Package ‘flatr’

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Type Package
Title Transforms Contingency Tables to Data Frames, and Analyses Them
Version 0.1.1
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Description Contingency Tables are a pain to work with when you want to run regressions.
This package takes them, flattens them into a long data frame, so you can more easily analyse them!
As well, you can calculate other related statistics. All of this is done so in a 'tidy' manner,
so it should tie in nicely with 'tidyverse' series of packages.
Depends R(>= 3.4.2), stats, dplyr, tibble, magrittr
Suggests testthat
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**flatten_ct**

Flatten i*j*k contingency tables into tidy data.

**Description**

`flatten_ct()` takes a i*j*k array, and turns it into a tibble.

**Usage**

`flatten_ct(data)`

**Arguments**

- `data` An i*j*k array.

**Value**

A tibble with 3 columns.

**Examples**

`flatten_ct(lung_cancer)`

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**goodness_of_fit**

Calculate the Chi^2 and G^2 Statistics

**Description**

Calculates the goodness of fit test statistics for contingency tables.

**Usage**

`goodness_of_fit(model, type = "Chisq", ...)`

**Arguments**

- `model` a GLM regression model.
- `type` either "Chisq" or "Gsq", which determines the type of goodness of fit test that is ran. Defaults to "Chisq".
- `...` Further arguments passed to or from other methods.
Value

A list with class "ct_goodness_of_fit" containing the following components:

- **test**: the type of test used.
- **model**: the name of the inputted model.
- **statistic**: The value of the test statistic as determined by the type parameter.
- **df**: The number of degrees of freedom. This equals the number of combinations for explanatory variables less the number of parameters in the model.
- **p.value**: The p-value calculated under a Chi-Squared distribution.

Examples

```r
lung_logit <- 
  lung_cancer %>% 
  flatten_ct() %>% 
  glm( 
    Lung ~ Smoking, 
    family = binomial, 
    data = . 
  )

goodness_of_fit(model = lung_logit, type = "chisq")

lung_logit %>% 
  goodness_of_fit(type = "gsq")

lung_cancer %>% 
  flatten_ct() %>% 
  glm( 
    Lung ~ City + Smoking, 
    family = binomial, 
    data = . 
  ) %>% 
  goodness_of_fit()
```

---

**Description**


**Usage**

```r
lung_cancer
```
Format

- An Array with 2*2*8 dimensions
- **Smoking** Whether or not a person smokes.
- **Lung** Whether or not a person has lung cancer.
- **City** Name of the city a person lives in.

Examples

- `lung_cancer`

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**print.ct_goodness_of_fit**

*Print method for goodness_of_fit()*

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Description

- Creates a nice looking output for the goodness_of_fit() function

Usage

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

Arguments

- `x` A list
- `...` Further arguments passed to or from other methods.
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