Package ‘hsdar’

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Type Package

Title Manage, Analyse and Simulate Hyperspectral Data

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Depends R (>= 3.3.1), raster (>= 2.5-8), rgdal (>= 1.1-10), signal, methods, caret

Suggests rgl (>= 0.98.1), RCurl, foreach, hyperSpec

Description
Transformation of reflectance spectra, calculation of vegetation indices and red edge parameters, spectral resampling for hyperspectral remote sensing, simulation of reflectance and transmittance using the leaf reflectance model PROSPECT and the canopy reflectance model PROSAIL.

License GPL

LazyLoad yes

BuildVignettes yes

URL http://vhrz669.hrz.uni-marburg.de/lcrs/, http://teledetection.ipgp.jussieu.fr/prosail/

R topics documented:

`hsdar-package` *Manage, analyse and simulate hyperspectral data in R*

Description

The **hsdar** package contains classes and functions to manage, analyse and simulate hyperspectral data. These might be either spectrometer measurements or hyperspectral images through the interface of **raster**.

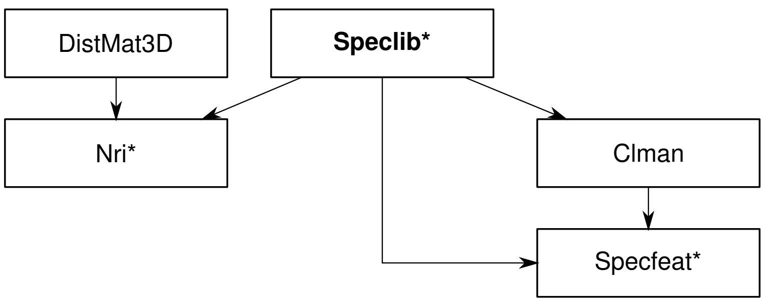
Details

hsdar provides amongst others the following functionality.

- Data handling: **hsdar** is designed to handle even large sets of spectra. Spectra are stored in a `Speclib` containing, amongst other details, the wavelength and reflectance for each spectrum. **hsdar** further contains functions for `plot`ting spectral data and `apply`ing functions to spectra.

- Data manipulation: A variety of established methods for data manipulation such as filter functions (`noiseFiltering`) for noise reduction, resampling of bands to various satellite sensors (`spectralResampling`), continuum removal (`transformSpeclib`), calculations of derivations (`derivative.speclib`) and extraction of absorption features (`cut_specfeat`) are implemented.
- Data analysis: Supported methods to analyse vegetation spectra are the calculation of red edge parameters (`rededge`), vegetation (`vegindex`) and soil (`soilindex`, `smgm`) indices as well as ndvi-like narrow band indices (`nri`). **hsdar** further enables to perform linear spectral unmixing of spectra (`unmix`) by use of endmember spectra. Note that some functions allow the parallel execution using the **doMPI**-, **doMC**- and **foreach**-packages. Execute '`hsdar_parallel()`' to get supporting functions.
- Data simulation: **hsdar** has implemented the models PROSAIL 5B (`PROSAIL`, Jacquemoud et al. 2009) and PROSPECT 5 and D (`PROSPECT`, Jacquemoud and Baret 1990, Feret et al. 2017) to simulate spectra of canopy and plants.

Several classes are defined and used in **hsdar**. Most of the classes are used and respective objects are created internally. However, the following figure gives an overview which class is used at which stage of processing.



Note that the asterisk marks all classes for which wrapper functions for the **caret** package exist.

To see the preferable citation of the package, type `citation("hsdar")`.

Acknowledgements

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Author(s)

Lukas Lehnert, Hanna Meyer, Jörg Bendix

References

Feret J.B., Gitelson A.A., Noble S.D., & Jacquemoud S. (2017), PROSPECT-D: towards modeling leaf optical properties through a complete lifecycle, Remote Sensing of Environment, 193, 204-215.

Jacquemoud, S., Verhoef, W., Baret, F., Bacour, C., Zarco-Tejada, P.J., Asner, G.P., Francois, C., and Ustin, S.L. (2009): PROSPECT + SAIL models: a review of use for vegetation characterization, Remote Sensing of Environment, 113, S56-S66.

Jacquemoud, S. and Baret, F. (1990). PROSPECT: A model of leaf optical properties spectra, Remote Sensing of Environment 34: 75 - 91.

`addcp` *Manually add fix point to continuum line*

Description

This function is used to add an additional fix point to a manually created hull of a single spectrum. This fix point is then used to re-construct a continuum line.

Usage

```
addcp(x, ispec, cpadd)
```

Arguments

`x`	Object of class `Clman`.
`ispec`	ID or index of spectrum to be modified.
`cpadd`	Single value or vector of wavelength containing new fix point(s).

Details

In some cases, it might be desirable to manually adapt automatically constructed segmended hulls (`transformSpeclib`). For example local maxima could be removed because they are very small and maybe afflicted with uncertainties which might legitimate it to manipulate the continuum line. Therefore, hsdar provides functions to remove and add "continuum points" from or to a continuum line. Manually adapted continuum lines can then be used to update band depth or ratio transformation. Handle these functions with care to avoid continuum lines too much build by subjective decisions. In the typical workflow, spectra are first transformed (`transformSpeclib`). Continuum points can then be retrieved (`getcp`) and manually adapted by adding `addcp` and deleting (`deletecp`) of points. Use `checkhull` to check for errors. If all uncertainties are removed, recalculate the hull (`makehull`) and update the transformed spectrum (`updatecl`).

Value

Object of class `Clman` containing the updated version of x.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `deletecp`, `getcp`, `checkhull`, `makehull`, `updatecl`,

`idSpeclib`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, xlim = c(2480, 2500), ylim=c(0.022,0.024))

## Add fix point at 4595 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2495)

## Plot new line
plot(spec_clman, ispec = 1, xlim = c(2480, 2500), ylim=c(0.022,0.024))

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error
```

`apply.DistMat3D` *Apply function for class DistMat3D*

Description

Apply function to values in a 3-D distance matrix. The 3-D distance matrix is an S4-class in **hsdar** to efficiently store distance values in hyperspectral datasets.

Usage

```
## S4 method for signature 'DistMat3D'
apply(X, MARGIN, FUN, ...)
```

Arguments

`X`	Object of class '`DistMat3D`'.
`MARGIN`	A vector giving the subscripts (dimensions) of the `DistMat3D`-object which the function will be applied over (see examples).
`FUN`	Function to be applied. Matched with `match.fun`.
`...`	Further arguments passed to FUN.

Value

Depending on the length of the return value of the specified function, objects of classes numeric or matrix are returned.

Author(s)

Lukas Lehnert

See Also

apply, match.fun, DistMat3D

Examples

```
data(spectral_data)

## Part I: Create an object of class DistMat3D
## Calculate all possible NRI - combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Get all NRI-values as numeric vector
nri_values <- as.numeric(t(as.matrix(getNRI(nri_WV,
                                            getFiniteNri(nri_WV)))))

## Create object of class DistMat3D
dmat <- distMat3D(nri_values, 8, 45)


## Part II: Apply function mean to values in the new object
## Calculate mean value of all samples for all indices
meanIndexVals <- apply(dmat, MARGIN = 1, FUN = mean)
## Convert to DistMat3D
meanIndexVals <- distMat3D(meanIndexVals, 8, 1)

## Same but for array
nri_WV_dat <- as.array(dmat)
meanIndexVals_arr <- apply(nri_WV_dat, MARGIN = c(1, 2), FUN = mean)
## Convert to DistMat3D
meanIndexVals_arr <- distMat3D(meanIndexVals_arr)

## Test if equal
all(meanIndexVals_arr == meanIndexVals)


## Calculate mean value of all indices wihtin each sample
meanSampleVals <- apply(dmat, MARGIN = 3, FUN = mean)
meanSampleVals_arr <- apply(nri_WV_dat, MARGIN = 3, FUN = mean,
                            na.rm = TRUE)
## Test if equal
all(meanSampleVals == meanSampleVals_arr)

## User-defined function (in this case the median)
quant <- function(x)
  return(quantile(x,  probs = 0.5))
## Apply user defined function to all samples for all indices
```

```
medianIndexVals <- apply(dmat, MARGIN = 1, FUN = quant)
```

---

apply.Speclib *Apply function for class Speclib*

Description

Apply function over all spectra or a subset of spectra in a Speclib.

Usage

```
## S4 method for signature 'Speclib'
apply(X, FUN, bySI = NULL, ...)
```

Arguments

X	Object of class Speclib
FUN	Function to be applied. Matched with match.fun.
bySI	Character string giving the name of the column in the SI to be used as subsets to apply function FUN on.
...	Further arguments passed to FUN.

Value

Object of class Speclib.

Author(s)

Lukas Lehnert

See Also

apply, match.fun, Speclib

Examples

```
data(spectral_data)

mean_spectrum <- apply(spectral_data, FUN = mean)
plot(mean_spectrum)

## Same as above but seperately for both seasons
mean_spectra <- apply(spectral_data, FUN = mean, bySI = "season")
plot(mean_spectra[1, ], ylim = c(0,50))
plot(mean_spectra[2, ], new = FALSE)
SI(mean_spectra)
```

`as.hyperSpec` *hyperSpec*

Description

Conversion from `Speclib`- to `hyperSpec`-object. The `hyperSpec`-class is the most important class in package **hyperSpec** which provides methods to analyze spectroscopic datasets.

Usage

```
as.hyperSpec(object)
```

Arguments

`object`	Object of class `Speclib`.

Value

Object of class `hyperSpec`.

Note

Package **hyperSpec** must be installed.

Author(s)

Lukas Lehnert

See Also

`Speclib`

`bandnames` *Handling names of bands*

Description

Returning and setting names of bands in `Speclib`

Usage

```
bandnames(x)
bandnames(x) <- value
```

Arguments

x	Object of class Speclib.
value	Character vector of the same length as nbands(x), or NULL.

Value

For bandnames<-, the updated object. Otherwise a vector giving the name of each band in Speclib is returned.

Note

Bandnames are not mandatory in Speclibs. If not set, the default names are in the form V+index of bands.

Author(s)

Lukas Lehnert

See Also

Speclib

Examples

```
data(spectral_data)

## Return band names
bandnames(spectral_data)

## Change band names
bandnames(spectral_data) <- paste("Band", wavelength(spectral_data),
                                  sep = "_")

## Return new band names
bandnames(spectral_data)
```

---

bdri *Band depth ratio indices*

Description

Calculate band depth ratio indices for objects of class Specfeat.

Usage

```
bdri(x, fnumber, index = "ndbi")
```

Arguments

`x`	Object of class `Specfeat`.
`fnumber`	Integer. Index of feature to modify.
`index`	Method to be applied. Currently, `"bdr"`, `"ndbi"` and `"bna"` are available.

Details

Method `"bdr"` calculates the normalised band depth ratio as

$$bdr = \frac{BD}{Dc},$$

with BD is the band depth calculated by `transformSpeclib` and Dc is the maximum band depth called band centre. Method `"ndbi"` calculates the the normalised band depth index as

$$ndbi = \frac{BD - Dc}{BD + Dc}.$$

Method `"bna"` calculates the band depth normalised to band area as

$$bna = \frac{BD}{Da},$$

where Da is the area of the absorption feature (see `feature_properties`). For further information see Mutanga and Skidmore (2004).

Value

Object of class `specfeat` containing the updated version of x.

Author(s)

Lukas Lehnert and Hanna Meyer

References

Mutanga, O. and Skidmore, A. (2004): Hyperspectral band depth analysis for a better estimation of grass biomass (*Cenchrus ciliaris*) measured under controlled laboratory conditions. International Journal of applied Earth Observation and Geoinformation, 5, 87-96

See Also

`transformSpeclib`, `specfeat`

Examples

```
data(spectral_data)

## Transform speclib
bd <- transformSpeclib(subset(spectral_data, season == "summer"),
                       method = "sh", out = "bd")
```

```
## Isolate the features around 450nm, 700nm, 1200nm and 1500nm and
## convert to specfeat.
featureSelection <- specfeat(bd, c(450,700,1200,1500))

## Plot features
plot(featureSelection,1:4)

## Calculate normalized band depth index for first feature
featureSelection_bdri <- bdri(featureSelection, 1, index = "ndbi")

## Plot result
plot(featureSelection_bdri)
```

`cancer_spectra` *Hyperspectral samples*

Description

Hyperspectral samples from the human larynx

Usage

```
data(cancer_spectra)
```

Format

An object of class `Speclib`

Details

This dataset contains hyperspectral data from the human larynx. The data were acquired in a project aiming to test the feasibility to use hyperspectral imaging for the non-invasive detection of cancer of the human larynx (head-and-neck squamous cell carcinoma). In **hsdar**, a subset of the total dataset is kindly provided by the project. This subset includes hyperspectral images from 25 patients including 10 cases with histopathological diagnosis of cancer. The images were acquired using an endoscope which was coupled with a monochromatic CCD camera. As light source, a special Polychrome V light machine was used. This allowed to change the wavelength of the impinging radiation so that hyperspectral cubes could be acquired by combining several images taken under different illuminations. The images were preprocessed using the methodology proposed by Regeling et al. (2015). The spectra were manually classified into cancerous and non-cancerous tissue by medical experts which is included in the SI of the data.

Author(s)

Bianca Regeling, Lukas Lehnert

References

Regeling, B., Laffers, W., Gerstner, A.O.H., Westermann, S., Mueller, N.A., Schmidt, K., Bendix, J., Thies, B. (2015): Development of an Image Pre-processor for Operational Hyperspectral Laryngeal Cancer Detection. Journal of Biophotonics, 1-11.

`caret::createDataPartition-methods`

Methods for Function `createDataPartition`

Description

Methods for function `createDataPartition` in package **caret**. Please refer to help pages in the **caret**-package for further information.

Methods

`signature(y = ".CaretHyperspectral")` Wrapper method for `createDataPartition`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri, Specfeat.

`caret::createFolds-methods`

Methods for Function `createFolds` *and* `createMultiFolds`

Description

Methods for functions `createFolds` and `createMultiFolds` in package **caret**

Methods

`signature(y = ".CaretHyperspectral")` Wrapper methods for `createFolds` and `createMultiFolds`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri, Specfeat.

`caret::createResample-methods`

Methods for Function `createResample`

Description

Methods for function `createResample` in package **caret**

Methods

`signature(y = ".CaretHyperspectral")` Wrapper method for `createResample`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri, Specfeat.

caret::featurePlot-methods *Methods for Function* `featurePlot`

Description

Methods for function `featurePlot` in package **caret**

Methods

`signature(x = ".CaretHyperspectral")` Wrapper method for `featurePlot`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri, Specfeat.

caret::gafs *Methods for Function* `gafs`

Description

Methods for function `gafs` in package **caret**. Please refer to help pages in the **caret**-package for further information.

Usage

```
## S4 method for signature 'Speclib'
gafs(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Nri'
gafs(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Specfeat'
gafs(x, y, cutoff = 0.95, returnData = TRUE, ...)

get_gafs(x)
```

Arguments

`x`	Object of class `Speclib`, `Nri` or `Specfeat`. For `get_gafs`, `x` must be the output of `gafs` as `Speclib` or `Nri`.
`y`	A numeric or factor vector containing the outcome for each sample. If missing, the response variable set by `setResponse` is used.
`cutoff`	The cutoff value of the correlation coefficients between response variables.
`returnData`	Logical. If TRUE, the updated object of `x` is returned, otherwise only the result of `gafs` is returned.
`...`	Further aruments passed to `gafs`.

Value

If `returnData == TRUE`, an object of class `Speclib` or `Nri`, otherwise an object of class `gafs`. Note that if `x` is an object of class `Specfeat`, the function returns an object of class `Speclib` containing the relevant transformed band values.

Author(s)

Lukas Lehnert

See Also

`gafs`

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Set additional predictor variables from the SI
spectral_data <- setPredictor(spectral_data, "season")

## Feature selection using genetic algorithms
## Note that this may take some time!
gafs_res <- gafs(spectral_data)

get_gafs(gafs_res)

## End(Not run)
```

`caret::preProcess-methods`

Methods for Function `preProcess`

Description

Methods for function `preProcess` in package **caret**. The function is mainly internally required, but can be also used to transform the reflectance values and the SI e.g., by centering, scaling etc.

Methods

`signature(x = ".CaretHyperspectral")` Wrapper method for `preProcess`.

Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri, Specfeat.

caret::rfe *Methods for Function* rfe

Description

Methods for function rfe in package **caret**. Please refer to help pages in the **caret**-package for further information.

Usage

```
## S4 method for signature 'Speclib'
rfe(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Nri'
rfe(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Specfeat'
rfe(x, y, cutoff = 0.95, returnData = TRUE, ...)

get_rfe(x)
```

Arguments

x	Object of class Speclib, Nri or Specfeat. For get_rfe, x must be the output of rfe as Speclib or Nri.
y	A numeric or factor vector containing the outcome for each sample. If missing, the response variable set by setResponse is used.
cutoff	The cutoff value of the correlation coefficients between response variables.
returnData	Logical. If TRUE, the updated object of x is returned, otherwise only the result of rfe is returned.
...	Further aruments passed to rfe.

Value

If returnData == TRUE, an object of class Speclib or Nri, otherwise an object of class rfe. Note that if x is an object of class Specfeat, the function returns an object of class Speclib containing the relevant transformed band values.

Author(s)

Lukas Lehnert

See Also

rfe

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Set additional predictor variables from the SI
spectral_data <- setPredictor(spectral_data, "season")

## Recursive feature selection
## Note that this may take some time!
rfe_res <- rfe(spectral_data)

get_rfe(rfe_res)

plot(get_rfe(rfe_res))

## End(Not run)
```

---

caret::safs *Methods for Function* safs

Description

Methods for function safs in package **caret**. Please refer to help pages in the **caret**-package for further information.

Usage

```
## S4 method for signature 'Speclib'
safs(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Nri'
safs(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Specfeat'
safs(x, y, cutoff = 0.95, returnData = TRUE, ...)

get_safs(x)
```

Arguments

x	Object of class Speclib, Nri or Specfeat. For get_safs, x must be the output of safs as Speclib or Nri.
y	A numeric or factor vector containing the outcome for each sample. If missing, the response variable set by setResponse is used.
cutoff	The cutoff value of the correlation coefficients between response variables.

`returnData` Logical. If TRUE, the updated object of `x` is returned, otherwise only the result of `safs` is returned.

`...` Further aruments passed to `safs`.

Value

If `returnData == TRUE`, an object of class `Speclib` or `Nri`, otherwise an object of class `safs`. Note that if `x` is an object of class `Specfeat`, the function returns an object of class `Speclib` containing the relevant transformed band values.

Author(s)

Lukas Lehnert

See Also

`safs`

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Set additional predictor variables from the SI
spectral_data <- setPredictor(spectral_data, "season")

## Supervised feature selection using simulated annealing
## Note that this may take some time!
safs_res <- safs(spectral_data)

get_safs(safs_res)

plot(get_safs(safs_res))

## End(Not run)
```

`caret::sbf` *Methods for Function* `sbf`

Description

Methods for function `sbf` in package **caret**. Please refer to help pages in the **caret**-package for further information.

Usage

```
## S4 method for signature 'Speclib'
sbf(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Nri'
sbf(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Specfeat'
sbf(x, y, cutoff = 0.95, returnData = TRUE, ...)

get_sbf(sbf_obj)
```

Arguments

`x`	Object of class `Speclib`, `Nri` or `Specfeat`.
`y`	A numeric or factor vector containing the outcome for each sample. If missing, the response variable set by `setResponse` is used.
`cutoff`	The cutoff value of the correlation coefficients between response variables.
`returnData`	Logical. If TRUE, the updated object of `x` is returned, otherwise only the result of `sbf` is returned.
`...`	Further aruments passed to `sbf`.
`sbf_obj`	Object of class `Speclib`, `Nri` or `Specfeat` as output of `sbf`-function.

Value

If `returnData == TRUE`, an object of class `Speclib` or `Nri`, otherwise an object of class `sbf`. Note that if `x` is an object of class `Specfeat`, the function returns an object of class `Speclib` containing the relevant transformed band values.

