



## Announcements

### Some tips for HW10:

Posted on: Monday, December 1, 2014 12:26:35 PM EST

Tips for getting your program to run faster:

1. We slightly changed line 6 of the simulated annealing pseudocode to eliminate the "max" function --- this will make your programs run faster.
2. In the simulated annealing code, if you find a new structure with the \*same\* energy, don't switch to it.

Tips for making the code easier to write:

3. For the drawing (201 extra credit; 601 required): you can use any format you want for the drawing so long as it shows the structure in a reasonable way.
4. The data structure the solution uses for laying out the fold is `[] []string`. Then `M[x][y]` lists all the residues that are in that position (if crossings are allowed). You can use `strings.Contains(M[x][y], "H")` to check if a cell position contains an H amino acid.
5. If you'd prefer, you can simply reject structures that have crossings (i.e. they have infinite energy)
6. Don't try to track which amino acids are adjacent to one another. Rather, lay them out in a 2d array, compute the score ignoring which residues are adjacent in the walk, and then subtract 2 for every H in the middle of the sequence, and 1 for every H at the ends of the sequence.

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Posted to: F14-  
Programming for  
Scientists