Some benefits of writing your manuscripts in R markdown: A short tutorial

Daniel Noble[1,2] and Diego Barneche[1]

[1] Department of Biology, Macquarie University

[2] Author to whom you should maybe not bother contacting

Introduction

R markdown provides a really cool platform for embedding your R script directly into your manuscript. You can then evaluate functions, figures, tables, numbers and objects directly in the manuscript, which means that if your data changes no more updating your values, tables and figures painfully by hand! In this manuscript we will show you how to do all this and incorperate references.

Methods

Maybe you want to write how many males and females you collected. So we collected 50 males and 50 females. This will be evaluated by knitR to indicate the numbers 50 for males and 50 for females. Which you will see later will be problematic when the data gets updated. We created some data using the following equation:

$$Y \approx \beta_0 + \Delta_{sex} + \beta_1 * X_1 + \beta_2 * X_2 + \epsilon$$

where Y is our response variable, Δ_{sex} are sex-driven devitions in our intercept β_0, and β_1 and β_2 are the coefficients for our predictor variables X_1 and X_2. To reference this equation we can consult [1].

Results

The average Y for males was 182.8924 and for females 182.8924. Y was strongly related to x1 (Fig 1 & Table 1).

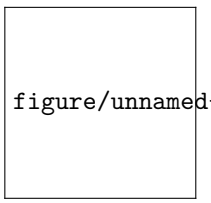
[htbp] 

Figure 1: Relationship between Y and x1

Table 1: Table 1

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	3.53	4.08	0.87	0.39
sexM	5.34	0.21	25.85	0.00
x1	1.80	0.10	17.98	0.00
x2	5.65	0.12	45.83	0.00

References

1. Ackerman JL, Bellwood DR, Brown JH (2004) The contribution of small individuals to density-body size relationships: examination of energetic equivalence in reef fishes. Oecologia 139: 568–571. Available: \T1\textless{}GotoISI\T1\textgreater{}://000221235800010.