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Creating E-Content Using NTSYspc Software for the Students of Plant Taxonomy

Usama K Abdel-Hameed[1,2]
[1]Biology Department, Faculty of Science, Taibah University, Saudi Arabia
[2]Botany Department, Faculty of Science, Ain Shams University, Egypt

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***Corresponding author**
Usama K Abdel-Hameed

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Abstract: The author has made an approach to develop e-content for hypothetical taxa as a case study in the present paper. The objective is to elucidate the interrelationships between the taxa under investigation using NTSyspc software. NTSyspc is a system of programs that is used to find and display structure in multivariate data. Using such computational software technology, complex understanding of taxonomical interrelationships becomes more understandable. In the current paper author has discussed sequence of steps to create dataset using NTSyspc and run the modules to generate a phenogram illustrating the interrelationships among the taxa under study.
Keywords: NTSyspc, phenetic analysis, digital learning environment.

INTRODUCTION

The request of new information and communication technology (ICT) in the educational systems are increased to acquire students skills needed for the current century and the digital learning environment nowadays becomes an urgent need. So, ICT at all levels of education is important issue, the lack of a high-quality e-contents is a barrier against intended learning outputs [1].

The computer has made it possible to consider large numbers of characteristics in classifying many phenomena, notably living organisms, fossil organisms, and even imaginary organisms [2]. NTSyspc is a system of programs that is used to find and display structure in multivariate data [3].

The program was originally developed for use in biology in the context of the field of numerical taxonomy, but it has also been widely used in morphometrics, ecology and in many other disciplines in the natural sciences, engineering, and the humanities, the terms mathematical taxonomy and automatic classification have also been used to describe this field of application [4].

Using such computational software technology, complex identification process becomes more user's friendly, and interrelationships more understandable. In this paper author has discussed sequence of steps to generate dataset using NTSyspc.

MATERIALS AND METHODS

Downloading NTSyspc

Numerical Taxonomy System [3] can be downloaded through
http://www.exetersoftware.com/cat/ntsyspc/ntsyspc.html

Creating a dataset

The dataset begins with building a taxon/characters states matrix as binary state (0/1) for each character state (Table 1).

Table-1: Data matrix of taxa and characters states

No.	Taxa	Characters states
1.	*Alpha*	1 1 0 0
2.	*Beta*	1 0 0 0
3.	*Gamma*	1 1 0 1
4.	*Delta*	0 1 1 1
5.	*Epsilon*	1 1 0 0
6.	*Zeta*	0 0 1 1
7.	*Eta*	0 1 0 1

Entering taxa and characters

To start a new matrix, click the NTedit.exe, NTedit window is displayed (Fig. 1, a), the window is initially empty, to start a new matrix, select File > New matrix (Fig. 1,b), then enter the values of No. rows (taxa number) and No. cols (Characters number).

Saving the dataset

Select File > Save file, that can be used for the proceeding computations (Fig. 1, c).

Running the modules

The first step is running Ntsys.exe, press ok on the displayed window (Fig. 1,d), three successive steps should be performed; General>Stand, detect the names of input and output files then let the module to compute, finally close the displayed windows (Fig. 1, e), the second step is choosing Similarity>SimInt, detect the names of the output and input files then let the module to compute (Fig. 1, f), the third step; choose Clustering>SAHN and detect the names of files then press compute (Fig. 2,a).

Obtaining the phenogram

The last step to obtain the phenogram is pressing on Graphics> Tree plot, detect the input file then compute (Fig. 2, b), the tree will be displayed that you can edit through Options> Plot Options (Fig. 2,c & d).

The estimation of character states variation was done by Unweighted Pair-Group Method using Arithmetic Averages with SAHN function due to [2] and characters states were analyzed as binary states. The grouping process was depended on the similarity values. All computations were performed by the aid of NTSYS-PC version 2.02 [3].

RESULTS AND DISCUSSION

The produced phenogram (Fig. 2, e) indicates that all the taxa under investigation are distributed in two series at similarity coefficient 1.48, the first one divided into two clusters at similarity coefficient less than 1.18 containing five taxa, the first cluster comprises *Alpha* and *Epsilon* as a sister taxa while *Beta* is delimited, *Gamma* and *Eta* are isolated in the second cluster, on the other hand, *Delta* and *Zeta* showed high affinity and nested in the second series at similarity coefficient less than 0.89**.**

Several phenetic analysis on families of flowering plants were conducted using NTSyspc software indicating that the used characters were likely to be useful and valuable taxonomic traits to cite but a few; [5 ,6]

In conclusion, the present paper discussed about skillful utilization of NTSyspc, for creating learning resources which is useful for graduate and postgraduate students. Teachers may incorporate more taxa and more characters and build phenogram for the interrelationships among the studied taxa.

