hyperSpec Plotting functions

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February 13, 2020

Reproducing the Examples in this Vignette

All spectra used in this manual are installed automatically with hyperSpec.
Note that some definitions are executed in vignette.defs, and others invisibly at the beginning of the file in order to have the code as similar as possible to interactive sessions.

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Suggested Packages

latticeExtra: available
deldir: available
rgl: available
ggplot2: available

In addition tripack, and latticist are mentioned, but not used in this vignette.

Preliminary Calculations

For some plots of the chondro dataset, the pre-processed spectra and their cluster averages ± one standard deviation are more suitable:

```r
> chondro.preproc <- chondro - spc.fit.poly.below (chondro)
> chondro.preproc <- chondro.preproc / rowMeans (chondro)
> chondro.preproc <- chondro.preproc - quantile (chondro.preproc, 0.05)
> cluster.cols <- c ("dark blue", "orange", "#C02020")
> cluster.meansd <- aggregate (chondro.preproc, chondro$clusters, mean_pm_sd)
> cluster.means <- aggregate (chondro.preproc, chondro$clusters, mean)
```

For details about the pre-processing, please refer to the example workflow in vignette ("chondro"), or the help ? chondro.

1 Predefined functions

hyperSpec comes with 6 major predefined plotting functions.
plot main switchyard for most plotting tasks
levelplot hyperSpec has a method for lattice[?] function levelplot
plotspc plots spectra
plotmat plots the spectra matrix
plotc calibration plot, time series, depth profile
plotc is a lattice function
plotmap more specialized version of levelplot for map or image plots.
plotmap is a lattice function
plotvoronoi more specialized version of plotmap that produces Voronoi tessellations.
plotvoronoi is a lattice function
plotmap, plotvoronoi, and levelplot are *lattice* functions. Therefore, in loops, functions, Sweave chunks, etc. the lattice object needs to be printed explicitly by e.g. `print (plotmap (object))` (R FAQ: Why do lattice/trellis graphics not work?).
plots the spectra, i.e. the intensities $spc$ over the wavelengths $\lambda$.

> plotspc (flu)

plots the spectra, i.e. the colour coded intensities $spc$ over the wavelengths $\lambda$ and the row number.

> plotmat (flu)

plots an intensity over a single other data column, e.g.

- calibration
- time series
- depth profile

> plotc (flu)

plots a false colour map, defined by a formula.

> levelplot (spc ~ x * y, chondro, aspect = "iso")

Warning: Only first wavelength is used for plotting
plotmap

plotmap is a specialized version of levelplot. It uses a single value (e.g., average intensity or cluster membership) over two data columns (default $x$ and $y$)

> plotmap (chondro)

plotvoronoi

Function plotvoronoi is a special version of plotmap that produces Voronoi diagram of the hyperSpec object.

> plotvoronoi (sample (chondro, 300), clusters ~ x * y)

2 Arguments for plot

hyperSpec’s plot method uses its second argument to determine which of the specialized plots to produce. This allows some handy abbreviations. All further arguments are handed over to the function actually producing the plot.

plot (x, "spc")

is equivalent to plotspc (flu)

> plot (flu, "spc")
plot (x, "spcmeansd") plots mean spectrum ± 1 standard deviation
> plot (chondro.preproc, "spcmeansd")

plot (x, "spcprctile") plots median, 16th and 84th percentile for each wavelength. For Gaussian distributed data, 16th, 50th and 84th percentile are equal to mean ± standard deviation. 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.preproc, "spcprctile")

plot (x, "spcprctl5") like "spcprct1" plus 5th and 95th percentile.
> plot (chondro.preproc, "spcprctl5")

plot (x, "c")
> plot (flu, "c") is equivalent to plotc (flu)
plots a time series plot

\[ \text{plot (laser [, , 405], "ts")} \]

 equivalent to plotc (laser, spc \sim t)

plots a depth profile plot

\[ \text{depth.profile <- new ("hyperSpec",}
\text{ + spc = as.matrix (rnorm (20) + 1:20),}
\text{ + data = data.frame (z = 1 : 20),}
\text{ + labels = list (spc = "I / a.u.",}
\text{ + z = expression (z / (\mu \text{m}))},
\text{ + .wavelength = expression (lambda)))}
\text{ > plot (depth.profile, "depth")}
\text{ the same as plotc (laser, spc \sim z)}

plots the spectra matrix.

