https://dx.doi.org/10.22161/ijaers.68.28 *ISSN: 2349-6495(P) | 2456-1908(O)*

Implementation of Bayesian tests *pbayes* and *dbayes* for randomized block design in R code.

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Abstract**—** *In the experimental statistic it is necessary to determine, after performing an experiment, which treatments differ wich other. In this context, Bayesian tests pbayes and dbayes allow the identification of these differences for data with or without balancing and for valid or not variance analysis hypotheses. The implementation of these tests in the context of completely randomized designs has already been performed in code R. Due to the importance of these tests, their extension to other designs is of great relevance. The purpose of the work is to expand them to a randomized block design. The implementation of the tests in R code for the randomized block design was successful. The programming was validated with three experiments: data with valid variance analysis assumption, balanced heterogeneous data and unbalanced data. The results were satisfactory, presented higher or equivalent sensitivity to traditional tests, evidencing the importance and versatility of pbayes and dbayes tests.*

Keywords**— Analysis of variance, Differences between averages, Experimental statistic, Heterogeneous data, Unbalanced data.**

I. INTRODUCTION

A recurring problem in researchers' daily lives in several areas of knowledge is to determine differences between treatments by means of a pairwise comparison of means. To solve this problem for qualitative treatments multiple comparisons tests (MCP) are used.

Ronald Fisher developed the first method for the analysis of experimental data, called analysis of variance (ANAVA), by means of the test F [1]. It detects if there is difference between treatments, however, it does not designate which average differ from one another. The MCP are used for qualitative treatments, when the F test is significant and there are more than two treatments. These compare the differences between the means at the end of the experiment, analyze these differences and identify which of these treatments differ from one another [2-5].

Furthermore, the analysis of variance must satisfy four assumptions to be valid: independence and normality of residues, homogeneity of variances and additivity of the effects allowed in the model [6]. If some of these assumptions are not satisfied, the F-test is not valid and consequently traditional tests such as *Tukey* [7], *Duncan* [8], *Scott-Knott (SK)* [9] e *Student-Newman-Keuls (SNK)* [10] are not suitable for use as a statistical analysis technique.

Andrade et al [11] implemented in R code the *Bayes* function, which allows Bayesian tests (*pbayes* and *dbayes*) to be performed in the context of completely randomized design (CRD). These were proposed by Andrade and Ferreira [12] and can be used for both balanced and unbalanced data, with analysis of variance being valid or not, for both types of data.

Pbayes and *dbayes* tests are of great relevance in the statistical analysis, since unbalanced data cases and with one or more unsatisfied F-test, assumptions are recurrent. Therefore, it is important to implement these tests for other experimental designs, for example, randomized block design (RBD). This model allows local control beyond repetition and randomization. This control consists of the subdivision of the plots (blocks) in cases where the experimental conditions are heterogeneous, allowing greater homogeneity within the blocks. It is the most used

https://dx.doi.org/10.22161/ijaers.68.28 *ISSN: 2349-6495(P) | 2456-1908(O)*

experimental design [13]. Therefore, implementation in this context is notorious.

II. METHODOLOGY

2.1 *Bayes* function in DBC

The *Bayes* function was programmed in R [14] code to perform the *dbayes* and *pbayes* tests in the context of a randomized block design. This is made up of three parameters, sample size to be simulated (N), *alpha* is the significance level and the file contains the data set.

To use the *Bayes* function, the file construction has the following order: treatments, blocks and data. Subsequently, there is the change of the names of these vectors, allowing them to be manipulated throughout the code. Then the file is automatically sorted by the function, organizing it incrementally in relation to the treatments.

After, the function then enables the installation and/or automatic loading of some packages required to perform the tests that analyze the assumptions of the analysis of variance. For this purpose, conditional structures have been developed that verify whether the package has been installed. If it has not been installed, installation and loading takes place. If it has already been installed, there is only loading.

