

# Package ‘provenance’

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**Title** Statistical Toolbox for Sedimentary Provenance Analysis

**Version** 1.5

**Description** Bundles a number of established statistical methods to facilitate the visual interpretation of large datasets in sedimentary geology. Includes functionality for adaptive kernel density estimation, multidimensional scaling, generalised procrustes analysis and individual differences scaling using a variety of dissimilarity measures. Univariate provenance proxies, such as single-grain ages or (isotopic) compositions are compared with the Kolmogorov-Smirnov dissimilarity and Sircombe-Hazelton L2-norm. Categorical provenance proxies, such as mineralogical, petrographic or chemical compositions are compared with the Aitchison and Bray-Curtis distances. Also included are tools to plot compositional data on ternary diagrams, to calculate the sample size required for specified levels of statistical precision, and to assess the effects of hydraulic sorting on detrital compositions. Includes an intuitive query-based user interface for users who are not proficient in R.

**Author** Pieter Vermeesch [aut, cre]

**Maintainer** Pieter Vermeesch <p.vermeesch@ucl.ac.uk>

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---

amalgamate

*Group components of a composition*


---

## Description

Adds several components of a composition together into a single component

**Usage**

```

amalgamate(X, ...)

## Default S3 method:
amalgamate(X, ...)

## S3 method for class 'compositional'
amalgamate(X, ...)

## S3 method for class 'SRDcorrected'
amalgamate(X, ...)

```

**Arguments**

X	a compositional dataset
...	a series of new labels assigned to strings or vectors of strings denoting the components that need amalgamating

**Value**

an object of the same class as X with fewer components

**Examples**

```

data(Namib)
HMcomponents <- c("zr", "tm", "rt", "TiOx", "sph", "ap", "ep",
                  "gt", "st", "amp", "cpx", "opx")
am <- amalgamate(Namib$PTHM, feldspars=c("KF", "P"),
                 lithics=c("Lm", "Lv", "Ls"), heavies=HMcomponents)
plot(ternary(am))

```

---

as.acomp

*create an acomp object*


---

**Description**

Convert an object of class `compositional` to an object of class `acomp` for use in the `compositions` package

**Usage**

```
as.acomp(x)
```

**Arguments**

x	an object of class <code>compositional</code>
---	---

**Value**

a data.frame

**Examples**

```
data(Namib)
qfl <- ternary(Namib$PT,c('Q'),c('KF','P'),c('Lm','Lv','Ls'))
plot(qfl,type="QFL.dickinson")
qfl.acomp <- as.acomp(qfl)
## uncomment the next two lines to plot an error
## ellipse using the compositions package:
# library(compositions)
# ellipses(mean(qfl.acomp),var(qfl.acomp),r=2)
```

---

as.compositional	<i>create a compositional object</i>
------------------	--------------------------------------

---

**Description**

Convert an object of class matrix, data.frame or acomp to an object of class compositional

**Usage**

```
as.compositional(x, method = NULL, colmap = "rainbow")
```

**Arguments**

x	an object of class matrix, data.frame or acomp
method	dissimilarity measure, either 'aitchison' for Aitchison's CLR-distance or 'bray' for the Bray-Curtis distance.
colmap	the colour map to be used in pie charts.

**Value**

an object of class compositional

**Examples**

```
data(Namib)
PT.acomp <- as.acomp(Namib$PT)
PT.compositional <- as.compositional(PT.acomp)
print(Namib$PT$x - PT.compositional$x)
## uncomment the following lines for an illustration of using this
## function to integrate the \code{provenance} package with \code{compositions}
# library(compositions)
# data(Glacial)
# a.glac <- acomp(Glacial)
# c.glac <- as.compositional(a.glac)
# summaryplot(c.glac,ncol=8)
```

---

```
as.data.frame.compositional
      create a data.frame object
```

---

**Description**

Convert an object of class `compositional` to a `data.frame` for use in the `robCompositions` package

**Usage**

```
## S3 method for class 'compositional'
as.data.frame(x, ...)
```

**Arguments**

`x`                      an object of class `compositional`  
`...`                    optional arguments to be passed on to the generic function

**Value**

a `data.frame`

**Examples**

```
data(Namib)
qfl <- ternary(Namib$PT,c('Q'),c('KF','P'),c('Lm','Lv','Ls'))
plot(qfl,type="QFL.dickinson")
qfl.frame <- as.data.frame(qfl)
## uncomment the next two lines to plot an error
## ellipse using the robCompositions package:
# library(robCompositions)
# pca <- pcaCoDa(qfl.frame)
# plot(pca,xlabs=rownames(qfl.frame))
```

---

```
botev                      Compute the optimal kernel bandwidth
```

---

**Description**

Uses the diffusion algorithm of Zdravko Botev (2011) to calculate the bandwidth for kernel density estimation

**Usage**

```
botev(x)
```

**Arguments**

x                      a vector of ordinal data

**Value**

a scalar value with the optimal bandwidth

**Author(s)**

Dzdravko Botev

**References**

Botev, Z. I., J. F. Grotowski, and D. P. Kroese. "Kernel density estimation via diffusion." *The Annals of Statistics* 38.5 (2010): 2916-2957.

