

```

T-TEST GROUPS=GROUP(0 1)
/MISSING=ANALYSIS
/VARIABLES=age1ªCO Parity caesarean abortion transverseconewidth anterop
osteriorconewidth conedepth conizationtimeuntilhysterectom
ymonth
/CRITERIA=CI(.95).

```

T-Test

Notes

Input	Output Created	05-Mai-2019 10h38min48s
	Comments	
	Data	F:\artigos completos joao\para envio novos\artigo cone pos revisao\plos one\review 1\reposta 1 para enviar\RESULTADOS PARA SITE\databaseconization.sav
	Active Dataset	DataSet1
	Filter	<none>
	Weight	<none>
	Split File	<none>
Missing Value Handling	N of Rows in Working Data File	128
	Definition of Missing	User defined missing values are treated as missing.
	Cases Used	Statistics for each analysis are based on the cases with no missing or out-of-range data for any variable in the analysis.
	Syntax	T-TEST GROUPS=GROUP(0 1) /MISSING=ANALYSIS /VARIABLES=age1ªCO Parity caesarean abortion transverseconewidth anteroposteriorconewidth conedepth conizationtimeuntilhysterectomymonth /CRITERIA=CI(.95).
Resources	Processor Time	0:00:00.015
	Elapsed Time	0:00:00.017

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[DataSet1] F:\artigos completos joao\para envio novos\artigo cone pos rev
isao\plos one\review 1\reposta 1 para enviar\RESULTADOS PARA SITE\databasec
onization.sav

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Group Statistics

GROUP		N	Mean
age 1ª CO	NO residual disease	37	42,38
	Residual disease	43	47,37
parity	NO residual disease	37	3,92

Group Statistics

GROUP		Std. Deviation	Std. Error Mean
age 1ª CO	NO residual disease	11,368	1,869
	Residual disease	13,352	2,036
parity	NO residual disease	2,420	,398

Group Statistics

GROUP		N	Mean
parity	Residual disease	39	3,62
caesarian	NO residual disease	37	,59
	Residual disease	39	,51
abortion	NO residual disease	37	,38
	Residual disease	39	,36
transverseconewidth	NO residual disease	35	22,63
	Residual disease	41	23,02
anteroposteriorconewidth	NO residual disease	29	17,00
	Residual disease	33	15,36
cone depth	NO residual disease	35	20,09
	Residual disease	41	21,98
conizationtimeuntilhysterectomy-month	NO residual disease	37	4,193
	Residual disease	43	7,428

Group Statistics

GROUP		Std. Deviation	Std. Error Mean
parity	Residual disease	2,988	,478
caesarian	NO residual disease	,798	,131
	Residual disease	,854	,137
abortion	NO residual disease	,924	,152
	Residual disease	,537	,086
transverseconewidth	NO residual disease	6,112	1,033
	Residual disease	6,740	1,053
anteroposteriorconewidth	NO residual disease	6,256	1,162
	Residual disease	5,273	,918
cone depth	NO residual disease	6,176	1,044
	Residual disease	9,501	1,484
conizationtimeuntilhysterectomy-month	NO residual disease	4,3952	,7226
	Residual disease	13,3661	2,0383

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means
		F	Sig.	t
age 1ª CO	Equal variances assumed	4,982	,028	-1,785

Independent Samples Test

		t-test for Equality of Means		
		df	Sig. (2-tailed)	Mean Difference
age 1 ^a CO	Equal variances assumed	78	,078	-4,994

Independent Samples Test

		t-test for Equality of Means
		Std. Error Difference
age 1 ^a CO	Equal variances assumed	2,798

Independent Samples Test

		t-test for Equality of Means	
		95% Confidence Interval of the Difference	
		Lower	Upper
age 1 ^a CO	Equal variances assumed	-10,563	,576

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means
		F	Sig.	t
age 1 ^a CO	Equal variances not assumed			-1,807
parity	Equal variances assumed	,176	,676	,485
	Equal variances not assumed			,488
caesarian	Equal variances assumed	,055	,815	,431
	Equal variances not assumed			,431
abortion	Equal variances assumed	,603	,440	,113
	Equal variances not assumed			,111
transverseconewidth	Equal variances assumed	,496	,484	-,266
	Equal variances not assumed			-,268
anteroposteriorconewidth	Equal variances assumed	1,336	,252	1,118
	Equal variances not assumed			1,105
cone depth	Equal variances assumed	6,032	,016	-1,008
	Equal variances not assumed			-1,042
conizationtimeuntilhysterectomy-month	Equal variances assumed	3,587	,062	-1,407
	Equal variances not assumed			-1,496