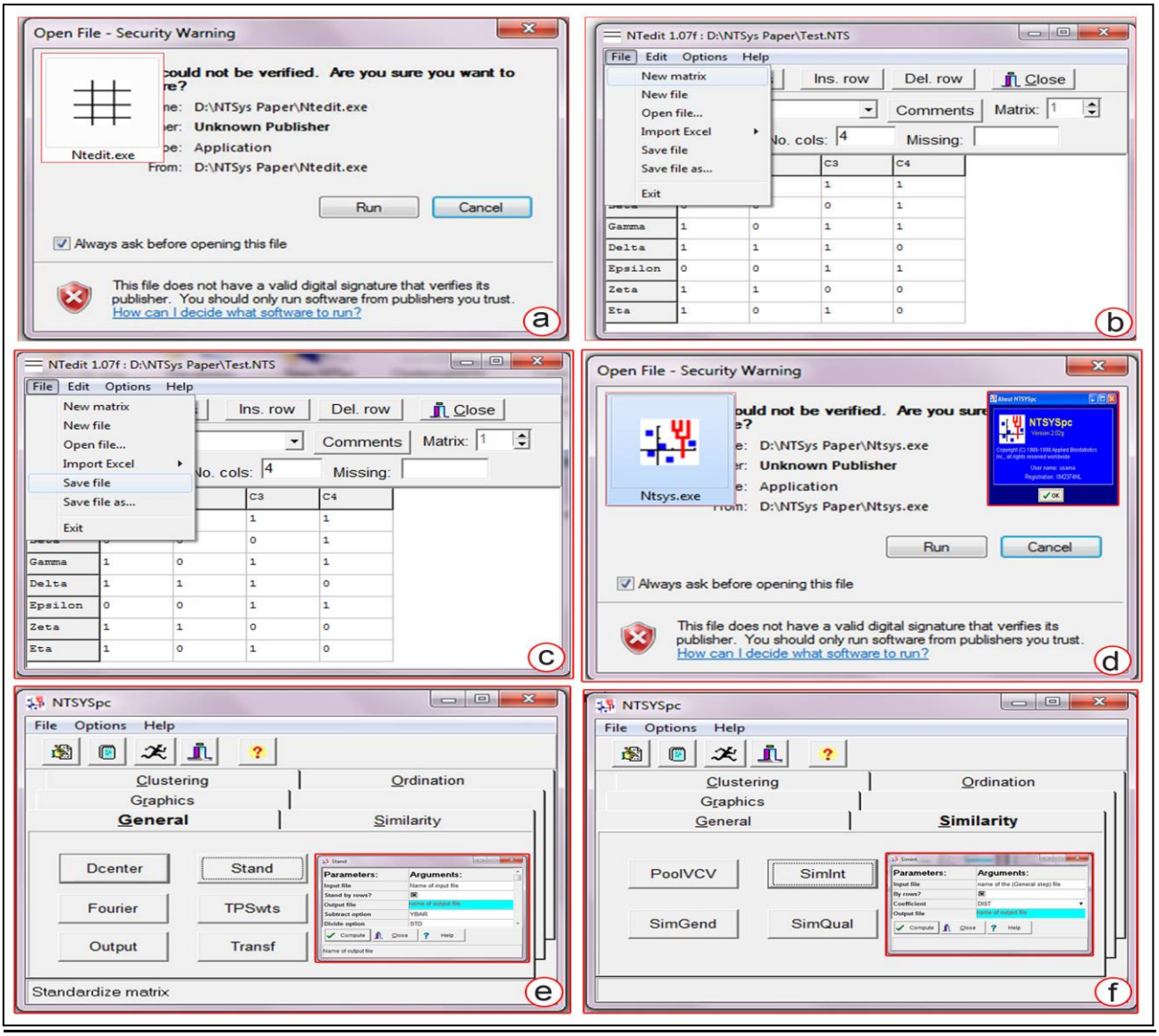

Fig-1: Screen shots of the NTSyspc software; a. Running Ntedit.exe. b. Input file format for NTedit. c. Saving the matrix file. d. Running NTsys.exe. e. General, Stand module. f. Similarity, SimInt module

