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## *m\_integr*

**a computer program for the  
measure of morphological  
integration based on  
correlation matrix.**

by INGO SCHINDLER, Berlin

### **Part I**

File: m\_integr.exe  
a computer program for Windows PCs

### **Part II**

UserNotes

# PART II

## USER NOTES

### DISCLAIMER

This VB-program is provided without any explicit or implicit warranty of correct functioning. To use this program on your computer is your own risk. The program has been developed for my own research program. Researchers can use this program for scientific and research purposes, but intellectual property and copyright for the source code and program remains the property of Ingo Schindler.

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### 1. Description

The program *m\_integr.exe* calculate the index of morphological integration *I* proposed by CHEVERUD et al. (1983). This measure of the degree of morphological integration is based on the fact that the eigenvalues of a correlation matrix give the amount of variance associated with the corresponding eigenvector (Wagner 1990). The Index of a symmetric correlation matrix *R* of size *n* is defined as

$$I = 1 - (\det R)^{1/n}$$

(CHEVERUD et al. 1983, WAGNER 1990, NEMESCHKAL 1991). In cases of high degree of morphological integration the Index *I* is near to 1. In the opposite case (low degree of morphological integration) the value of *I* is nearer to zero (NEMESCHKAL 1991).

### 2. Input file

The correlation matrix is in ASCII (\*.txt or \*.cor), square (n x n) with a proceeding line for the value of n followed by the number of matrices. No column or row headings are allowed (see 'Test Run' for further information).

### 3. Procedure

- a) Select input file (use drive-, directory- and file-box).
- b) Press 'DATA' to load the selected file.
- c) Press 'Start' to start the calculation.
- d) Press 'Save' to store the results in a file (saved in the same directory shown in the directory-box).
- e) Press 'Show' to observe the results on the screen.
- f) Select new file to restart or press 'close' to stop the program.

## 4. Test run

The data used in this test run are the same as in Schindler (2003). The notes in brackets are only for explanation and not part of the data file.

### Input file:

```
5 [number of n]
4 [number of matrix in the file]
[no line between these numbers and the first matrix]
1 .585 .658 .616 .555 [correlation matrix]
.585 1 .663 .634 .689
.658 .663 1 .697 .626
.616 .634 .697 1 .598
.555 .689 .626 .598 1

1 .685 .758 .716 .755
.685 1 .663 .634 .689
.758 .663 1 .697 .626
.716 .634 .697 1 .198
.755 .689 .626 .198 1

1 .785 .958 .616 .155
.785 1 .663 .634 .689
.958 .663 1 .697 .626
.616 .634 .697 1 .598
.155 .689 .626 .598 1

1 .685 .758 .716 .655
.685 1 .663 .634 .689
.758 .663 1 .697 .626
.716 .634 .697 1 .598
.655 .689 .626 .598 1
```

### Output :

#### Results:

```
=====
No. 1 = 0.43223 *      Determinant = 0.059
No. 2 = 0.78967      Determinant = 0.00041
No. 3 = 0.62285      Determinant = -0.00763
No. 4 = 0.48023 *    Determinant = 0.03794
=====
```

DATUM:15.05.04

Created with the program m\_integr. (C) 2004 by INGO SCHINDLER, Berlin

## 5. Notes

- 1) The program doesn't check the input file format. If it is not correct the program terminate automatically.
- 2) The program save the results in the file with the name 'm\_i-resultsX' (x = number of runs). The program doesn't check if this file name already exists. Thus, it may happen that your old data file is deleted.
- 3) If the correlation matrix is not sufficient for the calculation of the determinant the results can be wrong.
- 4) The limitation for the correlation matrix is 150 x 150 and the limit of the number of matrix in a file is 50.
- 5) The program creates a 'miPfad.ini' file, which contain the start path and the running number (see above).

## 6. Literature

CHEVERUD, J. M., J. J. RUTLEDGE, W. R. ATCHLEY (1983): Quantitative genetics of development – genetic correlations among age-specific trait values and the evolution of ontogeny. *Evolution* 37: 895-905.

HAINER, K. (1983): Numerik mit BASIC Tischrechnern. MikroComputer-Praxis. Teuber, Stuttgart. 251pp. [the program No. 36 "GAUSS-ELIMINATION FUER EIN LINEARES GLEICHUNGSSYSTEM  $A \cdot X = F$ " p. 149-151 is used in the source code]

NEMESCHKAL, H. L. (1991): Shell size in Land Snails (*Arianta*, Helicidae) as a so-called simple system of characters – A systems-analysis by means of classification an morphological integration. *Zool. Jb. Syst.* 118: 149-192.

SCHINDLER, I (2003): MSA-me, a Visual-Basic program for the measure of sampling adequacy. IS-Online-Public. No. 5.

WAGNER, G. P. (1990): A comparative study of morphological integration in *Apis mellifera* (Insecta, Hymenoptery). *Z. zool. Syst. Evolut.-forsch.* 28: 48-61

If you find bugs or mistakes in this program, please contact me immediately!  
Any help and suggestions are welcome.  
I apologize for my little English.

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