\[ \text{plot (laser, "mat")} \]

Equivalent to

\[ \text{plotmat (laser)} \]

A lattice alternative is:

\[ \text{levelplot (spc \sim .wavelength \times .row, laser)} \]

is equivalent to plotmap (chondro)

\[ \text{plot (chondro, "map")} \]
3 Spectra

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

- **particular wavelength range**

  ```r
  > plotspc(paracetamol[, 700:1200])
  > plotspc(paracetamol[, 700:1200], x.offset = 750)
  ```

  If only one wavelength range is needed, the extract command (see vignette("introduction")) is handiest:

  ```r
  > plotspc(paracetamol[, 700:1200])
  ```

- **more wavelength ranges**

  ```r
  > plotspc(paracetamol, +
  >       wl.range = list(600:1800, 2800:3100), +
  >       x.offset = 750)
  ```

  If available, the package `plotrix[1]` is used to produce the cut mark.

- **with reversed abscissa**

  ```r
  > plotspc(paracetamol, wl.reverse = TRUE)
  ```

  ```r
  > plotspc(paracetamol, +
  >       wl.reverse = TRUE)
  ```
in different colours

use \texttt{col} = \texttt{vector.of.colours}
> \texttt{plotspc (flu, col = matlab.dark.palette (6))}

dots instead of lines

use \texttt{lines.args} = \texttt{list (pch = 20, type = "p")}
> \texttt{plotspc (paracetamol \[,, 2800 ~ 3200\],}
+ \texttt{lines.args = list (pch = 20, type = "p"))}

mass spectra

use \texttt{lines.args} = \texttt{list (type = "h")}
> \texttt{plot (barbiturates \[[1]\], lines.args = list (type = "h"))}

more spectra into an existing plot

use \texttt{add} = \texttt{TRUE}
> \texttt{plotspc (chondro \[300,,\])}
> \texttt{plotspc (chondro \[300,,\], add = TRUE, col = "blue")}
Summary characteristics

\[
\begin{array}{cccccc}
600 & 800 & 1000 & 1300 & 1600 \\
0.00 & 0.04 & 0.08 & & \\
\Delta \nu \text{ cm}^{-1} & I / \text{a.u.} & \\
\end{array}
\]

\(\Delta \nu \sim \text{cm}^{-1}
\]

\[I / \text{a.u.}
\]

\[
\begin{array}{cccc}
600 & 800 & 1000 & 1300 & 1600 \\
0.00 & 0.04 & 0.08 & & \\
\Delta \nu \text{ cm}^{-1} & I / \text{a.u.} & \\
\end{array}
\]

func may be used to calculate summary characteristics prior to plotting. To plot e.g. the standard deviation of the spectra, use:

\>
plotspc (chondro.preproc, func = sd)

with different line at \(I = 0\)

\[
\begin{array}{cccc}
0 & 500 & 1500 & 2500 \\
0 & 20000 & 50000 & \\
\Delta \nu \text{ cm}^{-1} & I / \text{a.u.} & \\
\end{array}
\]

\[\Delta \nu \sim \text{cm}^{-1} / \text{a.u.}
\]

zeroline takes a list with parameters to abline, NA suppresses the line.

\>
plotspc (paracetamol,
+
zeroline = list (col = "red"))

adding to a spectra plot

\[
\begin{array}{cccc}
404.6 & 404.9 & 405.2 & 405.5 & 405.8 \\
0 & 40000 & & & \\
\lambda / \text{nm} & I / \text{a.u.} & \\
\end{array}
\]

\[\lambda / \text{nm} \sim \text{a.u.}
\]

plotspc uses base graphics. After plotting the spectra, more content may be added to the graphic by abline, lines, points, etc.

