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AMACID: A COMPUTER GENERATED PROGRAM FOR AMINO ACID DETECTION

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ABSTRACT:

Biomolecules are lifeless. Yet, in appropriate complexity and number, molecules compose living things. Amino acid is the chemical subunits of polypeptides and proteins, and therefore one of the fundamental building blocks of life, as we know it. Proteins are sequenced by identification of Amino acid. Amino acids are detected by chromatographic methods. Amino acid detection by chromatography is the critical method because the range of R_f value of amino acid is tedious and difficult to interpret. Many researcher and students found difficulty to identify the amino acid by R_f value due the range of standard R_f values. AMACID, an Amino acid detector is the software used to identify the amino acid on the basis of chromatographic result.
This software helps to different people working in various fields of life science to detect accurate amino acid on the basis of R_f values obtained by chromatographic techniques. Visual Basic is a popular platform for developing the software; hence this language was used for developing this software.

Keywords: *R_f value, Amino acids, Solvent system*

[I] INTRODUCTION

The idea that the organic compounds that serve as the basis of life were formed when the earth had an atmosphere of methane, ammonia, water, and hydrogen instead of carbon dioxide, nitrogen, oxygen and water suggested by Oparin[1] and has given emphasis recently by Urey[2] and Bernal [3]. Chromatography techniques employ mild conditions and separate molecule on the basis of differences of size, shape, mass, charge, solubility and adsorption properties. The term chromatography derived from the Greek meaning "colored writing" and was first used by the Russian Botanist Tswett to describe the separation of colored pigment [2]. Peptides may be considered the larger building blocks of proteins and as such are of interest in studies on the structure of proteins. In addition, numerous free peptides of biological importance have been observed. Cellulose in the form of paper sheets makes an ideal support medium where water is adsorbed between the cellulose fibres and forms a stationary hydrophilic phase.

Computer Simulation is a powerful alternative approach to solve numerical iteration using a high level language of interest. Simulation is a very useful research tool and is a legitimate, disciplined approach to scientific investigation and its value needs to be

recognized and appreciated. Simulation analysis offers a variety of benefits; it can be useful in developing theory and in guiding empirical work. It can provide insight into the operation of complex systems and explore their behavior. It can examine the consequence of theoretical arguments and assumptions generate alternative explanations and hypothesis, test the validity of explanations [4].

- Visual Basic is integrated development environment.
- Visual Basic is a fourth Generation Language.
- It allows direct connectivity with database.
- It supports different controls for database connectivity.
- It is simple to use software with any other program in windows environment.

[II] MATERIALS AND METHODS:

2.1 Wet Lab Preparation:

The standard amino acid sample was prepared by mixing amino acids in 1M HCL. The Whatman No. 1 (2cm X 10cm) paper was used for analytical purpose. The paper must be impregnated with a buffer solution before use.

Butanol acetic acid water 4:1:5 (v/v) Solvent and phenol-water 80:20 (v/v) was used to obtain the standard R_f values. The mixture was spotted on paper dried and the chromatogram developed by allowing the solvent to flow along the sheet. The solvent front was marked and, after drying the paper, the position of the compounds present in the mixture was visualized by a suitable staining method (detection spray). Detection spray was prepared by dissolving 200mg of ninhydrin in 100ml of 95% of alcohol and 1.5 ml pyridine. The paper was placed in an oven at 110^0 C. the spots was visualized. The distance was calculated. The data obtained by the above method & data given by the book fundamentals of Biochemistry J. L. Jain and an introduction to Practical Biochemistry David Plummer [5] was used as standard R_f values of standard amino acids in the database of software.

2.1 Program development:

The program was developed in V.B. by using protocols given in the book Guide to Visual Basic by Peter Norton [6].

To use the software, click on the icon appeared at desktop and follow the steps

1) Choose the solvent system used.
2) Choose the parameter as R_f value or distance traveled by solvent and solute.
3) Add the values of the field
4) The result will appear on the screen
5) User can also use the menus as File menu, View menu, Help menu for different task.

