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| * **draw the substrate and product molecules of your molecular system using any chemical drawing tool. For example, Maestro.** * **Run QM calculations to obtain the RESP charges. You can use any QM program, but here are some examples on how to do it with GAMESS or Gaussian – done with maestro** * **Generate the parameters with antichamber for the OPLS force field (of course it will depend on the FF you use in your calculations), including the charges.** * **convert into ffld – (convert all maestro files in ffld) - You will obtain an ffld file with the ffld\_server program in Maestro and you keep it for later.** * **Install VMD, Maestro** * **Running EVB** * **get Q6. Compile it and get the executables.** * **get also the qtools package to help you with running the simulations. Check the tutorial within the package to learn the different steps. Qpyl is difficult to use and develop, but qscripts-cli are very useful for setting up your simulations - check python 3 – github, check manual for Q, check q slides** * **convert FFLD parameters into Q format using q\_ffld2q.py file in qtools.** * **You will get the prm and lib file, needed for Q for each molecule in substrate and products. When running Q you will need a single .prm file but you can still have the different .lib files for each molecule.** * **(lib (topology) and prm file (parameter, force constants being added to the ff, except the charges) for running the simulations) add now water molecules around your system.** * **Check the gas simulation file**   **STEPS:**  **Prepare – pdb, charges, product, substrate, (ffld, lib, pdb, prm, prm.chk)**  **Relax – pef, relax (10)**  **Fep – replicas (10)**  **Calibration – qplots for all replicas (fep analysis)**  **Convergence - Equilibration steps, Constraints types and magnitudes, Sampling time per window, Number of replicas, Initial lambda step** |

a python library to visualize data. See examples here <https://matplotlib.org/2.0.2/gallery.html>

**What you need to get is the data to plot, and then such data can be plotted with python+matplotlib, with R, or with any graphing software. For example, in cygwin you will find gnuplot, which is the historical tool to plot things from unix/linux. It is pretty straightforward once you have a file with data in CSV format.**

**Let us start with something and you will get used to it. For example, try to plot the energies from the EVB calculation as a function of any parameter that gives your idea of the progress of the reaction. Check the energy files and try to understand their structure and the information they contain. Then use any of the named tools to plot the graph of the reaction coordinate you choose vs energy**

Find here a pretty neat paper on EVB application by a group different than warshel’s, which helps understanding better how to use it. the objective is to get plots like those in figure 4 of the article <https://www.researchgate.net/publication/301246394_Insights_into_enzyme_point_mutation_effect_by_molecular_simulation_Phenylethylamine_oxidation_catalyzed_by_monoamine_oxidase_A/fulltext/5b48fef245851519b4b8561f/Insights-into-enzyme-point-mutation-effect-by-molecular-simulation-Phenylethylamine-oxidation-catalyzed-by-monoamine-oxidase-A.pdf?origin=figuresDialog_download>In the meanwhile, try to plot any parameter that can give you an idea of the reaction coordinate vs the energy (for example, vs E1 or E2, which refer to reactants and products. These kinds of plots will help you understanding the MD runs