Chi-Square test calculator

Goodness of fit test, Test of independence, McNemar test

Video Information Chi-squared test for variance Chi-Square Calculator

Test calculation

Right-tailed - for the goodness of fit test, the test of independence / the test for association, or the McNemar test, you can use only the right tail test.
The calculator includes results from the Fisher calculator, binomial test, McNemar Mid-p, simulation.

right (H_1: after ≥ before)

Test:	Goodness of fit	Name:	Population
Significance level (α):	0.05	m:	0
Effect:	Medium	Effect size (w):	0.3
Continuity correction:	False	Simulation repeats:	100000
Digits:	4		

The continuity correction tends to overcorrect and increase the possibility of a type II error. Hence the resulting p-value is usually **too large**. It's controversial, so we recommend to leave it as false

Step by step

Enter raw data directly
Enter raw data from excel

McNemar chi-square test

Matched pairs

A to B:

12

Changes from group A to group B

B to A:

23

Changes from group B to group A

Before \ After	A	B
A	a	12
B	23	d

Enter sample data

Categories	Conventional	Assertiveness-based
Low	1 1 2 2 1 1 2 2 1 2 1 1 2 2 1 2	1 1 2 1 1 2 1 2 1 1 1 1 1 2 3 3 2
Medium	3 2 3 3 3 2 2 2 2 3 2 3 3 3 2	3 2 3 3 3 3 2 3 2 2 2 3 3 2 3
High	5 4 5 4 5 5 4 4 5 5 5 5 5 5 5	5 4 5 4 5 4 3 4 5 5 5 5 5 5 5

Enter sample data

You may copy data from Excel, Google sheets or any tool that separate data with **Tab** and **Line Feed**.
Copy the data, **one block** of **3** consecutive columns includes the top **header row** and left **header column**, and paste below. example

It is okay to leave empty cells, empty cells or non numeric cells won't be counted

*Choose **Expected Frequencies** or **Expected Probabilities**.
The sum of the **expected values** must be equal to the sum of the observed frequencies or to one.

Calculate | Insert row | Delete row | Insert column | Delete column | Clear

How to do with R?

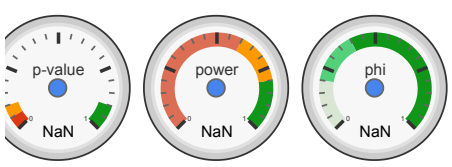
Results

The expected values should be at least 1 for all the values, and at least 5 for 80% of the values
Blue - less than 5, but still okay.
Red - potential issue.

$$\chi^2=\frac{(NaN-NaN)^2}{NaN}+\frac{(NaN-NaN)^2}{NaN}+\frac{(NaN-NaN)^2}{NaN}=NaN$$

P-value = 1 - p($\chi^2(2) \leq NaN$).

k	3	Number of categories
n	NaN	Sample size
χ^2	NaN	Chi square test statistic
DF	2	df = k-m-1 =3-0-1 = 2
Phi effect (Φ)	NaN	$\Phi=\sqrt{(\chi^2/n)}$



Goodness of fit, using χ^2 distribution (DF=2) (right-tailed) (validation)

