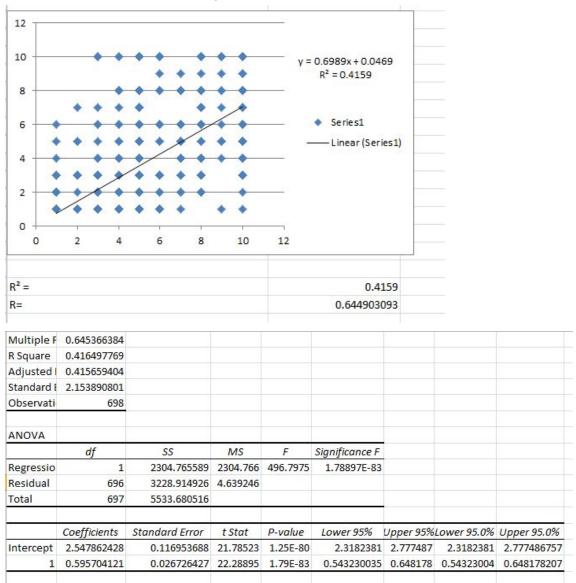
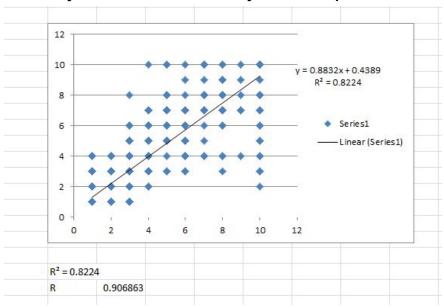
			+
Correlation Between	Correlation Coefficient	Result	ı
Clump Thickness & Uniformity of Cell Size	0.644912504	moderately correlated	Ť
Uniformity of Cell Size & Uniformity of Cell Shape	0.906881913	highly correlated	
Uniformity of Cell Shape & Marginal Adhesion	0.6830792	moderately correlated	
Marginal Adhesion & Single Epithelial Cell Size	0.599599068	moderately correlated	
Single Epithelial Cell Size & Bare Nuclei	0.57757338	moderately correlated	
Bare Nuclei & Bland Chromatin	0.676390294	moderately correlated	
Bland Chromatin & Normal Nucleoli	0.665877809	moderately correlated	
Normal Nucleoli & Mitosis	0.428335749	weakly correlated	
Clump Thickness & Mitosis	0.350033856	weakly correlated	F

Clump Thickness vs Uniformity of Cell Size Correlation



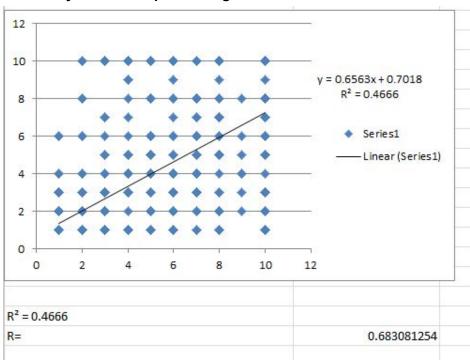
Uniformity of Cell Size vs Uniformity of Cell Shape correlation



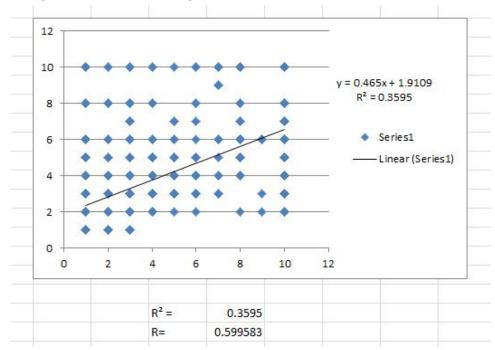
Regression Analysis

SUMMARY	OUTPUT							
Daggassi	n Ctatistics							
	on Statistics							
Multiple F								
R Square	0.82231103							
Adjusted I	0.82205573							
Standard (1.287681307							
Observati	698							
ANOVA								
	df	SS	MS	F	Significance F			
Regressio	1	5340.74285	5340.743	3220.957	2.539E-263			
Residual	696	1154.053712	1.658123					
Total	697	6494.796562						
	Coefficients	Standard Error	t Stat	P-value	Lower 95%	Upper 95%	Lower 95.0%	Upper 95.0%
Intercept	0.148057229	0.071764689	2.063093	0.039474	0.007156	0.2889585	0.007156	0.288958458
1	0.9311272	0.016406524	56.75347	2.5E-263	0.898914988	0.9633394	0.898914988	0.963339411

