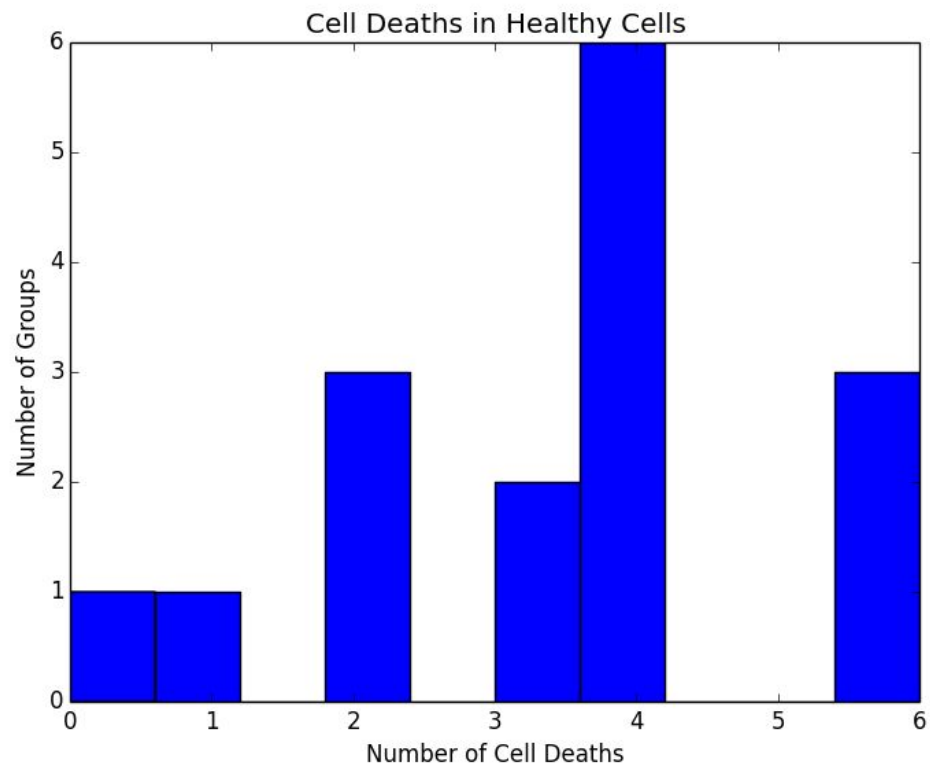


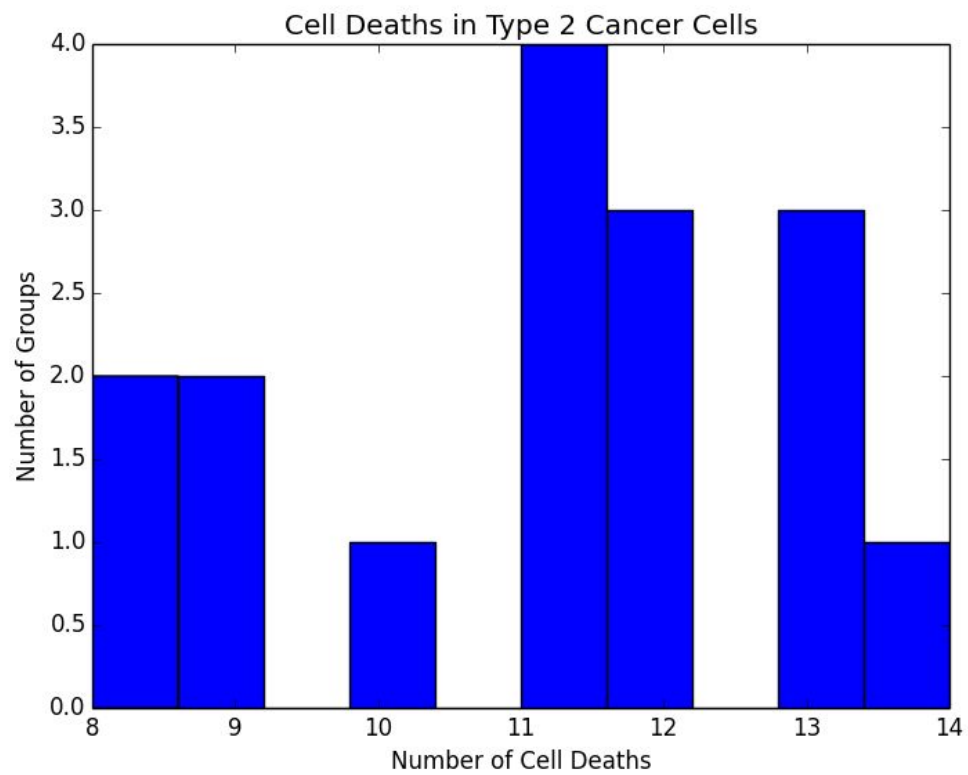
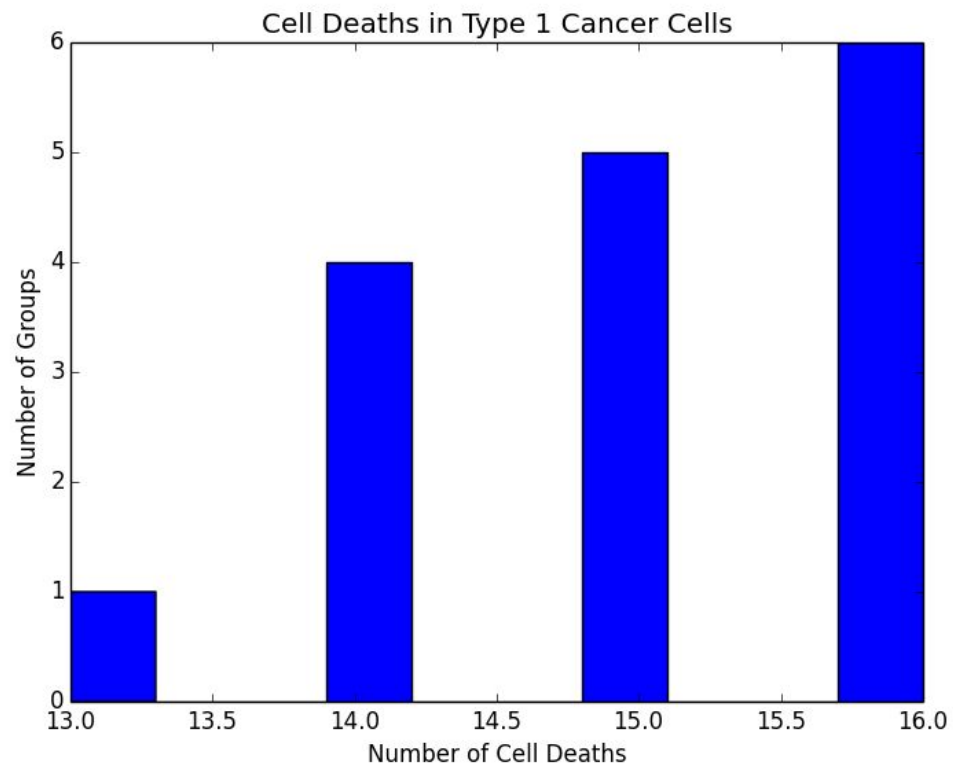
Bio Homework 9/10

- Shaan Chopra (2015090)

1. TRAIL (TNF-Related Apoptosis Inducing Ligand) is a cytokine that is secreted by most normal tissue cells. It has the ability to selectively trigger cancer cell death. It causes apoptosis primarily in tumor cells by binding to certain death receptors. A decoy receptor is a receptor that is able to recognize and bind to specific growth factors or cytokines efficiently, but it is not structurally able to signal or activate the intended receptor complex. It acts as an inhibitor, binding to a ligand and keeping it away from binding to the regular receptor. These decoy receptors participate in common methods of signal inhibition and are also abundant in malignant tissues.
2. Kinetic Monte Carlo Simulation: For the input file, we check the caspase 3 level after each monte carlo run (that is, 6th column of bottom row of each file). If the value is greater than equal to 50, which is the threshold value for the monte carlo simulation, then there is a cell death, else, the cell survives. This is how we carry out the kinetic monte carlo simulation. We count the number of cell deaths for 16 groups containing results of 16 MC runs (chosen randomly from the 64 given inputs of each type) for each cell type (healthy, cancer type 1, cancer type 2) and plot a histogram for each cell type.
3. Monte Carlo runs using bootstrapping is generated (16 groups with 16 MC runs) for each cell type. (See Code)
4. Caspase 3 level is used to determine kinetic Monte Carlo simulation as described in part 2. (See Code)