**Examples**

```
fname <- system.file("DZ.csv", package="provenance")
bw <- botev(read.distributional(fname)$x$N1)
print(bw)
```

---

bray.diss

*Bray-Curtis dissimilarity*


---

**Description**

Calculates the Bray-Curtis dissimilarity between two samples

**Usage**

```
bray.diss(x, y)
```

**Arguments**

x                      a vector containing the first compositional sample  
y                      a vector of length(x) containing the second compositional sample

**Value**

a scalar value

**Examples**

```
data(Namib)
print(bray.diss(Namib$HM$x["N1",], Namib$HM$x["N2",]))
```

---

CLR	<i>Centred logratio transformation</i>
-----	--

---

**Description**

Calculates Aitchison's centered logratio transformation for a dataset of class compositional

**Usage**

```
CLR(x)
```

**Arguments**

x                      an object of class compositional

**Value**

a matrix of CLR coordinates

**Examples**

```
# The following code shows that applying provenance's PCA function
# to compositional data is equivalent to applying R's built-in
# princomp function to the CLR transformed data.
data(Namib)
plot(PCA(Namib$Major))
dev.new()
clrdat <- CLR(Namib$Major)$x
biplot(princomp(clrdat))
```

---

combine	<i>Combine samples of distributional data</i>
---------	---

---

**Description**

Lumps all single grain analyses of several samples together under a new name

**Usage**

```
combine(X, ...)
```

**Arguments**

X                      a distributional dataset  
 ...                    a series of new labels assigned to strings or vectors of strings denoting the samples that need amalgamating

**Value**

a distributional data object with fewer samples than X

**Examples**

```
data(Namib)
combined <- combine(Namib$DZ,east=c('N3','N4','N5','N6','N7','N8','N9','N10'),
                    west=c('N1','N2','N11','N12','T8','T13'))
summaryplot(KDEs(combined))
```

---

densities

*A list of rock and mineral densities*


---

**Description**

List of rock and mineral densities using the following abbreviations: Q (quartz), KF (K-feldspar), P (plagioclase), F (feldspar), Lvf (felsic/porfiritic volcanic rock fragments), Lvm (microlithic / porfiritic / trachitic volcanic rock fragments), Lcc (calcite), Lcd (dolomite), Lp (marl), Lch (chert), Lms (argillaceous / micaceous rock fragments), Lmv (metavolcanics), Lmf (metasediments), Lmb (metabasites), Lv (volcanic rock fragments), Lc (carbonates), Ls (sedimentary rock fragments), Lm (metamorphic rock fragments), Lu (serpentine), mica, opaques, FeOx (Fe-oxides), turbids, zr (zircon), tm (tourmaline), rt (rutile), TiOx (Ti-oxides), sph (titanite), ap (apatite), mon (monazite), oth (other minerals), ep (epidote), othLgM (prehnite + pumpellyite + lawsonite + carpholite), gt (garnet), ctd (chloritoid), st (staurolite), and (andalusite), ky (kyanite), sil (sillimanite), amp (amphibole), px (pyroxene), cpx (clinopyroxene), opx (orthopyroxene), ol (olivine), spinel and othHM (other heavy minerals).

**Author(s)**

Alberto Resentini and Pieter Vermeesch

**References**

Resentini, A, Malusa M G and Garzanti, E. "MinSORTING: An Excel worksheet for modelling mineral grain-size distribution in sediments, with application to detrital geochronology and provenance studies." *Computers & Geosciences* 59 (2013): 90-97.

Garzanti, E, Ando, S and Vezzoli, G. "Settling equivalence of detrital minerals and grain-size dependence of sediment composition." *Earth and Planetary Science Letters* 273.1 (2008): 138-151.

**See Also**

restore, minsorting

**Examples**

```
data(Namib,densities)
N8 <- subset(Namib$HM,select="N8")
distribution <- minsorting(N8,densities,phi=2,sigmaphi=1,medium="air",by=0.05)
plot(distribution)
```



---

diss	<i>Calculate the dissimilarity matrix between two distributional or compositional datasets</i>
------	--

---

### Description

Calculate the dissimilarity matrix between two datasets of class distributional or compositional using the Kolmogorov-Smirnov, Sircombe-Hazelton, Aitchison or Bray Curtis distance

### Usage

```
diss(x, method)

## S3 method for class 'distributional'
diss(x, method = NULL)

## S3 method for class 'compositional'
diss(x, method = NULL)
```

### Arguments

x	an object of class distributional or compositional
method	(optional) either "KS", "SH", "aitchison" or "bray"

### Value

an object of class diss

### Examples

```
data(Namib)
print(round(100*diss(Namib$DZ)))
```

---

endmembers	<i>Petrographic end-member compositions</i>
------------	---

---

### Description

A compositional dataset comprising the mineralogical compositions of the following end-members: undissected\_magmatic\_arc, dissected\_magmatic\_arc, ophiolite, recycled\_clastic, undissected\_continental\_block, transitional\_continental\_block, dissected\_continental\_block, subcreted\_axial\_belt and subducted\_axial\_belt

### Author(s)

Alberto Resentini and Pieter Vermeesch

## References

Resentini, A, Malusa M G and Garzanti, E. "MinSORTING: An Excel worksheet for modelling mineral grain-size distribution in sediments, with application to detrital geochronology and provenance studies." Computers & Geosciences 59 (2013): 90-97.

Garzanti, E, Ando, S and Vezzoli, G. "Settling equivalence of detrital minerals and grain-size dependence of sediment composition." Earth and Planetary Science Letters 273.1 (2008): 138-151.

