

## Crosstabs

### Notes

Output Created		11-JUL-2024 17:47:39
Comments		
Input	Data	D:\Works\DNA\Bacteria Data.sav
	Active Dataset	DataSet0
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	44
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=Ward BY Shape Gram_Stain Catalase_Test Methyl_Red_Test Citrate_Test IndoleKovac_Test Possible_Organism /FORMAT=AVALUE TABLES /CELLS=COUNT /COUNT ROUND CELL /BARCHART.
Resources	Processor Time	00:00:05.92
	Elapsed Time	00:00:05.45
	Dimensions Requested	2
	Cells Available	524245

## Case Processing Summary

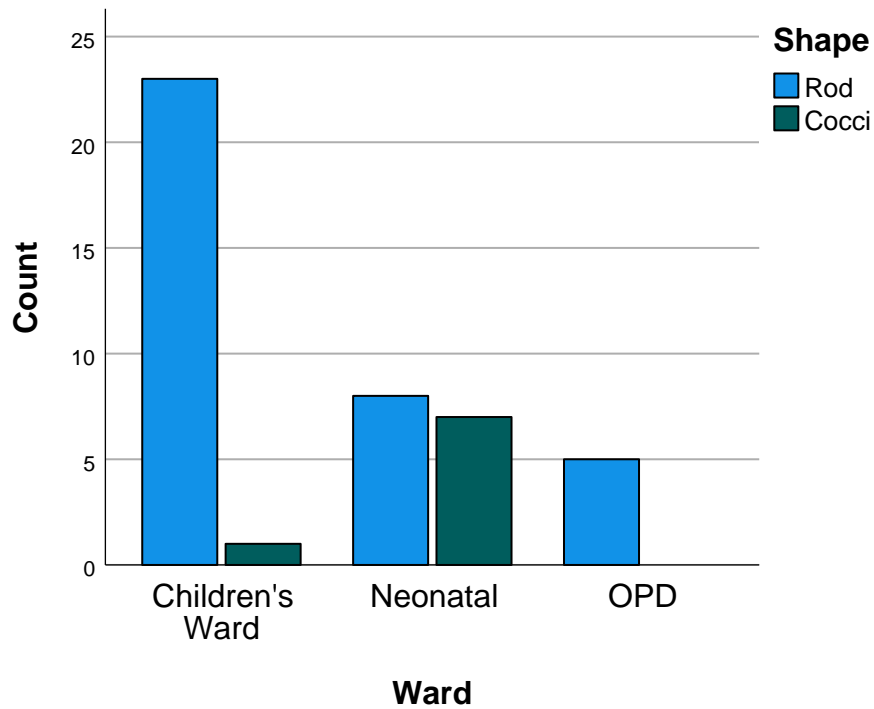
	Valid		Cases Missing		Total	
	N	Percent	N	Percent	N	Percent
Ward * Shape	44	100.0%	0	0.0%	44	100.0%
Ward * Gram Staining	44	100.0%	0	0.0%	44	100.0%
Ward * Catalase Test	44	100.0%	0	0.0%	44	100.0%
Ward * Methyl Red Test	44	100.0%	0	0.0%	44	100.0%
Ward * Citrate Test	44	100.0%	0	0.0%	44	100.0%
Ward * Indole/Kovac Test	44	100.0%	0	0.0%	44	100.0%
Ward * Possible_Organism	44	100.0%	0	0.0%	44	100.0%

## Ward \* Shape Crosstabulation

Count

		Shape		Total
		Rod	Cocci	
Ward	Children's Ward	23	1	24
	Neonatal	8	7	15
	OPD	5	0	5
Total		36	8	44