Independent Samples Test

		t-test for Equality of Means		
		df	Sig. (2-tailed)	Mean Difference
age 1ª CO	Equal variances not assumed	77,994	,075	-4,994
parity	Equal variances assumed	74	,629	,304
	Equal variances not assumed	72,251	,627	,304
caesarian	Equal variances assumed	74	,668	,082
	Equal variances not assumed	73,983	,667	,082
abortion	Equal variances assumed	74	,911	,019
	Equal variances not assumed	57,249	,912	,019
transverseconewidth	Equal variances assumed	74	,791	-,396
	Equal variances not assumed	73,711	,789	-,396
anteroposteriorconewidth	Equal variances assumed	60	,268	1,636
	Equal variances not assumed	55,084	,274	1,636
cone depth	Equal variances assumed	74	,317	-1,890
	Equal variances not assumed	69,394	,301	-1,890
conizationtimeuntilhysterectomy-month	Equal variances assumed	78	,163	-3,2352
	Equal variances not assumed	52,256	,141	-3,2352

Independent Samples Test

		t-test for Equality of Means
		Std. Error Difference
age 1 ^a CO	Equal variances not assumed	2,764
parity	Equal variances assumed	,626
	Equal variances not assumed	,622
caesarian	Equal variances assumed	,190
	Equal variances not assumed	,190
abortion	Equal variances assumed	,172
	Equal variances not assumed	,175
transverseconewidth	Equal variances assumed	1,486
	Equal variances not assumed	1,475
anteroposteriorconewidth	Equal variances assumed	1,464
	Equal variances not assumed	1,481
cone depth	Equal variances assumed	1,874
	Equal variances not assumed	1,814
conizationtimeuntilhystere ctomy-month	Equal variances assumed	2,2990
	Equal variances not assumed	2,1626

Independent Samples Test

		t-test for Equality of Means	
		95% Confidence Interval of the Difference	
		Lower	Upper
age 1 ^a CO	Equal variances not assumed	-10,496	,509
parity	Equal variances assumed	-,943	1,550
	Equal variances not assumed	-,937	1,544
caesarian	Equal variances assumed	-,297	,460
	Equal variances not assumed	-,296	,459
abortion	Equal variances assumed	-,324	,363
	Equal variances not assumed	-,330	,369
transverseconewidth	Equal variances assumed	-3,358	2,566
	Equal variances not assumed	-3,335	2,543
anteroposteriorconewidth	Equal variances assumed	-1,293	4,565
	Equal variances not assumed	-1,331	4,603
cone depth	Equal variances assumed	-5,624	1,844
	Equal variances not assumed	-5,509	1,729
conizationtimeuntilhystere ctomy-month	Equal variances assumed	-7,8122	1,3418
	Equal variances not assumed	-7,5742	1,1039

CROSSTABS

```

/TABLES=Race menopausalstatus colposcopy conizationtechnique BY GROUP
/FORMAT=AVALUE TABLES
/STATISTICS=CHISQ CORR KAPPA RISK MCNEMAR CMH(1)
/CELLS=COUNT EXPECTED ROW COLUMN TOTAL RESID
/COUNT ROUND CELL
/METHOD=EXACT TIMER(5) .

```

Crosstabs

Notes

Output Created	05-Mai-2019 10h40min25s
Comments	

Notes

Input	Data	F:\artigos completos joao\para envio novos\artigo cone pos revisao\plos one\review 1\reposta 1 para enviar\RESULTADOS PARA SITE\databaseconization.sav
	Active Dataset	DataSet1
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	128
Missing Value Handling	Definition of Missing	User-defined missing values are treated as missing.
	Cases Used	Statistics for each table are based on all the cases with valid data in the specified range(s) for all variables in each table.
	Syntax	CROSSTABS /TABLES=Race menopausalstatus colposcopy conizationtechnique BY GROUP /FORMAT=AVALUE TABLES /STATISTICS=CHISQ CORR KAPPA RISK MCNEMAR CMH(1) /CELLS=COUNT EXPECTED ROW COLUMN TOTAL RESID /COUNT ROUND CELL /METHOD=EXACT TIMER(5).
Resources	Processor Time	0:00:00.156
	Elapsed Time	0:00:00.159
	Dimensions Requested	2
	Cells Available	174762
	Time for Exact Statistics	0:00:00.100

