RESULTS

The **results** section provides a description of the data using words often combined with visual representations, such as tables and/or figures. While the specific way to analyze data will vary depending on the hypothesis and experimental design, some components of the results are consistent across all scientific writing.

Results SHOULD ...

- Summarize the findings in text
- Provide the results in the framework of the experiment
- Be written in paragraph form with reference to the appropriate tables and figures within the paragraphs of text

Results SHOULD NOT ...

- Provide descriptions on how to perform the experiment (protocols belong in **Methods** section)
- Include raw data (data that have not been summarized)
- Include data analysis or interpretation (interpretation of data belongs in **Discussion** section)

Types of Results

Results may be qualitative (not numeric) or quantitative (numeric).

Qualitative data are often used in diagnostic tests such as determining a biochemical pathway, mutation, or other important biological feature. Genetic analysis, microbial testing, and immunological assays utilize qualitative data.

Quantitative data are used to describe samples, as well as relationships. **Summary** (descriptive) statistics, used to describe a population or data set, are the most commonly used numeric results in biology and can be used for **categorical** or **continuous** data.

- **Categorical** data are those that are divided into groups (categories), such as by sex (male/female), size (small/medium/large), or demographic (aquatic/terrestrial) features.
- **Continuous** data are those that can take any value, such as height, weight, or temperature. Other data may be collected with regard to time.

Qualitative Results

Qualitative results contain data describing the outcome of the observational study. In the qualitative analysis, readers will note that no manipulation of data occurred; however, the author(s) provide both paragraph text and supportive visuals in the form of tables and/or figures to illustrate what was discovered in the study.

Example of Qualitative Results Text: Of the 25 restriction enzymes that were screened for use in this study, only five digested the amplified mtDNA completely and provided polymorphic results (Table 1.) Restriction enzymes *Fnu4H* I and *Hae* III each produced two distinct haplotypes while *Mse* I and *Tsp*509 I each produced three distinct haplotypes. *Hinf I* created four distinct haplotypes, the highest of any of the restriction enzymes used in this study.

Table 1. Five restriction enzymes that produced variable restriction fragment patterns for *Rana luteiventris* with haplotype name, fragment pattern and total length of each restriction fragment length polymorphism (RFLP) product. (Taken from Seitz 1999.)

Restriction	Haplotype		Total length of RFLP
enzyme	name	Fragment pattern	product
Fnu4H I	А	1650, 490, 470, 230, 210	3050
	В	1650, 700, 470, 230	3050
<u>Hae</u> III	А	620, 610, 540, 315, 275, 250, 210, 180, 50	3050
	В	620, 610, 540, 430, 315, 275, 210, 50	3050
<u>Hinf</u> I	А	850, 670, 570, 300, 230, 220, 210	3050
	В	1420, 670, 300, 230, 220, 210	3050
	С	850, 670, 570, 300, 230, 220, 170, 40	3050
	D	970, 850, 570, 230, 220, 210	3050
<u>Mse</u> I	А	280, 270, 240, 230, 190, 160, 150, 140, 135, 130, 115, 90, 80, 70, 60, 40	2380
	В	300, 280, 270, 240, 190, 160, 150, 140, 135, 130, 115, 90, 80, 60, 40	2380
	С	280, 240, 230, 210, 190, 160, 150, 140, 135, 130, 115, 90, 80, 70, 60, 50, 40	2380
Tsp509 I	А	400, 330, 280, 270, 260, 250, 150	1940
	В	400, 300, 280, 270, 260, 250, 150	1910
	С	400, 330, 280, 260, 250, 170, 150	1840

Quantitative Results: Summary / Descriptive Statistics

When working with numeric data, summary or descriptive statistics provide an easy way for the reader to visualize the relationship between the samples. Summary statistics may include sample size, minimum value, maximum value, range, mean, median, and standard deviation.