For the case of balanced data, the function tests the normality of the residues through the Durbin-Watson test [15], the independence of residues using the *Shapiro-Wilk* test [16], homogeneity of variances by means of the *Bartlett* test [17] and the *Tukey add* [18] test verifies the additivity of the allowed effects in the model. In case of unbalanced data, the assumptions are not tested and performs directly the *pbayes* and *dbayes* tests.

In addition, the *qpostbayes* function generates a sample of size *n* of the multivariate *t* distribution, this step is essential for performing the *pbayes* and *dbayes* tests. By means of the Monte Carlos method, *k* chains of means based on the multivariate a *posteriori* distribution are obtained [12]. After, densities of the standardized amplitude distribution *q*, expression (1), are obtained by means of the same function. Finally, the harmonic mean of the variances (σ_h) according to the expression (2) is obtained and upper quantile $100\alpha\%$ (q_α) by the return of the function *qpostbayes*. Therefore, the least significant difference (*lsd*) is calculated according to expression (3).

$$q = \frac{máx(\mu_i) - mín(\mu_i)}{\sigma_h} \quad (1)$$

$$\sigma_h = \sqrt{\frac{1}{\frac{1}{k}\left(\frac{n_1}{s_1^2} + \frac{n_2}{s_2^2} + \cdots + \frac{n_k}{s_k^2}\right)}} \quad (2)$$

$$\Delta = \sigma_h \cdot q_h \quad (3)$$

Furthermore, the *Yb* and *Syb* parameters of the *qposbayes* function (*N*, *Yb*, *Syb*, *nu*) allow the use of data with or without balancing. The parameter *Yb* is a vector whose entries are the means of each treatment. When there are unbalanced data the calculation of each mean differs with the amount of parcel of each treatment, as shown in equation (4). *Syb* parameter is a diagonal matrix. This matrix stores the values of the mean square of the error divided by the number of repetitions of each treatment, denoted by equation (5).

$$\sum_{i=1}^{n} \frac{d_i}{n_i} \quad (4)$$

where, d_i means the treatment data *i* and n_i the repeat number of the treatment *i*.

$$\begin{bmatrix} \frac{\text{Mean Sq}}{n_1} & 0 & \cdots & 0 \\ 0 & \frac{\text{Mean Sq}}{n_2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{\text{Mean Sq}}{n_k} \end{bmatrix} \quad (5)$$

For the calculation of these parameters it is necessary a vector that stores number of repetitions of each treatment. This vector is called *nrt*.

2.2 *dbayes* test

The *dbayes* test calculates the difference between the pairs of the means and compares the absolute value with the least significant difference *(lsd).* The null hypothesis, H_0: $\mu_i = \mu_i$', is rejected when the modulus of the difference between the pairs is greater than the *lsd* [12].

2.3 *Pbayes* test

The *pbayes* test calculates the probability of the intervals to contain the value zero, if the zero is contained in the interval, the treatments are considered equal. These intervals are determined by the lower (LI^{ii}') and upper (LS^{ii}') limits according to expression (6) [12]:

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$$\begin{cases} LI^{ii'} = \mu_{ij} - \mu_{i'j} - q_j\sigma_h \\ LS^{ii'} = \mu_{ij} - \mu_{i'j} + q_j\sigma_h \end{cases} \quad (6)$$

2.4 Validations

To validate *dbayes* and *pbayes* tests in the context of randomized block design (RBC) three experiments were used. Each experiment presents a different scenario in order to observe the behavior of the tests. In addition, some cases allow the use of other tests for comparison.

The first study consists of a data set provided by Johnson [19] which presents measurements of phosphorus pentoxide from five fertilizers analyzed in five laboratories. The interest of the experiment are the differences between fertilizers. In this data set all, the assumptions of the analysis of variance were met, so it was possible to compare the test results *dbayes* and *pbayes* with the traditional tests: *Tukey* [7], *Calinski* and *Corsten (CCF)* [20] and *Bootstrap (CCBOOT)* [21].

