

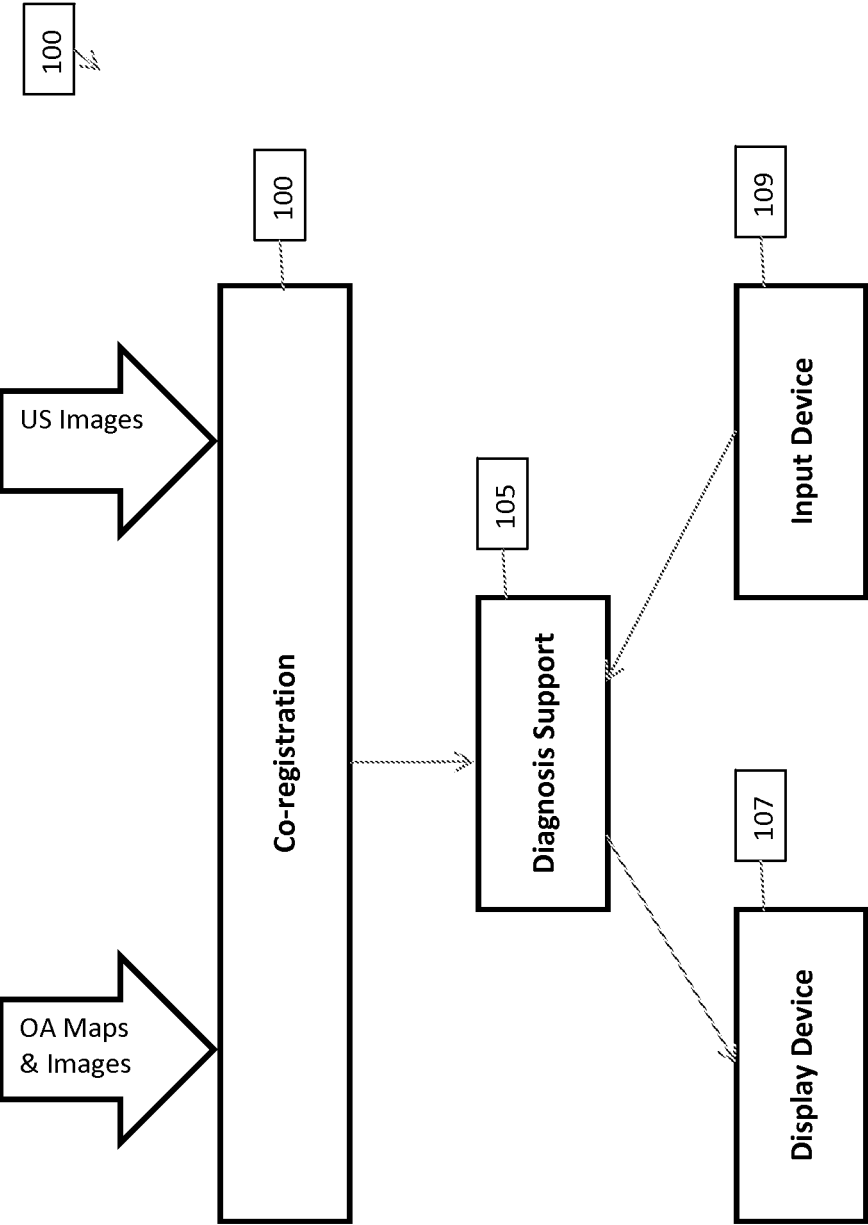


FIG. 1

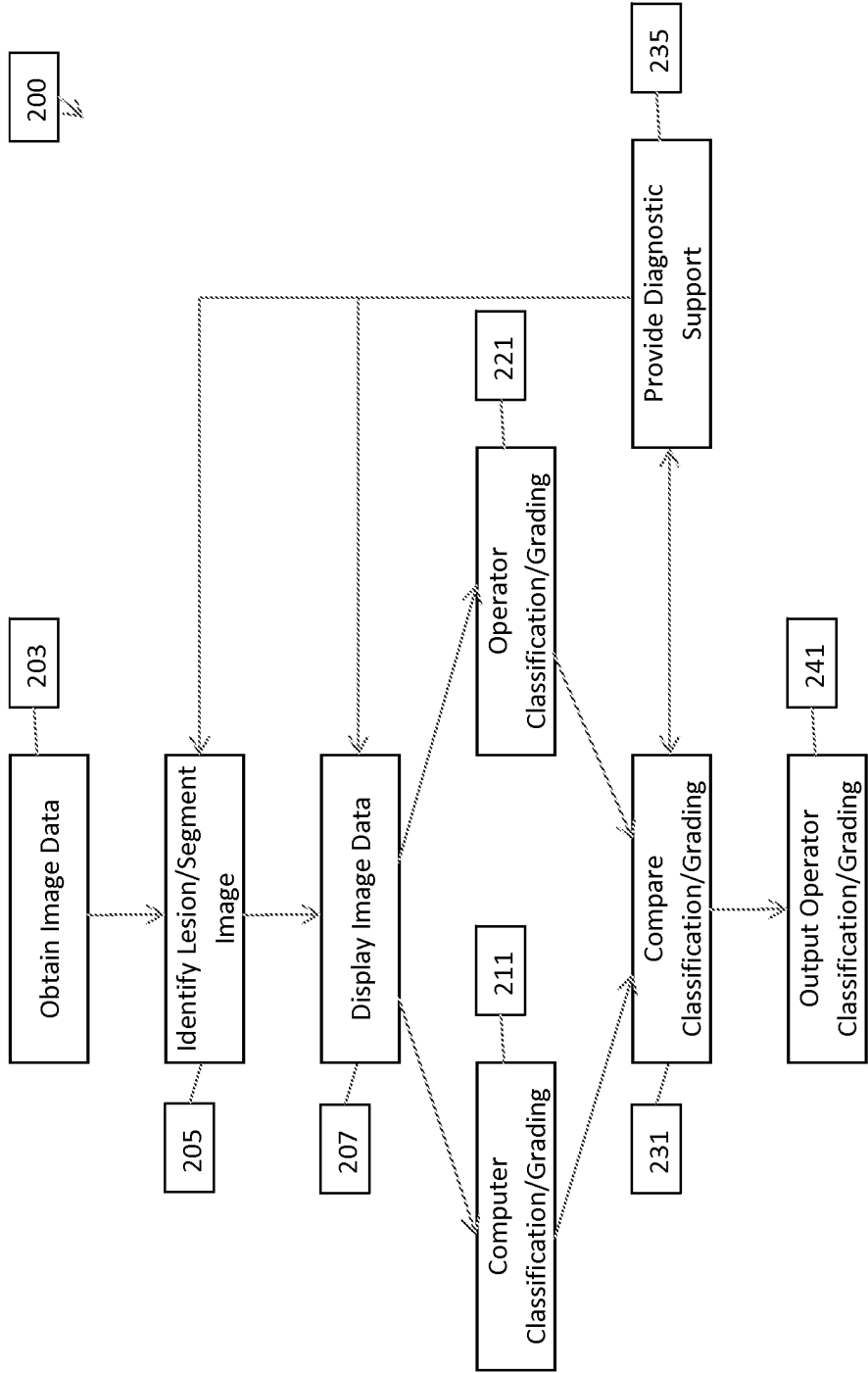


FIG. 2



FIG. 3

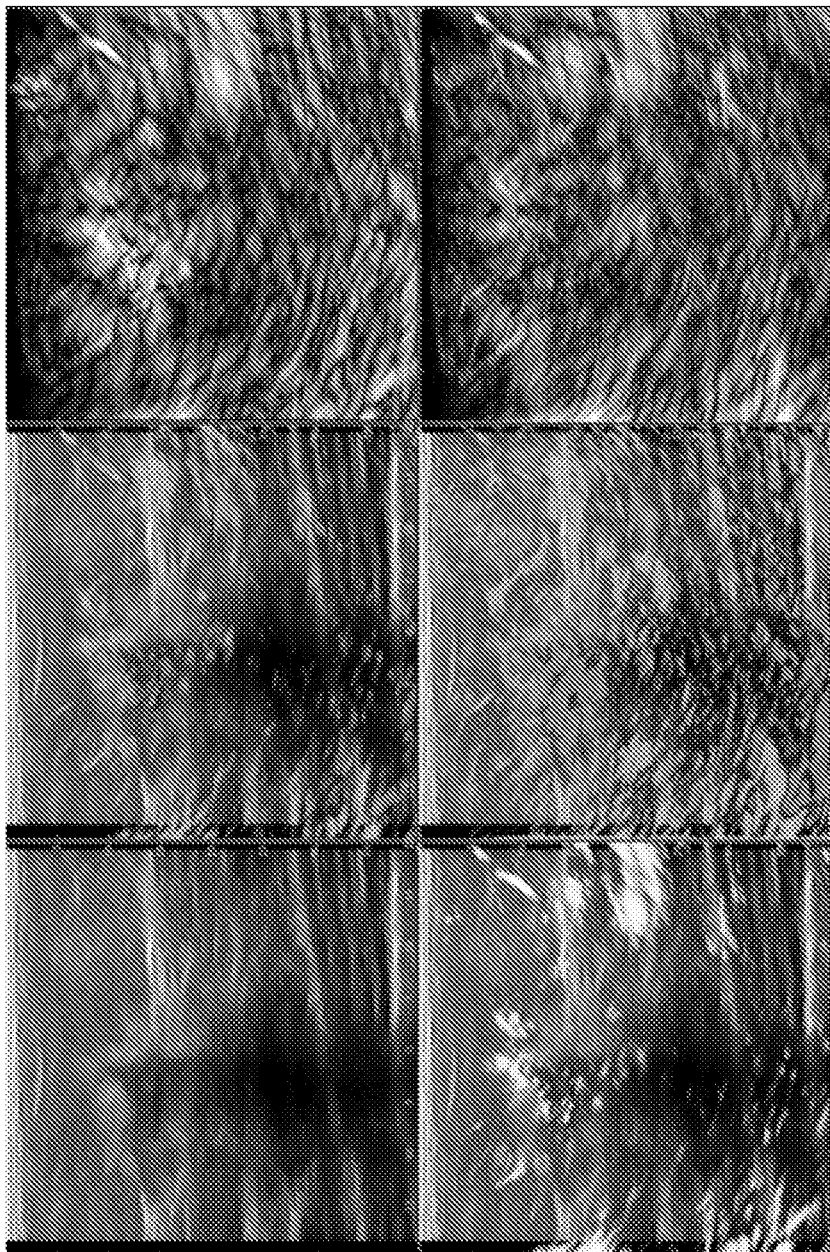


