

Prism Manual

Categorical Data Analysis

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This lab will introduce categorical data analysis using Prism. For more analysis for categorical data analysis in Prism, please check chapter in [Prism statistics guide](#). To learn more about categorical data analysis, please check another BCBB workshop – Categorical data analysis.

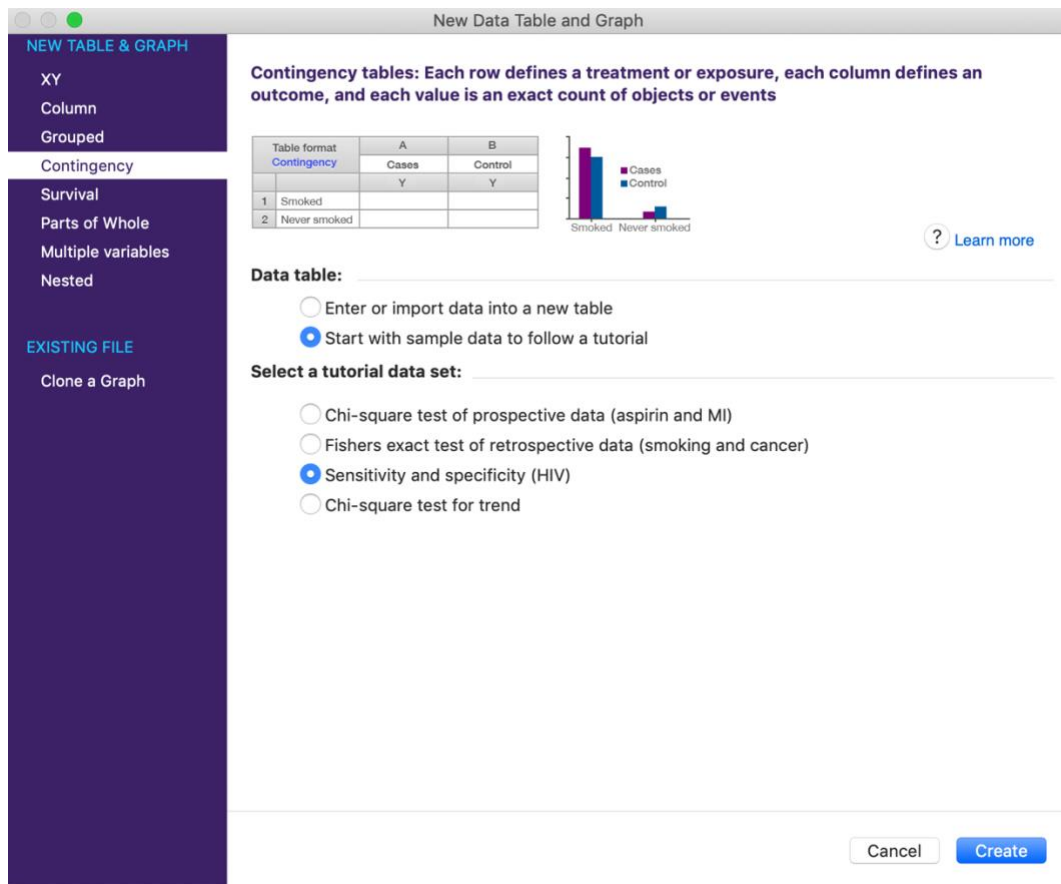
0. Outline:

- 1) Create a contingency table
- 2) Calculation - relative risk, difference between proportion, odds ratio, sensitivity etc (All of these applies to 2×2 tables)
- 3) Perform statistical testing for contingency table