## See Also

minsorting

## Examples

```
data(endmembers,densities)
ophiolite <- subset(endmembers,select="ophiolite")
plot(minsorting(ophiolite,densities,by=0.05))
```

---

get.f

*Calculate the largest fraction that is likely to be missed*

---

## Description

For a given sample size, returns the largest fraction which has been sampled with  $p \times 100$

## Usage

```
get.f(n, p = 0.05)
```

## Arguments

n	the number of grains in the detrital sample
p	the required level of confidence

## Value

the largest fraction that is sampled with at least  $100 \times p$  certainty

## References

Vermeesch, Pieter. "How many grains are needed for a provenance study?." Earth and Planetary Science Letters 224.3 (2004): 441-451.

## Examples

```
print(get.f(60))
print(get.f(117))
```

---

get.n	<i>Calculate the number of grains required to achieve a desired level of sampling resolution</i>
-------	--

---

## Description

Returns the number of grains that need to be analysed to decrease the likelihood of missing any fraction greater than a given size below a given level.

## Usage

```
get.n(p = 0.05, f = 0.05)
```

## Arguments

p	the probability that all n grains in the sample have missed at least one fraction of size f
f	the size of the smallest resolvable fraction ( $0 < f < 1$ )
n,	the number of grains in the sample

## Value

the number of grains needed to reduce the chance of missing at least one fraction f of the total population to less than p

## References

Vermeesch, Pieter. "How many grains are needed for a provenance study?." Earth and Planetary Science Letters 224.3 (2004): 441-451.

## Examples

```
# number of grains required to be 99% that no fraction greater than 5% was missed:  
print(get.n(0.01))  
# number of grains required to be 90% that no fraction greater than 10% was missed:  
print(get.n(p=0.1,f=0.1))
```

---

<code>get.p</code>	<i>Calculate the probability of missing a given population fraction</i>
--------------------	---

---

**Description**

For a given sample size, returns the likelihood of missing any fraction greater than a given size

**Usage**

```
get.p(n, f = 0.05)
```

**Arguments**

<code>n</code>	the number of grains in the detrital sample
<code>f</code>	the size of the smallest resolvable fraction ( $0 < f < 1$ )

**Value**

the probability that all `n` grains in the sample have missed at least one fraction of size `f`

**References**

Vermeesch, Pieter. "How many grains are needed for a provenance study?." *Earth and Planetary Science Letters* 224.3 (2004): 441-451.

**Examples**

```
print(get.p(60))
print(get.p(117))
```

---

GPA	<i>Generalised Procrustes Analysis of configurations</i>
-----	--

---

**Description**

Given a number of (2D) configurations, this function uses a combination of transformations (reflections, rotations, translations and scaling) to find a 'consensus' configuration which best matches all the component configurations in a least-squares sense.

**Usage**

```
GPA(X, scale = TRUE)
```

**Arguments**

<code>X</code>	a list of dissimilarity matrices
<code>scale</code>	boolean flag indicating if the transformation should include the scaling operation

**Value**

a two column vector with the coordinates of the group configuration

**See Also**

procrustes

---

indscal

*Individual Differences Scaling of provenance data*


---

**Description**

Performs 3-way Multidimensional Scaling analysis using Carroll and Chang (1970)'s INdividual Differences SCALing method as implemented using De Leeuw and Mair (2011)'s stress majorization algorithm.

**Usage**

```
indscal(..., type = "ordinal")
```

**Arguments**

... a sequence of datasets of class distributional or compositional  
 type is either "ratio" or "ordinal"

**Value**

an object of class INDSCAL, i.e. a list containing the following items:

delta: Observed dissimilarities

obsdiss: List of observed dissimilarities, normalized

confdiss: List of configuration dissimilarities

conf: List of matrices of final configurations

gspace: Joint configurations aka group stimulus space

cweights: Configuration weights

stress: Stress-1 value

spp: Stress per point

sps: Stress per subject (matrix)

ndim: Number of dimensions

model: Type of smacof model

niter: Number of iterations

nobj: Number of objects

**Author(s)**

Jan de Leeuw and Patrick Mair

**References**

de Leeuw, J., & Mair, P. (2009). Multidimensional scaling using majorization: The R package smacof. Journal of Statistical Software, 31(3), 1-30, < <http://www.jstatsoft.org/v31/i03/>>

**Examples**

```
data(Namib)
plot(indscal(Namib$DZ,Namib$HM))
```

---

KDE

---

*Create a kernel density estimate*


---

**Description**

Turns a vector of numbers into an object of class KDE using a combination of the Botev (2010) bandwidth selector and the Abramson (1982) adaptive kernel bandwidth modifier.

**Usage**

```
KDE(x, from = NA, to = NA, bw = NA, adaptive = TRUE, log = FALSE,
    n = 512, ...)
```

**Arguments**

x	a vector of numbers
from	minimum age of the time axis. If NULL, this is set automatically
to	maximum age of the time axis. If NULL, this is set automatically
bw	the bandwidth of the KDE. If NULL, bw will be calculated automatically using <code>botev()</code>
adaptive	boolean flag controlling if the adaptive KDE modifier of Abramson (1982) is used
log	transform the ages to a log scale if TRUE
n	horizontal resolution of the density estimate
...	optional arguments to be passed on to <code>density</code>

**Value**

an object of class KDE, i.e. a list containing the following items:

x: horizontal plot coordinates

y: vertical plot coordinates

bw: the base bandwidth of the density estimate

ages: the data values from the input to the KDE function

See Also

KDEs

Examples

```
data(Namib)
samp <- Namib$DZ$x[['N1']]
dens <- KDE(samp,0,3000,kernel="epanechnikov")
plot(dens)
```

---

KDEs	<i>Generate an object of class KDEs</i>
------	---

---

Description

Convert a dataset of class distributional into an object of class KDEs for further processing by the summaryplot function.