[DataSet1] F:\artigos completos joao\para envio novos\artigo cone pos revisao\plos one\review 1\reposta 1 para enviar\RESULTADOS PARA SITE\databaseconization.sav

Warnings

The Tests for Homogeneity of the Odds Ratio table and the Mantel-Haenszel Common Odds Ratio Estimate table are not computed for race * GROUP, because either (1) the group variable does not have exactly two distinct non-missing values or/and (2) the response variable does not have exactly two distinct non-missing values.

Case Processing Summary

	Cases					
	Valid		Missing		Total	
	N	Percent	N	Percent	N	Percent
race * GROUP	80	62,5%	48	37,5%	128	100,0%
menopausalstatus * GROUP	80	62,5%	48	37,5%	128	100,0%
colposcopy * GROUP	80	62,5%	48	37,5%	128	100,0%
conization technique * GROUP	80	62,5%	48	37,5%	128	100,0%

race * GROUP

Crosstab

			GROUP		
			NO residual disease	Residual disease	Total
race	white	Count	18	22	40
		Expected Count	18,5	21,5	40,0
		% within race	45,0%	55,0%	100,0%
		% within GROUP	48,6%	51,2%	50,0%
		% of Total	22,5%	27,5%	50,0%
		Residual	-,5	,5	
	latin american	Count	18	19	37
		Expected Count	17,1	19,9	37,0
		% within race	48,6%	51,4%	100,0%
		% within GROUP	48,6%	44,2%	46,3%
		% of Total	22,5%	23,8%	46,3%
		Residual	,9	-,9	
	african american	Count	1	2	3
		Expected Count	1,4	1,6	3,0
		% within race	33,3%	66,7%	100,0%
		% within GROUP	2,7%	4,7%	3,8%
		% of Total	1,3%	2,5%	3,8%
		Residual	-,4	,4	
Total	Count	37	43	80	
	Expected Count	37,0	43,0	80,0	
	% within race	46,3%	53,8%	100,0%	
	% within GROUP	100,0%	100,0%	100,0%	
	% of Total	46,3%	53,8%	100,0%	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	,312 ^a	2	,856	,927	
Likelihood Ratio	,317	2	,853	,927	
Fisher's Exact Test	,415			,927	
Linear-by-Linear Association	,002 ^b	1	,965	1,000	,560
McNemar-Bowker Test	.	.	. ^c		
N of Valid Cases	80				

a. 2 cells (33,3%) have expected count less than 5. The minimum expected count is 1,39.

b. The standardized statistic is -,044.

c. Computed only for a PxP table, where P must be greater than 1.

Chi-Square Tests

	Point Probability
Linear-by-Linear Association	,155

Symmetric Measures

		Value	Asymp. Std. Error ^a	Approx. T ^b
Interval by Interval	Pearson's R	-,005	,111	-,044
Ordinal by Ordinal	Spearman Correlation	-,014	,112	-,125
Measure of Agreement	Kappa	d		
	N of Valid Cases	80		

a. Not assuming the null hypothesis.

b. Using the asymptotic standard error assuming the null hypothesis.

d. Kappa statistics cannot be computed. They require a symmetric 2-way table in which the values of the first variable match the values of the second variable.

Symmetric Measures

		Approx. Sig.	Exact Sig.
Interval by Interval	Pearson's R	,965 ^c	1,000
Ordinal by Ordinal	Spearman Correlation	,901 ^c	,918

c. Based on normal approximation.

