SBf12, Assignment 1 Solutions

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1 Problem 1

There were many different answers to these questions. Here are a few from the class (used with permission):

1.1 Part (a) from Nathan Olson

According to the article "Synthetic Biology Moving into the Clinic", synthetic biology could be used to decrease the virulence of cholera. Cholera bacteria produce less toxins at high population density. The cholera bacteria could be tricked into thinking there was a high population density by a harmless engineered organism that lives in the human gut and produces the signaling molecules that the cholera bacteria use to determine population density. The cholera bacteria would act as if there was a high cholera density and decrease toxin secretion.

1.2 Part (b) from Julianus Pfeuffer

When it gets to biofuels, it is the algae that the synthetic biologists put their focus on. These single-celled organisms can grow very fast, in many different kinds of water and produce oils for biodiesel which contain much more energy than bioethanol from plants like corn.

The problem with algae is that although they are not highly fastidious organisms, it is hard to get the oil out of them, once it is produced. In deep water, you have to process a tremendous amount of water per liter oil, which is very expensive. In shallow water however you have to face the issue, that the algae are living together in a small volume and therefore are often shading each other, causing them to be much less productive because of the missing sunlight for photosynthesis.

Additionally, you have to fight viruses or bacteria infecting the algae. But the algae are not only affected by other species, since they compete among themselves. Their light absorbing antennas are consuming much more light than they need for photosynthesis just to get an advantage over the other cells, which leads to lesser productivity.

Then, algae are limited in the amount of oil they can keep in their cells. Natural, i.e. unengineered algae strains can only produce oil up to 40% of their weight which is limiting the production again. [2]

1.3 Part (c) from "Anonymous SBf12 Student"

I didnt notice a lot of personal recommendations from the authors, but the policy review article mentioned one interesting regulation: the screening of polynucleotides (DNA custom-made to order) for potentially dangerous sequences, such as the genes of extinct but deadly pathogens. I think this is a reasonable precaution that would prevent the majority of students from acquiring potentially dangerous DNA. However, I doubt it would be an effective deterrent for someone who is truly dedicated. For example, it would be possible to order such genes in very small pieces (perhaps flanked by introns), with randomized codons, and from different vendors, without any simple alignment software spotting their potential danger. In addition, the price of DNA synthesis may eventually decrease to the point where a personal synthesis machine is easy to obtain, limiting governmental oversight.

2 Problem 2

Screen captures shown in Figure 1.

Here is a well detailed description of *edge.gro* from class (used with permission):

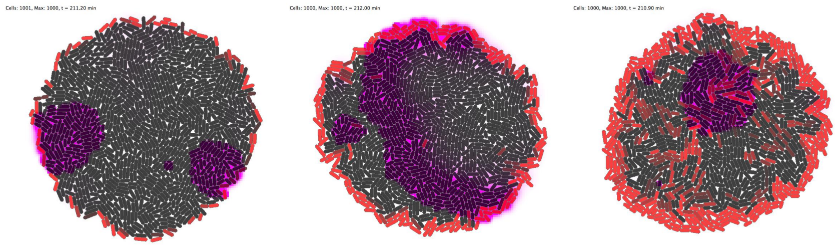
2.1 Solution text from "Anonymous SBf12 Student"

The intent of this program is for the ecoli cells that form the outer edge/perimeter of the colony to glow with rfp.

- The program begins by defining a few key parameters: wave emit rate, refraction period, detection time, signal emit magnitude, signal detect threshold for wave, and signal detect threshold for edge detection. It also declares a new signal of molecule ahl with diffusion and degradation rates of 1.
- To begin, we use the ecoli() command to create one ecoli bacteria at coordinates 0,0 in our grid, with which we associate the edge program so that the bacteria exhibits the properties defined in edge.
- In the edge program, we initialize a few parameters for the first cell of ecoli that we create: rfp is initially 0 and edge detected is initially false. We also initialize a recorder variable r.t to the value of refraction period. This is done so that we can control the variable in the program and use it as a local variable of sorts for control purposes; so we can keep track of the state of the program without worrying about gro degrading our variable upon cell division.

- The edge program is then constructed from a series of guarded commands that define the behavior of the cells. We start by randomly emitting the ahl signal. From here on, any cell that detects the ahl signal at a strength greater than 0.1 after a delay of 6 simulation time steps (refraction period), will itself emit ahl to propagate the signal through the colony of cells. If enough time has passed after ahl has been emitted (detection time), then the cells check the concentration of ahl theyre receiving. If this concentration is relatively low (below 0.2), then the cell assumes it is on the edge of the colony. If it has detected that its on the edge of the colony, then it increases production of rfp. If however, the ahl signal strength (concentration) that it detected was relatively strong, it determines that it is not on the edge and ,if it had previously been making rfp, degrades production of rfp.
- This is how the cells keep track of whether theyre on the edge of the colony or not.