FIG. 4

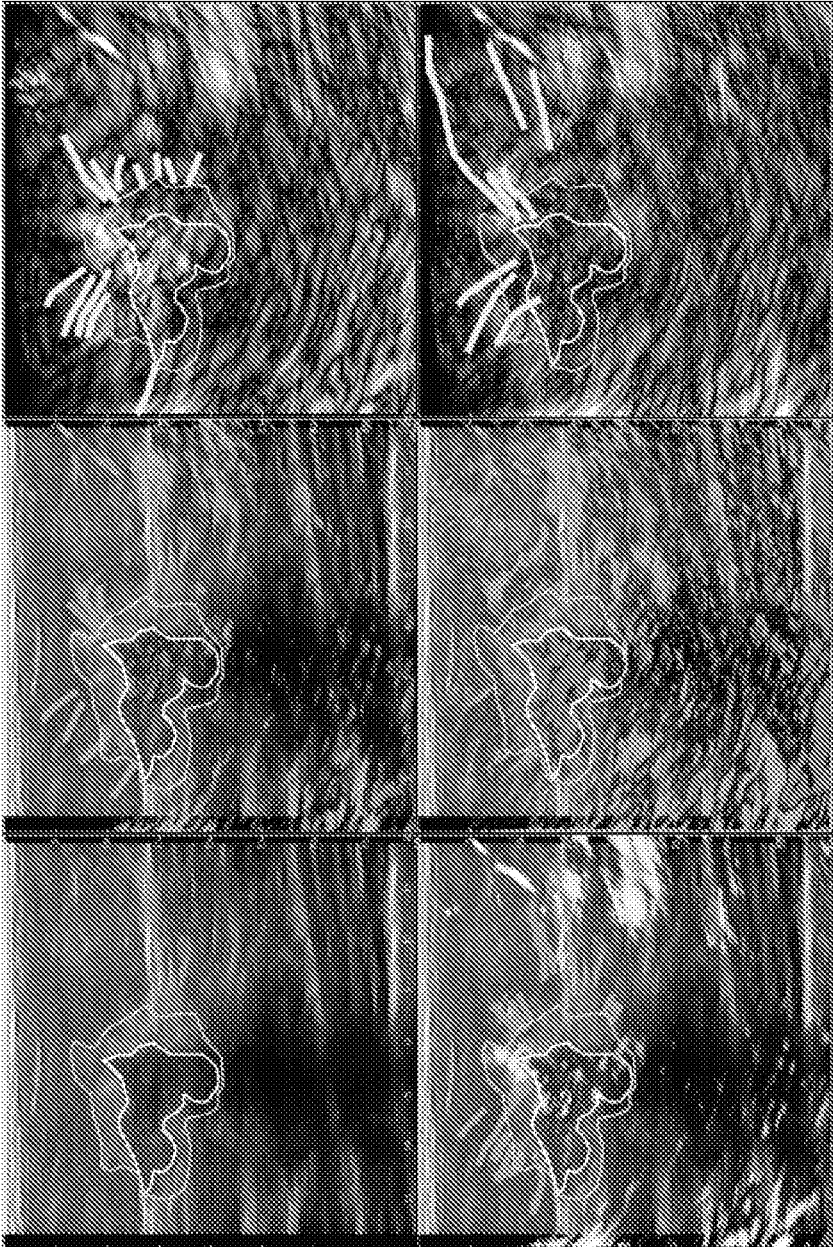


FIG. 5

Image Data	Examples of Feature Grades						
	Grade 0						
	Grade 1						
	Grade 2						
	Grade 3						
	Grade 4						
	Grade 5						
	Lesion Classification	Feature Grading					
		Feature 1	Feature 2	Feature 3	Feature 4	Feature 5	Feature 6

