Package 'FieldSpec'

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Type Package

Title Functions useful for processing field spectroscopy data

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Description A field spectroscopy package containing functions to process spectral files collected using Analytical Spectral Devices (ASD) instruments. The goal is to stream line and standardize spectral data processing for use in ecology, remote sensing, and plant ecophysiological research.

Depends XML, Hmisc

Suggests testthat, Rprospect, signal

SystemRequirements

OS_type Windows, unix, mac

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LazyLoad yes

LazyData FALSE

Collate 'import.asd.R' 'read.asd.R' 'spec.utils.R' 'average.spec.R''jump.correction.R'

R topics documented:

`average.spec` *average replicate spectra within a directory of spectra files*

Description

Function to average replicate spectra within a directory of spectra files

Usage

```
average.spec(file.dir = NULL, out.dir = NULL,
  start.wave = NULL, end.wave = NULL, step.size = NULL,
  bias.threshold = NULL, suffix.length = NULL,
  output.file.ext = NULL, spec.dataframe = FALSE,
  settings.file = NULL)
```

Arguments

`file.dir`	directory of spectra files to process
`out.dir`	output directory for processed spectra files
`start.wave`	starting wavelength of spectra files. Not needed if specified in XML settings file.
`end.wave`	ending wavelength of spectra files. Not needed if specified in XML settings file.
`step.size`	resolution of spectra files. E.g. 1 for 1nm, 5 for 5nm. Not needed if specified in XML settings file.
`bias.threshold`	reflectance/transmittance cutoff to remove spectra with anartificial bias (shift) due to improper spectral collection
`suffix.length`	length of auto numbering attached to ASD file names. This number of characters will be removed from the filename when averaged.
`output.file.ext`	optional setting to set file extension of output files. Defaults to .csv
`spec.dataframe`	option to return a data frame with the converted spectra files
`settings.file`	settings file used for spectral processing options (OPTIONAL). Contains information related to the spectra collection instrument, output directories, and processing options such as applying a jump correction to the spectra files. Options in the settings file take precedent over options selected in the function call.

Author(s)

Shawn P. Serbin

Examples

```
## Not run:
average.spec()
average.spec(file.dir,out.dir, start.wave=350,end.wave=2500,step.size=1,bias.threshold=0.06,
suffix.length=5,output.file.ext=".csv",spec.dataframe = TRUE,)

## End(Not run)
```

concat.spectra *Concatenate a directory of spectra files into a single .csv file. Works on a single directory or a series of directories*

Description

Concatenate a directory of spectra files into a single .csv file. Works on a single directory or a series of directories

Usage

```
concat.spectra(file.dir = NULL, out.dir = NULL,
  out.filename = NULL, in.file.ext = ".csv",
  out.file.ext = ".csv", transpose = FALSE,
  spec.dataframe = FALSE)
```

Arguments

file.dir	directory of spectra files to process. Currently works on spectra files formatted where each row is a wavelength and associated spectral observation.
out.dir	output directory for concatenated spectra files. If not set then the output directory defaults to file.dir (input directory)
out.filename	filename for concatenated spectra files
in.file.ext	file extension for individual spectra files. Defaults to ".csv"
out.file.ext	option to set the output extension. Defaults to ".csv"
transpose	option to transpose the spectra to/from row/column major output. This will be applied to both the returned dataframe (optional) and output file. TRUE/FALSE. Default FALSE
spec.dataframe	option toreturn a R dataframe containing the concatenated spectral data. TRUE/FALSE

Author(s)

Shawn P. Serbin

Examples

```
## Not run:
concat.spectra()
spectra <- concat.spectra(file.dir=file.dir,out.dir=out.dir,out.filename="concat.spectra",
out.file.ext=".csv",transpose=FALSE,spec.dataframe=FALSE)

## End(Not run)
```

`import.asd` *Import raw binary ASD spectra files*

Description

A wrapper function to import raw binary ASD spectra files, apply jump correction to the imported files and average replicate files into a single spectrum. Calls read.asd(), jump.correction(), and average.spec() functions.

