

# hyperSpec Introduction

Claudia Beleites ([cbeleites@units.it](mailto:cbeleites@units.it))  
CENMAT, DMRN, University of Trieste

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## Reproducing the Examples in this Vignette

All spectra used in this manual are installed automatically with *hyperSpec*.

The source data files of the `flu` and `laser` data sets as well as of the paracetamol spectrum are shipped with the package. For reproducing the examples in a live session, the full file names of the spectra can be found with the command:

```
> Sys.glob (paste (.libPaths ()), "hyperSpec/doc/rawdata/*.txt", sep = "/")
```

The source data file of the `chondro` data, however, needs to be obtained separately. It is available for download as a .zip file at *hyperSpec*'s home page (<http://r-forge.r-project.org/projects/hyperspec/>, ca. 8.5 MB). The original file (ca. 31 MB) is far too large to be included in the package.

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## 1 Introduction

*hyperSpec* is a R package that allows convenient handling of (hyper)spectroscopic data sets, i. e. data sets comprising spectra together with further data on a per-spectrum basis. Likewise, the spectra can be anything that is recorded over a common discretized axis, the wavelength axis. Throughout

the documentation of the package, the terms intensity and wavelength refer to the spectral ordinate and abscissa, respectively.

However, *hyperSpec* works perfectly fine with any data that fits in that general scheme, so that the three terms may also be used for:

wavelength: frequency, wavenumbers, chemical shift, Raman shift,  $\frac{m}{z}$ , etc.

intensity: transmission, absorbance,  $\frac{e^-}{s}$ , ...

extra data: spatial information (spectral images, maps, or profiles), temporal information (kinetics, time series), concentrations (calibration series), class membership information, etc.  
Note that there is no restriction on the number of extra data columns.

This vignette gives an introduction on basic working techniques using the R package *hyperSpec*. It comes with three data sets,

**chondro**      a Raman map of chondrocytes in cartilage,  
**flu**            a set of fluorescence spectra of a calibration series, and  
**laser**        a time series of an unstable laser emission

In this vignette, all three data sets are used in an intermixed way to illustrate appropriate procedures for different tasks.

In addition, each of the data sets is accompanied by an vignette that shows an exemplary work flow how to analyze the data.

This document describes how to accomplish spectroscopic tasks. It does not give a complete reference on particular functions. It is therefore recommended to look up the methods in R's help system using `? command`.

## 1.1 Notation

This vignette demonstrates working techniques mostly from a spectroscopic point of view: rather than going through the functions provided by *hyperSpec*, it is organized more closely on spectroscopic tasks. However, the functions discussed are printed on the margin for a fast overview.

In R, slots of a S4 class can be accessed directly by the `@` operator. In this vignette, the notation `@xxx` will thus mean “slot *xxx* of an object” see figure 1 on page 5).

Likewise, named elements of a *list*, like the columns of a *data.frame*, are accessed by the `$` operator, and `$xxx` will be used for “column *xxx*”, and as an abbreviation for “column *xxx* of the *data.frame* in slot *data* of the object” see figure 1 on page 5) .

## 2 Remarks on R

### 2.1 Generic Functions

*Generic Functions* are functions that apply to a wide range of data types or classes, e. g. *plot*, *print*, mathematical operators, etc. These functions can be implemented in a specialized way by each class.

*hyperSpec* implements with a variety of such functions, see table 1 on page 6.

## 2.2 Functionality Can be Extended at Runtime

The concept of functions in R offers much flexibility. Functions may be added or changed by the user in his *workspace* at any time. This is also true for methods belonging to a certain class. Neither restart of R nor reloading of the package or anything the like is needed. At the same time, the original function is not deleted, it is just masked by the user's new function but stays accessible if the change should be reverted.

This offers the opportunity of easily writing specialized functions that are adapted to specific tasks. As an example, see the setup of the plotting function for the spectra matrix in section 10.2 (page 18)

## 2.3 Validity Checking

S4 classes have a mechanism to define and enforce that the data actually stored in the object is appropriate for this class. In other words, there is a mechanism of *validity checking*.

The functions provided by *hyperSpec* check the validity of *hyperSpec* objects at the beginning, and — if the validity could be broken by inappropriate arguments — also before leaving the function.

It is highly recommended to use validity checking also for user-defined functions. In addition, non-generic functions need to ensure that the argument actually is a *hyperSpec* object. The two tasks are accomplished by:

```
> .is.hy (object)
> validObject (object)
```

The first line checks whether `object` is a *hyperSpec* object, the second checks its validity. Both functions return TRUE if the checks succeed, otherwise they raise an error and stop.

## 3 Loading the package

To load *hyperSpec*, use

```
> library (hyperSpec)
```

## 4 The structure of hyperSpec objects

*hyperSpec* is a S4 (or new-style) class. It has four so-called *slots* that hold the data:

|                          |   |
|--------------------------|---|
| <code>@wavelength</code> | containing a numeric vector with the wavelength axis of the spectra.                      |
| <code>@data</code>       | a <i>data.frame</i> with the spectra and all further information belonging to the spectra |
| <code>@label</code>      | a list with appropriate labels (particularly for axis annotations)                        |
| <code>@log</code>        | a <i>data.frame</i> keeping track of what is done with the object                         |

However, it is good practice to use the functions provided by *hyperSpec* to handle the objects rather than accessing the slots directly. This also helps ensuring that proper (*valid*) objects are retained.

Most of the data is stored in `@data`. This *data.frame* has one special column, `$spec`. It is the column that actually contains the spectra. The spectra are stored in a matrix inside this column, as

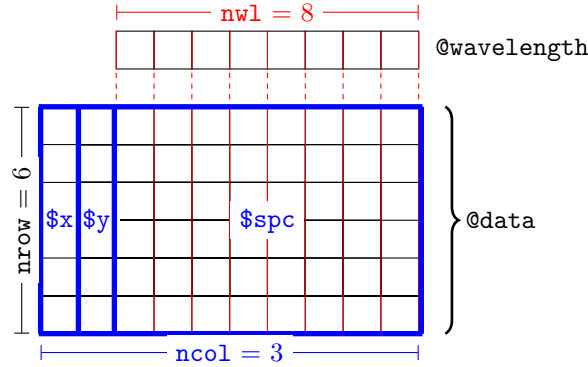


Figure 1: The structure of the data in a *hyperSpec* object.

illustrated in figure 1. Even if there are no spectra, `$spc` must still be present but it can contain a matrix with zero columns.

Slot `@label` contains an element for each of the columns in `@data` plus one holding the label for the wavelength axis, `.wavelength`. The elements of the list may be anything suitable for axis annotations, i. e. they should be either character strings or expressions for prettier axis annotations (see figure 3 on page 17). To get familiar with expressions for axis annotation, see

```
> ? plotmath
```

and

```
> demo (plotmath)
```

## 5 Functions provided by *hyperSpec*

Table 1 and 2 give an overview of the functions implemented by *hyperSpec*. 2 is a reference card providing an overview which functions help to accomplish what (spectroscopic) task.

