5th percentile.
- **p.q25** The slice-wise 25th percentile
- **p.q50** The slice-wise 50th percentile (median)
- **p.q75** The slice-wise 75th percentile
- **p.q95** The slice-wise 95th percentile
- **top** The slab top boundary.
- **bottom** The slab bottom boundary.
- **contributing_fraction** The fraction of profiles contributing to the aggregate value, ranges from $1/n\_profiles$ to 1.

When a single factor variable is used, slice-wise probabilities for each level of that factor are returned as:

- **variable** The names of variables included in the call to `slab`.
- **groupname** The name of the grouping variable when provided, otherwise a fake grouping variable named 'all.profiles'.
- A  The slice-wise probability of level A
- B  The slice-wise probability of level B
- ...  
- n  The slice-wise probability of level n
- **top** The slab top boundary.
- **bottom** The slab bottom boundary.
- **contributing_fraction** The fraction of profiles contributing to the aggregate value, ranges from $1/n\_profiles$ to 1.

Methods

- `data = "SoilProfileCollection"` Typical usage, where input is a `SoilProfileCollection`.

Note

Arguments to `slab` have changed with aqp 1.5 (2012-12-29) as part of a code clean-up and optimization. Calculation of weighted-summaries was broken in aqp 1.2-6 (2012-06-26), and removed as of aqp 1.5 (2012-12-29). `slab` replaced the previously defined `soil.slots.multiple` function as of aqp 0.98-8.58 (2011-12-21).
**slab-methods**

**Author(s)**

D.E. Beaudette

**References**


**See Also**

`slice`, `hdquantile`

**Examples**

```r
## basic examples
library(lattice)
library(grid)

# load sample data, upgrade to SoilProfileCollection
data(sp1)
depths(sp1) <- id ~ top + bottom

# aggregate entire collection with two different segment sizes
a <- slab(sp1, fm = ~ prop)
b <- slab(sp1, fm = ~ prop, slab.structure=5)

# check output
str(a)

# stack into long format
ab <- make.groups(a, b)
ab$which <- factor(ab$which, levels=c('a','b'),
                  labels=c('1-cm interval', '5-cm interval'))

# plot median and IQR
# custom plotting function for uncertainty viz.
xyplot(top ~ p.q50 | which, data=ab, ylab='Depth',
       xlab='median bounded by 25th and 75th percentiles',
       lower=ab$p.q25, upper=ab$p.q75, ylim=c(250,-5),
       panel=panel.depth_function,
       prepanel=prepanel.depth_function,
       cf=ab$contributing_fraction,
       layout=c(2,1), scales=list(x=list(alternating=1))
)

## categorical variable example
```
library(reshape)

# normalize horizon names: result is a factor
sp1$name <- generalize.hz(sp1$name,
new=c('O','A','B','C'),
pat=c('O','^A','^B','^C'))

# compute slice-wise probability so that it sums to contributing fraction, from 0-150
a <- slab(sp1, fm=- name, cpm=1, slab.structure=0:150)

# reshape into long format for plotting
a.long <- melt(a, id.vars=c('top','bottom'), measure.vars=c('O','A','B','C'))

# plot horizon type proportions using panels
xyplot(top ~ value | variable, data=a.long, subset=value > 0,
ylim=c(150, -5), type=c('S','g'), horizontal=TRUE, layout=c(4,1), col=1 )

# again, this time using groups
xyplot(top ~ value, data=a.long, groups=variable, subset=value > 0,
ylim=c(150, -5), type=c('S','g'), horizontal=TRUE, asp=2)

# adjust probability to size of collection, from 0-150
a.1 <- slab(sp1, fm= ~ name, cpm=2, slab.structure=0:150)

# reshape into long format for plotting
a.1.long <- melt(a.1, id.vars=c('top','bottom'), measure.vars=c('O','A','B','C'))

# combine aggregation from 'cpm' modes 1 and 2
g <- make.groups(cmp.mode.1=a.long, cmp.mode.2=a.1.long)

# plot horizon type proportions
xyplot(top ~ value | variable, groups=which, data=g, subset=value > 0,
ylim=c(240, -5), type=c('S','g'), horizontal=TRUE, layout=c(4,1),
auto.key=list(lines=TRUE, points=FALSE, columns=2),
par.settings=list(superpose.line=list(col=c(1,2))),
scales=list(alternating=3))

# apply slice-wise evaluation of max probability, and assign ML-horizon at each slice
(gen.hz.ml <- get.ml.hz(a, c('O','A','B','C')))
# upgrade to SPC
depths(sp3) <- id ~ top + bottom
site(sp3) <- ~ group

# custom 'slab' function, returning mean +/- 1SD
mean.and.sd <- function(values) {
  m <- mean(values, na.rm=TRUE)
  s <- sd(values, na.rm=TRUE)
  upper <- m + s
  lower <- m - s
  res <- c(mean=m, lower=lower, upper=upper)
  return(res)
}

# aggregate several variables at once, within 'group'
a <- slab(sp3, fm=group ~ L + A + B, slab.fun=mean.and.sd)

# check the results:
# note that 'group' is the column containing group labels
library(lattice)
xyplot(
  top ~ mean | variable, data=a, groups=group,
  lower=a$lower, upper=a$upper, sync.colors=TRUE, alpha=0.5,
  cf=a$contributing_fraction,
  ylim=c(125,-5), layout=c(3,1), scales=list(x=list(relation='free')),
  par.settings=list(superpose.line=list(lwd=2, col=c('RoyalBlue', 'Orange2'))),
  panel=panel.depth_function,
  prepanel=prepanel.depth_function,
  auto.key=list(columns=2, lines=TRUE, points=FALSE)
)

# compare a single profile to the group-level aggregate values
a.1 <- slab(sp3[1, ], fm=group ~ L + A + B, slab.fun=mean.and.sd)

# manually update the group column
a.1$group <- 'profile 1'

# combine into a single data.frame:
g <- rbind(a, a.1)

# plot with customized line styles
xyplot(
  top ~ mean | variable, data=g, groups=group, subscripts=TRUE,
  lower=a$lower, upper=a$upper, ylim=c(125,-5),
  layout=c(3,1), scales=list(x=list(relation='free')),
  panel=panel.depth_function,
  prepanel=prepanel.depth_function,
  sync.colors=TRUE, alpha=0.25,
  par.settings=list(superpose.line=list(col=c('orange', 'royalblue', 'black'),
    lwd=2, lty=c(1,1,2))),
  auto.key=list(columns=3, lines=TRUE, points=FALSE)
)
Slicing of SoilProfileCollection Objects

Description

Slicing of SoilProfileCollection Objects

Usage

# method for SoilProfileCollection objects
slice(object, fm, top.down=TRUE, just.the.data=FALSE, strict=TRUE)
slice-methods

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>a SoilProfileCollection</td>
</tr>
<tr>
<td>fm</td>
<td>A formula: either ‘integer.vector ~ var1 + var2 + var3’ where named variables are sliced according to ‘integer.vector’ OR where all variables are sliced according to ‘integer.vector ~.’.</td>
</tr>
<tr>
<td>top.down</td>
<td>Logical, should slices be defined from the top-down? The default is usually what you want.</td>
</tr>
<tr>
<td>just.the.data</td>
<td>Logical, return just the sliced data or a new SoilProfileCollection object.</td>
</tr>
<tr>
<td>strict</td>
<td>Logical, should the horizonation be strictly checked for self-consistency?</td>
</tr>
</tbody>
</table>

Value

Either a new SoilProfileCollection with data sliced according to fm, or a data.frame.