## Bar Chart

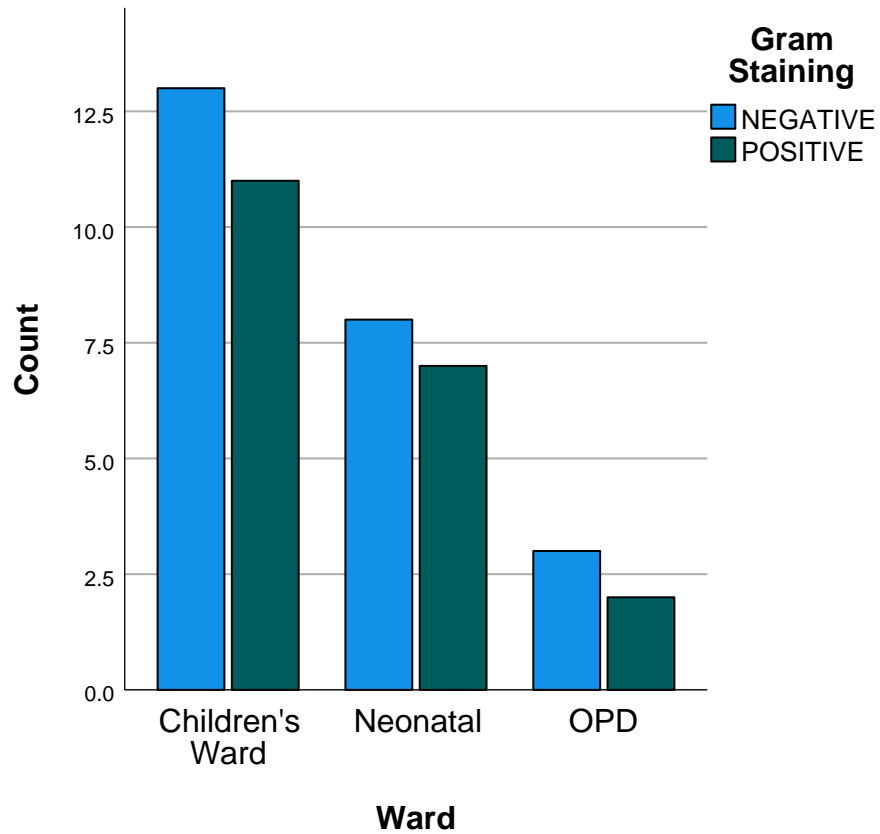


### Ward \* Gram Staining Crosstabulation

Count

		Gram Staining		Total
		NEGATIVE	POSITIVE	
Ward	Children's Ward	13	11	24
	Neonatal	8	7	15
	OPD	3	2	5
Total		24	20	44