The second experiment consists of comparing fungicides used in the control of *Diplodia spp*. in seeds. The study consists of six blocks and eight treatments. This data set was provided by Steel and Torrie [22] and presents data with heterogeneous variances.

The latter study consists of unbalanced data provided by Milliken and Johnson [23]. The objective is to compare three models of girder divided into ten blocks. The data consist of the amount of force required to fracture the girder. In order to compare, the *Tukey-Kramer* test [24] was used.

III. RESULTS AND DISCUSSION

3.1 *Bayes* Function

Figure 1 shows the way that the user must create the file: treatment, blocks and data, respectively. The columns names apresented are already modify by the function *Bayes*, allowing the manipulation of these vectors.

	trt	bloc	y
1	A	1	24
2	B	2	13
3	C	1	41
4	B	3	20
5	A	3	12
6	C	2	32
7	B	1	10
8	C	3	9
9	A	2	25

Fig. 1: Bayes function output in input file R code.

After the input of data, the ordination of them is required. On the figure 2 have the File organized by the function of ordination. Note that the disposition of data occur in crescent order compare to the treatments.

	trt	bloc	y
1	A	1	24
9	A	2	25
5	A	3	12
7	B	1	10
2	B	2	13
4	B	3	20
3	C	1	41
6	C	2	32
8	C	3	9

Fig. 2: Output in R after the ordination.

However, using the function *Bayes* the ensuing packages must been installed and charged. On the Table 1 is presented the names of the packages and your finality.

Table 1: Packages used by the function Bayes.

Packages	Finality
lmtest	Realization of Durbin-Watson test
asbio	Realization of *Tukey add* test
multcomp	Realization of Multiple Comparison test
mvtnorm	Generation of data string
stringr	Tables formatting
dplyr	Data ordination
car	Data ordenation

Due of the number of packages required, as shown in Table 1, the *Bayes* function automatically installs and / or loads those packages. Therefore, have programmed a conditional structure that performs this installation and / or loading. This Structure facilitates the use of the function and allows the operation to the lay users of R.

Firstly, the analysis of variance was performed to data balanced. For this type of data, it is necessary to verify the

https://dx.doi.org/10.22161/ijaers.68.28 *ISSN: 2349-6495(P) | 2456-1908(O)*

homogeneity assumptions of the variances, additivity of the effects allowed in the model, normality and independence of residues. Figure 3 shows the output of the R, presenting the assumption evaluated, the test used, the p-value found and whether the assumption was or was not met.

```
-----------------------------------------------------------------------
Test validity table
-----------------------------------------------------------------------
                                Test  p_value       Result
Normality                    Shapiro 0.270037 Not Violated
Independence of residues  Durbin-Watson 0.185493 Not Violated
Homogeneity                  Bartlett 0.029701     Violated
Additivity                      Tukey 0.260154 Not Violated
-----------------------------------------------------------------------
```

Fig. 3: Output of the Bayes function in R which presents the test results for the experiment provided by Steel and Torrie [22].

The Tables 2 and 3 show code sections to calculate the parameter *Yb* and *Syb* used as input to the *qpostbayes* function. In addition, the stretch of the nrt vector code that is used to calculate these parameters is presented in Table 4.

Table 2: Fragments of the R code developed for parameter Yb.

```
for(i in 1:nlevels(file$trt))
{
  mean[i]=0
  sum=0
  for(l in: length(file$trt))
  {
    if(file$trt[marker] == file$trt[l])
    {
      if(is.na(file$y[l]))
      {
      }
     else
     {
       sum= sum+file$y[l]
     }
      counter = counter+1
    }
  }
  mean[i] = sum/nrt[i]
}
```

Table 3. Fragments of the R code developed for the parameter Syb.

```
for(i in 1:nlevels(file$trt))
{
  for(l in 1:nlevels(file$trt))
  {
    if(i == l)
    {
      mvariance[i,l]= vvariance[i]/nrt[i]
    }
    if(i != l)
    {
      mvariance[i,l] = 0
    }
  }
}
```