Methods

| data = "SoilProfileCollection" | Typical usage, where input is a SoilProfileCollection. |

Note

slab() and slice() are much faster and require less memory if input data are either numeric or character.

Author(s)

D.E. Beaudette

References


See Also

slab

Examples

```
# simulate some data, IDs are 1:20
library(plyr)
d <- ldply(1:20, random_profile)

# init SoilProfilecollection object
depths(d) <- id ~ top + bottom
head(horizons(d))

# generate single slice at 10 cm
# output is a SoilProfilecollection object
s <- slice(d, 10 ~ name + p1 + p2 + p3)
```
# generate single slice at 10 cm, output data.frame
s <- slice(d, 10 - name + p1 + p2 + p3, just.the.data=TRUE)

# generate integer slices from 0 - 25 cm
s <- slice(d, 0:25 - name + p1 + p2 + p3)
plot(s)

# generate slices from 0 - 10 cm, for all variables
s <- slice(d, 0:10 - .)
print(s)

# note that pct missing is computed for each slice,
# if all vars are missing, then NA is returned
d$p1[1:10] <- NA
s <- slice(d, 10 - ., just.the.data=TRUE)
print(s)

##
## check sliced data
##

## test that mean of 1 cm slices property is equal to the
## hz-thickness weighted mean value of that property
data(sp1)
depths(sp1) <- id ~ top + bottom

# get the first profile
sp1.sub <- sp1[which(profile_id(sp1) == 'P009'), ]

# compute hz-thickness wt. mean
hz.wt.mean <- with(horizons(sp1.sub),
  sum((bottom - top) * prop) / sum(bottom - top))

# hopefully the same value, calculated via slice()
s <- slice(sp1.sub, 0:max(sp1.sub) ~ prop)
hz.slice.mean <- mean(s$prop, na.rm=TRUE)

# same?
if(!all.equal(hz.slice.mean, hz.wt.mean))
  stop('there is a bug in slice() !!!')

---

soilColorSignature  Soil Profile Color Signatures

**Description**

Generate a color signature for each soil profile in a collection.
soilColorSignature

Usage
soilColorSignature(spc, r = "r", g = "g", b = "b",
method=’colorBucket’, pam.k=3, RescaleLightnessBy = 1, useProportions=TRUE,
pigmentNames=c(’.white.pigment’, ’.red.pigment’, ’.green.pigment’,
’yellow.pigment’, ’.blue.pigment’))

Arguments
spc a SoilProfileCollection object
r horizon level attribute containing soil color (sRGB) red values
g horizon level attribute containing soil color (sRGB) green values
b horizon level attribute containing soil color (sRGB) blue values
method algorithm used to compute color signature, ’colorBucket’, ’depthSlices’, or ’pam’
pam.k number of classes to request from cluster::pam()
RescaleLightnessBy rescaling factor for CIE LAB L-coordinate
useProportions use proportions or quantities, see details
pigmentNames names for resulting pigment proportions or quantities

Details
details pending...

Value
For the ’colorBucket’ method, a data.frame object containing:

id column set according to idname(spc)
.white.pigment proportion or quantity of CIE LAB L-values
.red.pigment proportion or quantity of CIE LAB positive A-values
.green.pigment proportion or quantity of CIE LAB negative A-values
.yellow.pigment proportion or quantity of CIE LAB positive B-values
.blue.pigment proportion or quantity of CIE LAB negative B-values

Column names can be adjusted with the pigmentNames argument.
For the ’depthSlices’ method ...
For the ’pam’ method ...

Author(s)
D.E. Beaudette

References
https://en.wikipedia.org/wiki/Lab_color_space
SoilProfileCollection-class

See Also

munsell2rgb

Examples

# trivial example, not very interesting
data(sp1)
depths(sp1) <- id ~ top + bottom

# convert Munsell -> sRGB triplets
rgb.data <- munsell2rgb(sp1$hue, sp1$value, sp1$chroma, return_triplets = TRUE)
sp1$r <- rgb.data$r
sp1$g <- rgb.data$g
sp1$b <- rgb.data$b

# extract color signature
pig <- soilColorSignature(sp1)

SoilProfileCollection-class

SoilProfileCollection Class

Description

Basic class for storing soil profile collections, associated site data, and metadata.

Objects from the Class

Objects can be created by calls of the form new("SoilProfileCollection", ...).

Slots

idcol: Object of class "character" the name of the column used to uniquely identify profiles
depthcols: Object of class "character" with the names of columns containing the horizon top and bottom boundaries
metadata: Object of class "data.frame" with collection-level metadata, having a single row, and user-defined columns
horizons: Object of class "data.frame" with 1 or more rows per profile
site: Object of class "data.frame" with 1 row per profile
sp: Object of class "SpatialPoints" with 1 row per profile
diagnostic: Object of class "data.frame" with 0 or more rows per profile
Methods

$ signature(x = "SoilProfileCollection")": ...  
$< signature(x = "SoilProfileCollection")": ...  
[ signature(x = "SoilProfileCollection", i = "ANY", j = "ANY")": ...  
[[ signature(x = "SoilProfileCollection", i = "ANY", j = "ANY")": ...  
[[< signature(x = "SoilProfileCollection", i = "ANY", j = "ANY")": ...  
coordinates<- signature(object = "SoilProfileCollection")": ...  
horizonDepths signature(object = "SoilProfileCollection")": ...  
horizons signature(object = "SoilProfileCollection")": ...  
horizons<- signature(object = "SoilProfileCollection")": ...  
idname signature(object = "SoilProfileCollection")": ...  
names signature(x = "SoilProfileCollection")": ...  
horizonNames signature(object = "SoilProfileCollection")": ...  
siteNames signature(object = "SoilProfileCollection")": ...  
length signature(x = "SoilProfileCollection")": ...  
max signature(x = "SoilProfileCollection")": ...  
metadata signature(object = "SoilProfileCollection")": ...  
metadata<- signature(object = "SoilProfileCollection")": ...  
min signature(x = "SoilProfileCollection")": ...  
profile_id signature(object = "SoilProfileCollection")": ...  
profile_plot signature(object = "SoilProfileCollection")": ...  
show signature(object = "SoilProfileCollection")": ...  
site signature(object = "SoilProfileCollection")": ...  
site<- signature(object = "SoilProfileCollection")": ...  
slab signature(data = "SoilProfileCollection")": ...  
units signature(object = "SoilProfileCollection")": ...  
units<- signature(object = "SoilProfileCollection")": ...

Author(s)
Pierre Roudier and Dylan E. Beaudette

Examples

# concatenate SoilProfileCollection objects
## Not run:
require(plyr)
d <- ldply(1:10, random_profile)

# promote to SoilProfileCollection and plot
depths(d) <- id - top + bottom
plot(d)

# split into new SoilProfileCollection objects by index
d.1 <- d[1,]
d.2 <- d[2,]
d.345 <- d[3:5,]

# recombine, note that profiles are sorted according to ID
d.new <- rbind(d.345, d.1, d.2)
plot(d.new)

## End(Not run)

## Not run:
# these next examples should throw an error
# insert a missing horizon boundary
data(sp1)
sp1$top[1] <- NA
depths(sp1) <- id ~ top + bottom

## End(Not run)

---

SoilProfileCollection-plotting-methods

Profile Plot

Description

Generate a simple diagram of a soil profile, with annotated horizon names.