## 6 Obtaining Basic Information about *hyperSpec* Objects

As usual, the *print* and *show* methods display information about the object, and *summary* yields some additional details about the data handling done so far:

```
> chondro
```

```
hyperSpec object
 869 spectra
 4 data columns
300 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 300] 602 606 ... 1798
data: (869 rows x 4 columns)
(1) y: y/(mu * m) [numeric 869] range -4.77 -3.77 ... 19.23
(2) x: x/(mu * m) [numeric 869] range -11.55 -10.55 ... 22.45
(3) spc: I / a.u. [matrix 869 x 300] range 80.04420 81.75761 ... 1858.881
(4) clusters: clusters [factor 869] range cell lacuna matrix
```

Table 1: Generic methods implemented by *hyperSpec* and some closely related functions. *Emphasized* names indicate non-generic functions.

| Function  | Explanation   |
|---|---|
| <code>new ("hyperSpec", ...),<br/>initialize</code>                 | create and initialize an object   |
| <code>validObject</code>  | validity checking   |
| <b>Display</b>  |   |
| <code>print, show, summary</code>                                   | print information about the object  |
| <code>plot</code>   | plotting  |
| <b>Basic information</b>  |   |
| <code>dim, ncol, nrow, nwl</code>                                   | the dimensions of the object  |
| <code>dimnames, colnames, rownames</code>                           | names of the spectra, data columns, and both plus the names of the wavelengths  |
| <b>Parts of the object</b>  |   |
| <code>[, [, \$</code>   | extract parts of an object  |
| <code>[&lt;-, [[&lt;-, \$&lt;-</code>                               | assign parts of an object   |
| <code>labels, labels&lt;-</code>                                    | labels for axis annotations etc.  |
| <code>wl, wl&lt;-</code>  | access to the wavelength axis   |
| <code>logbook, logentry</code>                                      | logbook and adding a logbook entry  |
| <b>Calculations on the spectra matrix</b>                           |   |
| <code>+ - * ^ %% %/% / %*%</code>                                   | arithmetical operators work on <code>\$spc</code>   |
| <code>&gt; &lt; == &gt;= &lt;=</code>                               | comparison operators work on <code>\$spc</code> yielding a logic matrix   |
| <code>all.equal</code>  | checking equality of <i>hyperSpec</i> objects on different levels   |
| <code>log, log10, exp, etc.</code>                                  | basic math functions work on <code>\$spc</code> , see also: ? "hyperSpec Math"  |
| <code>min, max, range</code>  | minimum, maximum, and range of the intensities in <code>\$spc</code>  |
| <b>Combining and splitting</b>                                      |   |
| <code>cbind, rbind, cbind2, rbind2,<br/>bind</code>                 | combine two objects by columns or rows  |
| <code>split</code>  | split an object into a list of objects  |
| <b>Vectorization of calculations</b>                                |   |
| <code>apply</code>  | apply a function row- or column-wise, calculate e.g. the mean spectrum or normalization factors   |
| <code>aggregate (ave)</code>  | calculate sum characteristics for groups of spectra, e.g. cluster mean spectra. <i>hyperSpec</i> 's <b>aggregate</b> method covers also the functionality of <b>ave</b> . |
| <code>sweep</code>  | "sweep" a sum characteristic over rows or columns, e.g. centre the data by subtracting the mean spectrum.   |
| <b>Type conversion</b>  |   |
| <code>as.character, as.matrix,<br/>as.data.frame, as.long.df</code> | type conversion functions   |
| <code>[[, \$</code>   | extract parts of an object as data.frame, matrix, or vector   |

Table 2: Further functions implemented by *hyperSpec*. *Emphasized* names indicate related functions provided by other R packages (package name before the colons).

| Function   | Explanation  |
|--|--|
| <b>Baseline fitting</b>  |  |
| <code>spc.fit.poly</code>  | least squares fit of a polynomial  |
| <code>spc.fit.poly.below</code>  | least squares fit of a polynomial with automatically determined supporting points (see <code>vignette("baselinebelow")</code> )    |
| <b>Working with the wavelength axis</b>  |  |
| <code>spc.bin</code>   | spectral binning   |
| <code>spc.loess</code>   | <code>loess</code> smoothing interpolation of wavelengths  |
| <code>orderwl</code>   | sort columns of spectra matrix according to the wavelengths  |
| <code>wl2i, i2wl</code>  | convert wavelengths to column indices for the spectra matrix and vice versa  |
| <b>R internal import</b>   |  |
| <code>decomposition</code>   | re-import results of decomposition techniques (scores or loadings/latent variables) into a <i>hyperSpec</i> object                 |
| <b>Data import/export</b>  |  |
| <code>read.txt.long</code> ,<br><code>read.txt.wide</code> ,<br><code>write.txt.long</code> ,<br><code>write.txt.wide</code> | ASCII file import and export   |
| <code>scan.txt.Renishaw</code>   | import ASCII files written by Renishaw Wire software   |
| <code>read.ENVI</code>   | import ENVI hyperspectral images (works also with missing header files)  |
| <code>read.ENVI.Nicolet</code>   | import ENVI files written by Nicolet spectrometer software.  |
| <code>read.spc</code>  | import binary spectra files in Thermo Galactic's <code>spc</code> format.  |
| <code>read.spc.KaiserMap</code>  | import a collection of <code>.spc</code> files that belong to a Raman map obtained with Kaiser Optical Systems' Hologram software. |
| <code>R.matlab::readMat</code> ,<br><code>R.matlab::writeMat</code>  | package <i>R.Matlab</i> <sup>[1]</sup> provides <code>.mat</code> file import and export   |
| <b>Specialized plotting</b>  |  |
| <code>plotspc</code>   | spectra plots  |
| <code>plotc</code>   | intensity over one other dimension: calibration plots, depth profiles, time series, etc.   |
| <code>plotmap</code>   | color-coded intensity over two other dimensions: spectral images and maps, etc.  |
| <code>plotmat</code>   | color-coded intensity over wavelength axis and one other dimension: spectra matrix of time series, depth profiles, etc.            |
| <code>stacked.offsets</code>   | calculate offset values for stacking spectra or groups of spectra  |
| <code>index.grid</code>  | calculate a grid matrix holding the indices of the respective spectra (row indices)  |
| <code>spc.identify, map.identify</code>  | identify spectra and wavelength indices by clicking into plots produced by <code>plotspc</code> and <code>plotmap</code>           |