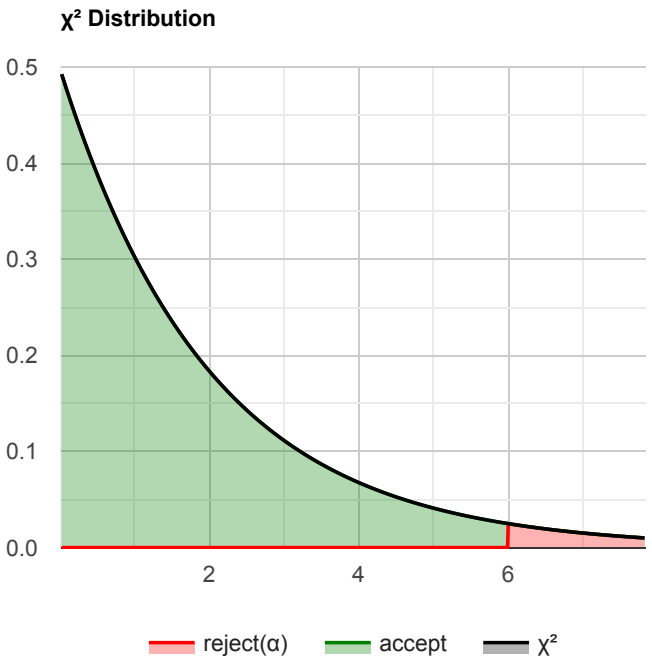
. H_0 hypothesis
Since p-value < α, H_0 is rejected.
The statistical model does not fit the observations

. P-value
The p-value equals NaN, ($p(x \leq \chi^2) = NaN$). It means that the chance of type I error (rejecting a correct H_0) is small: NaN (NaN%).
The smaller the p-value the more it supports H_1.

. The statistics
The test statistic χ^2 equals NaN, which is not in the 95% region of acceptance: [-∞ : 5.9915].

. Effect size
The observed effect size phi is **large**, **NaN**. This indicates that the magnitude of the difference between the observed data and the expected data is large.

If you like the page, please share or like. Questions, comments and suggestions are appreciated. (statskingdom@gmail.com)



More tests

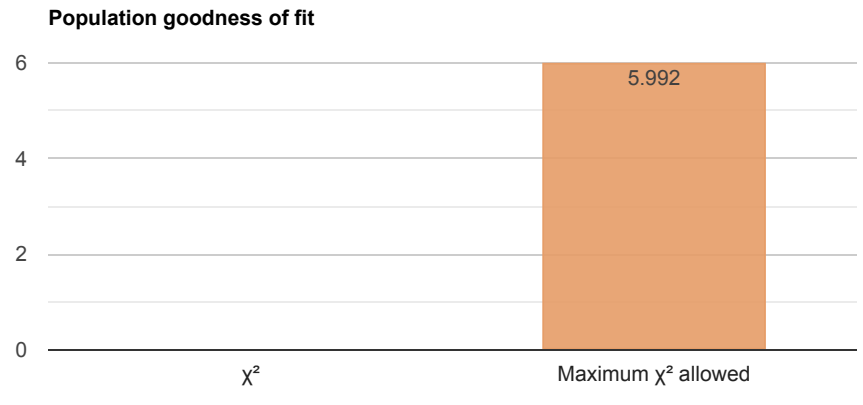
[What test should I choose?]

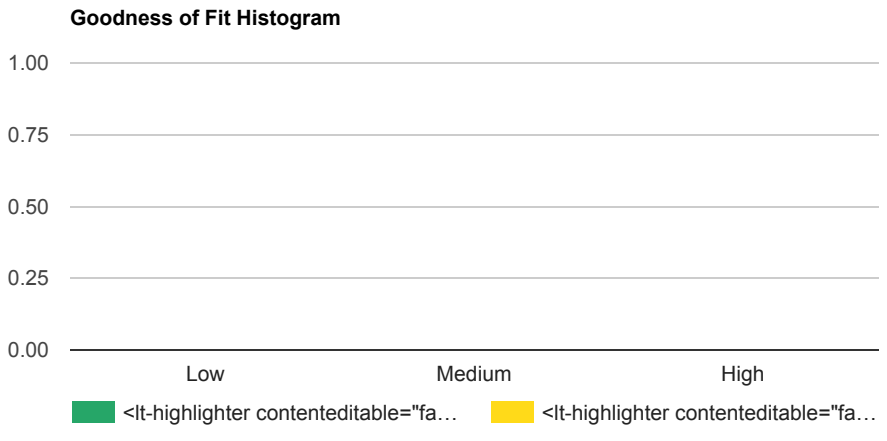
Simulation test

The simulation run 100,000 times, the duration is 0.07 seconds. Running more times will have better accuracy, but the default should be sufficient.
Since the simulation is random, each run will have a slightly different result.

