Package 'GenTag'

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Type Package

Title Generate Color Tag Sequences

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Description Implement a coherent and flexible protocol for animal color tagging. 'GenTag' provides a simple computational routine with low CPU usage to create color sequences for animal tag. First, a single-color tag sequence is created from an algorithm selected by the user, followed by verification of the combination uniqueness. Three methods to produce color tag sequences are provided. Users can modify the main function core to allow a wide range of applications.

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Contents

`GenTag-package` *Generate Color Tag Sequences*

Description

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Details

The DESCRIPTION file:

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Title:	Generate Color Tag Sequences
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Index of help topics:

`GenTag-package`	`Generate Color Tag Sequences`
`allequal`	`All equal tag sequence sample`
`erc`	`Estimates remaining color`
`escode`	`Empty synonym code`
`escombination`	`Empty synonym combination`
`esdataset`	`Empty synonym dataset`
`genseq`	`Color tag combination generator`
`lifexp`	`Life expectancy tag sequence sample`
`pre_used`	`Pre-used combinations combinations`
`scy`	`Summary color year`
`vfrequency`	`Variable frequency tag sequence sample`

Implement a coherent and flexible protocol for animal color tagging. 'GenTag' provides a simple computational routine with low CPU usage to create color sequences for animal tag. First, a single-color tag sequence is created from an algorithm selected by the user, followed by verification of the combination uniqueness. Three methods to produce color tag sequences are provided. Users can modify the main function core to allow a wide range of applications.

Author(s)

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Examples

```
genseq(30, 4,c("Black","Blue","Brown","Gray","Green"))
```

`allequal` *All equal tag sequence sample*

Description

Create combinations with equal sample probability to all colors.

Usage

```
allequal(ntag, colorsname, nspecial = 0, name1 = "Metal", name2 = "EMPTY", location1 = 1,
location2 = 2, nspecial1 = 1, nspecial2 = 1)
```

Arguments

`ntag`	Number of tag to be used in each animal.
`colorsname`	Names/Code of color tags to be sample.
`nspecial`	Number of special tags/codes, such as metallic, "EMPTY", or flag (min 0, max 2).
`name1`	Name of special tag 1.
`name2`	Name of special tag 2.
`location1`	Position (or group of positions) to special band 1.
`location2`	Position (or group of positions) to special band 2.
`nspecial1`	Number of special tag 1 that will be present in all sequences genetated.
`nspecial2`	Number of special tag 2 that will be present in all sequences genetated.

Value

A sequencie of tags

Author(s)

Biagolini-Jr.

See Also

genseq vfrequency lifexp

Examples

```
# Create an object contain the name/code of tag colors
tcol<-c("Black","Blue","Brown","Gray","Green","Pink","Purple","Red","White","Yellow")
# Generate color tag combination without especial tags
genseq(30, 4, colorsname= tcol)
#Generate color tag combination with especial color (ex metallic tag for numeric identification)
genseq(30, 4, tcol, nspecial=1, name1="Metal",location1=c(2,4))
# For ongoing works, use the argument usedcombinations to informe the previus used combinations
data(pre_used) # Data example
genseq(100, 4, tcol, usedcombinations=pre_used[,1:4])
```

`erc` *Estimates remaining color*

Description

Estimates number of remaining color tags in the field

Usage

```
erc(usedcombinations, yearusedcombinations, currentyear = NA,
  yearsurvival = NA, lifespan = NA, hide_color = NA)
```

Arguments

`usedcombinations`	Pre used combinations
`yearusedcombinations`	The year in which the combination was used.
`currentyear`	Current year.
`yearsurvival`	An estimation of the proportion of animals that survive between years.
`lifespan`	Combinations older the lifespan will be automatically disregard.
`hide_color`	Color(s) to be hide in the estimation of remain colors tags present in nature.

Value

A estimation of the number of remaining color tags in the field.

Author(s)

Biagolini-Jr.

