Package 'LCF'

October 12, 2022

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Title Linear Combination Fitting
Version 1.7.0
Date 2017-11-22
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Description Baseline correction, normalization and linear combination fitting (LCF) of X-ray absorption near edge structure (XANES) spectra. The package includes data loading of .xmu files exported from 'ATHENA' (Ravel and Newville, 2005) <doi:10.1107 s0909049505012719="">. Loaded spectra can be background corrected and all standards can be fitted at once. Two linear combination fitting functions can be used: (1) fit_athena(): Simply fitting combinations of standards as in ATHENA, (2) fit_float(): Fitting all standards with changing baseline correction and edgestep normalization parameters.</doi:10.1107>
Depends R (>= $3.2.1$)
License GPL-3
Imports quadprog
Repository CRAN
LazyData true
RoxygenNote 6.0.1
NeedsCompilation no
Date/Publication 2017-11-22 14:10:01 UTC
R topics documented:
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bkg_corr

Background correction function

Description

This function allows you to base-line correct and edge-step normalize XANES spectra (background correction). Raw spectra are loaded, then base-line corrected and edge-step normalized. The spectrum is flattened after E0. The function returns the corrected, normalized and flattened spectrum

Usage

```
bkg_corr(raw.spec, corr.norm)
```

Arguments

raw.spec Raw spectrum

corr.norm Vector of the base-line correction and edge-step normalization values (vector of

length 4)

Examples

```
data(stdmix)
corr.spec.samples <- initial_load(specdat[5:8],
   corr.norm = c(-36, -15, 37, 58))
corr.spec <- bkg_corr(raw.spec = corr.spec.samples[[1]],
   corr.norm = c(-36, -15, 37, 58))
print(corr.spec)</pre>
```

fit_athena

Porting of 'ATHENA' linear combination fitting

Description

The function can be used to check which combinations of standards produce a good fit and if output from 'ATHENA' is similar.

Usage

```
fit_athena(all.samples, all.standards, LC.vals, amoSTD, ex.smaller = NULL,
  file.output = NULL, best.fits = NULL)
```

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Arguments

all.samples	List of all samples
all.standards	List of all standards
LC.vals	The fitting range values for the linear combination fitting
amoSTD	Use at most X standards
ex.smaller	Exclude portions smaller than a given value (decimal form), default to NULL
file.output	Possibility to have a file output, default to NULL
best.fits	Possibility to output more than the best fit (e.g. the first 10 best fits), default to 1

Examples

```
data(stdmix)
corr.spec.standards <- initial_load(specdat[1:4],
    corr.norm = c(-36, -15, 37, 58))
corr.spec.samples <- initial_load(specdat[5:8],
    corr.norm = c(-36, -15, 37, 58))
athena.fit <- fit_athena(all.samples = corr.spec.samples,
    all.standards = corr.spec.standards, LC.vals = c(-14, 46), amoSTD = 4)
## exclude portions smaller 5% = 0.05
athena.fit.exlcude <- fit_athena(all.samples = corr.spec.samples,
    all.standards = corr.spec.standards,
    LC.vals = c(-14, 46), amoSTD = 4, ex.smaller = 0.05)</pre>
```

fit_float

Central fitting function with float environment

Description

This function allows to process all samples, especially written for the float environment.

Usage

```
fit_float(all.samples, all.standards, LC.vals, float, ex.smaller = NULL,
  file.output = NULL, best.fits = NULL)
```

Arguments

all.samples	List of all samples
all.standards	List of all standards
LC.vals	The fitting range values for the linear combination fitting
float	Let vary the energy range parameters
ex.smaller	Exclude portions smaller than a given value (decimal form), default to NULL
file.output	Possibility to have a file output, default to NULL
best.fits	Possibility to output more than the best fit (e.g. the first 10 best fits), default to