Usage

```
import.asd(asd.dir = NULL, output.dir = NULL,
  jump.correction = FALSE, average = FALSE,
  start.wave = NULL, end.wave = NULL, step.size = NULL,
  jumploc1 = NULL, jumploc2 = NULL, asd.file.ext = NULL,
  output.file.ext = NULL, settings.file = NULL)
```

Arguments

`asd.dir`	directory containing raw ASD files or sub-directories to be processed. Not needed if specified in settings file.
`output.dir`	main ouput directory. Not needed if specified in settings file.
`jump.correction`	option to apply a jump correction to the imported spectra files. Not needed if specified in settings file.
`average`	option to average imported spectra files. Will use jump corrected files if exist. Not needed if specified in settings file.
`start.wave`	starting wavelength of spectra files. Not needed if specified in settings file.
`end.wave`	ending wavelength of spectra files. Not needed if specified in settings file.
`step.size`	resolution of spectra files. E.g. 1 for 1nm, 5 for 5nm. Not needed if specified in settings file.
`jumploc1`	location of the first jump in the spectra to correct. Not needed if jump.correction=FALSE or if specified in settings file.
`jumploc2`	location of the second jump in the spectra to correct. Not needed if jump.correction=FALSE or if specified in settings file.
`asd.file.ext`	file extension for input binary asd spectra files
`output.file.ext`	optional setting to set file extension to output files. Defaults to .csv
`settings.file`	settings file used for spectral processing options (OPTIONAL). Contains information related to the spectra collection instrument, output directories, and processing options such as applying a jump correction to the spectra files. Options in the settings file take precedent over options selected in the function call.

Author(s)

Shawn P. Serbin

`jump.correction` *apply a jump (splice) correction to imported ASD spectra files. This splice or jump occurs at the boundaries between detectors*

Description

A function to apply a jump (splice) correction to imported spectra files

Usage

```
jump.correction(file.dir = NULL, out.dir = NULL,
  start.wave = NULL, end.wave = NULL, step.size = NULL,
  jumploc1 = NULL, jumploc2 = NULL, firstJumpMax = NULL,
  secondJumpMax = NULL, output.file.ext = NULL,
  settings.file = NULL)
```

Arguments

`file.dir`	directory of spectra files to process
`out.dir`	output directory for processed spectra files
`start.wave`	starting wavelength of spectra files. Not needed if specified in XML settings file.
`end.wave`	ending wavelength of spectra files. Not needed if specified in XML settings file.
`step.size`	resolution of spectra files. E.g. 1 for 1nm, 5 for 5nm. Not needed if specified in settings file.
`jumploc1`	location of the first jump in the spectra to correct. Not needed if jump.correction=FALSE or if specified in XML settings file.
`jumploc2`	location of the second jump in the spectra to correct. Not needed if jump.correction=FALSE or if specified in XML settings file.
`firstJumpMax`	maximum jump threshold for the first jump location. Determines whether spectra will be corrected or flaged as bad. (Optional. Default is 0.02)
`secondJumpMax`	maximum jump threshold for the second jump location. Determines whether spectra will be corrected or flaged as bad. (Optional. Default is 0.02)
`output.file.ext`	option to set file extension of the output files. Defaults to .csv
`settings.file`	settings file used for spectral processing options (OPTIONAL). Contains information related to the spectra collection instrument, output directories, and processing options such as applying a jump correction to the spectra files.

Value

output list containing processed spectra and associated diagnostic information

Author(s)

Shawn P. Serbin

Examples

```
## Not run:
jump.correction()
jump.correction(file.dir,out.dir, start.wave=350,end.wave=2500,step.size=1,jumploc1=651,jumploc2=1451,
output.file.ext=".csv",settings.file=NULL)

## End(Not run)
```

`read.asd` *A function to import raw ASD binary files*

Description

A function to import raw ASD binary files to ascii flat file format

Usage

```
read.asd(file.dir = NULL, out.dir = NULL,
  start.wave = NULL, end.wave = NULL, step.size = NULL,
  asd.file.ext = ".asd", output.file.ext = ".csv",
  spec.dataframe = FALSE, settings.file = NULL)
```