Changing st from 0.2 to 0.3 in the program increases the threshold of edge detection for the ahl signal. The ahl signal, as it propagates outwards in a wave degrades over time. In the original edge.gro program a threshold of edge detection of 0.2 meant that if the cells receive the ahl signal and detect the strength of that signal to be 0.2 or less (relatively weak) then they can be sure that theyre far enough away from whoever first emitted that signal to be at the edge of the colony. When we increase the threshold to 0.3 in newedge.gro, the cells that read a signal strength of 0.3 (somewhat strong) or less now think that theyre on the edge, when in fact they are still somewhat closer to the center of the colony than the actual perimeter. This is why you see many more cells producing rfp in the newedge.gro program. In conclusion, in relation to the degradation rate specified for ahl, the refraction period of the wave, the magnitude of the ahl signal emitted, and the growth rate of e.coli; it seems 0.2 is the best ahl signal strength value to denote that a cell is on the edge of the colony. Below is a chart of the state of the cells with st=0.2 and st=0.3 at 200 cells, 500 cells, 700 cells, and at 1000 cells.


Cells: 1001, Max: 1000, t = 211.20 min
Cells: 1000, Max: 1000, t = 212.00 min
Cells: 1000, Max: 1000, t = 210.90 min

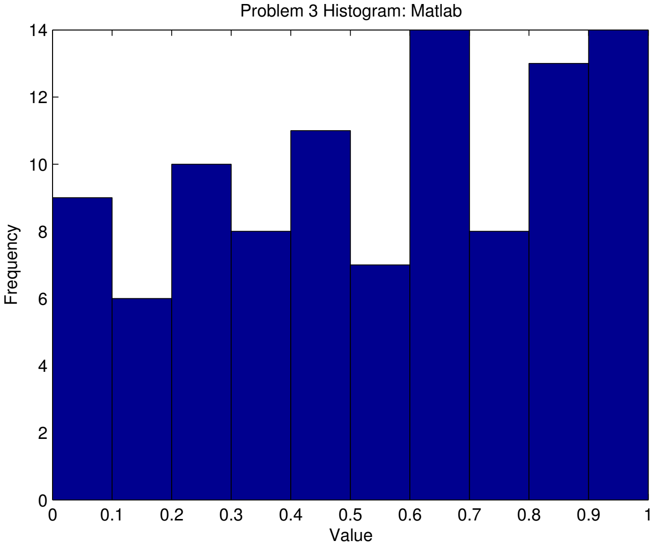
(a) $st = 0.1$ (b) $st = 0.2$ (c) $st = 0.3$

Figure 1: Screenshots of newedge.gro at 1000 cells for $st = 0.1, 0.2, 0.3$.

3 Problem 3

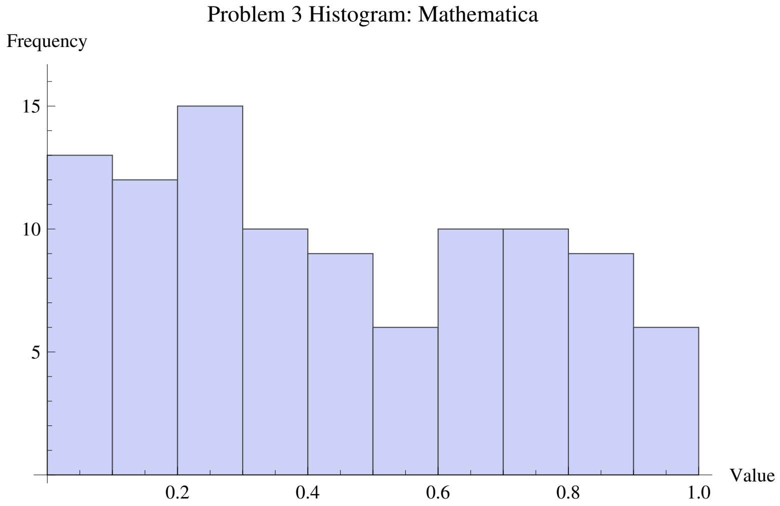
3.1 MATLAB

```
x=rand(1,100);
h=figure;
hist(x,0.05:0.1:1);
xlabel('Value');
ylabel('Frequency');
title('Problem␣3␣Histogram:␣MATLAB');
hgexport(h,'a1-3_matlab.eps');
```



