**Demo (Windows 10)**

* Tutorial to do re-docking, cross-docking, lead-optimization. Manually (build and) protonate a **small set** of compounds for evaluation.
* All the ligands and receptors must be protonated before subjected to docking
* From now on, use .sdf instead of .pdb to store ligand coordinates. This help to keep the correct bond order and allow direct usage of molecule files downloaded from externa molecular databases.

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| Select pdb for cross-docking |  |
|  |  |
| Retrieve receptor pdb for cross-docking. |  |
| Alignment of reference pdb receptors |  |
| Save aligned receptor (no H) |  |
|  |  |
| Pdb2pqr and restore metal  Save the pdb in “receptor” (change format to mol2/sdf?) |  |
| Mini-screening for similar ligands (PDB) and download ligand sdf |  |
| For the re-, cross-docking ligands and small set of similar ligands on PDB, manually fix protonation. |  |
| Build a new ligand or two |  |
| Save all the ligands as sdf in “ligand” |  |
| From the aligned reference pdb, choose the ligand of largest molecular size and save it as reference.sdf in a directory a level on top of “ligand” and “receptor” |  |
| Copy scripts from scripts/standard |  |
| Do the necessary modification |  |
| Check the directory tree |  |
| Run the calculation |  |
| Visualize the output |  |
| Analysis |  |
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| Usage of the current protocol |  |
| Summary of the practical workflow |  |

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| Further Discussion |
| Pros and cons of the current protocol  Tedious when you need to work on a large dataset  Why the virtual screening protocol in the next exercise |

Reference