Due: September 21, 2018 **Homework 1** CPSC 475/BENG 475

In this assignment you will use MATLAB to explore ideas from class. **Important:** please use the attached file `hw1answer.m` as a template. Before submitting, make sure your file can be *publish*ed without any errors.

Image manipulation: the image as a matrix

1 a Open the image `Paolina.tiff` with `imread` and convert it to a matrix with double precision numbers (`im2double`). Display the image with `imshow` and with `imagesc`. What is the difference between the two visualizations? (If you want to compare the images side-by-side, you can use the `figure` function to open multiple figure windows, or create two subplots side by side. Also, it might be a good idea to refer back to the MATLAB tutorial script.)

— b Plot the image level sets using the `contour` function. You will need to adjust the axes by typing `axis ij`. This is the image coordinate axis in which the y-axis decreases from top to bottom, opposite to the default direction `axis xy`. Comment briefly on what you see. What does the `contour` function do?

— c Display the gradient vector field for the image (use the `quiver` function, as well as `axis ij` as in b). Use the zoom tool in the figure window to zoom in on the vector field around the nose until you can see the direction of individual vectors. Explain briefly why the length and directions of the vector are what they are in this region. You may use the `gradient` function to calculate the gradient, but be sure you understand what it's doing!

— d Compute the image gradient magnitudes (lengths of the gradient vectors) at each image location as the matrix `gmag`. The magnitude (length) of a vector $\mathbf{v}$ is given by the formula

$$\|\mathbf{v}\| = \sqrt{v_x^2 + v_y^2}.$$

Display `gmag` in color code with `imagesc`, and comment briefly on what information this

image conveys. What do the gradient magnitudes tell us?

A. coli

Make sure you have `acoli_hist.m` in your working directory. Use `help acoli_hist` to figure out how to invoke it. Note that the `acoli_hist` function returns multiple outputs (the histogram, and the ground truth food function). To get both, you will have to supply two output variables! In other words, your call to `acoli_hist` should resemble `[histm, food] = acoli_hist(...)`.

When visualizing histograms or food functions, you can either use the `imagesc` function (be sure to use the `axis xy` command to display the images rightside up), or the `surf` function (to remove the annoying grid lines, write `surf(histm, 'EdgeColor', 'none')`).

2 a In your simulations, A. coli will move through an environment where the food concentration is fixed over time and is a smooth function of the position coordinates; we can write it as $f = (x, y)$. Visualize food function 1 in three different ways: using `imagesc`, `surf`, and `contour`. Then, do the same for food function 2. What is the main difference between the two?

— b Now display the gradient vector field for food functions 1 and 2 using the same procedure as in 1-c. Comment on the results.

— c Using food function 1 (you can pick the starting location), experiment with different values for the run-to-tumble (`rttp`) and tumble-to-run (`ttrp`) transition probabilities. How do they affect A. coli's behavior? In particular,

- what happens when both are low?
- both are high?
- one is high, the other low?

· either one of the probabilities is 0?

To see the behavior of A. coli during the simulation, set the `visualize` parameter to true. (Note that if you want to abort a long-running MATLAB command, you can use CTRL+C.)

— d Given your results from part c, what are good values to pick if your goal is to maximize the average value of the food function seen by A. coli over a long period of time? Why?

— e Using an initial position of $(0, 0)$ for A. coli, try running the simulation several times on food function 2, using the values chosen in part d. Could different values do better for food function 2? Why or why not? If you find values you think are better, confirm this empirically by calculating the average value of the food function seen by A. coli over 50 runs with 300 steps each, for both the old values from b and your new values. (Hint: You can calculate this average easily using only the `histm` and `food` matrices.) For the purposes of calculating the average, you may either pretend the food function is zero outside the area covered by the `food` and `histm` matrices (underestimating the true average), or simply ignore any steps that occur outside this area (overestimating the true average).

— f For some choice of parameters, use `acoli_hist` to obtain histograms with 10, 50, 100 and 500 bins along each axis. Plot the histograms with `imagesc` (use `axis xy`). Describe the relationship between the number of bins used and the resulting histogram. Are more bins better?

— g Would happen if we used the Paolina image as the food function for A. coli? What would determine the amount of "food" in this case? Choose an initial position for A. coli and describe what you expect its trajectory to be like, if you used the optimal parameters found in e.