Package 'FieldSpectra'

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Type Package

Title Functions for processing field spectroscopy data

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Description A field spectroscopy package containing functions to process spectral files collected with an Analytical Spectral Devices (ASD) or Spectral Evolution instrument. The goal is to streamline and standardize spectral data processing for use in remote sensing, ecology, and plant ecophysiological research.

Depends XML, Hmisc, signal, Rcpp

Suggests testthat, devtools, Rprospect

SystemRequirements

OS_type Windows, unix, mac

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LazyLoad yes

LazyData FALSE

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`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, metadata.file = NULL,
  image = 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
`metadata.file`	Option to select custom metadata file for use in processing. If not set then the information is either read from default metadata file, the settings file or at the function call. Need to set this as the full qualified path to the spectral metadata file is using a custom file/location
`image`	Logical. Whether to produce .png images of each spectrum (TRUE) or not (FALSE). Default is FALSE. Useful for diagnosing spectral observations during processing.
`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)
```

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

Description

Function to average replicate spectra within a directory of spectra files

Usage

```
average.spec.se(file.dir = NULL, out.dir = NULL, spec.type = NULL,
  spec.file.ext = NULL, start.wave = NULL, end.wave = NULL,
  step.size = NULL, bias.threshold = NULL, suffix.length = 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
`spec.type`	Option to set what type of spectra to average. Options: Reflectance, Transmittance. Can be set with abbreviations: e.g. "Refl" or "Tran" Default is "Reflectance"
`spec.file.ext`	Optional to set the input file extension. Default is ".sed"
`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
`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

concat.spectra *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)
```

convolve.spectra *Convolve field spectral observations to airborne/satellite spectral bands/channels.*

Usage

```
convolve.spectra(field.spectra = NULL, start.wave = NULL, end.wave = NULL,
  sensor = NULL, year = NULL, spc = NULL)
```

Arguments

field.spectra	Input field spectra. If a single spectra then the format can be either column or row major with the wavelengths either a column of data or the column headers. If multiple (i.e. a matrix of data) the input should be in row major format with the column headers as wavelength numbers. See examples below.
start.wave	Starting wavelength of field spectra
end.wave	ending wavelength of field spectra
sensor	The sensor (e.g. "AVIRIS", "Landsat 5", "Landsat 7", "MODIS"). Current options are: "AVIRIS" More to come in the future
year	[Optional] E.g. year=2011. If the AVIRIS sensor is selected this allows the user to select a specific spectral calibration based on the year of data aquisition. Defaults to 2011.
spc	[Optional] Option to use custom spectral calibration information. Format: band number, center wavelength, FWHM. NOT YET IMPLEMENTED
output.dir	[Optional] Directory to output the convolved spectral data. If not set the results are only pasesd back to the working environment

Value

output.spectra Returns a matrix of convolved spectra

Author(s)

Shawn P. Serbin

---

extract.metadata *Extract metadata for each spectra sample. Works on a single spectra or a directory.*

Usage

```
extract.metadata(file.dir = NULL, out.dir = NULL, instrument = NULL,
  spec.file.ext = NULL, output.file.ext = ".csv", tz = NULL,
  settings.file = NULL)
```

Arguments

file.dir	File directory or filename of single spectra for processing
out.dir	Output directory for metadata information file
instrument	What instrument was used to collect spectra. Current options: ASD, SE
spec.file.ext	[Optional] Input spectra file extension. E.g. .asd (ASD) or .sed (Spectral Evolution). Default for ASD instruments is .asd. Default for Spectral Evolution instruments is .sed
output.file.ext	[Optional] Output file extension of metadata information file. Default .csv
tz	[Optional] Set the timezone of the spectra file collection. Used to covert spectra collection time to UTC. If unused it is assumed that the correct timezone is the current system timezone.
settings.file	[Optional] Spectral settings file

Value

output Returns a dataframe of spectral metadata information

Author(s)

Shawn P. Serbin

Examples

```
# ASD
file <- system.file("extdata/PM01_TIAM_B_LC_REFL00005.asd",package="FieldSpectra")
output <- extract.metadata(file,instrument="ASD")