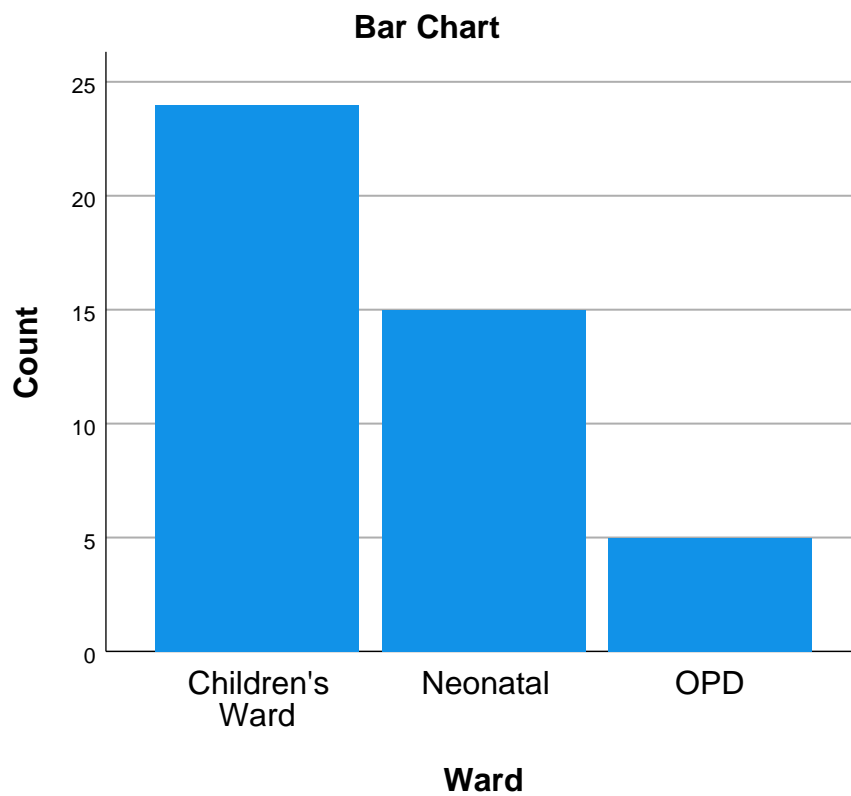
### Bar Chart



### Ward \* Catalase Test Crosstabulation

Count

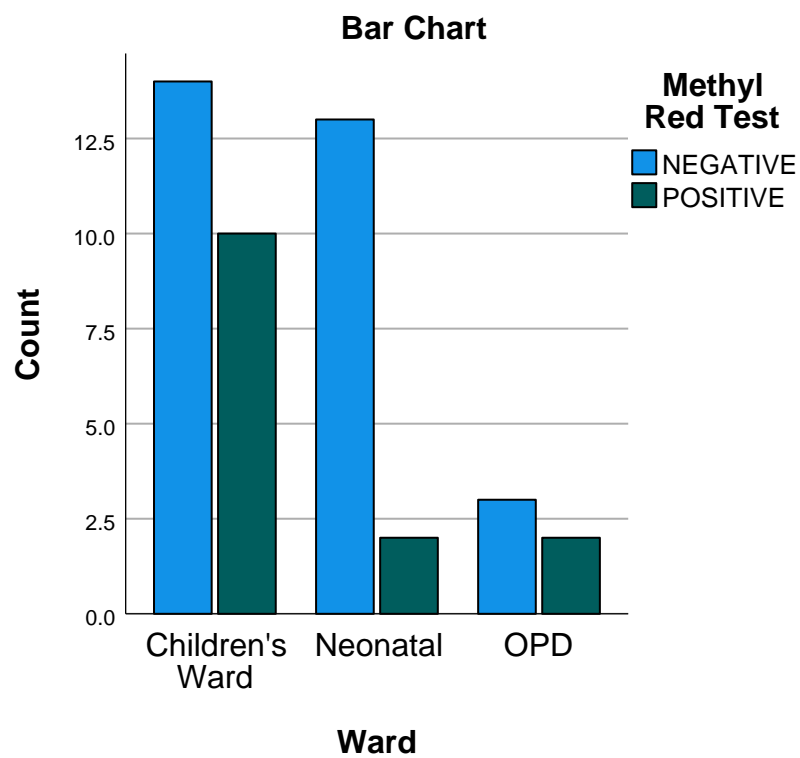
		Catalase Test	Total
		POSITIVE	
Ward	Children's Ward	24	24
	Neonatal	15	15
	OPD	5	5
Total		44	44