Usage

plotSPC(x, color='soil_color', width=0.2, name=NULL, label=idname(x),
alt.label=NULL, alt.label.col='black', cex.names=0.5,
cex.depth.axis=cex.names, cex.id=cex.names+(0.2*cex.names),
print.id=TRUE, id.style='auto', plot.order=1:length(x), add=FALSE,
scaling.factor=1, y.offset=0, x.idx.offset=0, n=length(x),
max.depth=ifelse(is.infinite(max(x)), 200, max(x)), n.depth.ticks=5,
shrink=FALSE, shrink.cutoff=3, abbr=FALSE, abbr.cutoff=5, divide.hz=TRUE,
hz.distinctness.offset=NULL, hz.distinctness.offset.col='black',
hz.distinctness.offset.lty=2, axis.line.offset=-2.5,
plot.depth.axis=TRUE, density=NULL, col.label=color,
col.palette = rev(brewer.pal(10, 'Spectral')), col.legend.cex=1,
lwd=1, lty=1,
default.color=grey(0.95), ...)
Arguments

- **x**: a SoilProfileCollection object
- **color**: the name of the column containing R-compatible color descriptions, or a column containing numeric or categorical data; see details
- **width**: scaling of profile widths
- **name**: the name of the (horizon-level) attribute containing horizon designation labels
- **label**: the name of the (site-level) attribute used to identify profiles in the plot
- **alt.label**: the name of a (site-level) attribute used for secondary annotation
- **alt.label.col**: color used when printing secondary annotation
- **cex.names**: character scaling applied to horizon names
- **cex.depth.axis**: character scaling applied to depth scale
- **cex.id**: character scaling applied to profile id
- **print.id**: should the profile id be printed above each profile? (TRUE)
- **id.style**: profile ID printing style: 'auto' (default) = simple heuristic used to select from: 'top' = centered above each profile, 'side' = 'along the top-left edge of profiles'
- **plot.order**: a vector describing the order in which individual SoilProfile objects from the parent should be plotted
- **add**: add to an existing figure
- **scaling.factor**: vertical scaling of the profile heights
- **y.offset**: vertical offset for top of profiles
- **x.idx.offset**: integer specifying horizontal offset from 0
- **n**: integer describing amount of space along x-axis to allocate, defaults to length(x)
- **max.depth**: suggested lower depth boundary of plot
- **n.depth.ticks**: suggested number of ticks in depth scale
- **shrink**: should long horizon names be shrunk by 80% ?
- **shrink.cutoff**: character length defining long horizon names
- **abbr**: should the profile ID be abbreviated?
- **abbr.cutoff**: suggested minimum length for abbreviated IDs
- **divide.hz**: should horizons be divided with a thin black line? (default is TRUE)
- **hz.distinctness.offset**: column name containing vertical offsets used to depict horizon boundary distinctness (same units as profiles)
- **hz.distinctness.offset.col**: color used to encode horizon distinctness (default is 'black')
- **hz.distinctness.offset.lty**: line style used to encode horizon distinctness (default is 2)
- **axis.line.offset**: horizontal offset applied to depth axis (default is -2.5)
- **plot.depth.axis**: plot depth axis? (default is TRUE)
density fill density used for horizon color shading, either a single integer or a column name containing integer values (default is NULL, no shading)
col.label text printed above the color-coded legend
col.palette color palette used to plot numeric data
col.legend.cex scaling of color legend
lwd single numeric value: line width multiplier
lty single integer: line style
default.color default horizon fill color used when ‘color’ attribute is NA
...
other arguments passed into lower level plotting functions

Details

Depth limits (max.depth) and number of depth ticks (n.depth.ticks) are *suggestions* to the pretty function. You may have to tinker with both parameters to get what you want.

The ‘side’ id.style is useful when plotting a large collection of profiles, and/or, when profile IDs are long.

If the column containing horizon designations is not specified (the name argument), a column (presumed to contain horizon designation labels) is guessed based on regular expression matching of the pattern ‘name’– this usually works, but it is best to manual specify the name of the column containing horizon designations.

The color argument can either name a column containing R-compatible colors, possibly created via munsellRrgb, or column containing either numeric or categorical (either factor or character) values. In the second case, values are converted into colors and displayed along with a simple legend above the plot. Note that this functionality makes several assumptions about plot geometry and is most useful in an interactive setting.

The x.idx.offset argument can be used to shift a collection of pedons from left to right in the figure. This can be useful when plotting several different SoilProfileCollection objects within the same figure. Space must be pre-allocated in the first plotting call, with an offset specified in the second call. See examples below.

Value

A new plot of soil profiles is generated, or optionally added to an existing plot.

Methods

signature(x = "SoilProfileCollection")

Author(s)

Dylan E. Beaudette

References

http://casoilresource.lawr.ucdavis.edu/
See Also

SoilProfileCollection-class, pretty, hzDistinctnessCodeToOffset, addBracket, profileGroupLabels

Examples

data(sp1)

# usually best to adjust margins
par(mar=c(0,0,3,0))

# add color vector
sp1$soil_color <- with(sp1, munsell2rgb(hue, value, chroma))

# promote to SoilProfileCollection
depths(sp1) <- id ~ top + bottom

# plot profiles
plot(sp1, id.style='side')

# title, note line argument:
title('Sample Data 1', line=1, cex.main=0.75)

# plot profiles without horizon-line divisions
plot(sp1, divide.hz=FALSE)

# add dashed lines illustrating horizon boundary distinctness
sp1$hzD <- hzDistinctnessCodeToOffset(sp1$bound_distinct)
plot(sp1, hz.distinctness.offset='hzD')

# plot horizon color according to some property
data(sp4)
depths(sp4) <- id ~ top + bottom
plot(sp4, color='clay')

# another example
data(sp2)
depths(sp2) <- id ~ top + bottom
site(sp2) <- ~ surface

# label with site-level attribute: `surface'
plot(sp2, label='surface', plot.order=order(sp2$surface))

# example using a categorical attribute
plot(sp2, color = "plasticity")

# plot two SPC objects in the same figure
par(mar=c(1,1,1,1))
# plot the first SPC object and
# allocate space for the second SPC object
plot(sp1, n=length(sp1) + length(sp2))
# plot the second SPC, starting from the first empty space
plot(sp2, x.idx.offset=length(sp1), add=TRUE)
soil_minerals  Munsell Colors of Common Soil Minerals

Description

Munsell colors for some common soil minerals.

Usage

data(soil_minerals)

Format

A data frame with 20 observations on the following 5 variables.

<table>
<thead>
<tr>
<th>mineral</th>
<th>mineral name</th>
</tr>
</thead>
<tbody>
<tr>
<td>color</td>
<td>Munsell color</td>
</tr>
<tr>
<td>hue</td>
<td>Munsell hue</td>
</tr>
<tr>
<td>value</td>
<td>Munsell value</td>
</tr>
<tr>
<td>chroma</td>
<td>Munsell chroma</td>
</tr>
</tbody>
</table>

Details

Soil color and other properties including texture, structure, and consistence are used to distinguish and identify soil horizons (layers) and to group soils according to the soil classification system called Soil Taxonomy. Color development and distribution of color within a soil profile are part of weathering. As rocks containing iron or manganese weather, the elements oxidize. Iron forms small crystals with a yellow or red color, organic matter decomposes into black humus, and manganese forms black mineral deposits. These pigments paint the soil (Michigan State Soil). Color is also affected by the environment: aerobic environments produce sweeping vistas of uniform or subtly changing color, and anaerobic (lacking oxygen), wet environments disrupt color flow with complex, often intriguing patterns and points of accent. With depth below the soil surface, colors usually become lighter, yellower, or redder.