[III] RESULTS

Figure 1 shows the main interface of the program and like all figures illustrating the article, is a bitmap retrieved from the program running in the real time in an IBM PC-compatible computer. In Figure 1 user has to select solvent system used for running the amino acid sample, click next to follow the next step. In next step user has to insert either R_f value of amino acid or distance traveled by solvent and solute as shown in figure2 and figure3. When user click on next followed by values, user get the result as shown in figure4, figure5 and figure6 shows the more information of amino acids. File menu will open to show standard R_f values as in figure7. In figure8 the information of software will appear form help menu.

Fig.1 Main interphase

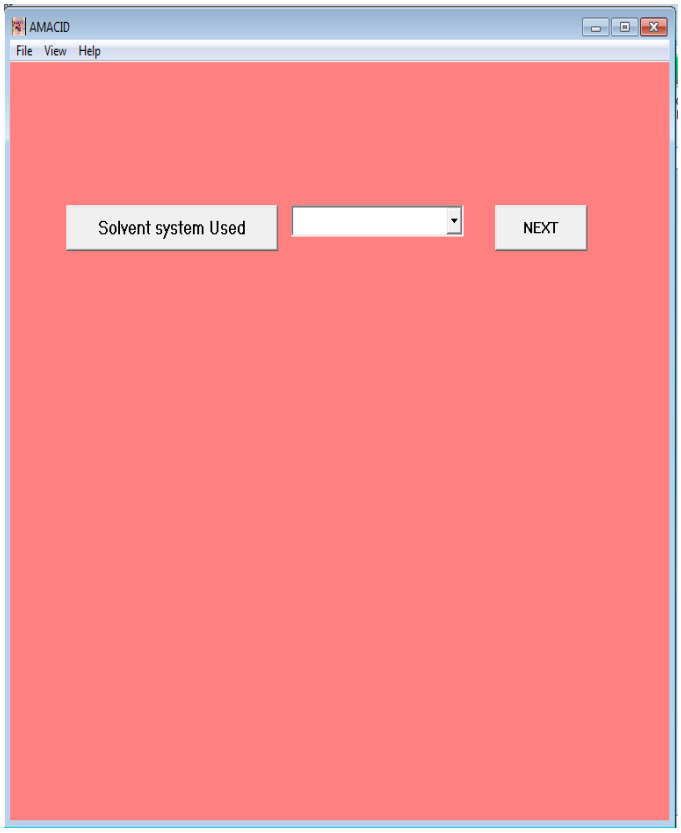


Fig.2 Enter the parameter as R_f value, or distance traveled by solvent and solute

