

# Package ‘PbPbRedux’

October 5, 2021

**Title** Pb-Pb data processing for meteorite geochronology

**Version** 0.1

**Description** The Pb-budget of meteorites consists of extraterrestrial and terrestrial components. The two components can be separated by spiking the sample with a solution that contains synthetic Pb-202 and Pb-205. The spike serves two purposes. First, the Pb-205 in it is used as a tracer to compare the sample (which is a mixture of extraterrestrial and terrestrial Pb) with a blank solution (which contains only terrestrial Pb). Second, if the true Pb-205/Pb-202 ratio of the spike is known, then this can be used to correct for mass-dependent fractionation. The package performs all these calculations in logratio space, so as to reduce the skewness of the mass spectrometer noise. It uses a maximum likelihood approach to ensure that blank corrections cannot result in negative values.

**License** `use\_gpl3\_license()`

**Depends** R (>= 3.1.0), IsoplotR

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

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## Description

High level function that takes samples, blanks and spikes as input and produces a table of Pb/Pb ratios, uncertainties and error correlations as output

**Usage**

```
process(samples, blanks, spikes, cblanks)
```

**Arguments**

<code>samples</code>	data frame with sample data. For an example, see <code>system.file("samples1.csv", package="PbPbRedux")</code>
<code>blanks</code>	data frame with blank data. For an example, see <code>system.file("blanks1.csv", package="PbPbRedux")</code>
<code>spikes</code>	data frame with spike data. For an example, see <code>system.file("spikes.csv", package="PbPbRedux")</code>
<code>cblanks</code>	data frame with replicate blank data. For an example, see <code>system.file("blanks2.csv", package="PbPbRedux")</code>

**Value**

a table with Pb concentrations, Pb/Pb ratios and error correlations

**Examples**

```
library(PbPbRedux)

s1 <- system.file("samples1.csv", package="PbPbRedux")
s2 <- system.file("samples2.csv", package="PbPbRedux")
b1 <- system.file("blanks1.csv", package="PbPbRedux")
b2 <- system.file("blanks2.csv", package="PbPbRedux")
sp <- system.file("spikes.csv", package="PbPbRedux")

spikes <- read.csv(sp, header=TRUE)

# example 1: all samples use the same blank:
samples <- read.csv(s1, header=TRUE)
blanks <- read.csv(b1, header=TRUE)
tab <- process(samples, blanks, spikes)

# example 2: each aliquot has its own blank:
samples <- read.csv('s2.csv', header=TRUE)
blanks <- read.csv('b2.csv', header=TRUE)
tab <- process(samples, blanks, spikes)

# example 3: individual blanks with shared covariance matrix:
samples <- read.csv('s2.csv', header=TRUE)
cblanks <- read.csv('b1.csv', header=TRUE)
blanks <- read.csv('b2.csv', header=TRUE)
tab <- process(samples, blanks, spikes, cblanks)
```

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