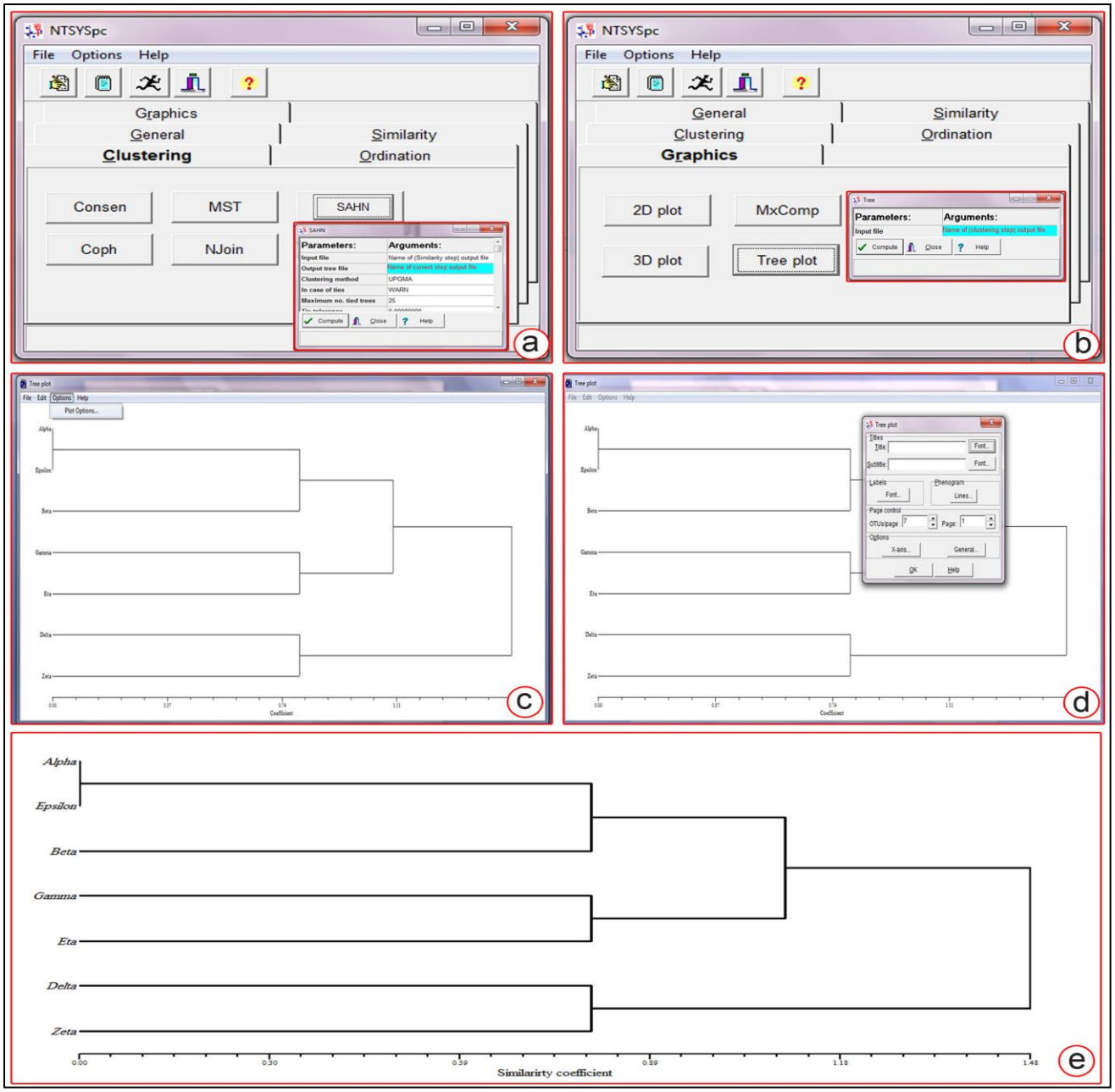

Fig-2: Screen shots of the NTSyspc software and resulted phenogram; a. Clustering, SAHN module. b. Graphics, tree plot module. c &d. Editing the resulted tree. e. The produced phenogram illustrating the interrelationships among the studied taxa

REFERENCES

1. Yadav U, Anjaria KB, Nairy R, Shirsath KB, Desai UN, Chaurasia RK, Bhat NN, Sapra BK. Differential killing and radio-modifying effects of iodoacetate in mammalian normal and cancer cells. Radiation and environmental biophysics. 2017 Aug 1;56(3):227-39.
2. Sneath PH, Sokal RR. Numerical taxonomy. Nature. 1962;193(4818):855-60.
3. Rolf FJ. NTSYSpc Numerical Taxonomy and Multi variate Analysis System: Version 2.0. User Guide. Applied Biostatistics. Inc. Setauret. New York. 1998:37.
4. Tanavar M, Kelestanie AR, Hoseni SA. Software Programs for analyzing genetic diversity. Int J Farming and Allied Sci. 2014;3(5):462-6.
5. Abdel-Hameed UK, Khdery GA, Tantawy ME, Abo-eleinein MM, Arafat SM, Aboelghar MA. A contribution of hyperspectral remote sensing criteria versus morphological traits in taxonomy of flowering plants. The egyptian journal of experimental biology (Botany). 2015;11(1):89-101.
6. Abdel-Hameed UK, Tantawy ME, Salim MA, Mourad MM, Ishak IF. Phenetic analysis of morphological and molecular traits in Acanthaceae Juss. Journal of Biosciences and Medicines. 2015 Mar 18;3(3):18-34.