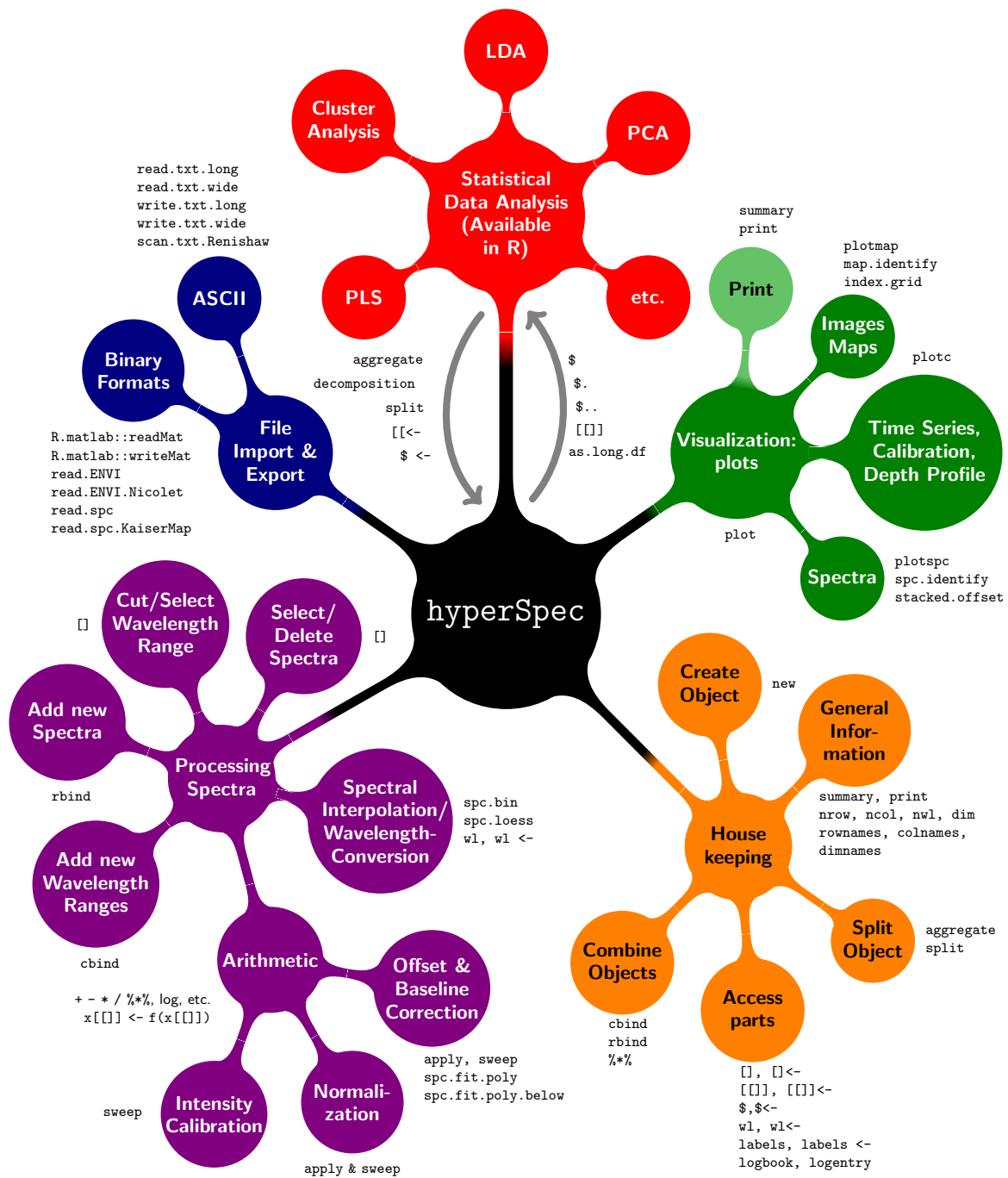


Figure 2: Overview of functions to accomplish common spectroscopic tasks.



Table 3: Utility functions provided by *hyperSpec* that are loosely related to working with spectra.

| Function  | Explanation   |
|---|---|
| <code>mean_pm_sd</code> , <code>mean_sd</code>                    | calculate mean and standard deviation, and mean $\pm$ 1 standard deviation, respectively. Convenience function for <code>plotspc</code> , <code>aggregate</code> , etc. |
| <code>pearson.dist</code>   | Pearson’s distance for use with cluster analysis  |
| <code>array2df</code>   | convert wide-format array into long-format matrix or data.frame   |
| <code>array2vec</code> , <code>vec2array</code>                   | index conversion between array and vector notation  |
| <code>wc</code>   | try to use <code>wc</code> (word count) if installed on the system  |
| <code>matlab.palette</code> ,<br><code>matlab.dark.palette</code> | color palettes resembling Matlab’s “jet” palette, and a version with darker green values  |

```
> summary (chondro)

hyperSpec object
  869 spectra
  4 data columns
  300 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 300]  602 606 ... 1798
data: (869 rows x 4 columns)
  (1) y: y/(mu * m) [numeric 869] range -4.77 -3.77 ... 19.23
  (2) x: x/(mu * m) [numeric 869] range -11.55 -10.55 ... 22.45
  (3) spc: I / a.u. [matrix 869 x 300] range 80.04420 81.75761 ... 1858.881
  (4) clusters: clusters [factor 869] range cell    lacuna matrix
log:
      short      long      date      user
1  scan.txt.Renishaw list(...) 2009-12-17 21:47:06 cb@cb
2      orderwl list(...) 2009-12-17 21:47:07 cb@cb
3      spc.loess list(...) 2009-12-17 21:47:29 cb@cb
4          [ list(...) 2009-12-17 21:47:47 cb@cb
5          $<- list(...) 2009-12-17 21:47:47 cb@cb
```

The data set `chondro` consists of 869 spectra with 300 data points each, and 4 data columns: two for the spatial information plus `$spc`. These informations can be directly obtained by

```
> nrow (chondro)

[1] 869

> nwl (chondro)

[1] 300

> ncol (chondro)

[1] 4

> dim (chondro)

nrow ncol  nwl
 869    4  300
```

The names of the columns in `@data` are accessed by

```
> colnames (chondro)
[1] "y"      "x"      "spc"    "clusters"
```

Likewise, `rownames` returns the names assigned to the spectra, and `dimnames` yields a list of these three vectors (including also the column names of `$spc`).

## 7 Creating a hyperSpec Object, Data Import and Export

### 7.1 ASCII Files

Currently, *hyperSpec* provides four functions for general ASCII data import and export:

```
read.txt.long    import long format ASCII files, i.e. one intensity value per row
read.txt.wide    import wide format ASCII files, i.e. one spectrum per row
write.txt.long   export long format ASCII files
write.txt.wide   export wide format ASCII files
```

```
read.txt.long
read.txt.wide
write.txt.long
write.txt.wide
```

The import functions immediately return a *hyperSpec* object.

### 7.2 Matlab Files

Matlab files can be read and written using the package *R.matlab*[1], which is available at CRAN and can be installed by `install.packages ("R.matlab")`.

### 7.3 ENVI Files

*hyperSpec* provides a function to read ENVI files, `read.ENVI`. ENVI files are binary data accompanied by an ASCII header file.

```
read.ENVI
```

As we experienced missing header files (Bruker's Opus software frequently produces header files without any content), the data that would usually be read from the header file can also be handed to `read.ENVI` as a list. The help page gives details on what elements the list should contain.

### 7.4 spc Files

Thermo Galactic's .spc file format can be read by `read.spc`.

### 7.5 Manufacturer Specific Import Functions

Many spectrometer manufacturers provide a function to export their spectra into ASCII files. The functions discussed above are written in a very general way, and are highly customizable. I recommend wrapping these calls with the appropriate settings for your spectra format in an import function. You may also consider contributing such import filters to *hyperSpec*: send me ([cbeleites@units.it](mailto:cbeleites@units.it)) the documented code (either .R + .Rd file or Roxygen commented .R).

### 7.5.1 Renishaw

For the long ASCII format written by Renishaw's converter, an optimized import function is already available: `scan.txt.Renishaw`.

`scan.txt.Renishaw`

```
> paracetamol <- scan.txt.Renishaw ("rawdata/paracetamol.txt", "spc")
> paracetamol

hyperSpec object
  1 spectra
  1 data columns
  4064 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 4064] 96.7865 98.1432 ... 3200.07
data: (1 rows x 1 columns)
  (1) spc: I / a.u. [AsIs matrix 1 x 4064] range 299.229 317.041 ... 49052.2
```

The converter also offers to write .spc files. We experienced however, that this conversion is not fully reliable: maps were saved as depth profile, loosing all spatial information. Also, an evenly spaced wavelength axis was produced, although this was de-selected in the converter. We therefore recommend using the ASCII format.

