Fractal Analysis of Breast Masses in Mammograms

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Breast Masses and Tumors

- Benign masses
  - Round or oval, smooth, macrolobulated
  - Homogeneous
  - Well-defined, well-circumscribed, sharp
- Malignant tumors (breast cancer)
  - Spiculated, rough, microlobulated
  - Heterogeneous
  - Ill-defined, ill-circumscribed, blurry

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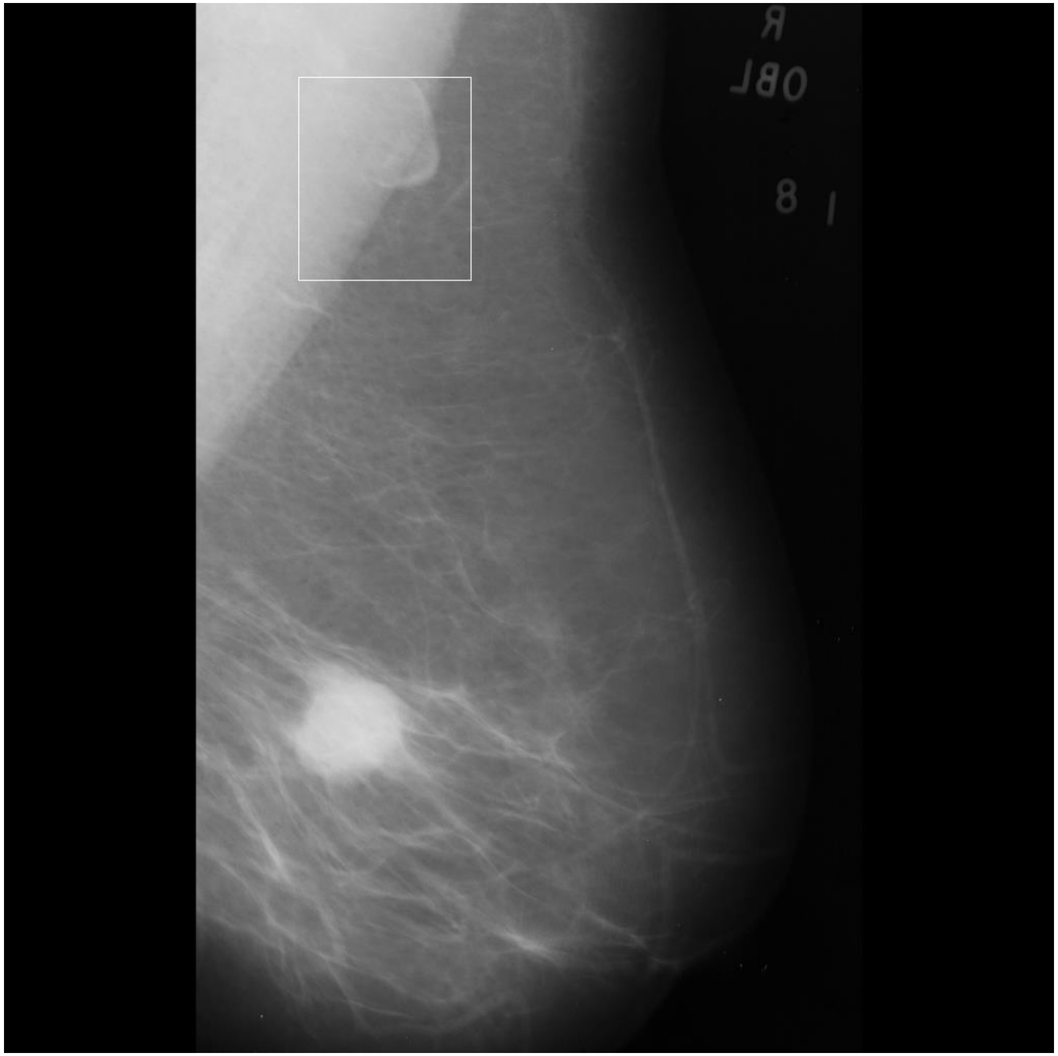
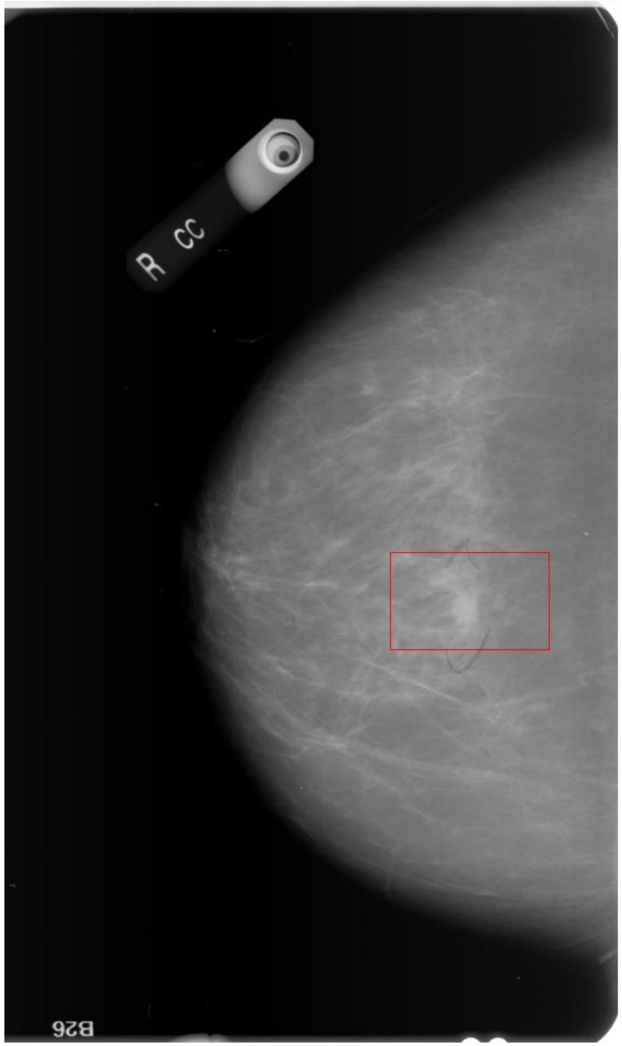
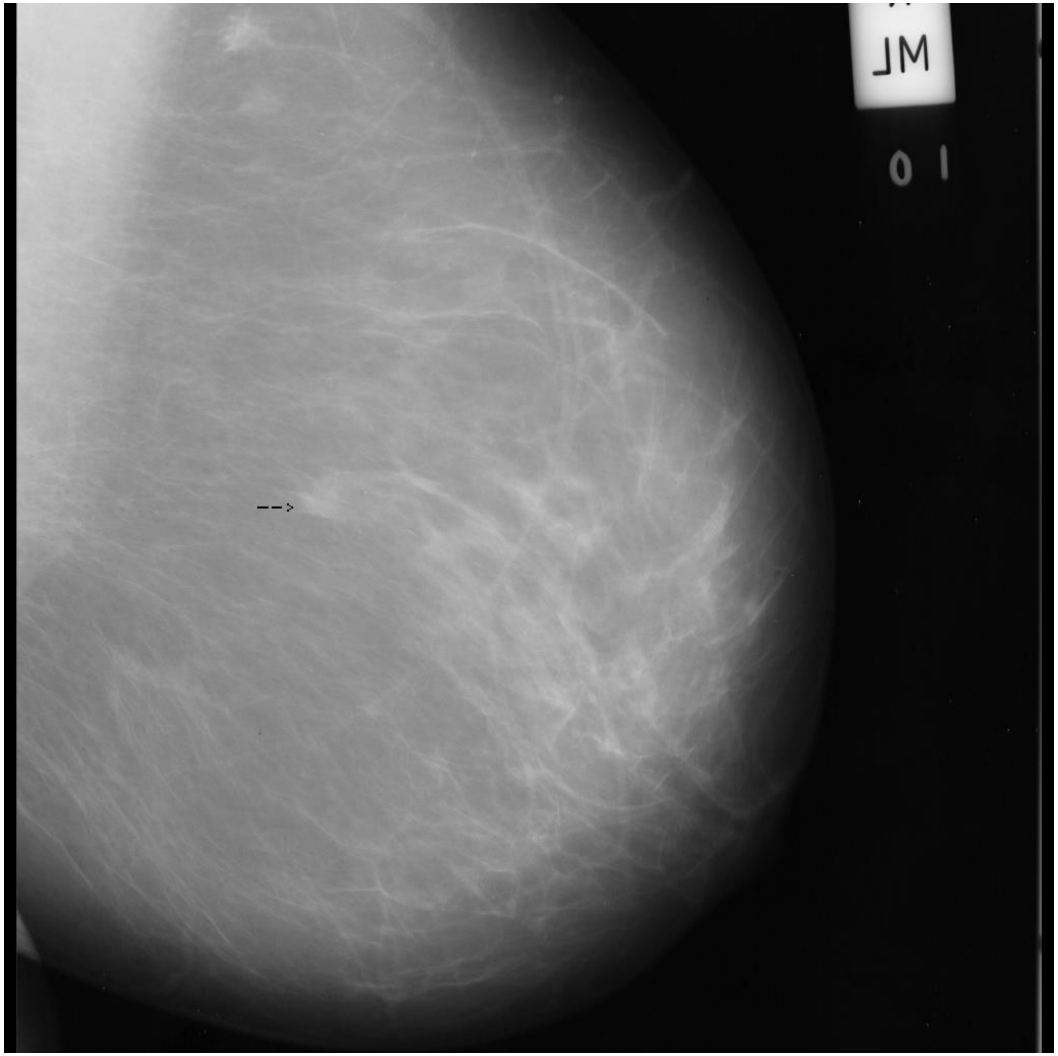
Mammogram with a Benign Mass



