This program was also incorporated into the BIOESTAT application, developed by the author, which includes 16 other statistical tests of current use in biological research. BIOESTAT can be obtained from the website of the Department of Statistics of UFPR, by downloading it at the address http://est.ufpr.br /'Recursos, Software' / 'Projetos Ativos, Bioestat').

It is also important to download a tutorial extensively illustrated with the prints of the screens, exemplifying in a very didactic way the routines of the calculations through examples developed for each test.

USING THE APPLICATION

The GADVDVC.F application was developed to calculate the degree of aggregation/discrimination (D) of a taxonomic character and also to calculate the weights of a weighting system (on a scale of 1 to 6) that informs the contribution of the character to the formation of subgroups in a group (that brings together 3 or more species) (WA) or for individualization of these same species (WD).

The term 'group' is being used in cases where the studied species do not represent the whole of a genus, but only part of it.

Thus, the conclusions will be valid only for the group studied and should not be extended to the corresponding gender. The methodological foundation for these calculations can be found int he bibliography cited at the end of this chapter.

These are two works that deal with the theme. Maia (2021) presents the methodology for discrete variables (counts and codifications), based on the calculation of the geometric average. Maia (2022) deals with the continuous variables formed by measurements using Analysis of Variance , F Test (one classification criterion), complemented by the Tukey test.

In the yellow boxes, we will reproduce the application's screens numbered in the sequence in which they appear during execution.

The green boxes will show explanatory comments about the screens reproduced.

If the analyzed variable is the result of counts or encodings, the application must be used as follows:

Screen 01

```
**************************************************************
*  INFORM THE TYPE OF VARIABLES THAT WILL BE ANALYZED       *
*  (1 =  Discrete Variables - Counting and Encoding)         *
*  (2 =  Continuous variables - Measurement (weights, measures)  *
**************************************************************
```

Type '1' for discrete variables   Type '2' for continuous variables

Screen 02

```
**************************************************
*                    ATTENTION                    *
*    Compound words must be written with a hyphen.    *
*         EX: Apis-melifera, light-yellow         *
**************************************************

**************************************************
*           Enter the number  'n' of species
*
**************************************************
```

- Names composed of species and taxonomic characters must be written with a hyphen.
- Inform the number of species that form the studied group.

Screen 03

```
**************************************************
*              Type the species name  1              *
**************************************************
```

Enter the name (or numerical code or letter, for identification) of each of the 'n' species. (1,2,....,n).

Screen 04

```
****************************************************
*          Which taxonomic character will be analyzed?          *
****************************************************
```

Enter the name of the taxonomic character for which the value of 'D' (degree of discrimination / aggregation) will be calculated.

Screen 05

```
****************************************************
*        How many status does this character have in the group?   *
****************************************************
```

Inform the number 'k' of different status of the taxonomic character in the analyzed group.

Screen 06

```
****************************************************
*            Which status will be identified by the code 1            *
****************************************************
```

In this step, inform the name of each status that will be identified by a sequential number (code) (1,2,3...k). Example: yellow color = code 1 / white color = code 2 / black color = code 3...

Screen 07

```
**************************************************
*     Code:  Labrum-color        in         Plebeia-juliani              *
**************************************************
```

The application will ask you to enter the code referring to the status of the analyzed character for each species.

Screen 08

```
**************************************************
*                    You informed      yellow                              *
*                    Is correct?  0=No  -  1=Yes                           *
**************************************************
```

If the information is correct, type 1 and the analysis continues. If not, enter 0 and the entry will be requested again.

Screen 09

```
**************************************************
*******        Degree of Discrimination / Aggregation       *******
*******************        D = 2.5       *********************
**************************************************

**************************************************
*                          Moderate  character                             *
**************************************************
*             Weight of Discriminative Potential: WD = 3 .5              *
*             Weight of Aggregate Potential:         WA =  3.5             *
**************************************************
```

- After informing the code referring to the status of the last species, the application calculates the value of the degree of discrimination / aggregation 'D', on a scale from zero to 5.
- It also informs the interpretation of 'D' (e.g. Moderate character).
- The discrimination (WD) and aggregation (WA) potential are calculated on a scale from 1 to 6. In this example (WD = 3.5 and WA = 3.5). The taxonomic character discriminates and aggregates with the same intensity.

Screen 10

```
************************************************************
* Do you want to analyze another character?   0=No  -   1=Yes       *
************************************************************
```

If the analysis involves several taxonomic characters, this routine must be repeated (from screen 04 onwards) as many times as there are characters.

Screen 01a

```
************************************************************
*   INFORM THE TYPE OF VARIABLES THAT WILL BE ANALYZED      *
*   (1 =   Discrete Variables - Counting and Encoding)      *
*   (2 =   Continuous variables - Measurement (weights, measures)   *
************************************************************
```

Type '2' for continuous variables

Screen 02a

```
************************************************************
*          How many species are part of the analyzed group?       *
************************************************************
```

Enter the number 'n' of species that are part of the group.

