CoVis-AR: Visually analysing COVID-19 variants in augmented reality

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Abstract: The recent COVID-19 pandemic had global health implications and sparked an unprecedented response from a broad range of scientific disciplines to mitigate implications of the virus. Data science played a significant role in analysing the vast amounts of data that were created by laboratories globally. Making sense of large databases and spreadsheets is often prohibitive though in understanding the behaviour of the virus especially given that it was novel and largely unexplored. To enable visual reasoning for scientists and other decision makers we previously developed an online web application called COVID-19 Visualiser, or CoVis, that facilitates investigating differences between structural proteins in COVID-19.

CoVis was designed to facilitate understanding of viral replication with a specific focus on COVID-19 variants. The interface was designed to be accessible to a broad range of end users with different levels of technical and scientific experience. Models are proportionally accurate with all point mutations highlighted and can be interacted with through rotation and zooming. Advanced information is accessible through a range of peripheral displays that can be hidden when not needed to minimize visual clutter. While CoVis provides useful insight into COVID-19 mutations it is limited in visually comprehending the 3D protein structure due to its 2D representation on screen.

Immersive technology such as virtual and augmented reality (AR) provides means to further leverage of the 3D perception of the human visual system. In the context of 3D model analysis this can prove valuable in gaining a better understanding of the model structure. We therefore more recently developed an AR extension referred to as CoVis-AR that can be enabled when using CoVis on a handheld device with a camera, such as a tablet or phone. In AR mode, the protein model is projected on a real-world surface as shown in Figure 1. The user can move around the model and use the same manipulations as in CoVis (rotate and zoom) in addition to moving the model around in space. The information displays are omitted as this mode is aimed for users to focus on understanding the 3D structure of the protein. In addition to the handheld device version of CoVis- AR we developed a HoloLens2 version, which provides the additional advantage of not having to hold a device in the user's hand. Thus, both hands can be used for interaction with the 3D model leading to an even more immersive experience of the 3D model structure.

Figure 1. View of an alpha spike protein model in CoVis-AR

We have not conducted formal user studies yet to evaluate CoVis and CoVis-AR but consider to do so in the future. Initial feedback from a couple of colleagues across CSIRO has been very positive though and value has been seen in using both the CoVis and CoVis-AR systems.
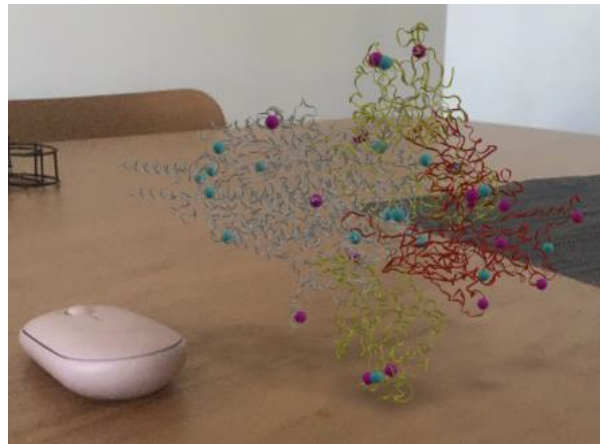
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