Usage

```
KDEs(x, from = NA, to = NA, bw = NA, samebandwidth = TRUE,
      adaptive = TRUE, pch = NA, normalise = FALSE, log = FALSE, n = 512,
      ...)
```

Arguments

x	an object of class distributional
from	minimum limit of the x-axis.
to	maximum limit of the x-axis.
bw	the bandwidth of the kernel density estimates. If bw = NA, the bandwidth will be set automatically using botev()
samebandwidth	boolean flag indicating whether the same bandwidth should be used for all samples. If samebandwidth = TRUE and bw = NULL, then the function will use the median bandwidth of all the samples.
adaptive	boolean flag switching on the adaptive bandwidth modifier of Abramson (1982)
pch	(optional) symbol to be used to mark the sample points along the x-axis
normalise	boolean flag indicating whether or not the KDEs should all integrate to the same value.
log	boolean flag indicating whether the data should be plotted on a logarithmic scale.
n	horizontal resolution of the density estimates
...	optional parameters to be passed on to density

**Value**

an object of class KDEs, i.e. a list containing the following items:

kdes: a named list with objects of class KDE

from: the beginning of the common time scale

to: the end of the common time scale

themax: the maximum probability density of all the KDEs

pch: the plot symbol to be used by plot.KDEs

xlabel: the x-axis label to be used by plot.KDEs

**See Also**

KDE

**Examples**

```
data(Namib)
KDEs <- KDEs(Namib$DZ, 0, 3000, pch=NA)
summaryplot(KDEs, ncol=3)
```

---

KS.diss

*Kolmogorov-Smirnov dissimilarity*


---

**Description**

Returns the Kolmogorov-Smirnov dissimilarity between two samples

**Usage**

```
KS.diss(x, y)
```

**Arguments**

x                      the first sample as a vector

y                      the second sample as a vector

**Value**

a scalar value representing the maximum vertical distance between the two cumulative distributions

**Examples**

```
data(Namib)
print(KS.diss(Namib$DZ$x[['N1']], Namib$DZ$x[['T8']]))
```



**Description**

Performs classical or nonmetric Multidimensional Scaling analysis

Multidimensional Scaling of compositional data

Multidimensional Scaling of distributional data

Multidimensional Scaling of a dissimilarity matrix

**Usage**

```
MDS(x, ...)
```

```
## S3 method for class 'compositional'
```

```
MDS(x, classical = FALSE, ...)
```

```
## S3 method for class 'distributional'
```

```
MDS(x, classical = FALSE, ...)
```

```
## S3 method for class 'diss'
```

```
MDS(x, classical = FALSE, ...)
```

**Arguments**

<code>x</code>	an object of class <code>distributional</code> , <code>compositional</code> or <code>diss</code>
<code>...</code>	optional arguments to be passed onto <code>diss</code> (if <code>x</code> is of class <code>compositional</code> or <code>distributional</code> ) or onto <code>cmdscale</code> or <code>isoMDS</code> (if <code>x</code> is of class <code>dist</code> ).
<code>classical</code>	boolean flag indicating whether classical (TRUE) or nonmetric (FALSE) MDS should be used

**Value**

an object of class `MDS`, i.e. a list containing the following items:

`points`: a two column vector of the fitted configuration

`classical`: a boolean flag indicating whether the MDS configuration was obtained by classical (TRUE) or nonmetric (FALSE) MDS.

`diss`: the dissimilarity matrix used for the MDS analysis

`stress`: (only if `classical=TRUE`) the final stress achieved (in percent)

**Examples**

```
data(Namib)
plot(MDS(Namib$Major,classical=TRUE))
```

minsorting

*Assess settling equivalence of detrital components***Description**

Models grain size distribution of minerals and rock fragments of different densities

**Usage**

```
minsorting(X, dens, sname = NULL, phi = 2, sigmaphi = 1,
          medium = "freshwater", from = -2.25, to = 5.5, by = 0.25)
```

**Arguments**

X	an object of class <code>compositional</code>
dens	a vector of mineral and rock densities
sname	sample name if unspecified, the first sample of the dataset will be used
phi	the mean grain size of the sample in Krumbein's phi units
sigmaphi	the standard deviation of the grain size distribution, in phi units
medium	the transport medium, one of either "air", "freshwater" or "seawater"
from	the minimum grain size to be evaluated, in phi units
to	the maximum grain size to be evaluated, in phi units
by	the grain size interval of the output table, in phi units

**Value**

an object of class `minsorting`, i.e. a list with two tables:

`mfract`: the grain size distribution of each mineral (sum of the columns = 1)

`mcomp`: the composition of each mineral (sum of the rows = 1)

**Author(s)**

Alberto Resentini and Pieter Vermeesch

**References**

Resentini, A, Malusa, M G and Garzanti, E. "MinSORTING: An Excel worksheet for modelling mineral grain-size distribution in sediments, with application to detrital geochronology and provenance studies." *Computers & Geosciences* 59 (2013): 90-97.

Garzanti, E, Ando, S and Vezzoli, G. "Settling equivalence of detrital minerals and grain-size dependence of sediment composition." *Earth and Planetary Science Letters* 273.1 (2008): 138-151.