Source

http://www.nrcs.usda.gov/wps/portal/nrcs/detail/soils/edu/?cid=nrcs142p2_054286

References

Examples

```r
## Not run:
library(aqp)
library(ape)
library(cluster)
library(colorspace)

# load common soil mineral colors
data(soil_minerals)
# convert Munsell to R colors
soil_minerals$col <- munsell2rgb(soil_minerals$hue, soil_minerals$value, soil_minerals$chroma)

# make a grid for plotting
n <- ceiling(sqrt(nrow(soil_minerals)))
# read from top-left to bottom-right
g <- expand.grid(x=1:n, y=n:1)[1:nrow(soil_minerals),]

# convert Munsell -> sRGB -> LAB
col.rgb <- munsell2rgb(soil_minerals$hue, soil_minerals$value, soil_minerals$chroma, return_triplets = TRUE)
col.lab <- as(sRGB(as.matrix(col.rgb)), 'LAB')@coords
row.names(col.lab) <- soil_minerals$mineral

# divisive hierarchical clustering of LAB coordinates
d <- daisy(col.lab)
h <- as.hclust(diana(d))
p <- as.phylo(h)

# plot grid of mineral names / colors
layout(matrix(c(1,2), nrow=1), widths = c(1.25,1))
par(mar=c(1,0,0,1))
plot(g$x, g$y, pch=15, cex=1.2, axes=FALSE, xlab='', ylab='',
col=rev(soil_minerals$col[order]), xlim=c(0.5,5.5), ylim=c(1.5,5.5))
text(g$x, g$y, rev(soil_minerals$color[order]), col='white', pos=1, cex=0.85, font=2)
title(main='Common Soil Minerals', line=-2, cex.main=2)
mtext('http://www.nrcs.usda.gov/wps/portal/nrcs/detail/soils/edu/?cid=nrcs142p2_054286',
side=1, cex=0.75, line=-1.5)
mtext('U. Schwertmann, 1993. SSSA Special Publication no. 31, pages 51--69', side=1, cex=0.75, line=-0.5)

# dendrogram + tip labels with mineral colors
plot(p, cex=0.85, label.offset=1, font=1)
tiplabels(pch=15, cex=4, col=soil_minerals$col)

## End(Not run)
```
Soil Profile Data Example 1

Description

Soil profile data from Pinnacles National Monument, CA.

Usage

data(sp1)

Format

A data frame with 60 observations on the following 21 variables.

- group: a numeric vector
- id: a character vector
- top: a numeric vector
- bottom: a numeric vector
- bound_distinct: a character vector
- bound_topography: a character vector
- name: a character vector
- texture: a character vector
- prop: a numeric vector
- structure_grade: a character vector
- structure_size: a character vector
- structure_type: a character vector
- stickiness: a character vector
- plasticity: a character vector
- field_ph: a numeric vector
- hue: a character vector
- value: a numeric vector
- chroma: a numeric vector

References

http://casoilresource.lawr.ucdavis.edu/
Examples

data(sp1)
# convert colors from Munsell to hex-encoded RGB
sp1$soil_color <- with(sp1, munsell2rgb(hue, value, chroma))

# promote to SoilProfileCollection
depths(sp1) <- id ~ top + bottom
site(sp1) <- ~ group

# re-sample each profile into 1 cm (thick) depth slices
# for the variables 'prop', 'name', 'soil_color'
# result is a SoilProfileCollection object
s <- slice(sp1, 0.25 ~ prop + name + soil_color)

# plot, note slices
plot(s)

# aggregate all profiles along 1 cm depth slices,
# using data from column 'prop'
s1 <- slab(sp1, fm= ~ prop)

# check median & IQR
library(lattice)
xyplot(top ~ p.q50 + p.q25 + p.q75,
data=s1, type='S', horizontal=TRUE, col=1, lty=c(1,2,2),
panel=panel.superpose, ylim=c(110,-5), asp=2)

---

sp2

Honcut Creek Soil Profile Data

Description

A collection of 18 soil profiles, consisting of select soil morphologic attributes, associated with a stratigraphic study conducted near Honcut Creek, California.

Usage

data(sp2)

Format

A data frame with 154 observations on the following 21 variables.

id profile id
surface dated surface
top horizon top in cm
bottom  horizon bottom in cm
bound_distinct horizon lower boundary distinctness class
bound_topography horizon lower boundary topography class
name  horizon name
texture  USDA soil texture class
prop  field-estimated clay content
structure_grade  soil structure grade
structure_size  soil structure size
structure_type  soil structure type
stickiness  stickiness
plasticity  plasticity
field_ph  field-measured pH
hue  Munsell hue
value  Munsell value
chroma  Munsell chroma
r  RGB red component
g  RGB green component
b  RGB blue component
soil_color  R-friendly encoding of soil color

Author(s)

Dylan E. Beaudette

Source

Busacca, Alan J.; Singer, Michael J.; Verosub, Kenneth L. 1989. Late Cenozoic stratigraphy of the Feather and Yuba rivers area, California, with a section on soil development in mixed alluvium at Honcut Creek. USGS Bulletin 1590-G.

References

http://casoilresource.lawr.ucdavis.edu/

Examples

data(sp2)

# convert into SoilProfileCollection object
depths(sp2) <- id ~ top + bottom

# transfer site-level data
site(sp2) <- ~ surface

# generate a new plotting order, based on the dated surface each soil was described on
p.order <- order(sp2$surface)

# plot
par(mar=c(1,0,3,0))
plot(sp2, plot.order=p.order)

# setup multi-figure output
par(mfrow=c(2,1), mar=c(0,0,1,0))

# truncate plot to 200 cm depth
plot(sp2, plot.order=p.order, max.depth=200)
abline(h=200, lty=2, lwd=2)

# compute numerical distances between profiles
# based on select horizon-level properties, to a depth of 200 cm
max_d <- profile_compare(sp2, vars=c('prop','field_ph','hue'),
                         max_d=200, k=0, sample.interval=5, rescale.result=TRUE)

# plot dendrogram with ape package:
if(require(ape) & require(cluster)) {
  h <- diana(d)
  p <- as.phylo(as.hclust(h))
  plot(p, cex=0.75, label.offset=0.01, font=1, direct='down', srt=90, adj=0.5, y.lim=c(-0.125, 0.5))

  # add in the dated surface type via color
  tiplabels(col=as.numeric(sp2$surface), pch=15)

  # based on distance matrix values, YMMV
  legend('topleft', legend=levels(sp2$surface), col=1:6, pch=15, bty='n', bg='white', cex=0.75)
}

---

**Soil Profile Data Example 3**

**Description**

Soil samples from 10 soil profiles, taken from the Sierra Foothill Region of California.

**Usage**

data(sp3)

**Format**

A data frame with 46 observations on the following 15 variables.

- id  soil id
- top  horizon upper boundary (cm)
- bottom  horizon lower boundary (cm)
clay  clay content
cec  CEC by ammonium acetate at pH 7
ph  pH in 1:1 water-soil mixture
tc  total carbon percent
hue  Munsell hue (dry)
value  Munsell value (dry)
chroma  Munsell chroma (dry)
mid  horizon midpoint (cm)
ln_tc  natural log of total carbon percent
L  color: l-coordinate, CIE-LAB colorspace (dry)
A  color: a-coordinate, CIE-LAB colorspace (dry)
B  color: b-coordinate, CIE-LAB colorspace (dry)
name  horizon name
soil_color  horizon color

Details

These data were collected to support research funded by the Kearney Foundation of Soil Science.

