Representational models of amino acid chemistry: The delivery medium as the message

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The use of educational technology for teaching and learning has received much attention over the past decade, and the introduction of apps for personal mobile devices is poised to make these technologies more accessible and widespread inside and outside the classroom. A question that comes along with the use of clickers, tablet devices, smart boards, online-only content delivery methods, etc. is how the technology in question is augmenting the teaching and learning process; in other words, is the educational technology being adopted for the sake of using some form of technology in the classroom or because of a genuine added value? If we accept educational technologies to be a new form and mechanism of content delivery, then these questions, although new in the context of electronic educational technology, are not new in the field of education research. For example, in 1927, O. M. Leland noted in the *Bulletin of the American Association of University Professors* that "it seems to be quite easy for a teacher to become so absorbed in the mechanism of measurement and tests as to lose sight of the importance of teaching…" One can therefore posit that challenges faced by educators in the past to prudently adapt forms of quantitative assessment in course syllabi could be comparable to challenges faced today in adapting the right form of educational technology to encourage and measure student engagement with the learning material. Moreover, challenges faced in delivering content to students enrolled in a 'massive open online course' (MOOC) may in some ways be compared to those in distance learning courses. Research on distance learning can rely on a rich set of historical evidence dating back at least to the University of London's first offering of its 'External Programme' in the mid-nineteenth century.

The aim of this project was to propose the use of an educational technology, namely three-dimensional molecular visualization software, not as a means of content delivery per se, but as an essential pedagogical element of a subsection of a theoretical/philosophical biology syllabus focused on the use and meaning of models in biochemistry. The software used in this exercise are ChemDraw (for structural drawing) and Chem3D (for structural visualization) (CambridgeSoft/PerkinElmer). Students will draw and then visualize the amino acid tyrosine (**Fig. 1A-B**). They will be asked to rotate the amino acid and consider (i) how the visualization would differ between the L- and D- forms of the amino acid and (ii) if the phenol side-chain can rotate freely for 360°. The students will also be asked to build a ball-and-stick model of tyrosine (**Fig. 1C**) and try to rotate the side-chain. While rotating the phenol group and holding the model in hand, students may notice that if the model is slightly bent, it would no longer be possible to rotate the side-chain fully (**Fig. 1D**). Students can hypothesize, among other possibilities, that under certain physiological conditions (such as a tyrosine residue's specific position in a given protein structure), the movement of the side-chain may be quite restricted (see for example, Gelin and Karplus, *Proc Natl Acad Sci USA* 1975 or Warncke, Babcock and McCracken, *J Phys Chem* 1996). This notion may not immediately be apparent in the three-dimensional visualization of the amino acid (**Fig. 1B**), and may probably become clear only when models or representations of tyrosine are compared across the electronic and physical mediums.

An extension of this exercise would be to include a water molecule. Not only is water important in the context of protein structures via its interaction with individual amino acids (Bartesaghi *et al.*, *Science* 2015), but its own structure is an active area of research in the field of physical chemistry (Pérez *et al.*, *Science* 2012). Students will be asked to make two physical models of water, a standard and a compact version (**Fig. 2A-B**). It would first become apparent that only the standard ball-and-stick model is suitable to show inter-molecular interactions of water, such as hydrogen bonding (**Fig. 2C**) and H-H bonding (**Fig. 2D**). These interactions will also be visualized using ChemDraw/Chem3D (**Fig. 2E**). Although the compact models, as noted earlier, cannot show these interactions clearly (**Fig. 2F**), they are indispensable in showing water interactions with the tyrosine molecular model built in the first module (**Fig. 2G**).

It is hoped that this exercise would (i) show the utility of comparing alternative representations of a molecular model across different mediums and (ii) demonstrate the nature of models as "metaphors" with inherent representational limitations and boundaries. Moreover, students can use this exercise to come up with new questions or hypotheses for further investigation. Overall, comparisons of two or more delivery mediums, to paraphrase the communication theorist Marshall McLuhan, would be the message of these exercises.