**See Also**

`restore`

## Examples

```
data(endmembers,densities)
distribution <- minsorting(endmembers,densities,sname='ophiolite',phi=2,
                           sigmaphi=1,medium="seawater",by=0.05)
plot(distribution,cumulative=FALSE)
```

---

Namib

*An example dataset*

---

## Description

A large dataset of provenance data from Namibia comprised of 14 sand samples from the Namib Sand Sea and 2 samples from the Orange River.

## Details

Namib is a list containing the following 6 items:

DZ: a distributional dataset containing the zircon U-Pb ages for ca. 100 grains from each sample, as well as their (1-sigma) analytical uncertainties.

PT: a compositional dataset with the bulk petrography of the samples, i.e. the quartz ('Q'), K-feldspar ('KF'), plagioclase ('P'), and lithic fragments of metamorphic ('Lm'), volcanic ('Lv') and sedimentary ('Ls') origin.

HM: a compositional dataset containing the heavy mineral composition of the samples, comprised of zircon ('zr'), tourmaline ('tm'), rutile ('rt'), Ti-oxides ('TiOx'), titanite ('sph'), apatite ('ap'), epidote ('ep'), garnet ('gt'), staurolite ('st'), andalusite ('and'), kyanite ('ky'), sillimanite ('sil'), amphibole ('amp'), clinopyroxene ('cpx') and orthopyroxene ('opx').

PTHM: a compositional dataset combining the variables contained in PT and HM plus 'mica', 'opaques', 'turbids' and 'other' transparent heavy minerals ('LgM'), normalised to 100.

Major: a compositional dataset listing the concentrations (in wt TiO<sub>2</sub>, P<sub>2</sub>O<sub>5</sub> and MnO).

Trace: a compositional data listing the concentrations (in ppm) of Rb, Sr, Ba, Sc, Y, La, Ce, Pr, Nd, Sm, Gd, Dy, Er, Yb, Th, U, Zr, Hf, V, Nb, Cr, Co, Ni, Cu, Zn, Ga and Pb.

## Author(s)

Pieter Vermeesch and Eduardo Garzanti

## References

Vermeesch, P. and Garzanti, E., Making geological sense of 'Big Data' in sedimentary provenance analysis, *Chemical Geology* 409 (2015) 20-27

## Examples

```
data(Namib)
samp <- Namib$DZ$x[['N1']]
dens <- KDE(samp,0,3000)
plot(dens)
```

---

PCA

*Principal Component Analysis*


---

**Description**

Performs PCA of compositional data using a centred logratio distance

**Usage**

```
PCA(x, ...)
```

**Arguments**

x                    an object of class compositional  
 ...                  optional arguments to R's princomp function

**Value**

an object of classes PCA, which is synonymous to the stats packages' princomp class.

**Examples**

```
data(Namib)
plot(MDS(Namib$Major,classical=TRUE))
dev.new()
plot(PCA(Namib$Major),asp=1)
print("This example demonstrates the equivalence of classical MDS and PCA")
```

---

plot.compositional

*Plot a pie chart*


---

**Description**

Plots an object of class compositional as a pie chart

**Usage**

```
## S3 method for class 'compositional'
plot(x, sname, annotate = TRUE, colmap = NULL, ...)
```

**Arguments**

x	an object of class compositional
sname	the sample name
annotate	a boolean flag controlling if the pies of the pie-chart should be labeled
colmap	an optional string with the name of one of R's built-in colour palettes (e.g., heat.colors, terrain.colors, topo.colors, cm.colors), which are to be used for plotting the data.
...	optional parameters to be passed on to the graphics object

**Examples**

```
data(Namib)
plot(Namib$HM, 'N1', colmap='heat.colors')
```

---

plot.distributional     *Plot continuous data as histograms or cumulative age distributions*

---

**Description**

Plot one or several samples from a distributional dataset as a histogram or Cumulative Age Distributions (CAD).

**Usage**

```
## S3 method for class 'distributional'
plot(x, snames = NULL, annotate = TRUE,
     CAD = FALSE, pch = NA, verticals = TRUE, colmap = NULL, ...)
```

**Arguments**

x	an object of class distributional
snames	a string or a vector of string with the names of the samples that need plotting if snames is a vector, then the function will default to a CAD.
annotate	boolean flag indicating whether the x- and y-axis should be labeled
CAD	boolean flag indicating whether the data should be plotted as a cumulative age distribution or a histogram. For multi-sample plots, the function will override this value with TRUE.
pch	an optional symbol to mark the sample points along the CAD
verticals	boolean flag indicating if the horizontal lines of the CAD should be connected by vertical lines
colmap	an optional string with the name of one of R's built-in colour palettes (e.g., heat.colors, terrain.colors, topo.colors, cm.colors), which are to be used for plotting the data.
...	optional arguments to the generic plot function

**Examples**

```
data(Namib)
plot(Namib$DZ,c('N1','N2'))
```

---

plot.GPA

---

*Plot a Procrustes configuration*


---

**Description**

Plots the group configuration of a Generalised Procrustes Analysis

**Usage**

```
## S3 method for class 'GPA'
plot(x, pch = NA, pos = NULL, col = "black", bg = "white",
     cex = 1, ...)
```

**Arguments**

x	an object of class GPA
pch	plot symbol
pos	position of the sample labels relative to the plot symbols if pch != NA
col	plot colour (may be a vector)
bg	background colour (may be a vector)
cex	relative size of plot symbols
...	optional arguments to the generic plot function

**See Also**

procrustes

**Examples**

```
data(Namib)
GPA <- procrustes(Namib$DZ,Namib$HM)
coast <- c('N1','N2','N3','N10','N11','N12','T8','T13')
snames <- names(Namib$DZ)
bgcol <- rep('yellow',length(snames))
bgcol[which(snames %in% coast)] <- 'red'
plot(GPA,pch=21,bg=bgcol)
```

---

plot.INDSCAL	<i>Plot an INDSCAL group configuration and source weights</i>
--------------	---

---

### Description

Given an object of class INDSCAL, generates two plots: the group configuration and the subject weights. Together, these describe a 3-way MDS model.

