Research Article

# Comparison with JMP, SAS, EXCEL and SPSS of Simple LabVIEW Software that Randomizes and Applies T-Student to Population Samples

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*Abstract*—In the present study we tried to apply the student's t-test for small samples, with LabVIEW software, which are compared against other programs that apply the same test such as JMP, Excel, SAS and SPSS. Considering the objective set forth in this study, as it is to provide postgraduate students and new researchers in their day to day, a simple, sufficient, fast and easy-to-apply instrument for their periodic investigations; a software was developed whose functionality allows randomizing samples, particularly for one sample (**1S**), two sample (**2S**) and related sample (**RS**);determining sample normality (Q-Q plots), differentiating variance homoscedasticity, calculating statistical variables such as: means, standard deviation, t-value, t-tabulated, p-value, F-calculated, F-tabulated, confidence intervals and generation of Excel-xls files; demonstrating that the labVIEW software tested in this work reveals, simplicity and easy operation with respect to the compared software, and whose efficiency was statistically verified by Pearson correlations ($p<0.05$) for the t value in all aspects ( one sample(**1S**) R =0,8517, two sample independent (**2S**) R =0,9986 and related sample (**RS**) R =0,6699).

*Keywords*—Randomized, samples, t-test, normality, t-value, Q-Q plot, software, LabVIEW.

## 1. Introduction

Sampling is an organized and systematic procedure that provides guidelines for selecting a small number of subjects or objects from a population for the purpose of descriptions and analyzes to make inferences, conclusions, and validation of the population being studied. This allows researchers to infer information about a population based on results from a portion of the population, ensuring that the subject or object individual is representative of the entire population.[1-4]
Random sampling or randomization process consists of balancing the groups involved in the study so that there is a uniform distribution of all known or unknown factors that may distort the results obtained. [5-10]

In this sense, the appropriate use of adequate sampling procedures and rigorous statistical analyzes guarantees safety and avoids bias in the results obtained. [11]

Several sampling techniques have been developed and the literature is extensive.[12-14]The sampling can be random (probabilistic), allowing the absence of bias, as well as displaying sampling distributions that justify the estimation of parameters with classical statistical tests or non-random (non-probabilistic).[15-20].

In biology, randomness occurs through simple random sampling (SRS). In this case, each element that makes up the universe is selected with the same probability of its stratified variant. In any case, a simple random sample with replacement (SRSWR) or without replacement (SRSWOR) can always be found. [21-23]

In simple sampling without replacement (SRSWOR), the subjects or objects selected for the sample no longer participate in the draw, that is, they appear only once in the draw. This condition is more suitable for processing biological samples, as there is no goal of replacing selected elements that may alter biological behavior. The purpose of this study was to use the LabVIEW graphical programming language to help graduate students and novice researchers determine the randomness of biological samples and apply the Student t test, in order to know certain characteristics of the population and thus infer about it.

## 2. Materials and Methods

### 2.1 Labview graphical programming language
LabVIEW software (a trademark of National Instruments of Austin TX, USA) is a graphical programming enviroment that uses icons instead of lines of text, used to develop applications. The user interface (known as the front panel) is

built from graphical code. The block diagram contains the connected lines guiding the flow of information from one code to the next. [24]

## 2.2 Randomization Process

To carry out the randomization process with the scheme proposed in this study, the user needs to create Excel files (-xls and –csv) that contain the samples to be used.

Although random features are included in many sampling programs, only two of the most common features in biology are: simple random sampling without replacement (**SRSWOR**) and variant stratified random sampling.

Techniques such as simple random sampling without replacement (**SRSWOR**) and stratified random sampling are applied in this study. Its probabilistic analysis is obtained by applying appropriate descriptive statistics techniques using the LabVIEW graphical programming language. [25]

## 2.3 Statistical Procedure

Sample statistics (means, medians, proportions, rates, etc.) help decide on the population to study. [26] Thus, statistical inference allows us to characterize or make decisions about a population using information obtained from a sample of that population. A test of statistical significance calculates the probability that the results between groups could be due to chance, assuming that both groups had the same behavior, that is, the null hypothesis is true. [27].

