

# Understanding the Brown-Forsythe Test in R: A Step-by-Step Guide

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The [one-way Analysis of Variance \(ANOVA\)](#) is a cornerstone of frequentist statistics, providing a robust framework for comparing the means of three or more independent groups. This powerful method is indispensable in experimental research across disciplines, from clinical trials and behavioral science to industrial engineering, where researchers need to assess if group membership significantly influences an outcome variable.

However, the validity of inferences drawn from an [ANOVA](#) hinges on satisfying several core statistical prerequisites. Paramount among these is the assumption of homogeneity of [variances](#), often referred to as homoscedasticity. This assumption mandates that the variability (spread) within each population, from which the samples are drawn, must be statistically equivalent.

When this critical assumption is potentially violated, researchers turn to specific diagnostic tests. The **Brown-Forsythe test** stands out as a highly reliable and robust alternative to the standard Levene test, particularly when dealing with data distributions that deviate from normality. The primary purpose of the [Brown-Forsythe test](#) is to formally evaluate the equality of [variances](#) across the groups by testing the following hypotheses:

**H<sub>0</sub>:** The population [variances](#) across all groups are equal (Homoscedasticity is assumed).

**H<sub>A</sub>:** At least one pair of population [variances](#) is not equal (Heteroscedasticity exists).

The decision rule is based on the resulting test statistic: if the calculated [p-value](#) falls below the chosen [significance level](#) (typically  $\alpha = .05$ ), we are compelled to reject the [null hypothesis](#) ( $H_0$ ). Rejecting  $H_0$  signals a statistically significant difference in [variances](#), confirming a violation of the fundamental assumption required for a standard [ANOVA](#). This comprehensive guide provides a detailed, step-by-step methodology for executing and interpreting the **Brown-Forsythe test** utilizing the powerful statistical environment, [R](#).

## Step 1: Establishing the Data Context and Setup in R

To provide a clear demonstration of the **Brown-Forsythe test**, we will simulate a realistic research scenario. Imagine a fitness study designed to compare the efficacy of three distinct weight loss programs--labeled Program A, Program B, and Program C. The central research question is whether these programs lead to different average weight loss outcomes over a standardized one-month period.

The experimental design involves a total of 90 participants, who are randomly and equally assigned to one of the three programs (30 participants per group). Following the conclusion of the intervention, the total weight loss achieved by each participant is meticulously recorded. This outcome variable, `weight_loss`, will serve as our dependent variable.

We will now use the [R](#) programming language to generate a simulated dataset that reflects these

outcomes. It is standard practice in reproducible research to utilize the `set.seed()` function prior to data generation. This ensures that anyone running the exact code will obtain the identical results, thereby guaranteeing the reproducibility of this example.

### #make this example reproducible

```
set.seed(0)
```

```
#create data frame
```

```
data <- data.frame(program = as.factor(rep(c("A", "B", "C"), each = 30)),
```

```
weight_loss = c(runif(30, 0, 3),
```

```
runif(30, 0, 5),
```

```
runif(30, 1, 7)))
```

```
#view first six rows of data frame
```

```
head(data)
```

```
# program weight_loss
```

```
#1 A 2.6900916
```

```
#2 A 0.7965260
```

```
#3 A 1.1163717
```

```
#4 A 1.7185601
```

```
#5 A 2.7246234
```

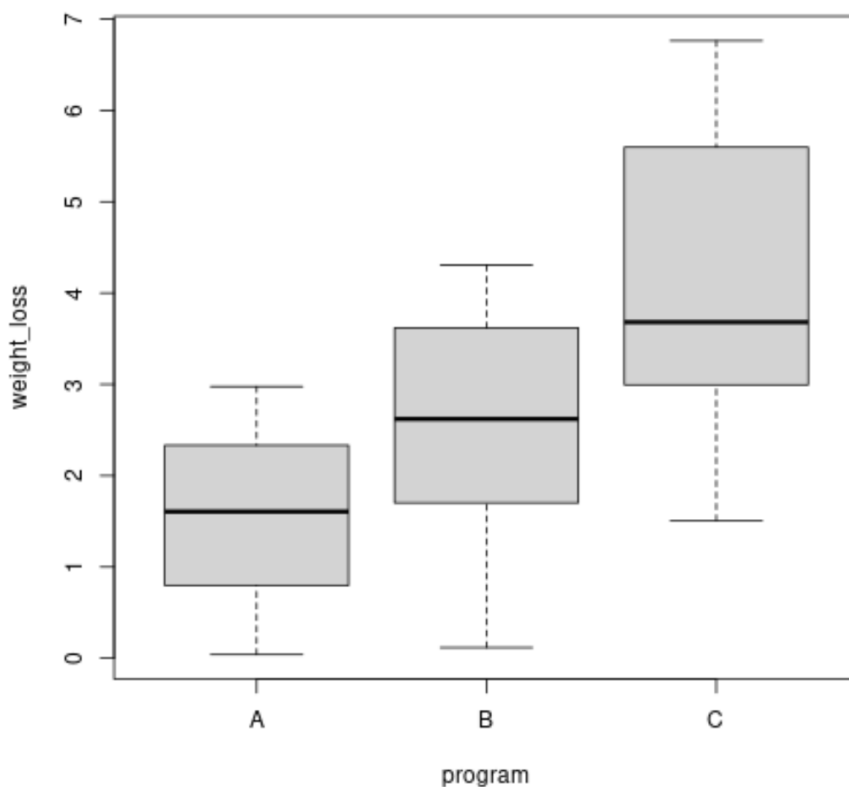
```
#6 A 0.6050458
```

## Step 2: Visualizing and Quantifying Variance Through Exploratory Data Analysis

Prior to engaging in formal inferential testing, a crucial precursor is conducting Exploratory Data Analysis (EDA). When assessing the assumption of homoscedasticity, EDA provides intuitive visual cues regarding potential differences in variability across the study groups. Visualizing the data spread can often give researchers an immediate indication of whether the assumption of equal [variances](#) is likely to hold.