### 7.5.2 Bruker FTIR Imaging

We use `read.ENVI` to import IR-Images collected with a Bruker Hyperion spectrometer with OPUS software. As mentioned above, the header files are frequently missing. We found the necessary information to be:

```
> header <- list (samples = 64 * no.images.in.row,
+               lines = 64 * no.images.in.column,
+               bands = no.data.points.per.spectrum,
+               `data type` = 4,
+               interleave = "bip")
```

No spatial information is given in the ENVI header (if correctly written). The lateral coordinates can be setup by specifying origin and pixel size for  $x$  and  $y$  directions. For details please see the help page.

### 7.5.3 Nicolet FTIR Imaging

Also Nicolet saves imaging data in ENVI files. These files use some non-standard keywords in the header file that should allow to reconstruct the lateral coordinates as well as the spectral axes' units.

There is indication that the position of the first spectrum is recorded in  $\hat{i}j\hat{m}$ , while the pixel size is in mm. Thus a flag `nicolet.correction` is provided that divides the pixel size by 1000. Also here, giving the correct offset and pixel size values as function arguments is possible.

### 7.5.4 Kaiser Raman Maps

Spectra obtained using Kaiser's Hologram software can be saved either in their own .hol format and imported into Matlab (from where the data may be written to a .mat file readable by *R.matlab*'s `readMat`). Alternatively, Hologram can write ASCII files and .spc files. We found working with .spc files the best option.

*hyperSpec* provides the function `read.spc.KaiserMap` to easily import spatial collections of .spc files written by Kaiser's Hologram software. The filenames of all .spc files to be read into one *hyperSpec* object can be provided either in a character vector or as a wildcard expression (e.g. "path/to/files/\*.spc").

## 7.6 Creating a hyperSpec Object from Spectra Matrix and Wavelength Vector

Once the data is in R's workspace, a *hyperSpec* object is created by:

```
spc <- new ("hyperSpec", spc = spectra.matrix, wavelength = wavelength.vector)
```

You will usually give the following arguments:

|                         |  |
|-------------------------|--|
| <code>spc</code>        | the spectra matrix   |
| <code>wavelength</code> | the wavelength axis vector   |
| <code>data</code>       | the extra data   |
| <code>label</code>      | a list with the proper labels. Do not forget the wavelength axis label in <code>\$.wavelength</code> and the spectral intensity axis label in <code>\$spc</code> . |

## 8 Combining hyperspec Objects

`cbind` `rbind`

*hyperspec* Objects can be bound together, either by rows to append a new spectral range or by columns to append new spectra

```
> cbind (chondro [, , 600 ~ 800], chondro [, , 1600 ~ 1800])
```

```
hyperSpec object
 869 spectra
 4 data columns
101 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 101] 602 606 ... 1798
data: (869 rows x 4 columns)
(1) y: y/(mu * m) [numeric 869] range -4.77 -3.77 ... 19.23
(2) x: x/(mu * m) [numeric 869] range -11.55 -10.55 ... 22.45
(3) spc: I / a.u. [matrix 869 x 101] range 80.04420 81.75761 ... 1541.625
(4) clusters: clusters [factor 869] range cell lacuna matrix
```

```
> rbind (chondro [, , 600 ~ 800], chondro [, , 600 ~ 800])
```

```
hyperSpec object
1738 spectra
 4 data columns
 50 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 50] 602 606 ... 798
data: (1738 rows x 4 columns)
(1) y: y/(mu * m) [numeric 1738] range -4.77 -3.77 ... 19.23
(2) x: x/(mu * m) [numeric 1738] range -11.55 -10.55 ... 22.45
(3) spc: I / a.u. [matrix 1738 x 50] range 195.5281 212.0432 ... 729.5765
(4) clusters: clusters [factor 1738] range cell lacuna matrix
```

There is also a more general function, `bind`, taking the direction ("r" or "c") as first argument and then all objects to bind either in separate arguments or in a list.

## 9 Access to the data

### 9.1 Selecting and Deleting Spectra

The extraction function `[]` (or `[[ ]]`, if the spectra *matrix* or the *data.frame* is needed rather than a *hyperSpec* object) takes the spectra as first argument (For detailed help: `? "[]"`). It may be a vector giving the indices of the spectra to extract (select), a vector with negative indices indicating which spectra should be deleted, or a logical

```
> flu [1 : 3]

hyperSpec object
  3 spectra
  2 data columns
 181 data points / spectrum
wavelength: lambda[f1]/nm [numeric 181] 405.0 405.5 ... 495
data: (3 rows x 2 columns)
  (1) c: c / (mg/l) [numeric 3] range 0.05 0.10 0.15
  (2) spc: I / a.u. [AsIs matrix 3 x 181] range 27.15000 32.34467 ... 336.5057

> flu [-3]

hyperSpec object
  5 spectra
  2 data columns
 181 data points / spectrum
wavelength: lambda[f1]/nm [numeric 181] 405.0 405.5 ... 495
data: (5 rows x 2 columns)
  (1) c: c / (mg/l) [numeric 5] range 0.05 0.10 0.20 0.25 0.30
  (2) spc: I / a.u. [AsIs matrix 5 x 181] range 27.15000 32.34467 ... 677.4947

> chondro [chondro$y > 10]

hyperSpec object
 350 spectra
  4 data columns
 300 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 300] 602 606 ... 1798
data: (350 rows x 4 columns)
  (1) y: y/(mu * m) [numeric 350] range 10.23 11.23 ... 19.23
  (2) x: x/(mu * m) [numeric 350] range -11.55 -10.55 ... 22.45
  (3) spc: I / a.u. [matrix 350 x 300] range 88.98556 89.99474 ... 1745.724
  (4) clusters: clusters [factor 350] range cell lacuna matrix
```

### 9.2 Accessing the Extra Data

The second argument of the extraction functions `[]` and `[[ ]]` specifies the (extra) data columns. They can be given like any column specification for a *data.frame*, i. e. numeric, logical, or by a vector of the column names:

```
> colnames(chondro)

[1] "y"      "x"      "spc"    "clusters"

> chondro [[1 : 3, 1]]
```

```

      y
1 -4.77
2 -4.77
3 -4.77

> chondro [[1 : 3, -3]]

      y      x clusters
1 -4.77 -11.55  matrix
2 -4.77 -10.55  matrix
3 -4.77  -9.55  matrix

> chondro [[1 : 3, "x"]]

      x
1 -11.55
2 -10.55
3  -9.55

> chondro [[1 : 3, c (TRUE, FALSE, FALSE)]]

      y clusters
1 -4.77  matrix
2 -4.77  matrix
3 -4.77  matrix

```

To select one column, the `$` operator is more convenient:

```

> flu$c

[1] 0.05 0.10 0.15 0.20 0.25 0.30

```

The extra data may also be set this way:

```

> flu$n <- list (1 : 6, label = "sample no.")

```

This function will append new columns, if necessary.

## 9.3 Wavelengths and Spectral Axis

### 9.3.1 Wavelength Indices

wl2i i2wl

Spectra in *hyperSpec* have always discretized wavelength axes, they are stored in a matrix with column corresponding to one wavelength. *hyperSpec* provides two conversion functions: `i2wl` returns the wavelength corresponding to the given indices and `wl2i` calculates index vectors from wavelengths.