Author(s)

Lukas Lehnert

See Also

`sbf`

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Set additional predictor variables from the SI
spectral_data <- setPredictor(spectral_data, "season")
```

```
## Selection by filtering
## Note that this may take some time!
sbf_res <- sbf(spectral_data)

get_sbf(sbf_res)

plot(get_sbf(sbf_res))

## End(Not run)
```

`caret::setPredictor` *Set predictor variable(s)*

Description

Set predictor variable(s) to be used in model-fitting functions of package **caret**. This function can be used to define additional predictor variables stored in the SI of a `Speclib`- or `Nri`-object. If the passed object is of class `Nri`, By default, all Nri-indices (if the passed object is of class `Nri`) or all bands (if the passed object is of class `Speclib`) are used as predictors.

Usage

```
## S4 method for signature '.CaretHyperspectral,character'
setPredictor(x, predictor)
```

Arguments

`x`	Object of one of the following classes: Speclib, Nri, Specfeat.
`predictor`	Character vector. Name of additional predictor variable(s) (from the SI).

Value

The updated object.

Author(s)

Lukas Lehnert

See Also

`showCaretParameters`, `setResponse`

Examples

```
## Not run:
data(spectral_data)

## Set "season" as additional predictor variable from the SI
spectral_data <- setPredictor(spectral_data, "season")

## Show caret related parameters stored in the Speclib
showCaretParameters(spectral_data)

## End(Not run)
```

`caret::setResponse` *Set response variable*

Description

Set response variable to be used in model-fitting functions of package **caret**. The response variable must be set upon any model training using a **hsdar**-object in **caret**.

Usage

```
## S4 method for signature '.CaretHyperspectral,character'
setResponse(x, response)
```

Arguments

`x`	Object of one of the following classes: Speclib, Nri, Specfeat.
`response`	Character. Name of response variable (from the SI).

Value

The updated object.

Author(s)

Lukas Lehnert

See Also

`showCaretParameters`, `setPredictor`

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Show caret related parameters stored in the Speclib
showCaretParameters(spectral_data)

## End(Not run)
```

`caret::showCaretParameters`

Show caret related parameters

Description

Show caret related parameters in objects of classes Speclib, Nri, Specfeat. Several parameters such as predictor and response variables are internally stored and used for model training and validation in the **caret**-package.

Usage

```
showCaretParameters(x)
```

Arguments

`x`	Object of one of the following classes: Speclib, Nri, Specfeat.

Author(s)

Lukas Lehnert

See Also

`sbf`

caret::train-methods *Methods for Function* train

Description

Methods for functions train and train.formula in package **caret**

Methods

signature(x = ".CaretHyperspectral") Wrapper method for train.
Note that ".CaretHyperspectral" is a class union containing classes Speclib, Nri, Specfeat.

signature(form = "formula", data = "Speclib") Wrapper method for train.formula to be used with objects of class Speclib.

checkhull *Check continuum line*

Description

Check if continuum line is intersecting the reflectance curve.

Usage

```
checkhull(x, ispec)
```

Arguments

x	Object of class clman.
ispec	ID or index of spectrum to be checked.

Details

In some cases, it might be desirable to manually adapt automatically constructed segmended hulls (transformSpeclib). For example local maxima could be removed because they are very small and maybe afflicted with uncertainties which might legitimate it to manipulate the continuum line. Therefore, hsdar provides functions to remove and add "continuum points" from or to a continuum line. Manually adapted continuum lines can then be used to update band depth or ratio transformation. Handle these functions with care to avoid continuum lines too much build by subjective decisions. In the typical workflow, spectra are first transformed (transformSpeclib). Continuum points can then be retrieved (getcp) and manually adapted by adding addcp and deleting (deletecp) of points. Use checkhull to check for errors. If all uncertainties are removed, recalculate the hull (makehull) and update the transformed spectrum (updatecl).

Value

Object of class list.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

transformSpeclib, addcp, deletecp, makehull, updatecl

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, xlim = c(2480, 2500), ylim=c(0.022,0.024))

## Add fix point at 4595 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2495)

## Plot new line
plot(spec_clman, ispec = 1, xlim = c(2480, 2500), ylim=c(0.022,0.024))

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error

## Add fix point at 4596 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2496)

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error
```

---

clman *Methods to create, manipulate and query objects of class 'Clman'.*

Description

Methods to create, manipulate and query objects of class 'Clman'. The class 'Clman' is used to store manually defined continuum lines and the associated spectra.

Usage

```
## Creation of objects
## S4 method for signature 'Clman'
initialize(.Object, ...)

## S4 method for signature 'Clman'
spectra(object, ...)

## S4 replacement method for signature 'Clman,data.frame'
spectra(object) <- value

## S4 replacement method for signature 'Clman,matrix'
spectra(object) <- value

## S4 replacement method for signature 'Clman,numeric'
spectra(object) <- value

## S4 method for signature 'Clman'
plot(x, ispec, subset = NULL, numeratepoints = TRUE,
    hull.style = NULL, points.style = list(), ...)
```

Arguments

`.Object,object`	Matrix, numeric or array in cases of creation of 'Clman' objects otherwise object of class 'Clman'.
`value`	Object of class numeric, matrix or array which is used for replacement of the values in x.
`...`	Arguments passed to `speclib` or `plot.default`.
`x`	Object of class `clman`.
`ispec`	Name or index of spectrum to be plotted.
`subset`	Lower and upper spectral limits used for plot.
`numeratepoints`	Flag if points should be numerated in plot.
`hull.style`	List of arguments passed to `lines` to construct the continuum line.
`points.style`	List of arguments passed to `points` to construct the continuum points. May be `NULL` to suppress plotting of fix points.

Value

For `spectra<-`, the updated object. Otherwise a matrix returning the spectra in the Clman object.

Note

The functions to create objects of class `Clman` are mainly internally needed by `transformSpeclib`.

Author(s)

Lukas Lehnert

See Also

dist.speclib, Clman, transformSpeclib, plot

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Return first spectrum
spectra(spec_clman)[1,]

## Plot clman
plot(spec_clman, ispec = 1, subset = c(400, 1000))
```

Clman-class ** Clman class*

Description

Class to store and handle manual continuum lines.

Details

The class is only required if a continuum line is manually adopted or entirely manually created. This is useful if the automatic approaches are not able to identify absorption features because, for instance, the spectrum has two pronounced maxima within the absortion feature of interest.

`Clman` is defined as `Speclib` extended by the following two slots:

- cp: Matrix containing the fix points (continuum points) of each spectrum.
- hull: Matrix containing the hull of each spectrum.

Normally, it is not necessary to manually change the values in any of the slots above. Use the functions `addcp` and `deletecp` to change the hulls manually. Functionality for conversion back to a `Speclib` with the final hull and the transformed spectra provides function `updatecl`.

Note

See figure in `hsdar-package` for an overview of classes in hsdar.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `plot`, `Speclib`, `addcp`, `deletecp`, `updatecl`

`cor.test` *Test for association/correlation between nri values and vector of samples*

Description

Test for association between paired samples (with one variable being nri-values), using one of Pearson's product moment correlation coefficient, Kendall's tau or Spearman's rho.

Usage

```
## S4 method for signature 'Nri'
cor.test(x, y, ...)
```

Arguments

`x`	Object of class `Nri` or numerical vector
`y`	Object of class `Nri` or numerical vector
`...`	Further arguments passed to `cor.test`

Details

NRI-values may be used as x and/or as y variable. If x and y are NRI-values the number of samples in both datasets must be equal. For additional information on correlation tests see details in `cor.test`.

Value

Object of class `Nri`

Author(s)

Lukas Lehnert

See Also

`plot`, `cor.test`, `glm.nri`, `lm.nri`, `getNRI`

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

cortestnri <- cor.test(nri_WV, SI(spec_WV)$chlorophyll)

cortestnri
```

---

cubePlot *cubePlot*

Description

Plotting 3D cube of hyperspectral data using **rgl**-package

Usage

```
cubePlot(x, r, g, b, ncol = 1, nrow = 1,
         sidecol = colorRamp(palette(heat.colors(100))), ...)
```

Arguments

`x`	Object of class `Speclib`.
`r`	Integer. Index of band used as red channel. If omitted, the band closest to 680 nm is selected.
`g`	Integer. Index of band used as green channel. If omitted, the band closest to 540 nm is selected.
`b`	Integer. Index of band used as blue channel. If omitted, the band closest to 470 nm is selected.
`ncol`	Integer giving the column(s) in `x` which is/are used to plot the spectral dimension.
`nrow`	Integer giving the row(s) in `x` which is/are used to plot the spectral dimension.
`sidecol`	ColorRamp used to illustrate spectral dimension.
`...`	Further arguments passed to `plotRGB` for the top of the cube. Currently, the following two arguments are supported: • `scale`: Maximum (possible) value in the three channels. Defaults to the maximum value in the red, green and blue band selected by arguments `r`, `g` and `b`. • `stretch`: Option to stretch the values to increase the contrast of the image: "lin" (default) or "hist"

Note

The function may take a lot of time if the images are large. Consider plotting a subset of the entire image instead of plotting the entire image. Please note that the example below demonstrates the functionality with a very small image.

For unknown reasons, it may be necessary to execute the function twice in order to get the right colors at the walls of the cube.

Author(s)

Lukas Lehnert

See Also

Speclib

Examples

```
## Not run:
## Create raster file using PROSPECT D
## Run PROSPECT for 1600 random chlorophyll content values
parameter <- data.frame(Cab = round(runif(1600, min = 10, max = 40), 0))
spectra <- PROSPECT(parameterList = parameter)
## Create SpatialPixelsDataFrame and fill data with spectra from PROSPECT
rows <- round(nspectra(spectra)/40, 0)
cols <- ceiling(nspectra(spectra)/rows)
grd <- SpatialGrid(GridTopology(cellcentre.offset = c(1,1,1),
cellsize = c(1,1,1),
cells.dim = c(cols, rows, 1)))
x <- SpatialPixelsDataFrame(grd, data = as.data.frame(spectra(spectra)))
## Write data to example file (example_in.tif) in workingdirectory
writeGDAL(x, fname = "example_in.tif", drivername = "GTiff")

## Read the raster and plot 3D cube
wavelength <- wavelength(spectra)
ras <- speclib("example_in.tif", wavelength)

cubePlot(ras)

## End(Not run)
```

`cut_specfeat` *Cut absorption features*

Description

Function cuts absorption features to a user-specified range. Since features may differ among spectra, it might be important to cut the features to specific wavelengths ranges.

Usage

```
cut_specfeat(x, ..., fnumber, limits)
```

Arguments

x	An object of class Specfeat containing isolated features determined by specfeat.
fnumber	A vector of the positions of the features in x to be cut.
limits	A vector containing the start and end wavelength for each fnumber. The corresponding feature will be cut to this specified range.
...	Further arguments passed to generic functions. Currently ignored.

Details

The typical workflow to obtain feature properties is to first calculate the band depth transformSpeclib, then isolate the absorption features specfeat. Optionally, cut_specfeat allows to cut the features at specified wavelengths. Finally use feature_properties to retrieve characteristics of the features.

Value

An object of class Specfeat containing the cut features.

Author(s)

Hanna Meyer and Lukas Lehnert

See Also

specfeat, Specfeat

Examples

```
data(spectral_data)

##Example to cut the features around 450nm and 700nm to a specific range
## Transform speclib
bd <- transformSpeclib(subset(spectral_data, season == "summer"),
                       method = "sh", out = "bd")

## Convert speclib to specfeat giving center wavelength of features
featureSelection <- specfeat(bd, c(450,700,1200,1500))

## Cut 1st and 2nd feature to [310 nm, 560 nm] and [589 nm, 800 nm]
featuresCut <- cut_specfeat(x = featureSelection, fnumber = c(1,2),
                            limits = c(c(310, 560), c(589, 800)))

## Plot result (1st and 2nd feature)
plot(featuresCut, fnumber = 1:2)
```

deletecp	*Delete fix point*

Description

Delete fix point from continuum line.

Usage

```
deletecp(x, ispec, cpdelete)
```

Arguments

x	Object of class `Clman`.
ispec	ID or index of spectrum to be modified.
cpdelete	Single value or vector of wavelength containing fix point(s) to be deleted.

Details

In some cases, it might be desirable to manually adapt automatically constructed segmended hulls (`transformSpeclib`). For example local maxima could be removed because they are very small and maybe afflicted with uncertainties which might legitimate it to manipulate the continuum line. Therefore, hsdar provides functions to remove and add "continuum points" from or to a continuum line. Manually adapted continuum lines can then be used to update band depth or ratio transformation. Handle these functions with care to avoid continuum lines too much build by subjective decisions. In the typical workflow, spectra are first transformed (`transformSpeclib`). Continuum points can then be retrieved (`getcp`) and manually adapted by adding `addcp` and deleting (`deletecp`) of points. Use `checkhull` to check for errors. If all uncertainties are removed, recalculate the hull (`makehull`) and update the transformed spectrum (`updatecl`).

Value

Object of class `Clman` containing the updated version of x.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `addcp`, `getcp`, `checkhull`, `makehull`, `updatecl`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)
## Mask parts not necessary for the example
mask(spec) <- c(1600, 2600)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, xlim = c(1100, 1300),ylim=c(0.17,0.21))

## Find wavelength of fix point to be deleted
getcp(spec_clman, 1, subset = c(1100, 1300))

## Delete all fix points between 1200 and 1240 nm
spec_clman <- deletecp(spec_clman, 1, c(1200:1240))

## Plot new line
plot(spec_clman, ispec = 1, xlim = c(1100, 1300),ylim=c(0.17,0.21))

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error
```

---

derivative.speclib *Derivation*

Description

Calculate derivations of spectra in `Speclib`.

Usage

```
derivative.speclib(x, m = 1, method = "sgolay", ...)
```

Arguments

`x`	Object of class `Speclib`.
`m`	Return the m-th derivative of the spectra.
`method`	Character string giving the method to be used. Valid options are `"finApprox"` or `"sgolay"`.
`...`	Further arguments passed to `sgolayfilt`.

Details

Two different methods are available:

- Finite approximation (`finApprox`):

$$\frac{dr}{d\lambda} = \frac{r(\lambda_i) - r(\lambda_{i+1})}{\Delta\lambda},$$

  where r_i is the reflection in band i and $\Delta\lambda$ the spectral difference between adjacent bands.
- Savitzky-Golay derivative computation (`sgolay`, default method)

Value

Object of class `Speclib`.

Author(s)

Lukas Lehnert

References

Tsai, F. & Philpot, W. (1998): Derivative analysis of hyperspectral data. Remote Sensing of Environment 66/1. 41-51.

See Also

`sgolayfilt`, `vegindex`, `soilindex`

Examples

```
data(spectral_data)

## Calculate 1st derivation
d1 <- derivative.speclib(spectral_data)

## Calculate 2nd derivation
d2 <- derivative.speclib(spectral_data, m = 2)

## Calculate 3rd derivation
d3 <- derivative.speclib(spectral_data, m = 3)

par(mfrow=c(2,2))
plot(spectral_data)
plot(d1)
plot(d2)
plot(d3)
```

dim.speclib *Dimensions of Speclib*

Description

Get dimension(s) of Speclib

Usage

```
## S4 method for signature 'Speclib'
dim(x)

nspectra(x)
nbands(x)
```

Arguments

x	Object of class `Speclib`.

Value

Vector of length = 2 for `dim` or single integer value for `nspectra` and `nbands`.

Author(s)

Lukas Lehnert

See Also

`Speclib`

Examples

```
data(spectral_data)

dim(spectral_data)
```

`dist.speclib` *Distance between spectra*

Description

Calculation of distance matrices by using one of the various distance measure to compute the distances between the spectra in `Speclib`. Spectral Angle Mapper (SAM) is calculated with `sam` giving reference spectra or with `sam_distance` taking all combinations between spectra in single Speclib into account.

Usage

```
dist.speclib(x, method = "sam", ...)

## Direct call to Spectral Angle Mapper function
sam(x, ref)
sam_distance(x)
```

Arguments

`x`	Object of class `Speclib`. Note that spectra in `x` must be in range [0,1].
`method`	The distance measure to be used. This must be one of "sam", "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski".
`ref`	Object of class `Speclib` containing reference spectra.
`...`	Further arguments, passed to other methods.

Details

Available distance measures are "spectral angle mapper" (`sam`, Kruse et al. 1993) and all distance measures available in `dist`. Spectral angle mapper is calculated with the following formula:

$$sam = \cos^{-1}\left(\frac{\sum_{i=1}^{nb} t_i r_i}{\sqrt{\sum_{i=1}^{nb} t_i^2}\sqrt{\sum_{i=1}^{nb} r_i^2}}\right)$$

nb is the number of bands in Speclib. t_i and r_i are the reflectances of target and reference spectrum in band i, respectively.

Value

The `dist-method` for Speclibs returns an object of class `"dist"`. See `dist` for further information on class `"dist"`. Both other functions return an object of class matrix.

Author(s)

Lukas Lehnert

References

Kruse, F. A.; Lefkoff, A. B.; Boardman, J. W.; Heidebrecht, K. B.; Shapiro, A. T.; Barloon, P. J. & Goetz, A. F. H. (1993). The spectral image processing system (SIPS) – interactive visualization and analysis of imaging spectrometer data. Remote Sensing of Environment, 44, 145-163.

See Also

dist, Speclib

Examples

```
data(spectral_data)

## Mask channel crossing part (around 1050 nm) and strong
## water absorption part (above 1350 nm)
mask(spectral_data) <- c(1045, 1055, 1350, 1706)

## Calculate distance between all spectra from spring
## using spectral angle mapper
dist.speclib(subset(spectral_data, season == "spring"))


## Calculate spectral angle mapper between reference spectrum
## and spectral_data
## Use first spectrum from summer as reference
distance <- sam(subset(spectral_data, season == "spring"),
                subset(spectral_data, season == "summer")[1,])
```

---

distMat3D *Methods to create, manipulate and query objects of class 'DistMat3D'.*

Description

Methods to create, manipulate and query objects of class 'DistMat3D'. The following relational operators are defined to compare values between 'DistMat3D'-object(s): `<, <=, ==, >, >=`

Usage

```
## Creation of objects
## S4 method for signature 'numeric'
distMat3D(x, ncol, nlyr)

## S4 method for signature 'matrix'
distMat3D(x, lower_tri = TRUE)

## S4 method for signature 'array'
```

```
distMat3D(x, lower_tri = TRUE)

## Conversion methods
## S4 method for signature 'DistMat3D'
as.array(x)

## S4 method for signature 'DistMat3D'
as.matrix(x, lyr = 1)

## Query of properties
## S4 method for signature 'DistMat3D'
dim(x)

## S4 method for signature 'DistMat3D'
ncol(x)

## S4 method for signature 'DistMat3D'
nrow(x)

## Manipulate and query data in objects
## S4 method for signature 'DistMat3D'
x[i, j, n]

## S4 replacement method for signature 'DistMat3D'
x[i, j, n] <- value


## S4 method for signature 'DistMat3D'
show(object)
```

Arguments

x,object	Matrix, numeric or array in cases of creation of 'DistMat3D' objects otherwise object of class 'DistMat3D'.
ncol	Number of columns in the new 'DistMat3D' object.
nlyr	Number of layer in the new 'DistMat3D' object.
lower_tri	Flag if only the lower triangle is used.
lyr	Layer in the 'DistMat3D' object to be transformed into matrix.
value	Object of class numeric, matrix or array which is used for replacement of the values in x.
i,j,n	Subscripts to access data.

