

Dice Roll Data Analysis

Sejin Kim

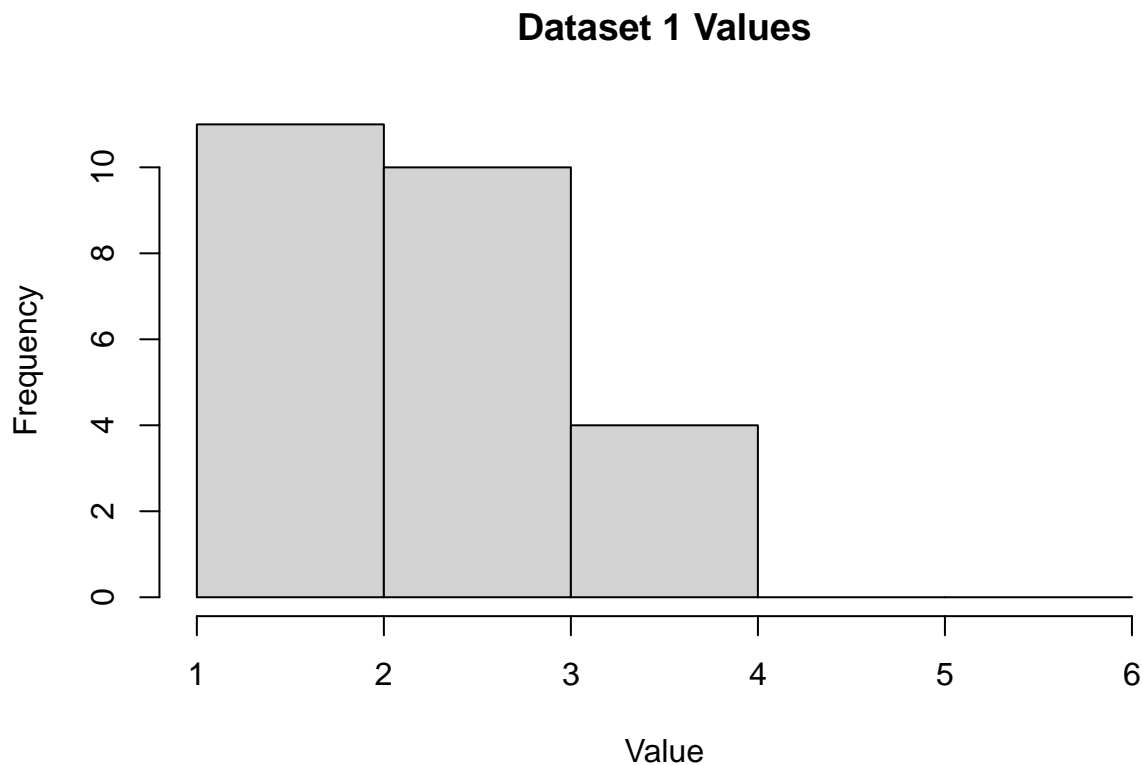
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Data