We will exemplify with the data of 6 species (n = 6) of the genus *Plebeia* (*P.juliani, P.meridionalis, P.droryana, P.emerina, P.remota and P.saiqui* represented by the letters J,M,D,E, R and S, respectively).

The analyzed variable is the measurement of the 'Jaw width' of 5 specimens (m = 5) of each species. See Maia (2022).

Table 1 - Width of the jaw of six species of the genus Plebeia

J	R	S	D	E	M
0.90	1.40	1.20	1.15	1.50	1.00
1.00	1.80	1.30	1.20	1.30	0.90
1.00	1.40	1.50	1.15	1.20	0.90
0.90	1.45	1.30	1.20	1.20	0.70
0.90	1.40	1.30	1.00	1.20	0.80

The application will then ask you to enter the name (or a numerical code, or alphabetic code, etc.) to identify each of the 'n' species. Remember that compound names (eg *Plebeia-juliani*) must be written with a hyphen.

Screen 03a

```
*****************************************************
*                  Enter species name 1                  *
*****************************************************
```

The application will ask you to enter the names of the 6 species (*Plebeia-juliani, Plebeia-meridionalis*, etc.)

Screen 04a

```
*****************************************************
*        Which taxonomic character will be analyzed?        *
*****************************************************
```

Type the character name. In this example 'jaw-width'. Compound names must be spelled with a hyphen.

Screen 05a

```
****************************************************
*            How many specimens of each species analyzed?            *
****************************************************
```

Each species will be represented by measurements originating from samples, all of the same size, with 'm' elements. In this example there will be 6 samples (n = 6), with 5 specimens each: (m = 5).

Screen 06a

```
****************************************************
*            Inform the table value of 'q' of the Tukey Test            *
*             Treatments =        -      Residual df =                 *
****************************************************
```

We need to inform the value of 'q' for the application of the Tukey Test to evaluate the differences between the means of the 6 samples. The value of 'q' can be obtained from the tables attached at the end of this tutorial.
In the horizontal header of the table we will inform the number of treatments. In this example each species is considered as a treatment in the Analysis of Variance. The app will tell us that n = 6.
The application also calculates the degrees of freedom of the residual variance: Residual df = n(m-1) where m is equal to the number of units of each sample (m = 5).
Therefore, Residual df = 6(5-1) or 6x4 = 24
We will use the two values provided by the application (horizontal header = 6 and vertical header = 24). Where the line meets the column is the number q = 4,373, which will be entered on screen 06a.

Screen 07a

****
* Enter specimen data 1 of species P.juliani *
****

Screen 08a

****
* Enter specimen data 2 of species P.juliani *
****

SCREEN 07a and SCREEN 08a show how the data will be requested by the application. After entering the last information of the first species, we will enter the information of the second species, and so on until the last species.

Screen 09a

****
* Analyzed character: Width-of-the-jaw *
****

****
******* Degree of Discrimination / Aggregation *******
****************** D = 2.6667 *******************
****

****
* Moderate character *
****
* Weight of Discriminative Potential: WD = 3.67 *
* Weight of Aggregate Potential: WA = 3.33 *
****

- This screen shows the results of the evaluation of the aggregative potential/discriminative of the taxonomic character 'Width-of-the-jaw'.
- The numerical value (on a scale from 0 to 5) equals 2.67.
- This value classifies the character as 'intermediate', that is, it aggregates and discriminates in approximately equal proportions.
- WD and WA values (on a scale between 1 and 6) express numerically the two similar potentials.

Screen 10a

```
***********************************************************
*    Do you want to analyze another character?  0=Nao - 1=Sim     *
***********************************************************
```

If you want to analyze another character, type '1' and the application will restart from SCREEN 04a.

TABLE VALUES FOR TUKEY'S TEST

On the following pages we transcribe two tables with the values of q'' for the application of the Tukey Test. We chose the 95% level because it is the most used in biological research.