### Usage

```
## S3 method for class 'INDSCAL'
plot(x, asp = 1, pch = NA, pos = NULL, col = "black",
     bg = "white", cex = 1, xlab = "X", ylab = "Y", xaxt = "n",
     yaxt = "n", ...)
```

### Arguments

x	an object of class INDSCAL
asp	the aspect ratio of the plot
pch	plot symbol (may be a vector)
pos	position of the sample labels relative to the plot symbols if pch != NA
col	plot colour (may be a vector)
bg	background colour (may be a vector)
cex	relative size of plot symbols
xlab	a string with the label of the x axis
ylab	a string with the label of the y axis
xaxt	if = 'y', adds ticks to the x axis
yaxt	if = 'y', adds ticks to the y axis
...	optional arguments to the generic plot function

### See Also

indscal

### Examples

```
data(Namib)
coast <- c('N1','N2','N3','N10','N11','N12','T8','T13')
snames <- names(Namib$DZ)
pch <- rep(21,length(snames))
pch[which(snames %in% coast)] <- 22
plot(indscal(Namib$DZ,Namib$HM),pch=pch)
```

---

plot.KDE	<i>Plot a kernel density estimate</i>
----------	---------------------------------------

---

**Description**

Plots an object of class KDE

**Usage**

```
## S3 method for class 'KDE'
plot(x, pch = "|", xlab = "age [Ma]", ylab = "", ...)
```

**Arguments**

x	an object of class KDE
pch	the symbol used to show the samples. May be a vector. Set pch = NA to turn them off.
xlab	the label of the x-axis
ylab	the label of the y-axis
...	optional parameters to be passed on to the graphics object

**See Also**

KDE

**Examples**

```
data(Namib)
samp <- Namib$DZ$x[['N1']]
dens <- KDE(samp, from=0, to=3000)
plot(dens)
```

---

plot.MDS	<i>Plot an MDS configuration</i>
----------	----------------------------------

---

**Description**

Plots the coordinates of a multidimensional scaling analysis as an X-Y scatter plot or 'map' and, if x\$classical = FALSE, a Shepard plot.

**Usage**

```
## S3 method for class 'MDS'
plot(x, nnlines = FALSE, pch = NA, pos = NULL, cex = 1,
     col = "black", bg = "white", xlab = "", ylab = "", xaxt = "n",
     yaxt = "n", ...)
```



**Arguments**

x	an object of class MDS
nnlines	if TRUE, draws nearest neighbour lines
pch	plot character (see ?plot for details). May be a vector.
pos	position of the sample labels relative to the plot symbols if pch != NA
cex	relative size of plot symbols (see ?par for details)
col	plot colour (may be a vector)
bg	background colour (may be a vector)
xlab	a string with the label of the x axis
ylab	a string with the label of the y axis
xaxt	if = 's', adds ticks to the x axis
yaxt	if = 's', adds ticks to the y axis
...	optional arguments to the generic plot function

**See Also**

MDS

**Examples**

```
data(Namib)
mds <- MDS(Namib$DZ)
coast <- c('N1', 'N2', 'N3', 'N10', 'N11', 'N12', 'T8', 'T13')
snames <- names(Namib$DZ)
bgcol <- rep('yellow', length(snames))
bgcol[which(snames %in% coast)] <- 'red'
plot(mds, pch=21, bg=bgcol)
```

plot.minsorting

*Plot inferred grain size distributions***Description**

Plot the grain size distributions of the different minerals under consideration

**Usage**

```
## S3 method for class 'minsorting'
plot(x, cumulative = FALSE, components = NULL, ...)
```

**Arguments**

x	an object of class minsorting
cumulative	boolean flag indicating whether the grain size distribution should be plotted as a density or cumulative probability curve.
components	string or list of strings with the names of a subcomposition that needs plotting
...	optional parameters to be passed on to graphics::matplot (see ?par for details)

**See Also**

minsorting

**Examples**

```
data(endmembers,densities)
OPH <- subset(endmembers,select="ophiolite")
distribution <- minsorting(OPH,densities,phi=2,sigmaphi=1,medium="air",by=0.05)
plot(distribution,components=c('F','px','opaques'))
```

---

plot.PCA

---

*Compositional biplot*


---

**Description**

Plot the results of a principal components analysis as a biplot

**Usage**

```
## S3 method for class 'PCA'
plot(x, ...)
```

**Arguments**

x	an object of class PCA
...	optional arguments of the biplot function

**See Also**

PCA

**Examples**

```
data(Namib)
plot(PCA(Namib$Major))
```

---

plot.ternary	<i>Plot a ternary diagram</i>
--------------	-------------------------------

---

## Description

Plots triplets of compositional data on a ternary diagram

## Usage

```
## S3 method for class 'ternary'
plot(x, type = "empty", pch = NA, pos = NULL,
     labels = names(x), showpath = FALSE, bg = NA, col = "cornflowerblue",
     ...)
```