Based on the previous criteria, the following proposals can be made: 1. Formulate the null hypothesis (Ho) and the alternative hypothesis (Ha), 2. Determine the significance level (α), 3. Calculate the value of the statistical test .4. Determining the critical value, 5. Determining the confidence interval (CI), 6. Calculating the p-value, and 7. Expressing the decision. [28] In this way, the Student's t-test is used to draw conclusions from simple means, two socks or variances when the sample size is small and/or the population distribution is unknown. In this way, the distribution of (variable t) is obtained as follows:

$$t = \frac{\overline{x} - \mu}{\frac{s}{\sqrt{n}}} \qquad (1)$$

Where:    t= t-test

$\overline{x}$ = estimated parameter of the sample

$\mu$ = hypothetically estimated parameter

$\frac{s}{\sqrt{n}}$ = estimated standard error

Simply put, a t-test is a way of formulating a parametric hypothesis that is applied to real, non-categorical data to test whether the sample mean is significantly different from the expected value or whether the means of two groups differ. significantly different from each other (1). In these cases, we consider one sample (1S), two independent samples (2S) and two related samples (RS). A program developed in LabVIEW to obtain randomness of samples and perform statistical operations using the Student's t-test is proposed (see Table 1).

**Table 1**: Student's T-test formulas used in LabVIEW graphical programming language

| | | | |
|---|---|---|---|
| One Sample T-test | $t = \dfrac{\overline{x} - \mu_0}{\frac{s}{\sqrt{n}}}$ | $s = \sqrt{\dfrac{\sum_{i=1}^{n}(x_i - \overline{x})^2}{n-1}}$  $\overline{x} = \dfrac{\sum_{i=1}^{n} x_i}{n}$ | $CI_{1-\alpha} = \overline{x} \pm \left(t_{\frac{\alpha}{2}}, df\right)\left(\frac{s}{\sqrt{n}}\right)$ |
| Two Sample T-test | $t = \dfrac{(\overline{x_1} - \overline{x_2}) - (\mu_1 - \mu_2)}{\sqrt{s_p^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$ | $s_p^2 = \dfrac{(n_1-1)s_1^2 + (n_2-1)s_2^2}{n_1 + n_2 - 2}$ | $CI_{1-\alpha} = (\overline{x_1} - \overline{x_2}) \pm \left(t_{\frac{\alpha}{2}}, df\right)\left(\sqrt{s_p^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}\right)$ |
| Paired Sample T-test | $t = \dfrac{\overline{d} - (\mu_1 - \mu_2)}{\frac{s_d}{\sqrt{n}}}$ | | $CI_{1-\alpha} = \overline{d} \pm \left(t_{\frac{\alpha}{2}}, df\right)\left(\frac{s_d}{\sqrt{n}}\right)$ |

t(t value) t½(critical value) $\overline{x}$ (mean) s(standard deviation) $s_p^2$(pooled variance) μ(population mean) n(sample size) d(mean of difference) CI(confidence interval) $s_d$(standard deviation of the difference)

## 2.4 Software Operability
### 2.4.1 Inputs necessary to develop the proposed program

The front panel or connection matrix with the user must be carried out according to the following guidelines:
• The user must create an Excel-xls file that contains the data of their investigation.Said file must be converted into an Excel -csv file (required as a matrix to use the software).
• The created Excel -csv file should be pasted into the appropriate path specified in the Control Panel.
• According to the front panel diagram, for the program to start working, it must collect certain information contained in the three sections displayed on the front panel.
• Select the type of sample you want to contrast by activating the One Sample (1S), Two Independent Samples (2S), and Related Samples (RS) selection levers (see Figure 1, front panel)
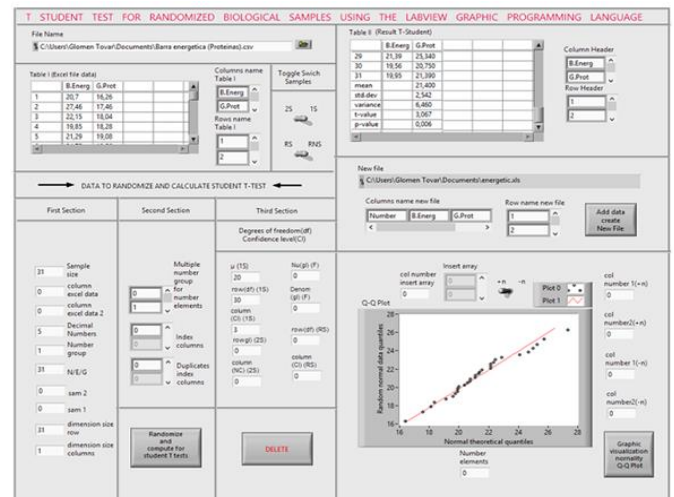


