Completely Randomized Design

In a **completely randomized design**, there is only one primary factor under consideration in the experiment. The test subjects are assigned to treatment levels of the primary factor at random.

**Example**

A fast food franchise is test marketing 3 new menu items. To find out if they the same popularity, 18 franchisee restaurants are randomly chosen for participation in the study. In accordance with the completely randomized design, 6 of the restaurants are randomly chosen to test market the first new menu item, another 6 for the second menu item, and the remaining 6 for the last menu item.

**Problem**

Suppose the following table represents the sales figures of the 3 new menu items in the 18 restaurants after a week of test marketing. At .05 level of significance, test whether the [mean](http://www.r-tutor.com/node/35)sales volume for the 3 new menu items are all equal.

 Item1 Item2 Item3   
    22    52    16   
    42    33    24   
    44     8    19   
    52    47    18   
    45    43    34   
    37    32    39

**Solution**

The solution consists of the following steps:

1. Copy and paste the sales figure above into a [table file](http://www.r-tutor.com/node/69) named "fastfood-1.txt" with a text editor.
2. Load the file into a [data frame](http://www.r-tutor.com/node/10) named df1 with the read.table function. As the first line in the file contains the column names, we set the header argument as TRUE.

> df1 = read.table("fastfood-1.txt", header=TRUE); df1   
  Item1 Item2 Item3   
1    22    52    16   
2    42    33    24   
3    44     8    19   
4    52    47    18   
5    45    43    34   
6    37    32    39

1. Concatenate the data rows of df1 into a single vector r .

> r = c(t(as.matrix(df1))) # response data   
> r   
 [1] 22 52 16 42 33 ...

1. Assign new variables for the treatment levels and number of observations.

> f = c("Item1", "Item2", "Item3")   # treatment levels   
> k = 3                    # number of treatment levels   
> n = 6                    # observations per treatment

1. Create a vector of treatment factors that corresponds to each element of r in step 3 with the gl function.

> tm = gl(k, 1, n\*k, factor(f))   # matching treatments   
> tm   
 [1] Item1 Item2 Item3 Item1 Item2 ...

1. Apply the function aov to a formula that describes the response r by the treatment factor tm.

> av = aov(r ~ tm)

1. Print out the ANOVA table with the summary function.

> summary(av)   
            Df Sum Sq Mean Sq F value Pr(>F)   
tm           2    745     373    2.54   0.11   
Residuals   15   2200     147

**Answer**

Since the p-value of 0.11 is greater than the .05 significance level, we do not reject the null hypothesis that the mean sales volume of the new menu items are all equal.

**Exercise**

Create the response data in step 3 above along *vertical*columns instead of horizontal rows. Adjust the factor levels in step 5 accordingly.