1. Create a contingency table

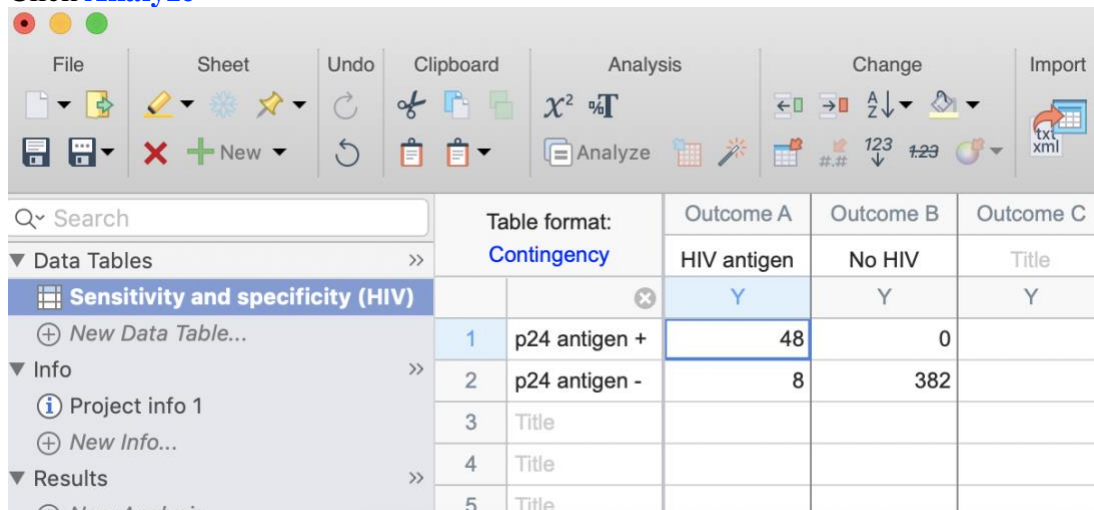
You must enter data in the form of a contingency table. Prism cannot cross-tabulate raw data to create a contingency table.

1.1 Select **Contingency** under “NEW TABLE & GRAPH” menu. Then select “**Start with sample data to follow a tutorial**” or the first option to enter your data. Select “**Sensitivity and specificity (HIV)**”. Click create.