**Ward \* Methyl Red Test Crosstabulation**

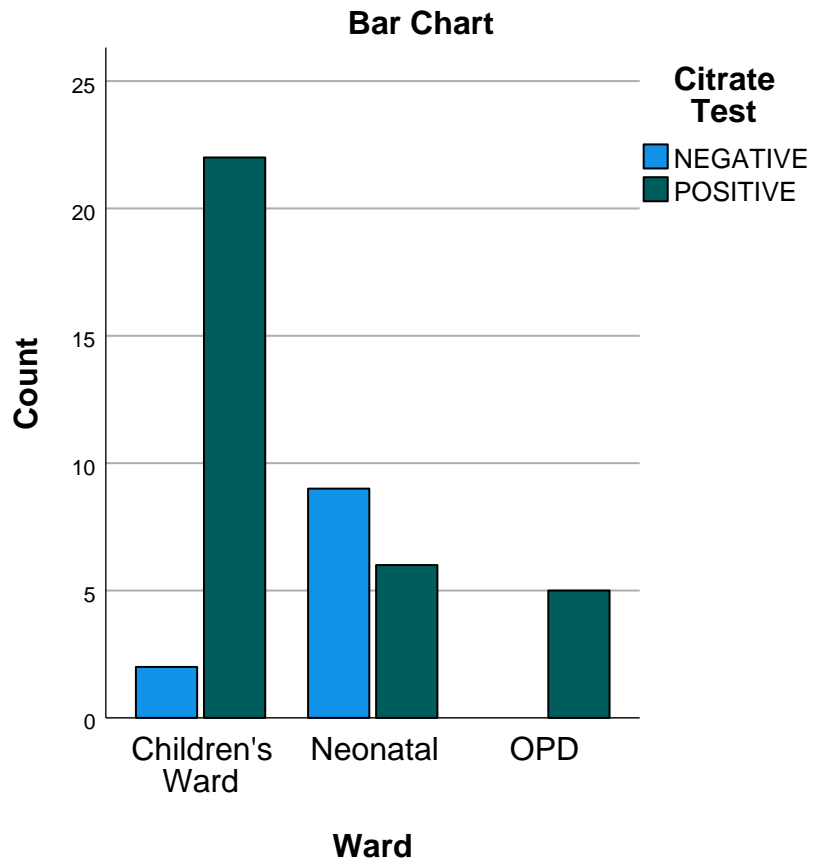
Count

		Methyl Red Test		Total
		NEGATIVE	POSITIVE	
Ward	Children's Ward	14	10	24
	Neonatal	13	2	15
	OPD	3	2	5
Total		30	14	44



**Ward \* Citrate Test Crosstabulation**

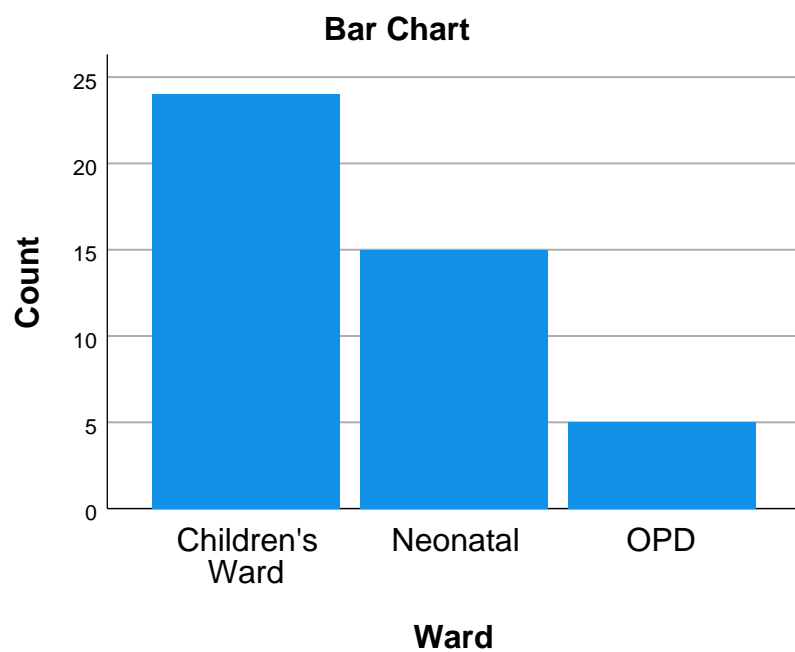
		Citrate Test		Total
		NEGATIVE	POSITIVE	
Ward	Children's Ward	2	22	24
	Neonatal	9	6	15
	OPD	0	5	5
Total		11	33	44



