

# 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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<code>flatten_ct</code>	<i>Flatten i*j*k contingency tables into tidy data.</i>
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**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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<code>goodness_of_fit</code>	<i>Calculate the <math>\chi^2</math> and <math>G^2</math> Statistics</i>
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**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**

<code>x</code>	A list
<code>...</code>	Further arguments passed to or from other methods.

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\* **datasets**

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