# Package 'IndRSA'

June 1, 2018

**Version** 0.0.0.9000

**Title** What the Package Does (One Line, Title Case)

**Description** What the package does (one paragraph).

**License** What license is it under?

**Encoding** UTF-8

**LazyData** true

**ByteCompile** true

**RoxygenNote** 6.0.1.9000

**Suggests** testthat

# R topics documented:

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aictab_ind                    *Perform model selection over all individuals*

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## Description

Perform AIC model selection over all individuals by adding up likelihood of individual model (based code partly taken from package AICcmodavg)

## Usage

```
aictab_ind(mod_ls, cutoff = -1)
```

## Arguments

mod_ls        A list of list of model generated by rsf_ind

cutoff        A cutoff value to exclude individuals with bad fit, default = -1 indicating model that did not converge will be excluded. Values > 0 will exclude based on coefficient values

## Value

A AIC model selection table

## Examples

```
Add something
```

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bad_fit                    *Identify potential individual with bad fits based on coefficients and model convergence*

---

## Description

Identify potential individual with bad fits based on coefficients and model convergence

## Usage

```
bad_fit(mod_ls, cutoff = 1000)
```

## Arguments

mod_ls        A list of list of model generated by rsf_ind

cutoff        Value a coeffiecient may take to indicate bad fit (default=1000)

## Value

A list with first element giving individuals with bad fits based on coefficients and second element containing individuals with bad fit based on convergence

## Examples

```
Add something
```

---

bad_fit1          *Identify potential individual with bad fits based on coefficients and model convergence for a specific model*

---

## Description

Identify potential individual with bad fits based on coefficients and model convergence

## Usage

```
bad_fit1(mod_ls, cutoff = 1000, m = 1)
```

## Arguments

| | |
|---|---|
| mod_ls | A list of list of model generated by rsf_ind |
| cutoff | Value a coeffiecient may take to indicate bad fit (default=1000) |
| m | model number (based on number in list of formula provided to rsf_ind) |

## Value

A list with first element giving individuals with bad fits based on coefficients and second element containing individuals with bad fit based on convergence

## Examples

```
Add something
```

---

cmodel          *Remove elements from glm object to save space*

---

## Description

Remove elements from glm objects (Taken from: https://www.r-bloggers.com/trimming-the-fat-from-glm-models-in-r/)

## Usage

```
cmodel(cm)
```

## Arguments

| | |
|---|---|
| cm | A glm object |

## Value

A glm object

---

| eval_ratio | *Evaluate ratio of used and random locations of individuals in a RSF table* |
|---|---|

---

## Description

Evaluate ratio of used and random locations of individuals in a RSF table

## Usage

```
eval_ratio(id, value)
```

## Arguments

| | |
|---|---|
| id | A vector of individual for each observation |
| value | A vector indicating if each observation is used (=1) or random(=0) |

## Value

A list indicating the range in ratio, range in random locations, and range in used location.

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| ind_coef | *Extract individual coefficients* |
|---|---|

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## Description

Extract individual coefficients.

## Usage

```
ind_coef(m = 1, mod_ls, cutoff = 0)
```

## Arguments

| | |
|---|---|
| m | model number (based on number in list of formula provided to rsf_ind) |
| mod_ls | A list of list of model generated by rsf_ind |
| cutoff | A cutoff value to exclude individuals with bad fit, default = -1 indicating model that did not converge will be excluded. Values > 0 will exclude based on coefficient |

## Value

A list containing a table population average with confidence intervals and a table of individual coefficients

## Examples

```
Add something
```

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kfoldRSF *Perform kfold cross-validation on a RSF output.*

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### Description

Perform kfold cross-validation on a RSF output. Similar to what is recommended in Boyce 2002. Function developped with Mathieu Basille

### Usage

```
kfoldRSF(mod, k = 5, nrepet = 10, nbins = 10, jitter = TRUE,
  random = TRUE, method = method, x = m, form_ls = ls,
  reproducible = TRUE)
```

### Arguments

| | |
|---|---|
| mod | A RSF model (glm or glmer) |
| k | number of fold (default = 5) |
| nrepet | Number of repetitions (default =10) |
| nbins | Number of bins (default =10) |
| jitter | Logical, whether to add some random noise to the predictions (useful when the model is fitted on categorica variables, which can produces error in the ranking process). |
| reproducible | Logical, whether to use a fixed seed for each repetition. |

### Value

A data frame with the correlations (cor) and the type of value (type).

---

kfold_ind *Perform kfold cross-validation at the individual level .*

---

### Description

Perform kfold cross-validation at the individual level and return histogram, mean kfold accros individual and min/max value

### Usage

```
kfold_ind(m = 1, mod_ls, ls = ls, cutoff = 0, k = 5, nrepet = 5,
  nbins = 10, grph = T)
```

## Arguments

| | |
|---|---|
| m | model number (based on number in list of formula provided to rsf_ind) |
| mod_ls | A list of list of model generated by rsf_ind |
| cutoff | A cutoff value to exclude individuals with bad fit, default = -1 indicating model that did not converge will be excluded. Values > 0 will exclude based on coefficient |
| k | number of fold (default = 5) |
| nrepet | Number of repetitions (default =10) |
| nbins | Number of bins (default =10) |
| jitter | Logical, whether to add some random noise to the predictions (useful when the model is fitted on categorica variables, which can produces error in the ranking process). |
| reproducible | Logical, whether to use a fixed seed for each repetition. |

## Value

A data frame with the correlations (cor) and the type of value (type).