**Figure 1:** (Fron Panel) Randomization process and T-student application

**Information that must be entered on the front panel (in the corresponding fields) to start program operation:**
• *First section*:
Enter the following in the corresponding fields for each sample:
For samples (**1S**)

Sample size, number of columns containing the excel file, number of decimals (always 5), number 1 for the group, number of elements per group (**NE/P/G**) 1, dimension of the rows and columns (always 1 for column and row related to group size)

For sample (**2S**):
Number of the column that contains the Excel file for each subsample (**sam1** and **sam2**), number of decimals (always 5), size for the subsamples (sam1 and sam2), number of elements per group (**NE/P/G**) 2, dimension of rows and columns, not applicable.

For sample (**RS**)
Number of the column that contains the Excel file for each subsample (**sam1** and **sam2**), number of decimals (always 5), size for the subsamples (sam1 and sam2), number of elements per group (**NE/P/G**) 2, dimension of rows and columns, not applicable

• *Second section:*
For sample (**1S**)
In the Multiples of Group Numbers by Number of Group Elements (NEP/G) column, begin by selecting a number after zero, divisible by each number of elements and that generates the numbers that include all elements in the group. This operation It will be carried out until the number of elements per group is completed.
For sample (**2S**) Does not apply. For sample (**RS**) Same sample (**1S**)

• Third Section:
For sample (**1S**)
 Assumed value of the population mean ($\mu$), values entered in the corresponding table [degrees of freedom (df) of the sample and column of the selected confidence level (significance level $\alpha$)] to obtain the t-value.
For sample (**2S**)
Values entered in the corresponding table [degrees of freedom (df) of the sample and column of the selected confidence level (significance level $\alpha$)] to obtain the t-value, values entered in the corresponding table (degrees of freedom (df) for the numerator and denominator) to obtain the Fisher F value.
For sample (**RS**) Idem sample (**1S**)
 • The name of the rows and columns that will accompany both Table I and Table II (front panel).  must be indicated.
• To verify that the sample values comply with normality (an essential requirement to apply a Student's t-test), a Q-Q plot was used; [29]
In the case of 1S and RS samples, the selective lever is used in the +n position;
For 2S samples if the samples have the same size +n is used if the samples are disparate the options +n and –n must be used, filling in the options of the rest of the boxes
• To verify that the values of independent samples (2S) comply with homoscedasticity, Fisher's standard F test will be used. The test statistic to test the hypothesis if $\sigma 21 = \sigma 22$ where $\sigma 21$ and $\sigma 22$ are the variances of two populations, is
$$F = s^2_1 / s^2_2 \quad (2)$$

• where s21 and s22 are the sample variances for two independent random samples of n1 and n2 observations from normally distributed populations with variances $\sigma 21$ and $\sigma 22$, respectively (2). In practical applications, the ratio F is usually calculated so that the largest sample variance is in the numerator, that is, s21 > s22. Therefore, the F statistic is always greater than one and only the upper critical values of the F distribution are used. At the $\alpha$ significance level, the test rejects the hypothesis that the variances are equal if $F > F(\alpha; n1-1; n2-1)$, where $F(\alpha, n1-1, n2-1)$ is the upper critical value of the F distribution with $(n1-1)$ and $(n2-1)$ degrees of freedom. [30]

• Click on ⇨ and activate the program ⇨ on the front panel.
• Once the program is activated, the data of the corresponding file will be displayed (see Table I front panel) which will be statistically contrasted.
• Next, the buttons are pressed to obtain the normality (Q-Q plot) of the sample and the calculations of the corresponding values for Student's T, whose data will be displayed in Table II front panel.
• Subsequently, the user can save their data by filing them in Excel-xls as new data   or data attached to another existing file, pressing the corresponding buttons.