\>
plot (laser, "spcmeansd")
>
abline (v = c(405.0063, 405.1121, 405.2885, 405.3591),
+
col = c("black", "blue", "red", "darkgreen"))

3.1 Stacked spectra

\[
\begin{array}{cccc}
1 & 2 & 3 & \\
600 & 800 & 1000 & 1300 & 1600 \\
\Delta \nu \text{ cm}^{-1} & I / \text{a.u.} & \\
\end{array}
\]

\[\Delta \nu \sim \text{cm}^{-1}
\]

\[I / \text{a.u.}
\]

use stacked = TRUE

\>
plotspc (cluster.means,
+
col = cluster.cols,
+
stacked = TRUE)
Stacking groups of spectra

The spectra to be stacked can be grouped: stacked = \texttt{factor}. Alternatively, the name of the grouping extra data column can be used:

\begin{verbatim}
> plot (cluster.meansd,
+ stacked = ".aggregate",
+ fill = ".aggregate",
+ col = cluster.cols)
\end{verbatim}

Manually giving yoffset

Stacking values can also be given manually as numeric values in yoffset:

\begin{verbatim}
> plotspc (cluster.meansd,
+ yoffset = rep (0:2, each = 3),
+ col = rep (cluster.cols, each = 3))
\end{verbatim}

Dense stacking

To obtain a denser stacking:

\begin{verbatim}
> yoffsets <- apply (cluster.means [[1]], 2, diff)
> yoffsets <- - apply (yoffsets, 1, min)
> plot (cluster.means, yoffset = c (0, cumsum (yoffsets)),
+ col = cluster.cols)
\end{verbatim}

Elaborate example

\begin{verbatim}
> yoffset <- apply (chondro.preproc, 2, quantile, c(0.05, 0.95))
> yoffset <- range (yoffset)
> plot (chondro.preproc[[1]],
+ plot.args = list (ylim = c (0, 2) * yoffset),
+ lines.args = list (type = "n"))
> yoffset <- (0:1) * diff (yoffset)
> for (i in 1 : 3){
+ plot (chondro.preproc, "spcprct15", yoffset = yoffset [i],
+ col = "gray", add = TRUE)
+ plot (chondro.preproc [[1]], yoffset = yoffset [i],
+ col = matlab.dark.palette (3) [[i]], add = TRUE,
+ lines.args = list (lwd = 2))
+ }
\end{verbatim}

\texttt{plotspc} allows fine grained customization of almost all aspects of the plot. This is possible by
giving arguments to the functions that actually perform the plotting. For setting up the plot area, lines for the plotting of the lines, axis for the axes, etc. The arguments for these functions should be given in lists as plot.args, lines.args, axis.args, etc.

4 Calibration Plots, (Depth) Profiles, and Time Series Plots

4.1 Calibration plots

Plots the Intensities of one wavelength over the concentration for univariate calibration:

```
> plotc (flu [, , 450])
```

The default is to use the first intensity only.

A function to compute a summary of the intensities before drawing can be used:

```
> plotc (flu, func = range, groups = .wavelength)
```

If func returns more than one value, the different results are accessible by .wavelength.

Conditioning: plotting more traces separately

```
> plotc (flu [, c (405, 445)], spc ~ c | .wavelength,
+     cex = .3, scales = list (alternating = c(1, 1)))
```
Grouping: plot more traces in one panel

> plotc (flu [, c (405, 445)], groups = .wavelength)

Changing Axis Labels (and other parameters)

Arguments for xyplot can be given to plotc:
> plotc (flu [, 450],
  + ylab = expression (I ["450 nm"] / a.u.),
  + xlim = range (0, flu$c + .01),
  + ylim = range (0, flu$spc + 10),
  + pch = 4)

Adding things to the plot: customized panel function

As plotc uses the lattice function xyplot, additions to the plot must be made via the panel function:
> panelcalibration <- function (x, y, ..., clim = range (x), level = .95) {
  + panel.xyplot (x, y, ...)
  + lm <- lm (y ~ x)
  + panel.abline (coef (lm), ...)
  + cx <- seq (clim [1], clim [2], length.out = 50)
  + cy <- predict (lm, data.frame (x = cx),
    + interval = "confidence",
    + level = level)
  + panel.lines (cx, cy [,2], col = "gray")
  + panel.lines (cx, cy [,3], col = "gray")
  + }
> plotc (flu [,405], panel = panelcalibration,
  + pch = 4, clim = c (0, 0.35), level = .99)

