

Package ‘AlphaPart’

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Title Partition/Decomposition of Additive Genetic Values by Paths of Information

Description Additive genetic (breeding) value represents a sum of additive gene effects over whole genome and can be inferred from phenotype values of relatives via pedigree based mixed models. The partitioning method is described in Garcia-Cortes et al. (2008) <DOI:10.1017/S175173110800205X>.

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AlphaPart	<i>AlphaPart.R</i>
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Description

A function to partition additive genetic values by paths. The partition method is described in García-Cortés et al., 2008: Partition of the genetic trend to validate multiple selection decisions. *Animal* : an international journal of animal bioscience. DOI: 10.1017/S175173110800205X

Usage

```
AlphaPart(x, pathNA = FALSE, recode = TRUE, unknown = NA,
  sort = TRUE, verbose = 1, profile = FALSE, printProfile = "end",
  pedType = "IPP", colId = 1, colFid = 2, colMid = 3,
  colPath = 4, colAGV = 5:ncol(x), colBy = NULL)
```

Arguments

x	data.frame , with (at least) the following columns: individual, father, and mother identification, and year of birth; see arguments colId, colFid, colMid, colPath, and colAgv; see also details about the validity of pedigree.
pathNA	Logical, set dummy path (to "XXX") where path information is unknown (missing).
recode	Logical, internally recode individual, father and, mother identification to 1:n codes, while missing parents are defined with 0; this option must be used if identifications in x are not already given as 1:n codes, see also argument sort.
unknown	Value(s) used for representing unknown (missing) parent in x; this options has an effect only when recode=FALSE as it is only needed in that situation.
sort	Logical, initially sort x using orderPed() so that children follow parents in order to make imputation as optimal as possible (imputation is performed within a loop from the first to the last unknown birth year); at the end original order is restored.
verbose	Numeric, print additional information: 0 - print nothing, 1 - print some summaries about the data.

profile	Logical, collect timings and size of objects.
printProfile	Character, print profile info on the fly ("fly") or at the end ("end").
pedType	Character, pedigree type: the most common form is "IPP" for Individual, Parent 1 (say father), and Parent 2 (say mother) data; the second form is "IPG" for Individual, Parent 1 (say father), and one of Grandparents of Parent 2 (say maternal grandfather).
colId	Numeric or character, position or name of a column holding individual identification.
colFid	Numeric or character, position or name of a column holding father identification.
colMid	Numeric or character, position or name of a column holding mother identification or maternal grandparent identification if pedType="IPG" .
colPath	Numeric or character, position or name of a column holding path information.
colAGV	Numeric or character, position(s) or name(s) of column(s) holding Additive Genetic Values.
colBy	Numeric or character, position or name of a column holding group information (see details).

Details

Pedigree in `x` must be valid in a sense that there are:

- no directed loops (the simplest example is that the individual identification is equal to the identification of a father or mother)
- no bisexuality, e.g., fathers most not appear as mothers
- father and/or mother can be unknown (missing) - defined with any "code" that is different from existing identifications

Unknown (missing) values for additive genetic values are propagated down the pedigree to provide all available values from genetic evaluation. Another option is to cut pedigree links - set parents to unknown and remove them from pedigree prior to using this function - see [pedSetBase](#) function. Warning is issued in the case of unknown (missing) values.

In animal breeding/genetics literature the model with the underlying pedigree type "IPP" is often called animal model, while the model for pedigree type "IPG" is often called sire - maternal grand-sire model. With a combination of `colFid` and `colMid` mother - paternal grandsire model can be accommodated as well.

Argument `colBy` can be used to directly perform a summary analysis by group, i.e., `summary(AlphaPart(...), by="group")`. See [summary.AlphaPart](#) for more. This can save some CPU time by skipping intermediate steps. However, only means can be obtained, while `summary` method gives more flexibility.