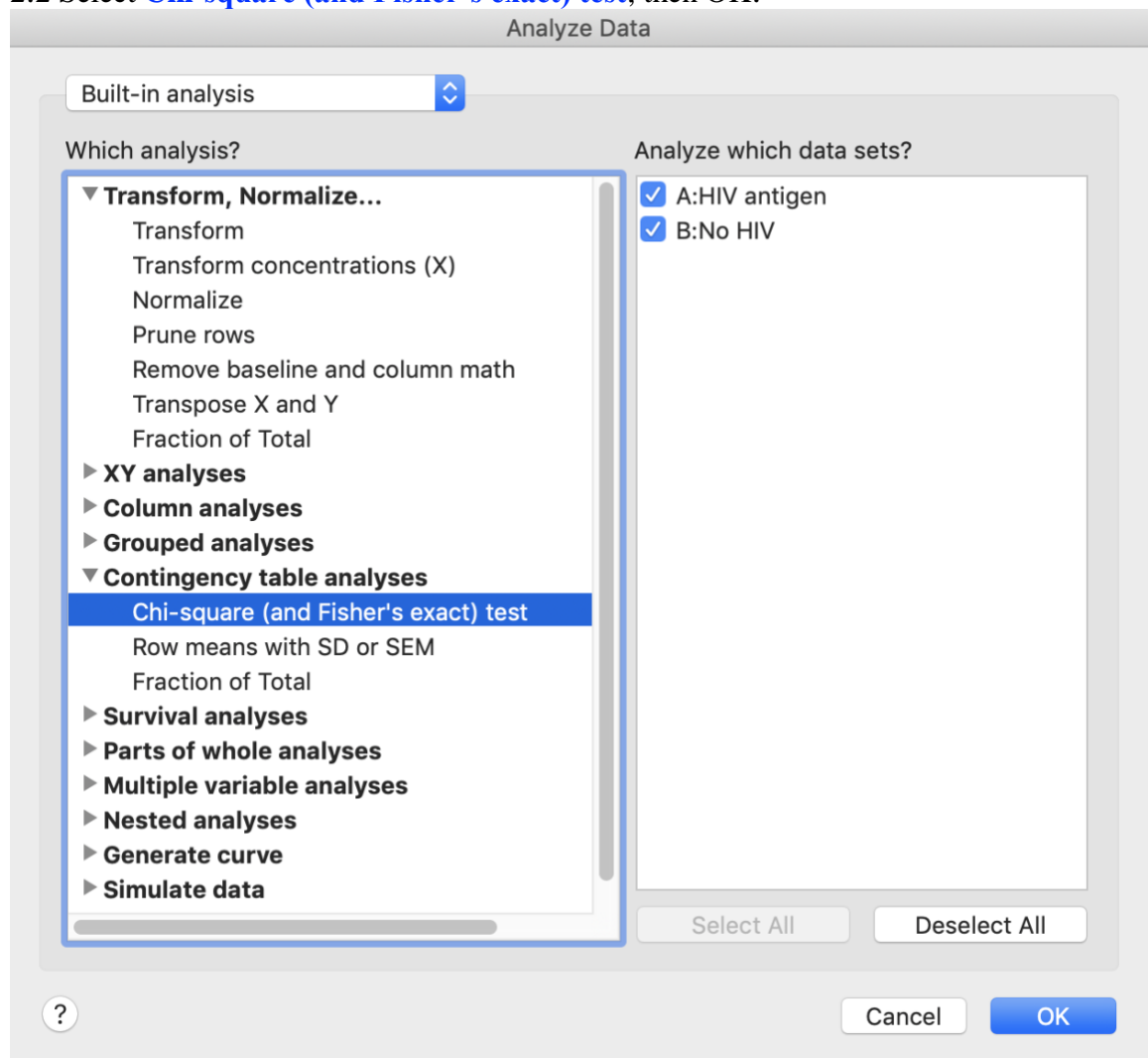


2. Calculation

2.1 Click **Analyze**



2.2 Select **Chi-square (and Fisher's exact) test**, then OK.



2.3 Select the **type of calculation** you want under Main Calculations. You could decide one sided or two sided from Options. Here we select **Sensitivity, specificity and predictive values** as an example.

Parameters: Chi-square (and Fisher's exact) test

Main Calculations Options

Effect sizes to report

☐ Relative Risk
Used for prospective and experimental studies

☐ Difference between proportions (attributable risk) and NNT
Used for prospective and experimental studies

☐ Odds ratio
Used for retrospective case-control studies

☒ Sensitivity, specificity and predictive values
Used for diagnostic tests

Method to compute the P value

☒ Fisher's exact test

☐ Yates' continuity corrected chi-square test

☐ Chi-square test

☐ Chi-square test for trend

Looking for the z test to compare proportions? Choose the chi-square test (with or without the Yates' correction). The chi-square and z tests are equivalent.

? Cancel OK

A two-sided P value is recommended unless you have a strong reason to choose a one-sided P value.

Parameters: Chi-square (and Fisher's exact) test

Main Calculations Options

Calculations options

P values: ☐ One-sided ☒ Two-sided

Confidence Interval: 95%

Method to calculate CI:

Relative risk:
Koopman asymptotic score (recommended)

Difference between proportions:
N/W score with CC (recommended)

Odds ratio:
Baptista-Pike method (recommended)

Sensitivity, specificity, etc.:
Wilson/Brown (recommended)

Output

Show this many significant digits (for everything except P values): 4

P value style: GP: 0.1234 (ns), 0.0332 (*), 0.0021 (**), 0... N= 6

☐ Make these choices be the default for future analyses.

? Cancel OK

2.4 Result are circled. More details about reporting the result could be found at [here](#).

Contingency				
1	Table Analyzed	Sensitivity and specificity (HIV)		
2				
3	P value and statistical significance			
4	Test	Fisher's exact test		
5	P value	<0.0001		
6	P value summary	****		
7	One- or two-sided	Two-sided		
8	Statistically significant (P < 0.05)?	Yes		
9				
10	Effect size	Value	95% CI	
11	Sensitivity	0.8571	0.7426 to 0.92	
12	Specificity	1.000	0.9900 to 1.00	
13	Positive Predictive Value	1.000	0.9259 to 1.00	
14	Negative Predictive Value	0.9795	0.9601 to 0.98	
15	Likelihood Ratio			
16				
17	Methods used to compute CIs			
18	Sensitivity, specificity, etc.	Wilson-Brown		
19				
20	Data analyzed	HIV antigen	No HIV	Total
21	p24 antigen +	48	0	48
22	p24 antigen -	8	382	390
23	Total	56	382	438
24				
25	Percentage of row total	HIV antigen	No HIV	
26	p24 antigen +	100.00%	0.00%	
27	p24 antigen -	2.05%	97.95%	
28				
29	Percentage of column total	HIV antigen	No HIV	
30	p24 antigen +	85.71%	0.00%	
31	p24 antigen -	14.29%	100.00%	
32				
33	Percentage of grand total	HIV antigen	No HIV	
34	p24 antigen +	10.96%	0.00%	
35	p24 antigen -	1.83%	87.21%	

When testing the independence of categorical data, different tests could be selected based on data characteristic:

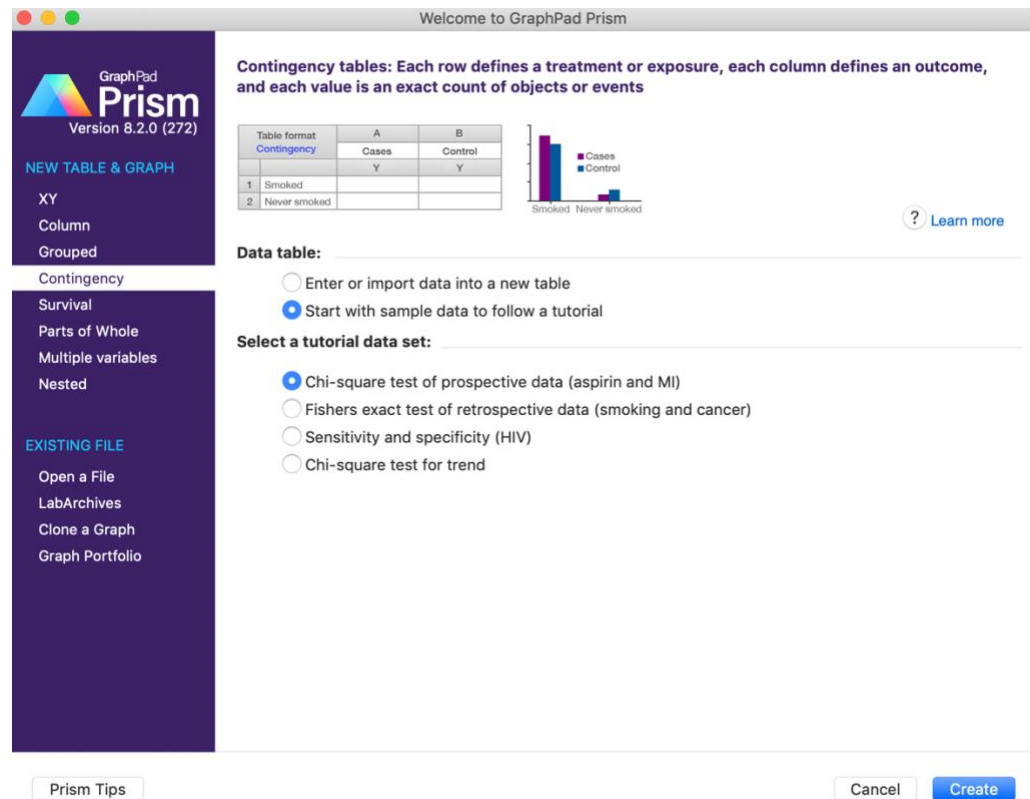
For example, if we have data with large sample size and independence, Pearson chi-square test and likelihood ratio test can be used. Fisher's exact test uses when sample size of data is small and conditioned. Cochran-Mantel-Haenszel test uses with stratified data. McNemar's test or CMH test uses with paired data. Linear trend test with ordinal data.


Among these, Chi-square test and Fisher's exact test are available in Prism software and McNemar test is available in the Prism online calculator. The null hypothesis of the test is no association, alternative hypothesis is there is association.

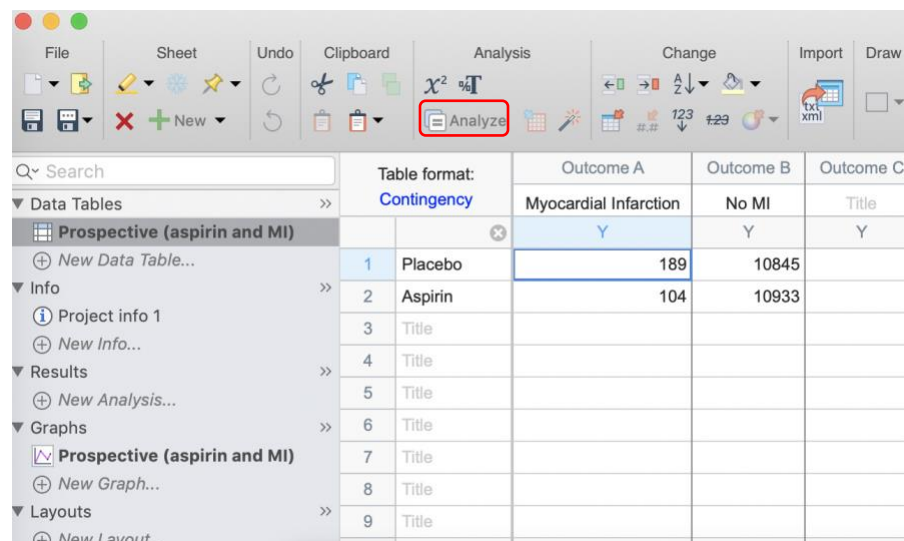
3.1 Pearson Chi-square test

The chi-squared test is used to determine whether there is a significant difference between the expected frequencies and the observed frequencies in one or more categories.