Author(s)

Lukas Lehnert

See Also

DistMat3D, apply, Nri

Examples

```
data(spectral_data)

## Mask channel crossing part (around 1050 nm) and strong
## water absorption part (above 1350 nm)
mask(spectral_data) <- c(1045, 1055, 1350, 1706)

## Calculate SAM distances (object of class 'dist')
sam_dist <- dist.speclib(subset(spectral_data, season == "summer"))

## Convert to class 'distMat3D'
sam_dist <- distMat3D(as.matrix(sam_dist))

## Default print of DistMat3D-object
sam_dist

## Convert back to matrix
as.matrix(sam_dist)

## Get number of rows and samples
dim(sam_dist)

## Compare values in DistMat3D-object
small_dists <- sam_dist < 0.02

## Convert small_dists-object to DistMat3D
distMat3D(as.numeric(small_dists), 15, 1)
```

DistMat3D-class ** DistMat3D class*

Description

Class to store effectively (large) distance matrices (up to 3D), which can be interpreted as a stack of traditional 2-D distance matrices. Therefore, the first two dimensions are of equal length and usually describe the wavelength in **hsdar**. This third dimension is normally the number of samples or pixels. In **hsdar**, objects of class DistMat3D are used e.g., to store nri-values. In this case, the first and second dimensions store the information which band #1 is substraced by which band #2, respectively. The third dimension is the sample. Since it usually does not matter if band #1 is substracted from band #2 or vice versa, the nri-matrix would contain the same absolute values on both triangles (as 2-D distance matrices would do). Therefore, **hsdar** defines and uses the class DistMat3D in which only one triangle is stored and memory demand is considerably reduced.

Details

S4-class with 3 slots:

- values: Numerical vector containing distance values
- ncol: Number of columns in the 3D-matrix. Number of columns equals always the number of rows
- nlyr: Number of layers in the 3D-matrix

The data in the values slot is organized as follows: The first value is the distance at band #1 and band #2 for sample number #1, the second one is for band #1 and band #3 (sample #1) and so forth. Methods to create objects of class `DistMat3D` for matrix and array objects exist. Additionally, methods to apply functions to the values exist.

Note

See figure in `hsdar-package` for an overview of classes in **hsdar**.

Author(s)

Lukas Lehnert

See Also

`distMat3D`, `apply.DistMat3D`

`Extract Speclib by index` *Indexing Speclib*

Description

Access subsets of data in Speclibs both in spectrals and sample dimensions

Usage

```
## S4 method for signature 'Speclib'
x[i, j, ...]
```

Arguments

`x`	Object of class `Speclib` to be indexed.
`i`	Samples to be returned.
`j`	Bands to be returned.
`...`	Further arguements (currently ignored).

Details

The first index represents the sample dimension and the second one is the band dimension. If the sample dimension is indexed, care is taken that the SI and the id is indexed as well.

Value

Object of class `Speclib` containing the updated version of x.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `subset.speclib`, `SI`, `idSpeclib`

Examples

```
data(spectral_data)

## Get the first five spectra
spec_1_5 <- spectral_data[1:5,]
spec_1_5

## Get the first ten bands
spec_1_10 <- spectral_data[,1:10]
spec_1_10

## Get the bands number 20 to 30 for the third and fifth spectra
spec_20_30 <- spectral_data[c(3,5),20:30]
spec_20_30
```

`feature_properties` *Calculation of properties of features*

Description

Function to calculate feature properties such as the area, the position of the maximum and several other parameters. This function can only be used for spectral data transformed using any kind of continuum removal (see `transformSpeclib`).

Usage

```
feature_properties(x)
```

Arguments

x	Object of class `Specfeat`

Details

The function calculates several parameters:

- *area*: The feature area is calculated by

$$area_{F_i} = \sum_{k=min(\lambda)}^{max(\lambda)} BD\lambda,$$

  with $area_{F_i}$ is the area of the feature i, $min(\lambda)$ is the minimum wavelength of the spectrum, $max(\lambda)$ is the maximum wavelength of the spectrum and BD is the band depth.
- *max*: Wavelength position of the maximum value observed in the feature.
- Parameters based on half-max values:
  - *lo* and *up*: Wavelength position of the *lo*wer and *up*per half-max value.
  - *width*: Difference between wavelength positions of *up*per and *lo*wer half-max values.
  - *gauss_lo*: Similarity of the Gauss distribution function and the feature values between the *lo*wer half-max and the *max*imum position. As similarity measurement, the root mean square error is calculated.
  - *gauss_up*: Same as above but for feature values between the *max*imum position and the *up*per half-max.

The typical workflow to obtain feature properties is to first calculate the band depth `transformSpeclib`, then isolate the absorption features `specfeat`. Optionally, `cut_specfeat` allows to cut the features at specified wavelengths. Finally use `feature_properties` to retrieve characteristics of the features.

Value

An object of class `Specfeat` containing the properties as (part of the) SI table.

Author(s)

Hanna Meyer & Lukas Lehnert

See Also

`specfeat`

Examples

```
data(spectral_data)

## Example calculating the areas of the features around 450nm,
## 700nm, 1200nm and 1500nm.
bd <- transformSpeclib(subset(spectral_data, season == "summer"),
                       method = "sh", out = "bd")

## Convert speclib to specfeat giving center wavelength of features
featureSelection <- specfeat(bd, c(450,700,1200,1500))
```

```
## Calculate properties of features
featureProp <- feature_properties(featureSelection)

## See resulting feature property variables
head(SI(featureProp))
```

---

get.gaussian.response *Gaussian response function*

Description

Simulate Gaussian response function for band(s) of a (satellite) sensor. Each band is either defined by center and full-width-half-maximum values or by passing its upper and lower border.

Usage

```
get.gaussian.response(fwhm)
```

Arguments

fwhm	Object of class data.frame with three columns. See details and examples sections.

Details

The characteristics of the sensor must be passed as a data.frame with three columns: first column is used as name for bands, second with lower bounds of channels and third column with upper bounds (5% sensitivity). Alternatively, the data.frame may encompass band centre wavelength and full-width-half-maximum values of the sensor. Function will check the kind of data passed by partially matching the names of the data frame: If any column is named "fwhm" or "center", it is assumed that data are band centre and full-width-half-maximum values.

Value

Data frame with response values for all bands covering the entire spectral range of sensor passed to the function.

Author(s)

Lukas Lehnert

See Also

get.sensor.characteristics, spectralResampling

Examples

```
par(mfrow=c(1,2))
## Plot response function of RapidEye
plot(c(0,1)~c(330,1200), type = "n", xlab = "Wavelength [nm]",
     ylab = "Spectral response")
data_RE <- get.gaussian.response(get.sensor.characteristics("RapidEye"))
xwl_response <- seq.int(attr(data_RE, "minwl"),
                        attr(data_RE, "maxwl"),
                        attr(data_RE, "stepsize"))
for (i in 1:ncol(data_RE))
  lines(xwl_response, data_RE[,i], col = i)

## Plot original response function
data_RE <- get.sensor.characteristics("RapidEye", TRUE)

plot(c(0,1)~c(330,1200), type = "n", xlab = "Wavelength [nm]",
     ylab = "Spectral response")
xwl_response <- seq.int(attr(data_RE$response, "minwl"),
                        attr(data_RE$response, "maxwl"),
                        attr(data_RE$response, "stepsize"))
for (i in 1:nrow(data_RE$characteristics))
  lines(xwl_response, data_RE$response[,i], col = i)

## Simulate gaussian response for arbitrary sensor with 3 bands
sensor <- data.frame(Name = paste("Band_", c(1:3), sep = ""),
                     center = c(450, 570, 680),
                     fwhm = c(30, 40, 30))

## Plot response function
par(mfrow=c(1,1))
plot(c(0,1)~c(330,800), type = "n", xlab = "Wavelength [nm]",
     ylab = "Spectral response")
data_as <- get.gaussian.response(sensor)
xwl_response <- seq.int(attr(data_as, "minwl"),
                        attr(data_as, "maxwl"),
                        attr(data_as, "stepsize"))
for (i in 1:3)
  lines(xwl_response, data_as[,i], col = i)
```

`get.sensor.characteristics` *Sensor characteristics*

Description

Get channel wavelength of implemented (multispectral) satellite sensors.

Usage

```
get.sensor.characteristics(sensor, response_function = FALSE)
```

Arguments

sensor — Character or integer. Name or numerical abbreviation of sensor. See 'sensor="help"' or 'sensor=0' for an overview of available sensors.

response_function — If TRUE, the spectral response function is returned.

Details

The following sensors are currently implemented: ALI, EnMAP, Hyperion, Landsat4, Landsat5, Landsat7, Landsat8, MODIS, Quickbird, RapidEye, Sentinel2, WorldView2-4, WorldView2-8.

Spectral response functions are available for the following ones: Landsat4, Landsat5, Landsat7, Landsat8, Quickbird, RapidEye, Sentinel2, WorldView2-4, WorldView2-8.

Author(s)

Lukas Lehnert

See Also

spectralResampling

Examples

```
## Return implemented sensors
get.sensor.characteristics(0)

## RapidEye
data_wv <- get.sensor.characteristics("RapidEye", TRUE)

## Plot response functions
plot(c(0,1)~c(330,1200), type = "n", xlab = "Wavelength [nm]",
     ylab = "Spectral response")
xwl_response <- seq.int(attr(data_wv$response, "minwl"),
                        attr(data_wv$response, "maxwl"),
                        attr(data_wv$response, "stepsize"))
for (i in 1:nrow(data_wv$characteristics))
  lines(xwl_response, data_wv$response[,i], col = i)
```

---

getcp — *Get fix points*

Description

Get fix points of continuum line within spectral range.

Usage

```
getcp(x, ispec, subset = NULL)
```

Arguments

`x`	Object of class `Clman`.
`ispec`	ID or index of spectrum to be analysed.
`subset`	Vector of `length = 2` giving the lower and upper limit of spectral range.

Value

Object of class `list` containing two elements:

- ptscon: Data frame with wavelength and reflectance of fix points
- ispec: Index of analysed spectrum within passed `Clman`-object.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `deletecp`, `addcp`, `Clman`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Fix points
spec_cp <- getcp(spec_clman, 1, c(400, 800))
spec_cp
```

---

getNRI *Return nri-values*

Description

Return normalized ratio index values at a given wavelength combination.

Usage

```
getNRI(nri, wavelength)
```

Arguments

`nri`	Object of class 'Nri'
`wavelength`	Wavelength values where nri is returned. See details section.

Details

Wavelength can be passed in three ways. As the result of nri_best_performance, as a data frame with two columns or as a vector of length 2. In the first two cases, the result will be a data frame (if data frames contain more than one row) with the nri-values of each pair of wavelengths. In the latter case it will be a vector.

Author(s)

Lukas Lehnert

See Also

nri, Nri

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Build glm-models
glmnri <- glm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)

## Return best 5 models
BM <- nri_best_performance(glmnri, n = 5, coefficient = "p.value")

## Get nri values for the 5 models
nri_BM <- getNRI(nri_WV, BM)
```

`get_reflectance` *Get reflectance values*

Description

Returns weighted or unweighted reflectance values at wavelength position.

Usage

```
get_reflectance(spectra, wavelength, position, weighted = FALSE, ...)
```

Arguments

spectra	Object of class Speclib or data.frame with reflectance values.
wavelength	Vector with wavelength values. May be missing if spectra is object of class Speclib.
position	Numeric value passing the position of reflectance values to be returned in dimensions of the wavelength values.
weighted	Logical indicating if reflectance values should be interpolated to fit wavelength position. If FALSE the reflectance values of nearest neighbour to passed position are returned.
...	Arguments to be passed to specific functions. Currently ignored.

Value

A vector with reflectance values for each spectrum is returned. If position falls outside of spectral range of input values, NA values are returned.

Author(s)

Lukas Lehnert \& Hanna Meyer

See Also

spectra

Examples

```
data(spectral_data)

## Simulate multispectral sensor encompassing two bands
## to show effect of weighted and unweighted modes
spectral_data_res <- spectralResampling(spectral_data,
  sensor = data.frame(lb = c(400, 600), ub = c(500, 700)))

## Compare reflectance at 520 nm (in between both bands to
## show the difference between weighted and unweighted modes)
weighted_reflectance   <- get_reflectance(spectral_data_res,
                                          520, weighted = TRUE)
unweighted_reflectance <- get_reflectance(spectral_data_res,
                                          520, weighted = FALSE)

## Plot result
plot(weighted_reflectance, unweighted_reflectance,
     ylab = "Reflectance at 520 nm (unweighted)",
     xlab = "Reflectance at 520 nm (weighted)")
```

glm.nri *(Generalised) Linear models from normalised ratio indices*

Description

Build (generalised) linear models of normalised ratio indices as response and predictor variables usually stored in the SI.

Usage

```
lm.nri(formula, preddata = NULL, ...)
glm.nri(formula, preddata = NULL, ...)
```

Arguments

`formula`	Formula for (generalized) linear model
`preddata`	Data frame or speclib containing predictor variables
`...`	Further arguments passed to `lm`, `glm` and generic `print.default`

Details

NRI-values may be used as predictor or response variable. If NRI-values are predictors, the models are build only with one index as predictor instead of all available indices. In this case, only one predictor and one response variable is currently allowed. See help pages for `lm` and `glm` for any additional information. Note that this function does not store the entire information returned from a normal (g)lm-model. To get full (g)lm-models use either the function `nri_best_performance` to return best performing model(s) or extract nri-values with `getNRI` and build directly the model from respective index.

See details in Nri-`plot`-method for information about plotting.

Value

The function returns an object of class `Nri`. The list in the slot *multivariate* contains the new (g)lm information which depends on the kind of model which is applied:

1. `lm.nri`: The list contains the following items:
   - Estimate: Coefficient estimates for each index and term
   - Std.Error: Standard errors
   - t.value: T-values
   - p.value: P-values
   - r.squared: R^2 values
2. `glm.nri`: The list contains the following items (depending on formula used):
   - Estimate: Coefficient estimates for each index and term
   - Std.Error: Standard errors
   - t.value/z.value: T-values or Z-values
   - p.value: P-values

Author(s)

Lukas Lehnert

See Also

plot, lm, glm, getNRI

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

glmnri <- glm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)
glmnri

plot(glmnri)
```

---

hsdardocs *Load additional documents*

Description

Access help documents and references for different methods.

Usage

```
hsdardocs(doc)
```

Arguments

doc	Name of document to load. Currently, "Hsdar-intro.pdf", "References.pdf" and "Copyright" are available

Author(s)

Lukas Lehnert

Examples

```
## Not run:
## Open introduction to hsdar (PDF-file)
hsdardocs("Hsdar-intro.pdf")

## Open references of hyperspectral vegetation indices (PDF-file)
hsdardocs("References.pdf")
```

```
## See copyrights of routines and data used in hsdar-package (ascii-file)
hsdardocs("Copyright")

## End(Not run)
```

hsdar_parallel *hsdar_parallel*

Description

Get all functions which support parallel execution. Currently, the parallel backend functions in **doMPI** and **doMC** are supported.

Usage

```
hsdar_parallel()
```

Details

Parallel execution is performed via the **foreach**-package. Care is taken that a function will never run in parallel if the calling function is already using multicore processing.

Value

Vector containing supported function names

Author(s)

Lukas Lehnert

Examples

```
## Not run:
supported_functions <- hsdar_parallel()
supported_functions

data(spectral_data)

## Example for Windows and other systems where doMPI is available
## Load library
library(doMPI)
## Register number of workers
cl <- startMPIcluster(count = 3)
registerDoMPI(cl)

## Transform speclib using 3 cores
bd <- transformSpeclib(spectral_data)

## Close the cluster (important to get rid of processes)
```

```
closeCluster(cl)

## Example for Linux and other systems where doMC is available
## Load library
library(doMC)
## Register number of workers
registerDoMC(3)

## Transform speclib using 3 cores
bd <- transformSpeclib(spectral_data)

## End(Not run)
```

`HyperSpecRaster` *Handle hyperspectral cubes using raster package (deprecated)*

Description

The HyperSpecRaster-Class is deprecated. Use `Speclib` instead.

Usage

```
## S4 method for signature 'character,numeric'
HyperSpecRaster(x, wavelength, fwhm = NULL, SI = NULL, ...)

## S4 method for signature 'RasterLayer,numeric'
HyperSpecRaster(x, wavelength, fwhm = NULL, SI = NULL)

## S4 method for signature 'RasterBrick,numeric'
HyperSpecRaster(x, wavelength, fwhm = NULL, SI = NULL)

## S4 method for signature 'HyperSpecRaster'
HyperSpecRaster(x, wavelength)

## S4 method for signature 'Speclib'
HyperSpecRaster(x, nrow, ncol, xmn, xmx, ymn, ymx, crs)

## S4 method for signature 'HyperSpecRaster,character'
writeStart(x, filename, ...)

## S4 method for signature 'HyperSpecRaster'
getValuesBlock(x, ...)

## S4 method for signature 'RasterLayer,Speclib'
writeValues(x, v, start)

## S4 method for signature 'RasterBrick,Speclib'
writeValues(x, v, start)
```

```
## S4 method for signature 'HyperSpecRaster,Speclib'
writeValues(x, v, start)
```

Arguments

`x`	Raster* object
`wavelength`	Vector containing wavelength for each band
`fwhm`	Optional vector containing full-width-half-max values. If length == 1 the same value is assumed for each band. Note that function does not check the integrity of the values
`SI`	Optional data.frame containing SI data
`nrow`	Optional. Number of rows in HyperspecRaster. If omitted, function will try to get the information from the SI in Speclib (`attr(x, "rastermeta")`)
`ncol`	Optional. Number of colums in HyperspecRaster. See nrow above.
`xmn`	Optional. Minimum coordiante in x-dimension. See nrow above.
`xmx`	Optional. Maximum coordiante in x-dimension. See nrow above.
`ymn`	Optional. Minimum coordiante in y-dimension. See nrow above.
`ymx`	Optional. Maximum coordiante in y-dimension. See nrow above.
`crs`	Optional. Object of class `'CRS'` giving the coordinate system for HyperspecRaster. See nrow above.
`...`	Additional arguments as for `brick`
`filename`	Name of file to create
`v`	Speclib or matrix of values
`start`	Integer. Row number (counting starts at 1) from where to start writing `v`

Value

HyperSpecRaster or RasterBrick

Author(s)

Lukas Lehnert

`HyperSpecRaster-class` *HyperSpecRaster* class (deprecated)*

Description

This is a deprecated class. Use `Speclib`-class instead.

Details

Extension of *RasterBrick-class with three additional slots:

`wavelength`: A numeric vector giving the center wavelength for each band.

`fwhm` **(optional):** A numeric vector giving the full-width-half-max values for each band.

`SI` **(optional):** A `data.frame` containing additional information for each pixel.

The information in the three slots are used for the convertion to `Speclib`.

Author(s)

Lukas Lehnert

See Also

`brick`, `Speclib`

`idSpeclib` *Handling IDs of spectra*

Description

Returning and setting ID of spectra in Speclib

Usage

```
idSpeclib(x)
idSpeclib(x) <- value
```

Arguments

`x`	Object of class `Speclib`.
`value`	Character vector of the same length as `nspectra(x)`, or NULL.

Value

For `idSpeclib<-`, the updated object. Otherwise a vector giving the ID of each spectrum in Speclib is returned.

Author(s)

Lukas Lehnert

See Also

`Speclib`

Examples

```
data(spectral_data)

idSpeclib(spectral_data)
```

`import_USGS` *import USGS spectra*

Description

Import and download spectral data from USGS spectral library

Usage

```
USGS_get_available_files(url = NULL)

USGS_retrieve_files(avl = USGS_get_available_files(),
                    pattern = NULL, retrieve = TRUE,
                    loadAsSpeclib = TRUE, tol = 0.1)
```

Arguments

`url`	Character passing the url of the data. If NULL, the following URL is used: 'ftp://ftpext.cr.usgs.gov/pub/cr/co/denver/speclab/pub/spectral.library/splib06.library/ASCII/'
`avl`	List of available files. Typically the result of `USGS_get_available_files`.
`pattern`	Search pattern to define a subset of all available spectra.
`retrieve`	Logical. Should the data be downloaded?
`loadAsSpeclib`	Logical. If TRUE, an object of class "Speclib" is retured
`tol`	Discrepancy of the wavelength values between different spectra.

Author(s)

Lukas Lehnert

Examples

```
## Not run:
## Retrieve all available spectra
avl <- USGS_get_available_files()

## Download all spectra matching "grass-fescue"
grass_spectra <- USGS_retrieve_files(avl = avl, pattern = "grass-fescue")

plot(grass_spectra)

## End(Not run)
```

`makehull` *Re-calculate hull*

Description

Re-calculates the hull after it was manually adapted

Usage

```
makehull(x, ispec)
```

Arguments

`x`	Object of class `Clman`.
`ispec`	Name or index of spectrum to be checked.

Details

In some cases, it might be desirable to manually adapt automatically constructed segmended hulls (`transformSpeclib`). For example local maxima could be removed because they are very small and maybe afflicted with uncertainties which might legitimate it to manipulate the continuum line. Therefore, hsdar provides functions to remove and add "continuum points" from or to a continuum line. Manually adapted continuum lines can then be used to update band depth or ratio transformation. Handle these functions with care to avoid continuum lines too much build by subjective decisions. In the typical workflow, spectra are first transformed (`transformSpeclib`). Continuum points can then be retrieved (`getcp`) and manually adapted by adding `addcp` and deleting (`deletecp`) of points. Use `checkhull` to check for errors. If all uncertainties are removed, re-calculate the hull (`makehull`) and update the transformed spectrum (`updatecl`).

Value

Object of class `list`.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `addcp`, `deletecp`, `makehull`, `updatecl`

`Clman`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, xlim = c(2480, 2500), ylim=c(0.022,0.024))

## Add fix point at 4595 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2495)

## Plot new line
plot(spec_clman, ispec = 1, xlim = c(2480, 2500), ylim=c(0.022,0.024))

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error

## Add fix point at 4596 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2496)

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error

## Re-calculate hull
hull <- makehull(spec_clman, 1)

## Transform spectra using band depth
spec_bd <- transformSpeclib(spec, method = "sh", out = "bd")

## Update continuum line of first spectrum
spec_bd <- updatecl(spec_bd, hull)

## Plot modified transformed spectrum
plot(spec_bd, FUN = 1)
```

`mask` *Mask spectra*

Description

Returning and setting mask of spectra in `Speclib`. `interpolate.mask` linearly interpolates masked parts in spectra.

