STEREOSCOPIC 3D VERSUS 2D INTERACTION WITH A HAPTIC BIOMOLECULAR VISUALIZATION

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Molecular visualization is a crucial feature of learning progression in molecular biosciences. This is closely linked with learning about fundamental molecular recognition processes such as protein-ligand binding, which relies on grasping the importance of spatial molecular properties. Surface shape is pivotal for molecular recognition in terms of chemical and spatial complementarity, steric hindrance, molecular conformations, and distances between molecules. However, little is known about the impact of 3D stereoscopic vision on students’ understanding of complex biomolecular interactions. This study investigates tertiary students’ interaction with an immersive visualization. In addition to a visual representation of molecular structures, the studied system also represents intermolecular forces via force feedback. The effect of stereoscopic vision (termed “3D” here) on interaction and learning was examined by an experimental comparison between a 3D and a 2D condition. Data collected included pre- and post-tests, logged interaction data generated during performed docking tasks, and group interviews. Preliminary results indicate that students in the 2D condition tended to rely on a “ball-and-stick” mode of protein representation, while students in the 3D condition used other modes. The 3D group tended to ‘zoom in’ closer to the molecules, while the 2D group spent more time actively moving molecules. Written and verbal responses indicate that students may gain a more complex understanding of protein-ligand docking from using the system, and that 3D vision may complement understanding of molecular interactions.

Keywords: Representations, Dynamic Visualization Tools, Computer Supported Learning Environments

INTRODUCTION

Molecular visualization is a crucial feature of learning progression in the molecular biosciences, and tools such as PyMOL and Jmol are widely adopted in teaching. Apart from visual perception, the haptic sensory modality combines the kinaesthetic and cutaneous sensory pathways. In the molecular life sciences, computer interfaces that combine visual and haptic feedback have been developed since the 1960’s (Brooks, Oh-Young, Batter, & Kilpatrick, 1990). Research on the potential benefits of such visuohaptic interfaces on student learning has only recently been initiated (Jones, Minouge, Tretter, Negishi, & Taylor, 2005). Molecular recognition is a fundamental concept in molecular life science. One important example is protein-ligand binding, where surface shape is important for molecular recognition in terms of chemical and spatial complementarity, steric hindrance, molecular conformations, relative sizes of objects and distances between objects. Understanding these properties is crucial for learning about molecular interactions.

This work uses a recently developed desktop virtual reality system (MolDock) that provides a visuohaptic representation of biomolecular interactions (Fig. 1). Whereas our previous work has shown conceptual differences between haptic and no-haptic experiences of biomolecular interaction, little is known about the cognitive and conceptual impact of 3D stereoscopic visual representation in this area of molecular visualization technology. The aim of the study was to investigate any differences between students’ interaction with visuohaptic biomolecular visualization in a stereoscopic 3D and a 2D condition.
Figure 1. Components and features of the MolDock system. A: The user interacts with a hand-held haptic device. B: Stereoscopically viewing the interaction between a protein and ligand molecule. C: Various modes of representation of the biomolecules can be viewed – in this case both are in ball-and-stick mode. The haptic device (A) is used to choose available menu options, to move, zoom and rotate the molecules in virtual space, and to experience the force feedback corresponding to the interaction (C).

METHOD

Participants and Study Design

A total of 22 students (16 female and 6 male, mean age 25) participated in the study as part of a Masters biotechnology course at a Norwegian university. Random assignment into two experimental conditions (3D and 2D) involved creating matched pairs of students based on spatial ability (Bodner & Guay, 1997).