### 2.4.2 Algorithm to obtain the randomness of the samples (ARS)
This algorithm is originated in the so-called block diagram and using the Stacked Sequence Structure (Selector label 0) allows obtaining random values from the samples. This is obtained by starting to explore through the Random number programming function that acts on the size of the sample, whose iteration through a For Loop is associated with a While Loop and through a Search 1D array, its result is mediated by a ship register that binds it to an array via an Insert into Array. From these data obtained using another For Loop and by means of the Power Of 10 function, the values of the data are selected with the value of the previously determined decimals, which are subsequently discriminated into ordered values (Sort 1D Array) and not ordered.

The data obtained from a File Name as a csv-file is discriminated into several columns with which an array is built by the Build Array function, and through an iteration mediated by a For Loop, whose data once transposed by the Transpose 2D function Array are inserted in an array mediated by a ship register, the results obtained are associated with the ordered values (Sort 1D Array) and not ordered, which once iterated through two For Loop and selected by a Case Structure allows to obtain an array in an Index Array through which, and using successive Delete From Arrays, Delete portions are obtained that represent subarrays containing the randomized samples. (see Figure 2)
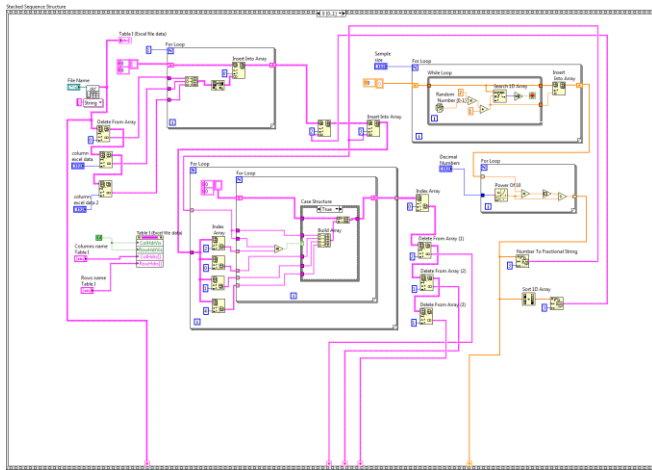
**Figure 2**: (Block Diagram) Algorithm to obtain the randomness in population samples (ARS)
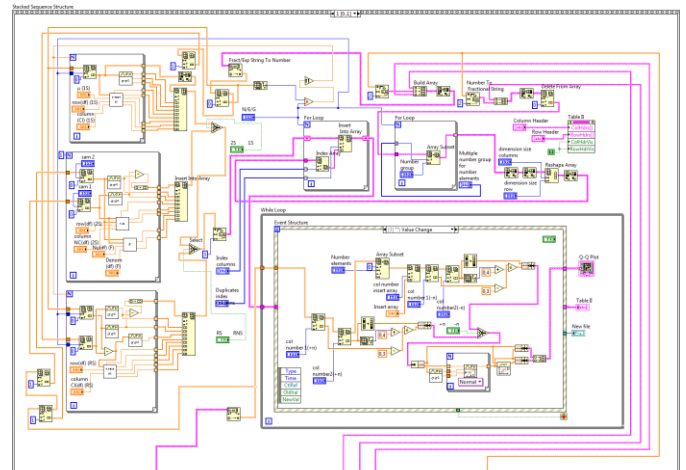
### 2.4.3 Algorithm for statistical quantification with the Student's T of the samples (ATS)