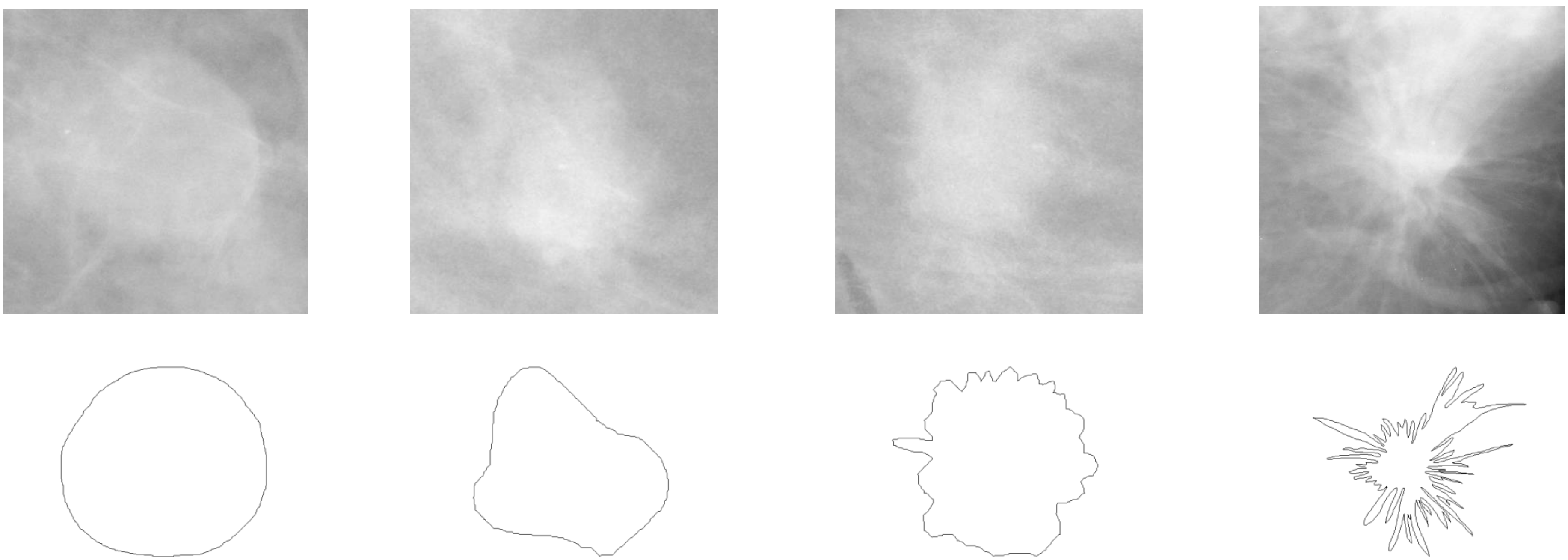
Mammogram with a Malignant Tumor



Mammogram with a Malignant Tumor



Examples of Breast Masses



Benign, round

Benign, macrolobulated

Malignant, microlobulated

Malignant, spiculated

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Fractals and Breast Masses

Self similarity at multiple scales:
macrolobulated versus