FIG. 6

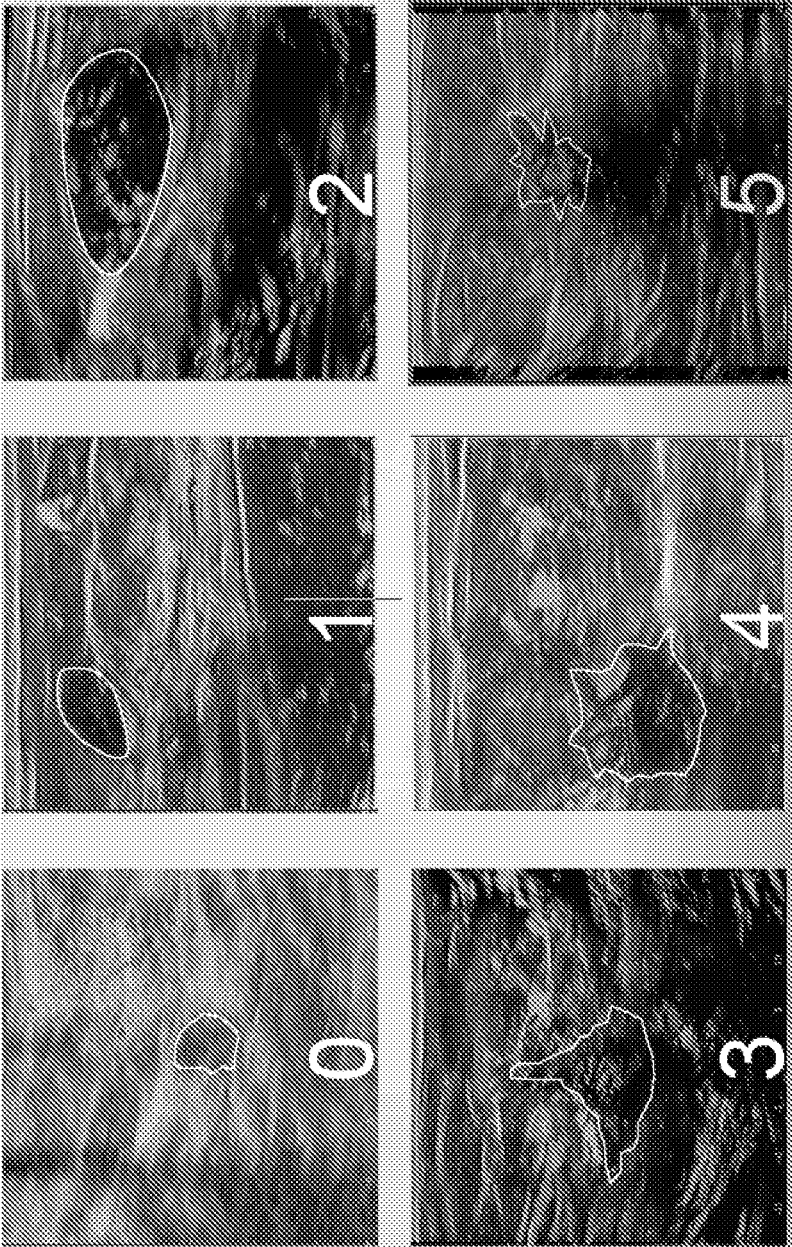


FIG. 7

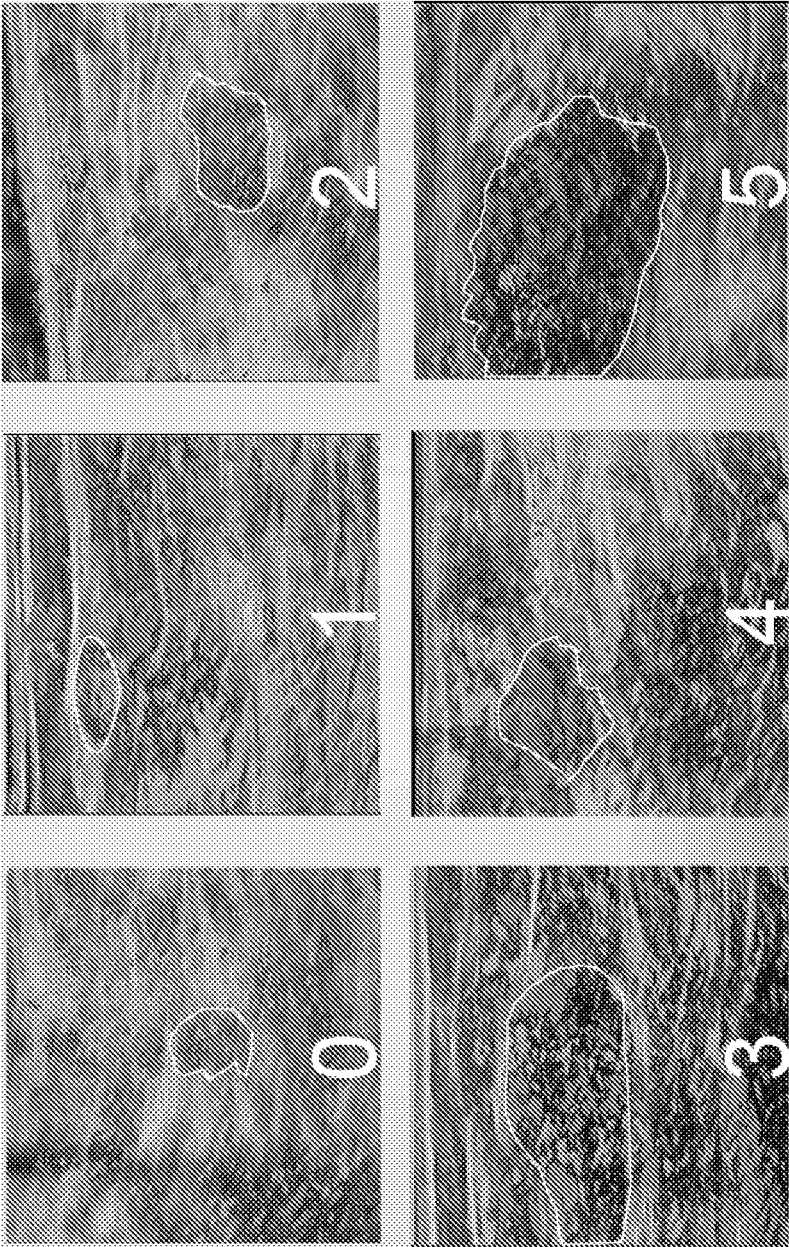


FIG. 8

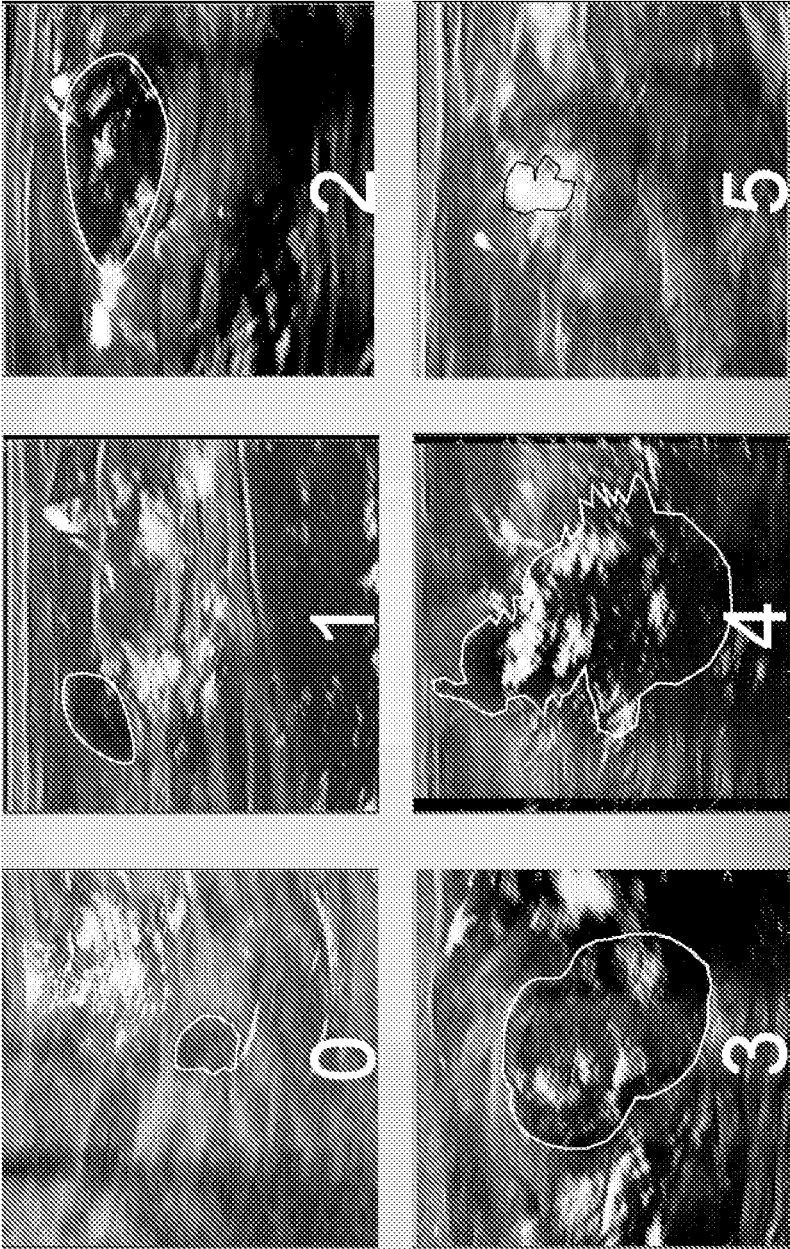


FIG. 9

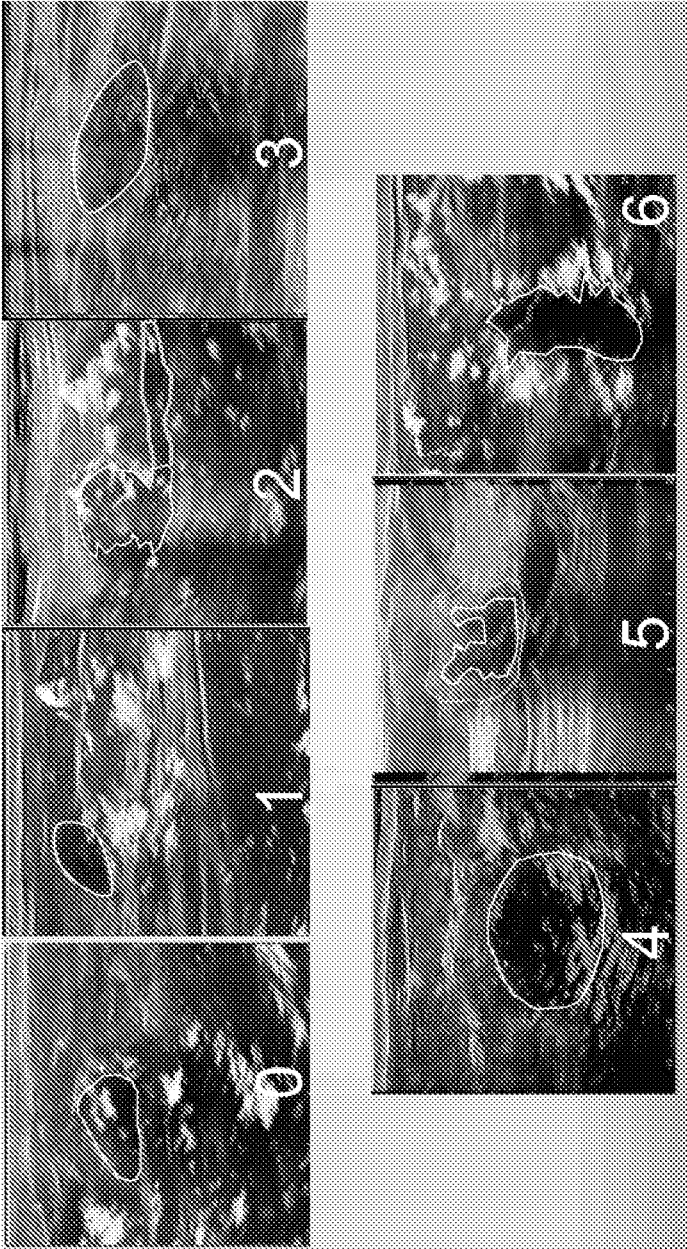


FIG. 10

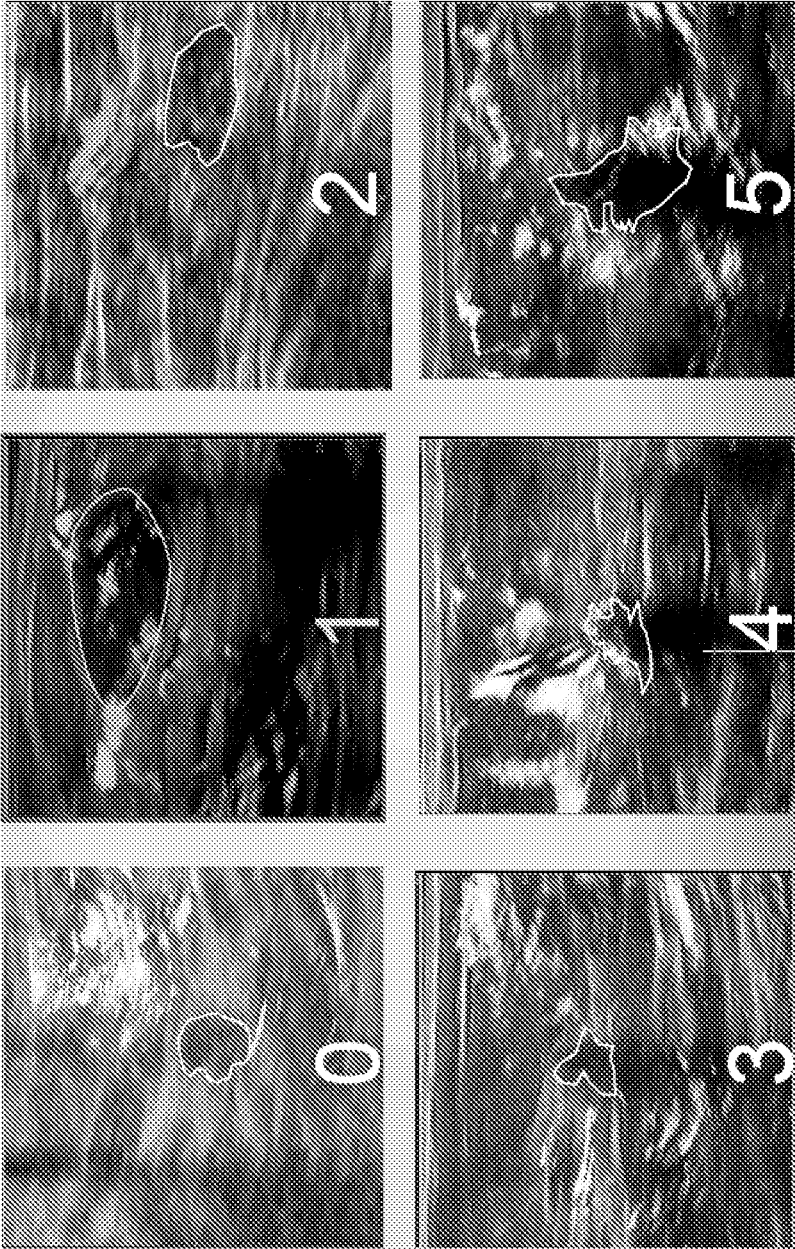


FIG. 11

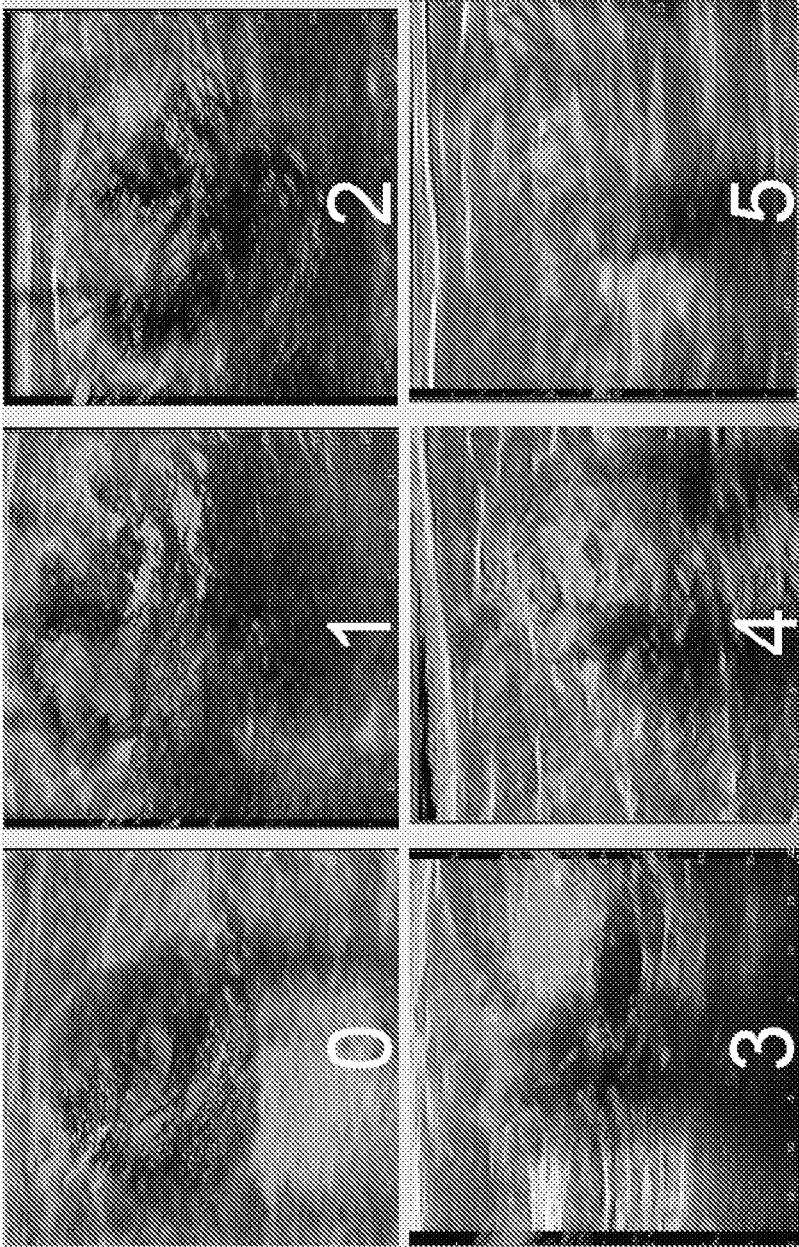


FIG. 12

feas-Pref	F = Feasibility pf = preFeasibility				
exclude	Y = yes N = no				
excl reason	MS = missing study WL = wrong lesion TI = technically inadequate EA = excessive artifact				
histo group	B = benign M = malignant H = high risk				
histo spec	IDC = invasive duct carcinoma ILC = invasive lobular carcinoma CIS = carcinoma in situ MC = mucinous (colloid) car MCC = mucinous(colloid) carcinoma LYM = lymphoma BCC = IPC = invasive papillary CA FA = fibroadenoma FCC = fibrocystic change IDP = large duct papilloma SCT = scar tissue FN = fat necrosis HEM = hematoma IMN = intramammary lymph node, normal ICC = indeterminate cyst/solid IFL = inflammation RS = radial scar ADH = PT = phyllodes tumor				
Histo grade	1 = low grade 2 = intermediate grade 3 = high grade				
CA subtype	ISM = micropapillary CIS ISO = solid CIS ICR = cribriform CIS				
b9 subtype	FAH = hyalinized FA FAJ = FA cellular stroma (juvenile) FAC = FA, complex CYS = cyst ACY = apocrine cyst CLM = clustered microcysts FSC = fibrosclerosis UDH = duct hyperplasia AD = adenosis SCA = sclerosing adenosis				
internal vv	0 = None 1 = up to one artery and one vein 2 = up to one art an one v with wnl branches 3) speckle red = green = bkgd 4) speckle, red > green > background 5) multiple red vessels				
boundary vv	0 = none 1 = up to 1 capsular art and v 2 = up to one capsular a and v wi wnl branches 3) specke red = green = bkgd 4) speckle, red > green > bkgd 5) multiple capsular vv (>2)				
internal blush	0 = None 1) minimal speckle, all green = bkgd 2) minimal speckle, red < green = bkgd 3) minimal speckle, red > green = background 4) signif speckle, red > green > bkgd 5) all red bl				
int blood	0 = None 1) minimal speckle = bkgd 2) minmal lagge vessel = bkgd 3) modeate, large vv = bkgd 4) lots of large vv > bkgd 5) mostly filled wi blood >>> bkgd				
surround vv	0 = None 1) up to one art and one v 2) multiple vessles (>2) random orientation 3) one or two radiating vessels 4) multiple radiating vessels, one side 5) multiple radiati				
signif artifact	0 = None 1) minimal, does not interfere 2) moderate, does not interfere 3) moderate, interferes 4) severe, interferes 5) severe, prevents interpretation				
