# 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

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**NeedsCompilation** no

**Repository** CRAN

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## R topics documented:

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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

```
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()
```

---

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
```

---

```
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. |

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