Advanced spectrolab for package developers and contributors

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Style guide and conventions

Genral

- object names are lower case
- assignment is done with equals `=` instead of arrow `<-`
- only really obvious abbreviations may be used
- names should be separated by undesrcore `_`, unless you're overloading an R generic e.g. `as.matrix`.
- internal functions should use the `i_` prefix. e.g `i_find_spectra()`
- all functions must be documented with roxygen2 comments
- strive for small functions.
- try to fail gracefully

Specific

- **Do not reach inside the `spectra` object's guts**. If you're accessing the internal data structuresdirectly, you're probably doing something wrong.
- If the only way you can implement something reasonably is gutting the `spectra` object, we did something wrong. Please report an issue and submit a pull request.
- **Do not** use a pattern of deconstructing and reconstructing the `spectra` object, even if doing so though the getters and setters.

```
library("spectrolab")
```

```
## spectrolab version: 0.0.7
##
## Please cite:
## Meireles J, Schweiger A, Cavender-Bares J (2018). spectrolab: Class
## and Methods for Hyperspectral Data. R package version 0.0.7, <URL:
## https://github.com/meireles/spectrolab>.
```

```
##
## Attaching package: 'spectrolab'
```

```
## The following objects are masked from 'package:stats':
##
##     sd, smooth, var
```

The spectra class

`spectrolab` defines a new S3 class called `spectra` that holds all of the different compnents of a spectral data.

Without diving too much into its implementation, a `spectra` object holds the important information needed for most spectral datasets: reflectance, wavelengths, etc. The class has a bunch of requirements in terms of both format and values.

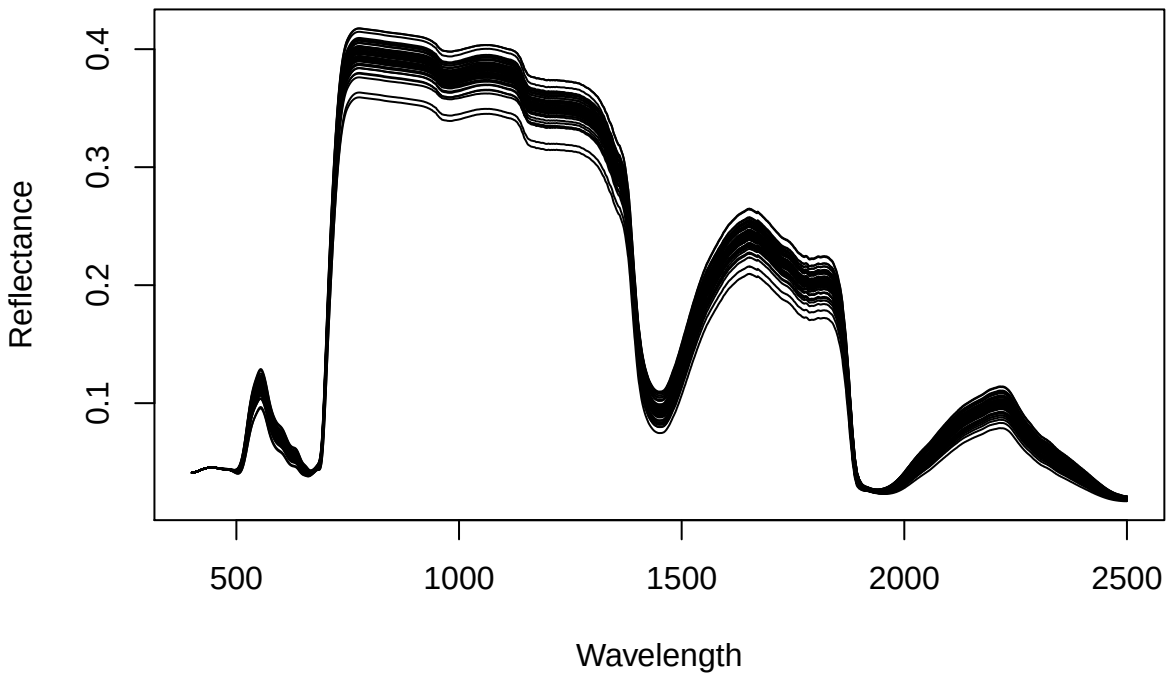
Constructing a `spectra` object *"by hand"*