**Ward \* Indole/Kovac Test Crosstabulation**

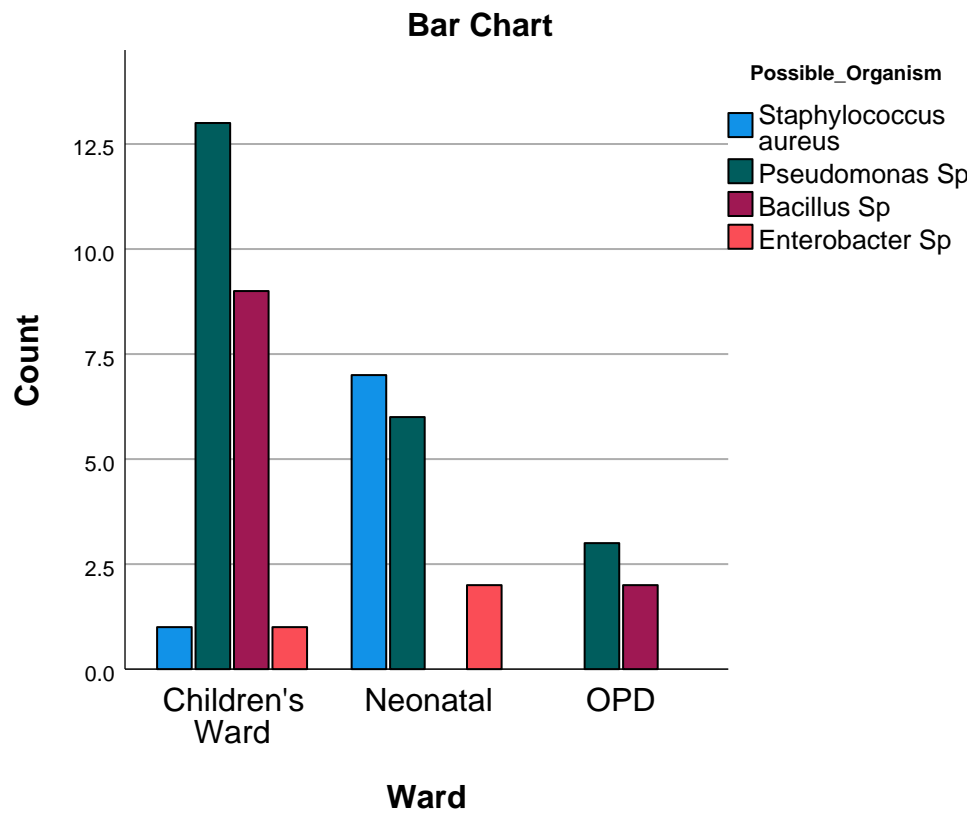
Count

		Indole/Kovac Test	
		NEGATIVE	Total
Ward	Children's Ward	24	24
	Neonatal	15	15
	OPD	5	5
Total		44	44



**Ward \* Possible\_Organism Crosstabulation**

		Possible_Organism				Total
		Staphylococcus aureus	Pseudomonas Sp	Bacillus Sp	Enterobacter Sp	
Ward	Children's Ward	1	13	9	1	24
	Neonatal	7	6	0	2	15
	OPD	0	3	2	0	5
Total		8	22	11	3	44



```
MEANS TABLES=Shape Gram_Stain Catalase_Test Methyl_Red_Test Citrate_Test IndoleKovac_T
est
```

```
    Possible_Organism BY Ward
/CELLS=MEAN STDDEV
/STATISTICS ANOVA LINEARITY.
```