Usage

```
## S4 method for signature 'Speclib'
mask(object)
## S4 replacement method for signature 'Speclib,data.frame'
mask(object) <- value
## S4 replacement method for signature 'Speclib,list'
mask(object) <- value
## S4 replacement method for signature 'Speclib,numeric'
mask(object) <- value

## Linear interpolation of masked parts
interpolate.mask(object)
```

Arguments

`object`	Object of class `Speclib`.
`value`	Numeric vector, data frame or list giving the mask boundaries in wavelength units. See details section.

Details

Value may be an object of class vector, data frame or list. Data frames must contain 2 columns with the first column giving the lower (lb) and the second the upper boundary (ub) of the wavelength ranges to be masked. List must have two items consisting of vectors of length = 2. The first entry is used as lower and the second as upper boundary value. Vectors must contain corresponding lower and upper boundary values consecutively. The masked wavelength range(s) as defined by the lower and upper boundaries are excluded from the object of class `Speclib`.

Interpolation of masked parts is mainly intended for internal use. Interpolation is only possible if mask does not exceed spectral range of `Speclib`.

Value

For `mask<-`, the updated object. Otherwise a data frame giving the mask boundaries.

`interpolate.mask` returns a new object of class `Speclib`.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`Speclib`

Examples

```
data(spectral_data)

mask(spectral_data) ## NULL
```

```
## Mask from vector
spectral_data_ve <- spectral_data
mask(spectral_data_ve) <- c(1040,1060,1300,1450)
mask(spectral_data_ve)


## Mask from data frame
spectral_data_df <- spectral_data
mask(spectral_data_df) <- data.frame(lb=c(1040,1300),ub=c(1060,1450))
mask(spectral_data_df)


## Mask from list
spectral_data_li <- spectral_data
mask(spectral_data_li) <- list(lb=c(1040,1300),ub=c(1060,1450))
mask(spectral_data_li)

## Linear interpolation
plot(spectral_data)
plot(interpolate.mask(spectral_data_li), new=FALSE)
```

`meanfilter` *Apply mean filter*

Description

Apply mean filter to spectra. Filter size is passed as number of bands averaged at both sides of the respective band value.

Usage

```
meanfilter(spectra, p = 5)
```

Arguments

`spectra`	Data.frame, matrix or Speclib containing spectra
`p`	Filter size.

Value

Filtered matrix or Speclib of same dimension as input matrix/Speclib

Author(s)

Lukas Lehnert

See Also

`noiseFiltering`

Examples

```
data(spectral_data)

spectra_filtered <- meanfilter(spectral_data, p = 10)
plot(spectra_filtered[1,])
plot(spectral_data[1,], new = FALSE)
```

---

merge *Merge speclibs*

Description

Merge two Speclibs and their SI data

Usage

```
## S4 method for signature 'Speclib,Speclib'
merge(x, y, ...)
```

Arguments

x	1st Object of class Speclib to be merged.
y	2nd Object of class Speclib to be merged.
...	Further (optional) objects of class Speclib.

Value

Object of class Speclib.

Author(s)

Lukas Lehnert

See Also

Speclib

Examples

```
data(spectral_data)
sp1 <- spectral_data[c(1:10),]
sp2 <- spectral_data[c(11:20),]

## Merge two Speclibs
speclib_merged_1 <- merge(sp1, sp2)
nspectra(speclib_merged_1)
```

```
## Merge multiple Speclibs
sp3 <- spectral_data[c(21:30),]
speclib_merged_2 <- merge(sp1, sp2, sp3)
nspectra(speclib_merged_2)
```

`noiseFiltering` *Smooth spectra*

Description

Smoothing of spectral data by Savitzky-Golay, lowess, spline, mean or user-defined filtering approaches.

Usage

```
noiseFiltering(x, method = "mean", ...)
```

Arguments

`x`	Object of class `Speclib`.
`method`	Character string giving the name of the method to be used. Predefined valid options are "sgolay", "lowess", "spline" and "mean". However, method can also be the (character) name of any other filter function (see examples).
`...`	Further arguments passed to the filter functions. The following arguments are important for the predefined methods: • `sgolay`: `n` sets the filter length (must be odd). • `lowess`: `f` defines the smoother span. This gives the proportion of bands in the spectrum which influence the smooth at each value. Larger values give more smoothness. • `spline`: `n` defines at how many equally spaced points spanning the interval interpolation takes place. • `mean`: `p` sets the filter size in number of bands. Note that larger values give more smoothness. Refer to the links in the details section, and see examples.

Details

Smoothing of spectra by filtering approaches is an essential technique in pre-processing of hyperspectral data with its contiguous spectra. By stepwise fitting of the spectral channels within a defined window size, it is used to minimize the variances caused by intrumental variations or the high noise levels resulting from the very fine wavelength resolution. Therefore, this function allows filtering using four different methods:

- Savitzky-Golay: Smoothing applying Savitzky-Golay-Filter. See `sgolayfilt` from signal-package for details.

- Lowess: Smoothing applying lowess-Filter. See lowess from stats-package for details.
- Spline: Smoothing applying spline-Filter. See spline from stats-package for details.
- Mean: Smoothing applying mean-Filter. See meanfilter for details.

Value

Object of class Speclib.

Author(s)

Lukas Lehnert, Wolfgang Obermeier

References

Tsai, F. & Philpot, W. (1998): Derivative analysis of hyperspectral data. Remote Sensing of Environment 66/1. 41-51.

Vidal, M. & Amigo, J. (2012): Pre-processing of hyperspectral images. Essential steps before image analysis. Chemometrics and Intelligent Laboratory Systems 117. 138-148.

See Also

sgolayfilt, lowess, spline, meanfilter

Examples

```
data(spectral_data)

## Example of predefined filter functions
## Savitzky-Golay
sgolay <- noiseFiltering(spectral_data, method="sgolay", n=25)

## Spline
spline <- noiseFiltering(spectral_data, method="spline",
                         n=round(nbands(spectral_data)/10,0))

## Lowess
lowess <- noiseFiltering(spectral_data, method="lowess", f=.01)

## Mean
meanflt <- noiseFiltering(spectral_data, method="mean", p=5)

par(mfrow=c(2,2))
plot(spectral_data, FUN=1, main="Savitzky-Golay")
plot(sgolay, FUN=1, new=FALSE, col="red", lty="dotted")
plot(spectral_data, FUN=1, main="Spline")
plot(spline, FUN=1, new=FALSE, col="red", lty="dotted")
plot(spectral_data, FUN=1, main="Lowess")
plot(lowess, FUN=1, new=FALSE, col="red", lty="dotted")
plot(spectral_data, FUN=1, main="Mean")
plot(meanflt, FUN=1, new=FALSE, col="red", lty="dotted")
```

```
## Example of a not predefined filter function (Butterworth filter)
bf <- butter(3, 0.1)
bf_spec <- noiseFiltering(spectral_data, method="filter", filt=bf)
plot(spectral_data, FUN=1, main="Butterworth filter")
plot(bf_spec, FUN=1, new=FALSE, col="red", lty="dotted")
```

---

nri *Normalised ratio index*

Description

Calculate normalised ratio index (nri) for a single given band combination or for all possible band combinations. Calculating nri is a frequently used method to standardize reflectance values and to find relationships between properties of the objects and their spectral data.

Usage

```
nri(x, b1, b2, recursive = FALSE, bywavelength = TRUE)
```

Arguments

`x`	List of class `Speclib` or of class `Nri` for print and as.matrix methods.
`b1`	Band 1 given as band number or wavelength.
`b2`	Band 2 given as band number or wavelength.
`recursive`	If TRUE indices for all possible band combinations are calculated. If FALSE, only a single nri for the given bands in `b1` and `b2` is calculated.
`bywavelength`	Flag to determine if b1 and b2 are band number (bywavelength = FALSE) or wavelength (bywavelength = TRUE) values.
`...`	Further arguments passed to generic functions. Currently ignored.

Details

Function performs the following calculation:

$$nri_{B1,\ B2} = \frac{R_{B1} - R_{B2}}{R_{B1} - R_{B2}};$$

with R being reflectance values at wavelength $B1$ and $B2$, respectively.

If recursive = TRUE, all possible band combinations are calculated.

Value

If recursive = FALSE, a data frame with index values is returned. Otherwise result is an object of class `Nri`. See `glm.nri` for applying a generalised linear model to an array of normalised ratio indices.

Author(s)

Lukas Lehnert

References

Sims, D.A.; Gamon, J.A. (2002). Relationships between leaf pigment content and spectral reflectance across a wide range of species, leaf structures and developmental stages. Remote Sensing of Environment: 81/2, 337 - 354.

Thenkabail, P.S.; Smith, R.B.; Pauw, E.D. (2000). Hyperspectral vegetation indices and their relationships with agricultural crop characteristics. Remote Sensing of Environment: 71/2, 158 - 182.

See Also

glm.nri, glm, Speclib, Nri

Examples

```
data(spectral_data)

## Calculate NDVI
ndvi <- nri(spectral_data, b1=800, b2=680)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)
nri_WV
```

Nri-class ** Nri class*

Description

Class to handle datasets containing normalized ratio indices of spectra.

Details

Object with slots:

- nri: Object of class DistMat3D containing nri values.
- fwhm: Vector or single numerical value giving the full-width-half-max value(s) for each band.
- wavelength: Vector with wavelength information.
- dimnames: Character vector containing band names used to calculate nri-values.
- multivariate: List defining the kind of test/model applied to the data and the model data. Only used after object has passed e.g. (g)lm.nri.
- SI: Data.frame containing additional data
- usagehistory: Vector giving information on history of usage of the object.

Note

See figure in hsdar-package for an overview of classes in hsdar.

Author(s)

Lukas Lehnert

See Also

Speclib

Nri-methods *Methods for * Nri-class*

Description

Methods to handle data in objects of class Nri.

Usage

```
## S4 method for signature 'Nri'
as.matrix(x, ..., named_matrix = TRUE)

## S4 method for signature 'Nri'
as.data.frame(x, na.rm = FALSE, ...)

## S4 method for signature 'Nri'
wavelength(object)

## S4 method for signature 'Nri'
dim(x)

getFiniteNri(x)
```

Arguments

x,object	Object of class 'Nri'
na.rm	Remove indices containing NA-values. Note that if TRUE, all indices are removed which have at least one NA value.
named_matrix	Flag if column and row names are set to band indices used for the calculation of the nri-values.
...	Further arguments passed to generic functions. Currently ignored.

Author(s)

Lukas Lehnert

See Also

glm.nri, glm, nri

nri_best_performance *Best performing model(s) with NRI*

Description

Get or mark best performing model(s) between narrow band indices and environmental variables

Usage

```
nri_best_performance(nri, n = 1, coefficient = "p.value",
                     predictor = 2, abs = FALSE, findMax = FALSE,
                     ...)
mark_nri_best_performance(best, glmnri, n = nrow(best$Indices),
                          uppertriang = FALSE, ...)
```

Arguments

`nri`	Object of class nri
`glmnri`	Object of class glmnri
`n`	Number of models to return or mark
`coefficient`	Name or index of coefficient to plot
`predictor`	Name or index of term to plot
`abs`	Use absolute value (e.g. for t-values)
`findMax`	Find maximum or minimum values
`best`	Output from `nri_best_performance`
`uppertriang`	Flag to mark the upper triangle
`...`	Further arguments passed to glm function. These must be the same as used for initial creation of glm.nri. For `mark_nri_best_performance` arguments are passed to polygon.

Details

See details in glm.nri and glm.

Author(s)

Lukas Lehnert

See Also

glm.nri, glm

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Build glm-models
glmnri <- glm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)

## Return best 5 models
BM <- nri_best_performance(glmnri, n = 5, coefficient = "p.value")

## Get nri values for the 5 models
nri_BM <- getNRI(nri_WV, BM)
```

`plot.Nri` *Plot function for (g)lm.nri and cor.test.nri*

Description

Plot values in (generalised) linear modes and correlation tests from narrow band indices

Usage

```
## S4 method for signature 'Nri'
plot(x, coefficient = "p.value", predictor = 2,
     xlab = "Wavelength band 1 (nm)",
     ylab = "Wavelength band 2 (nm)", legend = TRUE,
     colspace = "hcl", col = c(10, 90, 60, 60, 10, 80),
     digits = 2, range = "auto", constraint  = NULL,
     uppertriang = FALSE, zlog = FALSE, ...)
```

Arguments

`x`	Object to be plotted.
`coefficient`	Name or index of coefficient to plot.
`predictor`	Name or index of term to plot.
`xlab`	Label for x-axis.
`ylab`	Label for y-axis.
`legend`	Flag if legend is plotted. If `legend == "outer"` the legend is plotted in the outer margins of the figure. This is useful if both diagonals are used.
`colspace`	Either "hcl" or "rgb". Colour space to be used for the plots.

`col`	If colspace == "hcl", the vector is giving the minimum and maximum values of hue (element 1 & 2), chroma (element 3 & 4) and luminance (element 5 & 6). The optional element 7 is used as alpha value. See `hcl` for further explanation. If colspace == "rgb", a vector of length >=2 giving the colours to be interpolated using `colorRamp`.
`digits`	Precision of labels in legend.
`range`	"auto" or a vector of length = 2 giving the range of values to be plotted.
`constraint`	A character string giving a constraint which values should be plotted. See examples section.
`uppertriang`	Flag if upper triangle is used for the plot. Note that if `TRUE` the current plot is used instead of starting a new plot
`zlog`	Flag indicating if color should be logarithmically scaled. Useful e.g. for p-values.
`...`	Further arguments passed to `plot.default`.

Details

See details in `glm.nri` and `glm`.

Value

An invisible vector with minimum and maximum values plotted.

Author(s)

Lukas Lehnert

See Also

`nri`, `glm.nri`, `glm`, `cor.test`, `t.test`

Examples

```
## Not run:
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Fit generalised linear models between NRI-values and chlorophyll
glmnri <- glm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)

## Plot p-values
plot(glmnri, range = c(0, 0.05))
## Plot t-values
plot(glmnri, coefficient = "t.value")
## Plot only t-values where p-values < 0.001
```

```
plot(glmnri, coefficient = "t.value",
     constraint = "p.value < 0.001")

## Fit linear models between NRI-values and chlorophyll
lmnri <- lm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)

## Plot r.squared
plot(lmnri)

## Example for EnMAP (Attention: Calculation time may be long!)
spec_EM <- spectralResampling(spectral_data, "EnMAP",
                              response_function = FALSE)
mask(spec_EM) <- c(300, 550, 800, 2500)
nri_EM <- nri(spec_EM, recursive = TRUE)
glmnri <- glm.nri(nri_EM ~ chlorophyll, preddata = spec_EM)

## Plot T values in lower and p-values in upper diagonal
## of the plot
## Enlarge margins for legends
par(mar = c(5.1, 4.1, 4.1, 5))
plot(glmnri, coefficient = "t.value", legend = "outer")
plot(glmnri, coefficient = "p.value", uppertriang = TRUE, zlog = TRUE)
lines(c(400,1705),c(400,1705))

## End(Not run)
```

`plot.Specfeat` *Plot Specfeat*

Description

Plot spectra in objects of class `Specfeat`. Specfeats contain spectral data after applying a transformation such as continuum removal (see function `transformSpeclib`.

Usage

```
## S4 method for signature 'Specfeat'
plot(x, fnumber = 1, stylebysubset = NULL, changecol = TRUE,
        changetype = FALSE, autolegend = TRUE, new = TRUE, ...)
```

Arguments

`x`	Object to be plotted
`fnumber`	Subscript of feature(s) to be plotted
`stylebysubset`	Name of column in SI table to be used for colour.
`changecol`	Flag indicating if line colours change according to values in coloumn defined by stylebysubset

`changetype`	Flag indicating if line types change according to values in coloumn defined by stylebysubset
`autolegend`	Flag if legend is plotted.
`new`	Flag if a new plot should be started.
`...`	Further arguments passed to `plot.default`

Author(s)

Lukas Lehnert

See Also

`nri`, `glm.nri`, `glm`, `cor.test,Nri-method`, `t.test,Nri-method`, `Specfeat`

Examples

```
## Not run:
data(spectral_data)

## Transform speclib
bd <- transformSpeclib(spectral_data, method = "sh", out = "bd")

##Example to isolate the features around 450nm, 700nm, 1200nm and 1500nm.
featureSelection <- specfeat(bd, c(450,700,1200,1500))

## Plot features
plot(featureSelection, 1:4)

## Advanced plotting example
plot(featureSelection, 1:4, stylebysubset = "season")

plot(featureSelection, 1:4, stylebysubset = "season", changecol = FALSE,
     changetype = TRUE)

## End(Not run)
```

`plot.Speclib` *Plot speclib*

Description

Plot `Speclib` in a new plot or adding it to an existing plot.

Usage

```
## S4 method for signature 'Speclib'
plot(x, FUN = NULL, new = TRUE, ...)
```

Arguments

`x`	Object of class `Speclib`.
`FUN`	Name of a function (character) or index or ID of single spectrum to plot (integer).
`new`	If FALSE the plot is added to active existing plot.
`...`	Further arguments passed to internal plot functions.

Details

The function may work in a couple of modes. The default way is to plot mean values (solid line) of all spectra and the standard deviations within bands. If data is assumed to be continuous the standard deviations are plotted as dashed lines otherwise error bars will indicate standard deviations.

The user has various options to change the way things are looking: With argument `FUN` the name of a function, the ID or the index of a certain spectrum may be specified. Note that if `FUN` is a function, this function will be applied to all spectra. If function should be applied to a subset of spectra, use function `subset` to define rules excluding certain spectra.

By passing a subset, the user may specify a spectral range to plot. Limits for x- and y-axis will be found automatically or may be passed separately.

Author(s)

Lukas Lehnert

See Also

`Speclib`

Examples

```
data(spectral_data)

## Set mask for channel crossing and water absorption bands
mask(spectral_data) <- c(1040, 1060, 1350, 1450)

## Simple example
plot(spectral_data, legend = list(x = "topleft"))

## Example with groups
plot(spectral_data, bygroups = TRUE, legend = list(x = "topleft"))

## Example with function
par(mfrow = c(2,3))
plot(spectral_data, FUN = "min", main = "Minimum of speclib")
plot(spectral_data, FUN = "max", main = "Maximum of speclib")
plot(spectral_data, FUN = "median", main = "Median of speclib")
plot(spectral_data, FUN = "mean", main = "Mean of speclib")
plot(spectral_data, FUN = "var", main = "Variance of speclib")
```

predictHyperspec *Prediction based on train-object and Speclib*

Description

Perform predictions based on a train-object from the **caret**-package and a hyperspectral dataset from **hsdar**. See help file to function `predict.train` of the **caret**-package for general information on prediction with **caret**.

Usage

```
## S4 method for signature 'train,.CaretHyperspectral,missing'
predictHyperspec(object, newdata, preProcess, ...)