## Arguments

x	an object of class ternary
type	adds annotations to the ternary diagram, one of either empty, QFL.descriptive, QFL.folk or QFL.dickinson
pch	plot character, see ?par for details (may be a vector)
pos	position of the sample labels relative to the plot symbols if pch != NA
labels	vector of strings to be added to the plot symbols
showpath	if x has class SRDcorrected, and showpath==TRUE, the intermediate values of the SRD correction will be plotted on the ternary diagram as well as the final composition
bg	background colour for the plot symbols (may be a vector)
col	colour to be used for the background lines (if applicable)
...	optional arguments to the generic points function

## See Also

ternary

## Examples

```
data(Namib)
tern <- ternary(Namib$PT, 'Q', c('KF', 'P'), c('Lm', 'Lv', 'Ls'))
plot(tern, type='QFL.descriptive', pch=21, bg='red', labels=NULL)
```

---

procrustes

*Generalised Procrustes Analysis of provenance data*

---

### Description

Given a number of input datasets, this function performs an MDS analysis on each of these and the feeds the resulting configurations into the GPA() function.

### Usage

```
procrustes(...)
```

### Arguments

... a sequence of datasets of classes distributional and compositional

### Value

an object of class GPA, i.e. a list containing the following items:

points: a two column vector with the coordinates of the group configuration

labels: a list with the sample names

### Author(s)

Pieter Vermeesch

### References

Gower, J.C. (1975). Generalized Procrustes analysis, Psychometrika, 40, 33-50.

### See Also

GPA

### Examples

```
data(Namib)
gpa <- procrustes(Namib$DZ,Namib$HM)
plot(gpa)
```

---

provenance	<i>Menu-based interface for provenance</i>
------------	--

---

**Description**

For those less familiar with the syntax of the R programming language, the `provenance()` function provides a user-friendly way to access the most important functionality in the form of a menu-based query interface. Further details and examples are provided on <http://provenance.london-geochron.com>

**Usage**

```
provenance()
```

**Author(s)**

Pieter Vermeesch

**References**

Vermeesch, P., Resentini, A. and Garzanti, E., an R package for statistical provenance analysis, *Sedimentary Geology*, doi:10.1016/j.sedgeo.2016.01.009.

**See Also**

<http://provenance.london-geochron.com>

---

<code>read.compositional</code>	<i>Read a .csv file with categorical data</i>
---------------------------------	---

---

**Description**

Reads a data table containing categorical data (e.g. petrographic, heavy mineral or geochemical data)

**Usage**

```
read.compositional(fname, method = NULL, colmap = "rainbow")
```

**Arguments**

<code>fname</code>	a string with the path to the .csv file
<code>method</code>	either "bray" (for the Bray-Curtis distance) or "aitchison" (for Aitchison's central logratio distance). If omitted, the function defaults to 'aitchison', unless there are zeros present in the data.
<code>colmap</code>	an optional string with the name of one of R's built-in colour palettes (e.g., <code>heat.colors</code> , <code>terrain.colors</code> , <code>topo.colors</code> , <code>cm.colors</code> ), which are to be used for plotting the data.

**Value**

an object of class `compositional`, i.e. a list with the following items:

`x`: a data frame with the samples as rows and the categories as columns

`method`: either "aitchison" (for Aitchison's centred logratio distance) or "bray" (for the Bray-Curtis distance)

**Examples**

```
fname <- system.file("Major.csv", package="provenance")
Major <- read.compositional(fname)
plot(PCA(Major))
```

---

read.densities	<i>Read a .csv file with mineral and rock densities</i>
----------------	---

---

**Description**

Reads a data table containing densities to be used for hydraulic sorting corrections (`minsorting` and `srd` functions)

**Usage**

```
read.densities(fname)
```

**Arguments**

`fname`                      a string with the path to the .csv file

**Value**

a vector with mineral and rock densities

**Examples**

```
data(Namib, densities)
N8 <- subset(Namib$HM, select="N8")
distribution <- minsorting(N8, densities, phi=2, sigmaphi=1, medium="air", by=0.05)
plot(distribution)
```

---

read.distributional     *Read a .csv file with continuous (detrital zircon) data*

---

## Description

Reads a data table containing continuous data (e.g. detrital zircon ages)

## Usage

```
read.distributional(fname, errorfile = NA, method = "KS",
  xlab = "age [Ma]", colmap = "rainbow")
```

## Arguments

fname	the path of a .csv file with the input data, arranged in columns.
errorfile	the (optional) path of a .csv file with the standard errors of the input data, arranged by column in the same order as fname. Must be specified if the data are to be compared with the Sircombe-Hazelton dissimilarity.
method	an optional string specifying the dissimilarity measure which should be used for comparing this with other datasets. Should be one of either "KS" (for Kolmogorov-Smirnov) or "SH" (for Sircombe and Hazelton). If method = "SH", then errorfile should be specified. If method = "SH" and errorfile is unspecified, then the program will default back to the Kolmogorov-Smirnov dissimilarity.
xlab	an optional string specifying the nature and units of the data. This string is used to label kernel density estimates.
colmap	an optional string with the name of one of R's built-in colour palettes (e.g., heat.colors, terrain.colors, topo.colors, cm.colors), which are to be used for plotting the data.