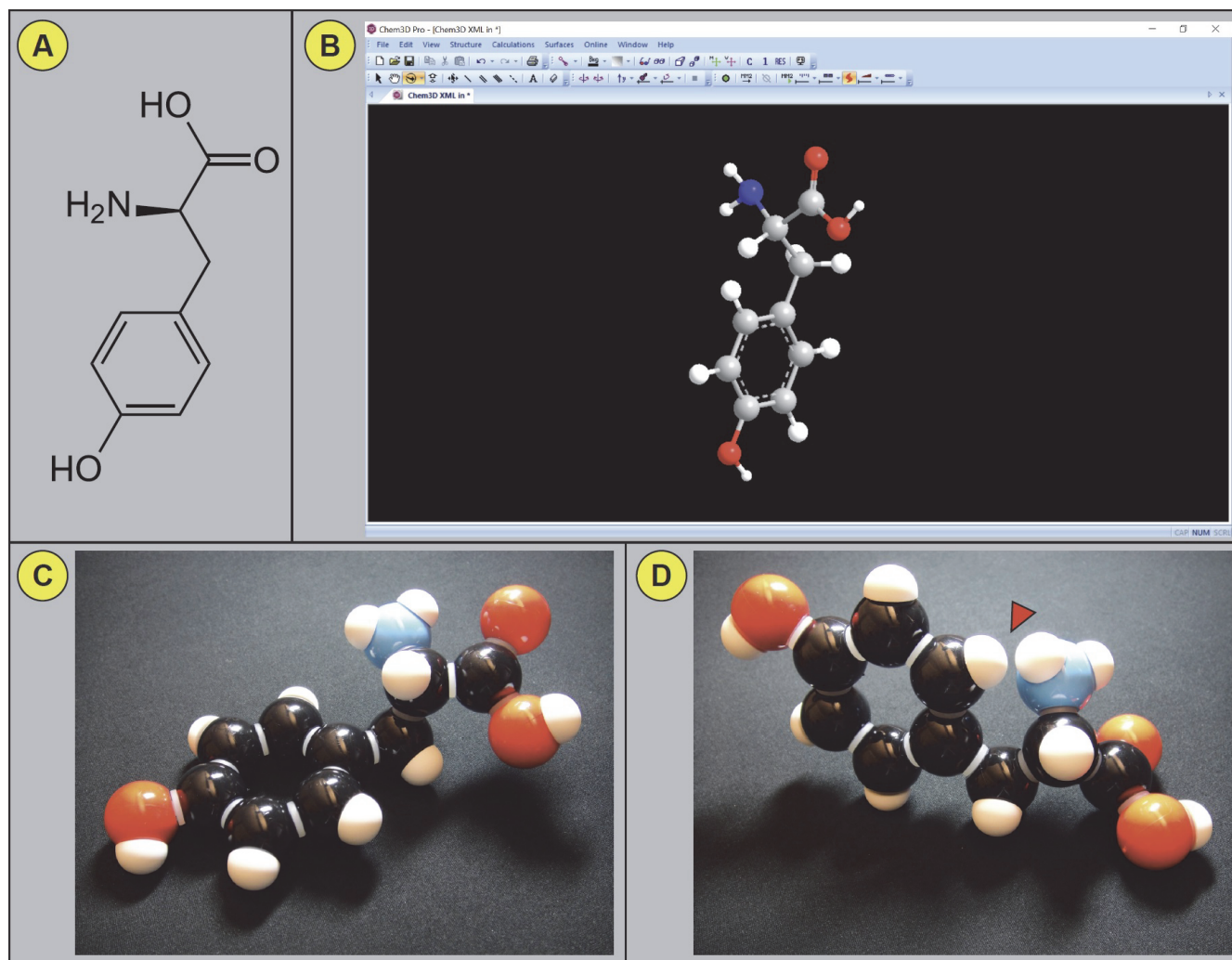
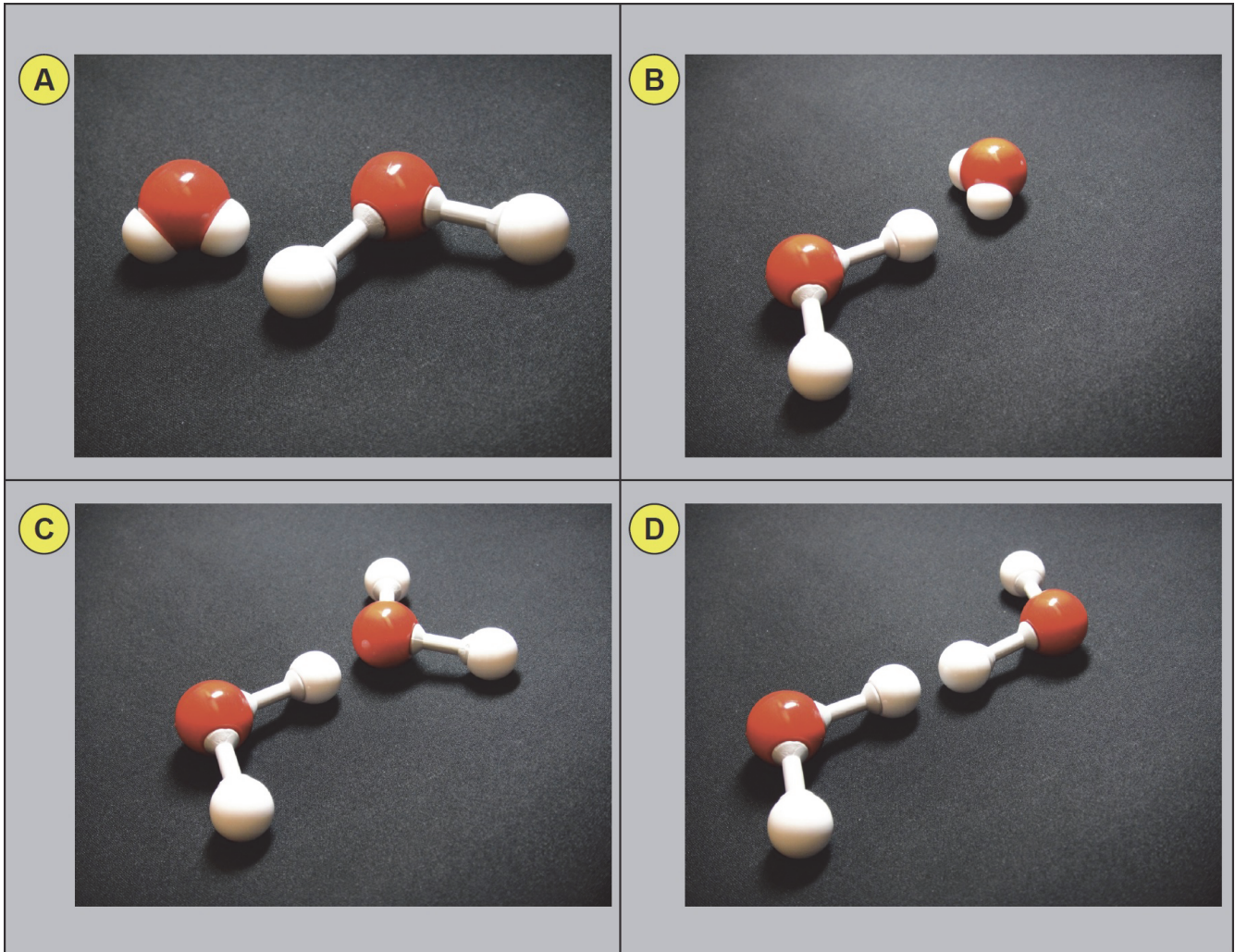**Figure 1. Representational models of the amino acid tyrosine.**

Figure 2. Representational models of water and its interaction with tyrosine.