P-value

P-value equals 0. It means that the chance of type1 error (rejecting a correct H_0) is small: 0 (0%)
The smaller the p-value, the more it supports H_1.





Test validation

The requested test was calculated, it is likely you chose the right test.

- **Test power** +

  Although the priori power is low (NaN), the H_0 is rejected.

Information

Hypotheses

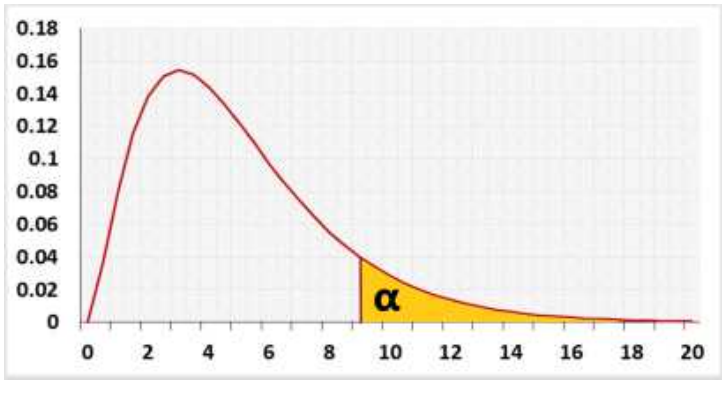
H_0: Model Fits

H_1: Model Doesn't Fit

Test statistic

$$\chi^2 = \sum_{i=1}^{n} \frac{(o_i - e_i)^2}{e_i}$$

χ^2 distribution



Target: Check if the statistical model fits the observations.
The test uses Chi-square distribution.

McNemar chi-square test

The test checks only the cases when the status of the dichotomous variable was changed.
The null assumption is that the probability to switch from A to B equals the probability to switch from B to A, equals 0.5.

Before \ After	A	B
A	No change	**A to B**
B	**B to A**	No change

The number of cases with no change, A to A or B to B, doesn't change the result of the McNemar test.

Chi-square test for independence

The null assumption is that the two categorical variables are independent.

R Code

The following R code should produce the same results:

```
obs<-c(1 1 2 2 1 1 2 2 1 2 1 1 2 2 1 2 2 1 2 2 1 2 1 1 1 1 1 1 1 1 2 2,3 2 3 3 3 2 2 2 2 3 2 3 3 3 2 3 4 2 3 2 2 4 2 2 4 2 1 2 2,5 4 5 4 5 5 4 4 5 5 5 5 5 5 5 5 5 5 4 4 5 5 4 2 4 5 5 5)
prob<-c(1 1 2 1 1 2 1 2 1 1 1 1 1 2 3 3 2 1 2 1 1 1 1 1 2 2 1 2 2,3 2 3 3 3 3 2 3 2 2 2 3 3 2 3 2 4 2 3 3 2 2 2 3 3 3 2 2 2,5 4 5 4 5 4 3 4 5 5 5 5 5 5 5 4 5 5 4 5 5 5 5 4 5 5 5)
prob = prob / sum(prob)
chisq.test(x=obs, y=NULL, correct = FALSE, p=prob)

#Compute p-values by Monte Carlo simulation
chisq.test(x=obs, y=NULL, correct=FALSE, p=prob, simulate.p.value = TRUE, B = 100000)
```

Goodness of fit example: checking a fair dice.
Model: the probability of each side is equal - 1/6.
H_0: fair dice.
H_1: unfair dice.

The **groups** are the dice's numbers (1,2,3,4,5,6).
In this example, you throw the dice n times.
Expected frequencies - for each group are n/6.
Observed frequencies - the actual times each number appears.