microlobulated contours

Nested patterns or complexity:

- smooth versus rough contours
- convex versus spiculated contours
- geometric versus space-filling curves

Cauliflower as a Fractal

Cauliflower as a Fractal

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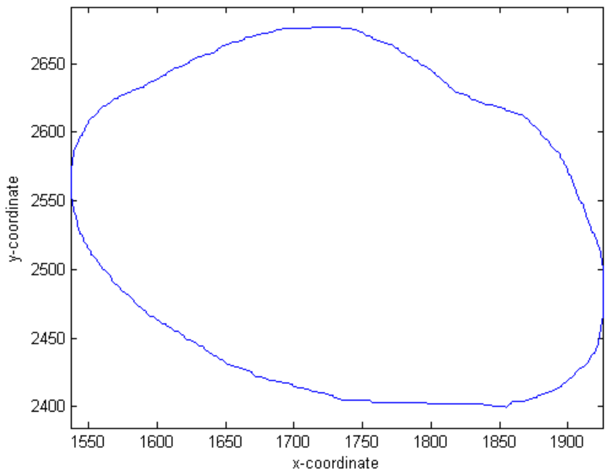
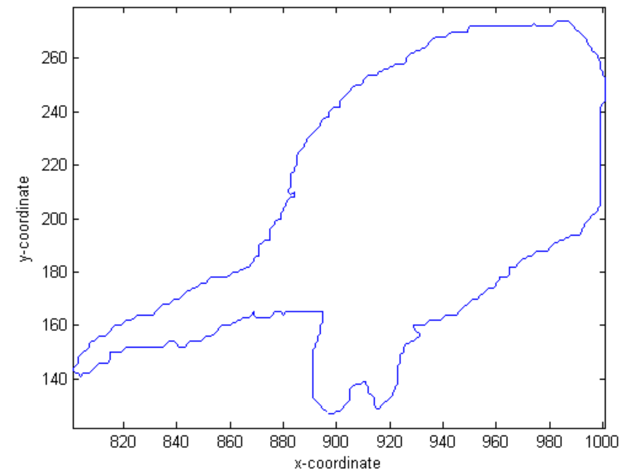
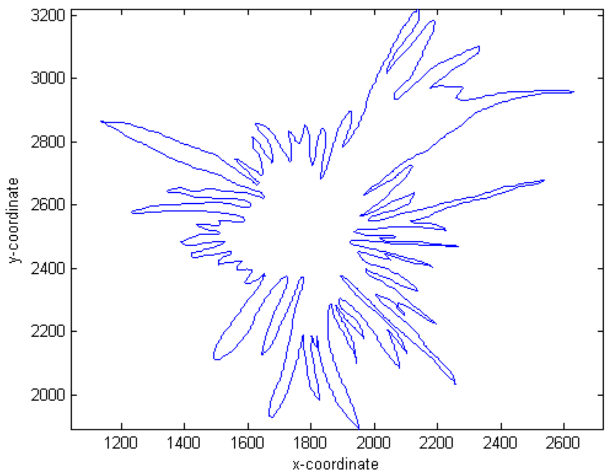