# Spectral Evolution
file <- system.file("extdata/cvars_grape_leaf1_lc_rg_01236.sed",package="FieldSpectra")
output <- extract.metadata(file,instrument="SE")
```

`extract.metadata.asd` *Extract metadata from raw binary ASD files. Called from extract.metadata*

Usage

```
extract.metadata.asd(file.dir, out.dir, spec.file.ext, output.file.ext, tz)
```

Arguments

`file.dir`	File directory or filename of single spectra for processing
`out.dir`	Output directory for meta-data information file
`spec.file.ext`	[Optional] Input spectra file extension. E.g. .asd (ASD) or .sed (Spectral Evolution). Default for ASD instruments is .asd. Default for Spectral Evolution instruments is .sed
`output.file.ext`	[Optional] Output file extension of meta-data information file. Default .csv
`tz`	[Optional] Set the timezone of the spectra file collection. Used to covert spectra collection time to UTC. If unused it is assumed that the correct timezone is the current system timezone.

Value

output Returns output dataframe of ASD metadata information

Author(s)

Shawn P. Serbin

`extract.metadata.se` *Extract metadata from Spectral Evolution files. Called from extract.metadata*

Usage

```
extract.metadata.se(file.dir, out.dir, spec.file.ext, output.file.ext, tz)
```

Value

output Returns output dataframe of SE metadata information

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, spec.type = NULL,
  start.wave = NULL, end.wave = NULL, step.size = NULL, jumploc1 = NULL,
  jumploc2 = NULL, firstJumpMax = NULL, secondJumpMax = NULL,
  output.file.ext = NULL, metadata.file = NULL, image = FALSE,
  settings.file = NULL)
```

Arguments

`file.dir`	directory of spectra files to process
`out.dir`	output directory for processed spectra files
`spec.type`	[Optional] Option to set the type of spectra being processed. Options: "Reflectance" or "Transmittance" Defaults to "Reflectance"
`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`	Wavelength location of the first jump in the spectra to correct. Not needed if specified in XML settings file.
`jumploc2`	Wavelength location of the second jump in the spectra to correct. Not needed 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
metadata.file	Option to select custom metadata file for use in processing. If not set then the information is either read from default metadata file, the settings file or at the function call. Need to set this as the full qualified path to the spectral metadata file is using a custom file/location
image	Logical. Whether to produce .png images of each spectrum (TRUE) or not (FALSE). Default is FALSE. Useful for diagnosing spectral observations during processing.
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(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, spec.type = NULL,
  start.wave = NULL, end.wave = NULL, step.size = NULL, image = FALSE,
  spec.file.ext = ".asd", output.file.ext = ".csv", get.metadata = TRUE,
  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. If not set then no output ASCII files are provided. If set then output ASCII files for each spectra are written to out.dir/ascii_files
spec.type	Optional. Option to set the type of spectra being processed. Options: "Reflectance" or "Transmittance" Defaults to "Reflectance"
start.wave	Optional. Selected starting wavelength of ASD binary spectra files. Depends on instrument. If not set then read from file header
end.wave	Optional. Selected ending wavelength of ASD binary spectra files. Depends on instrument. If not set then read from file header
step.size	Optional. Wavelength step size for ASD files. E.g. 1nm, 5nm, 10nm If not set then read from file header. If selected for larger size than raw data, spectrum is interpolated (not yet availible)
image	Logical. Whether to produce .png images of each spectrum (TRUE) or not (FALSE). Default is FALSE. Useful for diagnosing spectral observations during processing.
spec.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
get.metadata	Logical. Run extract.metadata when importing .asd files and place information in a metadata file? TRUE/FALSE. Default is TRUE
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 wavelength and spectra values for each input ASD file.

Author(s)

Shawn P. Serbin

Examples

```
# Set input file
file.dir <- system.file("extdata/PM01_TIAM_B_LC_REFL00005.asd",package="FieldSpectra")
spec <- read.asd(file.dir,out.dir=~,start.wave=350,end.wave=2500,step.size=1)

# Get info from file header
spec <- read.asd(file.dir,out.dir=~)

# Plot output
plot(spec$Wavelength,spec$Spectra,type="l",lwd=2,xlab="Wavelength (nm)", ylab="Reflectance (%)")
```

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.*

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	logical. 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.*

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	logical. Do/does the file(s) have a header line?

Author(s)

Shawn P. Serbin

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