References

http://casoilresource.lawr.ucdavis.edu/

Examples

```r
## this example investigates the concept of a "median profile"

# required packages
if(require(ape) & require(cluster)) {
  data(sp3)

  # generate a RGB version of soil colors
  # and convert to HSV for aggregation
  sp3$h <- NA ; sp3$s <- NA ; sp3$v <- NA
  sp3.rgb <- with(sp3, munsell2rgb(hue, value, chroma, return_triplets=TRUE))
  sp3[, c('h','s','v')] <- t(with(sp3.rgb, rgb2hsv(r, g, b, maxColorValue=1)))

  # promote to SoilProfileCollection
  depths(sp3) <- id ~ top + bottom

  # aggregate across entire collection
  a <- slab(sp3, fml= ~ clay + cec + ph + h + s + v, slab.structure=10)

  # check
  str(a)
```
# convert back to wide format
library(reshape)
a.wide.q25 <- cast(a, top + bottom ~ variable, value=c('p.q25'))
a.wide.q50 <- cast(a, top + bottom ~ variable, value=c('p.q50'))
a.wide.q75 <- cast(a, top + bottom ~ variable, value=c('p.q75'))

# add a new id for the 25th, 50th, and 75th percentile pedons
a.wide.q25$id <- 'Q25'
a.wide.q50$id <- 'Q50'
a.wide.q75$id <- 'Q75'

# combine original data with "mean profile"
vars <- c('top','bottom','id','clay','cec','ph','h','s','v')
# make data.frame version of sp3
sp3.df <- as(sp3, 'data.frame')
sp3.grouped <- rbind(
  sp3.df[, vars], a.wide.q25[, vars], a.wide.q50[, vars], a.wide.q75[, vars]
)

# re-constitute the soil color from HSV triplets
# convert HSV back to standard R colors
sp3.grouped$soil_color <- with(sp3.grouped, hsv(h, s, v))

# give each horizon a name
sp3.grouped$names <- paste(round(sp3.grouped$clay), '/', round(sp3.grouped$cec), '/', round(sp3.grouped$ph), 1))

### perform comparison, and convert to phylo class object
### D is rescaled to [0,]
d <- profile.compare(sp3.grouped, vars=c('clay','cec','ph'), max_d=100, k=0.01, replace_na=TRUE, add_soil_flag=TRUE, rescale.result=TRUE)

h <- agnes(d, method='ward')
p <- ladderize(as.phylo(as.hclust(h)))

# look at distance plot-- just the median profile
plot_distance_graph(d, 12)

# similarity relative to median profile (profile #12)
round(1 - (as.matrix(d)[12, ] / max(as.matrix(d)[12, ])), 2)

### make dendrogram + soil profiles
# first promote to SoilProfileCollection
depths(sp3.grouped) <- id ~ top + bottom

# setup plot: note that D has a scale of [0,1]
par(mar=c(1,1,1,1))
p.plot <- plot(p, cex=0.8, label.offset=3, direction='up', y.lim=c(2,0),
x.lim=c(1.25,length(sp3.grouped)+1), show.tip.label=FALSE)
# get the last plot geometry
lastPP <- get("last_plot.phylo", envir = .PlotPhyloEnv)

# the original labels, and new (indexed) order of pedons in dendrogram
d.labels <- attr(d, "Labels")

new_order <- sapply(1:lastPP$tip, 
  function(i) which(as.integer(lastPP$xx[1:lastPP$tip]) == i))

# plot the profiles, in the ordering defined by the dendrogram
# with a couple fudge factors to make them fit
plot(sp4.grouped, color="soil_color", plot.order=new_order, 
  scaling.factor=0.01, width=0.1, cex.names=0.5, 
  y.offset=max(lastPP$yy)+0.1, add=TRUE) 

sp4

---

Soil Chemical Data from Serpentinitic Soils of California

**Description**

Soil Chemical Data from Serpentinitic Soils of California

**Usage**

data(sp4)

**Format**

A data frame with 30 observations on the following 13 variables.

- **id**: site name
- **name**: horizon designation
- **top**: horizon top boundary in cm
- **bottom**: horizon bottom boundary in cm
- **K**: exchangeable K in cmol/kg
- **Mg**: exchangeable Mg in cmol/kg
- **Ca**: exchangeable Ca in cmol/kg
- **CEC_7**: cation exchange capacity (NH4OAc at pH 7)
- **ex_Ca_to_Mg**: extractable Ca:Mg ratio
- **sand**: sand content by weight percentage
- **silt**: silt content by weight percentage
- **clay**: clay content by weight percentage
- **CF**: >2mm fraction by volume percentage
Details
Selected soil physical and chemical data from (McGahan et al., 2009).

Source
https://www.soils.org/publications/sssaj/articles/73/6/2087

References

Examples
# setup environment
library(aqp)

# load sample data set, a simple data.frame object with horizon-level data from 10 profiles
data(sp4)
str(sp4)

# optionally read about it...
# ?sp4

# upgrade to SoilProfileCollection
# 'id' is the name of the column containing the profile ID
# 'top' is the name of the column containing horizon upper boundaries
# 'bottom' is the name of the column containing horizon lower boundaries
depths(sp4) <- id + top + bottom

# check it out
class(sp4) # class name
str(sp4) # internal structure

# inspect object properties
idname(sp4) # self-explanatory
horizon Depths(sp4) # self-explanatory

# you can change these:
depth_units(sp4) # defaults to 'cm'
metadata(sp4) # not much to start with

# alter the depth unit metadata
depth_units(sp4) <- 'inches' # units are really 'cm'

# more generic interface for adjusting metadata
md <- metadata(sp4) # save original metadata

# add columns
md$describer <- 'DGM'
md$date <- as.Date('2009-01-01')
md$citation <- 'McGahan, D.G., Southard, R.J, Claassen, V.P.'

# re-assign
metadata(sp4) <- md
depth_units(sp4) <- 'cm' # fix depth units, back to 'cm'

# further inspection with common function overloads
length(sp4) # number of profiles in the collection
nrow(sp4) # number of horizons in the collection
names(sp4) # column names
min(sp4) # shallowest profile depth in collection
max(sp4) # deepest profile depth in collection

# extraction of soil profile components
profile_id(sp4) # vector of profile IDs
horizons(sp4) # horizon data

# extraction of specific horizon attributes
sp4$clay # vector of clay content

# subsetting SoilProfileCollection objects
sp4[1, ] # first profile in the collection
sp4[, 1] # first horizon from each profile

# basic plot method, highly customizable: see manual page ?plotSPC
plot(sp4)
# inspect plotting area, very simple to overlay graphical elements
abline(v=1:length(sp4), lty=3, col='blue')
# profiles are centered at integers, from 1 to length(obj)
axis(1, line=-1.5, at=1:10, cex.axis=0.75, font=4, col='blue', lwd=2)
# y-axis is based on profile depths
axis(2, line=-1, at=pretty(1:max(sp4)), cex.axis=0.75, font=4, las=1, col='blue', lwd=2)