Risk Estimate

	Value
Odds Ratio for race (white / latin american)	a

a. Risk Estimate statistics cannot be computed. They are only computed for a 2*2 table without empty cells.

menopausalstatus * GROUP

Crosstab

			GROUP	
			NO residual disease	Residual disease
menopausalstatus	premenopausal	Count	34	30
		Expected Count	29,6	34,4

Crosstab

			Total
menopausalstatus	premenopausal	Count	64
		Expected Count	64,0

Crosstab

			GROUP	
			NO residual disease	Residual disease
menopausalstatus	premenopausal	% within menopausalstatus	53,1%	46,9%
		% within GROUP	91,9%	69,8%
		% of Total	42,5%	37,5%
		Residual	4,4	-4,4
	postmenopausal	Count	3	13
		Expected Count	7,4	8,6
		% within menopausalstatus	18,8%	81,3%
		% within GROUP	8,1%	30,2%
		% of Total	3,8%	16,3%
		Residual	-4,4	4,4
	Total	Count	37	43
		Expected Count	37,0	43,0
		% within menopausalstatus	46,3%	53,8%
		% within GROUP	100,0%	100,0%
		% of Total	46,3%	53,8%

Crosstab

			Total
menopausalstatus	premenopausal	% within menopausalstatus	100,0%
		% within GROUP	80,0%
		% of Total	80,0%
	postmenopausal	Count	16
		Expected Count	16,0
		% within menopausalstatus	100,0%
		% within GROUP	20,0%
		% of Total	20,0%
	Total	Count	80
		Expected Count	80,0
		% within menopausalstatus	100,0%
		% within GROUP	100,0%
		% of Total	100,0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	6,084 ^a	1	,014	,023	,013
Continuity Correction ^b	4,780	1	,029		
Likelihood Ratio	6,538	1	,011	,023	,013
Fisher's Exact Test				,023	,013
Linear-by-Linear Association	6,008 ^c	1	,014	,023	,013
McNemar Test				^d	
N of Valid Cases	80				

a. 0 cells (,0%) have expected count less than 5. The minimum expected count is 7,40.

b. Computed only for a 2x2 table

c. The standardized statistic is 2,451.

d. Both variables must have identical values of categories.

Chi-Square Tests

	Point Probability
Linear-by-Linear Association	,011

Symmetric Measures

		Value	Asymp. Std. Error ^a	Approx. T ^b
Interval by Interval	Pearson's R	,276	,096	2,534
Ordinal by Ordinal	Spearman Correlation	,276	,096	2,534
Measure of Agreement	Kappa	^d		
	N of Valid Cases	80		

a. Not assuming the null hypothesis.

b. Using the asymptotic standard error assuming the null hypothesis.

d. Kappa statistics cannot be computed. They require a symmetric 2-way table in which the values of the first variable match the values of the second variable.

Symmetric Measures

		Approx. Sig. ^c	Exact Sig.
Interval by Interval	Pearson's R	,013 ^c	,023
Ordinal by Ordinal	Spearman Correlation	,013 ^c	,023

c. Based on normal approximation.

Risk Estimate

	Value	95% Confidence Interval	
		Lower	Upper
Odds Ratio for menopausalstatus (premenopausal / postmenopausal)	4,911	1,276	18,906
For cohort GROUP = NO residual disease	2,833	,996	8,061
For cohort GROUP = Residual disease	,577	,406	,820
N of Valid Cases	80		

Tests of Homogeneity of the Odds Ratio

	Chi-Squared	df	Asymp. Sig. (2-sided)
Breslow-Day	,000	0	.
Tarone's	,000	0	.

Tests of Conditional Independence

	Chi-Squared	df	Asymp. Sig. (2-sided)
Cochran's	6,084	1	,014
Mantel-Haenszel	4,720	1	,030

Under the conditional independence assumption, Cochran's statistic is asymptotically distributed as a 1 df chi-squared distribution, only if the number of strata is fixed, while the Mantel-Haenszel statistic is always asymptotically distributed as a 1 df chi-squared distribution. Note that the continuity correction is removed from the Mantel-Haenszel statistic when the sum of the differences between the observed and the expected is 0.