artifact type					
teaching 1st	Y = yes, use YX = yes, already used N = no, don't use				
teaching 2nd	Y = yes, use YX = yes, already used N = no, don't use				
rerun algo	Y = yes, rerun YX = yes, already rerun N = no, don't rerun				
central path	YFN = yes, false neg YFP = yes, false pos YTP = yes, good true pos YTN = yes, good true neg N = no, no central path needed				

FIGURE 13

Figure 1 - Categories and Rankings.

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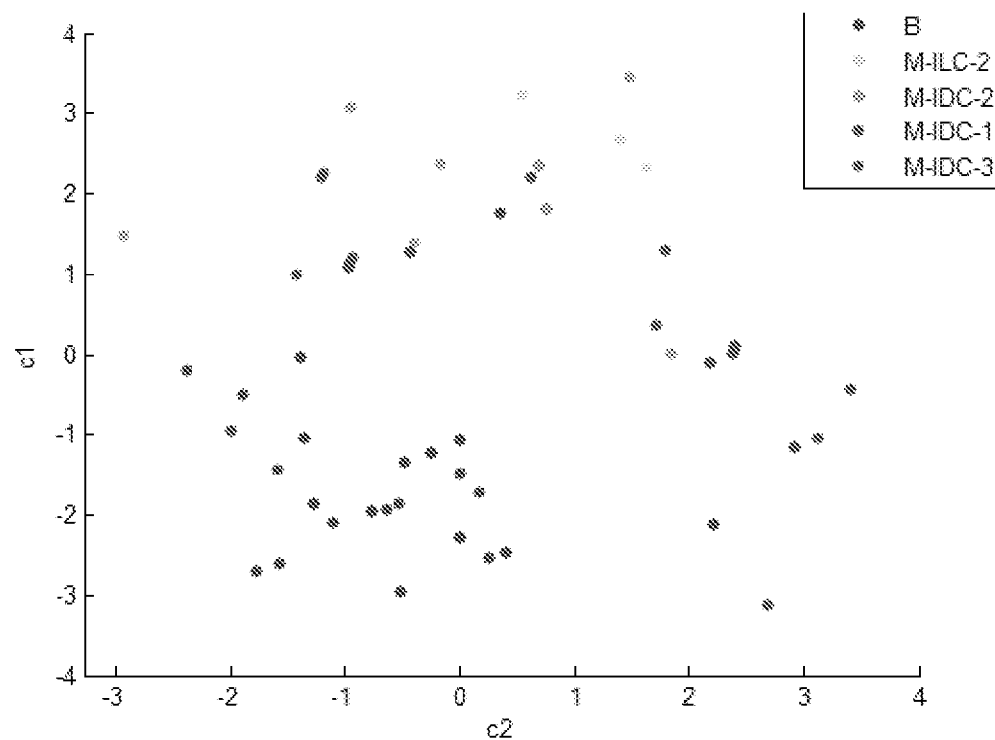


Figure 2a – Cluster of patients when categorized by features. Each axis represents a combination of features. Benign patients cluster in the bottom left. The value on is the score on feature vectors c_1 and c_2 which are shown in Figure 3. Benign is shown as red dots, malignant shown as other color dots.

