## Project Description & Requirement

#	Attribute	Domain
	1. Sample code number	id number
	2. Clump Thickness	1 - 10
	3. Uniformity of Cell Size	1 - 10
	4. Uniformity of Cell Shape	1 - 10
	5. Marginal Adhesion	1 - 10
	6. Single Epithelial Cell Size	1 - 10
	7. Bare Nuclei	1 - 10
	8. Bland Chromatin	1 - 10
	9. Normal Nucleoli	1 - 10
	10. Mitoses	1 - 10
	11. Class:	(2 for benign, 4 for malignant)
		`

Note: Missing attribute values: 16

There are 16 instances that contain a single missing

(i.e., unavailable) attribute value, now denoted by "?". You may just delete those instances.

Note: 11 attribute "Class" is our response.

## **Project Requirements:**

Write a report on your findings and try to answer the following questions:

- 1. Is the full model (including all 10 features) good? Is there any non-important feature? If so, how do you remove them?
- 2. Propose the best model in your mind. (hint: there could be many criteria like prediction error, goodness of fit and etc.) Remember there may not be unique solution for this question.