The following algorithm is developed in a Stacked Sequence Structure (Selector label 1) of the block diagram obtained by the information offered through Delete portions that are grouped by the Build Array function to be later transposed (Transposed Array String), and converted to their numeric form (Fract/Exp String to Number)). A similar process occurs but through a conversion to its string form (Number to Fraction String), thus becoming the input paths. First, the string form (Fract/Exp String To Number) is obtained from the Delete From Array ( 1 and 3) of the randomized sample and is converted to the numerical form by selecting said columns based on the number of elements per group. ; in this way, subsequent iterations via several For Loops, gather the corresponding statistical calculations: for the mean, standard deviation and variances that are coupled to other statistical determinations such as: t-calculated, t-tabulated, p-value and upper and lower limits of confidence intervals; obtained through several conformed Subvi (T1Svi, T2Svi, TRSvi and T-tab(CI)vi), through which the aforementioned calculations are made; which are expressed as a string according to the type of sample selected (Select). Secondly, the numerical form (Number To Fraction String) of the randomized samples is converted to the string form to associate with the Delete From Array (2) of the randomized samples, generating an array (Build Array) that is transposed (Transpose 2D Array) and from which is extracted (Delete From Array) to iterate (For Loop) with an Array Subset using Number group and Multiple number group for number elements to obtain a subarray that is doubly transposed to obtain an Output Array through a Reshape Array in function of the size of the column and the row whose result is subsequently transposed (Transpose 2D Array). (see Figure 3)



**Figure 3**: (Block Diagram) Algorithm for the application student's T in population samples (ATS)

The results obtained by a Fract/Exp String to Number and a Number to Fraction String are coupled through an Index Array (Index columns and Duplicate Index) and Insert into Array by a Ship Register in a For Loop generating an Output Array whose values are spliced into an Even Structure and a While Loop to produce a Table II (randomized sample and t-student calculation), a New File (Add data to generate new file), and a XY plot (Q-Q plot Normality).

## 3. Results and Discussion

Considering the objective set out in this work, which is to provide postgraduate students and new researchers with a simple, sufficient, fast and easy-to-apply instrument for their periodic research; A software was developed whose operability allowed to randomize and statistically analyze a set of samples which, once their normality was verified through the Q-Q graphic representation [29] and homoscedasticity (Fisher's F standard [30]), the t test was applied Student which constitutes the fundamental essence of this study. Its operability is verified when we compare the results obtained with the labview software, with the results of 4 statistical software routinely applied in research, such as: Excel (Microsoft Excel [31-33]), JMP (Java Memory Profiler [34-36]), SPSS (Statistical Package for Social Sciences [37-39]) and SAS (Statistical Analysis System [40-42]).

The procedure applied consisted of executing the data obtained from the indicated software in the labview software. The case presented in the front panel corresponds to the data obtained from the results of the JMP software of a sample that contained 31 data, from which the protein content of nutritional bars was determined and its sample mean value was contrasted ($\bar{x}$ ) with an assumed population value (μ) and verified its statistical significance by considering a null hypothesis (Ho) as one in which the value of the sample mean was equal to the value of the population mean and an alternative hypothesis (Ha) where the sample mean is different from the population mean. In this way, by running the LabVIEW software, statistical information was obtained based on the statistical analysis for a sample (1S), which

included a total of 7 tests such as: standard deviation (s), t value (calculated (t-v) and tabulated (t-t)), p value (p), confidence level (upper limit (U-I) and lower limit (L-I)) whose results closely coincided with the results of the JMP software (see table 2).

