

Package: GenTag (via r-universe)

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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.

License GPL (>= 2)

URL <https://github.com/biagolini/GenTag>

Depends R (>= 3.5.0), base

Encoding UTF-8

VignetteBuilder knitr

RoxygenNote 6.1.1

Suggests knitr, rmarkdown, covr, testthat (>= 2.1.0)

Repository <https://biagolini.r-universe.dev>

RemoteUrl <https://github.com/biagolini/gentag>

RemoteRef HEAD

RemoteSha 9d8e783acf5a5ad70adeed43b43b564663124da7

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allequal	<i>All equal tag sequence sample</i>
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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 sequeinc of tags

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 previous 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.

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	<i>Empty synonym code</i>
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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	<i>Empty synonym combination</i>
---------------	----------------------------------

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. For example, in a code of 6 colors for bird tag, tags from 1 to 3 belongs to the left leg, and tags from 4 to 6 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 4 to 6 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

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 4 to 6 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 4 to 6 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

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	<i>All equal tag sequence sample</i>
--------	--------------------------------------

Description

Create combinations with equal sample probability to all colors.

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 4 to 6 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 4 to 6 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

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

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	<i>Pre-used combinations combinations</i>
----------	---

Description

Pre-used combinations 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

scy	<i>Summary color year</i>
-----	---------------------------

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

Examples

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

vfrequency	<i>Variable frequency tag sequence sample</i>
------------	---

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

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)
```

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