Package 'GenTag'

May 7, 2026

Type Package

Title Generate Color Tag Sequences

Version 1.0

Date 2019-06-21

Author Carlos Biagolini-Jr.

Maintainer Carlos Biagolini-Jr.<c.biagolini@gmail.com>

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)

NeedsCompilation no

Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2019-06-24 14:20:03 UTC

Contents

GenTag-package 2
allequal 4
erc 5
escode 6
escombination 6
esdataset 7
genseq 8
lifexp 10
pre_used 12
scy 13
vfrequency 14

Index **15**

GenTag-package *Generate Color Tag Sequences*

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.

Details

The DESCRIPTION file:

Package:	GenTag
Type:	Package
Title:	Generate Color Tag Sequences
Version:	1.0
Date:	2019-06-21
Author:	Carlos Biagolini-Jr.
Maintainer:	Carlos Biagolini-Jr.<c.biagolini@gmail.com>
Description:	Implement a coherent and flexible protocol for animal color tagging. 'GenTag' provides a simple computationa
License:	GPL (>= 2)

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)

Carlos Biagolini-Jr.

Maintainer: Carlos Biagolini-Jr.<c.biagolini@gmail.com>

References

Alisauskas & Lindberg (2002). Effects of neckbands on survival and fidelity of White-fronted and Canada geese captured as non-breeding adults. doi: 10.1080/02664760120108575 Broughton (2015). Low incidence of leg and foot injuries in colour-ringed Marsh tits Poecile palustris. doi: 10.1080/03078698.2015.1059610 Burley (1986). Sex-ratio manipulation in color-banded populations of Zebra finches. doi: 10.1111/j.1558-5646.1986.tb05744.x Burley, Krantzberg & Radman (1982). Influence of colour-banding on the conspecific preferences of Zebra finches. doi: 10.1016/S0003-3472(82)80055-9 Calvo & Furness (1992). A review of the use and the effects of marks and devices on birds. doi: 10.1080/03078698.1992.9674036 Cresswell, Lind, Quinn, Minderman & Whitfield, (2007). Ringing or colour-banding does not increase predation mortality in Redshanks Tringa totanus. doi: 10.1111/j.2007.0908-8857.3925.x Cuthill, Hunt, Cleary, & Clark (1997). Colour bands, dominance, and body mass regulation in male Zebra finches (Taeniopygia guttata). doi: 10.1098/rspb.1997.0151 Fiske & Amundsen (1997). Female bluethroats prefer males with symmetric colour bands. doi: 10.1006/anbe.1996.0436 Gil, Graves, Hazon, & Wells, (1999). Male attractiveness and differential testosterone investment in Zebra finch eggs. doi: 10.1126/science.286.5437.126 Griesser, Schneider, Collis, Overs, Guppy, Guppy, Takeuchi, Collins, Peters & Hall (2012). Causes of ring-related leg injuries in birds - evidence and recommendations from four field studies. doi: 10.1371/journal.pone.0051891 Jennions (1998). The effect of leg band symmetry on female-male association in Zebra finches. doi: 10.1006/anbe.1997.0579 Johnsen, Fiske, Amundsen, Lifjeld, & Rohde (2000). Colour bands, mate choice and paternity in the Bluethroat. doi: 10.1006/anbe.1999.1274 Johnsen, Lifjeld, & Rohde (1997). Coloured leg bands affect male mate-guarding behaviour in the Bluethroat. doi: 10.1006/anbe.1996.0437 Johnson, Dalton & Burley (1993). Preferences of female American goldfinches (Carduelis tristis) for natural and artificial male traits. doi: 10.1093/beheco/4.2.138 Kosinski (2004). The removal of colour rings by Greenfinches Carduelis chloris. doi: 10.1080/03078698.2004.9674304 McCrea & Morgan (2014). Analysis of capture-recapture data. Boca Raton, Chapman and Hall/CRC. Nietmann & Ha (2018). Site-specific incidence of ring-related injuries in Rufous fantails Rhipidura rufifrons. doi: 10.1080/03078698.2018.1505109 Pierce, Stevens, Mulder & Salewski (2007). Plastic colour rings and the incidence of leg injury in Flycatchers (Muscicapidae, Monarchidae). doi: 10.1080/03078698.2007.9674365 Schlich & Kempenaers (2018). The immediate impact of ringing, blood sampling and PIT-tag implanting on the behaviour of Blue tits Cyanistes caeruleus. doi: 10.5253/arde.v106i1.a8 Sedgwick & Klus (1997). Injury due to leg bands in Willow flycatchers. Song, Liu, Booksmythe & Ding (2017). Effects of individual-based preferences for colour-banded mates on sex allocation in Zebra finches. doi: 10.1093/beheco/arx069 Sutherland (2006). Ecological census techniques: a handbook (2nd ed.). New York, Cambridge University Press. Weiser et al (2018). Effects of leg flags on nest survival of four species of Arctic-breeding shorebirds. doi: 10.1111/jofo.12264 Zann (1994). Effects of band color on survivorship, body condition and reproductive effort of free-living Australian Zebra finches. doi: 10.2307/4088512

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

∗ **animal behavior**
GenTag-package, 2
∗ **band**
GenTag-package, 2
∗ **color tagging**
GenTag-package, 2
∗ **datasets**
pre_used, 12
∗ **ecology methods**
GenTag-package, 2
∗ **field ecology**
GenTag-package, 2
∗ **marks**
GenTag-package, 2
∗ **ringing**
GenTag-package, 2
∗ **tagging**
GenTag-package, 2

allequal, 4

erc, 5
escode, 6
escombination, 6
esdataset, 7

genseq, 8
GenTag *(*GenTag-package*)*, 2
GenTag-package, 2

lifexp, 10

pre_used, 12

scy, 13

vfrequency, 14