**Table 2**: LabVIEW comparison with other software (JMP, SAS, EXCEL, SPSS). One Sample T-test

| T-test | | Software | | | | | | | |
|--------|---|------|------|--------|--------|--------|--------|------|------|
| | | Lab | JMP | Lab | SAS | Lab | EXCEL | Lab | SPSS |
| One Sample | n | 31 | 31 | 20 | 20 | 12 | 12 | 15 | 15 |
| | $\bar{x}$ | 21,4 | 21,39 | 311,15 | 311,22 | 14,33 | 14,33 | 62,73 | 62,73 |
| | μ | 20 | 20 | 200 | 200 | 15 | 15 | 58 | 58 |
| | s | 2,54 | 2,54 | 64,39 | 64,39 | 1,371 | 1,37 | 5,175 | 5,175 |
| | t-v | 3,067 | 3,07 | 7,719 | 7,72 | -1,68 | -1,68 | 3,542 | 3,542 |
| | t-t | 2,042 | 2,043 | 2,093 | 2,93 | 2,201 | 2,201 | 2,145 | 2,145 |
| | p | 0,006 | 0,005 | <0,000 | <0,000 | 0,098 | 0,1201 | 0,003 | 0,003 |
| | L-I | 20,47 | 20,46 | 281,01 | 280 | 13,412 | 13,46 | 59,86 | 57,55 |
| | U-I | 22,33 | 22,33 | 341,28 | 341,3 | 15,3 | 15,2 | 65,59 | 67,91 |

Lab(LabVIEW) JMP(Java Memory Profiler) SAS(Statistical Analysis System) EXCEL(Microsoft Excel) SPSS(Statistical Package for Social Sciences) n(sample size) $\bar{x}$(mean) μ(population mean) s(standard deviation) t-v(t-value) t-t(t-tabulated) p(p-value) L-I (lower limited) U-I(upper limited).

Subsequently, the LabVIEW software was applied to all the samples of the other programs in all their aspects, that is, for two independent samples (**2S**), which included a total of 9 tests such as: $\bar{x}_1$ (mean1, $\bar{x}_2$ (mean2 ), $\bar{x}_1 - \bar{x}_2$ (mean differences), s(standard deviation), t-v(t-value), t-t(t-tabulated), p(p-value), F-v(F-value), F-t(F- tabulated)(see table 3)

**Tabla 3**: LabVIEW comparison with other software (JMP, SAS, EXCEL, SPSS). Two Sample T-test

| T-test | Variables | Software | | | | | | | |
|--------|-----------|------|--------|-------|------|-------|-------|------|------|
| | | Lab | JMP | Lab | SAS | Lab | EXCEL | Lab | SPSS |
| TwoSample | $n_1$ | 10 | 10 | 12 | 12 | 20 | 20 | 12 | 12 |
| | $n_2$ | 15 | 15.0 | 12 | 12 | 20 | 20 | 12 | 12 |
| | $\bar{x}_1$ | 22,9 | 22,9 | 17 | 17 | 15,15 | 15,15 | 22,75 | 21 |
| | $\bar{x}_2$ | 14,94 | 14,95 | 19,33 | 19,33 | 15,8 | 15,8 | 21 | 22,75 |
| | $\bar{x}_1$-$\bar{x}_2$ | 7,344 | 7,34 | -2,33 | -2,33 | -0,45 | -0,45 | -1,75 | -1,75 |
| | s | 6,236 | 6,24 | 2,702 | 2,7 | 3,243 | 10,5 | 3,002 | --- |
| | t-v | -1,428 | 1,43 | -2,115 | -2,11 | -0,634 | -0,63 | -2,8 | -2,8 |
| | t-t | 2,08 | 2.08 | 2,074 | --- | 2,024 | 2,024 | 2,074 | --- |
| | p | 0,012 | 0,0107 | 0,047 | 0,046 | 0,323 | 0,53 | 0,142 | 0,167 |
| | F-v | 1,455 | 1,45 | 0.565 | 1,77 | 1,587 | 1,586 | 1,418 | 0,034 |
| | F-t | 3,073 | --- | 2,818 | 0,357 | 2,168 | --- | 2,818 | 0,855 |

Lab(LabVIEW) JMP(Java Memory Profiler) SAS(Statistical Analysis System) EXCEL(Microsoft Excel) SPSS(Statistical Package for Social Sciences) n1( sample size 1) n2(sample size 2) $\bar{x}_1$(mean1) $\bar{x}_2$(mean2)$\bar{x}_1 - \bar{x}_2$(mean differences) s(standard deviation) t-v(t-value) t-t(t-tabulated) p(p-value) F-v(F-value) F-t(F-tabulated) (---) (does not report)