Mantel-Haenszel Common Odds Ratio Estimate

Asymp. 95% Confidence Interval	Common Odds Ratio	Estimate	4,911
		ln(Estimate)	1,592
		Std. Error of ln(Estimate)	,688
		Asymp. Sig. (2-sided)	,021
		Lower Bound	1,276
		Upper Bound	18,906
		ln(Common Odds Ratio)	,244
		Upper Bound	2,939

The Mantel-Haenszel common odds ratio estimate is asymptotically normally distributed under the common odds ratio of 1,000 assumption. So is the natural log of the estimate.

colposcopy * GROUP

Crosstab

			GROUP		Total
			NO residual disease	Residual disease	
colposcopy	SCJ visible	Count	30	27	57
		Expected Count	26,4	30,6	57,0

Crosstab

			GROUP		Total
			NO residual disease	Residual disease	
colposcopy	SCJ visible	% within colposcopy	52,6%	47,4%	100,0%
		% within GROUP	81,1%	62,8%	71,3%
		% of Total	37,5%	33,8%	71,3%
		Residual	3,6	-3,6	
	SCJ not visible	Count	7	16	23
		Expected Count	10,6	12,4	23,0
		% within colposcopy	30,4%	69,6%	100,0%
		% within GROUP	18,9%	37,2%	28,8%
		% of Total	8,8%	20,0%	28,8%
		Residual	-3,6	3,6	
	Total	Count	37	43	80
		Expected Count	37,0	43,0	80,0
		% within colposcopy	46,3%	53,8%	100,0%
		% within GROUP	100,0%	100,0%	100,0%
		% of Total	46,3%	53,8%	100,0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	3,248 ^a	1	,072	,087	,059
Continuity Correction ^b	2,416	1	,120		
Likelihood Ratio	3,325	1	,068	,087	,059
Fisher's Exact Test				,087	,059
Linear-by-Linear Association	3,207 ^c	1	,073	,087	,059
McNemar Test				^d	
N of Valid Cases	80				

a. 0 cells (,0%) have expected count less than 5. The minimum expected count is 10,64.

b. Computed only for a 2x2 table

c. The standardized statistic is 1,791.

d. Both variables must have identical values of categories.

Chi-Square Tests

	Point Probability
Linear-by-Linear Association	,040

Symmetric Measures

		Value	Asymp. Std. Error ^a	Approx. T ^b
Interval by Interval	Pearson's R	,201	,106	1,817
Ordinal by Ordinal	Spearman Correlation	,201	,106	1,817
Measure of Agreement	Kappa	.		
	N of Valid Cases	80		

a. Not assuming the null hypothesis.

b. Using the asymptotic standard error assuming the null hypothesis.

d. Kappa statistics cannot be computed. They require a symmetric 2-way table in which the values of the first variable match the values of the second variable.

Symmetric Measures

		Approx. Sig. ^c	Exact Sig.
Interval by Interval	Pearson's R	,073 ^c	,087
Ordinal by Ordinal	Spearman Correlation	,073 ^c	,087

c. Based on normal approximation.

Risk Estimate

	95% Confidence Interval		
	Value	Lower	Upper
Odds Ratio for colposcopy (SCJ visible / SCJ not visible)	2,540	,907	7,108
For cohort GROUP = NO residual disease	1,729	,889	3,363
For cohort GROUP = Residual disease	,681	,463	1,000
N of Valid Cases	80		

Tests of Homogeneity of the Odds Ratio

	Chi-Squared	df	Asymp. Sig. (2-sided)
Breslow-Day	,000	0	.
Tarone's	,000	0	.

Tests of Conditional Independence

	Chi-Squared	df	Asymp. Sig. (2-sided)
Cochran's	3,248	1	,072
Mantel-Haenszel	2,386	1	,122

Under the conditional independence assumption, Cochran's statistic is asymptotically distributed as a 1 df chi-squared distribution, only if the number of strata is fixed, while the Mantel-Haenszel statistic is always asymptotically distributed as a 1 df chi-squared distribution. Note that the continuity correction is removed from the Mantel-Haenszel statistic when the sum of the differences between the observed and the expected is 0.

