Notes for Tumor Extraction Part

Main idea

Think of the procedure as split into two separate parts 1. Tumor Extraction -
Find separate tumors (90% done) 2. Tumor Pairing, within samples (0% done)

Things that Remain to be done for Tumor Extraction

1. Flip y-axis in graphical output, is erronously oriented.
2. Make sure that multiple arguments can be passed (nargs and "*" usage)
3. Change name of graph function
4. Returns error when having no input file, must fix this. Left "TODO" in
   code for marking
5. Coloring is weird when no tumor spots are present
6. Make sure that original tumor annotation is left in output for those regions
   that are "masked" out, incase of invasive spread out we still want to be
   able to use these for analysis
7. Include replicate and patient in input files.
8. Do not make dependent on patient name, remove regexp and replace with
   simple input handling

Things to be done for Tumor Pairing

1. Decide if this is to be separate or included in analysis
2. Need a way of aligning and pairing up tumors
3. One idea is to minimize the following objective function $\min v_i A u_j \quad \forall \quad i,j$