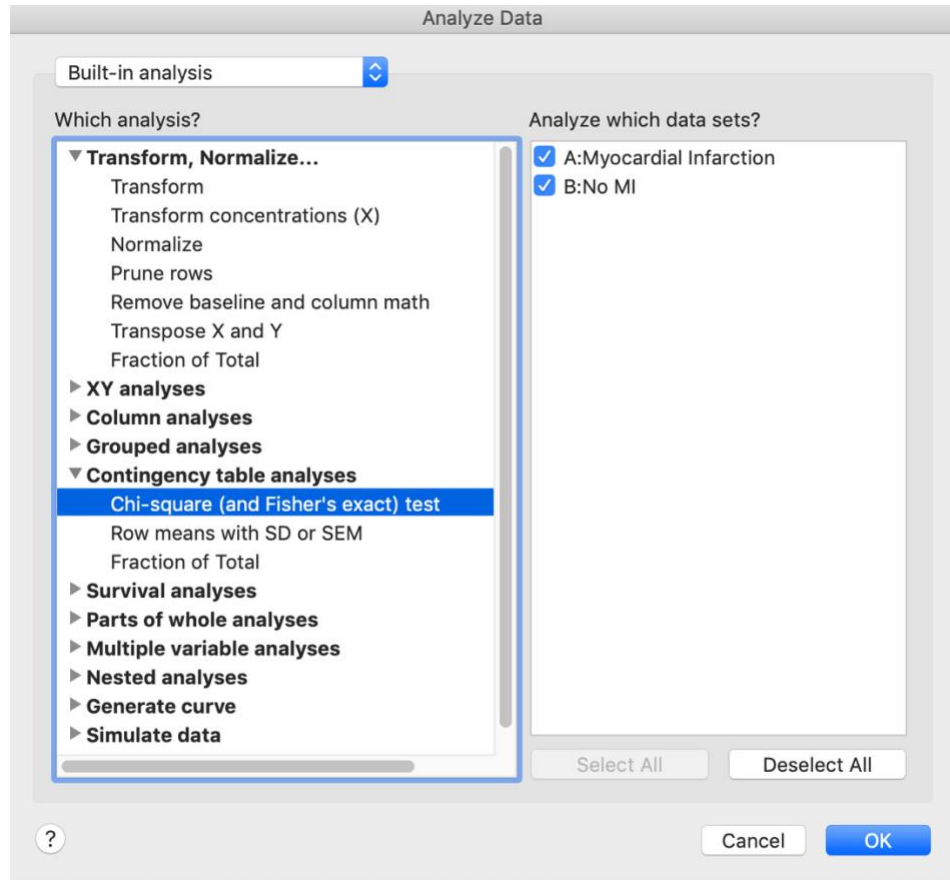
3.1.1 Select **Contingency** under "New Table & Graph"; Select **Start with sample data to follow a tutorial** and **Chi-square test of prospective data (aspirin and MI)**, then click **Create**.



3.1.2 Click **Analyze**  after sample data opened.



3.1.3 Select **Chi-square (and Fisher's exact) test** under Contingency table analyses list. Check the columns you want to analyze on the right side, then click **OK**.



3.1.4 Select test type under Method to compute P value and other report statistic under Effect sizes to report. Click **Chi-square test**, then **OK**.

Parameters: Chi-square (and Fisher's exact) test

Main Calculations Options

Effect sizes to report

☐ Relative Risk
Used for prospective and experimental studies

☐ Difference between proportions (attributable risk) and NNT
Used for prospective and experimental studies

☐ Odds ratio
Used for retrospective case-control studies

☐ Sensitivity, specificity and predictive values
Used for diagnostic tests

Method to compute the P value

☐ Fisher's exact test

☐ Yates' continuity corrected chi-square test

☒ Chi-square test

☐ Chi-square test for trend

Looking for the z test to compare proportions? Choose the chi-square test (with or without the Yates' correction). The chi-square and z tests are equivalent.

? Cancel OK

3.1.5 Result includes p-value, marginal table, and marginal percentage. Chi-square statistic, degree of freedom and p-value are circled. Test result is significant, which means we have 95% confidence to reject the null hypothesis and conclude that there is association between aspirin and MI.