These tables were originally published by H. Leon Harter, as indicated in the bibliography:

TABLE 3 (*Continued*)

P = .95

ν\n	2	3	4	5	6	7	8	9	10
1	17.97	26.98	32.82	37.08	40.41	43.12	45.40	47.36	49.07
2	6.085	8.331	9.798	10.88	11.74	12.44	13.03	13.54	13.99
3	4.501	5.910	6.825	7.502	8.037	8.478	8.853	9.177	9.462
4	3.927	5.040	5.757	6.287	6.707	7.053	7.347	7.602	7.826
5	3.635	4.602	5.218	5.673	6.033	6.330	6.582	6.802	6.995
6	3.461	4.339	4.896	5.305	5.628	5.895	6.122	6.319	6.493
7	3.344	4.165	4.681	5.060	5.359	5.606	5.815	5.998	6.158
8	3.261	4.041	4.529	4.886	5.167	5.399	5.597	5.767	5.918
9	3.199	3.949	4.415	4.756	5.024	5.244	5.432	5.595	5.739
10	3.151	3.877	4.327	4.654	4.912	5.124	5.305	5.461	5.599
11	3.113	3.820	4.256	4.574	4.823	5.028	5.202	5.353	5.487
12	3.082	3.773	4.199	4.508	4.751	4.950	5.119	5.265	5.395
13	3.055	3.735	4.151	4.453	4.690	4.885	5.049	5.192	5.318
14	3.033	3.702	4.111	4.407	4.639	4.829	4.990	5.131	5.254
15	3.014	3.674	4.076	4.367	4.595	4.782	4.940	5.077	5.198
16	2.998	3.649	4.046	4.333	4.557	4.741	4.897	5.031	5.150
17	2.984	3.628	4.020	4.303	4.524	4.705	4.858	4.991	5.108
18	2.971	3.609	3.997	4.277	4.495	4.673	4.824	4.956	5.071
19	2.960	3.593	3.977	4.253	4.469	4.645	4.794	4.924	5.038
20	2.950	3.578	3.958	4.232	4.445	4.620	4.768	4.896	5.008
24	2.919	3.532	3.901	4.166	4.373	4.541	4.684	4.807	4.915
30	2.888	3.486	3.845	4.102	4.302	4.464	4.602	4.720	4.824
40	2.858	3.442	3.791	4.039	4.232	4.389	4.521	4.635	4.735
60	2.829	3.399	3.737	3.977	4.163	4.314	4.441	4.550	4.646
120	2.800	3.356	3.685	3.917	4.096	4.241	4.363	4.468	4.560
∞	2.772	3.314	3.633	3.858	4.030	4.170	4.286	4.387	4.474

ν\n	11	12	13	14	15	16	17	18	19
1	50.59	51.96	53.20	54.33	55.36	56.32	57.22	58.04	58.83
2	14.39	14.75	15.08	15.38	15.65	15.91	16.14	16.37	16.57
3	9.717	9.946	10.15	10.35	10.53	10.69	10.84	10.98	11.11
4	8.027	8.208	8.373	8.525	8.664	8.794	8.914	9.028	9.134
5	7.168	7.324	7.466	7.596	7.717	7.828	7.932	8.030	8.122
6	6.649	6.789	6.917	7.034	7.143	7.244	7.338	7.426	7.508
7	6.302	6.431	6.550	6.658	6.759	6.852	6.939	7.020	7.097
8	6.054	6.175	6.287	6.389	6.483	6.571	6.653	6.729	6.802
9	5.867	5.983	6.089	6.186	6.276	6.359	6.437	6.510	6.579
10	5.722	5.833	5.935	6.028	6.114	6.194	6.269	6.339	6.405
11	5.605	5.713	5.811	5.901	5.984	6.062	6.134	6.202	6.265
12	5.511	5.615	5.710	5.798	5.878	5.953	6.023	6.089	6.151
13	5.431	5.533	5.625	5.711	5.789	5.862	5.931	5.995	6.055
14	5.364	5.463	5.554	5.637	5.714	5.786	5.852	5.915	5.974
15	5.306	5.404	5.493	5.574	5.649	5.720	5.785	5.846	5.904
16	5.256	5.352	5.439	5.520	5.593	5.662	5.727	5.786	5.843
17	5.212	5.307	5.392	5.471	5.544	5.612	5.675	5.734	5.790
18	5.174	5.267	5.352	5.429	5.501	5.568	5.630	5.688	5.743
19	5.140	5.231	5.315	5.391	5.462	5.528	5.589	5.647	5.701
20	5.108	5.199	5.282	5.357	5.427	5.493	5.553	5.610	5.663
24	5.012	5.099	5.179	5.251	5.319	5.381	5.439	5.494	5.545
30	4.917	5.001	5.077	5.147	5.211	5.271	5.327	5.379	5.429
40	4.824	4.904	4.977	5.044	5.106	5.163	5.216	5.266	5.313
60	4.732	4.808	4.878	4.942	5.001	5.056	5.107	5.154	5.199
120	4.641	4.714	4.781	4.842	4.898	4.950	4.998	5.044	5.086
∞	4.552	4.622	4.685	4.743	4.796	4.845	4.891	4.934	4.974

TABLE 3 (*Continued*)