## Means



## Notes

Output Created		11-JUL-2024 17:50:42
Comments		
Input	Data	D:\Works\DNA\Bacteria Data.sav
	Active Dataset	DataSet0
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	44
Missing Value Handling	Definition of Missing	For each dependent variable in a table, user-defined missing values for the dependent and all grouping variables are treated as missing.
	Cases Used	Cases used for each table have no missing values in any independent variable, and not all dependent variables have missing values.
Syntax		MEANS TABLES=Shape Gram_Stain Catalase_Test Methyl_Red_Test Citrate_Test IndoleKovac_Test Possible_Organism BY Ward /CELLS=MEAN STDDEV /STATISTICS ANOVA LINEARITY.
Resources	Processor Time	00:00:00.03
	Elapsed Time	00:00:00.03

### Case Processing Summary

	Included		Cases Excluded		Total	
	N	Percent	N	Percent	N	Percent
Shape * Ward	44	100.0%	0	0.0%	44	100.0%
Gram Staining * Ward	44	100.0%	0	0.0%	44	100.0%
Catalase Test * Ward	44	100.0%	0	0.0%	44	100.0%
Methyl Red Test * Ward	44	100.0%	0	0.0%	44	100.0%
Citrate Test * Ward	44	100.0%	0	0.0%	44	100.0%
Indole/Kovac Test * Ward	44	100.0%	0	0.0%	44	100.0%
Possible_Organism * Ward	44	100.0%	0	0.0%	44	100.0%

### Report

Ward		Shape	Gram Staining	Catalase Test	Methyl Red Test
Children's Ward	Mean	1.04	1.46	2.00	1.42
	Std. Deviation	.204	.509	.000	.504
Neonatal	Mean	1.47	1.47	2.00	1.13
	Std. Deviation	.516	.516	.000	.352
OPD	Mean	1.00	1.40	2.00	1.40
	Std. Deviation	.000	.548	.000	.548
Total	Mean	1.18	1.45	2.00	1.32
	Std. Deviation	.390	.504	.000	.471

### Report

Ward		Citrate Test	Indole/Kovac Test	Possible_Organism
Children's Ward	Mean	1.92	1.00	2.42
	Std. Deviation	.282	.000	.654
Neonatal	Mean	1.40	1.00	1.80
	Std. Deviation	.507	.000	1.014
OPD	Mean	2.00	1.00	2.40
	Std. Deviation	.000	.000	.548
Total	Mean	1.75	1.00	2.20
	Std. Deviation	.438	.000	.823

**ANOVA Table<sup>a,b</sup>**

			Sum of Squares	df
Shape * Ward	Between Groups	(Combined)	1.854	2
		Linearity	.290	1
		Deviation from Linearity	1.564	1
	Within Groups		4.692	41
	Total		6.545	43
Gram Staining * Ward	Between Groups	(Combined)	.017	2
		Linearity	.006	1
		Deviation from Linearity	.011	1
	Within Groups		10.892	41
	Total		10.909	43
Methyl Red Test * Ward	Between Groups	(Combined)	.779	2
		Linearity	.184	1
		Deviation from Linearity	.595	1
	Within Groups		8.767	41
	Total		9.545	43
Citrate Test * Ward	Between Groups	(Combined)	2.817	2
		Linearity	.364	1
		Deviation from Linearity	2.453	1
	Within Groups		5.433	41
	Total		8.250	43
Possible_Organism * Ward	Between Groups	(Combined)	3.726	2
		Linearity	.814	1
		Deviation from Linearity	2.912	1
	Within Groups		25.433	41
	Total		29.159	43

**ANOVA Table<sup>a,b</sup>**

			Mean Square	F
Shape * Ward	Between Groups	(Combined)	.927	8.100
		Linearity	.290	2.532
		Deviation from Linearity	1.564	13.668
	Within Groups		.114	
	Total			
Gram Staining * Ward	Between Groups	(Combined)	.009	.033
		Linearity	.006	.024
		Deviation from Linearity	.011	.042
	Within Groups		.266	
	Total			
Methyl Red Test * Ward	Between Groups	(Combined)	.389	1.821
		Linearity	.184	.859
		Deviation from Linearity	.595	2.783
	Within Groups		.214	
	Total			
Citrate Test * Ward	Between Groups	(Combined)	1.408	10.627
		Linearity	.364	2.744
		Deviation from Linearity	2.453	18.510
	Within Groups		.133	
	Total			
Possible_Organism * Ward	Between Groups	(Combined)	1.863	3.003
		Linearity	.814	1.312
		Deviation from Linearity	2.912	4.694
	Within Groups		.620	
	Total			