1

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Examples

```
data(stdmix)
corr.spec.standards <- initial_load(specdat[1:4],</pre>
  corr.norm = c(-36, -15, 37, 58))
corr.spec.samples <- initial_load(specdat[5:8],</pre>
  corr.norm = c(-36, -15, 37, 58))
## Select parameters for baseline correction and edge-step normalization
param.float <- expand.grid(pre.adj.1 = seq(-42, -30, 6),
  pre.adj.2 = seq(-19, -9, 5), post.adj.1 = seq(35, 40, 5),
  post.adj.2 = seq(50,65,5))
length(param.float[,1])
float.fit <- fit_float(all.samples = corr.spec.samples,</pre>
  all.standards = corr.spec.standards,
  LC.vals = c(-14, 46), float = param.float, best.fits = 20)
print(float.fit)
###### Using next configuration can be very time consuming
param.float.2 <- expand.grid(pre.adj.1 = seq(-43,-30,1),
  pre.adj.2 = seq(-19, -9, .5), post.adj.1 = seq(34, 40, .5),
  post.adj.2 = seq(50,65,1))
```

initial_load

Initial loading of spectra

Description

This function loads and initially normalizes the raw spectra. Output is a list with the raw and initially corrected spectra.

Usage

```
initial_load(raw.spec = NULL, file = NULL, corr.norm, use.eshift = NULL)
```

Arguments

raw.spec List of files already loaded with read_raw_spec()

file Vector with file names

corr.norm Initial correction and normalization parameters

use.eshift Set TRUE, if using energy shift value, defaults to NULL

```
data(stdmix)
corr.spec.standards <- initial_load(specdat[1:4],
  corr.norm = c(-36, -15, 37, 58))
corr.spec.samples <- initial_load(specdat[5:8],
  corr.norm = c(-36, -15, 37, 58))</pre>
```

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LCF_solve_QP

Linear combination fitting solve function

Description

Quadratic programming solution function for linear combination fitting (LCF)

Usage

```
LCF_solve_QP(LCF.stds, LCF.samp)
```

Arguments

LCF.stds Standards for LCF
LCF.samp Sample for LCF

```
data(stdmix)
corr.spec.standards <- initial_load(specdat[1:4],</pre>
  corr.norm = c(-36, -15, 37, 58))
corr.spec.samples
                     <- initial_load(specdat[5:8],</pre>
  corr.norm = c(-36, -15, 37, 58))
fit.standards <- std_df(sample = corr.spec.samples[[1]],</pre>
  all.standards = corr.spec.standards)
corr.spec <- bkg_corr(raw.spec = corr.spec.samples[[1]],</pre>
  corr.norm = c(-36, -15, 37, 58))
## set fitting range parameters relative to E zero
E.zero <- corr.spec.samples[[1]]$data$E0</pre>
LC.pre <- -14
LC.post <- 46
## find ranges that have to be fitted
abs.pre <- abs(corr.spec[["energy"]]-(E.zero+LC.pre))</pre>
abs.post <- abs(corr.spec[["energy"]]-(E.zero+LC.post))</pre>
range.pre <- which(abs.pre == min(abs.pre))</pre>
range.post <- which(abs.post == min(abs.post))</pre>
## extract standards and sample in given range
LC.sample <- corr.spec["cor.absorption"][range.pre:range.post,]</pre>
LC.standards <- fit.standards[range.pre:range.post,]</pre>
## actual fitting
fit.result <- LCF_solve_QP(LCF.stds = LC.standards, LCF.samp = LC.sample)</pre>
print(fit.result)
```

plot_LCF

LC_fit

Linear combination fitting function

Description

This function performs the LC fitting of the input sample/samples. It outputs the fitting results with the R-Factors as fitting statistics.