Uniformity of Cell Shape vs Marginal Adhesion correlation

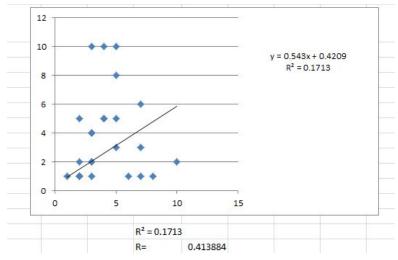


Marginal Adhesion & Single Epithelial Cell Size correlation

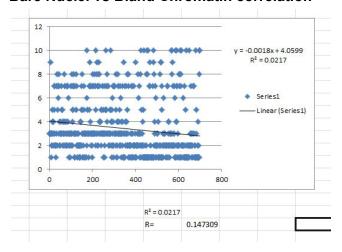


SUMMARY	OUTPUT							
Regressio	on Statistics							
Multiple F	0.599402347							
R Square	0.359283174							
Adjusted I	0.358362604							
Standard [2.288206244							
Observati	698							
ANOVA								
	df	SS	MS	F	Significance F			
Regressio	1	2043.48	2043.48	390.2833	2.63919E-69			
Residual	696	3644.178	5.235888					
Total	697	5687.658				0		
	Coefficients	andard Err	t Stat	P-value	Lower 95%	Upper 95%	Lower 95.0%	Upper 95.0%
Intercept	0.322492617	0.152803	2.110515	0.03517	0.022482927	0.622502	0.02248293	0.62250231
2	0.772885198	0.039122	19.75559	2.64E-69	0.696073215	0.849697	0.69607322	0.84969718

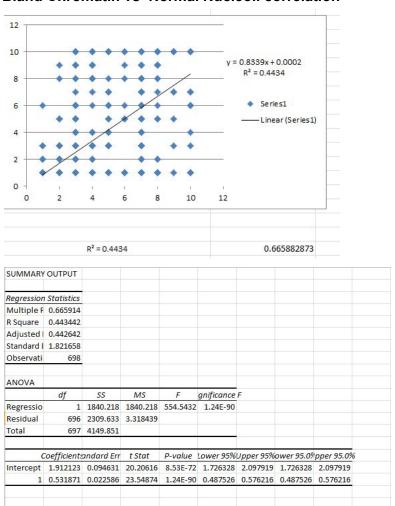
Single Epithelial Cell Size vs Bare Nuclei correlation



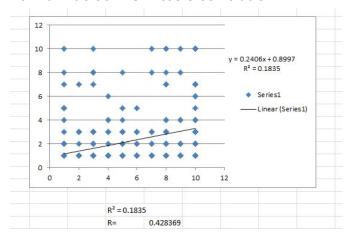
Bare Nuclei vs Bland Chromatin correlation



Bland Chromatin vs Normal Nucleoli correlation

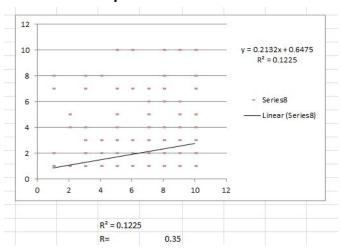


Normal Nucleoli vs Mitosis correlation



SUMMARY	OUTPUT							
Regression	Statistics							
Multiple F	0.428185							
R Square	0.183343							
Adjusted I	0.182169							
Standard I	2.762762							
Observati	698							
ANOVA			•					
	df	SS	MS	F	gnificance	F		
Regressio	1	1192.669	1192.669	156.2547	1.72E-32			
Residual	696	5312.467	7.632854					
Total	697	6505.136						
C	oefficients	andard Err	t Stat	P-value	Lower 95%	Upper 95%	ower 95.0%	pper 95.0%
Intercept	1.657487	0.142613	11.62228	1.16E-28	1.377484	1.937491	1.377484	1.937491
1	0.762229	0.060977	12.50019	1.72E-32	0.642507	0.88195	0.642507	0.88195

Mitosis vs Clump Thickness correlation



SUMMARY	OUTPUT							
Regression	Statistics							
Multiple F	0.350176							
R Square	0.122623							
Adjusted I	0.121363							
Standard I	2.641164							
Observati	698							
ANOVA								
	df	SS	MS	F	gnificance	F		
Regressio	1	678.5587	678.5587	97.27394	1.45E-21			
Residual	696	4855.122	6.97575					
Total	697	5533.681	- Herrita er					
C	oeffic <mark>i</mark> ents	andard Err	t Stat	P-value	Lower 95%	Upper 95%	ower 95.0%	pper 95.0%
Intercept	3.50261	0.136336	25.69099	6.8E-103	3.234931	3.77029	3.234931	3.77029
1	0.574935	0.058294	9.862755	1.45E-21	0.460483	0.689388	0.460483	0.689388