**ANOVA Table<sup>a,b</sup>**

			Sig.
Shape * Ward	Between Groups	(Combined)	.001
		Linearity	.119
		Deviation from Linearity	.001
	Within Groups		
	Total		
Gram Staining * Ward	Between Groups	(Combined)	.968
		Linearity	.878
		Deviation from Linearity	.839
	Within Groups		
	Total		
Methyl Red Test * Ward	Between Groups	(Combined)	.175
		Linearity	.359
		Deviation from Linearity	.103
	Within Groups		
	Total		
Citrate Test * Ward	Between Groups	(Combined)	.000
		Linearity	.105
		Deviation from Linearity	.000
	Within Groups		
	Total		
Possible_Organism * Ward	Between Groups	(Combined)	.061
		Linearity	.259
		Deviation from Linearity	.036
	Within Groups		
	Total		

a. No variance within groups - statistics for Catalase Test \* Ward cannot be computed.

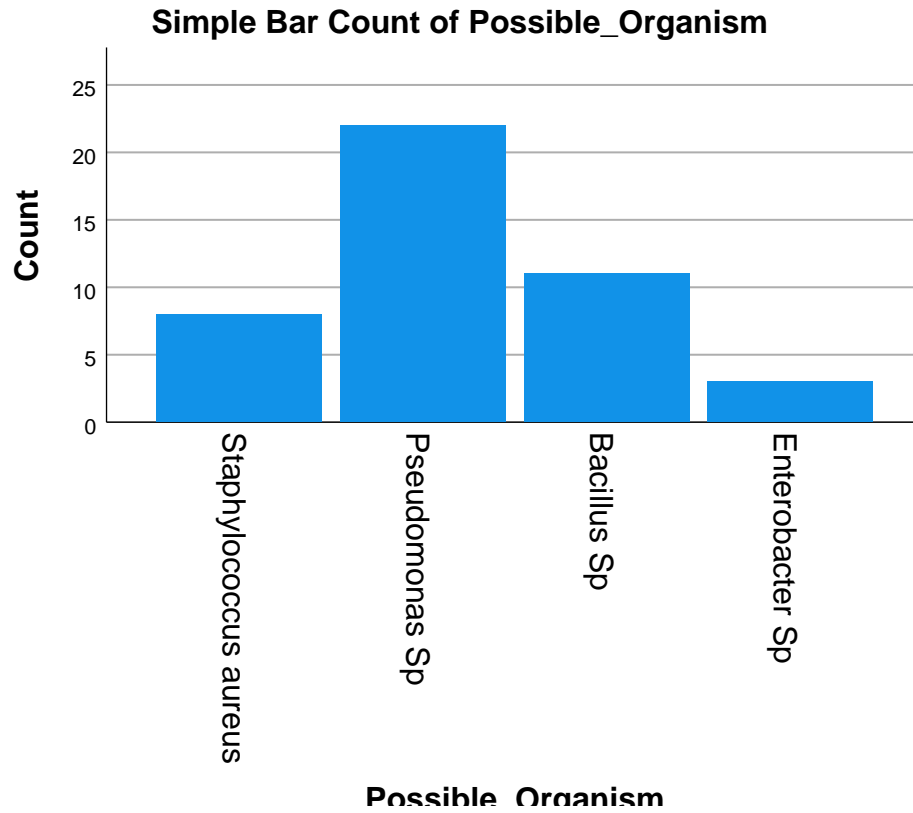
b. No variance within groups - statistics for Indole/Kovac Test \* Ward cannot be computed.