## Value

an object of class `distributional`, i.e. a list with the following items:

- x: a named list of vectors containing the numerical data for each sample
- err: an (optional) named list of vectors containing the standard errors of x
- method: either "KS" (for Kolmogorov-Smirnov) or "SH" (for Sircombe Hazelton)
- breaks: a vector with the locations of the histogram bin edges
- xlab: a string containing the label to be given to the x-axis on all plots

## Examples

```
agefile <- system.file("DZ.csv", package="provenance")
errfile <- system.file("DZerr.csv", package="provenance")
DZ <- read.distributional(agefile, errfile)
plot(KDE(DZ$x$N1))
```

---

restore	<i>Undo the effect of hydraulic sorting</i>
---------	---

---

### Description

Restore the detrital composition back to a specified source rock density (SRD)

### Usage

```
restore(X, dens, target = 2.71)
```

### Arguments

X	an object of class <code>compositional</code>
dens	a vector of rock and mineral densities
target	the target density (in g/cm <sup>3</sup> )

### Value

an object of class `SRDcorrected`, i.e. an object of class `compositional` which is a daughter of class `compositional` containing the restored composition, plus one additional member called `restoration`, containing the intermediate steps of the SRD correction algorithm.

### Author(s)

Alberto Resentini and Pieter Vermeesch

### References

Garzanti E, Ando, S and Vezzoli, G. "Settling equivalence of detrital minerals and grain-size dependence of sediment composition." *Earth and Planetary Science Letters* 273.1 (2008): 138-151.

### See Also

`minsorting`

### Examples

```
data(Namib,densities)
rescomp <- restore(Namib$PTHM,densities,2.71)
HMcomp <- c("zr","tm","rt","sph","ap","ep","gt",
            "st","amp","cpx","opx")
amcomp <- amalgamate(rescomp,Plag="P",HM=HMcomp,Opq="opaques")
plot(ternary(amcomp),showpath=TRUE)
```



SH.diss

*Sircombe and Hazelton distance***Description**

Calculates Sircombe and Hazelton's L2 distance between the Kernel Functional Estimates (KFEs, not to be confused with Kernel Density Estimates!) of two samples with specified analytical uncertainties

**Usage**

```
SH.diss(x, i, j, c.con = 0)
```

**Arguments**

x	an object of class <code>distributional</code>
i	index of the first sample
j	index of the second sample
c.con	smoothing bandwidth of the kernel functional estimate

**Value**

a scalar value expressing the L2 distance between the KFEs of samples i and j

**Author(s)**

Keith Sircombe and Martin Hazelton

**References**

Sircombe, K. N., and M. L. Hazelton. "Comparison of detrital zircon age distributions by kernel functional estimation." *Sedimentary Geology* 171.1 (2004): 91-111.

**See Also**

KS.diss

**Examples**

```
datfile <- system.file("DZ.csv",package="provenance")
errfile <- system.file("DZerr.csv",package="provenance")
DZ <- read.distributional(datfile,errfile)
d <- SH.diss(DZ,1,2)
print(d)
```

---

subset.compositional    *Get a subset of compositional data*

---

**Description**

Return a subset of provenance data according to some specified indices

**Usage**

```
## S3 method for class 'compositional'  
subset(x, subset = NULL, select = NULL,  
       components = NULL, ...)
```

**Arguments**

x	an object of class compositional
subset	logical expression indicating elements or rows to keep: missing values are taken as false.
select	a vector of sample names.
components	a vector specifying a subcomposition
...	optional arguments for the generic subset function

**Value**

an object of class compositional

**See Also**

read.compositional

---

subset.distributional    *Get a subset of distributional data*

---

**Description**

Return a subset of provenance data according to some specified indices

**Usage**

```
## S3 method for class 'distributional'  
subset(x, subset = NULL, select = NULL, ...)
```

**Arguments**

x	an object of class <code>distributional</code>
subset	logical expression indicating elements or rows to keep: missing values are taken as false.
select	a vector of sample names
...	optional arguments for the generic subset function

**Value**

an object of class `distributional`

**See Also**

`read.distributional`

**Examples**

```
data(Namib)
coast <- subset(Namib$HM,select=c("N1","N2","T8","T13","N12","N13"))
summaryplot(coast,ncol=2)
```

---

summaryplot

*Joint plot of several provenance datasets*


---

**Description**

Arranges kernel density estimates and pie charts in a grid format

**Usage**

```
summaryplot(..., ncol = 1)
```

**Arguments**

...	a sequence of datasets of class <code>compositional</code> , <code>KDEs</code> , or <code>distributional</code>
ncol	the number of columns

**Value**

a summary plot of all the data comprised of KDEs for the datasets of class `KDEs`, pie charts for those of class `compositional` and histograms for those of class `distributional`.

**See Also**

`KDEs`

**Examples**

```
data(Namib)
KDEs <- KDEs(Namib$DZ,0,3000)
summaryplot(KDEs,Namib$HM,Namib$PT,ncol=2)
```

---

ternary

---

*Define a ternary composition*


---

**Description**

Create an object of class ternary

**Usage**

```
ternary(X, x = NULL, y = NULL, z = NULL)
```

**Arguments**

X	an object of class compositional
x	string or a vector of strings indicating the variables making up the first sub-composition of the ternary system. If omitted, the first component of X is used instead.
y	second (set of) variables
z	third (set of) variables

**Value**

an object of class ternary, i.e. a list containing:

x: a three column matrix (or vector) of ternary compositions.

and (if X is of class SRDcorrected)

restoration: a list of intermediate ternary compositions inherited from the SRD correction

**See Also**

restore

**Examples**

```
data(Namib)
tern <- ternary(Namib$PT,c('Q'),c('KF','P'),c('Lm','Lv','Ls'))
plot(tern,type="QFL")
```

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