If the wavelengths are given as a numeric vector, they are each converted to the corresponding wavelength. In addition there is a more sophisticated possibility of specifying wavelength ranges using a *formula*. The basic syntax is *start*  $\sim$  *end*. This yields a vector *index of start* : *index of end*.

The result of the formula conversion differs from the numeric vector conversion in three ways:

- The colon operator for constructing vectors accepts only integer numbers, the tilde (for formulas) does not have this restriction.

- If the vector does not take into account the spectral resolution, one may get only every  $n^{th}$  point or repetitions of the same index:

```
> wl2i (flu, 405 : 410)
[1] 1 3 5 7 9 11

> wl2i (flu, 405 ~ 410)
[1] 1 2 3 4 5 6 7 8 9 10 11

> wl2i (chondro, 1000 : 1010)
[1] 100 101 101 101 101 102 102 102 102 103 103

> wl2i (chondro, 1000 ~ 1010)
[1] 100 101 102 103
```

- If the object's wavelength axis is not ordered, the formula approach doesn't work. In that (rare) case, use `orderwl` first to obtain an object with ordered wavelength axis.

*start* and *end* may contain the special variables `min` and `max` that correspond to the lowest and highest wavelengths of the object:

```
> wl2i (flu, min ~ 410)
[1] 1 2 3 4 5 6 7 8 9 10 11
```

Often, specifications like *wavelength  $\pm n$  data points* are needed. They can be given using complex numbers in the formula. The imaginary part is added to the index calculated from the wavelength in the real part:

```
> wl2i (flu, 450 - 2i ~ 450 + 2i)
[1] 89 90 91 92 93

> wl2i (flu, max - 2i ~ max)
[1] 179 180 181
```

To specify several wavelength ranges, use a list containing the formulas and vectors<sup>1</sup>:

```
> wl2i (flu, 450 - 2i ~ 450 + 2i)
[1] 89 90 91 92 93

> wl2i (flu, c (min ~ 406.5, max - 2i ~ max))
[1] 1 2 3 4 179 180 181
```

This mechanism also works for the wavelength arguments of `[]`, `[[ ]]`, and `plotspc`.

### 9.3.2 Wavelength Axis Conversion

## 9.4 Fast Access to Parts of the hyperSpec Object

[[]] \$. \$..

*hyperSpec* comes with three abbreviation functions for easy access to the data:

`x [[]]` returns the spectra matrix (`x$spc`).

`x [[i, , 1]]` the cut spectra matrix is returned if wavelengths are specified in *l*.

`x [[i, j, 1]]` If data columns are selected (second index), the result is a *data.frame*.

`x [[i, , 1]] <-` Also, parts of the spectra matrix can be set (only indices for spectra and wavelength are allowed for this function).

`x [i, j] <-` sets parts of `x@data`.

`x $.` returns the complete *data.frame* `x@data`, with the spectra in column `$spc`.

`x $..` returns the extra data (`x@data` without `x$spc`).

`x $.. <-` sets the extra data (`x@data` without `x$spc`). However, the columns must match exactly in this case.

## 10 Plotting

*hyperSpec* comes with three predefined plotting functions.

`plotspc` plots the spectra, i. e. the intensities `$spc` over the wavelengths `@wavelength`.

`plotmap` plots a false colour map: a single value (e. g. average intensity or cluster membership) over two data columns (default `$x` and `$y`).

`plotc` plots a time series or calibration plot: e. g. an intensity over a single other data column (like concentration, depth, or time).

All three plus some more handy abbreviations are also accessible via *plot*:

`plot`

`plot (flu, "spc")` is equivalent to `plotspc (flu)`

`plot (chondro, "spcmeansd")` plots mean spectrum  $\pm 1$  standard deviation

`plot (chondro, "spcprctl")` plots median, 16<sup>th</sup> and 84<sup>th</sup> percentile. This is similar to `"spcmeansd"`. Spectroscopic data frequently are not Gaussian distributed. The percentiles give a better idea of the true distribution. They are also less sensitive to outliers.

`plot (chondro, "spcprctl5")` like `"spcprctl"` plus 5<sup>th</sup> and 95<sup>th</sup> percentile.

`plot (chondro, "map")` is equivalent to `plotmap (chondro)`

`plot (flu, "c")` is equivalent to `plotc (flu)`

`plot (laser, "ts")` plots a time series plot, equivalent to `plotc (laser, use.c = "t")`

`plot (x, "depth")` plots a depth profile plot, equivalent to `plotc (laser, use.c = "z")`

Figure 3 shows some example plots.

`plot` uses its second argument to determine which of the three specialized plot functions to call. All further arguments are handed over to this function.



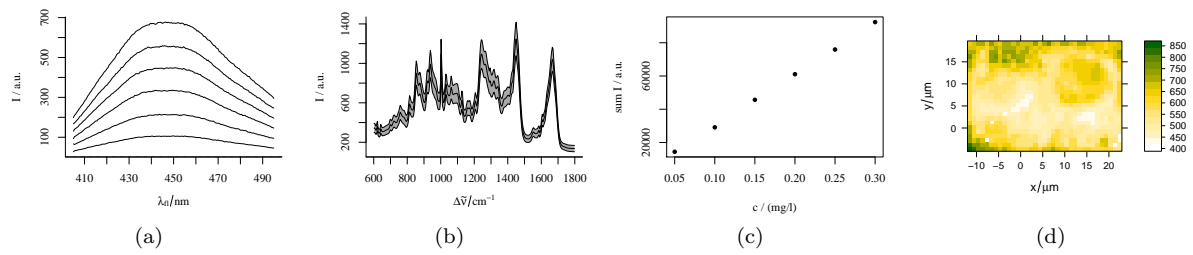


Figure 3: Some example plots. (a) `plotspc (flu)`, (b) `plot (chondro, "spcmeansd")`, (c) `plotc (flu)`, and (d) `plotmap (chondro, col.regions = YG (20))` (using a yellow-green palette).

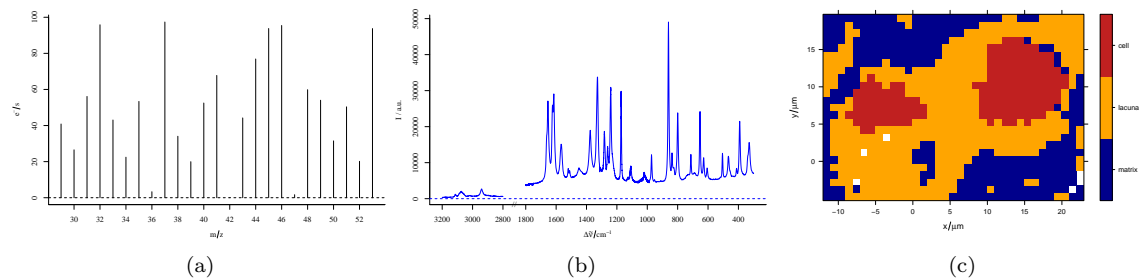


Figure 4: Arguments to `plotspc`. (a) `plot (fake.mass.spec, lines.args = list (type = "h"))` (b) `plotspc (paracetamol, wl.range = c (300 ~ 1800, 2800 ~ max), xoffset = 850, wl.reverse = TRUE)` (c) `plotmap` with a factor, see section 12.2.

## 10.1 Plotting Spectra

`plotspc`

`plotspc` offers a variety of parameters for customized plots. To plot ...