Arguments

`file.dir`	A single ASD binary file or directory of ASD files to import. Currently only supports single directory processing (i.e. no nested dir structures)
`out.dir`	main output directory for processed spectra files.
`start.wave`	starting wavelength of ASD binary spectra files. Depends on instrument.
`end.wave`	ending wavelength of ASD binary spectra files. Depends on instrument.
`step.size`	wavelength step size for ASD files. E.g. 1nm, 5nm, 10nm
`asd.file.ext`	file extension of ASD files. Usually ".asd" (Default)
`output.file.ext`	optional setting to set file extension to output files. Defaults to .csv
`spec.dataframe`	option to return a data frame with the converted spectra files
`settings.file`	settings file used for spectral processing options (OPTIONAL). Contains information related to the spectra collection instrument, output directories, and processing options such as applying a jump correction to the spectra files. Options in the settings file take precedent over options selected in the function call.

Value

output for a single file returns a list with wavelengths and measured reflectance or transmittance values. For a directory, outputs individual ascii text files with wavelenght and spectra values for each input ASD file.

Author(s)

Shawn P. Serbin

settings — *parse settings file used for spectra file import and processing*

Description

Read settings file for spectra import and processing

Usage

```
settings(input.file = NULL)
```

Arguments

input.file	settings file containing information needed for spectra processing

Author(s)

Shawn P. Serbin

Examples

```
## Not run:
settings <- settings()
settings <- settings('/home/$USER/settings.xml')

## End(Not run)
```

smooth.spectra — *Smooth spectra file with Savitsky-Golay smoothing filter. Works with either a single spectrum or array of spectral observations in row-major format.*

Description

Smooth spectra file with Savitsky-Golay smoothing filter. Works with either a single spectrum or array of spectral observations in row-major format.

Usage

```
smooth.spectra(file.dir = NULL, input.file = NULL,
  out.dir = NULL, out.filename = NULL, header = TRUE,
  p = NULL, n = NULL, length = "full", file.ext = ".csv")
```

Arguments

file.dir	Directory of spectra files to apply sgolay smoothing filter.
input.file	Spectra file to apply sgolay smoothing filter. If not set then all files in file.dir are processed.
out.dir	Output directory for smoothed spectra files. If not set then processed spectra will be output to file.dir
out.filename	Output filename for processed spectra file. If not set then the original filename(s) will be modified with the .sg suffix.
header	Does the spectra file(s) have a header line? Default = TRUE
p	SG filter order. Default 1.
n	SG filter length. Needs to be an odd value. Default 21
length	Apply sgolay smoothing filter to the entire (default=full) or subset of the spectrum. Define subset limits as (wavelength1,wavelength2), e.g. (2000,2500) in nanometers [NOT YET IMPLEMENTED]
file.ext	File extension for spectra files. Default '.csv'

Author(s)

Shawn P. Serbin

Examples

```
## Not run:
smooth.spectra()
smooth.spectra(file.dir=file.dir,input.file=input.file,out.dir=out.dir,out.filename=out.filename,
               header=TRUE,p=1,n=21,length=full)

## End(Not run)
```

---

transpose.spectra *Transpose spectra file(s) from/to row or column major format. Works with either a single spectrum or directory of spectral observations.*

Description

Transpose spectra file(s) from/to row or column major format. Works with either a single spectrum or directory of spectral observations.

Usage

```
transpose.spectra(file.dir = NULL, input.file = NULL,
  out.dir = NULL, out.filename = NULL,
  in.file.ext = ".csv", out.file.ext = ".csv",
  header = FALSE)
```

Arguments

file.dir	directory of spectra files to process
input.file	name of input spectra file. If ommitted then the function transposes all files in the input file.dir
out.dir	output directory for transposed spectra file(s)
out.filename	output filename of transposed spectra file(s). If using a directory then the original filenames are appended with the .t suffix
in.file.ext	file extension for individual spectra files. Defaults to ".csv"
out.file.ext	option to set the output extension. Defaults to ".csv"
header	TRUE/FALSE. Do/does the file(s) have a header line?

Author(s)

Shawn P. Serbin

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