# Package 'flatr'

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110 / 0111001 11, 2017
Type Package
Title Transforms Contingency Tables to Data Frames, and Analyses Them
<b>Version</b> 0.01.0
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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.
<b>Depends</b> R(>= 3.4.2), stats, dplyr, tibble, magrittr
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R topics documented:  flatten_ct
goodness_of_fit2lung_cancer3print.ct_goodness_of_fit4
Index 5
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)

2 goodness\_of\_fit

#### **Arguments**

data An i\*j\*k array.

#### Value

A tibble with 3 columns.

#### **Examples**

```
flatten_ct(lung_cancer)
```

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, response, type = "Chisq", ...)
```

#### **Arguments**

model a GLM regression model.

response a string with the same name as the response column in the data

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.

lung\_cancer 3

#### **Examples**

```
lung_logit <-</pre>
  lung_cancer %>%
  flatten_ct() %>%
   Lung ~ City + Smoking
    ,family = binomial
    , data = .
  )
goodness_of_fit(model = lung_logit, response = "Lung", type = "Chisq")
lung_logit %>%
  goodness_of_fit(response = "Lung", type = "Gsq")
lung_cancer %>%
  flatten_ct() %>%
  glm(
   Lung ~ City + Smoking
    ,family = binomial
    ,data = .
  ) %>%
  goodness_of_fit(response = "Lung", type = "Chisq")
```

lung\_cancer

Lung Cancer by whether or not a person smokes and City.

## Description

Based on data in Z. Liu, Int. J. Epidemiol., 21: 197-201, 1992.

## Usage

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

```
\label{eq:print.ct_goodness_of_fit} Print\ method\ for\ goodness\_of\_fit()
```

## Description

Creates a nice looking output for the goodness\_of\_fit() function

## Usage

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

## Arguments

x A list

... Further arguments passed to or from other methods.

## Index

```
*Topic datasets
    lung_cancer, 3

flatten_ct, 1
goodness_of_fit, 2
lung_cancer, 3
print.ct_goodness_of_fit, 4
```