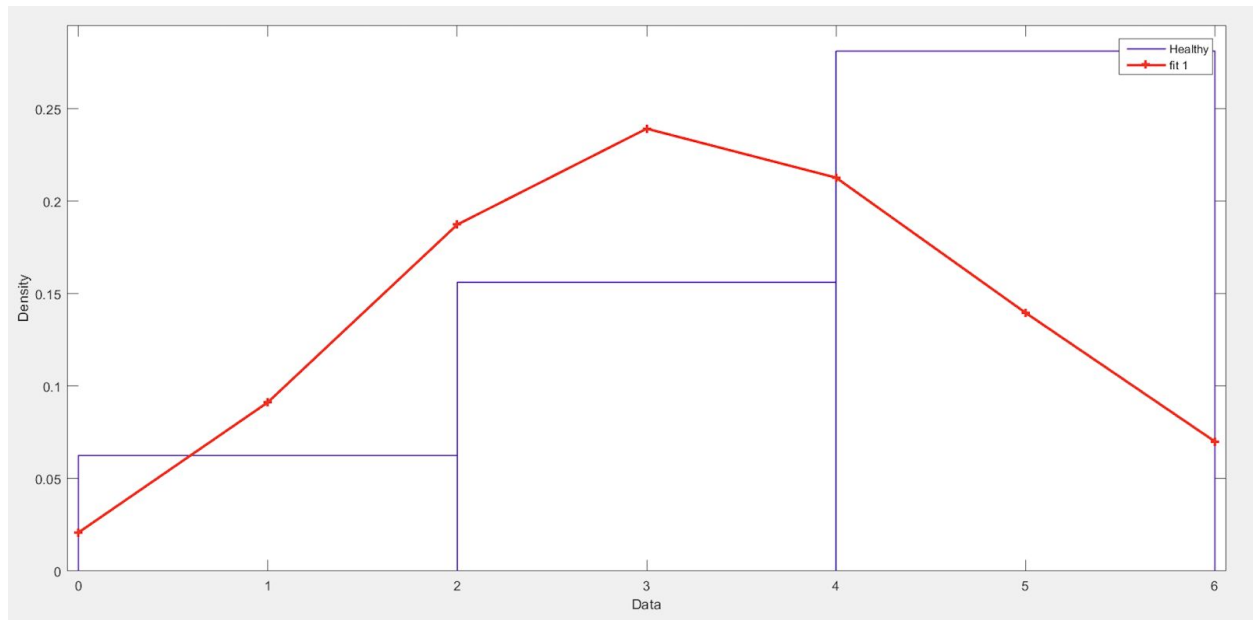
5. Histogram showing the number of cell deaths in each group for the 3 different cell types:



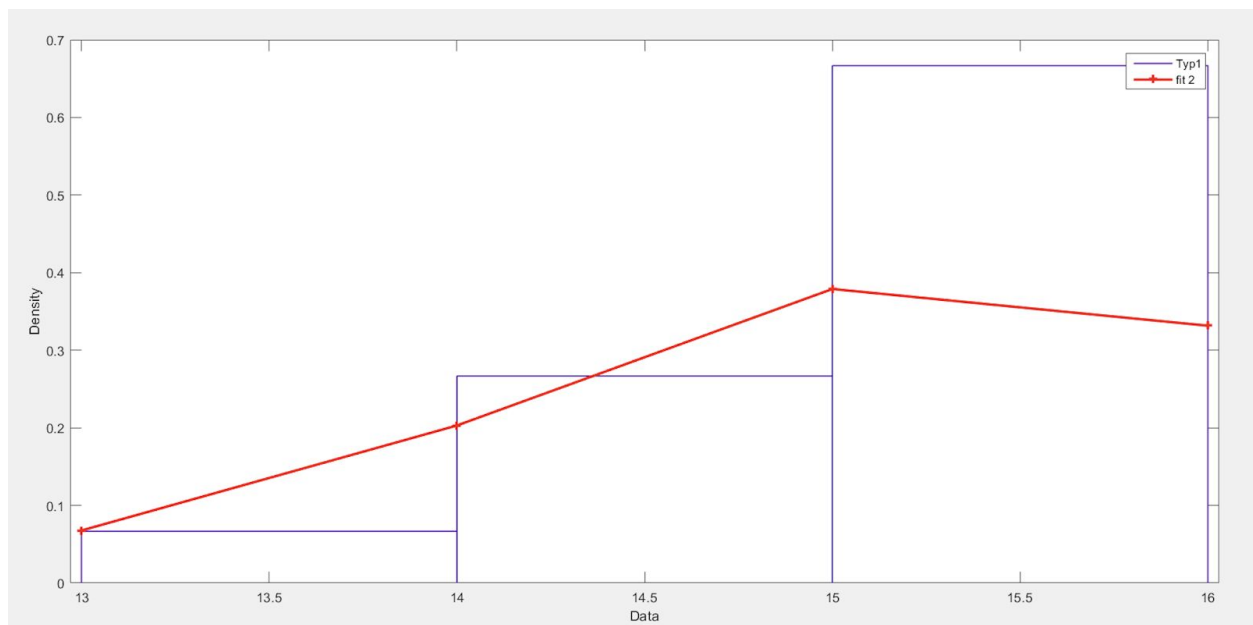


6. 3 histograms fit in binomial distribution using Binomial Fitting Tool of MATLAB