**with reversed abscissa** use `wl.reverse = TRUE`

**in different colours** colours use `col = vector.of.colours`

**dots instead of lines** use `lines.args = list (pch = 20, type = "p")`

**mass spectra** use `lines.args = list (type = "h")`

**particular wavelength ranges** use `wl.range = list (600 ~ 1800, 2800 ~ 3100)`

If `wl.range` already contains indices: use `wl.index = TRUE`

Cut the wavelength axis appropriately with `xoffset = 800`

**stacked spectra** use `stacked`

**more spectra into an existing plot** use `add = TRUE`

**with different line at  $I = 0$**  use `zeroline = list.of.arguments.to.abline`. NULL suppresses the line.

<sup>1</sup>Formulas are combined to a list by `c`.

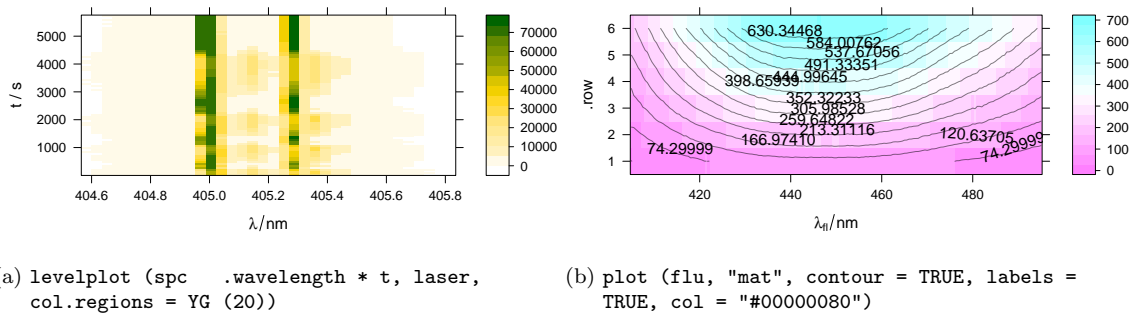


Figure 5: plotting the spectra matrix.

## 10.2 Plotting the Spectra Matrix

It is often useful to plot the spectra against an additional coordinate, e.g. the time for time series, the depth for depth profiles, etc.

This is done by `levelplot`, or by using `plot (object, "mat", model = spc ~ .wavelength * other.data.column)`. The actual plotting is done by `levelplot`, so the plots can be grouped or conditioned. See figure 5

```
> levelplot (spc ~ .wavelength * t, laser, col.regions = YG (20))
```

```
> print (plot (flu, "mat", contour = TRUE, labels = TRUE, col = "#00000080"))
```

## 10.3 Calibration Plots, (Depth) Profiles, and Time Series Plots

`plotc`

`plotc` plots an intensity over one of the extra data columns. The abscissa uses column `$c` by default, another column can be specified using `use.c = name`. The ordinate can be calculated as a sum characteristic (with parameter `func= function`, defaulting to `sum`). If parameter `z` is given, these values are used instead. `z` may be the name of an extra data column, or a *numeric* that should be used directly.

To customize the plot, give any arguments that you would usually supply to `plot` as a list using argument `plot.args`.

## 10.4 Plotting False-Colour Maps

`plotmap`

`plotmap` uses `levelplot`, a *lattice* function. Therefore, in loops, functions, Sweave chunks, etc. the lattice object needs to be printed explicitly by `print (plotmap (object))` ([R FAQ: Why do lattice/trellis graphics not work?](#)).

`plotmap` produces a 3d plot, with the `z` axis colour-coded. `plotmap`'s arguments `x` and `y` take the name of extra data columns.

**The colour-coded axis.** Also *z* can be used to select one column of the extra data by name. Alternatively, it may be a numeric or factor directly giving the values to be used. Each level of a factor will have one colour. It is also possible to plot a sum characteristic of the spectra: supply the function in argument *func*. The default setting is to plot the average intensity (no *z* and *func*=*mean*).

To plot with a different palette, use *trellis.args*= *list* (*col.regions* = *palette*).

**Conditioning.** Lattice graphics have a concept of conditioning a plot. Instead of plotting all data in one diagram, a diagram is produced for each of the groups specified by the condition. *plotmap*'s argument *cond* takes the name of the extra data column used for conditioning. This could e.g. be a column containing the sample number of a *hyperSpec* object that contains several samples.

## 11 Spectral (Pre)processing

### 11.1 Cutting the Spectral Range

□ □□

The extraction functions *[]* and *[] []* can be used to cut the spectra: Their third argument takes wavelength specifications as discussed above and also logicals (i.e. vectors specifying with TRUE/FALSE for each column of *\$spc* whether it should be included or not).

*[]* returns a *hyperSpec* object, *[] []* the spectra *matrix**\$spc* (or the *data.frame**@data* if data columns were specified, too) only.

```
> flu [, , min ~ 408.5]
```

hyperSpec object

6 spectra

3 data columns

8 data points / spectrum

wavelength: lambda[f1]/nm [numeric 8] 405.0 405.5 ... 408.5

data: (6 rows x 3 columns)

(1) c: c / (mg/l) [numeric 6] range 0.05 0.10 ... 0.3

(2) spc: I / a.u. [AsIs matrix 6 x 8] range 27.15000 32.34467 ... 256.8913

(3) n: sample no. [integer 6] range 1 2 ... 6

```
> flu [, , c (min ~ min + 2i, max - 2i ~ max)]
```

|      | 405       | 405.5     | 406       | 494       | 494.5     | 495       |
|------|-----------|-----------|-----------|-----------|-----------|-----------|
| [1,] | 27.15000  | 32.34467  | 33.37867  | 47.16267  | 46.41233  | 45.25633  |
| [2,] | 66.80133  | 63.71533  | 66.71200  | 96.60167  | 96.20600  | 94.61033  |
| [3,] | 93.14433  | 103.06767 | 106.19367 | 149.53900 | 148.52667 | 145.79333 |
| [4,] | 130.66367 | 139.99833 | 143.79767 | 201.48433 | 198.86733 | 195.86733 |
| [5,] | 167.26667 | 171.89833 | 177.47067 | 252.06567 | 248.06700 | 246.95200 |
| [6,] | 198.43033 | 209.45800 | 215.78500 | 307.51850 | 302.32550 | 294.64950 |

### 11.2 Spectral Interpolation and Smoothing

spc.bin  
spc.loess

Frequently, a *hyperSpec* object needs to be interpolated onto a new wavelength axis. e.g. because measurements resulted in slightly shifted wavelength axes. Or data from a grating spectrometer with unequal data point spacing should be interpolated onto an evenly spaced wavelength axis. Also, the spectra can be smoothed: reducing the spectral resolution allows to increase the signal to noise ratio.