Contingency				
1	Table Analyzed	Prospective (aspirin and MI)		
2				
3	P value and statistical significance			
4	Test	Chi-square		
5	Chi-square, df	25.01, 1		
6	z	5.001		
7	P value	<0.0001		
8	P value summary	****		
9	One- or two-sided	Two-sided		
10	Statistically significant (P < 0.05)?	Yes		
11				
12	Data analyzed	Myocardial Infarction	No MI	Total
13	Placebo	189	10845	11034
14	Aspirin	104	10933	11037
15	Total	293	21778	22071
16				
17	Percentage of row total	Myocardial Infarction	No MI	
18	Placebo	1.71%	98.29%	
19	Aspirin	0.94%	99.06%	
20				
21	Percentage of column total	Myocardial Infarction	No MI	
22	Placebo	64.51%	49.80%	
23	Aspirin	35.49%	50.20%	
24				
25	Percentage of grand total	Myocardial Infarction	No MI	
26	Placebo	0.86%	49.14%	
27	Aspirin	0.47%	49.54%	
28				

3.2 Fisher's exact test

Fisher's exact test is optimal to test association between small and conditioned sample size. It is named after its inventor, Ronald Fisher. It is an exact test because the significance of the deviation from a null hypothesis (e.g., P-value) can be calculated exactly, rather than relying on an approximation that becomes exact in the limit as the sample size grows to infinity.

3.2.1 Select **Contingency** under “New Table & Graph”; Select **Start with sample data to follow a tutorial** and **Fishers exact test of retrospective data (smoking and cancer)**, then click **Create**.

New Data Table and Graph

NEW TABLE & GRAPH

- XY
- Column
- Grouped
- Contingency**
- Survival
- Parts of Whole
- Multiple variables
- Nested

EXISTING FILE

- Clone a Graph

Contingency tables: Each row defines a treatment or exposure, each column defines an outcome, and each value is an exact count of objects or events

Table format	A	B
Contingency	Cases	Control
	Y	Y
1 Smoked		
2 Never smoked		

Smoked Never smoked

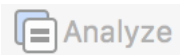
Enter or import data into a new table

☒ Start with sample data to follow a tutorial

Select a tutorial data set:

- ☐ Chi-square test of prospective data (aspirin and MI)
- ☒ Fishers exact test of retrospective data (smoking and cancer)
- ☐ Sensitivity and specificity (HIV)
- ☐ Chi-square test for trend

Cancel Create

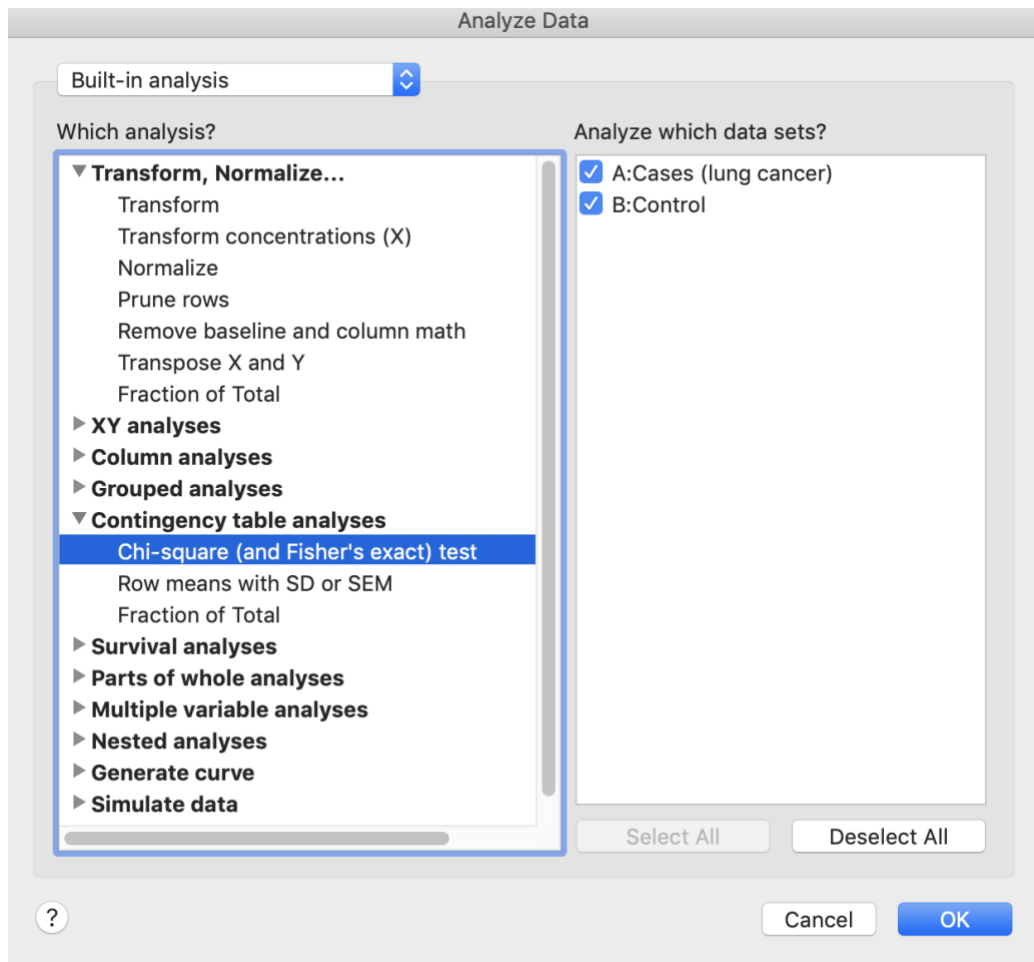
3.2.2 Click **Analyze**  after sample data opened.