P = .95

ν \ n	20	22	24	26	28	30	32	34	36
1	59.56	60.91	62.12	63.22	64.23	65.15	66.01	66.81	67.56
2	16.77	17.13	17.45	17.75	18.02	18.27	18.50	18.72	18.92
3	11.24	11.47	11.68	11.87	12.05	12.21	12.36	12.50	12.63
4	9.233	9.418	9.584	9.736	9.875	10.00	10.12	10.23	10.34
5	8.208	8.368	8.512	8.643	8.764	8.875	8.979	9.075	9.165
6	7.587	7.730	7.861	7.979	8.088	8.189	8.283	8.370	8.452
7	7.170	7.303	7.423	7.533	7.634	7.728	7.814	7.895	7.972
8	6.870	6.995	7.109	7.212	7.307	7.395	7.477	7.554	7.625
9	6.644	6.763	6.871	6.970	7.061	7.145	7.222	7.295	7.363
10	6.467	6.582	6.686	6.781	6.868	6.948	7.023	7.093	7.159
11	6.326	6.436	6.536	6.628	6.712	6.790	6.863	6.930	6.994
12	6.209	6.317	6.414	6.503	6.585	6.660	6.731	6.796	6.858
13	6.112	6.217	6.312	6.398	6.478	6.551	6.620	6.684	6.744
14	6.029	6.132	6.224	6.309	6.387	6.459	6.526	6.588	6.647
15	5.958	6.059	6.149	6.233	6.309	6.379	6.445	6.506	6.564
16	5.897	5.995	6.084	6.166	6.241	6.310	6.374	6.434	6.491
17	5.842	5.940	6.027	6.107	6.181	6.249	6.313	6.372	6.427
18	5.794	5.890	5.977	6.055	6.128	6.195	6.258	6.316	6.371
19	5.752	5.846	5.932	6.009	6.081	6.147	6.209	6.267	6.321
20	5.714	5.807	5.891	5.968	6.039	6.104	6.165	6.222	6.275
24	5.594	5.683	5.764	5.838	5.906	5.968	6.027	6.081	6.132
30	5.475	5.561	5.638	5.709	5.774	5.833	5.889	5.941	5.990
40	5.358	5.439	5.513	5.581	5.642	5.700	5.753	5.803	5.849
60	5.241	5.319	5.389	5.453	5.512	5.566	5.617	5.664	5.708
120	5.126	5.200	5.266	5.327	5.382	5.434	5.481	5.526	5.568
∞	5.012	5.081	5.144	5.201	5.253	5.301	5.346	5.388	5.427

ν \ n	38	40	50	60	70	80	90	100	
1	68.26	68.92	71.73	73.97	75.82	77.40	78.77	79.98	
2	19.11	19.28	20.05	20.66	21.16	21.59	21.96	22.29	
3	12.75	12.87	13.36	13.76	14.08	14.36	14.61	14.82	
4	10.44	10.53	10.93	11.24	11.51	11.73	11.92	12.09	
5	9.250	9.330	9.674	9.949	10.18	10.38	10.54	10.69	
6	8.529	8.601	8.913	9.163	9.370	9.548	9.702	9.839	
7	8.043	8.110	8.400	8.632	8.824	8.989	9.133	9.261	
8	7.693	7.756	8.029	8.248	8.430	8.586	8.722	8.843	
9	7.428	7.488	7.749	7.958	8.132	8.281	8.410	8.526	
10	7.220	7.279	7.529	7.730	7.897	8.041	8.166	8.276	
11	7.053	7.110	7.352	7.546	7.708	7.847	7.968	8.075	
12	6.916	6.970	7.205	7.394	7.552	7.687	7.804	7.909	
13	6.800	6.854	7.083	7.267	7.421	7.552	7.667	7.769	
14	6.702	6.754	6.979	7.159	7.309	7.438	7.550	7.650	
15	6.618	6.669	6.888	7.065	7.212	7.339	7.449	7.546	
16	6.544	6.594	6.810	6.984	7.128	7.252	7.360	7.457	
17	6.479	6.529	6.741	6.912	7.054	7.176	7.283	7.377	
18	6.422	6.471	6.680	6.848	6.989	7.109	7.213	7.307	
19	6.371	6.419	6.626	6.792	6.930	7.048	7.152	7.244	
20	6.325	6.373	6.576	6.740	6.877	6.994	7.097	7.187	
24	6.181	6.226	6.421	6.579	6.710	6.822	6.920	7.008	
30	6.037	6.080	6.267	6.417	6.543	6.650	6.744	6.827	
40	5.893	5.934	6.112	6.255	6.375	6.477	6.566	6.645	
60	5.750	5.789	5.958	6.093	6.206	6.303	6.387	6.462	
120	5.607	5.644	5.802	5.929	6.035	6.126	6.205	6.275	
∞	5.463	5.498	5.646	5.764	5.863	5.947	6.020	6.085	