Value

An object of class `AlphaPart`, which can be used in further analyses - there is a handy summary method ([summary.AlphaPart](#) works on objects of `AlphaPart` class) and a plot method for its output ([plot.summaryAlphaPart](#) works on objects of `summaryAlphaPart` class). Class `AlphaPart` is a list. The first `length(colAGV)` components (one for each trait and named with trait label, say `trt`) are data frames. Each data.frame contains:

x columns from initial data x
 trt_pa parent average
 trt_w Mendelian sampling term
 trt_path1, trt_path2, ...
 additive genetic value partitions

The last component of returned object is also a list named `info` with the following components holding meta information about the analysis:

path column name holding path information
 nP number of paths
 lP path labels
 nT number of traits
 lT trait labels
 warn potential warning messages associated with this object

If `colBy!=NULL` the resulting object is of a class `summaryAlphaPart`, see [summary.AlphaPart](#) for details.

If `profile=TRUE`, profiling info is printed on screen to spot any computational bottlenecks.

References

Garcia-Cortes, L. A. et al. (2008) Partition of the genetic trend to validate multiple selection decisions. *Animal*, 2(6):821-824. <http://dx.doi.org/10.1017/S175173110800205X>

See Also

[summary.AlphaPart](#) for summary method that works on output of AlphaPart, [pedSetBase](#) for setting base population, [pedFixBirthYear](#) for imputing unknown (missing) birth years, [orderPed](#) in **pedigree** package for sorting pedigree

Examples

```
## Small pedigree with additive genetic (=breeding) values
ped <- data.frame( id=c( 1,  2,  3,  4,  5,  6),
                  fid=c( 0,  0,  2,  0,  4,  0),
                  mid=c( 0,  0,  1,  0,  3,  3),
                  loc=c("A", "B", "A", "B", "A", "A"),
                  gen=c( 1,  1,  2,  2,  3,  3),
                  trt1=c(100, 120, 115, 130, 125, 125),
                  trt2=c(100, 110, 105, 100, 85, 110))

## Partition additive genetic values
tmp <- AlphaPart(x=ped, colAGV=c("trt1", "trt2"))
print(tmp)

## Summarize by generation
summary(tmp, by="gen")
```

```
## There are also two demos
demo(topic="AlphaPart_deterministic", package="AlphaPart", ask=interactive())
demo(topic="AlphaPart_stochastic", package="AlphaPart", ask=interactive())
```

AlphaPart.ped	<i>Sample pedigree for partition.</i>
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Description

A dataset containing pedigree information and additive genetic value for 48 individuals.

Usage

AlphaPart.ped

Format

A data frame with 48 rows and 9 variables:

id individual's ID

fid Father's ID

mid Mother's ID

loc Location

gen Generation

sex Individual's sex

loc.gen Interaction of location and generation

agv1 First additive genetic value

agv2 Second additive genetic value

Source

Stochastic simulation.

AlphaPartSubset	<i>AlphaPartSubset.R</i>
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Description

A function to choose the partition paths to keep.

Usage

```
AlphaPartSubset(x, paths = NULL)
```

Arguments

x	AlphaPart or summaryAlphaPart, object from the AlphaPart(...) or summary(AlphaPart(...), ...) call.
paths	Character, names of paths to be kept.

Details

Displaying results of partitions for many paths is often confusing. This function helps in selecting only paths of interest. Unspecified paths are removed from the input object x. Meta information is modified accordingly. Default setting does nothing.

Value

An object of class AlphaPart or summaryAlphaPart with only some paths. Meta information in slot "info" is modified as well.

See Also

[AlphaPart](#) for the main method, [summary.AlphaPart](#) for summary method that works on output of AlphaPart, [AlphaPartSum](#) for sum method.

Examples

```
## Small pedigree with additive genetic (=breeding) values
ped <- data.frame( id=c( 1,  2,  3,  4,  5,  6),
                  fid=c( 0,  0,  2,  0,  4,  0),
                  mid=c( 0,  0,  1,  0,  3,  3),
                  loc=c("A", "B", "A", "B", "A", "A"),
                  gen=c( 1,  1,  2,  2,  3,  3),
                  trt1=c(100, 120, 115, 130, 125, 125),
                  trt2=c(100, 110, 105, 100,  85, 110))

## Partition additive genetic values
(tmp <- AlphaPart(x=ped, colAGV=c("trt1", "trt2")))

## Keep some partitions (working on object of class AlphaPart)
(tmp2 <- AlphaPartSubset(x=tmp, paths="A"))
```

```
## Summarize by generation
(tmpS <- summary(tmp, by="gen"))

## Keep some partitions (working on object of class summaryAlphaPart)
(tmpS2 <- AlphaPartSubset(x=tmpS, paths="A"))

## ... must be equal to
(tmpS3 <- summary(tmp2, by="gen"))
```

AlphaPartSum

AlphaPartSum.R

Description

A function to sum partitions of several paths.

