Attribute Information:

1) ID number  
2) Diagnosis (M = malignant, B = benign)  
3-32)

Ten real-valued features are computed for each cell nucleus:

a) radius (mean of distances from center to points on the perimeter)  
b) texture (standard deviation of gray-scale values)  
c) perimeter  
d) area  
e) smoothness (local variation in radius lengths)  
f) compactness (perimeter^2 / area - 1.0)  
g) concavity (severity of concave portions of the contour)  
h) concave points (number of concave portions of the contour)  
i) symmetry  
j) fractal dimension ("coastline approximation" - 1)

The mean, standard error and "worst" or largest (mean of the three  
largest values) of these features were computed for each image,  
resulting in 30 features. For instance, field 3 is Mean Radius, field  
13 is Radius SE, field 23 is Worst Radius.

All feature values are recoded with four significant digits.

Missing attribute values: none

Class distribution: 357 benign, 212 malignant