4.2 Time series and other Plots of the Type Intensity-over-Something
Abscissae other than c

Other abscissae may be specified by explicitly giving the model formula:

```r
> plotc (laser [, , c(405.0063, 405.1121, 405.2885, 405.3591)],
+     spc ~ t,
+     groups = .wavelength,
+     type = "b",
+     col = c ("black", "blue", "red", "darkgreen"))
```

5 Levelplot

`hyperSpec`'s levelplot can use two special column names:

- `.wavelength` for the wavelengths
- `.row` for the row index (i.e. spectrum number) in the data

Besides that, it behaves exactly like `levelplot`. Particularly, the data is given as the second argument:

```r
> levelplot (spc ~ x * y, chondro)
```

Factors as z

If the colour-coded value is a factor, the display is adjusted to this fact:

```r
> levelplot (clusters ~ x * y, chondro)
```

6 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 can be done by `plot (object, "mat")`. The actual plotting is done by `image`, but `levelplot`
can produce spectra matrix plots as well and these plots can be grouped or conditioned.

**different palette**

> plot (laser, "mat", col = heat.colors (20))
> plotmat (laser, col = heat.colors (20))

**different y axis**

Using a different extra data column for the y axis:
> plotmat (laser, y = "t")
alternatively, y values and axis label can be given separately.
> plotmat (laser, y = laser$t, ylab = labels (laser, "t"))

**contour lines**

Contour lines may be added:
> plotmat (flu, col = "white",
>         contour = TRUE, add = TRUE)
> plotmat (flu, col = matlab.dark.palette (20))
> plotmat (flu, col = "white",
>         contour = TRUE, add = TRUE)

**colour-coded points: levelplot with special panel function**

> require ("latticeExtra")
> barb <- do.call (collapse, barbiturates[1:50])
> barb <- orderwl (barb)
> levelplot (spc ~ .wavelength * z, barb,
>         panel = panel.levelplot.points,
>         cex = .5, col.symbol = NA,
>         colregions = matlab.palette)
7 False-Colour Maps: plotmap

plotmap is a specialized version of levelplot. The spectral intensities may be summarized by a function before plotting (default: mean). The same scale is used for x and y axes (aspect = "iso").

plotting map

> plotmap (chondro)

plotting maps with other than x and y

specify the colour-coded variable, abscissa and ordinate as formula: colour.coded ~ abscissa * ordinate

> plotmap (chondro, spc ~ y * x)

colour-coded factors

> plotmap (chondro, clusters ~ x * y)

If the colour-coded variable is a factor, each level gets its own colour, and the legend is labeled accordingly.

different palette

To plot with a different palette, use argument col.regions.

> plotmap (chondro, clusters ~ x * y, 
+ col.regions = cluster.cols)
Fine tuning lattice parameters

The plotting of color maps is done via R package `lattice` (aka Trellis graphic approach), which is highly customizable. Use `trellis.par.get` and `trellis.par.set` to get/set the settings for the current graphics device.

```r
> my.theme = trellis.par.get()
> names(my.theme)    # note how many parameters are tunable
[1] "grid.pars" "fontsize" "background" "panel.background"
[5] "clip" "add.line" "add.text" "plot.polygon"
[9] "dot.symbol" "box.rectangle" "box.umbrella" "dot.line"
[13] "strip.background" "strip.shingle" "strip.border" "superpose.line"
[17] "superpose.symbol" "superpose.polygon" "regions" "shade.colors"
[21] "axis.line" "axis.text" "axis.components" "layout.heights"
[25] "layout.widths" "box.3d" "par.xlab.text" "par.ylab.text"
[29] "par.zlab.text" "par.main.text" "par.sub.text"
```

Any of these parameters can be fine-tuned to produce the desired output. For example, parameter `my.theme$region` is responsible for the appearance of color maps, and it contains elements `$alpha` and `$col`. By changing this parameters you can create your own theme for plotting and pass it to the plotting function via `par.settings`.