Usage

```
AlphaPartSum(x, map = NULL, remove = TRUE, zeroPath = TRUE,
  call = "AlphaPartSum")
```

Arguments

x	summaryAlphaPart, object from the AlphaPart(...) or summary(AlphaPart(...), ...) call.
map	List, a map of summing paths; see details and examples.
remove	Logical, remove original paths or not.
zeroPath	Logical, set called path to zero if it does not exist.
call	character, for internal use with AlphaPartSubset).

Details

Sometimes partitions of particular paths are very small or we want to sum paths that have some similarity. These actions are easy to achieve manually but this function provides a way to do this consistently with the given object x.

Arguments map must be a list of vectors of length at least two. Vectors of length one are skipped. The idea is that the first element is the new or existing path into which we add up all the remaining specified paths, say `list(c("A", "B"), c("X", "X", "Y"), c("Z", "X"))` would imply $A = B$, $X = X + Y$, and $Z = X + X + Y$. Note that once X is changed its changed value is used in further calculations. Specify different (new) names for new targets if you want to avoid this.

Be careful with `remove=TRUE`, which is the default setting, as all partitions defined after the first (target/new) partition in vector in list will be removed, for example with `list(c("A", "B"), c("X", "X", "Y"), c("Z", "X"))` partitions B and Y will be removed, while X will not be removed as it is defined as a target/new partition.

Value

An object of class `AlphaPart` or `summaryAlphaPart` with modified partitions. Meta information in slot "info" is modified as well.

See Also

[AlphaPart](#) for the main method, [summary.AlphaPart](#) for summary method that works on output of `AlphaPart`, [AlphaPartSubset](#) for subset/keep method

Examples

```
## Small pedigree with additive genetic (=breeding) values
ped <- data.frame( id=c( 1,  2,  3,  4,  5,  6),
                  fid=c( 0,  0,  2,  0,  4,  0),
                  mid=c( 0,  0,  1,  0,  3,  3),
                  loc=c("A", "B", "A", "B", "A", "A"),
                  gen=c( 1,  1,  2,  2,  3,  3),
                  trt1=c(100, 120, 115, 130, 125, 125),
                  trt2=c(100, 110, 105, 140, 85, 110))

## Partition additive genetic values
(tmp <- AlphaPart(x=ped, colAGV=c("trt1", "trt2")))

## Sum some partitions (working on object of class AlphaPart)
(tmp2 <- AlphaPartSum(x=tmp, map=list(c("X", "A", "B"), c("A", "B"))))

## Summarize by generation
(tmpS <- summary(tmp, by="gen"))

## Sum some partitions (working on object of class summaryAlphaPart)
(tmpS2 <- AlphaPartSum(x=tmpS, map=list(c("X", "A", "B"), c("A", "B"))))

## ... must be equal to
(tmpS3 <- summary(tmp2, by="gen"))
```

pedFixBirthYear

pedFixBirthYear.R

Description

A function to fix (impute) missing birth years in pedigree.

Usage

```
pedFixBirthYear(x, interval, down = FALSE, na.rm = TRUE, sort = TRUE,
               direct = TRUE, report = TRUE, colId = 1, colFid = 2,
               colMid = 3, colBY = 4)
```


Arguments

x	data.frame , with (at least) the following columns: individual, father, and mother identification, and year of birth; see arguments colId, colFid, colMid, and colBY
interval	Numeric, a value for generation interval in years.
down	Logical, the default is to impute birth years based on the birth year of children starting from the youngest to the oldest individuals, while with down=TRUE birth year is imputed based on the birth year of parents in the opposite order.
na.rm	Logical, remove NA values when searching for the minimal (maximal) year of birth in children (parents); setting this to FALSE can lead to decreased success of imputation
sort	Logical, initially sort x using orderPed() so that children follow parents in order to make imputation as optimal as possible (imputation is performed within a loop from the first to the last unknown birth year); at the end original order is restored.
direct	Logical, insert inferred birth years immediately so they can be used for successive individuals within the loop.
report	Logical, report success.
colId	Numeric or character, position or name of a column holding individual identification.
colFid	Numeric or character, position or name of a column holding father identification.
colMid	Numeric or character, position or name of a column holding mother identification.
colBY	Numeric or character, position or name of a column holding birth year.