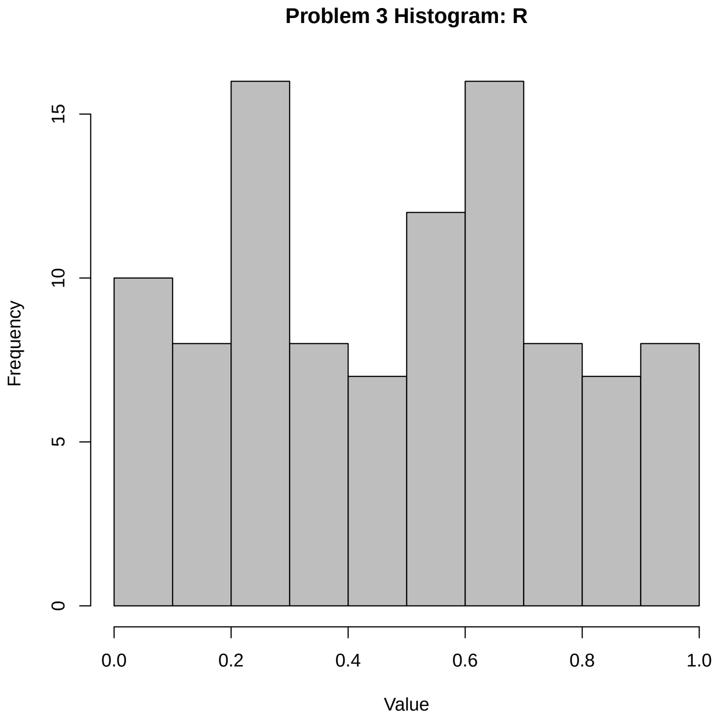
3.2 Mathematica

```
x = RandomReal[{0, 1}, 100];
h = Histogram[
   x, {0, 1, 0.1},
   AxesLabel -> {"Value", "Frequency"},
   PlotLabel -> "Problem␣3␣Histogram:␣Mathematica"
]
Export["a1-3_mathematica.eps", h]
```



3.3 R

```
x <- runif(100)
hist(
    x, breaks=seq(0,1,by=0.1)
    col=”grey”,
    xlab=”Value”,ylab=”Frequency”,
    main=”Problem␣3␣Histogram:␣R”
)
dev.copy(pdf,”a1−3_r.pdf”)
dev.off()
```



4 Problem 4: Extra Credit

Histograms illustrating rfp concentration per cell shown in Figures 2-3.

4.1 Modifications to *newedge.gro*

```
set("population_max",1001);
outfile := fopen("newedge_output.csv","w");

⋮

program main() := {
  L := {};
  stats("pop_size") >= 1000 & length(L) = 0 : {
    L := maptocells rfp/volume end,
    foreach l in L do fprint(outfile,l,"\n") end
  }
};
```

4.2 Generating histograms in Mathematica

```
data = Import["newedge_output.csv", "CSV"] // Flatten;
Histogram[data, 20, PlotLabel -> "Problem␣4:␣rfp/volume",
 AxesLabel -> {"Value", "Frequency"}]
Histogram[Select[data, # > 0 &], 20,
 PlotLabel -> "Problem␣4:␣rfp/volume␣>␣0",
 AxesLabel -> {"Value", "Frequency"}]
```

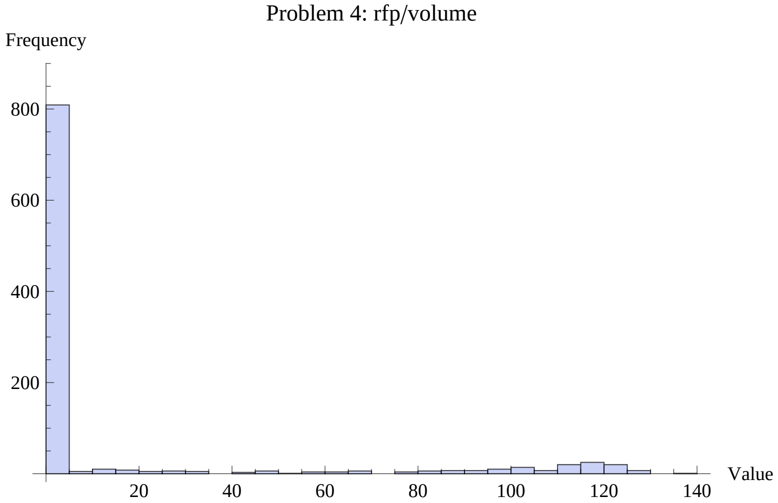


Figure 2: Histogram of $rfp/volume$ values at 1000 cells for *newedge.gro*.

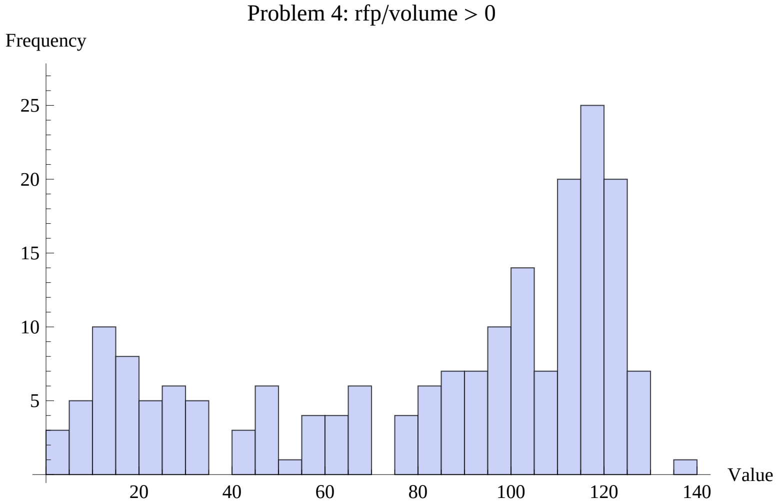


Figure 3: Histogram of nonzero $rfp/volume$ values at 1000 cells for $newedge.gro$