## S4 method for signature 'train,.CaretHyperspectral,function'
predictHyperspec(object, newdata, preProcess, ...)
```

Arguments

`object`	Object of class `train` from `caret`-package
`newdata`	Object of class Speclib or Nri to predict on.
`preProcess`	Optional function to be applied on newdata prior to the prediction.
`...`	Further arguments passed to original train function and/or to the preProcess-function.

Value

Depending on the settings either a vector of predictions if `type = "raw"` or a data frame of class probabilities for `type = "prob"`. In the latter case, there are columns for each class. For `predict.list`, a list results. Each element is produced by `predict.train`. See details in `predict.train` in the `caret`-package.

Author(s)

Lukas Lehnert

See Also

`predict.train`, `Speclib`

Examples

```
## Not run:
## The following example is taken from the journal paper
## "Hyperspectral Data Analysis in R: the hsdar Package"
## under review at the "Journal of Statistical Software"
```

```
data(spectral_data)

spectral_data <- noiseFiltering(spectral_data, method = "sgolay", p = 15)

## Convert the chlorophyll measurements stored in the SI dataframe
## from SPAD-values into mg.
SI(spectral_data)$chlorophyll <-
  (117.1 * SI(spectral_data)$chlorophyll) /
  (148.84 - SI(spectral_data)$chlorophyll)

## Mask spectra
spectral_data <- spectral_data[, wavelength(spectral_data) >= 310 &
  wavelength(spectral_data) <= 1000]

## Transform reflectance values into band depth applying a segmented upper hull
## continuum removal.
spec_bd <- transformSpeclib(spectral_data, method = "sh", out = "bd")

## Select the chlorophyll absorption features at 460 nm and 670 nm for further
## processing
featureSpace <- specfeat(spec_bd, c(460, 670))

## Calculate all parameters from both selected features such as area, distance
## to Gauss curve etc.
featureSpace <- feature_properties(featureSpace)

## Set response and additional predictor variables for random forest model
featureSpace <- setResponse(featureSpace, "chlorophyll")
featureSpace <- setPredictor(featureSpace,
  names(SI(featureSpace))[4:ncol(SI(featureSpace))])

## Define training and cross validation for random forest model tuning
ctrl <- trainControl(method = "repeatedcv", number = 10, repeats = 5)

## Partition data set for training and validation
training_validation <- createDataPartition(featureSpace)

## Train random forest model based on training-subset
rfe_trained <- train(featureSpace[training_validation$Resample1,],
                     trainControl = ctrl, method = "rf")

## Predict on the validation data set
pred <- predictHyperspec(rfe_trained, featureSpace[-training_validation$Resample1,])

## Plot result for visual interpretation
lim <- range(c(SI(featureSpace,i = -training_validation$Resample1)$chlorophyll,
               pred))
plot(SI(featureSpace,i = -training_validation$Resample1)$chlorophyll, pred,
     ylab = "Predicted chlorophyll content",
     xlab = "Estimated chlorophyll content",
     xlim = lim, ylim = lim)
lines(par()$usr[c(1,2)],par()$usr[c(3,4)], lty = "dotted")
```

```
## End(Not run)
```

PROSAIL *Simulate canopy spectrum*

Description

Simulate a canopy spectrum using PROSAIL 5B

Usage

```
PROSAIL(N = 1.5, Cab = 40, Car = 8, Cbrown = 0.0,
        Cw = 0.01, Cm = 0.009, psoil = 0, LAI = 1,
        TypeLidf = 1, lidfa = -0.35, lidfb = -0.15,
        hspot = 0.01, tts = 30, tto = 10, psi = 0,
        parameterList = NULL, rsoil = NULL)
```

Arguments

`N`	Structure parameter
`Cab`	Chlorophyll content
`Car`	Carotenoid content
`Cbrown`	Brown pigment content
`Cw`	Equivalent water thickness
`Cm`	Dry matter content
`psoil`	Dry/Wet soil factor
`LAI`	Leaf area index
`TypeLidf`	Type of leaf angle distribution. See details section
`lidfa`	Leaf angle distribution. See details section
`lidfb`	Leaf angle distribution. See details section
`hspot`	Hotspot parameter
`tts`	Solar zenith angle
`tto`	Observer zenith angle
`psi`	Relative azimuth angle
`parameterList`	An optional object of class `'data.frame'`. Function will iterate over rows of parameterList setting missing entries to default values. See examples section.
`rsoil`	An optional object of class `'Speclib'` containing the background (soil) reflectance. Note that reflectance values must be in range [0...1].

Details

This function uses the FORTRAN code of PROSAIL model (Version 5B). For a general introduction see following web page and the links to articles provided there:

http://teledetection.ipgp.jussieu.fr/prosail/

The following table summarises the abbreviations of parameters and gives their units as used in PROSAIL. Please note that default values of all parameters were included with the intention to provide an easy access to the model and should be used with care in any scientific approach!

Parameter	Description of parameter	Units
N	Leaf structure parameter	NA
Cab	Chlorophyll a+b concentration	μg/cm^2
Car	Carotenoid concentration	μg/cm^2
Caw	Equivalent water thickness	cm
Cbrown	Brown pigment	NA
Cm	Dry matter content	g/cm^2
LAI	Leaf Area Index	NA
psoil	Dry/Wet soil factor	NA
hspot	Hotspot parameter	NA
tts	Solar zenith angle	deg
tto	Observer zenith angle	deg
psi	Relative azimuth angle	deg

Functions for distribution of leaf angles within the canopy may work in two modes, which is controlled via `TypeLidf`:

1. `TypeLidf == 1` (default): `lidfa` is the average leaf slope and `lidfb` describes bimodality of leaf distribution. The following list gives an overview on typical settings:

LIDF type	`lidfa`	`lidfb`
Planophile	1	0
Erectophile	-1	0
Plagiophile	0	-1
Extremophile	0	1
Spherical (default)	-0.35	-0.15

2. `TypeLidf != 1`: `lidfa` is the average leaf angle in degree (0 = planophile / 90 = erectophile); `lidfb` is 0

Value

An object of class `Speclib`. If parameterList is used, the parameter are stored in SI table of `Speclib`.

Note

The function is based on the FORTRAN version of the PROSAIL-code initially developed by Stephane JACQUEMOUD, Jean-Baptiste FERET, Christophe FRANCOIS and Eben BROADBENT. SAIL component has been developed by Wout VERHOEF.

Author(s)

Lukas Lehnert

References

Jacquemoud, S., Verhoef, W., Baret, F., Bacour, C., Zarco-Tejada, P.J., Asner, G.P., Francois, C., and Ustin, S.L. (2009): PROSPECT + SAIL models: a review of use for vegetation characterization, Remote Sensing of Environment, 113, S56-S66.

See Also

PROSPECT, Speclib

Examples

```
## Single spectrum
spectrum <- PROSAIL(N = 1.3)
plot(spectrum)

## Example using parameterList
## Test effect of leaf structure and LAI on spectra
parameter <- data.frame(N = c(rep.int(seq(0.5, 1.5, 0.5), 2)),
                        LAI = c(rep.int(0.5, 3), rep.int(1, 3)))
spectra <- PROSAIL(parameterList = parameter)

## Print SI table
SI(spectra)

## Plot spectra
plot(subset(spectra, LAI == 0.5), col = "red", ylim = c(0, 0.3))
plot(subset(spectra, LAI == 1), col = "green", new = FALSE)
```

PROSPECT *Simulate plant spectrum*

Description

Simulate plant spectrum using PROSPECT 5b or PROSPECT D. The inversion uses the concept after Feret et al. (2008) based on PROSPECT 5B.

Usage

```
PROSPECT(N = 1.5, Cab = 40, Car = 8, Anth = 1.0, Cbrown = 0.0,
         Cw = 0.01, Cm = 0.009, transmittance = FALSE,
         parameterList = NULL, version = "D")
## Inversion
PROSPECTinvert(x, P0 = NULL, transmittance_spectra = NULL,
               sam = FALSE, ...)
```

Arguments

`N`	Structure parameter
`Cab`	Chlorophyll content
`Car`	Carotenoid content
`Anth`	Anthocyanin content
`Cbrown`	Brown pigment content
`Cw`	Equivalent water thickness
`Cm`	Dry matter content
`transmittance`	Logical flag, if transmittance instead of reflectance values are returned.
`parameterList`	An optional object of class `'data.frame'`. Function will iterate over rows of parameterList setting missing entries to default values. See examples section.
`version`	Sets the version of PROSPECT to be used (either "5B" or "D").
`x, transmittance_spectra`	Speclib(s) containing the reflectance/transmittance values to be simulated during inversion of PROSPECT.
`P0`	Initial set of parameters (N, Cab etc.).
`sam`	Logical if spectral angle mapper is used as distance measurement. If FALSE, the root mean square error is used. Note that this flag has only an effect if no transmittance spectra are passed.
`...`	Parameters passed to `optim`

Details

This function uses the FORTRAN code of PROSPECT model (Version 5B an D). For a general introduction see following web page and the links to articles provided there:

`http://teledetection.ipgp.jussieu.fr/prosail/`

The following table summarises the abbreviations of parameters and gives their units as used in PROSPECT. Please note that default values of all parameters were included with the intention to provide an easy access to the model and should be used with care in any scientific approach!

Parameter	Description of parameter	Units
N	Leaf structure parameter	NA
Cab	Chlorophyll a+b concentration	μg/cm^2

Car	Carotenoid concentration	$\mu g/cm^2$
Anth	Anthocyanin content	$\mu g/cm^2$
Cw	Equivalent water thickness	cm
Cbrown	Brown pigment	NA
Cm	Dry matter content	g/cm^2

The inversion uses the function `optim` and implements the Matlab-Code developed by Feret et al. (2008). Please note that the inversion currently only uses version 5B.

Value

An object of class `Speclib`.

Note

The function is based on the FORTRAN version of the PROSPECT-code initially developed by Jean-Baptiste FERET, Stephane JACQUEMOUD and Christophe FRANCOIS.

Author(s)

Lukas Lehnert

References

Feret J.B., Francois C., Asner G.P., Gitelson A.A., Martin R.E., Bidel L.P.R., Ustin S.L., le Maire G., & Jacquemoud S. (2008), PROSPECT-4 and 5: advances in the leaf optical properties model separating photosynthetic pigments. Remote Sensing of Environment, 112, 3030-3043.

Feret J.B., Gitelson A.A., Noble S.D., & Jacquemoud S. (2017), PROSPECT-D: towards modeling leaf optical properties through a complete lifecycle, Remote Sensing of Environment, 193, 204-215.

Jacquemoud, S. and Baret, F. (1990). PROSPECT: A model of leaf optical properties spectra, Remote Sensing of Environment 34: 75 - 91.

See Also

`PROSAIL`, `optim`, `Speclib`

Examples

```
## Single spectrum
spectrum <- PROSPECT(N = 1.3, Cab = 30, Car = 10, Cbrown = 0,
                     Cw = 0.01, Cm = 0.01)
plot(spectrum)

## Example using parameterList
## Test effect of leaf structure and chlorophyll content on
## spectra
parameter <- data.frame(N = c(rep.int(seq(0.5, 1.5, 0.5), 2)),
                        Cab = c(rep.int(40, 3), rep.int(20, 3)))
spectra <- PROSPECT(parameterList = parameter)
```

```
## Print SI table
SI(spectra)

## Plot spectra for range from 400 to 800 nm
spectra <- spectra[,wavelength(spectra) >= 400 &
                    wavelength(spectra) <= 800]

plot(subset(spectra, Cab == 20), col = "red", ylim = c(0, 0.5))
plot(subset(spectra, Cab == 40), col = "green", new = FALSE)

## Example for inversion
## Create spectrum using PROSAIL
spectrum <- PROSAIL(LAI = 4)

## Invert PROSPECT using Euclidean and SAM distances
param_rmse <- PROSPECTinvert(spectrum, transmittance_spectra = NULL)
param_sam <- PROSPECTinvert(spectrum, transmittance_spectra = NULL, sam = TRUE)

## Model spectrum based on parameters from inversion
pro_rmse <- PROSPECT(N = param_rmse$par[1], Cab = param_rmse$par[2],
                     Car = param_rmse$par[3], Cbrown = param_rmse$par[4],
                     Cw = param_rmse$par[5], Cm = param_rmse$par[6],
                     version = "5B")

pro_sam <- PROSPECT(N = param_sam$par[1], Cab = param_sam$par[2],
                    Car = param_sam$par[3], Cbrown = param_sam$par[4],
                    Cw = param_sam$par[5], Cm = param_sam$par[6],
                    version = "5B")

## Plot result
plot(spectrum, ylim = c(0,0.55))
plot(pro_rmse, new = FALSE, col = "red")
plot(pro_sam, new = FALSE, col = "blue")
legend("topright", legend = c("original spectrum", "inverted with RMSE",
                              "inverted with SAM"), lty = "solid",
       col = c("black", "red", "blue"))
```

`Raster-methods` *Rasterbased methods for spectra*

Description

Methods to manipulate, save, convert and plot spectra in Speclibs stored as RasterBrick

Usage

```
## S4 method for signature 'Speclib'
extract(x, y, ...)
```

```
## S4 method for signature 'Speclib,character'
writeRaster(x, filename, ...)

## S4 method for signature 'Speclib'
plotRGB(x, ...)

## S4 method for signature 'Speclib'
brick(x, ...)
```

Arguments

`x`	Speclib with RasterBrick-object for spectra
`y`	Object of any valid type to define area to extract
`filename`	Output filename
`...`	Additionaly arguments passed to basic funtions in the raster-package

Details

For `extract`, a `Speclib` is returned containing the data of `y` in the `SI`. Note that if `y` is a buffer, spatial lines or spatial polygon object, the respective data in `y` is copied for each spectrum so that the length of the `SI` equals the number of spectra.

For `writeRaster`, the Speclib is returned which is written to file. Please note that data in the SI and the wavelength information cannot be stored in a raster file at present. Therefore, it should be considered to store the entire Speclib as R-data file using the `save`-function in R.

Note for function `brick` that by default the values of the internal brick in the Speclib are copied to the new object. However, new brick objects with differing dimensions, bands etc. may be created if `values == FALSE` is passed as additional arguement.

Value

`Speclib` for `extract` and `writeRaster`. Object of class `Brick` for `brick`.

Author(s)

Lukas Lehnert

`rastermeta` *Create list containing rastermeta-information*

Description

Create valid objects for slot `rastermeta` in `Speclib`.

Usage

```
rastermeta(x, dim, ext, crs)
```

Arguments

`x`	Optional. Object of one of the following classes: "Raster", "RasterBrick", "RasterStack", "HyperSpecRaster".
`dim`	Optional. Vector with length == 2. The first and second elements give the number of rows and columns, respectively.
`ext`	Optional. Object of class `extent`.
`crs`	Optional. Object of class `CRS`.

Value

List with following elements (in exactly this order!):

- dim: Vector with length == 2. The first and second elements give the number of rows and columns, respectively.
- ext: Object of class `extent`.
- crs: Object of class `CRS`.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `HyperSpecRaster`

`rededge` *Red edge parameter*

Description

Derive red edge parameters from hyperspectral data. Red edge is the sharp increase of reflectance values in the near infrared.

Usage

```
rededge(x)
```

Arguments

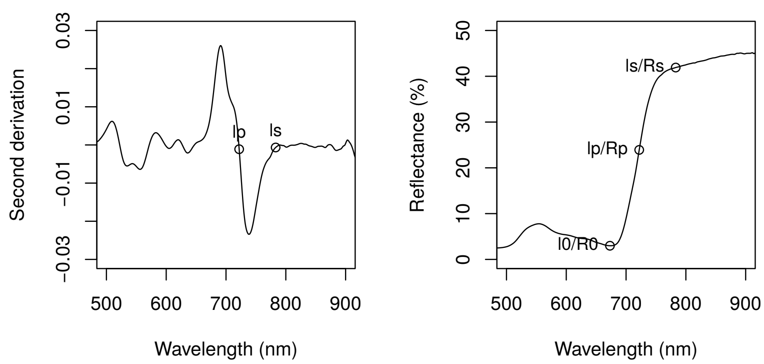
`x`	List of class `Speclib`

Details

Shape and location of the red edge are commonly described by four parameters:

- $\lambda 0$: wavelength of the minimum reflectance in the red spectrum
- λp: wavelength of the inflection point
- λs: wavelength of the reflectance shoulder
- $R0$: reflectance at l0
- Rp: Reflectance at lp
- Rs: Reflectance at ls

The red edge parameters are calculated as proposed in Bach (1995) from the spectral area between 550 and 900 nm. $\lambda 0$ is calculated as the last root before the maximum value of the 2nd derivation. The minimum reflectance is the reflectance at ($\lambda 0$). The inflection point is the root of the 2nd derivative function between the maximum value and the minimum value. The shoulder wavelength is the first root beyond the minimum value of the 2nd derivation. The following figure shows the locaqtion of the red edge parameters in an example second derivation and reflectance spectrum.



Value

A data frame containing parameters for each spectrum.

Author(s)

Hanna Meyer

References

Bach, H. (1995): Die Bestimmung hydrologischer und landwirtschaftlicher Oberflaechenparameter aus hyperspektralen Fernerkundungsdaten. Muenchner Geographische Abhandlungen Reihe B, Band B21.

See Also

`vegindex`, `derivative.speclib`, `noiseFiltering`

Examples

```
# compare R0 for spectra taken in different seasons
data(spectral_data)
rd <- rededge(spectral_data)
boxplot(rd$R0 ~ SI(spectral_data)$season, ylab = "R0")

# visualize red edge parameter of one spectrum
plot(spectral_data[1,],xlim=c(500,900),ylim=c(0,50))
plot(spectral_data[1,],xlim=c(500,900),ylim=c(0,50))
x <- c(rd$l0[1], rd$lp[1], rd$ls[1])
y <- c(rd$R0[1], rd$Rp[1], rd$Rs[1])
points(x, y)
text(x, y, c("l0", "lp", "ls"), pos = 3, offset = 1)
```

SI *Handling supplementary information (SI) of spectra*

Description

Supplementary information (SI) can be any additional data available for each spectrum in a `Speclib`- or `Nri`-object. These functions are used to set or return SI-data of a `Speclib` or `Nri`-object. Note that SI-data is automatically subsetted if indexing and extracting single spectra from a `Speclib`- or `Nri`-object. SI-data may encompass (several) raster files which must have the same extent, resolution and x- and y-dimensions as the raster file used as spectral information.

Usage

```
## S4 method for signature 'Speclib'
SI(object, i, j)