Details

Warnings are issued when there is no information to use to impute birth years or missing values (NA) are propagated.

Arguments down and na.rm allow for repeated use of this function, i.e., with down=FALSE and with down=TRUE (both in combination with na.rm=TRUE) in order to propagate information over the pedigree until "convergence".

This function can be very slow on large pedigrees with extensive missingness of birth years.

Value

Object x with imputed birth years based on the birth year of children or parents. If report=TRUE success is printed on the screen as the number of initially, fixed, and left unknown birth years is printed.

See Also

[orderPed](#) in **pedigree** package

Examples

```
## Example pedigree with missing (unknown) birth year for some individuals
ped0 <- data.frame(  id=c( 1, 2, 3,  4, 5, 6, 7,  8, 9, 10, 11, 12, 13, 14),
                    fid=c( 0, 0, 0,  1, 1, 1, 3,  3, 3, 5, 4, 0,  0, 12),
                    mid=c( 0, 0, 0,  2, 0, 2, 2,  2, 5, 0, 0, 0,  0, 13),
                    birth_dt=c(NA, 0, 1, NA, 3, 3, 3, 3, 4, 4, 5, NA, 6, 6) + 2000)

## First run - using information from children
ped1 <- pedFixBirthYear(x=ped0, interval=1)

## Second run - using information from parents
ped2 <- pedFixBirthYear(x=ped1, interval=1, down=TRUE)

## Third run - using information from children, but with no success
ped3 <- pedFixBirthYear(x=ped2, interval=1)
```

pedSetBase

pedSetBase.R

Description

A function to set the base population in the pedigree.

Usage

```
pedSetBase(x, keep = NULL, unknown = NA, report = TRUE, colId = 1,
           colFid = 2, colMid = 3)
```

Arguments

x	data.frame , with (at least) the following columns: individual, father, and mother identification, and year of birth; see arguments colId, colFid, colMid, and colBY
keep	Logical, indicator that defines which individuals should stay in the the pedigree; see details.
unknown	Value used to represent unknown/missing identification
report	Logical, report success.
colId	Numeric or character, position or name of a column holding individual identification.
colFid	Numeric or character, position or name of a column holding father identification.
colMid	Numeric or character, position or name of a column holding mother identification.

Details

Base population in the pedigree is set by removing rows for some individuals, while their presence as parents is also removed.

Arguments `down` and `na.rm` allow for repeated use of this function, i.e., with `down=FALSE` and with `down=TRUE` (both in combination with `na.rm=TRUE`) in order to propagate information over the pedigree until "convergence".

This function can be very slow on large pedigrees with extensive missingness of birth years.

Value

Object `x` with removed rows for some individuals and their presence as parents. If `report=TRUE` progress is printed on the screen.

See Also

[orderPed](#) in **pedigree** package

Examples

```
## Example pedigree
ped <- data.frame(
  id=1:10,
  fid=c(0, 0, 0, 1, 1, 1, 3, 3, 3, 5),
  mid=c(0, 0, 0, 2, 0, 2, 2, 2, 5, 0),
  birth_dt=c(0, 0, 1, 2, 3, 3, 3, 4, 4, 5) + 2000)

## Set base population as those individuals that were born after year 2002
pedSetBase(x=ped, keep=ped$birth_dt > 2002, unknown=0)
```

plot.summaryAlphaPart *plot.summaryAlphaPart.R*

Description

A function to plot summary of partitioned additive genetic values.

Usage

```
## S3 method for class 'summaryAlphaPart'
plot(x, sortValue = TRUE,
     sortValueFUN = sum, sortValueDec = TRUE, addSum = TRUE,
     paths = NULL, xlab = NULL, ylab = NULL, xlim = NULL,
     ylim = NULL, ylimRel = NULL, color, lineSize = 1, lineType = 1,
     lineTypeList = NULL, useDirectLabels = TRUE, method = list(last.qp,
     hjust = 0), labelPath = NULL, ...)
```