# symbolize soil properties via color
par(mar=c(0,0,0,0))
plot(sp4, color='clay')
plot(sp4, color='CF')

# apply a function to each profile, returning a single value per profile,
# in the same order as profile_id(sp4)
soil.depths <- profileApply(sp4, max) # recall that max() gives the depth of a soil profile

# check that the order is correct
all.equal(names(soil.depths), profile_id(sp4))

# a vector of values that is the same length as the number of profiles
# can be stored into site-level data
sp4$depth <- soil.depths
# check: looks good
max(sp4[1, ]) == sp4$depth[1]
# extract site-level data
site(sp4) # as a data.frame
sp4$depth # specific columns as a vector

# use site-level data to alter plotting order
new.order <- order(sp4$depth) # the result is an index of rank
par(mar=c(0,0,0,0))
plot(sp4, plot.order=new.order)

# deconstruct SoilProfileCollection into a data.frame, with horizon+site data
as(sp4, 'data.frame')

---

**Sample Soil Database #5**

**Description**

296 Soil Profiles from the La Rochelle region of France (F. Carre and Girard, 2002)

**Usage**

data(sp5)

**Format**

Formal class 'SoilProfileCollection' [package "aqp"] with 6 slots

...@ idcol : chr "soil"
...@ depthcols: chr [1:2] "top" "bottom"
...@ metadata : 'data.frame': 1 obs. of 1 variable:
  ..$ depth_units: chr "cm"
...@ horizons : 'data.frame': 1539 obs. of 17 variables:
  .. ..$ soil : soil ID
  .. ..$ sand : sand
  .. ..$ silt : silt
  .. ..$ clay : clay
  .. ..$ R25 : RGB r-coordinate
  .. ..$ G25 : RGB g-coordinate
  .. ..$ B25 : RGB b-coordinate
  .. ..$ pH : pH
  .. ..$ EC : EC
  .. ..$ CaCO3 : CaCO3 content
  .. ..$ C : C content
  .. ..$ Ca : Ca
  .. ..$ Mg : Mg
  .. ..$ Na : Na
  .. ..$ top : horizon top boundary (cm)
  .. ..$ bottom : horizon bottom boundary (cm)
  .. ..$ soil_color: soil color in r-friendly format
Details

These data are c/o F. Carre (Florence.CARRE@ineris.fr).

Source

296 Soil Profiles from the La Rochelle region of France (F. Carre and Girard, 2002). These data can be found on the OSACA project page (http://eusoils.jrc.ec.europa.eu/projects/OSACA/).

References


Examples

```r
library(scales)
data(sp5)
par(mar=c(1,1,1,1))
# plot a random sampling of profiles
s <- sample(1:length(sp5), size=25)
plot(sp5[s, ], divide.hz=FALSE)

# plot the first 100 profiles, as 4 rows of 25, hard-coding the max depth
layout(matrix(c(1,2,3,4), ncol=1), height=c(0.25,0.25,0.25,0.25))
plot(sp5[1:25, ], max.depth=300)
plot(sp5[26:50, ], max.depth=300)
plot(sp5[51:75, ], max.depth=300)
plot(sp5[76:100, ], max.depth=300)

# 4x1 matrix of plotting areas
layout(matrix(c(1,2,3,4), ncol=1), height=c(0.25,0.25,0.25,0.25))

# plot profiles, with points added to the mid-points of randomly selected horizons
sub <- sp5[1:25, ]
plot(sub, max.depth=300); mtext('Set 1', 2, line=0.5, font=2)
y.p <- profileApply(sub, function(x) {
  s <- sample(1:nrow(x), 1)
  h <- horizons(x); with(h[s, ], (top+bottom)/2)
})
points(1:25, y.p, bg='white', pch=21)

# plot profiles, with arrows pointing to profile bottoms
```
```r
sub <- sp5[26:50, ]
plot(sub, max.depth=300); mtext('Set 2', 2, line=-0.5, font=2)
y.a <- profileApply(sub, function(x) max(x))
arrows(1:25, y.a-50, 1:25, y.a, len=0.1, col='white')

# plot profiles, with points connected by lines: ideally reflecting some kind of measured data
sub <- sp5[51:75, ]
plot(sub, max.depth=300); mtext('Set 3', 2, line=-0.5, font=2)
y.p <- 20*(sin(1:25) + 2*cos(1:25) + 5)
points(1:25, y.p, bg='white', pch=21)
lines(1:25, y.p, lty=2)

# plot profiles, with polygons connecting horizons with max clay content (+/-) 10 cm
sub <- sp5[76:100, ]
y.clay.max <- profileApply(sub, function(x) {
  i <- which.max(x$c$clay)
  h <- horizons(x)
  with(h[i, ], (top+bottom)/2)
})

plot(sub, max.depth=300); mtext('Set 4', 2, line=-0.5, font=2)
polygon(c(1:25, 25:1), c(y.clay.max-10, rev(y.clay.max+10)),
    border='black', col=rgb(0,0,0.8, alpha=0.25))
points(1:25, y.clay.max, pch=21, bg='white')

# close plot
dev.off()

# plotting parameters
yo <- 100 # y-offset
sf <- 0.65 # scaling factor
# plot profile sketches
par(mar=c(0,0,0,0))
plot(sp5[1:25, ], max.depth=300, y.offset=yo, scaling.factor=sf)
# optionally add describe plotting area above profiles with lines
# abline(h=c(0,90,100, (300*sf)+yo), lty=2)
# simulate an environmental variable associated with profiles (elevation, etc.)
r <- vector(mode='numeric', length=25)
r[1] <- -50; for(i in 2:25) {r[i] <- r[i-1] + rnorm(mean=-1, sd=25, n=1)}
# rescale
r <- rescale(r, to=c(80, 0))
# illustrate gradient with points/lines/arrows
lines(1:25, r)
points(1:25, r, pch=16)
arrows(1:25, r, 1:25, 95, len=0.1)
# add scale for simulated gradient
axis(2, at=pretty(0:80), labels=rev(pretty(0:80)), line=-1, cex.axis=0.75, las=2)
# depict a secondary environmental gradient with polygons (water table depth, etc.)
polygon(c(1:25, 25:1), c((100-r)+150, rep((300*sf)+yo, times=25)),
    border='black', col=rgb(0,0,0.8, alpha=0.25))
```

# sample 25 profiles from the collection
s <- sp5[sample(1:length(sp5), size=25), ]
# compute pair-wise dissimilarity
d <- profile_compare(s, vars=c('R2S','pH','clay','EC'), k=0, 
replace_na=TRUE, add_soil_flag=TRUE, max.d=300)
# keep only the dissimilarity between profile 1 and all others
d.1 <- as.matrix(d)[1, ]
# rescale dissimilarities
d.1 <- rescale(d.1, to=c(80, 0))
# sort in ascending order
d.1.order <- rev(order(d.1))
# plotting parameters
yo <- 100 # y-offset
sf <- 0.65 # scaling factor
# plot sketches
par(mar=c(0,0,0,0))
plot(s, max.depth=300, y.offset=yo, scaling.factor=sf, plot.order=d.1.order)
# add dissimilarity values with lines/points
lines(1:25, d.1[d.1.order])
points(1:25, d.1[d.1.order], pch=16)
# add an axis for the dissimilarity scale
axis(2, at=pretty(0:80), labels=rev(pretty(0:80)), line=-1, cex.axis=0.75, las=2)

---

Soil Physical and Chemical Data from Manganiferous Soils

Description

Soil Physical and Chemical Data from Manganiferous Soils (Bourgault and Rabenhorst, 2011)

Usage

data(sp6)

Format

A data frame with 30 observations on the following 13 variables.

id  pedon name
name horizon designation
top horizon top boundary in cm
bottom horizon bottom boundary in cm
color moist soil color in Munsell notation
sp6

texture  USDA soil texture class
sand  sand content by weight percentage
silt  silt content by weight percentage
clay  clay content by weight percentage
Fe  DCB-extracted Fe in g/kg (see citation)
Mn  DCB-extracted Mn in g/kg (see citation)
C  total organic carbon as g/kg
pH  measured in 1:1 H2O slurry
Db  bulk density (g/cc), clod method

Details

Selected soil physical and chemical data from (Bourgault and Rabenhorst, 2011).

