157P A COMPUTER-BASED INTERACTIVE TUTORIAL PROGRAM TO TEACH THE PHYSIOLOGY OF THE HEART TO UNDERGRADUATE STUDENTS

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The use of computers in undergraduate teaching is now widespread and interactive software has been developed to enhance and sometimes replace traditional teaching methods. Computer-assisted learning (CAL) has many advantages: it promotes active learning, gives students control of when they learn and the pace of their learning, it may incorporate features which enhance the quality of presentation of material and promote better understanding, and it potentially saves staff time. Also the availability and user-friendliness of sophisticated authoring programs now makes it possible for academics with little programming knowledge to develop high quality courseware. Here we demonstrate an interactive tutorial which aims to teach the basic physiology of the heart. It is suitable for first year undergraduates from a range of biological science, medical and health-related courses and may be used for both primary learning, revision and as a remedial teaching resource.

The CAL program was developed using Authorware Professional® (Macromedia Inc.) to run on IBM PC compatibles (minimum delivery platform: 386 SX, 20 MHz PC running Windows™ (Microsoft), a sixteen colour VGA monitor and a mouse).

The main menu has three options: which may be accessed in any order: *aims and objectives*; *introduction*: (structure and function of the cardiovascular system) and *the heart*:. This latter section also has a submenu: *gross structure* (chambers and major blood vessels, the wall of the heart and the pericardium; *heart valves* (structure and function of atrioventricular and semi-lunar valves; *histology* (cardiac muscle cells and pacemaker cells); *excitation* (spread of depolarization and the electrocardiogram); *heart sounds*; *the cardiac cycle* (pressure and volume changes); *cardiac output* (control by autonomic nerves, hormones and autoregulation).

High quality colour graphics are used extensively throughout the program and features such as animation and a Hypertext facility are used to enhance student learning. For example animation sequences are used to explain the action of papillary muscles in preventing valve eversion, and to show the route taken by blood through the heart.The program is highly interactive and uses several features to promote this. For example students are required to: label diagrams by "dragging" labels from a list and "dropping" them into the box corresponding to the correct position on the diagram; interpret recordings of pacemaker cell action potentials to better understand the effect of autonomic nerves on heart rate. In addition they must answer a variety of questions included in each section. These may be multiple choice, selecting correct phrases from a list to complete a statement, true/false questions with feedback.

The learning package is intended for independent study and could be used as an alternative to resource-intensive, staff-led tutorials or lectures (the material covers approximately four one-hour lectures to first year students). It is estimated that it would occupy students for 3-5 hours of fairly intensive study and is suitable for primary learning or revision. The question-answer sections may also be useful for self-assessment.

Providing the program evaluates well in student use it will be extended to cover the circulatory vessels and blood pressure

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158P AN INTERACTIVE, COMPUTER-BASED TUTORIAL PROGRAM TO TEACH THE PHARMACOLOGY OF DOPAMINE TO UNDERGRADUATE STUDENTS

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The Pharma-CAL-ogy project is funded through the Teaching and Learning Technology Program (TLTP) which aims to facilitate the use of modern technology to make teaching and learning in higher education more productive and efficient. One of the major aims of this initiative is to promote the development of new teaching software in areas of the pharmacology curriculum where there is an identified need. Here we describe a computer-assisted learning (CAL) program which takes the form of an interactive tutorial and aims to teach the pharmacology of dopamine. It is suitable for undergraduates from science, medical and a range of biomedical courses which include basic pharmacology modules.

The CAL program was developed using Authorware Professional® (Macromedia Inc.) to run on IBM PC compatibles (minimum delivery platform: 386 SX, 20 MHz PC running Windows™ (Microsoft), a sixteen colour VGA monitor and a mouse).

The menu has six options which may be accessed in any order: *introduction*: (the physiological role of dopamine in the CNS and its clinical significance); *dopamine transmission*: (synthesis, storage, release, pre- and post-synaptic receptors, uptake and inactivation); *central dopaminergic pathways*: (main sites of dopaminergic neurones and pathways in the rat brain); *dopamine receptors*: (D_1 and D_2 family of receptors and their sub-types, transduction mechanisms); *dopaminergic drugs*: the action and clinical importance of selected drugs which interfere with synthesis (alpha-methyl p tyrosine, L-DOPA), storage (reserpine, D-amphetamine, amantidine), and neuronally-evoked release of dopamine (D_2 autoreceptor blockers); and dopamine receptor antagonists (chlorpromazine, haloperidol, spiperone, sulpiride, clozapine), dopamine-receptor agonists (pergolide, quinpirole, brompcriptine, apomorphine), and inhibitors of dopamine inactivation (antimuscarinics, COMT inhibitors, MAO_B inhibitors).