This plot uses a customized lattice theme.

```r
> my.theme$regions$col = grDevices::terrain.colors
> plotmap (chondro, par.settings = my.theme)
```

It is possible to persistently (i.e. inside of the current R session) set `lattice` parameters, so they would apply to all further plots. This is done via a call to `trellis.par.set`, for example `trellis.par.set(my.theme)`.

The current settings can be visualized via a call to `show.settings()`.

```r
> # Display current trellis parameters
> show.settings()
```
An overview of different color palettes, and ways to create your own, can be found in the R color cheatsheet.

To plot a map of the average intensity at particular wavelengths use extraction:

```r
> plotmap (chondro.preproc [, , c(728, 782, 1098, 1240, 1482, 1577)],
+ col.regions = matlab.palette)
```

Conditioning on wavelengths

```r
> plotmap (chondro,
+ spc ~ y * x | x > 5,
+ col.regions = matlab.palette(20))
```

Conditioning on `.wavelength`

```r
> pca <- prcomp (~ spc, data = chondro.preproc$.)
> scores <- decomposition (chondro, pca$x,
+ label.wavelength = "PC",
+ label.spc = "score / a.u."
)
> plotmap (scores [,1:2],
+ spc ~ y * x | as.factor(.wavelength),
+ func = NULL,
+ col.regions = matlab.palette(20))
```

plotmap automatically applies the function in `func` before plotting. This defaults to the `mean`. In order to suppress this, use `func = NULL`. This allows conditioning on the wavelengths.

To plot e.g. the first two score maps of a principal component analysis:

```r
> pca <- prcomp (~ spc, data = chondro.preproc$.)
> scores <- decomposition (chondro, pca$x,
+ label.wavelength = "PC",
+ label.spc = "score / a.u."
)
> plotmap (scores [,1:2],
+ spc ~ y * x | as.factor(.wavelength),
+ func = NULL,
+ col.regions = matlab.palette(20))
```
Conditioning on wavelength II

Alternatively, use `levelplot` directly:

```r
> levelplot (spc ~ y * x | as.factor(.wavelength),
+     scores [,1:2],
+     aspect = "iso",
+     col.regions = matlab.palette(20))
```

Voronoi plot

Voronoi uses `panel.voronoi` from `latticeExtra[2]`. The tessellation is calculated by default using `deldir[3]`, but `tripack[4]` can also be used. `tripack` seems to faster in general, but may “hang” with certain data sets (particularly regular grids with missing spectra as in this example). Furthermore, it is not FOSS (free and open source software), so users are kindly asked to review `tripack`’s license before using it.

Mark missing spectra

If the spectra come from a rectangular grid, missing positions can be marked with this panel function:

```r
> mark.missing <- function (x, y, z, ...){
+     panel.levelplot (x, y, z, ...)
+     miss <- expand.grid (x = unique (x), y = unique (y))
+     miss <- merge (miss, data.frame (x, y, TRUE),
+                     all.x = TRUE)
+     miss <- miss [is.na (miss[, 3]),]
+     panel.xyplot (miss [, 1], miss [, 2], pch = 4, ...)
+ }
> plotmap (sample (chondro, length(chondro) - 20),
+          col.regions = matlab.palette(20),
+          col = "black",
+          panel = mark.missing)
```

Unevenly spaced measurement grid

The panel function used by `plotmap` defaults to `panel.levelplot.raster` which assumes an evenly spaced measurement grid. Even if the spectra are measured on a nominally evenly spaced grid, the actual stage position may be slightly varying due to positioning inaccuracy and some manufacturers (e.g. Kaiser) record the position reported by the stage rather than the position requested by the stage control.
This leads to weird looking output with holes, and possibly wrong columns:

```
> plotmap (uneven)
```

The symptom of this situation are warnings about values in x and/or y not being equispaced; and that the output therefore may be wrong.