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| pop_avg | *Extract population average of top model and extract individual coefficients* |
|---|---|

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## Description

Extract population average of top model and extract individual coefficients. Population average can be calculated based on bootstrap (Prokopenko et al. 2016 JAppEco) or weighted based on standard errors (Murtaugh 2007 Ecology)

## Usage

```
pop_avg(m = 1, mod_ls, cutoff = 0, method = "boot", nboot = 1000)
```

## Arguments

| | |
|---|---|
| m | model number (based on number in list of formula provided to rsf_ind) |
| mod_ls | A list of list of model generated by rsf_ind |
| cutoff | A cutoff value to exclude individuals with bad fit, default = -1 indicating model that did not converge will be excluded. Values > 0 will exclude based on coefficient |
| method | If = "boot", population average is based on bootstrap, if = "murtaugh" based on standard errors weighting. See Prokopenko et al 2016 or Murtaugh 2007 for details. |
| nboot | Number of bootstrap iterations, default = 1000. Only applicable if method = "boot". |

## Value

A list containing a table population average with confidence intervals and a table of individual coefficients

## Examples

```
Add something
```

---

| | |
|---|---|
| resample_rsf | *Resample a RSF table to keep constant ratio of used/random locations accross individuals* |

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## Description

Resample a RSF table to keep constant ratio of used/random locations accross individuals. Resampling is done with replacement.

## Usage

```
resample_rsf(data, id = "Id_Year", value = "Value", ratio = 3)
```

## Arguments

| | |
|---|---|
| data | The RSF dataset to resample |
| id | A vector of individual for each observation |
| value | A vector indicating if each observation is used (=1) or random(=0) |
| ratio | The ratio of random:used location (default =3, meaning 3 random locations for each used location) |

## Value

A RSF dataset

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| | |
|---|---|
| rm_bad_fit | *Remove potential individual with bad fits based on coefficients* |

---

## Description

Remove potential individual with bad fits based on coefficients

## Usage

```
rm_bad_fit(mod_ls, cutoff = 1000)
```

## Arguments

| | |
|---|---|
| mod_ls | A list of list of model generated by rsf_ind |
| cutoff | Value a coeffiecient may take to indicate bad fit (default=1000) |

## Value

A list excluding individual with bad fits.

---

| rm_bad_fit1 | *Remove potential individual with bad fits based on coefficients for a specific model* |

---

## Description

Remove potential individual with bad fits based on coefficients

## Usage

```
rm_bad_fit1(mod_ls, cutoff = 1000, m = 1)
```

## Arguments

| | |
|---|---|
| mod_ls | A list of list of model generated by rsf_ind |
| cutoff | Value a coeffiecient may take to indicate bad fit (default=1000) |
| m | model number (based on number in list of formula provided to rsf_ind) |

## Value

A list excluding individual with bad fits.

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| rm_conv_fit | *Remove potential individual with bad fits based on model convergence* |

---

## Description

Remove potential individual with bad fits based on model convergence

## Usage

```
rm_conv_fit(mod_ls)
```

## Arguments

| | |
|---|---|
| mod_ls | A list of list of model generated by rsf_ind |

## Value

A list excluding individual with bad fits.

---

| rm_conv_fit1 | *Remove potential individual with bad fits based on model convergence for a specific model* |
|---|---|

---

## Description

Remove potential individual with bad fits based on model convergence

## Usage

```
rm_conv_fit1(mod_ls, m = 1)
```

## Arguments

m          model number (based on number in list of formula provided to rsf_ind)

## Value

A list excluding individual with bad fits.

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| rsf_ind | *Apply a list of candidate models to multiple individuals* |
|---|---|

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## Description

Apply rsf_mod to each individual of a dataset

## Usage

```
rsf_ind(id, data, form_ls, cleanModel = F, method = "glm.fit")
```

## Arguments

| | |
|---|---|
| id | A vector indicating the individuals |
| data | The dataset containing all data |
| form_ls | A list of formulas for the different candidate models |
| method | Weither typical glm or bias-reduction glm should be fitted (default="glm.fit) (see package brglm) |
| cleamModel | Whether the model should be "cleaned" to save memory space (default = F) |

## Value

A list of list of glm objects

## Examples

```
Add something
```

| rsf_mod | *Apply a list of candidate models to a single individual* |
|---|---|

## Description

Apply a list of candidate models to a single individual

## Usage

```
rsf_mod(sub, form_ls, cleanModel = F, method = method)
```

## Arguments

| | |
|---|---|
| sub | A subset of data from a single individual |
| form_ls | A list of formulas for the different candidate models |
| method | Weither typical glm or bias-reduction glm should be fitted (see package brglm) |
| cleamModel | Whether the model should be "cleaned" to save memory space |

## Value

A list of glm objects

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