Arguments

x	summaryAlphaPart, object from the AlphaPart(...) or summary(AlphaPart(...), ...) call.
sortValue	Logical, affect legend attributes via sort of paths according to sortValueFUN function; if not logical, then ordered paths are given as a character vector.
sortValueFUN	Function, that produces single value for one vector, say mean or sum.
sortValueDec	Logical, sort decreasing.
addSum	Logical, plot the overall trend.
paths	Character or list or characters, name of paths to plot; if NULL plot all paths; see examples.
xlab	Character, x-axis label.
ylab	Character, y-axis label; can be a vector of several labels if there are more traits in x (recycled!).
xlim	Numeric, a vector of two values with x-axis limits; use a list of vectors for more traits.
ylim	Numeric, a vector of two values with y-axis limits; use a list of vectors for more traits.
ylimRel	Numeric, a vector of two values with y-axis limits for relative values; use a list of vectors for more traits.
color	Character, color names; by default a set of 54 colors is predefined from the RColorBrewer package; in addition a black colour is attached at the beginning for the overall trend; if there are more paths than colors then recycling occurs.
lineSize	Numeric, line width.
lineType	Numeric, line type (recycled); can be used only if lineTypeList=NULL.
lineTypeList	List, named list of numeric values that help to point out a set of paths (distinguished with line type) within upper level of paths (distinguished by, color), e.g., lineTypeList=list("-1"=1, "-2"=2, def=1) will lead to use of line type 1 for paths having "-1" at the end of path name and line type 2, for paths having "-2" at the end of path name, while line type 1 (default) will, be used for other paths; specification of this argument also causes recycling of colors for the upper level of paths; if NULL all lines have a standard line type, otherwise lineType does not have any effect.
useDirectLabels	Logical, use directlabels package for legend.
method	List, method for direct.label.
labelPath	Character, legend title; used only if useDirectLabels=FALSE.
...	Arguments passed to other functions (not used at the moment).

Details

Information in summaries of partitions of additive genetic values can be overwhelming due to a large volume of numbers. Plot method can be used to visualise this data in eye pleasing way using ggplot2 graphics.

Value

A list of ggplot objects that can be further modified or displayed. For each trait in x there are two plots (one for absolute values and one for relative values).

Examples

```
## Load an example data
data("AlphaPart.ped")

## Partition additive genetic values by location
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc", colAGV=c("agv1", "agv2")))

## Summarize population by generation (=trend)
(ret <- summary(res, by="gen"))

## Plot the partitions
p <- plot(ret, ylab=c("AGV for trait 1", "AGV for trait 2"), xlab="Generation")
print(p[[1]]$abs)
print(p[[1]]$rel)
print(p[[2]])
print(p)

## Partition additive genetic values by location and sex
AlphaPart.ped$loc.sex <- with(AlphaPart.ped, paste(loc, sex, sep="-"))
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc.sex", colAGV=c("agv1", "agv2")))

## Summarize population by generation (=trend)
(ret <- summary(res, by="gen"))

## Plot the partitions
p <- plot(ret, ylab=c("AGV for trait 1", "AGV for trait 2"), xlab="Generation")
print(p)
p <- plot(ret, ylab=c("AGV for trait 1", "AGV for trait 2"), xlab="Generation",
          lineTypeList=list("-1"=1, "-2"=2, def=3))
print(p)
p <- plot(ret, ylab=c("AGV for trait 1", "AGV for trait 2"), xlab="Generation",
          lineTypeList=list("-1"=1, "-2"=2, def=3), useGgplot2=FALSE, useDirectLabels = FALSE)
print(p)

## Plot control (color and type of lines + limits)
p <- plot(ret, ylab=c("AGV for trait 1", "AGV for trait 2"), xlab="Generation",
          useGgplot2=TRUE, color=c("green", "gray"), lineType=c(2, 3),
          sortValue=FALSE, lineSize=4,
          xlim=c(-1, 7))
print(p)
```

Description

Print method for the output of AlphaPart function.

Usage

```
## S3 method for class 'AlphaPart'
print(x, n = 6, ...)
```

Arguments

`x` AlphaPart, output object from [AlphaPart](#) function.

`n` Integer, number of the first and last rows in `x` to print out using [head](#) and [tail](#).

`...` Arguments passed to other functions (not used at the moment).