Mantel-Haenszel Common Odds Ratio Estimate

		Estimate	2,540
		ln(Estimate)	,932
		Std. Error of ln(Estimate)	,525
		Asymp. Sig. (2-sided)	,076
Asymp. 95% Confidence Interval	Common Odds Ratio	Lower Bound	,907
		Upper Bound	7,108
	ln(Common Odds Ratio)	Lower Bound	-,097
		Upper Bound	1,961

The Mantel-Haenszel common odds ratio estimate is asymptotically normally distributed under the common odds ratio of 1,000 assumption. So is the natural log of the estimate.

conization technique * GROUP

Crosstab

			GROUP
			NO residual disease
conization technique	cold knife	Count	18
		Expected Count	21,3
		% within conization technique	39,1%
		% within GROUP	48,6%
		% of Total	22,5%
		Residual	-3,3
	electrosurgical knife	Count	19
		Expected Count	15,7
		% within conization technique	55,9%
		% within GROUP	51,4%
		% of Total	23,8%
		Residual	3,3

Crosstab

			GROUP	
			Residual disease	Total
conization technique	cold knife	Count	28	46
		Expected Count	24,7	46,0
		% within conization technique	60,9%	100,0%
		% within GROUP	65,1%	57,5%
		% of Total	35,0%	57,5%
		Residual	3,3	
	electrosurgical knife	Count	15	34
		Expected Count	18,3	34,0
		% within conization technique	44,1%	100,0%
		% within GROUP	34,9%	42,5%
		% of Total	18,8%	42,5%
		Residual	-3,3	

Crosstab

		GROUP
		NO residual disease
Total	Count	37
	Expected Count	37,0
	% within conization technique	46,3%
	% within GROUP	100,0%
	% of Total	46,3%

Crosstab

		GROUP	
		Residual disease	Total
Total	Count	43	80
	Expected Count	43,0	80,0
	% within conization technique	53,8%	100,0%
	% within GROUP	100,0%	100,0%
	% of Total	53,8%	100,0%

Symmetric Measures

		Value	Asymp. Std. Error ^a	Approx. T ^b
Interval by Interval	Pearson's R	-,166	,111	-1,488

a. Not assuming the null hypothesis.

b. Using the asymptotic standard error assuming the null hypothesis.

Symmetric Measures

		Approx. Sig. ^c	Exact Sig.
Interval by Interval	Pearson's R	,141 ^c	,175

c. Based on normal approximation.

Symmetric Measures

		Value	Asymp. Std. Error ^a	Approx. T ^b
Ordinal by Ordinal	Spearman Correlation	-,166	,111	-1,488
Measure of Agreement	Kappa	. ^d		
	N of Valid Cases	80		

a. Not assuming the null hypothesis.

b. Using the asymptotic standard error assuming the null hypothesis.

d. Kappa statistics cannot be computed. They require a symmetric 2-way table in which the values of the first variable match the values of the second variable.

Symmetric Measures

		Approx. Sig. ^c	Exact Sig.
Ordinal by Ordinal	Spearman Correlation	,141 ^c	,175

c. Based on normal approximation.

Risk Estimate

		95% Confidence Interval	
	Value	Lower	Upper
Odds Ratio for conization technique (cold knife / electrosurgical knife)	,508	,206	1,248
For cohort GROUP = NO residual disease	,700	,438	1,118
For cohort GROUP = Residual disease	1,380	,885	2,150
N of Valid Cases	80		

Tests of Homogeneity of the Odds Ratio

	Chi-Squared	df	Asymp. Sig. (2-sided)
Breslow-Day	,000	0	.
Tarone's	,000	0	.

Tests of Conditional Independence

	Chi-Squared	df	Asymp. Sig. (2-sided)
Cochran's	2,207	1	,137
Mantel-Haenszel	1,565	1	,211

Under the conditional independence assumption, Cochran's statistic is asymptotically distributed as a 1 df chi-squared distribution, only if the number of strata is fixed, while the Mantel-Haenszel statistic is always asymptotically distributed as a 1 df chi-squared distribution. Note that the continuity correction is removed from the Mantel-Haenszel statistic when the sum of the differences between the observed and the expected is 0.

Mantel-Haenszel Common Odds Ratio Estimate

		Estimate	,508
		ln(Estimate)	-,678
		Std. Error of ln(Estimate)	,459
		Asymp. Sig. (2-sided)	,139
Asymp. 95% Confidence Interval	Common Odds Ratio	Lower Bound	,206
		Upper Bound	1,248
	ln(Common Odds Ratio)	Lower Bound	-1,578
		Upper Bound	,221

The Mantel-Haenszel common odds ratio estimate is asymptotically normally distributed under the common odds ratio of 1,000 assumption. So is the natural log of the estimate.