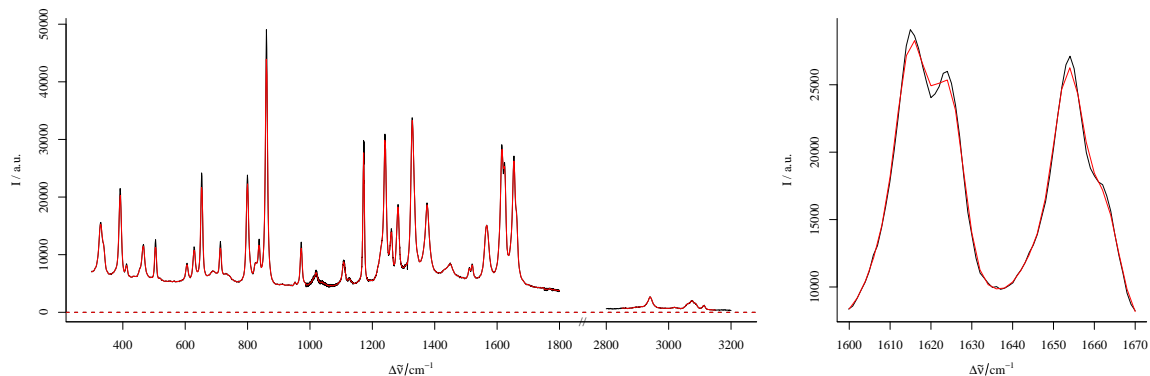


Figure 6: Smoothing interpolation by `spc.loess` with new data point spacing of  $2\text{ cm}^{-1}$ . The magnification on the right shows how interpolation may cause a loss in signal.

For chemometric data analysis reducing the number of data points per spectrum may be crucial as it reduces the dimensionality of the data.

*hyperSpec* provides two functions to change the wavelength axis of *hyperSpec* objects: `spc.bin` and `spc.loess`.

`spc.bin` bins the spectral axis by averaging every *by* data points.

```
> plot (paracetamol, wl.range = c (300 ~ 1800, 2800 ~ max), xoffset = 850)
> p <- spc.loess (paracetamol, c(seq (300, 1800, 2), seq (2850, 3150, 2)))
> plot (p, wl.range = c (300 ~ 1800, 2800 ~ max), xoffset = 850, col = "red", add = TRUE)
```

`spc.loess` applies R's `loess` function for spectral interpolation. Figure 6 shows the result of interpolating from 300 to 1800 and 2850 to 3150  $\text{cm}^{-1}$  with  $2\text{ cm}^{-1}$  data point distance. This corresponds to a spectral resolution of about  $4\text{ cm}^{-1}$ , and the decrease in spectral resolution can be seen at the sharp bands where the maxima are not reached (due to the fact that the interpolation wavelength axis does not necessarily hit the maxima. The original spectrum had 4064 data points with unequal data point spacing (between 0 and  $1.4\text{ cm}^{-1}$ ). The interpolated spectrum has 902 data points.

### 11.3 Background Correction

To subtract a background spectrum of each of the spectra in an object, use `sweep (spectra, 2, background.spectrum, "-")`.

### 11.4 Offset Correction

Calculate the offsets and sweep them off the spectra:

```
> offsets <- apply (chondro, 1, min)
> chondro.offset.corrected <- sweep (chondro, 1, offsets, "-")
```

## 11.5 Baseline Correction

*hyperSpec* comes with two functions to fit polynomial baselines.

`spc.fit.poly` fits a polynomial baseline of the given order. A least-squares fit is done so that the function may be used on rather noisy spectra. However, the user must supply an object that is cut appropriately. Particularly, the supplied wavelength ranges are not weighted.

`spc.fit.poly.below` tries to find appropriate support points for the baseline iteratively.

Both functions return a *hyperSpec* object containing the fitted baselines. They need to be subtracted afterwards:

```
> bl <- spc.fit.poly.below (chondro)

Fitting with npts.min = 15

> chondro <- chondro - bl
```

For details, see `vignette (baselinebelow)`.

## 11.6 Intensity Calibration

### 11.6.1 Correcting by a constant, e.g. Readout Bias

CCD cameras often operate with a bias, causing a constant value for each pixel. Such a constant can be immediately subtracted:

```
spectra - constant
```

### 11.6.2 Correcting Wavelength Dependence

This means that for each of the wavelengths the same correction needs to be applied to all spectra.

1. There might be wavelength dependent offsets (background or dark spectra). They are subtracted:  
`sweep (spectra, 2, offset.spectrum, "-")`
2. A multiplicative dependency such as a CCD's photon efficiency:  
`sweep (spectra, 2, photon.efficiency, "/")`

### 11.6.3 Spectra Dependent Correction

If the correction depends on the spectra (e.g. due to inhomogeneous illumination while collecting imaging data<sup>2</sup>), the *MARGIN* of the `sweep` function needs to be 1:

1. Pixel dependent offsets are subtracted:  
`sweep (spectra, 2, pixel.offsets, "-")`
2. A multiplicative dependency:  
`sweep (spectra, 2, illumination.factors, "*")`

---

<sup>2</sup>imaging (as opposed to mapping) refers to simultaneously collecting spatially resolved spectra, either 2d images or line imaging.

## 11.7 Normalization

1. Calculate appropriate normalization factors:

`factors <- 1 / apply (spectra, 1, sum)` for area normalization. `mean` gives equal results, just that the Intensities are on the same scale as before.

For minimum-maximum-normalization, first do an offset- or baseline correction, then calculate the *factors* using `max`.

You may calculate the factors using only a certain wavelength range, thereby normalizing on a particular band or peak.

2. Again, sweep the factor off the spectra:

```
normalized <- sweep (spectra, 1, factors, "*")
```

```
> factors <- 1 / apply (chondro, 1, mean)
> chondro <- sweep (chondro, 1, factors, "*")
```

## 11.8 Centering the Data

Centering means that the mean spectrum is subtracted from each of the spectra. Many data analysis techniques, like principal component analysis, partial least squares, etc., work much better on centered data.

However, from a spectroscopic point of view it depends on the particular data set whether centering does make sense or not.

It is perfectly fine to centre the `flu` data set: the interpretation is that centering the data cancels the offset (background spectrum etc.) of the calibration:

```
> flu.centered <- sweep (flu, 2, apply (flu, 2, mean), "-")

> plot (flu.centered)
```

On the other hand, the `chondro` data set consists of Raman spectra, so the spectroscopic interpretation of centering is getting rid of the the average chemical composition of the sample. But: what is the meaning of the “average spectrum” of an inhomogeneous sample? In this case it is better to subtract the minimum spectrum (which will hopefully have almost the same benefit on the data analysis) as it is the spectrum of that chemical composition that is underlying the whole sample.

One more point to consider is that the actual minimum spectrum will pick up lots of the negative noise. In order to avoid that, using e. g. the 5<sup>th</sup> percentile spectrum is more suitable:

```
> chondro <- sweep (chondro, 2, apply (chondro, 2, quantile, 0.05), "-")

> plot (chondro, "spcprct15")
```

## 11.9 Variance Scaling

Variance scaling is often used in multivariate analysis to adjust the influence and scaling of the variates (that are typically different physical values). However, it is hardly appropriate for spectra that do have the same scale of the same physical value.

## 11.10 Multiplicative Scatter Correction (MSC)

MSC can be done using `msc` from package *pls*<sup>[2]</sup>. It operates on the spectra matrix:

```
> library (pls)
> chondro.msc <- chondro
> chondro.msc [[]] <- msc (chondro [[]])
```

## 11.11 Spectral Arithmetic

Basic mathematical functions are defined for *hyperSpec* objects. You may convert spectra:  
`absorbance.spectra = - log10 (transmission.spectra)`

In this case, do not forget to adapt the label:

```
> labels (absorbance.spectra)$spc <- "A"
```

Be careful: R's `log` function calculates the natural logarithm if no base is given.

The basic arithmetic operators work element-wise in R. Thus they all need either a scalar, or a matrix (or *hyperSpec* object) of the correct size.

Matrix multiplication is done by `%*%`, again each of the operands may be a matrix or a *hyperSpec* object, and must have the correct dimensions.