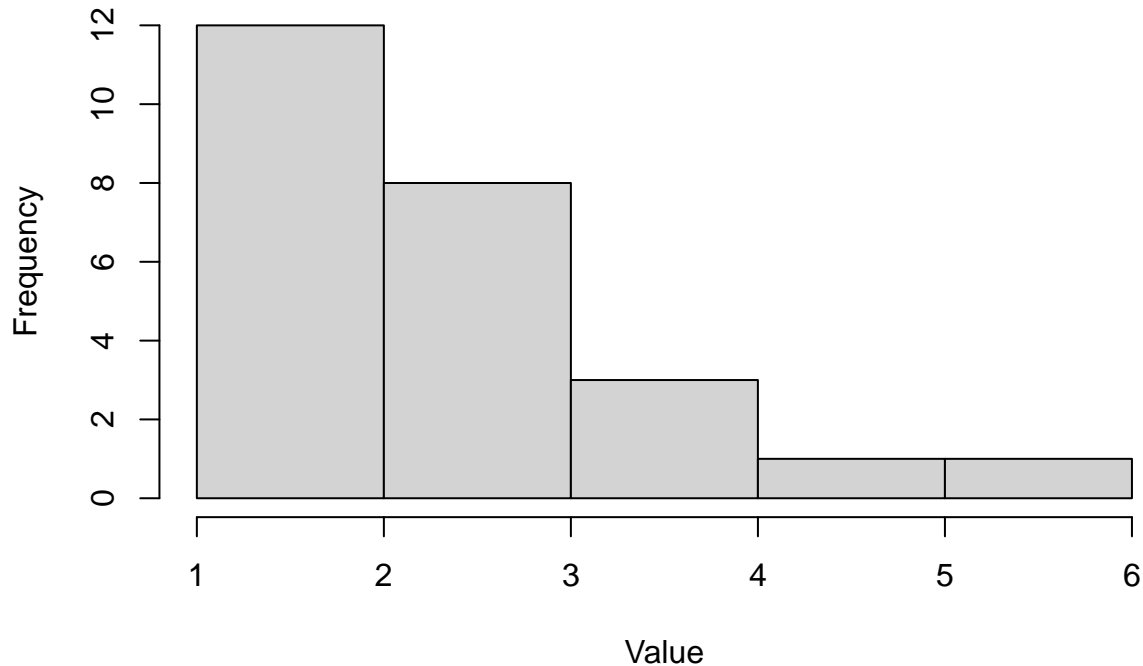
Two die were rolled, one of which was weighted and one of which was not. In the analysis, `die1` is the weighted die, and `die2` is the non-weighted die. The data were stored in a comma-separated value document (`.csv`) and in a R dataset (`.rds`) file, and both are available in the repository at <https://github.com/kim3-sudo/die-data-analysis>.

Analysis

After the data were imported and formatted as needed, a simple EDA was done visually, and a simple Tibble was created with counts, medians, and IQRs. Interestingly, both datasets look about the same from a summary statistic point of view. This is further reflected by the histograms.



Dataset 2 Values



However, the data are non-normal, so we cannot use an analysis of variance, which depends on normality. Rather, I used a Wilcoxon rank sum test. The assumptions for a Wilcoxon test are as follows.

- Each data is independent. That is, each die roll was not affected by the previous roll or will not influence the result of the next roll.
- The two populations have equal variance.

To test for equal variance, we can run a Fligner-Killeen test for homogeneity of variances. The hypotheses for the Fligner-Killeen test are as follows.

- H_0 (null hypothesis): There is evidence to suggest that the variances in die rolls are significantly different between the different treatment groups (the different dice).
- H_A (alternative hypothesis): There is no evidence to suggest that the variance in values are significantly different between the different treatment groups.

A test can be run using the following code.

```
fligner.test(value ~ group, data = diedata)
```

where `value` represents the value that was rolled, `group` represents the die that was rolled, and `diedata` is the dataset that holds the values for both die.

The results of the Fligner-Killeen test are as follows, as reported by R (v3.6.3).

Fligner-Killeen test of homogeneity of variances

```
data: value by group
Fligner-Killeen:med chi-squared = 0, df = 1, p-value = 1
```

Given a p -value of 1 and a median $\chi^2 = 0$ on 1 degree of freedom, we fail to reject the null hypothesis that the variances are significantly different and all conditions are met. Therefore, we can run a Wilcoxon rank sum test.

The hypotheses for the Wilcoxon rank sum test are as follows.

- H_0 (null hypothesis): The two datasets are derived from the same die.
- H_A (alternative hypothesis): There is some force acting on one of the die.

A Wilcoxon rank sum test can be run using the following code.

```
wtest <- wilcox.test(value ~ group, data = diedata, exact = FALSE, alternative = "less")
```

where `value` represents that value that was rolled, `group` indicates the die that was rolled, `diedata` is the dataset that holds the values for both die, `exact` mutes the warning that a Wilcoxon test's responses are continuous, and `alternative = "less"` indicates a test for whether the median roll value on die 1 is less than the median roll value on die 2.

The results of the Wilcoxon test are as follows, as reported by R (v3.6.3).

Wilcoxon rank sum test with continuity correction

```
data: value by group
W = 309, p-value = 0.4759
alternative hypothesis: true location shift is less than 0
```

With a W test statistic of 309 and a p -value of 0.4759, it would appear that both of the die were of the same type.

Conclusion

The test has concluded that the two dies are of the same type, and that statistically, there is no difference between the two. With a p -value of 0.4758, we must accept the null hypothesis that the two dies are of the same group.

While we know that the two die are not of the same type, the test has failed us. A more accurate conclusion would require many more die rolls.