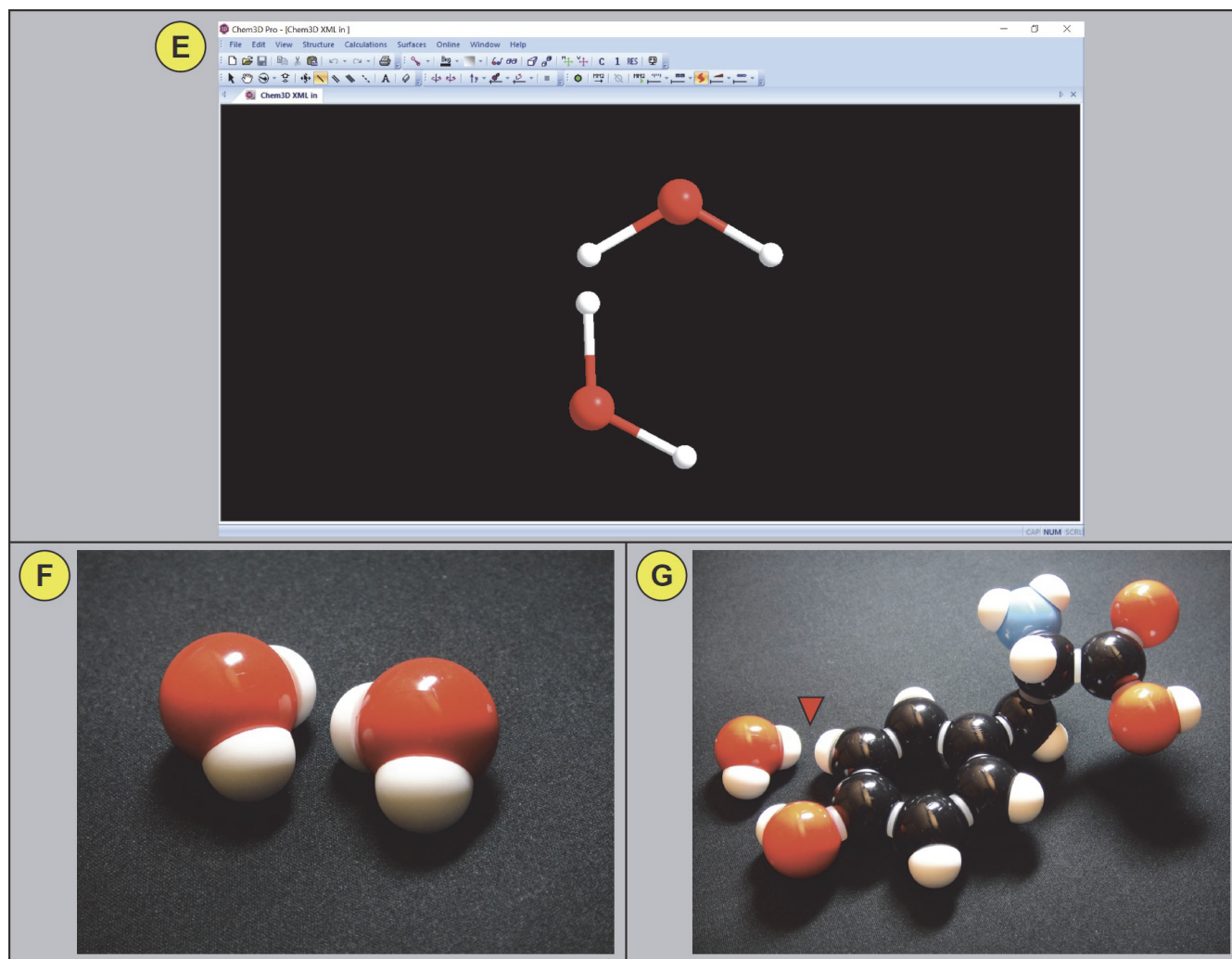
Figure 2. Cont'd.