Table 4. Fragments of the R code developed for the vector nrt.

```
for(i in 1:nlevels(file$trt))
{
  nrt[i]=0
  for(l in marker:length(file$trt))
  {
    if(file$trt[marker] == file$trt[l])
    {
      counter = conter+1
    }
  }
  for(i in 1:length(file$y))
  {
    if(is.na(file$y[i]))
    {
      for(l in 1:nlevels(file$trt))
      {
        if (l==1)
        {
          if(i<=pos[l])
          {
            nrt[l]=nrt[l]-1
          }
          }else
          {
            if((i>pos[l-1]) && (i<=pos[l]))
          {
            nrt[l]=nrt[l]-1
          }
        }
```

After, the *qpostbayes* function generates *k* chains of means by the *Monte Carlo* method and generates the standardized amplitude of the *posteriori*. Subsequently, the harmonic mean of the variances (σ_h) and the upper quantile 100α% (q_α) were obtained by the return of this function. The calculation of the least significant difference using these values is presented in Table 5.

Table 5. Fragments of the R code developed for the calculation of lsd.

```
conf = 1-alfa
q$q=sort(q$q)
q$q[N*conf]
```

https://dx.doi.org/10.22161/ijaers.68.28 *ISSN: 2349-6495(P) | 2456-1908(O)*

```
q$sigh
delta = (q$sigh)*(q$q[N*conf])
```

Posteriorly, the tests are performed Table 6 shows the code for the *dbayes* test. As a result presented to the user, *ns* indicates that there is no significant difference between treatments and * indicates that there is significant difference between treatments.

Table 6. Fragments of the R code developed to perform the dbayes test.

```
for(i in 1:(nlevels(file$trt)-1))
{
  for(j in (i+1):nlevels(file$trt))
  {
    counter = counter +1
    Y= mean[i] – mean[j]
    Y= abs(Y)
    if(Y<delta)
    {
      dif.letters[counter]="ns"
    }else
    {
      dif. letters [counter]="*"
    }
  }
}
```

Regarding to the *pbayes* test, the piece of code developed for this test is shown in Table 7. As with the *dbayes* test, the result presented to the user is given by *ns* and *.

Table 7. Fragments of the R code developed to perform the pbayes test.

```
for(i in 1:nlevels(file$trt))
{
  for(j in i:nlevels(file$trt))
  {
    if(i != j)
    {
LI[,n] = Chain1[,i] - Chain1[,j] -    Chain1[,kk]*q$sigh
LS[,n] = Chain1[,i] - Chain1[,j] + Chain1[,kk]*q$sigh
      comp1[n] = i
      comp2[n] = j
      n = n +1
    }
  }
}
```

3.2 *Bayes* function validations

The *Bayes* function inputs (*N*, *alpha*, *file*) for the three experiments were N = 10,000, α = 0.05 and the file with the data for each case. The first experiment provided by Johnson [19] has all the assumptions of the analysis of variance satisfied. The output of the *Bayes* function in the context of a randomized block design (DBC), presents the evaluated assumption, the test used, the p-value found and whether or not the assumption was met, according to Figure 4.

```
Test validity table
                                        Test p_value       Result
Normality                            Shapiro 0.45533 Not Violated
Independence of residues  Durbin-Watson 0.26989 Not Violated
Homogeneity                         Bartlett 0.91866 Not Violated
Additivity                             Tukey 0.41141 Not Violated
```

Fig. 4: Output of the Bayes function in R, presented the test results for the experiment provided by Johnson [19].

It was compared the results of the *dbayes* and *pbayes* t ests with the traditional tests *Tukey* [7], *Calinski* and *Cors ten* (CCF) [20] and *Bootstrap* (CCBOOT) [21], according to Table 8. This comparison was only possible because th e analysis of variance is valid.

Table 8. Comparison of the dbayes and pbayes tests with t raditional tests for the dataset presented by Johnson [19].