See Also

scy

Examples

```
## The function is currently defined as
data(pre_used) # Data example
erc(pre_used[,1:4],pre_used[,5],2019,0.85, hide_color="EMPTY")
```

`escode` *Empty synonym code*

Description

Find synonyms in a group of colors with code for empty tag.

Usage

```
escode(row_under_review, emptyname = NA, columns_set = NA)
```

Arguments

`row_under_review`	Color sequence to be analyzed.
`emptyname`	Code used to define empty code.
`columns_set`	Range of codes which belong to the same tag region.

Value

Matrix with all synonym

Examples

```
# Example of a full sequence
combination<- c("EMPTY","Red","Yellow","Red","Blue","Green")
# See synonym for the code group 1 to 3
escode(combination,"EMPTY",columns_set=1:3)
```

`escombination` *Empty synonym combination*

Description

Find synonyms of a sequence with code for empty tag.

Usage

```
escombination(row_under_review, emptyname,
g1 = NA, g2 = NA, g3 = NA, g4 = NA, g5 = NA, g6 = NA)
```

Arguments

`row_under_review`	Color sequence to be analyzed.
`emptyname`	Code used to define empty code.
`g1`	Group of tags from group 1.
`g2`	Group of tags from group 2.
`g3`	Group of tags from group 3.
`g4`	Group of tags from group 4.
`g5`	Group of tags from group 5.
`g6`	Group of tags from group 6.

Value

Matrix with all synonyms

Author(s)

Biagolini-Jr

See Also

escode esdataset

Examples

```
# Example of a full sequence
combination<- c("EMPTY","Red","Yellow","Red","Blue","Green")  # See synonym for the full sequence
escombination(combination,"EMPTY",g1=1:3,g2=4:6)
```

`esdataset` *Empty synonym dataset*

Description

Find synonyms in a dataset contain combination with code for empty tag.

Usage

```
esdataset(tag_sheet, emptyname, g1 = NA, g2 = NA, g3 = NA, g4 = NA, g5 = NA, g6 = NA)
```

Arguments

`tag_sheet`	Dataset contain sequences to be analyzed.
`emptyname`	Code used to define empty code.
`g1`	Group of tags from group 1. For example, in a code of 6 colors for bird tag, tags from 1 to 3 belongs to the left leg, and tags from 1 to 3 belongs to the right. g1 must to address the left leg, and g2 must to address right leg. Thus: "g1=1:3" and "g2=4:6".
`g2`	Group of tags from group 2. For example, in a code of 6 colors for bird tag, tags from 1 to 3 belongs to the left leg, and tags from 1 to 3 belongs to the right. g1 must to address the left leg, and g2 must to address right leg. Thus: "g1=1:3" and "g2=4:6".
`g3`	Group of tags from group 3.
`g4`	Group of tags from group 4.
`g5`	Group of tags from group 5.
`g6`	Group of tags from group 6.

Value

Matrix with all synonyms for from entire dataset

Author(s)

Biagolini-Jr.

See Also

escode escombination

Examples

```
(combination<- matrix(c(”EMPTY”,”Red”,”Blue”,”Green”),4,6,TRUE)) # Example of a dataset
esdataset(combination,”EMPTY”,g1=1:3,g2=4:6)
```

`genseq` *Color tag combination generator*

Description

Create sequences of color tags for animal identification.

Usage

```
genseq(ncombinations = 100, ntag = 4, colorsname, gen_method = "allequal",
usedcombinations = NA, colorsf = NA, nspecial = 0, name1 = "Metal", name2 = "EMPTY",
location1 = 1, location2 = 2, nspecial1 = 1, nspecial2 = 1, emptyused = FALSE,
emptyname = "EMPTY", currentyear = NA, yearsurvival = 1, lifespan = NA, iotf = FALSE,
yearusedcombinations = NA, speed = 1, ignorecolor = NA,
g1 = NA, g2 = NA, g3 = NA, g4 = NA, g5 = NA, g6 = NA, parameterslist = NA)
```