## S4 replacement method for signature 'Speclib,data.frame'
SI(object) <- value

## S4 replacement method for signature 'Speclib,matrix'
SI(object) <- value

## S4 method for signature 'Nri'
SI(object)

## S4 replacement method for signature 'Nri,data.frame'
SI(object) <- value

## S4 replacement method for signature 'Nri,matrix'
SI(object) <- value
```

Arguments

- `object` — Object of class `Speclib` or `Nri`.
- `i` — Index of rows to keep. Note that in combination with raster files in the SI, it is MUCH faster to pass row index instead of cutting the resulting data frame. Thus, `SI(object, i)` should be used instead of `SI(object)[i,]`.
- `j` — Index of columns to keep. See comment above for usage with raster files in the SI.
- `value` — Data frame with `nrow(value) == nspectra(object)`, NULL or vector with length `nspectra(object)`. Alternatively, objects of class `RasterLayer` are accepted. Please note that the function does not check for integrity in the latter case (e.g., no error will occur if number of spectra does not match number of pixel in the `RasterLayer`-object).

Details

Names of items in `SI` are used within the function `subset` to select/deselect spectra via logical expression. Values can be accessed via the "\$"-sign (see examples). Note that the function does not check the integrity of the data stored in the SI (e.g., if there are values for each spectrum).

Value

For `SI<-`, the updated object. `SI` returns a data frame with SI data.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `Nri`

Examples

```
data(spectral_data)

## Returning SI
si_spec <- SI(spectral_data)
head(si_spec)

## Adding new SI item
SI(spectral_data)$MeasurementID <- c(1:nspectra(spectral_data))
head(SI(spectral_data))

## Replacing SI
SI(spectral_data) <- SI(spectral_data)[,c(1:3)]
head(SI(spectral_data))

## Adding SI to a Speclib without SI
spec_new <- speclib(spectra(spectral_data), wavelength(spectral_data))
## This throws an error
```

```
#SI(spec_new)$NewColumn <- 1:nspectra(spec_new)
## This works:
SI(spec_new) <- data.frame(NewColumn = 1:nspectra(spec_new))
## Now, you can add a column as explained above:
SI(spec_new)$SecondCol <- c(1:nspectra(spec_new))*100
## Print SI
SI(spec_new)

## Not run:
## Example for raster file in SI

## Create raster file using PROSAIL
## Run PROSAIL
parameter <- data.frame(N = c(rep.int(seq(0.5, 1.4, 0.1), 6)),
                        LAI = c(rep.int(0.5, 10), rep.int(1, 10),
                                rep.int(1.5, 10), rep.int(2, 10),
                                rep.int(2.5, 10), rep.int(3, 10)))
spectra <- PROSAIL(parameterList = parameter)

## Create SpatialPixelsDataFrame and fill data with spectra from
## PROSAIL
rows <- round(nspectra(spectra)/10, 0)
cols <- ceiling(nspectra(spectra)/rows)
grd <- SpatialGrid(GridTopology(cellcentre.offset = c(1,1,1),
                                cellsize = c(1,1,1),
                                cells.dim = c(cols, rows, 1)))
x <- SpatialPixelsDataFrame(grd,
                            data = as.data.frame(spectra(spectra)))

## Write data to example file (example_in.tif) in workingdirectory
writeGDAL(x, fname = "example_in.tif", drivername = "GTiff")

infile <- "example_in.tif"
wavelength <- wavelength(spectra)
ra <- speclib(infile, wavelength)
tr <- blockSize(ra)

## Write LAI to separate raster file
LAI <- SI(spectra)$LAI
SI_file <- "example_SI.tif"
SI_raster <- setValues(raster(infile), LAI)
SI_raster <- writeRaster(SI_raster, SI_file)

## Read LAI file and calculate NDVI for each pixel where LAI >= 1
outfile <- "example_result_ndvi.tif"
SI(ra) <- raster(SI_file)
names(SI(ra)) <- "LAI"
res <- writeStart(ra, outfile, overwrite = TRUE, nl = 1)
for (i in 1:tr$n)
{
  v <- getValuesBlock(ra, row=tr$row[i], nrows=tr$nrows[i])
  mask(v) <- c(1350, 1450)
  LAI <- SI(v)$LAI
```

```
  v <- as.matrix(vegindex(v, index="NDVI"))
  v[LAI <= 1] <- NA
  res <- writeValues(res, v, tr$row[i])
}
res <- writeStop(res)

## End(Not run)
```

---

smgm *SMGM*

Description

Calculate Gaussian model on soil spectra

Usage

```
smgm(x, percentage = TRUE, gridsize = 50)
```

Arguments

`x`	Object of class Speclib.
`percentage`	Flag if spectra in x are in range [0, 100]. If FALSE, the spectra are scaled to [0,100].
`gridsize`	Size of the grid used to perform least squares approximation.

Details

The algorithm fits a Gaussian function to the continuum points of the spectra in the spectral region between approx. 1500 to 2500 nm. The continuum points are derived constructing the convex hull of the spectra (see `transformSpeclib`). The Gaussian function requires three parameter: (1) the mean values which is set to the water fundamental of 2800 nm, (2) the absorption depth at 2800 nm, and (3) the distance to the inflection point of the function. The latter two parameters are iteratively chosen using a grid search. The mesh size of the grid can be adjusted with the `gridsize` parameter. Note that the function requires the spectral reflectance values to be in interval [0, 100].

Value

Object of class `Speclib` containing the fitted Gaussian spectra and the parameters derived from the Gaussian curve. The three parameters (absorption depth, R0; distance to the inflection point, sigma; area between the curve and 100 % reflectance, area) are stored in the SI of the new Speclib. Additionally, the function returns the final root mean square error of the Gaussian fit.

Note

The code is based on the IDL functions written by Michael L. Whiting.

Author(s)

Lukas Lehnert

References

Whiting, M. L., Li, L. and Ustin, S. L. (2004): Predicting water content using Gaussian model on soil spectra. Remote Sensing of Environment, 89, 535-552.

See Also

soilindex, Speclib

Examples

```
## Use PROSAIL to simulate spectra with different soil moisture content
Spektr.lib <- noiseFiltering(PROSAIL(parameterList = data.frame(psoil = seq(0,1,0.1),
                                                                  LAI = 0)))

smgm_val <- smgm(Spektr.lib)

for (i in 1:nspectra(smgm_val))
  plot(smgm_val, FUN = i, new = i==1, col = i)

SI(smgm_val)
```

---

soilindex *soilindex*

Description

Function calculates a variety of hyperspectral soil indices

Usage

```
soilindex(x, index, returnHCR = "auto", weighted = TRUE, ...)
```

Arguments

x	Object of class Speclib
index	Character string. Name or definition of index or vector with names/definitions of indices to calculate. See Details section for further information.
returnHCR	If TRUE, the result will be of class HyperSpecRaster, otherwise it is a data frame. If "auto", the class is automatically determined by passed Speclib.
weighted	Logical indicating if reflectance values should be interpolated to fit wavelength position. If FALSE the reflectance values of nearest neighbour to passed position are returned. See get_reflectance for further explanation.
...	Further arguments passed to derivative functions. Only used for indices requiring derivations.

Details

Index must be a charater vector containing pre-defined indices (selected by their name) or self defined indices or any combination of pre- and self-defined indices.

Pre-defined indices: The following indices are available:

Name	**Formula**	**Reference***
BI_TM	$((TM\_1^2 + TM\_2^2 + TM\_3^2)/3)^{0.5}$**	Mathieu et al. (1998)
CI_TM	$(TM\_3 - TM\_2)/(TM\_3 + TM\_2)$**	Escadafal and Huete (1991)
HI_TM	$(2 \cdot TM\_3 - TM\_2 - TM\_1)/(TM\_2 - TM\_1)$**	Escadafal et al. (1994)
NDI	$(R_{840} - R_{1650})/(R_{840} + R_{1650})$	McNairn, H. and Protz, R. (1993)
NSMI	$(R_{1800} - R_{2119})/(R_{1800} + R_{2119})$	Haubrock et al. (2008)
RI	$R_{693}^2/(R_{447} \cdot R_{556}^3)$	Ben-Dor et al. (2006)
RI_TM	$TM\_3^2/(TM\_1 \cdot TM\_2^3)$**	Madeira et al. (1997), Mathieu et al. (1998)
SI_TM	$(TM\_3 - TM\_1)/(TM\_3 + TM\_1)$**	Escadafal et al. (1994)
SWIR SI	$-41.59 \cdot (R_{2210} - R_{2090}) + 1.24 \cdot (R_{2280} - R_{2090}) + 0.64$	Lobell et al. (2001)

* For references please type: `hsdardocs("References.pdf")`.
** TM_1 denotes the first band of Landsat Thematic Mapper. Consequently, the hyperspectral data is resmapled to Landsat TM using `spectralResampling` prior to the calculation of the index. For resampling, the spectral response function is used.

Self-defining indices:
Self-defined indices may be passed using the following syntax:

- Rxxx: Reflectance at wavelength 'xxx'. Note that R must be upper case.
- Dxxx: First derivation of reflectance values at wavelength 'xxx'. Note that D must be upper case.

Using this syntax, complex indices can be easily defined. Note that the entire definition of the index must be passed as one character string. Consequently, the NSMI would be written as "(R1800-R2119)/(R1800+R2119)".

Value

A vector containing indices values. If index is a vector with length > 1, a data frame with ncol = length(index) and nrow = number of spectra in x is returned.

If function is called without any arguments, return value will be a vector containing all available indices in alphabetical order.

Author(s)

Lukas Lehnert

References

See hsdardocs("References.pdf")

See Also

vegindex, get_reflectance

Examples

```
data(spectral_data)
## Example calculating all available indices
## Get available indices

avl <- soilindex()
vi <- soilindex(spectral_data, avl)
```

---

specfeat — *Function to isolate absorption features*

Description

Function isolates absorption features from band depth or ratio transformed reflectance spectra.

Usage

```
specfeat(x, FWL, tol = 1.0e-7)
```

Arguments

x	Object of class Speclib containing the band depth or ratio transformed reflectance spectra.
FWL	A vector containing one wavelength included in each feature to be isolated, e.g. the major absorption features. Features which include these specified wavelengths will be isolated.
tol	The tolerance of the band depth which defines a wavelength as a start or end point of a feature. Usually a band depth of 0 or a ratio of 1 indicates feature limits, however, better results are achieved if slightly deviating values are tolerated.

Details

A feature is defined as the part of the spectrum between two fix points in the transformed spectra (band depth values of 0). This function separates features at wavelengths of interest according to this rule. Hence it allows a subsequent characterization of the features of interest, e.g. via feature_properties or visual inspection via plot.Specfeat. The typical workflow to obtain feature properties is to first calculate the band depth transformSpeclib, then isolate the absorption features specfeat. Optionally, cut_specfeat allows to cut the features at specified wavelengths. Finally use feature_properties to retrieve characteristics of the features.

Value

An object of class Specfeat containing the isolated features.

Author(s)

Hanna Meyer and Lukas Lehnert

See Also

transformSpeclib, cut_specfeat, Specfeat, plot.Specfeat, feature_properties

Examples

```
data(spectral_data)

## Transform speclib
bd <- transformSpeclib(spectral_data, method = "sh", out = "bd")

##Example to isolate the features around 450nm, 700nm, 1200nm and 1500nm.
featureSelection <- specfeat(bd, c(450,700,1200,1500))

## Plot features
plot(featureSelection, fnumber = 1:4)

## Advanced plotting example
plot(featureSelection, fnumber = 1:4, stylebysubset = "season")

plot(featureSelection, fnumber = 1:4, stylebysubset = "season",
     changecol = FALSE, changetype = TRUE)
```

Specfeat-class   ** Specfeat class*

Description

Class to handle spectral feature data. Spectral features are absorption (transmission or reflection) bands defined e.g. by continuum removal (see transformSpeclib).

Details

Class extends Speclib-class and adds two additional slots:

- features: List containing the spectra according to the features.
- featureLimits: List containing limits of features defined by specfeat.

Note

See figure in hsdar-package for an overview of classes in **hsdar**.

Author(s)

Lukas Lehnert

See Also

Speclib, specfeat

---

speclib *Methods to create objects of class Speclib*

Description

Methods to create objects of class Speclib from various data sources such as matrixes and raster files (e.g. GeoTiff).

Usage

```
## S4 method for signature 'matrix,numeric'
speclib(spectra, wavelength, ...)

## S4 method for signature 'SpatialGridDataFrame,numeric'
speclib(spectra, wavelength, ...)

## S4 method for signature 'numeric,numeric'
speclib(spectra, wavelength, ...)

## S4 method for signature 'matrix,data.frame'
speclib(spectra, wavelength, ...)

## S4 method for signature 'SpatialGridDataFrame,data.frame'
speclib(spectra, wavelength, ...)

## S4 method for signature 'numeric,data.frame'
speclib(spectra, wavelength, ...)

## S4 method for signature 'matrix,matrix'
speclib(spectra, wavelength, ...)

## S4 method for signature 'SpatialGridDataFrame,matrix'
speclib(spectra, wavelength, ...)

## S4 method for signature 'numeric,matrix'
speclib(spectra, wavelength, ...)
```

```
## S4 method for signature 'hyperSpec'
speclib(spectra, wavelength, ...)

## S4 method for signature 'character,numeric'
speclib(spectra, wavelength, ...)

## S4 method for signature 'Speclib,numeric'
speclib(spectra, wavelength, ...)

## S4 method for signature 'Speclib'
print(x)

## S4 method for signature 'Speclib'
show(object)

is.speclib(x)
```

Arguments

- `spectra` — Data frame, matrix of raster object of class 'RasterBrick' or 'SpatialGridDataFrame' with spectral data. Alternatively, spectra may be the path to a raster file containing hyperspectral data.
- `x,object` — Object to be converted to or from Speclib. For conversion to Speclib it can be a of class `'data frame'`, `'matrix'`, `'list'` or `'character string'`. In the latter case `x` is interpreted as path to raster object and read by `readGDAL`. For conversion from `Speclib` the object must be of class `Speclib`.
- `wavelength` — Vector with corresponding wavelength for each band. A matrix or data.frame may be passed giving the upper and lower limit of each band. In this case, the first column is used as lower band limit and the second as upper limit, respectively.
- `...` — Further arguments passed to specific (generic) functions. Theey encompass particularly the following additional parameters:
  - `fwhm`: Vector containing full-width-half-max values for each band. Default: NULL
  - `SI`: Data frame with supplementary information to each spectrum. Default: NULL
  - `transformation`: Kind of transformation applied to spectral data (character). See `transformSpeclib` for available ones. If `transformation = NULL`, no transformation is assumed (default).
  - `usagehistory`: Character string or vector used for history of usage. Default: NULL
  - `continuousdata`: Flag indicating if spectra are quasi continuous or discrete sensor spectra (deprecated). Default: "auto"
  - `wlunit`: Unit of wavelength in spectra. Default: "nm". See datails how other units are treated.

- `xlabel`: Label of wavelength data to be used for plots etc. Default: "Wavelength"
- `ylabel`: Label of spectral signal to be used for plots etc. Default: "Reflectance"
- `rastermeta`: List of meta information for SpatialGridDataFrame. If missing, meta data in speclib is used. Use function `rastermeta` to create valid objects. Default: NULL

Details

Spectral data: The spectral data (usually reflectance values) are stored in an object of class `'.Spectra'`. This object may eiter contain the spectral data as a `RasterBrick` or as a `matrix` with columns indicating spectral bands and rows different samples, respectively. The Speclib-class provides converting routines to and from `RasterBrick`-class allowing to read and write geographic raster data via `brick`. Since R is in general not intended to be used for VERY large data sets, this functionality should be handled with care. If raster files are large, one should split them in multiple smaller ones and process each of the small files, separately. See the excellent tutorial 'Writing functions for large raster files' available on `https://CRAN.R-project.org/package=raster` and section '2.2.2 Speclibs from raster files' in 'hsdar-intro.pdf'.

Spectral information: Speclib contains wavelength information for each band in spectral data. This information is used for spectral resampling, vegetation indices and plotting etc. Since spectra can be handled either as continuous lines or as discrete values like for satellite bands, spectral information is handled in two principle ways:

- Continuous spectra: Data of spectrometers or hyperspectral (satellite) sensors. This data is plotted as lines with dotted lines indicating standard deviations by default.
- Non-continuous spectra: Data of multispectral satellite sensors. Here, data is plotted as solid lines and error bars at the mean position of each waveband indicating standard deviations by default.

The kind of data may be chosen by the user by setting the flag `"continuousdata"` (`attr(x, "continuousdata")`) or passing `continuousdata = TRUE/FALSE`, when initially converting data to `Speclib`-class. Take care of doing so, because some functions as `spectralResampling` may only work correctly with continuous data!

The internal and recommended wavelength unit is nm. If Speclibs are created with wavelength values in other units than nm as passed by `wlunit`-argument, wavelength values are automatically converted to nm. In this case, functions requiring to pass wavelength information (e.g., `mask` etc) expect the unit to match the one initially set. The only exception is the Nri-class which always uses and expects nm as unit of passed wavelength values. The following units are automatically detected: mu, μm, nm, mm, cm, dm, m.

Technical description: An object of class `Speclib` contains the following slots:

- wavelength: Vector with wavelength information. Always stored in nm.
- fwhm: Vector or single numerical value giving the full-width-half-max value(s) for each band.
- spectra: Object of class '.Spectra' with three slots:
  - fromRaster: logical, indicating if spectral data is read from a RasterBrick-object.

  - spectra_ma: Matrix with ncol = number of bands and nrow = number. Used if fromRaster == FALSE
  - spectra_ra: RasterBrick-object which is used if fromRaster == TRUE.

  Contains reflectance, transmittance or absorbance values. Handle with function `spectra`.
- SI: Data frame containing additional data to each spectrum. May be used for linear regression etc. Handle with function `SI`.
- usagehistory: Vector giving information on history of usage of speclib. Handle with function `usagehistory`.

Value

An object of class `Speclib` containing the following slots is returned:

- wavelength: Vector with wavelength information. Always stored in nm.
- fwhm: Vector or single numerical value giving the full-width-half-max value(s) for each band.
- spectra: Object of class '.Spectra' with three slots:
  - fromRaster: logical, indicating if spectral data is read from a RasterBrick-object.
  - spectra_ma: Matrix with ncol = number of bands and nrow = number. Used if fromRaster == FALSE
  - spectra_ra: RasterBrick-object which is used if fromRaster == TRUE.

  Contains reflectance, transmittance or absorbance values. Handle with function `spectra`.
- SI: Data frame containing additional data to each spectrum. May be used for linear regression etc. Handle with function `SI`.
- usagehistory: Vector giving information on history of usage of speclib. Handle with function `usagehistory`.
- rastermeta: List containing meta information to create *Raster objects from Speclib. Handle with function `rastermeta`.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `plot`, `readGDAL`, `mask`,

`idSpeclib`, `dim`, `spectra`,

`SI`

Examples