In addition to `read_spectra()` and `as.spectra()`, you can create a `spectra` object "by hand"" using the more flexible `spectra()` constructor, which takes at least arguments: (1) a reflectance matrix, (2) a vector of wavelengths and (3) the sample names.

```
# (1) Create a reflectance matrix.
#     In this case, by removing the first column that holds the species name
rf = spec_matrix_example[ , -1]

# (2) Create a vector with wavelength labels that match
#     the reflectance matrix columns.
wl = colnames(rf)

# (3) Create a vector with sample labels that match
#     the reflectance matrix rows.
#     In this case, use the first colum of spec_matrix_example
sn = spec_matrix_example[ , 1]

# Finally, construct the spectra object using the `spectra` constructor
spec = spectra(reflectance = rf, wavelengths = wl, names = sn)

# And hopefully this worked fine
is_spectra(spec)
```

```
## [1] TRUE
```

```
plot(spec)
```



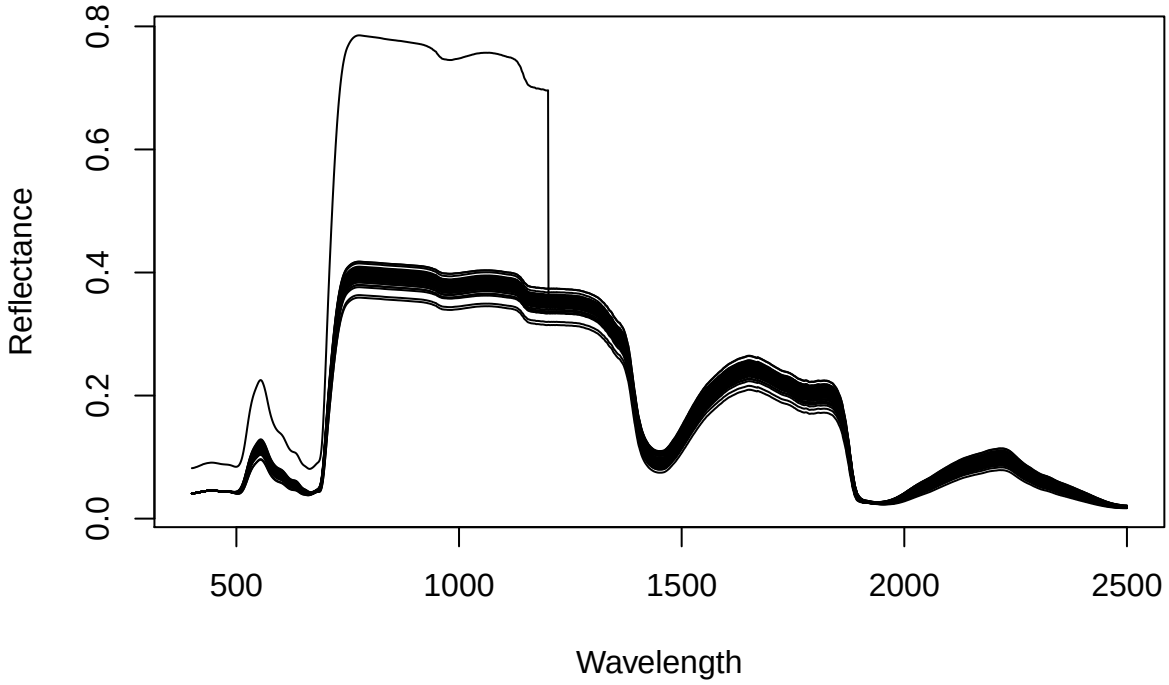
Getting and Setting

`spectrolab` gives you acess to get and set functions for most `spectra` components. The `names()`, `wavelengths()` functions do both getting and setting. For example:

```
# Getters
names(spec)[1:4]
wavelengths(spec)[1:4]

# Setters
names(spec)       = toupper(names(spec))
wavelengths(spec) = wavelengths(spec) / 1000
```

Reflectances are set using the `[` notation. For instance:

```
spec[1, 400:1200] = spec[1, 400:1200] * 2
plot(spec)
```


Reflectance
0.0
0.2
0.4
0.6
0.8
500
1000
1500
2000
2500
Wavelength