Arguments

`ncombinations`	Number of combinations to be generated.
`ntag`	Number of tag to be used in each animal.
`colorsname`	Names/Code of color tags to be sample.
`gen_method`	method used for sample colors for tag sequence.
`usedcombinations`	Pre used combinations.
`colorsf`	Frequencies/ratio for color sample.
`nspecial`	Number of special tags/codes, such as metallic, "EMPTY", or flag (min 0, max 2).
`name1`	Name of special tag 1.
`name2`	Name of special tag 2.
`location1`	Position (or group of positions) to special band 1.
`location2`	Position (or group of positions) to special band 2.
`nspecial1`	Number of special tag 1 that will be present in all sequences genetated.
`nspecial2`	Number of special tag 2 that will be present in all sequences genetated.
`emptyused`	If pre-used combination has code for empty set as TRUE, otherwise FALSE
`emptyname`	Code used to define empty code.
`currentyear`	Current year.
`yearsurvival`	An estimation of the proportion of animals that survive between years.
`lifespan`	Combinations older the lifespan will be automatically disregard.
`iotf`	Ignore older than lifespan. If TRUE ignore pre-used combinations older than lifespan
`yearusedcombinations`	The year in which the combination was used.
`speed`	Speed for color frequency adjustment.
`ignorecolor`	Color to be ignored on lifexp.
`g1`	Group of tags from group 1. For example, in a code of 6 colors for bird tag, tags from 1 to 3 belongs to the left leg, and tags from 1 to 3 belongs to the right. g1 must to address the left leg, and g2 must to address right leg. Thus: "g1=1:3" and "g2=4:6".

`g2`	Group of tags from group 2. For example, in a code of 6 colors for bird tag, tags from 1 to 3 belongs to the left leg, and tags from 1 to 3 belongs to the right. g1 must to address the left leg, and g2 must to address right leg. Thus: "g1=1:3" and "g2=4:6".
`g3`	Group of tags from group 3.
`g4`	Group of tags from group 4.
`g5`	Group of tags from group 5.
`g6`	Group of tags from group 6.
`parameterslist`	parameters for methods not provide by 'GenTag'

Value

A list of combinations

Author(s)

Biagolini-Jr.

See Also

allequal vfrequency lifexp

Examples

```
# Create an object contain the name/code of tag colors
tcol<-c("Black","Blue","Brown","Gray","Green","Pink","Purple","Red","White","Yellow")
# Generate color tag combination without especial tags
genseq(30, 4, colorsname= tcol)
#Generate color tag combination with especial color (ex metallic tag for numeric identification)
genseq(30, 4, tcol, nspecial=1, name1="Metal", location1=c(2,4))
# For ongoing works, use the argument usedcombinations to informe the previus used combinations
data(pre_used) # Data example
genseq(30, 4, colorsname= tcol, usedcombinations=pre_used[,1:4])
combinations<-genseq(100, 4, tcol) # save combinations into an object
```

`lifexp` *Life expectancy tag sequence sample*

Description

Create combinations with variable sample probability.

Usage

```
lifexp(ntag, colorsname, nspecial = 0, name1 = "Metal", name2 = "EMPTY",
location1 = 1, location2 = 2, nspecial1 = 1, nspecial2 = 1, currentyear = NA,
 yearsurvival = 1, lifespan = NA, yearusedcombinations,
usedcombinations, speed = 1, ignorecolor = NA)
```

Arguments

`ntag`	Number of tag to be used in each animal.
`colorsname`	Names/Code of color tags to be sample.
`nspecial`	Number of special tags/codes, such as metallic, "EMPTY", or flag (min 0, max 2).
`name1`	Name of special tag 1.
`name2`	Name of special tag 2.
`location1`	Position (or group of positions) to special band 1.
`location2`	Position (or group of positions) to special band 2.
`nspecial1`	Number of special tag 1 that will be present in all sequences genetated.
`nspecial2`	Number of special tag 2 that will be present in all sequences genetated.
`currentyear`	Current year.
`yearsurvival`	An estimation of the proportion of animals that survive between years.
`lifespan`	Combinations older the lifespan will be automatically disregard.
`yearusedcombinations`	The year in which the combination was used.
`usedcombinations`	Pre used combinations.
`speed`	Speed for color frequency adjustment.
`ignorecolor`	Color to be ignored on lifexp.