Usage

```
LC_fit(sample, standards, LC.vals, float = NULL, E.zero = NULL,
ex.smaller = NULL)
```

Arguments

sample	The sample spectrum
standards	The standards spectra
LC.vals	Values for ranges of linear combination fitting, with respect to the edge-step
float	Set float parameters, defaults to NULL
E.zero	Set E0, defaults to NULL
ex.smaller	Set value to exclude small portions (as portion of 1), defaults to NULL

Examples

```
data(stdmix)
corr.spec.standards <- initial_load(specdat[1:4],
   corr.norm = c(-36, -15, 37, 58))
corr.spec.samples <- initial_load(specdat[5:8],
   corr.norm = c(-36, -15, 37, 58))
fit.standards <- std_df(sample = corr.spec.samples[[1]],
   all.standards = corr.spec.standards)
fit.result <- LC_fit(sample = corr.spec.samples[[1]],
   standards = fit.standards, LC.vals = c(-14, 46))
print(fit.result)</pre>
```

plot_LCF

Plot sample data, linear combination fit and residual spectrum

Description

This function allows plotting (png or tiff image files) of the corrected sample spectrum, the linear combination fit and the residual.

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Usage

```
plot_LCF(all.samples, all.standards, LCF.res, LC.vals, corr.norm,
  float = NULL, exclude = NULL, use.tiff = NULL, E.zero = NULL,
  set.plot.ymax = NULL, file.output = NULL)
```

Arguments

all.samples	List of all samples
all.standards	List of all standards
LCF.res	Results from function fit_float()
LC.vals	The fitting range values for the linear combination fitting
corr.norm	Vector of the base-line correction and edge-step normalization values (vector of length 4)
float	Logical, default to FALSE
exclude	Logical, default to FALSE
use.tiff	Logical, default to FALSE
E.zero	Set E0, defaults to NULL
set.plot.ymax	Set maximum of plot y axis, defaults to NULL
file.output	Logical, default to FALSE

```
data(stdmix)
corr.spec.standards <- initial_load(specdat[1:4],</pre>
  corr.norm = c(-36, -15, 37, 58))
corr.spec.samples <- initial_load(specdat[5:8],</pre>
  corr.norm = c(-36, -15, 37, 58))
param.float <- expand.grid(pre.adj.1 = seq(-45, -30, 5),
  pre.adj.2 = seq(-19, -9, 5), post.adj.1 = seq(34, 40, 2),
  post.adj.2 = seq(50,65,5))
float.fit <- fit_float(all.samples = corr.spec.samples[1],</pre>
  all.standards = corr.spec.standards, LC.vals = c(-14, 46),
  float = param.float, ex.smaller = 0.05)
par(pty="s")
plot_LCF(all.samples = corr.spec.samples[1],
  all.standards = corr.spec.standards,
  LCF.res = float.fit[1,], LC.vals = c(-14,46),
  corr.norm = c(-36, -15, 37, 58))
```

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read_raw_spec

Read raw spectra

Description

This function reads the raw .xmu file, extracts E0 and energy shift and returns a list with name, E0, energy shift, and the raw spectrum

Usage

```
read_raw_spec(file, use.eshift = NULL)
```

Arguments

file

The raw .xmu file

use.eshift

Set TRUE, if using energy shift value, defaults to NULL

Examples

```
## any .xmu file as output from ATHENA (>=0.9.25)
```

specdat

Phosphorus K-edge XANES spectral data for LCF

Description

Data from an experiment on the quality of XANES spectrscopy for phosphorus speciation

Usage

```
data(stdmix)
```

Format

List of four standard spectra comounds and four spectra of mixtures of these standard compounds, output objects of function read_raw_spec().

References

```
Werner & Prietzel 2015, Environ. Sci. Technol. (49), 10521-10528 (DOI)
```

```
data(stdmix)
specdat[[1]]
specdat[[5]]
```

std_df

std_df

Create a data frame of all standards

Description

The function creates a data frame with all standards in one data frame. The data frame has the same energy values as the sample that is loaded.

Usage

```
std_df(sample, all.standards)
```

Arguments

```
sample A raw sample all.standards List of all standards
```

```
data(stdmix)
corr.spec.standards <- initial_load(specdat[1:4],
   corr.norm = c(-36, -15, 37, 58))
corr.spec.samples <- initial_load(specdat[5:8],
   corr.norm = c(-36, -15, 37, 58))
fit.standards <- std_df(sample = corr.spec.samples[[1]],
   all.standards = corr.spec.standards)
print(fit.standards)</pre>
```

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