```
data(spectral_data)
spectra <- spectra(spectral_data)
wavelength <- spectral_data$wavelength

spectra <- speclib(spectra,wavelength)
```

Speclib-class *Speclib class*

Description

Class to store and handle hyperspectral data in R

Details

Spectral data: The spectral data (usually reflectance values) are stored in an object of class `'.Spectra'`. This object may eiter contain the spectral data as a `RasterBrick` or as a `matrix` with columns indicating spectral bands and rows different samples, respectively. The Speclib-class provides converting routines to and from `RasterBrick`-class allowing to read and write geographic raster data via `brick`. Since R is in general not intended to be used for VERY large data sets, this functionality should be handled with care. If raster files are large, one should split them in multiple smaller ones and process each of the small files, separately. See the excellent tutorial 'Writing functions for large raster files' available on `https://CRAN.R-project.org/package=raster` and section '2.2.2 Speclibs from raster files' in 'hsdar-intro.pdf'.

Spectral information: Speclib contains wavelength information for each band in spectral data. This information is used for spectral resampling, vegetation indices and plotting etc. Since spectra can be handled either as continuous lines or as discrete values like for satellite bands, spectral information is handled in two principle ways:

- Continuous spectra: Data of spectrometers or hyperspectral (satellite) sensors. This data is plotted as lines with dotted lines indicating standard deviations by default.
- Non-continuous spectra: Data of multispectral satellite sensors. Here, data is plotted as solid lines and error bars at the mean position of each waveband indicating standard deviations by default.

The kind of data may be chosen by the user by setting the flag `"continuousdata"` (`attr(x, "continuousdata")`) or passing `continuousdata = TRUE/FALSE`, when initially converting data to `Speclib`-class. Take care of doing so, because some functions as `spectralResampling` may only work correctly with continuous data!

The internal and recommended wavelength unit is nm. If Speclibs are created with wavelength values in other units than nm as passed by `wlunit`-argument, wavelength values are automatically converted to nm. In this case, functions requiring to pass wavelength information (e.g., `mask` etc) expect the unit to match the one initially set. The only exception is the Nri-class which always uses and expects nm as unit of passed wavelength values. The following units are automatically detected: mu, μm, nm, mm, cm, dm, m.

Technical description: An object of class `Speclib` contains the following slots:

- wavelength: Vector with wavelength information. Always stored in nm.
- fwhm: Vector or single numerical value giving the full-width-half-max value(s) for each band.
- spectra: Object of class '.Spectra' with three slots:
  - fromRaster: logical, indicating if spectral data is read from a RasterBrick-object.

  - spectra_ma: Matrix with ncol = number of bands and nrow = number. Used if fromRaster == FALSE
  - spectra_ra: RasterBrick-object which is used if fromRaster == TRUE.

  Contains reflectance, transmittance or absorbance values. Handle with function `spectra`.
- SI: Data frame containing additional data to each spectrum. May be used for linear regression etc. Handle with function `SI`.
- usagehistory: Vector giving information on history of usage of speclib. Handle with function `usagehistory`.

Note

See figure in `hsdar-package` for an overview of classes in hsdar.

Author(s)

Lukas Lehnert

See Also

`plot`, `readGDAL`, `mask`, `idSpeclib`,

`dim`, `spectra`, `SI`

---

speclib_raster-methods

Functions for processing large hyperspectral raster files

Description

Functions for processing large hyperspectral raster files using the low-level functions provided by the **raster**-package. For a detailed overview see the vignette "Writing functions for large raster files" shipped along with the **raster**-package.

Usage

```
## S4 method for signature 'Speclib'
blockSize(x)

## S4 method for signature 'Speclib,character'
writeStart(x, filename, ...)

## S4 method for signature 'Speclib'
getValuesBlock(x, ...)

## S4 method for signature 'Speclib,Speclib'
writeValues(x, v, start)

## S4 method for signature 'Speclib,matrix'
```

```
writeValues(x, v, start)

## S4 method for signature 'Speclib,numeric'
writeValues(x, v, start)

## S4 method for signature 'Speclib'
writeStop(x)
```

Arguments

`x`	Object of class Speclib.
`filename`	Name of the new file to create.
`v`	Object to write the data to file. May be one of the following classes: "Speclib", "matrix" or "numeric".
`start`	Integer. Row number (counting starts at 1) from where to start writing v.
`...`	Further arguements passed to respective functions in the **raster**-packages.

Author(s)

Lukas Lehnert

Examples

```
## Not run:
## Create raster file using PROSAIL
## Run PROSAIL
parameter <- data.frame(N = c(rep.int(seq(0.5, 1.4, 0.1), 6)),
                        LAI = c(rep.int(0.5, 10), rep.int(1, 10),
                                rep.int(1.5, 10), rep.int(2, 10),
                                rep.int(2.5, 10), rep.int(3, 10)))
spectra <- PROSAIL(parameterList = parameter)

## Create SpatialPixelsDataFrame and fill data with spectra from PROSAIL
rows <- round(nspectra(spectra)/10, 0)
cols <- ceiling(nspectra(spectra)/rows)
grd <- SpatialGrid(GridTopology(cellcentre.offset = c(1,1,1),
                                cellsize = c(1,1,1),
                                cells.dim = c(cols, rows, 1)))
x <- SpatialPixelsDataFrame(grd, data = as.data.frame(spectra(spectra)))

## Write data to example file (example_in.tif) in workingdirectory
writeGDAL(x, fname = "example_in.tif", drivername = "GTiff")

## Examples for Speclib using file example_in.tif
## Example 1:
## Noise reduction in spectra
infile <- "example_in.tif"
outfile <- "example_result_1.tif"
wavelength <- spectra$wavelength
```

```
ra <- speclib(infile, wavelength)
tr <- blockSize(ra)

res <- writeStart(ra, outfile, overwrite = TRUE)
for (i in 1:tr$n)
{
  v <- getValuesBlock(ra, row=tr$row[i], nrows=tr$nrows[i])
  v <- noiseFiltering(v, method="sgolay", n=25)
  res <- writeValues(res, v, tr$row[i])
}
res <- writeStop(res)

## Example 2:
## masking spectra and calculating vegetation indices
outfile <- "example_result_2.tif"
n_veg <- as.numeric(length(vegindex()))
res <- writeStart(ra, outfile, overwrite = TRUE, nl = n_veg)
for (i in 1:tr$n)
{
  v <- getValuesBlock(ra, row=tr$row[i], nrows=tr$nrows[i])
  mask(v) <- c(1350, 1450)
  v <- as.matrix(vegindex(v, index=vegindex()))
  res <- writeValues(res, v, tr$row[i])
}
res <- writeStop(res)

## End(Not run)
```

---

spectra *Handling spectra*

Description

Returning and setting spectra in Speclib

Usage

```
## S4 method for signature 'Speclib'
spectra(object, i, j, ...)

## S4 replacement method for signature 'Speclib,data.frame'
spectra(object) <- value

## S4 replacement method for signature 'Speclib,matrix'
spectra(object) <- value

## S4 replacement method for signature 'Speclib,numeric'
spectra(object) <- value
```

```
## S4 replacement method for signature 'Speclib,RasterBrick'
spectra(object) <- value
```

Arguments

object	Object of class Speclib.
i	Index of spectra to return. If missing all spectra are returned.
j	Index of bands to return. If missing all bands are returned.
...	Passed to internal function. Currently only one parameter is accepted: return_names: Logical indicating, if names of columns and rows should be set to bandnames and idSpeclib.
value	Matrix or RasterBrick-object containing spectral values. If value is a matrix, columns are band values and rows are spectra.

Details

For spectra<-, the function does not check if dimensions of spectra match dimensions of Speclib. Additionally, no conversion into matrix is performed! If spectra are not correctly stored, errors in other functions may arise. Thus check always carefully, if spectra are modified by hand.

Value

For spectra<-, the updated object. Otherwise a matrix of the spectra in x is returned.

Author(s)

Lukas Lehnert

See Also

Speclib

Examples

```
data(spectral_data)

## Manual plot of the first spectrum
plot(wavelength(spectral_data), spectra(spectral_data)[1,], type="l")
```

`spectralResampling` *Spectral resampling*

Description

Resample spectra to (satellite) sensors

Usage

```
spectralResampling(x, sensor, rm.NA = TRUE, continuousdata = "auto",
                   response_function = TRUE)
```

Arguments

- `x` Object of class `Speclib`. Data to be spectrally resampled.
- `sensor` Character or `data.frame` containing definition of sensor characteristics. See details section for further information.
- `rm.NA` If `TRUE`, channels which are not covered by input data wavelength are removed
- `continuousdata` Definition if returned `Speclib` is containing continuous data or not.
- `response_function` If `TRUE`, the spectral response function of the sensor is used for integration, if `FALSE` a Gaussian distribution is assumed and if `NA` the mean value of `spectra[min(ch):max(ch)]` is calculated. If `response_function` is an object of class `Speclib` the function assumes that the spectra in the object are spectral response values. In this case the wavelength dimension determines the spectral response values for the respective wavelength and the sample dimension separates between the different bands. Note that if `response_function` is an object of class `Speclib`, `sensor` may be missing. In this case the function calculates the central wavelength and the fwhm-values from the spectral response functions.

Details

The characteristics of (satellite) sensor to integrate spectra can be chosen from a list of already implemented sensors. See `get.sensor.characteristics` for available sensors.

Otherwise the characteristics can be passed as a `data.frame` with two columns: first column with lower bounds of channels and second column with upper bounds. Alternatively, the `data.frame` may encompass band centre wavelength and full-width-half-maximum values of the sensor. Function will check the kind of data passed by partially matching the names of the data frame: If any column is named `"fwhm"` or `"center"`, it is assumed that data are band centre and full-width-half-maximum values.

The third option is to use a `Speclib` containing the spectral response values instead of reflectances. In this case, the `sensor`-argument may be missing and the function automatically determines the sensor's central wavelength and the fwhm-values based on the spectral response values. See examples.

If sensor characteristics are defined manually and no `Speclib` with spectral response values is passed, a Gaussian response is assumed.

Value

Object of class Speclib

Note

The spectral response functions are kindly provided by the operators of the satellites. See hsdardocs("Copyright") for copyright information on spectral response functions.

- Quickbird: Copyright by DigitalGlobe, Inc. All Rights Reserved
- RapidEye: Copyright by RapidEye AG
- WorldView-2: Copyright by DigitalGlobe, Inc. All Rights Reserved

Author(s)

Lukas Lehnert

See Also

get.sensor.characteristics, get.gaussian.response

Examples

```
## Load example data
data(spectral_data)

## Resample to RapidEye
data_RE <- spectralResampling(spectral_data, "RapidEye",
                              response_function = TRUE)

## Plot resampled spectra
plot(data_RE)

## Compare different methods of spectral resampling
par(mfrow=c(1,3))
ga <- spectralResampling(spectral_data, "RapidEye",
                         response_function = FALSE)
plot(ga)
re <- spectralResampling(spectral_data, "RapidEye",
                         response_function = TRUE)
plot(re)
no <- spectralResampling(spectral_data, "RapidEye",
                         response_function = NA)
plot(no)

## Usage of Speclib with spectral response values
## Define 3 bands (RGB)
center <- c(460, 530, 600)
fwhm   <- 70
wl     <- c(310:750)

## Create spectral response with gaussian density function
```

```
response <- speclib(t(sapply(center, function(center, wl, fwhm)
{
  a <- dnorm(wl, mean = center, sd = fwhm/2)
  a <- (a-min(a))/(max(a) - min(a))
  return(a)
}, wl, fwhm)), wl)

## Plot response functions
for (i in 1:3)
  plot(response[i,], new = i == 1, col = c("blue", "green", "red")[i])

## Perform resampling
rgb_data <- spectralResampling(spectral_data, response_function = response)
```

`spectral_data` *Hyperspectral samples*

Description

Hyperspectral samples from a FACE experiment in Germany

Usage

```
data(spectral_data)
```

Format

An object of class `Speclib`

Details

Data has been sampled during vegetation period 2014 in spring and summer. Measurements were taken with a HandySpec Field portable spectrometer (tec5 AG Oberursel, Germany). This device has two channels measuring incoming and reflected radiation simultaneously between 305 and 1705 nm in 1 nm steps.

Author(s)

Wolfgang A. Obermeier, Lukas Lehnert, Hanna Meyer `subset.nri` *Subsetting* `Nri`*-objects*

Description

Return subsets of `Nri`-objects which meet conditions.

Usage

```
## S4 method for signature 'Nri'
subset(x, subset, ...)
```

Arguments

`x`	Object of class 'Nri'.
`subset`	Logical expression indicating spectra to keep: missing values are taken as false. See details section.
`...`	Further arguments passed to `agrep`.

Details

Matchable objects are SI data. Use column names to identify the respective SI. See `SI` to access SI of a `Nri`. IDs of samples may be accessed using "id.nri" as variable name.

Value

Object of class `Nri`.

Author(s)

Lukas Lehnert

See Also

`Nri`, `SI`

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Return names of SI data
names(SI(nri_WV))
```

```
## Divide into both seasons
sp_summer <- subset(nri_WV, season == "summer")
sp_spring <- subset(nri_WV, season == "spring")

## Print both Nri-objects
sp_summer
sp_spring

## Divide into both seasons and years
sp_summer_14 <- subset(nri_WV, season == "summer" & year == 2014)
sp_spring_14 <- subset(nri_WV, season == "spring" & year == 2014)

## Print both Nri-objects
sp_summer_14
sp_spring_14
```

`subset.speclib` *Subsetting speclibs*

Description

Function to return subsets of `Speclibs` by defined conditions.

Usage

```
## S4 method for signature 'Speclib'
subset(x, subset, ...)
```

Arguments

`x`	Object of class 'Speclib'.
`subset`	Logical expression indicating spectra to keep: missing values are taken as false. Multiple expressions can be applied using logical operators AND and OR. See details section.
`...`	Further arguments passed to `agrep`.

Details

Matchable objects are SI data. Use column names to identify the respective SI. See `SI` to access SI of a `Speclib`. IDs of spectra may be accessed using "id.speclib" as variable name. To subset certain wavelength ranges of a `Speclib` refer to `mask`.

Value

Object of class `Speclib`.

Author(s)

Lukas Lehnert, Wolfgang Obermeier

See Also

Speclib, SI, mask

Examples

```
data(spectral_data)

## Return names of SI data
names(SI(spectral_data))

## Divide into both seasons
sp_summer <- subset(spectral_data, season == "summer")
sp_spring <- subset(spectral_data, season == "spring")

## Divide into both seasons and years
sp_summer_14 <- subset(spectral_data, season == "summer" & year == 2014)
sp_spring_14 <- subset(spectral_data, season == "spring" & year == 2014)

## Plot all speclibs
plot(sp_spring_14, col="green", ylim = c(0,80))
plot(sp_summer_14, col="red", new = FALSE)
```

`t.test` *t-test for nri values*

Description

Performs Student's t-tests for normalized ratio index values.

Usage

```
## S4 method for signature 'Nri'
t.test(x, ...)
```

Arguments

`x`	Object of class `'nri'`.
`...`	Arguments to be passed to `t.test`.

Value

An object of class "data.frame"

Author(s)

Lukas Lehnert & Hanna Meyer

See Also

`t.test`, `cor.test`,`Nri-method`, `Nri`

Examples

```
data(spectral_data)


## Calculate nri-values for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Perform t.tests between nri-values of both sites
season <- SI(spec_WV)$season
ttestres <- t.test(x = nri_WV, y = season, alternative = "two.sided")
ttestres

## Plot p.values of t.tests
plot(ttestres)
```

`transformSpeclib` *Transform spectra*

Description

Transform spectra by using convex hull or segmented upper hull

Usage

```
transformSpeclib(data, ..., method = "ch", out = "bd")
```

Arguments

`data`	Speclib to be transformed
`method`	Method to be used. See details section.
`out`	Kind of value to be returned. See details section.
`...`	Further arguments passed to generic functions. Currently ignored.

Details

Function performs a continuum removal transformation by firstly establishing a continuum line/hull which connects the local maxima of the reflectance spectrum. Two kinds of this hull are well established in scientific community: the convex hull (e.g. Mutanga et al. 2004) and the segmented hull (e.g. Clark et al. 1987). Both hulls are established by connecting the local maxima, however, the precondition of the convex hull is that the resulting continuum line must be convex whereas considering the segmented hull it might be concave or convex but the algebraic sign of the slope is not allowed to change from the global maximum of the spectrum downwards to the sides. In contrast to a convex hull, the segmented hull is able to identify small absorption features.

Specify `method = "ch"` for the convex hull and `method = "sh"` for the segmented hull. The output might be `"raw"`, `"bd"` or `"ratio"`:

- "raw": the continuum line is returned
- "bd": the spectra are transformed to band depth by

  $$BD_\lambda = 1 - \frac{R_\lambda}{CV_\lambda},$$

  where BD is the band depth, R is the reflectance and CV is the continuum value at the wavelength λ.
- "ratio": the spectra are transformed by

  $$BD_\lambda = \frac{R_\lambda}{CV_\lambda}.$$

In some cases it might be useful to apply `noiseFiltering` before the transformation if too many small local maxima are present in the spectra. Anyway, a manual improvement of the continuum line is possible using `addcp` and `deletecp`.

Value

If `out != "raw"` an object of class `Speclib` containing transformed spectra is returned. Otherwise the return object will be of class `Clman`.

Note

For large Speclibs, it may be feasible to run the function on multiple cores. See `hsdar_parallel()` for further information.

Author(s)

Hanna Meyer and Lukas Lehnert

References

Clark, R. N., King, T. V. V. and Gorelick, N. S. (1987): Automatic continuum analysis of reflectance spectra. Proceedings of the Third Airborne Imaging Spectrometer Data Analysis Workshop, 30. 138-142.

Mutanga, O. and Skidmore, A. K. (2004): Hyperspectral band depth analysis for a better estimation of grass biomass (Cenchrus ciliaris) measured under controlled laboratory conditions International Journal of applied Earth Observation and Geoinformation, 5, 87-96.

See Also

Clman, addcp, deletecp, checkhull

Examples

```
## Example spectrum for wavelength values
## between 400 and 1000 nm
example_spectrum <- PROSPECT()[,c(1:600)]

## Default (convex hull and band depth)
ch_bd <- transformSpeclib(example_spectrum)

## Construct convex hull but calculate ratios
ch_ratio <- transformSpeclib(example_spectrum, out = "ratio")

## Return continuum line of convex hull
ch_raw <- transformSpeclib(example_spectrum, out = "raw")

## Plot results
par(mfrow=c(2,2))
plot(example_spectrum)
plot(ch_raw, ispec = 1, main = "Continuum line",
     ylim = c(0,0.5))
plot(ch_bd, main = "Band depth")
plot(ch_ratio, main = "Ratio")

## Same example but with segmented hull

## Segmented hull and band depth
sh_bd <- transformSpeclib(example_spectrum, method = "sh",
                          out = "bd")

## Segmented hull and ratios
sh_ratio <- transformSpeclib(example_spectrum, method = "sh",
                             out = "ratio")

## Return continuum line of segmented hull
sh_raw <- transformSpeclib(example_spectrum, method = "sh",
                           out = "raw")

## Plot results
par(mfrow=c(2,2))
plot(example_spectrum)
plot(sh_raw, ispec = 1, main = "Continuum line",
     ylim = c(0,0.5))
plot(sh_bd, main = "Band depth")
plot(sh_ratio, main = "Ratio")
```

---

unmix *Unmix spectra*

Description

Perform linear spectral unmixing on hyperspectral data or spectra resampled to satellite bands using endmember spectra.

Usage

```
unmix(spectra, endmember, returnHCR = "auto", scale = FALSE, ...)
```

Arguments

`spectra`	Input spectra of class 'Speclib'
`endmember`	Endmember spectra of class 'Speclib'
`returnHCR`	Set class of value. If TRUE, value will be of class '`HyperSpecRaster`', otherwise a list is returned. If `auto`, function will switch to mode depending on input data characteristics.
`scale`	Flag to scale spectra to [0,1] if necessary.
`...`	Further arguments passed to `HyperSpecRaster` (ignored if returnHCR = FALSE).

Details

Linear spectral unmixing is a frequently used method to calculate fractions of land-cover classes (endmembers) within the footprint of pixels. This approach has originally been intended to be used for multispectral satellite images. The basic assumption is that the signal received at the sensor (ρ_{mix}) is a linear combination of n pure endmember signals (ρ_i) and their cover fractions (f_i):

$$\rho_{mix} = \sum_{i=1}^{n} \rho_i f_i,$$

where $f_1, f_2, ..., f_n >= 0$ and $\sum_{i=1}^{n} f_i = 1$ to fulfill two constraints:

1. All fractions must be greater or equal 0
2. The sum of all fractions must be 1

Since this linear equation system is usually over-determined, a least square solution is performed. The error between the final approximation and the observed pixel vector is returned as vector (`error`) in list (`returnSpatialGrid = FALSE`) or as last band if `returnSpatialGrid = TRUE`.

Value

A list containing the fraction of each endmember in each spectrum and an error value giving the euclidean norm of the error vector after least square error minimisation.

Note

Unmixing code is based on "i.spec.unmix" for GRASS 5 written by Markus Neteler (1999).