One possibility to obtain a correct map is using `plotvoronoi` instead which will construct a mosaic-like image with the respective “pixel” areas being centered around the actually recorded $x$ and $y$ position:

```
> plotvoronoi (uneven)
```

Another possibility that underlines a point shape of the measurements is switching to `latticeExtra::panel.levelplot.points`:

```
> plotmap (uneven, panel = panel.levelplot.points,
      + cex = 0.75, col.symbol=NA)
```

Alternatively, the measurement raster positions can be rounded to their nominal raster, e.g.:

```
> rx <- makeraster (uneven$x, start = -11.55, d = 1, tol = 0.3)
> uneven$x <- rx$x
> ry <- makeraster (uneven$y, start = -4.77, d = 1, tol = 0.3)
> uneven$y <- ry$y
> plotmap (uneven)
```

8 3D plots (with rgl)
rgl[5] offers fast 3d plotting in R. As rgl’s axis annotations are sometimes awkward, they may better be set manually:

```r
> laser <- laser [, , 404.8:405.6] / 10000
> laser$t <- laser$t / 3600
> cols <- rep(matlab.palette(nrow(laser)), nwl(laser))
> surface3d(y = wl(laser), x = laser$t, z = laser$spc, col = cols)
> aspect3d(c(1, 1, 0.25))
> axes3d(c('x+-', 'y--', 'z--'))
> axes3d('y--', nticks = 25, labels = FALSE)
> mtext3d('t / h', 'x+-', line = 2.5)
> mtext3d('lambda / nm', 'y--', line = 2.5)
```

9 Using ggplot2 with hyperSpec objects

hyperSpec objects do not yet directly support plotting with ggplot2[6]. Nevertheless, ggplot2 graphics can easily be obtained, and qplot* equivalents to plotspc and plotmap are defined:

```
plot spectra with as.long.df

> qplotspc (flu) + aes (colour = c)

Map with ggplot2

> qplotmap (chondro) +
  + scale_fill_gradientn("spc", colours = matlab.palette ())
```

The two special columns .wavelength and .rownames contain the wavelength axis and allow to distinguish the spectra.

For more general plotting, as.long.df transforms a hyperSpec object into a long-form data.frame that is suitable for qplot, while as.t.df produces a data.frame where each spectrum is one column, and an additional first column gives the wavelength (see “plotting mean ± sd” below for an example).
Long data frames can be very memory consuming as they are of size \( nrow \cdot nwl \times (ncol + 2) \) with respect to the dimensions of the hyperSpec object. Thus, e.g. the chondro data set (2 MB) as hyperSpec object) needs 28 MB as long-format data.frame. It is therefore highly recommended to calculate the particular data to be plotted beforehand.

Mean ± standard deviation with ggplot2

\[
\begin{align*}
  &> \text{qplotspc (mean (chondro)) +} \\
  &\quad \text{geom_ribbon (aes (ymin = mean + sd,} \\
  &\quad \quad \text{ymax = mean - sd,} \\
  &\quad \quad \text{y = 0, group = NA),} \\
  &\quad \text{alpha = 0.25,} \\
  &\quad \text{data = as.t.df (mean_sd (chondro)))}
\end{align*}
\]

Note that qplotspc specifies aesthetics \( y = \text{spc} \) and \( \text{groups = .rownames} \), which do not have corresponding columns in the data.frame returned by as.t.df. These aesthetics must therefore be set manually in the aesthetics definition in geom_ribbon (or any other geom_ that uses as.t.df). Otherwise, errors occur that object spc (and/or .rownames) cannot be found.

Cut spectra with ggplot2

Cut axes can be implemented by faceting:

\[
\begin{align*}
  &> \text{qplotspc (paracetamol / 1e4,} \\
  &\quad \text{wl.range = c ( min ~ 1800, 2800 ~ max)) +} \\
  &\quad \text{scale_x_continuous (breaks = seq (0, 3200, 400))}
\end{align*}
\]

10 Troubleshooting

10.1 No output is produced

plotmap, plotvoronoi, levelplot, and plotc use lattice functions. 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?). The same holds for ggplot2 graphics.

For suggestions how the lattice functions can be redefined so that the result is printed without external print command, see the file vignettes.defs.

11 Interactive Graphics

hyperSpec offers basic interaction, spc.identify for spectra plots, and map.identify and map.sel.poly for maps. The first two identify points in spectra plots and map plots, respectively. map.sel.poly selects the part of a hyperSpec object that lies inside the user defined polygon.
11.1 spc.identify: finding out wavelength, intensity and spectrum

spc.identify allows to measure points in graphics produced by plottspc. It works correctly with reversed and cut wavelength axes.

