

Package: hyperSpec (via r-universe)

September 27, 2026

Encoding UTF-8

Type Package

Title Work with Hyperspectral Data, i.e. Spectra + Meta Information
(Spatial, Time, Concentration, ...)

Version 0.200.0.9000

Date 2024-05-01

Description Comfortable ways to work with hyperspectral data sets,
i.e. spatially or time-resolved spectra, or spectra with any
other kind of information associated with each of the spectra.
The spectra can be data as obtained in XRF, UV/VIS,
Fluorescence, AES, NIR, IR, Raman, NMR, MS, etc. More
generally, any data that is recorded over a discretized
variable, e.g. absorbance = f(wavelength), stored as a vector
of absorbance values for discrete wavelengths is suitable.

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LazyLoad yes

LazyData yes

Additional_repositories <https://r-hyperspec.github.io/pkg-repo/>

Depends R (>= 3.6.0), lattice, grid, ggplot2 (>= 2.3.0)

Imports dplyr, hySpc.testthat, latticeExtra (>= 0.6-30), lazyeval,
methods, rlang, utils, xml2

Suggests baseline, bookdown, caTools, colorspace, covr, digest,
kableExtra, knitr, MASS, matrixStats, mvtnorm, plotrix, pls,
R.matlab, reshape, reshape2, rgl, rmarkdown, sessioninfo, sp,
styler, tibble, vdiff (>= 1.0.0)

URL <https://r-hyperspec.github.io/hyperSpec>,
<https://github.com/r-hyperspec/hyperSpec>

BugReports <https://github.com/r-hyperspec/hyperSpec/issues>

VignetteBuilder knitr

RoxygenNote 7.3.3

Roxygen list(markdown = TRUE)

Collate 'hy_validate.R' 'hyperspec-class.R' 'paste_row.R' 'expand.R'
 'Arith.R' 'Compare.R' 'DEPRECATED-chk.hy.R'
 'DEPRECATED-count_lines.R' 'DEPRECATED-dist_pearson.R'
 'hy_options.R' 'constants-regexps.R' 'extract_numbers.R'
 'DEPRECATED-extract_numbers.R' 'DEPRECATED-ggplot2.R'
 'DEPRECATED-hy_options.R' 'DEPRECATED-isample.R'
 'mark_groups_in_dendrogram.R' 'DEPRECATED-mark.dendrogram.R'
 'mark_peak.R' 'DEPRECATED-markpeak.R'
 'DEPRECATED-normalize01.R' 'raster.R' 'DEPRECATED-plotc.R'
 'DEPRECATED-plotmap.R' 'DEPRECATED-plotmat.R'
 'DEPRECATED-plotspc.R' 'DEPRECATED-plotvoronoi.R'
 'cov_pooled.R' 'DEPRECATED-pooled.cov.R' 'DEPRECATED-raster.R'
 'DEPRECATED-read.ENVI.R' 'DEPRECATED-read.ENVI.HySpex.R'
 'DEPRECATED-read.ENVI.Nicolet.R'
 'spc_io_postprocess_optional.R' 'DEPRECATED-read.txt.Witec.R'
 'DEPRECATED-read.asc.Andor.R'
 'DEPRECATED-read.asc.PerkinElmer.R' 'DEPRECATED-read.ini.R'
 'DEPRECATED-read.jdx.R' 'DEPRECATED-read.mat.Cytospec.R'
 'DEPRECATED-read.mat.Witec.R' 'DEPRECATED-read.spc.Kaiser.R'
 'DEPRECATED-read.spc.R' 'DEPRECATED-read.spe.R'
 'DEPRECATED-read.txt.Horiba.R' 'DEPRECATED-read.txt.Renishaw.R'
 'DEPRECATED-read.txt.Shimadzu.R' 'DEPRECATED-read.txt.long.R'
 'DEPRECATED-read.txt.wide.R' 'DEPRECATED-scan.R'
 'identify_spc.R' 'DEPRECATED-spc.identify.R'
 'DEPRECATED-spc_bin.R' 'spc_fit_poly.R'
 'DEPRECATED-spc_fit_poly.R' 'DEPRECATED-spc_fix_colnames.R'
 'DEPRECATED-spc_loess.R' 'DEPRECATED-spc_na_approx.R'
 'spc_rubberband.R' 'DEPRECATED-spc_rubberband.R'
 'DEPRECATED-spc_spline.R' 'DEPRECATED-stacked.offsets.R'
 'DEPRECATED-wc.R' 'DEPRECATED-wl_convert_units.R' 'wl_eval.R'
 'DEPRECATED-wl_eval.R' 'DEPRECATED-wl_sort.R'
 'DEPRECATED-write_txt_long.R' 'DEPRECATED-write_txt_wide.R'
 'Math.R' 'Summary.R' 'aggregate.R' 'all.equal.R' 'apply.R'
 'as.data.frame.R' 'as_hyperSpec.R' 'barbiturates.R' 'bind.R'
 'colMeans.R' 'collapse.R' 'decomposition.R' 'dim.R'
 'dimnames.R' 'dist_pearson.R' 'droplevels.R' 'empty.R' 'wl2i.R'
 'extract.R' 'initialize.R' 'faux_cell.R' 'flu.R'
 'generate-test-data.R' 'hy_attach.R' 'hy_auto_completion.R'
 'hy_browse_homepage.R' 'hy_deprecation-messages.R'
 'hy_list_available_hySpc_packages.R'
 'hy_list_installed_hySpc_packages.R' 'hy_paste_names.R'
 'paracetamol.R' 'laser.R' 'hyperspec-package.R' 'labels.R'
 'plot_map.R' 'levelplot.R' 'map_identify.R' 'mean_sd.R'
 'merge.R' 'mergeextra.R' 'normalize_01.R'
 'palette_colorblind.R' 'palette_matlab.R' 'plot.R'
 'plot_and_get.R' 'plot_c.R' 'plot_mat.R' 'plot_spc.R'
 'plot_voronoi.R' 'quantile.R' 'rbind.fill.R' 'read_txt_long.R'

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'read_txt_wide.R' 'replace.R' 'rmmvnorm.R' 'sample.R' 'scale.R'
'seq.R' 'show.R' 'spc_bin.R' 'spc_fix_colnames.R' 'spc_loess.R'
'spc_na_approx.R' 'spc_spline.R' 'split.R' 'subset.R' 'sweep.R'
'trellis_factor_key.R' 'vandermonde.R' 'wl.R'
'wl_fix_unit_name.R' 'wl_convert_units.R'
'wl_create_label_from_units.R' 'wl_sort.R' 'write_txt_long.R'
'write_txt_wide.R' 'zzz.R'
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Config/pak/sysreqs cmake make libjpeg-dev libpng-dev libuv1-dev libxml2-dev

Repository <https://r-hyperspec.r-universe.dev>

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RemoteUrl <https://github.com/r-hyperspec/hyperspec>

RemoteRef HEAD

RemoteSha 8f875352f6eaf092e27e777303ad488f0b141c4d