Details

Partitioning of additive genetic values is often performed on quite large datasets, which quickly fills in the whole screen. Print method therefore prints out paths, number of individuals and the first and the last few lines for each trait to quickly see what kind of data is in `x`.

See Also

[AlphaPart](#), [head](#), [tail](#).

Examples

```
## Small pedigree with additive genetic (=breeding) values
ped <- data.frame( id=c( 1,  2,  3,  4,  5,  6),
                  fid=c( 0,  0,  2,  0,  4,  0),
                  mid=c( 0,  0,  1,  0,  3,  3),
                  loc=c("A", "B", "A", "B", "A", "A"),
                  gen=c( 1,  1,  2,  2,  3,  3),
                  trt1=c(100, 120, 115, 130, 125, 125),
                  trt2=c(100, 110, 105, 100,  85, 110))

## Partition additive genetic values
tmp <- AlphaPart(x=ped, colAGV=c("trt1", "trt2"))
print(tmp)

## Summarize by generation
summary(tmp, by="gen")

## There are also two demos
demo(topic="AlphaPart_deterministic", package="AlphaPart", ask=interactive())
demo(topic="AlphaPart_stochastic",   package="AlphaPart", ask=interactive())
```

```
print.plotSummaryAlphaPart  
    print.plotSummaryAlphaPart.R
```

Description

#' Print method for objects of the class plotSummaryAlphaPart (result of plot(summary(AlphaPart(...)))).

Usage

```
## S3 method for class 'plotSummaryAlphaPart'  
print(x, ask = interactive(), ...)
```

Arguments

x	plotSummaryAlphaPart, output object from plot.summaryAlphaPart function
ask	Logical, ask before printing another plot?
...	Arguments passed to other functions (not used at the moment).

Details

TODO: DETAILS

See Also

[plot.summaryAlphaPart](#)

Examples

```
## Load an example data  
data("AlphaPart.ped")  
  
## Partition additive genetic values  
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc", colAGV=c("agv1", "agv2")))  
  
## Summarize population by generation (=trend)  
(ret <- summary(res, by="gen"))  
  
## Plot the partitions  
p <- plot(ret, ylab=c("AGV for trait 1", "AGV for trait 2"), xlab="Generation")  
print(p[[1]]$abs)  
print(p[[1]]$rel)  
print(p[[2]]$abs)  
print(p[[2]])  
print(p)
```

```
print.summaryAlphaPart
      print.summaryAlphaPart.R
```

Description

Print method for objects of the class `summaryAlphaPart`.

Usage

```
## S3 method for class 'summaryAlphaPart'
print(x, ...)
```

Arguments

```
x          summaryAlphaPart, output object from summary.AlphaPart function.
...        Arguments passed to other functions (not used at the moment).
```

Details

Print method for objects of the class `summaryAlphaPart` (result of `summary(AlphaPart(...))`).

See Also

[summary.AlphaPart](#)

Examples

```
## Load an example data
data("AlphaPart.ped")

## --- Partition additive genetic values by loc ---
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc", colAGV=c("agv1", "agv2")))

## Summarize whole population
(ret <- summary(res))

## Summarize population by generation (=trend)
(ret <- summary(res, by="gen"))

## Summarize population by generation (=trend) and location 1
(ret <- summary(res, by="loc.gen"))

## Summarize population by generation (=trend) but only for location 1
(ret <- summary(res, by="gen", subset=res[[1]]$loc == 1))

## --- Partition additive genetic values by loc and sex ---
AlphaPart.ped$loc.sex <- with(AlphaPart.ped, paste(loc, sex, sep="-"))
```



```
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc.sex", colAGV=c("agv1", "agv2")))

## Summarize population by generation (=trend)
(ret <- summary(res, by="gen"))

## Summarize population by generation (=trend) and location 1
(ret <- summary(res, by="loc.gen"))

## Summarize population by generation (=trend) but only for location 1
(ret <- summary(res, by="gen", subset=res[[1]]$loc == 1))
```

savePlot

savePlot.plotSummaryAlphaPart.R

Description

Save plot objects on the disk for permanent storage. Function `savePlot` from the **grDevices** package works for current page on graphical device. This is an attempt to make this function generic so that one can define `savePlot` methods for particular needs.