And for related or paired samples (**RS**) which included 10 tests such as: $\bar{x}_1$ (mean1), $\bar{x}_2$ (mean2), $\bar{x}_1 - \bar{x}_2$ (mean differences), $\bar{d}$ (mean differences), sd(standard deviation differences). ), t-v(t-value), t-t(t-tabulated), p(p-value), L-I (lower limited), U-I(upper limited) (see table 4)

**Tabla 4**: LabVIEW comparison with other software (JMP, SAS, EXCEL, SPSS). Paired Sample T-test

| T-test | Variables | Software | | | | | | | |
|--------|-----------|------|-------|-------|-------|-------|-------|-------|-------|
| | | Lab | JMP | Lab | SAS | Lab | EXCEL | Lab | SPSS |
| PairedSample | $n_1$ | 16 | 16 | 15 | 15 | 20 | 20 | 12 | 12 |
| | $n_2$ | 16 | 16 | 15 | 15 | 20 | 20 | 12 | 12 |
| | $\bar{x}_1$ | 79,43 | 79,4 | 84,6 | 84,33 | 85,25 | 85,4 | 21 | 21 |
| | $\bar{x}_2$ | 78,25 | 78,1 | 86,66 | 86,6 | 87,1 | 87,2 | 22,75 | 22,75 |
| | $\bar{d}$ | 1,18 | 1,31 | 2,067 | -2,3 | 1,85 | -1,8 | 1,75 | -1,75 |
| | sd | 6,9 | 7 | 3,32 | 3,03 | 2,925 | --- | 2,7 | --- |
| | t-v | -0,68 | -0,75 | -2,4 | -2,97 | -2,82 | -2,78 | -2,24 | -2,24 |
| | t-t | 2,131 | 2,131 | 2,145 | --- | 2,093 | 2,09 | 2,201 | --- |
| | p | 0,307 | 0,465 | 0,029 | 0,01 | 0,012 | 0,0119 | 0,041 | 0,046 |
| | L-I | 74,56 | --- | 83,41 | --- | 84,3 | --- | 20,68 | --- |
| | U-I | 84,31 | --- | 89,91 | --- | 89,89 | --- | 24,81 | --- |

Lab(LabVIEW) JMP(Java Memory Profiler) SAS(Statistical Analysis System) EXCEL(Microsoft Excel) SPSS(Statistical Package for Social Sciences) n1( sample size 1) n2(sample size 2) $\bar{x}_1$(mean1) $\bar{x}_2$(mean2) $\bar{x}_1 - \bar{x}_2$(mean differences) $\bar{d}$(mean differences) sd(standard deviation differences) t-v(t-value) t-t(t-tabulated) p(p-value)　L-I (lower limited) U-I(upper limited) (---) (does not report).

Immediately after knowing the previous results, to check the fidelity and efficiency of the labVIEW software, Pearson correlations for the t value were applied to all samples (**1S**, **2S** and **RS**) between the different programs analyzed (Excel, JMP, SPSS and SAS); obtaining significantly positive correlations (P<0.05) for a one-sample t-test (1S r=0,8517), for a two-independent samples t-test (2S r=0,9986) and for a two-sample t-test related. test (RS r= 0,6699) (see Figure 4).



**Figure 4**: Correlation T-value LabVIEW vs EXCEL, JMP, SPSS and SAS: A) One Sample T-Test　B) Two Sample T-Test and C) Paired Sample T-Test

## 4. Conclusions and Future Scope

An application has been developed for the evaluation of biological samples with the Student t test using the LabVIEW graphical programming language, generating a tool that provides statistical support to the data obtained from daily work in the field of life sciences and to new graduate and undergraduate students. similar. By drawing statistical conclusions based on the results obtained when applying LabVIEW software, researchers can make decisions about the behavior of the population they are studying. This application allows you to integrate acquired data directly into files saved in Excel, display it on the front panel of the LabVIEW software, and view results generated by the application.

After activating the application, by clicking a button on the control panel, you can quickly and accurately retrieve the randomization of the selected sample from an Excel file and test the normality of the sample using Q-Q plots or homoscedasticity of variances. To then perform a Student's T, for a sample (**1S**), independent sample (**2S**) and related sample (**RS**). This will allow the calculation of several variables such as the mean, standard deviation, variance, confidence level, calculated t value and tabulated t value. p value, among others.

