URAP CA and mouse pods: plans for fall semester 2018

Each pod is now aiming for a major paper that will include new data, include some mixture data, have an experimental biologist as first author, could perhaps be widely read in the radiobiology community, and might lead to further substantial papers. The basic computational approach to both papers is in principle very similar. What follows describes some corresponding coding plans for Fall 2018 and beyond.

1. The mouse Monte Carlo code takes less than 10 minutes to run even for 500 sample paths and multi-ion mixtures. First priority for the CA pod is making the Monte Carlo about that fast. Edward is working on adapting to the CA data the methods he, Yimin, and Peter used to speed up the mouse Monte Carlo.

2. The mouse code is modular: data is entered and passed to a synergy modeling script which makes the one-ion models and does the synergy calculations. The results are passed to a Monte-Carlo script, which in turn passes its results to a plotting script which does nothing but make graphs and some numerical output. The modularity makes the calculations much easier to adapt to new needs. In the long run the same modularity will be needed for the CA script, though for the moment that still has fairly low priority.

3. While entering mixture data I realized that one-ion data and mixture data should be in 2 different data bases. One-ion data is needed for almost everything we do. Mixture data will be used only in the plotting module.

4. Edward: My plan is to use 2 separate excel .csv files, have the data_and_info module turn them into separate dataframes, pass the 1-ion data to the synergy module as now, but have data_and_info pass the mixture data directly to the plotting module, leapfrogging over the synergy and monte carlo modules. Then the flow is no longer strictly linear but modules do often have multiple output assignments so that seems OK to me. Do you agree?