The screenshot shows a software interface with a top toolbar containing various icons and buttons. The 'Analyze' button is highlighted with a red rectangle. Below the toolbar, there is a sidebar on the left with a search bar and a list of data tables. The 'Retrospective (smoking and cancer)' table is selected. The main area displays a contingency table with the following data:

Table format: Contingency		Outcome A	Outcome B	Outcome C
		Cases (lung cancer)	Control	Title
		Y	Y	Y
1	Smoked	688	650	
2	Never smoked	21	59	
3	Title			
4	Title			
5	Title			
6	Title			
7	Title			

3.2.3 Select **Chi-square (and Fisher's exact) test** under Contingency table analyses list.

Check the columns you want to analyze on the right side, then click **OK**.



3.2.4 Select **Fisher's exact test**, then go to **Options**, select **Two-sided** under Calculations options, then click **OK**.

Parameters: Chi-square (and Fisher's exact) test

Main Calculations

Options

Effect sizes to report

☐ Relative Risk

Used for prospective and experimental studies

☐ Difference between proportions (attributable risk) and NNT

Used for prospective and experimental studies

☐ Odds ratio

Used for retrospective case-control studies

☐ Sensitivity, specificity and predictive values

Used for diagnostic tests

Method to compute the P value

☒ Fisher's exact test

☐ Yates' continuity corrected chi-square test

☐ Chi-square test

☐ Chi-square test for trend

Looking for the z test to compare proportions? Choose the chi-square test (with or without the Yates' correction). The chi-square and z tests are equivalent.



Cancel

OK

Parameters: Chi-square (and Fisher's exact) test

Main Calculations Options

Calculations options

P values: ☐ One-sided ☒ Two-sided

Confidence Interval: 95%

Method to calculate CI:

Relative risk:
Koopman asymptotic score (recommended)

Difference between proportions:
N/W score with CC (recommended)

Odds ratio:
Baptista-Pike method (recommended)

Sensitivity, specificity, etc.:
Wilson/Brown (recommended)

Output

Show this many significant digits (for everything except P values): 4

P value style: GP: 0.1234 (ns), 0.0332 (*), 0.0021 (**), 0... N= 6

☐ Make these choices be the default for future analyses.

? Cancel OK

3.2.5 Result includes p-value, marginal table, and marginal percentage. p-value is circled. P-value is less than 0.05, we reject null hypothesis at 0.05 significance level and conclude that there is association between smoking and lung cancer.