+ - \* / ^ log  
log10

labels

%\*%

## 12 Data Analysis

### 12.1 Data Analysis Methods using a `data.frame`

#### e.g. Principal Component Analysis with `prcomp`

The `$.` notation is handy, if a data analysis function expects a *data.frame*. The column names can then be used in the formula:

```
> pca <- prcomp (~ spc, data = chondro$. , centre = FALSE)
```

Results of such a decomposition can be put again into *hyperSpec* objects. This allows to plot e.g. the loading like spectra, or score maps, see figure 7.

```
> scores <- decomposition (chondro, pca$x, label.wavelength = "PC", label.spc = "score / a.u.")
> loadings <- decomposition (chondro, t(pca$rotation), scores = FALSE, label.spc = "loading I / a.u.")
```

### 12.2 Data Analysis Methods using a matrix

#### e.g. Hierarchical Cluster Analysis

```
> dist <- pearson.dist (chondro [[]])
> dendrogram <- hclust (dist, method = "ward")
```

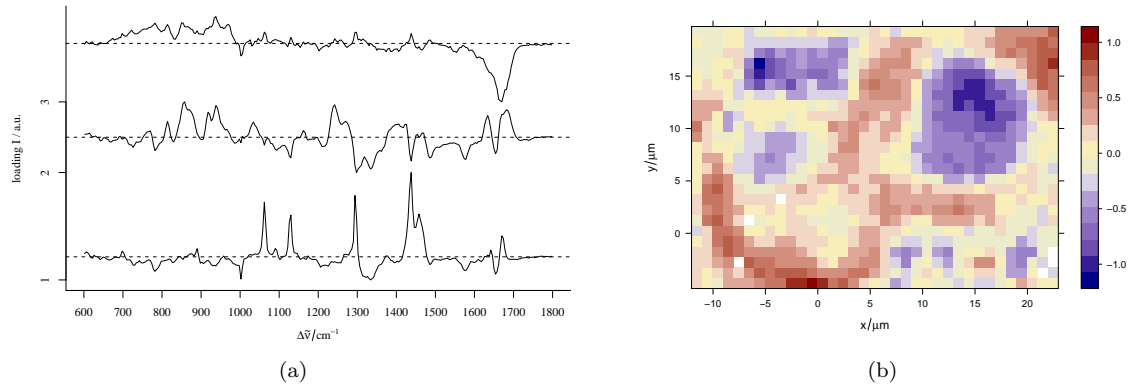


Figure 7: (a) The first three loadings: `plot (loadings [1 : 3], stacked = TRUE)`. (b) The second score map: `plotmap (scores [, , 2])`

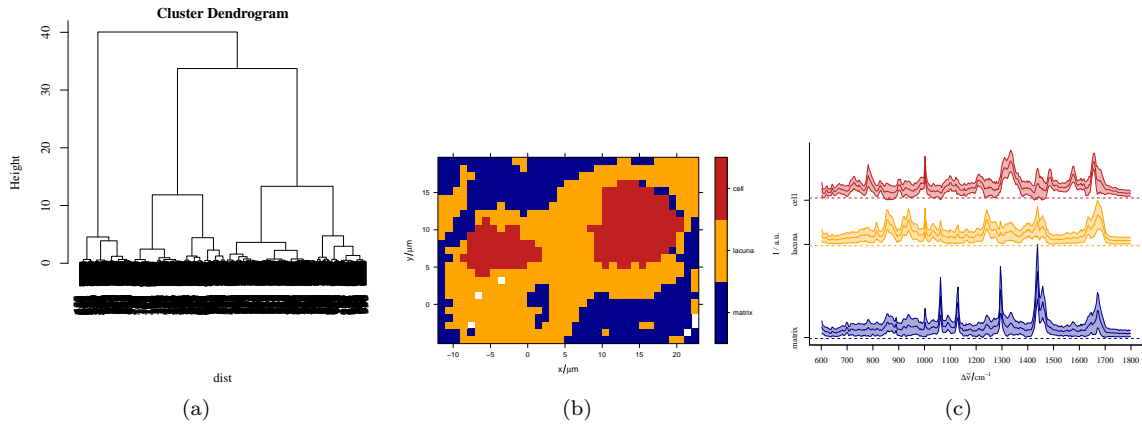


Figure 8: The results of the cluster analysis: (a) the dendrogram (b) the map of the 3 clusters (c) the mean spectra.

```
> plot (dendrogram)
```

In order to plot a cluster map, the cluster membership needs to be calculated from the dendrogram. First, cut the dendrogram so that three clusters result:

```
> chondro$clusters <- as.factor (cutree (dendrogram, k = 3))
```

As the cluster membership was stored as factor, the levels can be meaningful names, which are displayed in the color legend.

```
> levels (chondro$clusters) <- c ("matrix", "lacuna", "cell")
```

Then the result may be plotted (figure 8b):



## 12.3 Calculating group-wise Sum Characteristics

### e.g. Cluster Mean Spectra

`aggregate` applies the function given in *FUN* to each of the groups of spectra specified in *by*.

`aggregate`

So we may plot the cluster mean spectra:

```
> means <- aggregate (chondro, by = chondro$clusters, mean_pm_sd)
> plot (means, col = cluster.cols, stacked = ".aggregate", fill = ".aggregate")
```

## 12.4 Splitting an Object

A *hyperSpec* object may also be split into a list of *hyperSpec* objects:

```
> clusters <- split (chondro, chondro$clusters)
> clusters

$matrix
hyperSpec object
  285 spectra
  4 data columns
  300 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 300] 602 606 ... 1798
data: (285 rows x 4 columns)
  (1) y: y/(mu * m) [numeric 285] range -4.77 -3.77 ... 19.23
  (2) x: x/(mu * m) [numeric 285] range -11.55 -10.55 ... 22.45
  (3) spc: I / a.u. [matrix 285 x 300] range -0.1361023 -0.1294874 ... 0.9382975
  (4) clusters: clusters [factor 285] range matrix

$lacuna
hyperSpec object
  424 spectra
  4 data columns
  300 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 300] 602 606 ... 1798
data: (424 rows x 4 columns)
  (1) y: y/(mu * m) [numeric 424] range -4.77 -3.77 ... 19.23
  (2) x: x/(mu * m) [numeric 424] range -11.55 -10.55 ... 22.45
  (3) spc: I / a.u. [matrix 424 x 300] range -0.1178416 -0.1175710 ... 0.481894
  (4) clusters: clusters [factor 424] range lacuna

$cell
hyperSpec object
  160 spectra
  4 data columns
  300 data points / spectrum
wavelength: Delta * tilde(nu)/cm^-1 [numeric 300] 602 606 ... 1798
data: (160 rows x 4 columns)
  (1) y: y/(mu * m) [numeric 160] range 4.23 5.23 ... 16.23
  (2) x: x/(mu * m) [numeric 160] range -8.55 -7.55 ... 20.45
  (3) spc: I / a.u. [matrix 160 x 300] range -0.1372812 -0.1364245 ... 0.4372353
  (4) clusters: clusters [factor 160] range cell
```

Splitting can be reversed by `rbind` (see section 8, page 12).

## References

- [1] Henrik Bengtsson and Jason Riedy. *R.matlab: Read and write of MAT files together with R-to-Matlab connectivity*, 2008. URL <http://www.braju.com/R/>. R package version 1.2.4.
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