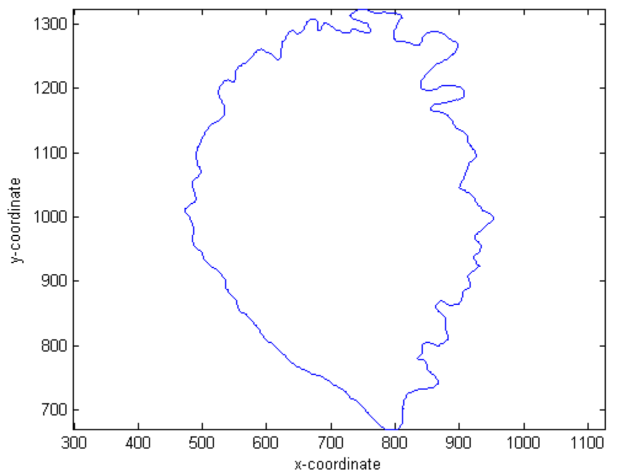
Circumscribed Benign (CB)



Spiculated Benign (SB)



Spiculated Malignant (SM)



Circumscribed Malignant (CM)

Fractal Dimension: Application to Breast Masses

- Fractal dimension can characterize the shape differences between benign masses and malignant tumors

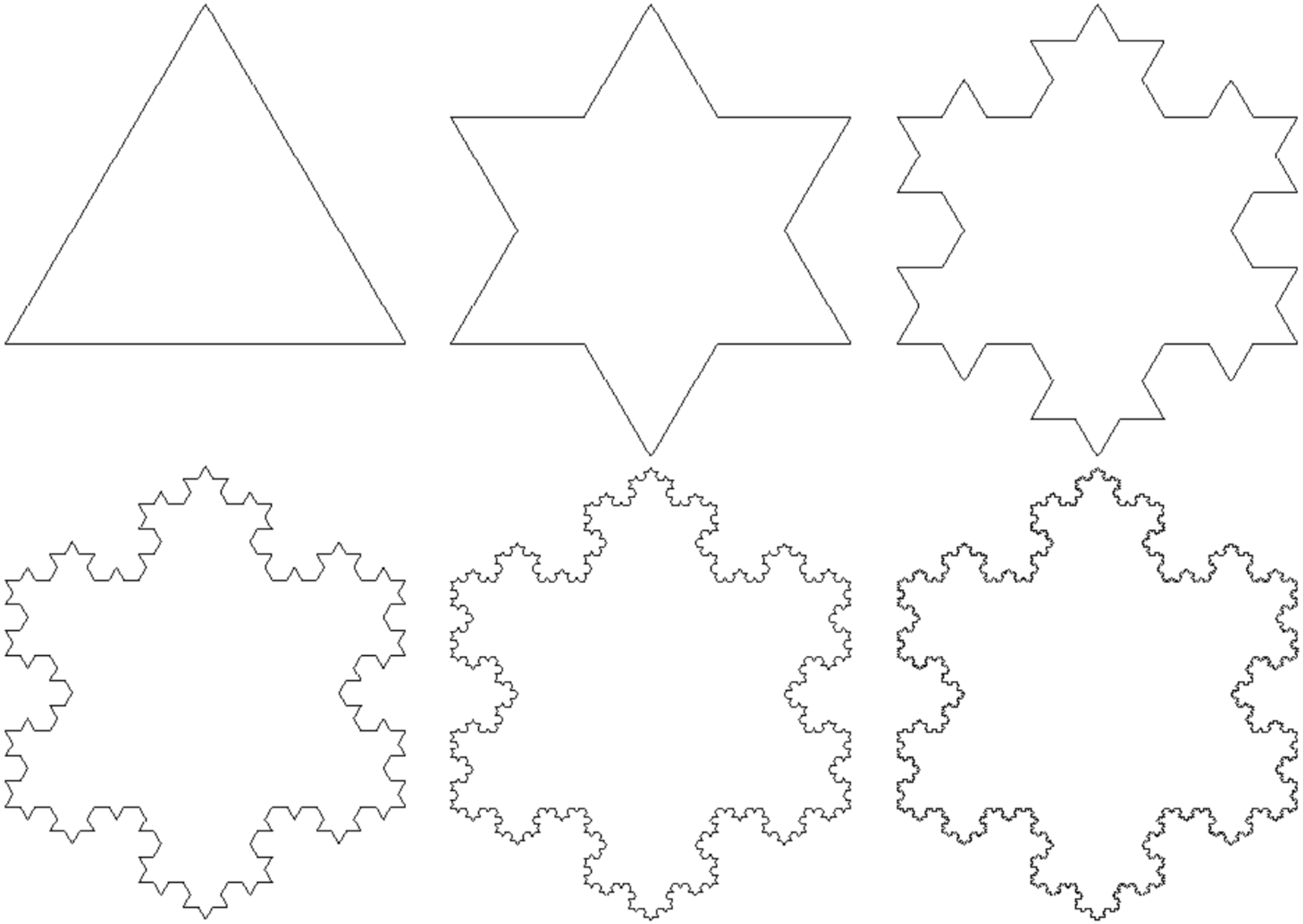
- Fractal analysis can also be used to characterize the texture of suspicious regions in mammograms