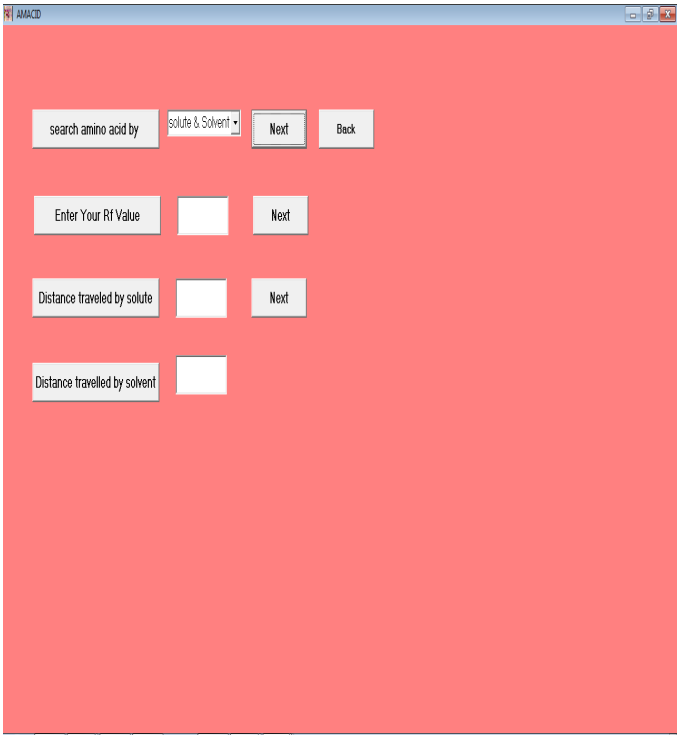


Fig.3 Write the values & click next

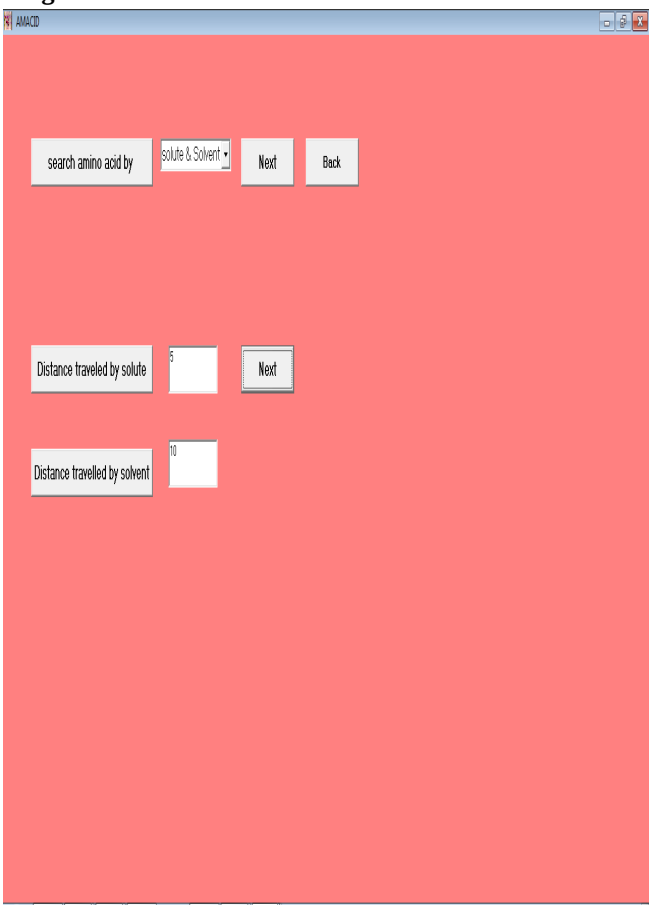


Fig.4 Display result from distance values

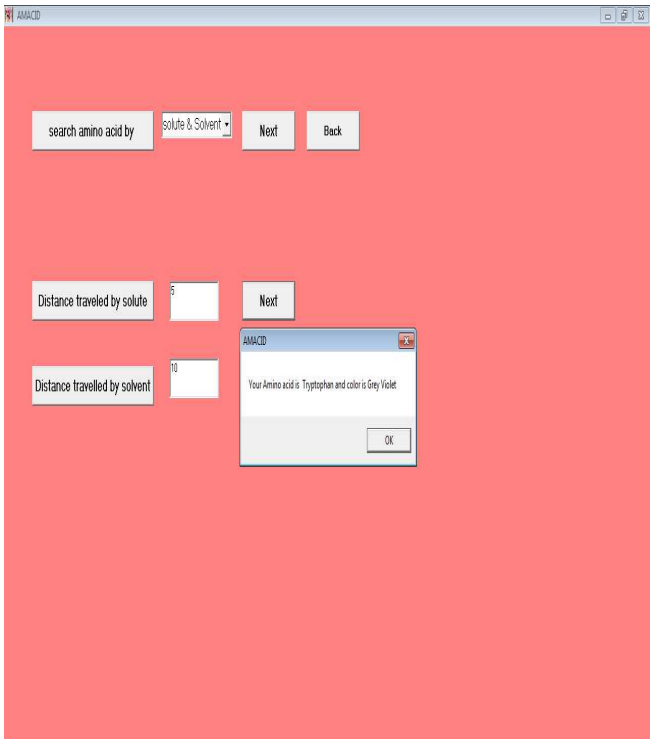


Fig.5 Display result by entered R_f value

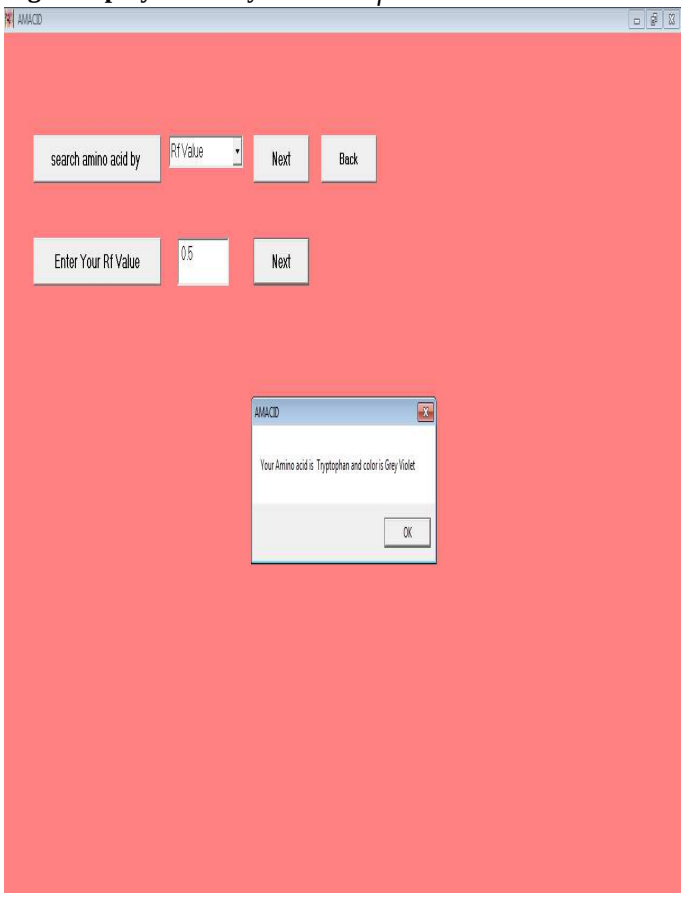


Fig.6 Information related Amino acids from menu bar

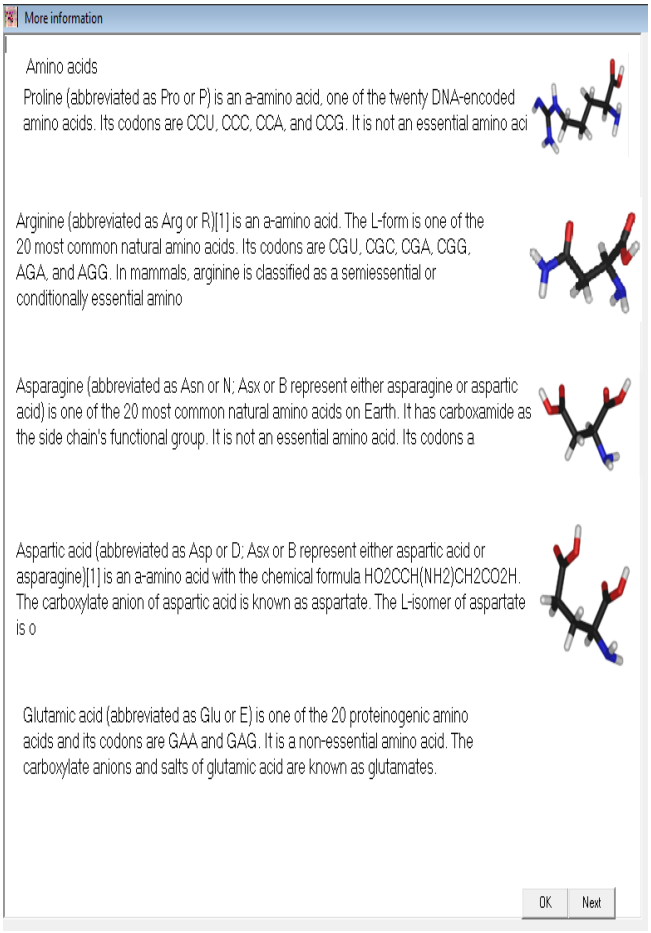


Fig.7 Standard R_f values from file menu

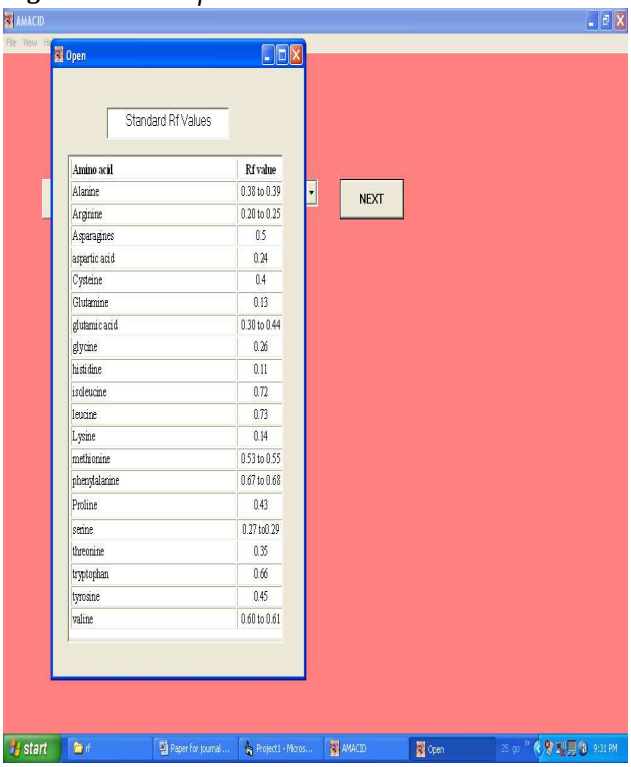
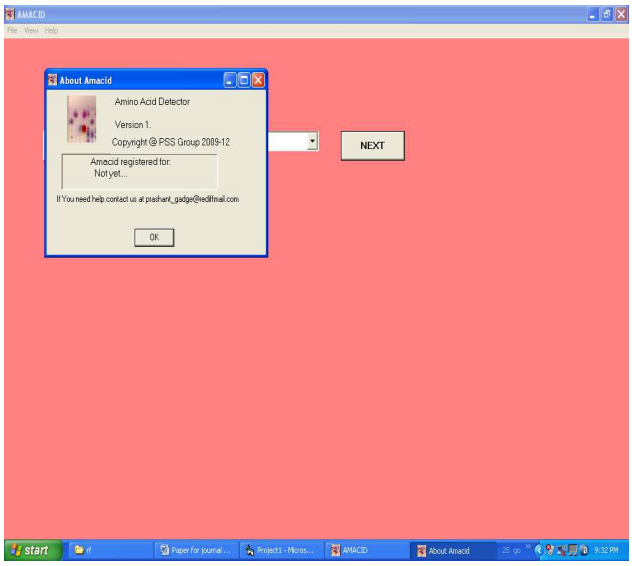


Fig.8 Details of the software from help menu



CONCLUSION:

Our results confirmed and compare with manual methods and we can summarize the results as follows

1) Software is useful to obtained result from R_f value or Distance traveled by solute and solvent.
2) It provides the information of amino acids.
3) The software provides techniques for amino acid separation by different chromatographic techniques.
4) User can save result.

REFERENCES:-

[1] OPARIN, A.I. The Origin of Life. New York : Macmillan (1938).

[2] UREY, H.C. *Proc. Natl. Acad. Sci.* U.S., 38, 351 (1952); The Planets. New Haven : Yale University press.

[3] BERNAL, J.D. Physical Basis of Life *Proc. Phys. Soc.* (London), 62A, 537 (1949); 62B, 597 (1949).

[4] ABDUL KADIR BABA HASSAN, MATTHEW SUNDAY ABOLARIN, ONAWOLA HASSAN JIMOH, The Application of Visual Basic Computer Programming Language to Simulate Numerical Iteration, Leonardo *Journal of Sciences*, 125-126, 2006.

[5] DAVID PLUMMER An Introduction to Practical Biochemistry (2007), Tata McGraw-Hill Publishing company Limited.

[6] PETER NORTON's Guide to Visual Basic 6 (1998) BPB Publication New Delhi.

[7] EVANGELOS PETROUTSOS, Mastering Visual Basic (2005) BPB Publication New Delhi.

(Reference No. 6th and 7th was used for the development of the program in V.B.)