Usage

```
savePlot(x, filename = paste("Rplot", type, sep = "."), type = c("pdf",
  "png", "jpeg", "tiff", "bmp"), device = dev.cur(), ...)
```

```
## S3 method for class 'plotSummaryAlphaPart'
savePlot(x, filename = paste("Rplot",
  type, sep = "."), type = c("pdf", "png", "jpeg", "tiff", "bmp"),
  device = dev.cur(), pre.hook = NULL, traitsAsDir = FALSE, ...)
```

Arguments

<code>x</code>	Object on which to chose savePlot method.
<code>filename</code>	Character, filename to save to.
<code>type</code>	Character, file/device type.
<code>device</code>	Device, the device to save from. TODO
<code>...</code>	Arguments passed to type specific methods, say width and height for type="pdf" etc.
<code>pre.hook</code>	Function, call some code before calling print method for plots (see examples).
<code>traitsAsDir</code>	Logical, should plots be saved within trait folders; the construction is <code>file.path(dirname(file), trait)</code> folders are created if they do not exist.

Value

Beside the side effect of saving plots to disk, filenames are printed on screen during the process and at the end invisibly returned.

Methods (by class)

- plotSummaryAlphaPart: Save plot objects of class plotSummaryAlphaPart on the disk for permanent storage.

See Also

[savePlot](#) help page on the default savePlot method in the **grDevices** package; [savePlot.plotSummaryAlphaPart](#) help page on the method for the objects of plotSummaryAlphaPart class; and [plot.summaryAlphaPart](#) for plotting results of summaryAlphaPart object.

Examples

```
## Load an example data
data("AlphaPart.ped")

## --- Partition additive genetic values by loc ---
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc", colAGV=c("agv1", "agv2")))

## Summarize whole population
(ret <- summary(res))

## Summarize population by generation (=trend)
(ret <- summary(res, by="gen"))

## Summarize population by generation (=trend) and location 1
(ret <- summary(res, by="loc.gen"))

## Summarize population by generation (=trend) but only for location 1
(ret <- summary(res, by="gen", subset=res[[1]]$loc == 1))

## --- Partition additive genetic values by loc and sex ---

AlphaPart.ped$loc.sex <- with(AlphaPart.ped, paste(loc, sex, sep="-"))
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc.sex", colAGV=c("agv1", "agv2")))

## Summarize population by generation (=trend)
(ret <- summary(res, by="gen"))

## Summarize population by generation (=trend) and location 1
(ret <- summary(res, by="loc.gen"))

## Summarize population by generation (=trend) but only for location 1
(ret <- summary(res, by="gen", subset=res[[1]]$loc == 1))
```

summary.AlphaPart

summary.AlphaPart.R

Description

A function to summarize AlphaPart object.

Usage

```
## S3 method for class 'AlphaPart'
summary(object, by = NULL, FUN = mean,
        labelSum = "Sum", subset = NULL, sums = FALSE, ...)
```

Arguments

object	AlphaPart, output object from AlphaPart function.
by	Character, the name of a column by which summary function FUN should be applied; if NULL (default) summary is given for the whole table.
FUN	Function, which function should be used in summary; function should return single value per each level of by.
labelSum	Character, label used for the overall additive genetic value.
subset	Logical, perform summary only on a subset of object subsetted by this argument.
sums	Logical, link between AlphaPart and summary.AlphaPart() (only for internal use!).
...	Arguments passed to other functions (not used at the moment).

Details

Additive genetic values of individuals are often summarized, either by year of birth or some other classification. Function `summary.AlphaPart` provides a way to ease the computation of such summaries on partitions of additive genetic values.

Value

An object of class `summaryAlphaPart`, which is a list of data frames with summary statistics on additive genetic value partitions. For each trait there is a list component holding two dataframes. The first data.frame is called `abs` and holds summary for the "whole/original" additive genetic value and its partitions, while the second data.frame is called `rel` and holds relative values of `abs` counterpart. In addition another list is added (named `info`) with the following components holding meta info:

path	column name holding path information
nP	number of paths
lP	path labels
nT	number of traits
lT	trait labels
by	column name of variable by which summary was performed
warn	potential warning messages associated with this object
labelSum	column name of summary for "whole/original" additive genetic values

There is a handy plot method (`plot.summaryAlphaPart`) for output.