Self-similarity Dimension

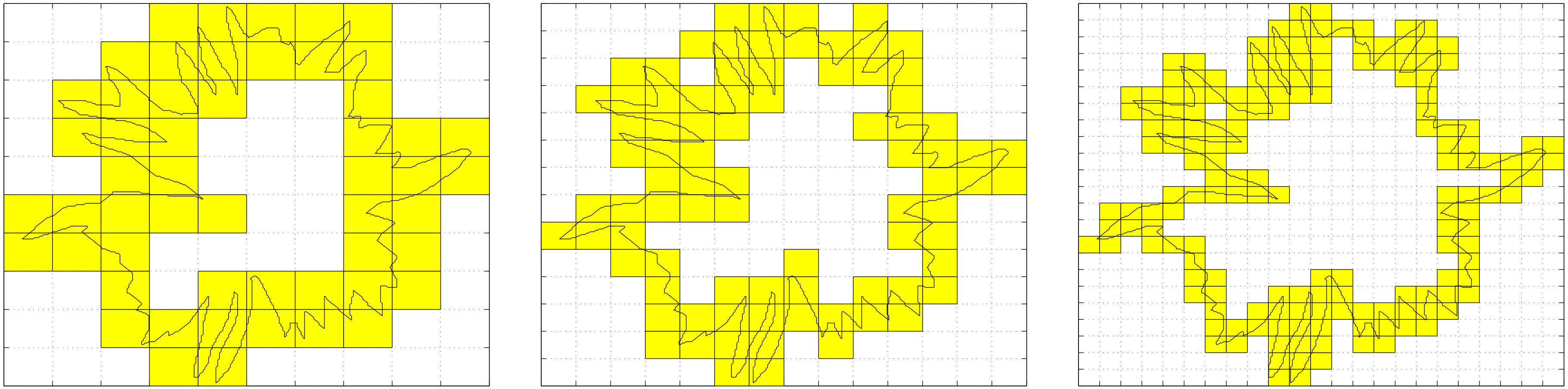
a = number of self-similar pieces
1/s = reduction factor
D = self-similarity dimension