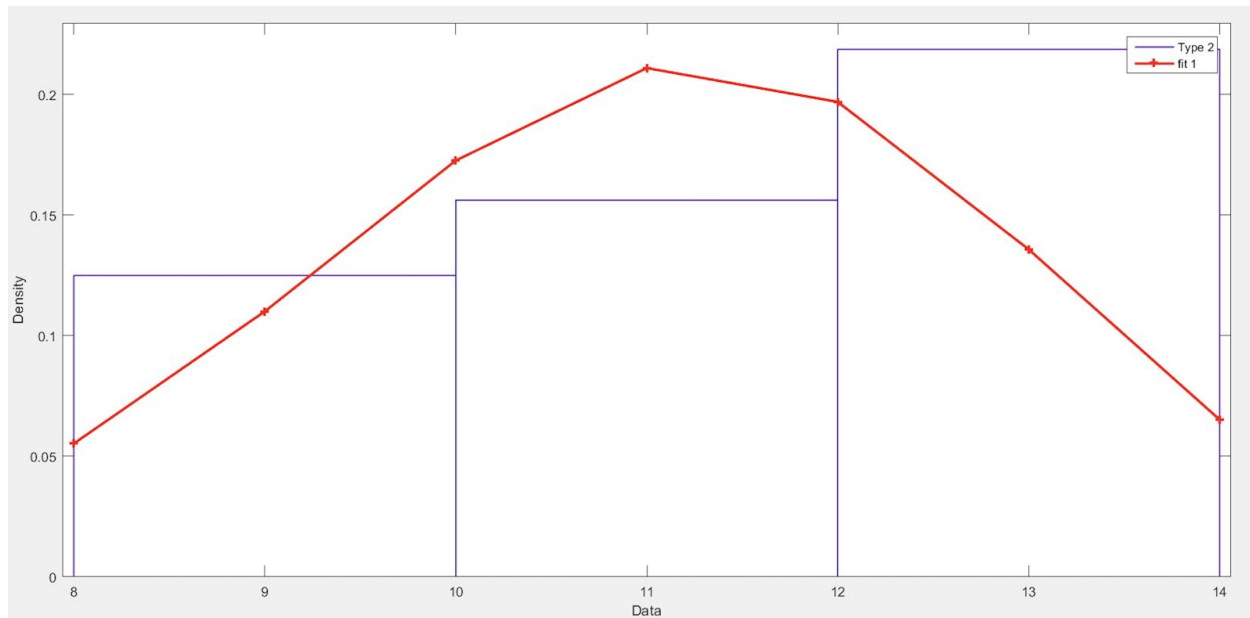
Healthy Cells



Type 1 Cancer Cells



Type 2 Cancer Cells



Healthy

Distribution: Binomial
Log likelihood: -31.4027
Domain: $0 \leq y < \text{Inf}$
Mean: 3.4375
Variance: 2.69897

Parameter	Estimate	Std. Err.
N	16	0
p	0.214844	0.0256696

Estimated covariance of parameter estimates:

	N	p
N	0	0
p	0	0.000658929

Type1 Cancer

Distribution: Binomial
Log likelihood: -19.4424
Domain: $0 \leq y < \text{Inf}$
Mean: 14.9333
Variance: 0.995556

Parameter	Estimate	Std. Err.
N	16	0
p	0.933333	0.0161015

Estimated covariance of parameter estimates:

	N	p
N	0	0
p	0	0.000259259

Type2 Cancer

Distribution: Binomial
Log likelihood: -31.778
Domain: $0 \leq y < \text{Inf}$
Mean: 11.0625
Variance: 3.41382

Parameter	Estimate	Std. Err.
N	16	0
p	0.691406	0.0288696

Estimated covariance of parameter estimates:

	N	p
N	0	0
p	0	0.000833452

7. Selective Activation of Cell Deaths: As we can see from the above probabilities that number of cell deaths are more in Cancer cells due to high caspase 3 level in such cells. In healthy cells, the cell deaths are less as caspase 3 level in such cells is generally low. Thus, in healthy cells, the probability of death is least. We also see that the probability of cell death in Type 1 cancer cells is more than the probability of cell death in Type 2 cancer cells. Thus, Type 1 is even more harmful than Type 2. But probability of cell death in both type of cancer cells is much higher than the probability of cell death in healthy cells.