> spc.identify (plotspc (paracetamol, wl.range = c (600 ~ 1800, 2800 ~ 3200), xoffset = 800))

The result is a data.frame with the indices of the spectra, the wavelength, and its intensity.

11.2 map.identify: finding a spectrum in a map plot

map.identify returns the spectra indices of the clicked points.

> map.identify (chondro)

11.3 map.sel.poly: selecting spectra inside a polygon in a map plot

map.sel.poly returns a logical indicating which spectra are inside the polygon drawn by the user:

> map.sel.poly (chondro)

11.4 Related functions provided by base graphics and lattice

For base graphics (as produced by plottspc), locator may be useful as well. It returns the clicked coordinates. Note that these are not transformed according to xoffset & Co.

For lattice graphics, grid.locator may be used instead. If it is not called in the panel function, a preceding call to trellis.focus is needed:

> plot (laser, "mat")
> trellis.focus ()
> grid.locator ()

identify (or panel.identify for lattice graphics) allows to identify points of the plot directly. Note that the returned indices correspond to the plotted object.

References

Session Info

sysname "Linux"
release "4.15.0-76-generic"
version "#86-Ubuntu SMP Fri Jan 17 17:24:28 UTC 2020"
nodename "cx17007"
machine "x86_64"
login "unknown"
user "cb"
effective_user "cb"

R version 3.6.2 (2019-12-12)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 18.04.4 LTS

Matrix products: default
BLAS: /usr/lib/x86_64-linux-gnu/openblas/libblas.so.3
LAPACK: /usr/lib/x86_64-linux-gnu/libopenblaslapack.so.0

locale:
[1] LC_CTYPE=de_DE.UTF-8 LC_NUMERIC=C LC_TIME=de_DE.UTF-8
[4] LC_COLLATE=C LC_MONETARY=de_DE.UTF-8 LC_MESSAGES=de_DE.UTF-8
[7] LC_PAPER=de_DE.UTF-8 LC_NAME=C LC_ADDRESS=C
[10] LC_TELEPHONE=C LC_MEASUREMENT=de_DE.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] tools grid stats graphics grDevices utils datasets methods base

other attached packages:
[1] latticeExtra_0.6-28 RColorBrewer_1.1-2 baseline_1.2-2 MASS_7.3-51.5
[5] hyperSpec_0.99-20200213 xml2_1.2.2 ggplot2_3.2.1 lattice_0.20-38

loaded via a namespace (and not attached):
[1] tidyselect_0.2.5 xfun_0.11 reshape2_1.4.3 purrr_0.3.3
[5] colorspace_1.4-1 testthat_2.3.1 miniUI_0.1.1.1 htmltools_0.4.0
[9] rlang_0.4.2 R.oo_1.23.0 manipulateWidget_0.10.0 pillar_1.4.2
[13] later_1.0.0 glue_1.3.1 withr_2.1.2 R.utils_2.9.2
[17] plyr_1.8.5 R.cache_0.14.0 lifecycle_0.1.0 stringr_1.4.0
[21] munsell_0.5.0 gtable_0.3.0 R.methodsS3_1.17.1 htmlwidgets_1.5.1
[25] mvtnorm_1.0-11 labeling_0.3 knitr_1.26 fastmap_1.0.1
[29] SparseM_1.78 httpuv_1.5.2 crosstalk_1.0.0 Rcpp_1.0.3
[33] tibble_1.8-4 scales_1.1.0 promises_1.1.0 plotrix_3.7-7
[37] webshot_0.5.2 jsonlite_1.6 delimr_0.1-23 mime_0.7
[41] farver_2.0.1 R.rsp_0.43.2 digest_0.6.23 stringi_1.4.3
[45] dplyr_0.8.3 shiny_1.4.0 magrittr_1.5 lazyeval_0.2.2
[49] tibble_2.1.3 crayon_1.3.4 pkgconfig_2.0.3 assertthat_0.2.1
[53] R6_2.4.1 compiler_3.6.2