See Also

[AlphaPart](#) for partitioning additive genetic values, [plot.summaryAlphaPart](#) for plotting output of summary method

Examples

```
## Load an example data
data("AlphaPart.ped")

## --- Partition additive genetic values by loc ---
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc", colAGV=c("agv1", "agv2")))

## Summarize whole population
(ret <- summary(res))

## Summarize population by generation (=trend)
(ret <- summary(res, by="gen"))

## Summarize population by generation (=trend) and location 1
(ret <- summary(res, by="loc.gen"))

## Summarize population by generation (=trend) but only for location 1
(ret <- summary(res, by="gen", subset=res[[1]]$loc == 1))

## --- Partition additive genetic values by loc and sex ---

AlphaPart.ped$loc.sex <- with(AlphaPart.ped, paste(loc, sex, sep="-"))
(res <- AlphaPart(x=AlphaPart.ped, colPath="loc.sex", colAGV=c("agv1", "agv2")))

## Summarize population by generation (=trend)
(ret <- summary(res, by="gen"))

## Summarize population by generation (=trend) and location 1
(ret <- summary(res, by="loc.gen"))

## Summarize population by generation (=trend) but only for location 1
(ret <- summary(res, by="gen", subset=res[[1]]$loc == 1))
```

write.csv

write.csv.R

Description

Save summaries of partitioned additive genetic values to CSV files on disk for further analyses of processing with other software or just for saving (backing up) results.

Usage

```
write.csv(...)

## Default S3 method:
write.csv(...)

## S3 method for class 'AlphaPart'
write.csv(x, file, traitsAsDir = FALSE,
          csv2 = TRUE, row.names = FALSE, ...)

## S3 method for class 'summaryAlphaPart'
write.csv(x, file, traitsAsDir = FALSE,
          csv2 = TRUE, row.names = FALSE, ...)
```

Arguments

...	Other options passed to write.csv2 or write.csv .
x	AlphaPart, object returned from AlphaPart function or summaryAlphaPart, object returned from summary.AlphaPart function.
file	Character, file name with or without .csv extension, e.g., both "file" and "file.csv" are valid.
traitsAsDir	Logical, should results be saved within trait folders; the construction is <code>file.path(dirname(file), trait)</code> , folders are created if they do not exist.
csv2	Logical, export using write.csv2 or write.csv .
row.names	Logical, export row names as well?

Details

Function [write.csv](#) from the [utils](#) package works when exported object is a [data.frame](#) or a [matrix](#). This is an attempt to make this function generic so that one can define `write.csv` methods for other objects.

Value

`write.csv` See [write.csv](#) for details.
`write.csv.AlphaPart`

For each trait (list component in `x`) a file is saved on disk with name "file_trait.csv", where the file will hold original data and additive genetic value partitions. With `traitsAsDir=TRUE` files are saved as "trait/file_trait.csv". File names are printed on screen during the process of export and at the end invisibly returned.

`litemwrite.csv.summaryAlphaPart` For each trait (list component in `x`) two files are saved on disk with names "file_trait_abs.csv" and "file_trait_rel.csv", where the first file will hold absolute values and the second file will hold relative values of additive genetic value partitions. With `traitsAsDir=TRUE` files are saved as "trait/file_trait_*.csv". File names are printed on screen during the process of export and at the end invisibly returned.

Methods (by class)

- default: Default write.csv method.
- AlphaPart: Save partitioned additive genetic values to CSV files on disk on disk for further analyses or processing with other software or just for saving (backing up) results.
- summaryAlphaPart: Save summaries of partitioned additive genetic values to CSV files on disk for further analyses of processing with other software or just for saving (backing up) results.

See Also

[write.csv](#) help page on the default write.csv and write.csv2 methods in the **utils** package; [summary.AlphaPart](#) and [AlphaPart](#) help pages on the objects of summaryAlphaPart and AlphaPart classes.

Examples

```
## Load an example data
data("AlphaPart.ped")

## Partition additive genetic values
res <- AlphaPart(x=AlphaPart.ped, colPath="loc", colAGV=c("agv1", "agv2"))

## Write summary on the disk and collect saved file names
fileName <- file.path(tempdir(), "AlphaPart")
ret <- write.csv(x=res, file=fileName)
print(ret)
file.show(ret[1])

## Clean up
files <- dir(path=tempdir(), pattern="AlphaPart*")
unlink(x=files)
```

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