### Measures of Association

	R	R Squared	Eta	Eta Squared
Shape * Ward	.210	.044	.532	.283
Gram Staining * Ward	-.024	.001	.040	.002
Methyl Red Test * Ward	-.139	.019	.286	.082
Citrate Test * Ward	-.210	.044	.584	.341
Possible_Organism * Ward	-.167	.028	.357	.128

## Notes

Output Created		11-JUL-2024 17:59:11
Comments		
Input	Data	D:\Works\DNA\Bacteria Data.sav
	Active Dataset	DataSet0
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	44
Syntax		<pre> GGRAPH   /GRAPHDATASET   NAME="graphdataset"   VARIABLES=Possible_Or ganism COUNT()[name=" COUNT"]   MISSING=LISTWISE   REPORTMISSING=NO   /GRAPHSPEC   SOURCE=INLINE. BEGIN GPL   SOURCE: s=userSource (id("graphdataset"))   DATA: Possible_Organism=col (source(s), name ("Possible_Organism"), unit.category())   DATA: COUNT=col (source(s), name ("COUNT"))   GUIDE: axis(dim(1), label ("Possible_Organism"))   GUIDE: axis(dim(2), label ("Count"))   GUIDE: text.title(label ("Simple Bar Count of Possible_Organism"))   SCALE: cat(dim(1), include("1", "2", "3", "4"))   SCALE: linear(dim(2), include(0))   ELEMENT: interval (position (Possible_Organism*COU NT), shape.interior(shape. square)) END GPL. </pre>
Resources	Processor Time	00:00:02.59
	Elapsed Time	00:00:03.14



```
MEANS TABLES=Possible_Organism BY Ward
/CELLS=MEAN STDDEV
/STATISTICS ANOVA LINEARITY.
```

## Means

## Notes

Output Created		11-JUL-2024 18:37:54
Comments		
Input	Data	D:\Works\DNA\Bacteria Data.sav
	Active Dataset	DataSet0
	Filter	<none>
	Weight	<none>
	Split File	<none>
	N of Rows in Working Data File	44
Missing Value Handling	Definition of Missing	For each dependent variable in a table, user-defined missing values for the dependent and all grouping variables are treated as missing.
	Cases Used	Cases used for each table have no missing values in any independent variable, and not all dependent variables have missing values.
Syntax		MEANS TABLES=Possible_Organism BY Ward /CELLS=MEAN STDDEV /STATISTICS ANOVA LINEARITY.
Resources	Processor Time	00:00:00.03
	Elapsed Time	00:00:00.09

## Case Processing Summary

	Included		Excluded		Total	
	N	Percent	N	Percent	N	Percent
Possible_Organism * Ward	44	100.0%	0	0.0%	44	100.0%

## Report

Possible\_Organism

Ward	Mean	Std. Deviation
Children's Ward	2.42	.654
Neonatal	1.80	1.014
OPD	2.40	.548
Total	2.20	.823



**ANOVA Table**

			Sum of Squares	df
Possible_Organism * Ward	Between Groups	(Combined)	3.726	2
		Linearity	.814	1
		Deviation from Linearity	2.912	1
	Within Groups		25.433	41
	Total		29.159	43

**ANOVA Table**

			Mean Square	F
Possible_Organism * Ward	Between Groups	(Combined)	1.863	3.003
		Linearity	.814	1.312
		Deviation from Linearity	2.912	4.694
	Within Groups		.620	
	Total			

**ANOVA Table**

			Sig.
Possible_Organism * Ward	Between Groups	(Combined)	.061
		Linearity	.259
		Deviation from Linearity	.036
	Within Groups		
	Total		

**Measures of Association**

	R	R Squared	Eta	Eta Squared
Possible_Organism * Ward	-.167	.028	.357	.128