Source


References


Examples

# setup environment
library(aqp)
data(sp6)

# init SPC
depths(sp6) <- id ~ top + bottom
# convert non-standard Munsell colors
sp6$soil_color <- getClosestMunsellChip(sp6$color)

# profile sketches
par(mar=c(0,0,3,0))
plot(sp6, color='soil_color')
plot(sp6, color='Mn')
plot(sp6, color='Fe')
plot(sp6, color='pH')
plot(sp6, color='texture')
SPC-utils  

Getters, Setters, and Utility Methods for SoilProfileCollection Objects

Description

Getters, Setters, and Utility Methods for SoilProfileCollection Objects

Methods

signature(object = "SoilProfileCollection")

Author(s)

Dylan E. Beaudette

References

http://casoilresource.lawr.ucdavis.edu/

Examples

data(sp1)

## init SoilProfileCollection objects from data.frame
depths(sp1) <- id ~ top + bottom

## depth units
(du <- depth_units(sp1))
depth_units(sp1) <- 'in'
depth_units(sp1) <- du

## get/set metadata on SoilProfileCollection objects
# this is a 1-row data.frame
m <- metadata(sp1)
m$sampler <- 'Dylan'
metadata(sp1) <- m

## extract horizon data from SoilProfileCollection objects as data.frame
h <- horizons(sp1)

# also replace horizon data in SoilProfileCollection objects
# original order and length must be preserved!
horizons(sp1) <- h

# get number of horizons
nrow(sp1)

## getting site-level data
site(sp1)
subsetProfiles-methods

Subset SoilProfileCollection Objects.

Description

This function is used to subset SoilProfileCollection objects using either site-level or horizon-level attributes, or both.

Details

The \texttt{s} argument supplies a fully-quoted search criteria for matching via site-level attributes. The \texttt{h} argument supplies a fully-quoted search criteria for matching via horizon-level attributes. All horizons associated with a single horizon-level match (i.e. out of several, only a single horizon matches the search criteria) are returned. See examples for usage.

Value

A SoilProfileCollection class object.

Methods

signature(object = "SoilProfileCollection", s = 'character', h = 'character', ...)

See Also

profileApply, site, horizons

Examples

\begin{verbatim}
data(sp1)
depths(sp1) <- id ~ top + bottom
site(sp1) <- ~ group

# save par settings, and setup plot for 3 columns
\end{verbatim}
op <- par(mar=c(1,1,8,1), mfcol=c(1,3))

# subset sp1 via site-level attributes
# note quoting style
plot(group.1 <- subsetProfiles(sp1, s="group == '1'"))

# subset sp1 via horizon-level attributes
# note quoting style
plot(coarse.soils <- subsetProfiles(sp1, h="texture == 'LS'"))

# re-combine subsets, note that duplicates are removed
g <- rbind(group.1, coarse.soils)
plot(g)

# reset plot area
par(op)

# subset sp1 via horizon and site-level attributes
plot(tiny.set <- subsetProfiles(sp1, s="group == 2", h='prop < 8'))

## other ways to subset SoilProfileCollection objects, via index
## more interesting sample data
data(sp2)
depths(sp2) <- id ~ top + bottom
site(sp2) <- ~ surface

# subset by integer index, note that this does not re-order the profiles
plot(sp2[1:5, ])

# generate an integer index via pattern-matching
idx <- grep('modesto', sp2$surface, ignore.case=TRUE)
plot(sp2[idx, ])

# generate an index via profileApply:
# subset those profiles where: min(ph) < 5.6
idx <- which(profileApply(sp2, function(i) min(i$field_ph, na.rm=TRUE) < 5.6))
plot(sp2[idx, ])

---

**Description**

tau: Computes: (1) unweighted naïve, (2) weighted naïve, (3) unweighted tau, (4) weighted tau accuracy statistics
summaryTauf: prints a summary of the results from tauW
xtableTauf: formats a LaTeX table with results from tauW and saves it as a .tex file for import into a LaTeX document.
Usage

tauw(CM, W = diag(sqrt(length(as.matrix(CM)))))
   P = rep(1/nrow(as.matrix(CM)), nrow(as.matrix(CM))))

summaryTauW(result.tau)

xtableTauW(result.tau, file.name="tau_results_table.tex")

Arguments

CM  a square confusion (cross-classification) matrix (rows: allocation, columns: reference)
W  weights: 1 on diagonals, [-1..1] off giving partial credit to this error
P  prior probability vector, length = number of rows/columns in CM and W
result.tau results returned by tauw
file.name output LaTeX file

Details

Input matrices CM and W may be in data.frame format and will be converted
Weights matrix W: 0 = no credit; 1 = full credit; -1 = maximum penalty/ If absent, default is no partial credit, i.e., unweighted.
Prior probabilities vector P: If absent, P are equal priors for each class. Special value P = 0 is interpreted as P = column marginals.
Error checks: CM must be square; P must have correct number of classes and sum to 1 +/- 0.0001; W & CM must be conformable

Value

Results are returned in a list with obvious R names

Author(s)

D G Rossiter

References


Examples

# example confusion matrix
# rows: allocation (user's counts)
# columns: reference (producer's counts)
crossclass <- matrix(data=c(2,1,0,5,0,0,
                            1,74,2,1,3,6,
                            0,5,8,6,1,3,
                            6,1,3,91,0,0,
                            0,4,0,0,0,4,
                            0,6,2,2,4,38),
nrow=6, byrow=TRUE)
row.names(crossclass) <- c("OP", "SA", "UA", "UC", "AV", "AC")
colnames(crossclass) <- row.names(crossclass)

# build the weights matrix
# how much credit for a mis-allocation
weights <- matrix(data=c(1.00,0.05,0.05,0.15,0.05,0.05,
                          0.05,1.00,0.05,0.05,0.05,0.35,
                          0.05,0.05,1.00,0.20,0.15,0.15,
                          0.15,0.05,0.25,1.00,0.10,0.25,
                          0.05,0.10,0.15,0.10,1.00,0.15,
                          0.20,0.30,0.10,0.25,0.20,1.00),
nrow=6, byrow=TRUE)

# unweighted accuracy
summaryTauW(nnaive <- tauW(crossclass))

# unweighted tau with equal priors, equivalent to Foody (1992) modified Kappa
tauW(crossclass)$tau

# unweighted tau with user's = producer's marginals, equivalent to original kappa
(priors <- apply(crossclass, 2, sum)/sum(crossclass))
tauW(crossclass, P=priors)$tau

# weighted accuracy; tau with equal priors
summaryTauW(weighted <- tauW(crossclass, W=weights))

# weighted accuracy; tau with user's = producer's marginals
summaryTauW(tauW(crossclass, W=weights, P=priors))

# change in accuracy statistics weighted vs. non-weighted
(weighted$overall.weighted - weighted$overall.naive)
(weighted$user.weighted - weighted$user.naive)
(weighted$prod.weighted - weighted$prod.naive)

---

test_hz_logic  Test Horizon Logic

Description

Simple tests for horizon logic, based on a simple data.frame of ordered horizons.
Usage

test_hz_logic(i, topcol, bottomcol, strict = FALSE)

Arguments

i
  a data.frame associated with a single soil profile, ordered by depth

topcol
  character, giving the name of the column in i that describes horizon top depth

bottomcol
  character, giving the name of the column in i that describes horizon bottom depth

strict
  logical, should continuity tests be performed—i.e. for non-contiguous horizon boundaries

Details

By default, this function tests for NA and overlapping horizons. If any either are encountered, FALSE is returned.