Value

A sequencie of tags

Author(s)

Biagolini-Jr.

See Also

allequal genseq vfrequency

Examples

```
data(pre_used) # Data example
# Create an object contain the name/code of tag colors
tcol<-c("Black","Blue","Brown","Gray","Green","Pink","Purple","Red","White","Yellow")
genseq(30, 4,tcol, "lifexp", pre_used[,1:4],
yearusedcombinations=pre_used[,5], yearsurvival= 0.8, lifespan=5, currentyear=2019)
```

`pre_used` *Pre-used combinations combinations*

Description

Simulated data of pre-used combinations

Usage

```
data("pre_used")
```

Format

A data frame with 1200 observations on the following 5 variables.

`Tag_1` a factor with levels `Black` `Brown` `Dark_Blue` `EMPTY` `Gray` `Green` `Light_Blue` `Orange` `Pink` `Red` `White` `Yellow`

`Tag_2` a factor with levels `Black` `Brown` `Dark_Blue` `Gray` `Green` `Light_Blue` `Metal` `Orange` `Pink` `Red` `White` `Yellow`

`Tag_3` a factor with levels `Black` `Brown` `Dark_Blue` `EMPTY` `Gray` `Green` `Light_Blue` `Orange` `Pink` `Red` `White` `Yellow`

`Tag_4` a factor with levels `Black` `Brown` `Dark_Blue` `Gray` `Green` `Light_Blue` `Metal` `Orange` `Pink` `Red` `White` `Yellow`

`Year` a numeric vector

Details

Simulated database to example of registers of color tag sequences usage. Columns 1, 2 ,3 and 4 represent the tag code, and column 5 is the date of tagging.

Source

Simulated database

Examples

```
data(pre_used)
```

`scy` *Summary color year*

Description

Summary the number of each color tag used per year.

Usage

```
scy(usedcombinations, yearusedcombinations, hide_color = NA)
```

Arguments

`usedcombinations`	Pre used combinations.
`yearusedcombinations`	The year in which the combination was used.
`hide_color`	Color(s) to be hide in the estimation of remain colors tags present in nature.

Value

A summary of the numeber of tag colors used by year

Author(s)

Biagolini-Jr.

See Also

erc

Examples

```
data(pre_used) # Data example
scy(pre_used[,1:4],pre_used[,5], hide_color="EMPTY")
```

`vfrequency` *Variable frequency tag sequence sample*

Description

Create combinations with defined sample probability to each colors.

Usage

```
vfrequency(ntag, colorsname, colorsf, nspecial = 0, name1 = "Metal",
name2 = "EMPTY", location1 = 1, location2 = 2, nspecial1 = 1, nspecial2 = 1)
```

Arguments

`ntag`	Number of tag to be used in each animal.
`colorsname`	Names/Code of color tags to be sample.
`colorsf`	Frequencies/ratio for color sample.
`nspecial`	Number of special tags/codes, such as metallic, "EMPTY", or flag (min 0, max 2).
`name1`	Name of special tag 1.
`name2`	Name of special tag 2.
`location1`	Position (or group of positions) to special band 1.
`location2`	Position (or group of positions) to special band 2.
`nspecial1`	Number of special tag 1 that will be present in all sequences genetated.
`nspecial2`	Number of special tag 2 that will be present in all sequences genetated.

Value

A sequencie of tags

Author(s)

Biagolini-Jr

See Also

allequal genseq lifexp

Examples

```
tcol<-c("Black","Blue","Brown","Gray","Green","Pink","Purple","Red","White","Yellow")
p<-c(1,2,5,1,2,2,4,5,8,5)
genseq(30, 4, tcol, gen_method="vfrequency", colorsf=p)
```

Index