Treatments	Tests				
	Tukey	*CCF*	*CCBOOT*	*dbayes*	*pbayes*
G – F	*	*	*	*	*
H – F	*	*	*	*	*
I – F	*	*	*	*	*
J – F	*	*	*	*	*
H – G	ns	ns	ns	ns	ns
I – G	*	*	*	*	*
J – G	*	*	*	*	*
I – H	*	*	*	*	*
J – H	*	*	*	*	*
J – I	*	*	*	*	*

https://dx.doi.org/10.22161/ijaers.68.28 *ISSN: 2349-6495(P) | 2456-1908(O)*

Analyzing Table 8 it is observed that all the tests used presented the same result. Therefore, the response of the *dbayes* and *pbayes* tests in this situation were satisfactory, presenting the same sensitivity as the traditional tests.

Regarding to the second experiment provided by Steel and Torrie [22], the analysis of variance is not valid; since the data present heterogeneous variances, according to the *Bayes* function output (Figure 3). Table 9 presents the results of the *pbayes* and *dbayes* tests. In this case, it is not possible to compare them with the traditional tests as in the first experiment, since the analysis of variance is not valid.

Table 9. Results of the dbayes and pbayes tests for the dataset presented by Steel and Torrie [23].

Treatments	Repetitions	
	dbayes	*pbayes*
B – A	*	*
C – A	*	*
D – A	ns	ns
E – A	ns	ns
F – A	ns	ns
G – A	ns	ns
H – A	ns	ns
C – B	*	ns
D – B	*	*
E – B	*	*
F – B	*	*
G – B	*	*
H – B	*	*
D – C	ns	ns
E – C	*	*
F – C	*	*
G – C	*	*
H – C	ns	ns
E – D	ns	ns
F – D	ns	ns
G – D	ns	ns
H – D	ns	ns
F – E	ns	ns
G – E	ns	ns
H – E	*	ns
G – F	ns	ns
H – F	ns	ns
H – F	ns	ns

It is observed that the *dbayes* test presents a greater sensitivity than the *pbayes* test since it detected a greater number of differences between the treatments. The violation of the hypothesis of homogeneity of variances can affect the performance of traditional methods and compromise the results [25-27]. Therefore, it is observed the importance of *dbayes* and *pbayes* tests, since they are valid on such circumstance.

Finally, Table 10 shows the comparisons of the *dbayes* and *pbayes* tests with the *Tukey-Kramer* test for the data set presented by Milliken and Johnson [23]. This study consists of unbalanced data and the Tukey-Kramer test [18] is valid under these circumstances.

Table 10. Comparison of the dbayes and pbayes tests with the Tukey-Kramer test for the data set presented by Milliken and Johnson [23].

Treatments	Tests		
	Tukey-Kramer	*dbayes*	*pbayes*
2 – 1	ns	*	ns
3 – 1	*	*	*
3 – 1	ns	ns	ns

According to table 10, it can be observed that the dbayes test presented a higher sensitivity than both tests compared, whereas the *pbayes* test had the same result as the *Tukey-Kramer* test [18]. Therefore, the *dbayes* test presents a better performance in unbalanced data than the *pbayes* test. However, the result of the *pbayes* test is also satisfactory, since it shows the same sensitivity as the *Tukey-Kramer* test [18].

IV. CONCLUSION

The *Bayes* function for the randomized block design (DBC) was successfully implemented in R code. Satisfactory results were obtained for the three cases: assumptions served with balanced data; assumptions not fully met; unbalanced data.

The *pbayes* and *dbayes* tests presented good performance for the DBC model. They presented results compatible with the traditional tests in the case of balanced data in which the assumptions are met and the superior performance of the *dbayes* test in relation to the *Tukey-Kramer* test [18] in the case of unbalanced data.

By means of the obtained results it was possible to perceive and to observe the importance of the *pbayes* and dbayes tests, since these can be used for cases in which the most popular tests are not valid. Therefore, the expansion of tests for other designs and analysis schemes is of utmost importance.

ACKNOWLEDGEMENTS

To FAPEMIG for the Scientific Initiation scholarship.

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