Value

logical: TRUE -> pass, FALSE -> fail

Author(s)

D.E. Beaudette

References

http://casoilresource.lawr.ucdavis.edu/

See Also

depths<-

Examples

```r
## simple example: just one profile
data(sp1)
depths(sp1) <- id ~ top + bottom
s <- horizons(sp1[1, ])

## check
# fails due to missing hz boundary
s$bottom[6] <- NA # missing horizon boundary, common on bottom-most hz
test_hz_logic(s, 'top', 'bottom', strict=FALSE)

# fails due to inconsistent hz boundary
s$bottom[3] <- 30 # inconsistent hz boundary
test_hz_logic(s, 'top', 'bottom', strict=TRUE)
```
textureTriangleSummary

Soil Texture Low-RV-High as Defined by Quantiles

Description

This function accepts soil texture components (sand, silt, and clay percentages) and plots a soil texture triangle with a "representative value" (point) and low-high region (polygon) defined by quantiles (estimated with \texttt{Hmisc::hquantile}). Marginal quantiles of sand, silt, and clay are used to define the boundary of a low-high region that encloses several likely soil texture classes based on the values in \texttt{ssc}. The default settings place the RV symbol at the texture defined by marginal medians of sand, silt, and clay. The default low-high region is defined by the 5th and 95th marginal percentiles of sand, silt, and clay.

Usage

\begin{verbatim}
textureTriangleSummary(ssc, p=c(0.05, 0.5, 0.95), delta=1, texture.names=FALSE, pop.rv.col='red', range.col='RoyalBlue', range.alpha=75, sim=FALSE, sim.n=1000, sim.rv.col='yellow', sim.col=grey(0.95), sim.alpha=150, legend.cex=0.75, ...)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{ssc} a matrix-like object with columns: 'sand', 'silt', 'clay', values are percentages that should add to 100.
  \item \texttt{p} percentiles defining 'low', 'representative value', and 'high'
  \item \texttt{delta} step-size used to form low-high region
  \item \texttt{texture.names} logical, should soil texture names be added to the figure?
\end{itemize}
pop.rv.col the symbol color used to denote the population representative value on the texture triangle
range.col color of the polygon enclosing the low-high region
range.alpha transparency of the low-high range polygon (0-255)
sim optional simulation of low-rv-high values based on a composition drawn from normal distributions, this requires the ‘compositions’ package
sim.n number of simulated sand, silt, and clay values
sim.rv.col the symbol color used to denote the simulated representative value on the texture triangle
sim.col color of the simulated low-high range polygon
sim.alpha transparency of the simulated low-high range polygon (0-255)
legend.cex scaling factor for legend
... further arguments passed to triax.points

Details
Simulated sand, silt, and clay values are based on sampling from a normal distribution as performed by rnorm.acomp in the ‘compositions’ package. The mean vector of the sand, silt, and clay values, along with covariance matrix derived from ssc are used to parametrize sampling.

Value
A high-level plot as generated by soil.texture.

Note
Simulation of sand, silt, and clay values requires the ‘compositions’ package. When using this function within .Rmd, be sure to explicitly load the ‘compositions’ package via library and use the chunk option fig.keep='last'. For some reason, the soil.texture function generates two figures when used within a .Rmd, hence the strange hack.

Author(s)
D.E. Beaudette

See Also
triax.points, soil.texture

Examples
# sample data
data(loafercreek, package='soilDB')

# extract sand, silt, clay proportions
x <- na.omit(data.frame(sand=loafercreek$sand, silt=loafercreek$silt, clay=loafercreek$clay))

# test out the function
textureTriangleSummary(x, p=c(0.05, 0.5, 0.95))
textureTriangleSummary(x, p=c(0.25, 0.5, 0.75), range.col='darkgreen')

# simulate compositional data from source mean / var-covar matrix
if(require(compositions)) {
  # add simulated low-rv-high
  textureTriangleSummary(x, p=c(0.05, 0.5, 0.95), sim=TRUE)
}

unique-methods

Get Indices to Unique Soil Profiles Within a Collection

Description

This function returns a set of indices to a subset of profiles within a SoilProfileCollection object that are uniquely defined by a named set of horizon and site level attributes.

Usage

uniqueSPC(x, vars)

Arguments

x 
  a SoilProfileCollection

vars 
  a character vector naming those horizon and site level attributes that will be used to test for duplication

Details

Duplicates are identified via MD5 hash of select horizon and site level attributes.

Value

A vector of integer indices that can be used to subset unique profiles from the original SoilProfileCollection object.

Methods

signature(x = "SoilProfileCollection")

Author(s)

D.E. Beaudette
Examples

```r
## use the digest library to detect duplicate data
data(sp1)

# make a copy, make new IDs, and stack
s.1 <- sp1
s.2 <- sp1
s.2$id <- paste(s.2$id, '-copy', sep='
')
s <- rbind(s.1, s.2)
depths(s) <- id ~ top + bottom

# digests are computed from horizon-level data only
# horizon boundaries and 'prop'
# result is an index of unique profiles
u <- unique(s, vars=c('top', 'bottom', 'prop'))

# compare with and without dupes:
# note subsetting of SoilProfileCollection
cbind(dupes=length(s), no.dupes=length(s[u, ]))
```

---

**unroll**

*Unroll Genetic Horizons*

**Description**

Generate a descretized vector of genetic horizons along a user-defined pattern.

**Usage**

```r
unroll(top, bottom, prop, max_depth, bottom_padding_value = NA, strict=FALSE)
```

**Arguments**

- `top`: vector of upper horizon boundaries, must be an integer
- `bottom`: vector of lower horizon boundaries, must be an integer
- `prop`: vector of some property to be "unrolled" over a regular sequence
- `max_depth`: maximum depth to which missing data is padded with NA
- `bottom_padding_value`: value to use when padding missing data
- `strict`: should horizons be strictly checked for self-consistency? defaults to FALSE

**Details**

This function is used internally by several higher-level components of the aqp package. Basic error checking is performed to make sure that bottom and top horizon boundaries make sense. Note that the horizons should be sorted according to depth before using this function. The `max_depth` argument is used to specify the maximum depth of profiles within a collection, so that data from any profile shallower than this depth is padded with NA.
Value

a vector of "unrolled" property values

Author(s)

Dylan E. Beaudette

References

http://casoilresource.lawr.ucdavis.edu/

Examples

data(sp1)

# subset a single soil profile:
sp1.1 <- subset(sp1, subset=id == 'P001')

# demonstrate how this function works
x <- with(sp1.1, unroll(top, bottom, prop, max_depth=50))
plot(x, 1:length(x), ylim=c(90,0), type='b', cex=0.5)
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