Data Collection and Analysis

A pre-/post-test targeted students’ perceptions of the binding process, molecular visualization, and conceptual understanding of non-covalent bonding. Captured data also included logged information about states of the system (e.g. position of protein and ligand, calculated intermolecular forces, activated visual representations, and interaction with menu artefacts). The study commenced with the pre-test followed by interacting with MolDock where students worked individually for 30 minutes. The session consisted of a task sequence requiring students to interact with the visualization to deduce optimal protein-ligand interactions (Fig. 1). Examples included locating an area on the protein surface where a ligand is likely to bind, and to compare how strongly two ligands bind based on experienced haptic forces. After completing a post-test, students rated perceived difficulty and cognitive load required to solve the docking tasks on a nine-point scale. Four weeks later, discussions were conducted in groups of 3-6 students, where students reflected on their experiences with the system. Quantitative and qualitative methods adopted in our previous work (e.g. Schönborn, Bivall, & Tibell, 2011) were used to mine the data logs and perform thematic analyses.

RESULTS AND DISCUSSION

Understanding of Biomolecular Interaction before and after Interaction with the System

An example of a student’s pre- and post-test responses regarding protein-ligand binding was as follows:

“As it [ligand] comes closer to its designated enzyme, the enzyme changes its conformational state and the active site becomes visible. Through electrochemical force it is dragged into the now suitable active site and locks into the enzyme...” [Pre-test, 3D, C6].

“As the ligand closes into the protein there is an abundance of trial and error in order to correctly manage to find its way into the binding site. An abundance of interactions is causing the ligand to shift and turn in its attempt to properly bind. If it is not properly structured before making its way into the active site, proper binding is most difficult, and it will likely result in a weak interaction... When at last bound, one can really see how the term "key and lock" describes it...” [Post-test, 3D, C6].

As opposed to initially perceiving a ligand as being “dragged”, and “locked” into an active site, the student shows a more intricate interpretation that incorporates the stochastic nature of the biomolecular interaction.
Interaction with the Visuohaptic System during the Task

Table 1 presents data obtained from students’ direct interaction with the haptic device to move molecules (by engaging a stylus button), zooming activity, and relative interaction activity with protein representations.

<table>
<thead>
<tr>
<th>Group</th>
<th>Molecular interaction activity (%)</th>
<th>Zooming</th>
<th>Proportional interaction activity with protein representations (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Space-fill</td>
</tr>
<tr>
<td>3D</td>
<td>19.5</td>
<td>1.336</td>
<td>17.4</td>
</tr>
<tr>
<td>2D</td>
<td>25.7</td>
<td>1.178</td>
<td>1.3</td>
</tr>
</tbody>
</table>

In comparison with the 3D condition, students in the 2D condition spent a greater proportion of activity on moving and rotating the molecules, and the 3D group tended to ‘zoom’ closer. While the 3D group varied their viewing of different modes of protein representation, the 2D group relied mostly on the ball-and-stick representation. The ball-and-stick representation was the preferred mode of representation in both groups.

Group Discussions following Students’ Interaction with the System

Examples of responses obtained during group discussions were as follows:

“I could feel different forces, but… when I placed the substrate or the ligand, I saw it in 2D, when I turned the protein and the active site, I saw that I was actually far away from the active site, and it took a long time before I could get into the active site. I guess that if I experienced it in 3D I maybe would have got a different point-of-view from all the forces…” [2D, A7, 18:55-19:51]

“…It also depends what [re]presentation you have of the protein […] I used sticks most of the time and what you could see on the protein isn’t always the same as your experience of what you feel when you move it around… I zoomed a lot in and out… that was very cool to be able to zoom into the protein… you had an overview of what was there…” [3D, C8, 26:31-28:17].

The first utterance indicates how perceived tactile feedback was not always in congruence with visual interpretation of ligand position, which provides evidence for combining 3D visual and haptic modalities. The second utterance reflects students’ engagement of the ‘zooming in’ function during the 3D experience.

CONCLUSION

Results suggest that although experiencing 3D is associated with a higher degree of visual feature use (i.e. representations and zooming), it may decrease a user’s direct manipulation of molecules. Qualitative analysis indicates positive changes in understanding the stochastic nature of biomolecular interactions.

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REFERENCES


