HYDRA:

A WEB-BASED VISUALIZER FOR HIGH-THROUGHPUT LIGAND DOCKING ANALYSIS

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Project Overview

- This project aims to create a browser-based program that can simultaneously display many molecular interactions in a dynamically sized grid of molecular viewers.
 - Simulated interactions will be obtained from high-throughput simulation programs.
 - Yuan Zhao, a former student of Dr Haga's, previously created the framework for this program in Webix, a JavaScript library, and HTML5/CSS.
- This will enable almost any device with internet access to be used for data analysis with no end user setup.
- My specific focus will be on creating a functional graphical user interface (GUI)

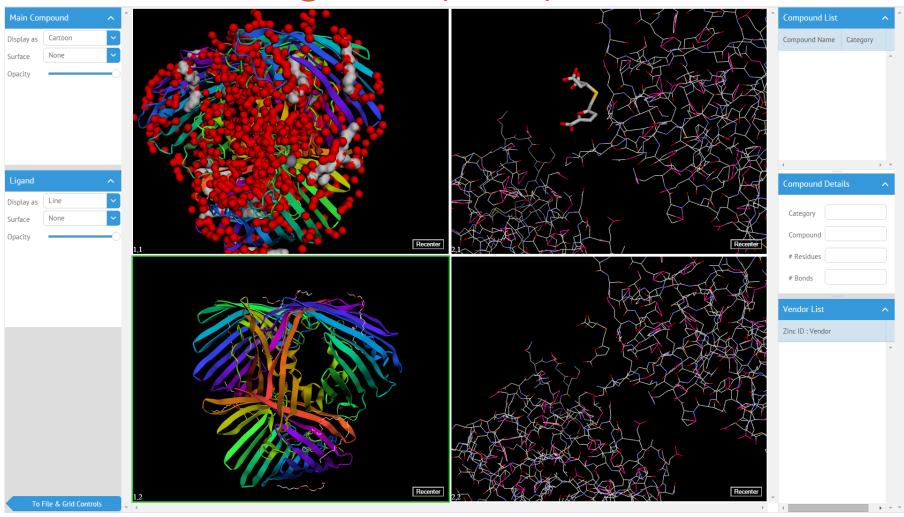
Week 6 Progress

- 30 July Met with Dr Haga, Ichikawa-sensei, Watashiba-sensei, and collaborating student Shelby Matlock
 - Discussed progress and future direction
 - Feedback on Shelby's poster and paper drafts
- Added styling to the "active viewer"
 - The border around the last clicked viewer now turns lime-green to mark which viewer the compound controls will target
- Many bug fixes with 3Dmol viewers and the Webix GUI
 - Currently working with the 3Dmol developer to fix a final issue with deleting molecular surfaces from the viewers
 - Have applied a temporary patch until this is resolved within 3Dmol.js

Week 6 Progress (cont)

- Added distinct display settings for ligands
 - Ligands are identified by the 'HETATM' tag in .pdb files
 - The alternative method of identifying ligands in .pdb files involves setting them as a different "chain" (eg chain "B" if the main compound is chain "A"). However, this will not be supported as it does not have consistent implementation
 - With the exception of the "cartoon structure", all the display settings available for proteins may also be applied to ligands
- Changed mechanism for switching between panes in the left panel
 - Replaced the tabbed view
 - Clicking a single button on the bottom will now switch between the panes. Currently uses a sliding animation

Week 6 Progress (cont)



Development snapshot: The same files are loaded on the top and bottom with different ligand settings. As marked by the green border, the bottom-left viewer is currently selected.

31 July 2015

Week 7 Plans

Implement

- Script to process the raw output of molecular docking programs
 - Protein and ligand models may be in separate files
 - Ligand atoms may not be formatted with the 'HETATM' tag
 - Will add option to allow user to batch upload raw output files and have them processed
 - This will streamline usage of Hydra for the average user
- Pull fixes to 3Dmol.js into Hydra

Investigate

 Saving lists of compounds for future study or for simple record keeping

Plans for the remaining weeks

- The essential functionality of Hydra has now been successfully implemented
 - Models can now be uploaded and have their display settings adjusted
 - Notably, Hydra has also been made more computationally efficient by processing files asynchronously and by replacing GLmol with 3Dmol
- Areas to improve:
 - Allow Hydra to handle the raw output of molecular docking simulations to reduce work required of the end-user
 - Potentially allow users to save lists of compounds
 - No longer quite as necessary since Shelby Matlock's work links compounds uploaded to Hydra directly to manufacturers
 - Add JSDoc style comments to each function
 - Will aid future developers and debugging and will streamline documentation generation
 - Write more detailed documentation and usage instructions

Exploration

Clockwise from the near right:

Omukae Dolls at
Tenmangu Shrine;
Moyōshi-Taiko
ceremony before the
procession of floats
at Tenjin Matsuri;
bustling Tenjinbashi
2-Chōme; friendly
ceremonial ox; view
of Tenjin Matsuri
fireworks from
Keihan National
Highway



Exploration



Counter-clockwise from above:

Namba Parks at night; Tenjin Matsuri Fireworks; Namba Parks statue; noodles and tempura dinner set; on the bridge leaving the Tenjin Matsuri fireworks area (it was like a military evacuation in the movies)

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