High quality colour graphics are used extensively throughout the program and features such as animation and a Hypertext facility are used to enhance student learning. For example animation sequences are used to explain the steps in dopamine transmission, and the action and clinical significance of drugs which interfere with these processes. The program is highly interactive and uses several interactive features described in a previous demonstration to the Society (Collins, *et al*, 1995). The main sections all have associated questions, mostly of the true/false variety with feedback. These are designed to allow students to assess their understanding of the section they have completed and also to present additional information and explanations through the feedback. The computer also keeps a tally of correct/incorrect answers

The learning package is intended for independent study and could be used as an alternative to resource-intensive, staff-led tutorials. It is estimated that it would occupy students for 2-3 hours of fairly intensive study and is suitable for primary learning or revision. The question-answer sections may also be useful for self-assessment.

G.G.S. Collins, D. G. Dewhurst & R.T. Ullyott (1995) Brit. J. Pharmac. Proc. suppl. (in press)

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The use of computer-based learning techniques provides a powerful, interactive tool for the teaching of complicated aspects of many sciences. In biology the effective teaching of the concept of cellular drug targets and their associated signal transduction mechanisms occupies a major part of many degree courses in pharmacology and related disciplines. In particular, students report difficulty in visualising the molecular structure of these targets and the sequence of events occurring as a result of target activation. This program aims to allow students to explore the basic structure and molecular functions of cellular drug targets: to understand the mechanisms by which their activation is converted into biological effects within cells and to investigate the effects of agonists on these processes.

'Drug Targets and Transduction Systems' is a Windows-based computer-assisted learning package developed under the Teaching and Learning Technology Programme (TLTP2) by members of the Pharma-CAL-ogy consortium. It is written in Authorware and will run on any IBM-compatible 386-based PC, having a VGA (16-colour) monitor and Windows 3.1.
Currently, the package is divided into four main sections: namely Introduction, Target Synthesis and Turnover, G-Protein Coupled Receptors and Ligand-gated Ion Channels. It incorporates a high level of student interaction and students are free to explore the package at their own pace.

Each major section is presented as a number of 'concept screens', some of which also have 'extra knowledge level'screens, should the student wish to explore further. In this way, the student is provided with basic level material that may be completed in about 90 min, or a more comprehensive study that would occupy about 3 h. Throughout the package the level of student interaction is high, involving the use of 'hot text' and animation to expand the student's understanding. The package is intended either for primary teaching or tutorial-based study.

The Introduction explores the need for intercellular communication and identifies candidate sites for cellular recognition of messages between cells. Seven screens are presented, each introducing a major concept in the understanding of the need for intercellular communication. Target Synthesis and Turnover explores the processes of protein synthesis, movement and destruction within the cell and the mechanisms by which these processes result in the availabiliy of suitable recognition sites and potential drug targets within the cell. G-Protein Coupled Receptors are investigated using the β_2-adrenoceptor in the lung as an example. Eleven screens explore the structure and function of the receptor, the binding of the stimulating ligand, coupling to the second messenger system and the binding of antagonists. The section on Ligand-Gated Ion Channels comprises eight screens and explores the structure and function of this type of cell membrane receptor, using the nicotinic acetylcholine receptor as the main example.

160P ROBOFIT: A VERSATILE MACRO-DRIVEN TEMPLATE FOR CURVE FITTING, ANALYSIS AND PRESENTATION IN MICROSOFT EXCEL

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We have described previously a method of simultaneously fitting concentration-response data using the solver function within Microsoft Excel™ (Bowen *et al.*, 1994). We now describe the development and utility of 'RoboFit', a macro-driven template developed for the routine curve-fitting, analysis and high quality presentation of experimental concentration-effect data.

RoboFit employs a format that is capable of handling up to eight pairs of experimental data. However, the template can be easily customised to suit individual experimental protocols. Data are entered either manually or electronically onto a standard form, and then manipulated according to preference, e.g. normalized as a percentage of maximum response. Data are represented graphically, either as a simple line plots, or as curves fitted using the three parameter equation shown below. Where E represents response and [A] is agonist concentration.

$$E = \frac{\alpha}{1+(EC_{50}/[A])^{n}}$$

This allows estimation of agonist potency (EC_{50}), maximum response (α) and mid-point slope factor (n). Curve location parameters obtained in the absence and presence of an antagonist can be analysed to provide estimates of antagonist affinity. Data are presented in a concise format which includes tables of raw data and derived curve parameters, and graphical figures with curve fits. Data are stored as an Excel file which is easily accessed by many software packages on both IBM-compatible and Macintosh computers. In addition, RoboFit has the ability to fit paired data simultaneously to the Operational Model of Agonism (Black & Leff, 1983). RoboFit may also exploit simultaneous-fitting to estimate antagonist and partial agonist affinity (Leff, 1993; Lazareno & Birdsall, 1993).

RoboFit provides an inexpensive and an easily accessible method for routine data analysis, and provides a framework that can be easily modified to accommodate other pharmacological models.

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