Author(s)

Lukas Lehnert

References

Sohn, Y. S. & McCoy, R. M. (1997): Mapping desert shrub rangeland using spectral unmixing and modeling spectral mixtures with TM data. Photogrammetric Engineering and Remote Sensing, 63, 707-716

Examples

```
## Not run:
## Use PROSAIL to generate some vegetation spectra with different LAI
parameter <- data.frame(LAI = seq(0, 1, 0.01))
spectral_data <- PROSAIL(parameterList = parameter)

## Get endmember spectra
## Retrieve all available spectra
avl <- USGS_get_available_files()

## Download all spectra matching "grass-fescue"
grass_spectra <- USGS_retrieve_files(avl = avl, pattern = "grass-fescue")
limestone <- USGS_retrieve_files(avl = avl, pattern = "limestone")

## Integrate all spectra to Quickbird
grass_spectra_qb <- spectralResampling(grass_spectra[1,], "Quickbird")
limestone_qb <- spectralResampling(limestone, "Quickbird")
spectral_data_qb <- spectralResampling(spectral_data, "Quickbird")


em <- speclib(spectra = rbind(spectra(grass_spectra_qb),
                              spectra(limestone_qb))/100,
              wavelength = wavelength(limestone_qb))

## Unmix
unmix_res <- unmix(spectral_data_qb, em)

unmix_res

plot(unmix_res$fractions[1,] ~ SI(spectral_data_qb)$LAI, type = "l",
     xlab = "LAI", ylab = "Unmixed fraction of vegetation")

## End(Not run)
```

`updatecl` *Check transformed Speclib*

Description

Update a transformed Speclib with a re-calculated hull

Usage

```
updatecl(x, hull)
```

Arguments

x	Object of class Speclib transformed by transformSpeclib.
hull	Hull to be applied to x. Output of function makehull.

Details

In some cases, it might be desirable to manually adapt automatically constructed segmended hulls (transformSpeclib). For example local maxima could be removed because they are very small and maybe afflicted with uncertainties which might legitimate it to manipulate the continuum line. Therefore, hsdar provides functions to remove and add "continuum points" from or to a continuum line. Manually adapted continuum lines can then be used to update band depth or ratio transformation. Handle these functions with care to avoid continuum lines too much build by subjective decisions. In the typical workflow, spectra are first transformed (transformSpeclib). Continuum points can then be retrieved (getcp) and manually adapted by adding addcp and deleting (deletecp) of points. Use checkhull to check for errors. If all uncertainties are removed, recalculate the hull (makehull) and update the transformed spectrum (updatecl).

Value

Object of class Speclib.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

transformSpeclib, makehull, Speclib

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, xlim = c(2480, 2500), ylim=c(0.022,0.024))

## Add fix point at 4595 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2495)

## Plot new line
plot(spec_clman, ispec = 1, xlim = c(2480, 2500), ylim=c(0.022,0.024))

## Check new hull
hull <- checkhull(spec_clman, 1)
```

```
hull$error

## Add fix point at 4596 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2496)

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error

## Re-calculate hull
hull <- makehull(spec_clman, 1)

## Transform spectra using band depth
spec_bd <- transformSpeclib(spec, method = "sh", out = "bd")

## Update continuum line of first spectrum
spec_bd <- updatecl(spec_bd, hull)

## Plot modified transformed spectrum
plot(spec_bd, FUN = 1)
```

---

usagehistory *History of usage*

Description

Function to read and write history of usage for `Speclibs`. Similar to a log file, the history of usage records processing steps applied to a `Speclib`.

Usage

```
usagehistory(x)
usagehistory(x) <- value
```

Arguments

`x`	Object of class Speclib
`value`	Character string to be added to usagehistory or NULL, if usagehistory should be deleted.

Value

For `usagehistory<-`, the updated object. Otherwise a vector containing the history of usage of `Speclib` is returned.

Author(s)

Lukas Lehnert

See Also

Speclib

Examples

```
data(spectral_data)

## Return history of usage
usagehistory(spectral_data)

## Deleting history of usage
usagehistory(spectral_data) <- NULL
spectral_data

## Adding entries
usagehistory(spectral_data) <- "New entry"   ## Adding new entry
usagehistory(spectral_data) <- "New entry 2" ## Adding second entry
spectral_data
```

`vegindex` *vegindex*

Description

Function calculates a variety of hyperspectral vegetation indices

Usage

```
vegindex(x, index, returnHCR = "auto", L = 0.5,
          weighted = TRUE, ...)
```

Arguments

`x`	Object of class `Speclib`
`index`	Character string. Name or definition of index or vector with names/definitions of indices to calculate. See Details section for further information.
`returnHCR`	If TRUE, the result will be of class HyperSpecRaster, otherwise it is a data frame. If "auto", the class is automatically determined by passed Speclib.
`L`	Factor for SAVI index. Unused for other indices.
`weighted`	Logical indicating if reflectance values should be interpolated to fit wavelength position. If `FALSE` the reflectance values of nearest neighbour to passed position are returned. See `get_reflectance` for further explanation.
`...`	Further arguments passed to derivative functions. Only used for indices requiring derivations.

Details

Index must be a charater vector containing pre-defined indices (selected by their name) or self defined indices or any combination of pre- and self-defined indices.

Pre-defined indices: The following indices are available:

Name	**Formula**	**Reference***
Boochs	D_{703}	Boochs et al. (1990)
Boochs2	D_{720}	Boochs et al. (1990)
CAI	$0.5 \cdot (R_{2000} + R_{2200}) - R_{2100}$	Nagler et al. (2003)
CARI	$a = (R_{700} - R_{550})/150$ $b = R_{550} - (a \cdot 550)$ $R_{700} \cdot \text{abs}(a \cdot 670 + R_{670} + b)/R_{670} \cdot$ $(a^2 + 1)^{0.5}$	Kim et al. (1994)
Carter	R_{695}/R_{420}	Carter (1994)
Carter2	R_{695}/R_{760}	Carter (1994)
Carter3	R_{605}/R_{760}	Carter (1994)
Carter4	R_{710}/R_{760}	Carter (1994)
Carter5	R_{695}/R_{670}	Carter (1994)
Carter6	R_{550}	Carter (1994)
CI	$R_{675} \cdot R_{690}/R_{683}^2$	Zarco-Tejada et al. (2003)
CI2	$R_{760}/R_{700} - 1$	Gitelson et al. (2003)
ClAInt	$\int_{600nm}^{735nm} R$	Oppelt and Mauser (2004)
CRI1	$1/R_{515} - 1/R_{550}$	Gitelson et al. (2003)
CRI2	$1/R_{515} - 1/R_{770}$	Gitelson et al. (2003)
CRI3	$1/R_{515} - 1/R_{550} \cdot R_{770}$	Gitelson et al. (2003)
CRI4	$1/R_{515} - 1/R_{700} \cdot R_{770}$	Gitelson et al. (2003)
D1	D_{730}/D_{706}	Zarco-Tejada et al. (2003)
D2	D_{705}/D_{722}	Zarco-Tejada et al. (2003)
Datt	$(R_{850} - R_{710})/(R_{850} - R_{680})$	Datt (1999b)
Datt2	R_{850}/R_{710}	Datt (1999b)
Datt3	D_{754}/D_{704}	Datt (1999b)
Datt4	$R_{672}/(R_{550} \cdot R_{708})$	Datt (1998)
Datt5	R_{672}/R_{550}	Datt (1998)
Datt6	$(R_{860})/(R_{550} \cdot R_{708})$	Datt (1998)
Datt7	$(R_{860} - R_{2218})/(R_{860} - R_{1928})$	Datt (1999a)
Datt8	$(R_{860} - R_{1788})/(R_{860} - R_{1928})$	Datt (1999a)
DD	$(R_{749} - R_{720}) - (R_{701} - R_{672})$	le Maire et al. (2004)
DDn	$2 \cdot (R_{710} - R_{660} - R_{760})$	le Maire et al. (2008)
DPI	$(D_{688} \cdot D_{710})/D_{697}^2$	Zarco-Tejada et al. (2003)
DWSI1	R_{800}/R_{1660}	Apan et al. (2004)

DWSI2	R_{1660}/R_{550}	Apan et al. (2004)
DWSI3	R_{1660}/R_{680}	Apan et al. (2004)
DWSI4	R_{550}/R_{680}	Apan et al. (2004)
DWSI5	$(R_{800}+R_{550})/(R_{1660}+R_{680})$	Apan et al. (2004)
EGFN	$(\max(D_{650:750})-\max(D_{500:550}))/$ $(\max(D_{650:750})+\max(D_{500:550}))$	Penuelas et al. (1994)
EGFR	$\max(D_{650:750})/\max(D_{500:550})$	Penuelas et al. (1994)
EVI	$2.5\cdot((R_{800}-R_{670})/$ $(R_{800}-(6\cdot R_{670})-(7.5\cdot R_{475})+1))$	Huete et al. (1997)
GDVI	$(R_{800}^n-R_{680}^n)/(R_{800}^n+R_{680}^n)$**	Wu (2014)
GI	R_{554}/R_{677}	Smith et al. (1995)
Gitelson	$1/R_{700}$	Gitelson et al. (1999)
Gitelson2	$(R_{750}-R_{800}/R_{695}-R_{740})-1$	Gitelson et al. (2003)
GMI1	R_{750}/R_{550}	Gitelson et al. (2003)
GMI2	R_{750}/R_{700}	Gitelson et al. (2003)
Green NDVI	$(R_{800}-R_{550})/(R_{800}+R_{550})$	Gitelson et al. (1996)
LWVI_1	$(R_{1094}-R_{983})/(R_{1094}+R_{983})$	Galvao et al. (2005)
LWVI_2	$(R_{1094}-R_{1205})/(R_{1094}+R_{1205})$	Galvao et al. (2005)
Maccioni	$(R_{780}-R_{710})/(R_{780}-R_{680})$	Maccioni et al. (2001)
MCARI	$((R_{700}-R_{670})-0.2\cdot(R_{700}-R_{550}))\cdot$ (R_{700}/R_{670})	Daughtry et al. (2000)
MCARI/OSAVI		Daughtry et al. (2000)
MCARI2	$((R_{750}-R_{705})-0.2\cdot(R_{750}-R_{550}))\cdot$ (R_{750}/R_{705})	Wu et al. (2008)
MCARI2/OSAVI2		Wu et al. (2008)
mND705	$(R_{750}-R_{705})/(R_{750}+R_{705}-2\cdot R_{445})$	Sims and Gamon (2002)
mNDVI	$(R_{800}-R_{680})/(R_{800}+R_{680}-2\cdot R_{445})$	Sims and Gamon (2002)
MPRI	$(R_{515}-R_{530})/(R_{515}+R_{530})$	Hernandez-Clemente et al. (2011)
mREIP	Red-edge inflection point using Gaussain fit	Miller et al. (1990)
MSAVI	$0.5\cdot(2\cdot R_{800}+1-$ $((2\cdot R_{800}+1)^2-8\cdot(R_{800}-R_{670}))^{0.5})$	Qi et al. (1994)
MSI	R_{1600}/R_{817}	Hunt and Rock (1989)
mSR	$(R_{800}-R_{445})/(R_{680}-R_{445})$	Sims and Gamon (2002)
mSR2	$(R_{750}/R_{705})-1/(R_{750}/R_{705}+1)^{0.5}$	Chen (1996)
mSR705	$(R_{750}-R_{445})/(R_{705}-R_{445})$	Sims and Gamon (2002)
MTCI	$(R_{754}-R_{709})/(R_{709}-R_{681})$	Dash and Curran (2004)
MTVI	$1.2\cdot(1.2\cdot(R_{800}-R_{550})-$ $2.5\cdot(R_{670}-R_{550}))$	Haboudane et al. (2004)
NDLI	$(log(1/R_{1754})-log(1/R_{1680}))/$ $(log(1/R_{1754})+log(1/R_{1680}))$	Serrano et al. (2002)
NDNI	$(log(1/R_{1510})-log(1/R_{1680}))/$ $(log(1/R_{1510})+log(1/R_{1680}))$	Serrano et al. (2002)
NDVI	$(R_{800}-R_{680})/(R_{800}+R_{680})$	Tucker (1979)
NDVI2	$(R_{750}-R_{705})/(R_{750}+R_{705})$	Gitelson and Merzlyak (1994)
NDVI3	$(R_{682}-R_{553})/(R_{682}+R_{553})$	Gandia et al. (2004)
NDWI	$(R_{860}-R_{1240})/(R_{860}+R_{1240})$	Gao (1996)

NPCI	$(R_{680} - R_{430})/(R_{680} + R_{430})$	Penuelas et al. (1994)
OSAVI	$(1 + 0.16) \cdot (R_{800} - R_{670})/$ $(R_{800} + R_{670} + 0.16)$	Rondeaux et al. (1996)
OSAVI2	$(1 + 0.16) \cdot (R_{750} - R_{705})/$ $(R_{750} + R_{705} + 0.16)$	Wu et al. (2008)
PARS	R_{746}/R_{513}	Chappelle et al. (1992)
PRI	$(R_{531} - R_{570})/(R_{531} + R_{570})$	Gamon et al. (1992)
PRI_norm	$\text{PRI} \cdot (-1)/(\text{RDVI} \cdot R_{700}/R_{670})$	Zarco-Tejada et al. (2013)
PRI*CI2	$\text{PRI} \cdot \text{CI2}$	Garrity et al. (2011)
PSRI	$(R_{678} - R_{500}/R_{750}$	Merzlyak et al. (1999)
PSSR	R_{800}/R_{635}	Blackburn (1998)
PSND	$(R_{800} - R_{470})/(R_{800} - R_{470})$	Blackburn (1998)
PWI	R_{900}/R_{970}	Penuelas et al. (1997)
RDVI	$(R_{800} - R_{670})/\sqrt{R_{800} + R_{670}}$	Roujean and Breon (1995)
REP_LE	Red-edge position through linear extrapolation.	Cho and Skidmore (2006)
REP_Li	$R_{re} = (R_{670} + R_{780})/2$ $700 + 40 \cdot ((R_{re} - R_{700})/(R_{740} - R_{700}))$	Guyot and Baret (1988)
SAVI	$(1 + L) \cdot (R_{800} - R_{670})/(R_{800} + R_{670} + L)$	Huete (1988)
SIPI	$(R_{800} - R_{445})/(R_{800} - R_{680})$	Penuelas et al. (1995), Penuelas et al. (1995a)
SPVI	$0.4 \cdot 3.7 \cdot (R_{800} - R_{670}) - 1.2\cdot$ $((R_{530} - R_{670})^2)^{0.5}$	Vincini et al. (2006)
SR	R_{800}/R_{680}	Jordan (1969)
SR1	R_{750}/R_{700}	Gitelson and Merzlyak (1997)
SR2	R_{752}/R_{690}	Gitelson and Merzlyak (1997)
SR3	R_{750}/R_{550}	Gitelson and Merzlyak (1997)
SR4	R_{700}/R_{670}	McMurtey et al. (1994)
SR5	R_{675}/R_{700}	Chappelle et al. (1992)
SR6	R_{750}/R_{710}	Zarco-Tejada and Miller (1999)
SR7	R_{440}/R_{690}	Lichtenthaler et al. (1996)
SR8	R_{515}/R_{550}	Hernandez-Clemente et al. (2012)
SRPI	R_{430}/R_{680}	Penuelas et al. (1995)
SRWI	R_{850}/R_{1240}	Zarco-Tejada et al. (2003)
Sum_Dr1	$\sum_{i=626}^{795} D1_i$	Elvidge and Chen (1995)
Sum_Dr2	$\sum_{i=680}^{780} D1_i$	Filella and Penuelas (1994)
SWIR FI	$R_{2133}^2/(R_{2225} \cdot R_{2209}^3$	Levin et al. (2007)
SWIR LI	$3.87 \cdot (R_{2210} - R_{2090}) -$ $27.51 \cdot (R_{2280} - R_{2090}) - 0.2$	Lobell et al. (2001)
SWIR SI	$-41.59 \cdot (R_{2210} - R_{2090}) +$ $1.24 \cdot (R_{2280} - R_{2090}) + 0.64$	Lobell et al. (2001)

SWIR VI	$37.72 \cdot (R_{2210} - R_{2090}) + 26.27 \cdot (R_{2280} - R_{2090}) + 0.57$	Lobell et al. (2001)
TCARI	$3 \cdot ((R_{700} - R_{670}) - 0.2 \cdot (R_{700} - R_{550}) \cdot (R_{700}/R_{670}))$	Haboudane et al. (2002)
TCARI/OSAVI	TCARI/OSAVI	Haboudane et al. (2002)
TCARI2	$3 \cdot ((R_{750} - R_{705}) - 0.2 \cdot (R_{750} - R_{550}) \cdot (R_{750}/R_{705}))$	Wu et al. (2008)
TCARI2/OSAVI2	TCARI2/OSAVI2	Wu et al. (2008)
TGI	$-0.5(190(R_{670} - R_{550}) - 120(R_{670} - R_{480}))$	Hunt et al. (2013)
TVI	$0.5 \cdot (120 \cdot (R_{750} - R_{550}) - 200 \cdot (R_{670} - R_{550}))$	Broge and Leblanc (2000)
Vogelmann	R_{740}/R_{720}	Vogelmann et al. (1993)
Vogelmann2	$(R_{734} - R_{747})/(R_{715} + R_{726})$	Vogelmann et al. (1993)
Vogelmann3	D_{715}/D_{705}	Vogelmann et al. (1993)
Vogelmann4	$(R_{734} - R_{747})/(R_{715} + R_{720})$	Vogelmann et al. (1993)

* For references please type: `hsdardocs("References.pdf")`.
** For GDVI n must be defined appending an underscore and the intended exponent to the index name. E.g., for n = 2, the correct index name would be "GDVI_2". Note that GDVI-indices with n = 2, 3, 4 will be derived if all available indices are calculated.

Self-defining indices:

Self-defined indices may be passed using the following syntax:

- Rxxx: Reflectance at wavelength 'xxx'. Note that R must be upper case.
- Dxxx: First derivation of reflectance values at wavelength 'xxx'. Note that D must be upper case.

Using this syntax, complex indices can be easily defined. Note that the entire definition of the index must be passed as one character string. Consequently, the NDVI would be written as "(R800-R680)/(R800+R680)".

Value

A vector containing indices values. If index is a vector with length > 1, a data frame with ncol = length(index) and nrow = number of spectra in x is returned.

If function is called without any arguments, return value will be a vector containing all available indices in alphabetical order.

Author(s)

Hanna Meyer and Lukas Lehnert

References

See `hsdardocs("References.pdf")`

See Also

`soilindex`, `derivative.speclib`, `rededge`, `get_reflectance`

Examples

```
## Example calculating NDVI
data(spectral_data)
ndvi <- vegindex(spectral_data, "NDVI")


## Example calculating all available indices
## Get available indices
avl <- vegindex()
vi <- vegindex(spectral_data, avl)

## Self-defined indices
## NDVI
vi <- vegindex(spectral_data, "(R800-R680)/(R800+R680)")
## NDNI
vi <- vegindex(spectral_data,
               "(log(1/R1510) - log(1/R1680))/(log(1/R1510) + log(1/R1680))")
## D1
vi <- vegindex(spectral_data, "D730/D706")
```

`wavelength` *Handling wavelength and fwhm*

Description

Methods to access and set wavelength (band center) and full-width-half-max (fwhm) values for class `Speclib`.

Usage

```
## S4 method for signature 'Speclib'
wavelength(object)

## S4 replacement method for signature 'Speclib,data.frame'
wavelength(object) <- value

## S4 replacement method for signature 'Speclib,numeric'
wavelength(object) <- value

## S4 method for signature 'Speclib'
fwhm(object)

## S4 replacement method for signature 'Speclib,numeric'
fwhm(object) <- value
```

Arguments

`object`	Object of class `Speclib`.
`value`	Numeric vector or data.frame containing wavelength values. Must always be in nm!

Details

Wavelength (band center) and full-width-half-max (fwhm) values are given for each spectral band. The wavelength is mandatory for creation of `Speclib` and is used within the whole functionality of the package (e.g., `noiseFiltering`, `spectralResampling`, `vegindex`, `nri`, `plot.Speclib`, `mask`).

Value

For `wavelength<-` and `fwhm<-`, the updated object. Otherwise a numeric vector of the wavelength and fwhm-values in nm is returned.

Author(s)

Lukas Lehnert

See Also

`Speclib`

Examples

```
data(spectral_data)

wavelength(spectral_data)
```

Index