This application, obtained through a graphical programming language, provides users with effective and easy-to-use tools based on data obtained from field or laboratory tests and stored in Excel files. The advantage and scope of this tool is to allow new programs to be designed with other statistical aspects such as: Chi-square, unifactor and bifactor analysis of variance, multiple range, correlation coefficient, coefficient of variation, etc.

The operability of the application was verified, when its results were compared with other software (Excel, JMP, SAS and SPSS) and whose results showed a significant correlation (p<0.05)

## Data Availability
There is no data to provide other than that given in the Article
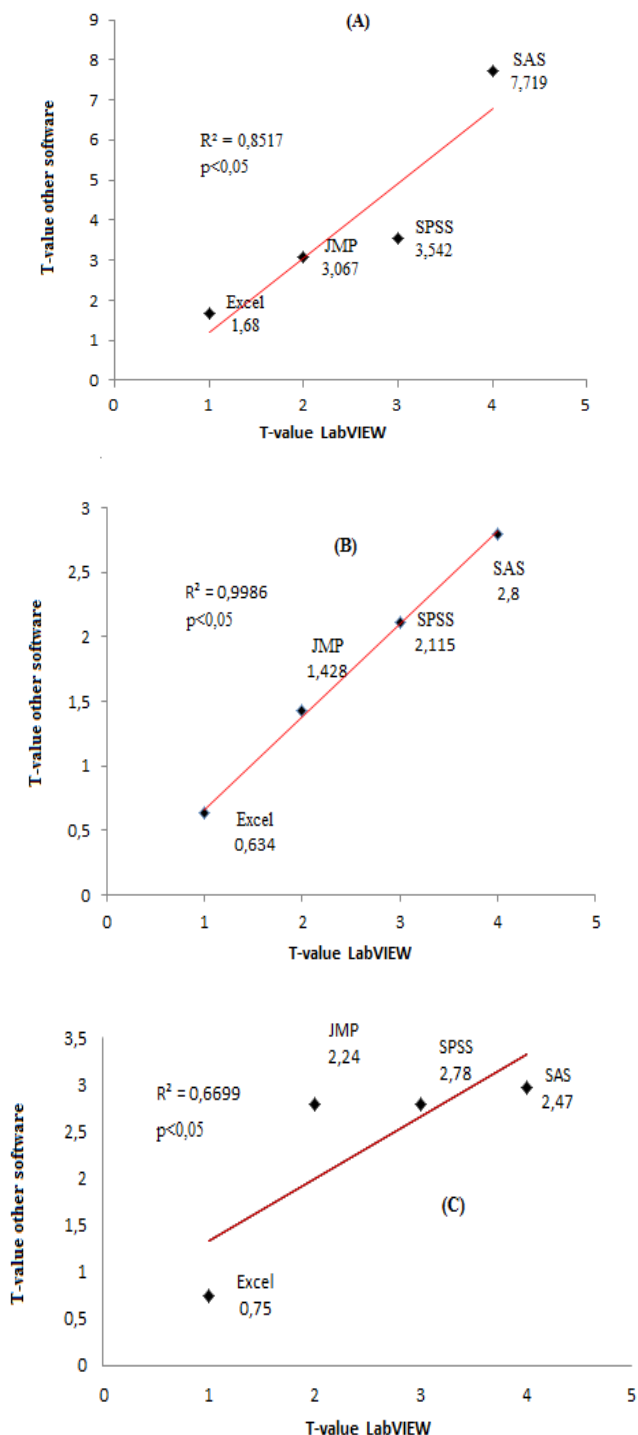
## Conflict of interest
Author declare no conflict of interest

## Funding Sources
The Research leading to this Article is funded by Author's own resources

## Author's Contribution

The complete article, is contributed by the author, is prepared from my own knowledge of the aspects developed on the topic and as such, there is no room for any charge of plagiarism.

## Acknowledgements

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