- **Sample size** is the number of samples per treatment or group often indicated by the letter (n)
- The **minimum** value is the smallest value or minimum.
- The **maximum** value is the largest value or maximum.
- The **range** is the difference between the maximum value and the minimum value (maximum minimum value).
- The **median** value is the middle value. This value separates the higher half of the data from the lower half of the data.
- The **mean** is the arithmetic average. It is calculated by adding all the scores together and dividing by the number of scores.
- **Standard deviation** is the square root of the variance. This can be calculated by hand or through the use of computer programs, such as Excel or JMP.

While all of the above summary statistics are frequently provided by statistical software, the five that should be included in biological papers at this level are *sample size, minimum value, maximum value, mean, and standard deviation.* These values provide a good overview data set. It is possible to provide all of the summary statistics clearly and concisely in a single sentence. The example below is based on an experiment performed in a MTH 280 - Biometry course. Students surveyed pet owners and non-pet owners regarding their happiness levels. Surveyors used a happiness scale of 1-10 and allowed individuals to categorize their own level of happiness.

Example of Summary Statistics Text: Of the 19 people who own pets, the happiness level ranged from 4.5 - 10 with a mean of 7.34 and a standard deviation of 1.59 (Figure 1). Of the 21 people who do not own pets, the happiness level ranged from 4-9 with a mean of 7.52 and a standard deviation of 1.47.

Note that sample size, minimum, maximum, mean, and standard deviation were provided for pet owners and those that don't own pets. Also note that the figure illustrating this information is cited in the text. If a table or figure is included in a paper, **it must be cited in the text**.

Results for Categorical Data

Categorical data are types of data that can be divided into groups. Typically **bar charts** are useful for illustrating categorical data, as the categories are listed along the **x-axis**, and the quantitative dependent variable is shown along the **y-axis**. Example such as comparing height based on sex of individuals or counting number of eggs laid based on where a bird lives would fall in to the categorical data analysis.



Figure 1. Mean happiness score for individuals who do not own pets (No) and who do own pets (Yes). Error bars represent one standard deviation from the mean.

While the **summary statistics** are useful in providing an overall description of the results, they do not indicate whether there is a **statistically significant difference** in the dependent variable based on the treatment (independent variable). Therefore, **statistical tests** may be performed to identify the level of confidence that a difference exists. This is most commonly expressed with a **p-value**.

Example of Results with Statistical Test Results for Categorical Data: Within the ring of observation, the mean lichen coverage was 48.3% with a minimum of 35% to a maximum of 60% and a standard deviation of 9.0% across the nine rough-barked trees examined. The nine smooth-barked trees had a mean average lichen coverage at 68.9% with a minimum of 30% coverage to a maximum of 90% coverage with a standard deviation of 19.2% (Figure 2). A nonparametric Wilcoxon test indicated that the lichen coverage was significantly higher on the smooth-barked trees than those with rough bark. (p = 0.02)



Figure 2. Mean lichen coverage within the ring of observation. Error bars represent one standard deviation from the mean.

Results for Continuous Data

Continuous data are quantitative data that can have any number value including decimals or fragments. Scientists often examine the relationship that a continuous independent variable has (if any) with the dependent variable. If the relationship is linear, then how close the points are to the **regression line** indicates how well the independent variable predicts the dependent variable. Note that this type of analysis does NOT reveal cause/effect but instead **correlation**.

Example of Results with Statistical Test Results for Continuous Data: Cricket chirp rate was positively correlated with ambient temperature (Figure 3). From 15 samples, the data indicated that at lower temperatures (6.0°C - 13°C), chirp rates were in the 14 to 16 chirps per minute range while at higher temperatures (14.0°C - 20°C), cricket chirp rates were in the 16 to 20 chirps per minute range. A regression analysis provided an r² value of 0.697 with a p-value of 0.0001.



Figure 3. Cricket chirp rate in response to ambient temperature. The blue line represents a linear fit of the data.

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