Contingency				
1	Table Analyzed	Retrospective (smoking and cancer)		
2				
3	P value and statistical significance			
4	Test	Fisher's exact test		
5	P value	<0.0001		
6	P value summary	****		
7	One- or two-sided	Two-sided		
8	Statistically significant (P < 0.05)?	Yes		
9				
10	Data analyzed	Cases (lung cancer)	Control	Total
11	Smoked	688	650	1338
12	Never smoked	21	59	80
13	Total	709	709	1418
14				
15	Percentage of row total	Cases (lung cancer)	Control	
16	Smoked	51.42%	48.58%	
17	Never smoked	26.25%	73.75%	
18				
19	Percentage of column total	Cases (lung cancer)	Control	
20	Smoked	97.04%	91.68%	
21	Never smoked	2.96%	8.32%	
22				
23	Percentage of grand total	Cases (lung cancer)	Control	
24	Smoked	48.52%	45.84%	
25	Never smoked	1.48%	4.16%	
26				

3.3 McNemar's test

McNemar's test is applied to paired categorical data. It is available via Prism web. (<https://www.graphpad.com/quickcalcs/>)

In the usual kind of case-control study, the investigator compares a group of controls with a group of cases. As a group, the controls are supposed to be similar to the cases (except for the absence of disease). Another way to perform a case-control study is to match individual cases with individual controls based on age, gender, occupation, location and other relevant variables. This is the kind of study McNemar's test is designed for.

		Control		
		+	-	Total
Case	+	13	25	38
	-	4	92	96
	Total	17	117	134

3.3.1 Click in the website above, select Categorical data, select **McNemar's test to analyze a matched case-control study**, then click **Continue**.

[1. Select category](#)

2. Choose calculator

[3. Enter data](#)

[4. View results](#)

Analyze categorical data

- ☐ Confidence interval of a proportion or count.
- ☐ Chi-square. Compare observed and expected frequencies.
- ☐ Fisher's and chi-square. Analyze a 2x2 contingency table.
- ☒ McNemar's test to analyze a matched case-control study.
- ☐ Binomial and sign test. Compare observed and expected proportions.
- ☐ NNT (Number Needed to Treat) with confidence interval.
- ☐ Predictive values from sensitivity, specificity, and prevalence.
- ☐ Kappa. Quantify interrater agreement.

CONTINUE ➤

3.3.2 **Input # of pairs of case and control.** Consider “Yes” as positive, “No” as negative, input the data in the contingency table. Then click **Calculate**.

QuickCalcs

[1. Select category](#)

[2. Choose calculator](#)

3. Enter data

[4. View results](#)

McNemar's test to analyze a matched case-control study

McNemar's test is used to compare paired proportions. It can be used to analyze retrospective case-control studies, where each case is matched to a particular control. Or it can be used to analyze experimental studies, where the two treatments are given to matched subjects. [Read an example with explanation.](#)

Risk Factor?

Control Case # of pairs

No	Yes	<input type="text" value="25"/>
Yes	No	<input type="text" value="4"/>
Yes	Yes	<input type="text" value="13"/>
No	No	<input type="text" value="92"/>

Calculate

Use McNemar's test (and this calculator) only when you are analyzing matched pairs. Each value you enter above represents a number of PAIRS. The total number of subjects in the study is twice the total of the values you enter above.

Note that the calculations are based entirely on the first two numbers you enter. Enter the remaining two numbers in order to document your full results.

3.3.3 Results include summary, p-value, odds ratio and contingency table. P-value is less than 0.05, we can reject the null hypothesis that there is association between risk factor and disease.

QuickCalcs

[1. Select category](#)

[2. Choose calculator](#)

[3. Enter data](#)

4. View results

Results of McNemar's test for a case-control study

Summary:

If there were no association between the risk factor and the disease, you'd expect the number of pairs where cases were exposed to the risk factor but control was not to equal the number of pairs where the control was exposed to the risk factor but the case did not. In this study, there were 29 discordant pairs (case and control had different exposure to the risk factor). There were 4 (13.793%) pairs where the control was exposed to the risk factor but the case was not, and 25 (86.207%) pairs where the case was exposed to the risk factor but the control was not.

P Value:

The two-tailed P value equals 0.0002

By conventional criteria, this difference is considered to be extremely statistically significant.

The P value was calculated with McNemar's test with the continuity correction.

Chi squared equals 13.793 with 1 degrees of freedom.

The P value answers this question: If there is no association between risk factor and disease, what is the probability of observing such a large discrepancy (or larger) between the number of the two kinds of discordant pairs? A small P value is evidence that there is an association between risk factor and disease.

Odds ratio:

The odds ratio is 6.250, with a 95% confidence interval extending from 2.158 to 24.710

Review your data:

		Control		
		+	-	
Case	+	13	25	38
	-	4	92	96
Total		17	117	134

In the end, if you have any questions regarding to this topic, please contact me (jingwen.gu@nih.gov) or submit a request to BCBB (bioinformatics@niaid.nih.gov).