A highly effective visualization technique for this purpose is the use of boxplots. By plotting the distribution of `weight_loss` against the factor variable `program`, we can graphically compare the interquartile range and overall spread of the data for each group. If a boxplot appears significantly wider or taller than the others, it visually suggests higher variability, potentially indicating unequal variances.

```
boxplot(weight_loss ~ program, data = data)
```



To complement this visualization, we should calculate the empirical sample [variances](#) for each program group. Using the functionality provided by the `dplyr` package, we can efficiently group the data by `program` and summarize the variance of the `weight_loss` variable. This quantitative summary is essential for confirming the visual assessment and setting the stage for the formal test.

### #load dplyr package

```
library(dplyr)
```

```
#calculate variance of weight loss by group
```

```
data %>%
```

```
group_by(program) %>%
```

```
summarize(var=var(weight_loss))
```

```
# A tibble: 3 x 2
```

```
program var
```

```
1 A 0.819
```

```
2 B 1.53
```

```
3 C 2.46
```

The quantitative results clearly indicate noticeable differences in variability: Program C exhibits the

largest variance (2.46), nearly triple the variance observed in Program A (0.819). This substantial disparity strongly suggests that the homogeneity of [variances](#) assumption is likely violated, thus justifying the formal execution of the **Brown-Forsythe test**.

### Step 3: Executing the Brown-Forsythe Test in R

To implement the **Brown-Forsythe test** within [R](#), we must utilize specialized statistical packages that extend R's base functionality. The required function, `bf.test()`, is conveniently located within the [onewaytests](#) package. If this package has not been previously installed in your environment, you would first need to install it using the command `install.packages("onewaytests")`.

Once the package is loaded, the test is applied using the standard R formula syntax: `dependent_variable ~ independent_variable`. In our example, we are testing how the variance of `weight_loss` is distributed across the levels of the grouping factor `program`. The [Brown-Forsythe test](#) is computationally efficient and provides a clear output summary for hypothesis testing.

```
#load onewaytests package
```

```
library(onewaytests)
```

```
#perform Brown-Forsythe test
```

```
bf.test(weight_loss ~ program, data = data)
```

```
Brown-Forsythe Test (alpha = 0.05)
```

```
-----  
data : weight_loss and program
```

```
statistic : 30.83304
```

```
num df : 2
```

```
denom df : 74.0272
```

```
p.value : 1.816529e-10
```

```
Result : Difference is statistically significant.  
-----
```

The statistical output provides the key metrics necessary for drawing a formal conclusion, including the test statistic (30.83304), the degrees of freedom, and most importantly, the [p-value](#). In this specific analysis, the [p-value](#) is reported as  $1.816529 \times 10^{-10}$ . This value is exceptionally small, effectively translating to  $p < 0.0001$ .

Since this minuscule [p-value](#) is significantly lower than our conventional [significance level](#) of

$\alpha = 0.05$ , we must definitively reject the [null hypothesis](#) ( $H_0$ ). The formal conclusion is that the differences in variability (variances) across the three weight loss programs are statistically significant, confirming that the data violates the assumption of homoscedasticity.

## Step 4: Interpreting Results and Strategically Addressing Violations

The outcome of the [Brown-Forsythe test](#) is a critical juncture that determines the appropriate path for subsequent mean comparison analyses. Had the test failed to reject the [null hypothesis](#), we would proceed confidently with a standard [one-way ANOVA](#), knowing the homogeneity assumption was met.

However, when the [null hypothesis](#) is rejected, as demonstrated by our statistically significant result, researchers must decide how to proceed with the primary analysis (comparing means). Two primary strategies are commonly employed when facing this violation of equal [variances](#):

### Assessing ANOVA Robustness.

Despite the violation, the [one-way ANOVA](#) is known to be remarkably robust to minor deviations from the homogeneity assumption, especially when the sample sizes across all groups are equal (balanced design). A widely accepted practical heuristic suggests that the [ANOVA](#) remains reliable as long as the ratio of the largest group variance to the smallest group variance does not exceed 4.

We must revisit the variances calculated in Step 2 to perform this robustness check:

Smallest Variance (Program A): 0.819

Largest Variance (Program C): 2.46

The ratio calculation yields  $2.46 / 0.819 = 3.003$ . Since the resulting ratio (3.003) is less than the critical threshold of 4, a researcher could ethically and statistically justify proceeding with the standard one-way ANOVA, arguing that the violation is not severe enough to invalidate the test results in this balanced design.

### Adopting the Non-Parametric Alternative.

If the calculated variance ratio were found to be significantly greater than 4, or if the researcher sought a more conservative approach that requires fewer distributional assumptions, the preferred statistical method would be the [Kruskal-Wallis Test](#). This procedure serves as the non-parametric equivalent to the [one-way ANOVA](#) and is entirely non-reliant on the assumptions of population normality or equal variability (homoscedasticity). The [Kruskal-Wallis Test](#) is highly recommended when the data are strongly skewed, ordinal, or when the variance ratio severely exceeds the established robustness threshold.