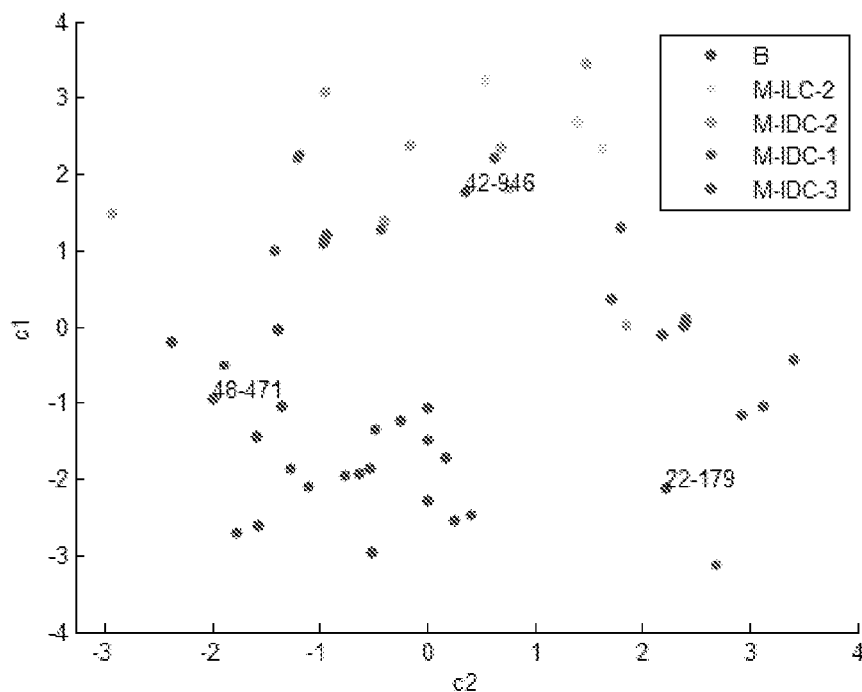


Figure 2a – Same as Figure 2, but assigning the patient IDs to the outliers.

FIGURE 14

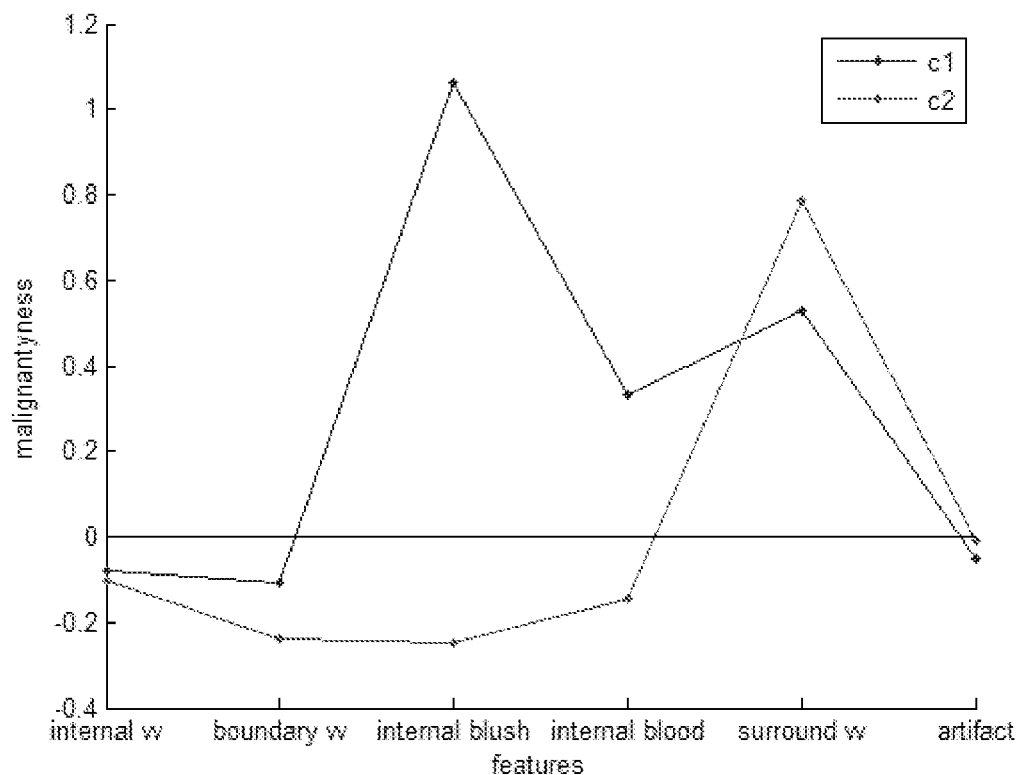


FIGURE 15

Figure 3 – Feature vectors showing strongest correlation between features. A positive value for a feature means that the feature is correlated malignancy score, a negative value means that it correlated with benign. A scatterplot using axes generated by the feature vectors c1 and c2 was shown in Figure 2. In other words, this figure shows the weighting of each feature that gives a coordinate in Figure 2 (the x-axis is given by c1, the y-axis given by c2). (Technical explanation: Multiplying the number represented by each dot (weights) by the corresponding features that were scored for a given patient will give a number, it is that number which gets plotted on the axis in Figure 2.)