

Virtual Screening Procedure

- First, I transferred the files to Bridges using sync_virtual_screen.sh
- Then, I logged onto Bridges and executed the command `sbatch vina_multithread.job`
- Next, I transferred the results to my own computer using sync_virtual_screen.sh
- Finally, I performed some preliminary analysis on an ipython notebook, AnalyzeVS.ipynb, also exported to html format.

References

- Awale, M.; van Deursen, R.; Reymond, J.-L. MQN-Mapplet: Visualization of Chemical Space with Interactive Maps of DrugBank, ChEMBL, PubChem, GDB-11, and GDB-13. *J. Chem. Inf. Model.* 2013, 53 (2), 509–518. <https://doi.org/10.1021/ci300513m>.
- Cross, J. B.; Thompson, D. C.; Rai, B. K.; Baber, J. C.; Fan, K. Y.; Hu, Y.; Humblet, C. Comparison of Several Molecular Docking Programs: Pose Prediction and Virtual Screening Accuracy. *Journal of Chemical Information and Modeling* 2009, 49 (6), 1455–1474. <https://doi.org/10.1021/ci9000056c>.
- [Morris et al, 2008a] Presentation: Using AutoDock 4 for Virtual Screening (Handouts, PDF document, 1.1 MB)
 - <http://autodock.scripps.edu/faqs-help/tutorial/using-autodock4-for-virtual-screening/VSTutorial2.2008.pdf>
 - This presentation also describes some virtual screening success stories
- [Morris et al, 2008b] Instructions: Using AutoDock 4 for Virtual Screening (PDF document, 464 KB)
 - http://autodock.scripps.edu/faqs-help/tutorial/using-autodock4-for-virtual-screening/UsingAutoDock4forVirtualScreening_v4.pdf
- Sterling, T.; Irwin, J. J. ZINC 15 – Ligand Discovery for Everyone. *J. Chem. Inf. Model.* 2015, 55 (11), 2324–2337. <https://doi.org/10.1021/acs.jcim.5b00559>.