$$a = \frac{1}{s^D} \Rightarrow D = \left| \frac{\log(a)}{\log(1/s)} \right|$$

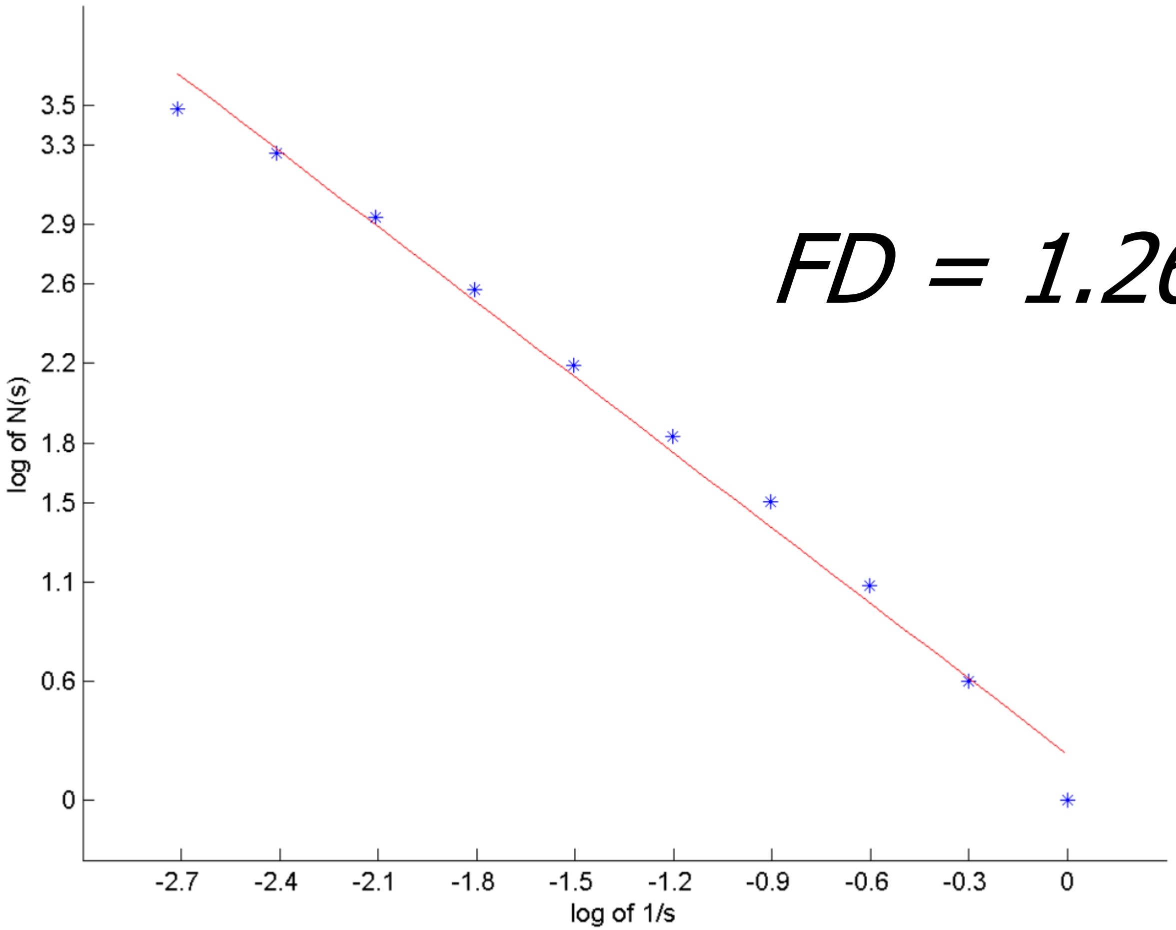
The Koch Snowflake
Fractal Dimension = 1.262



The Box-counting Method



Result of Box-counting for the Koch Snowflake



FD = 1.264

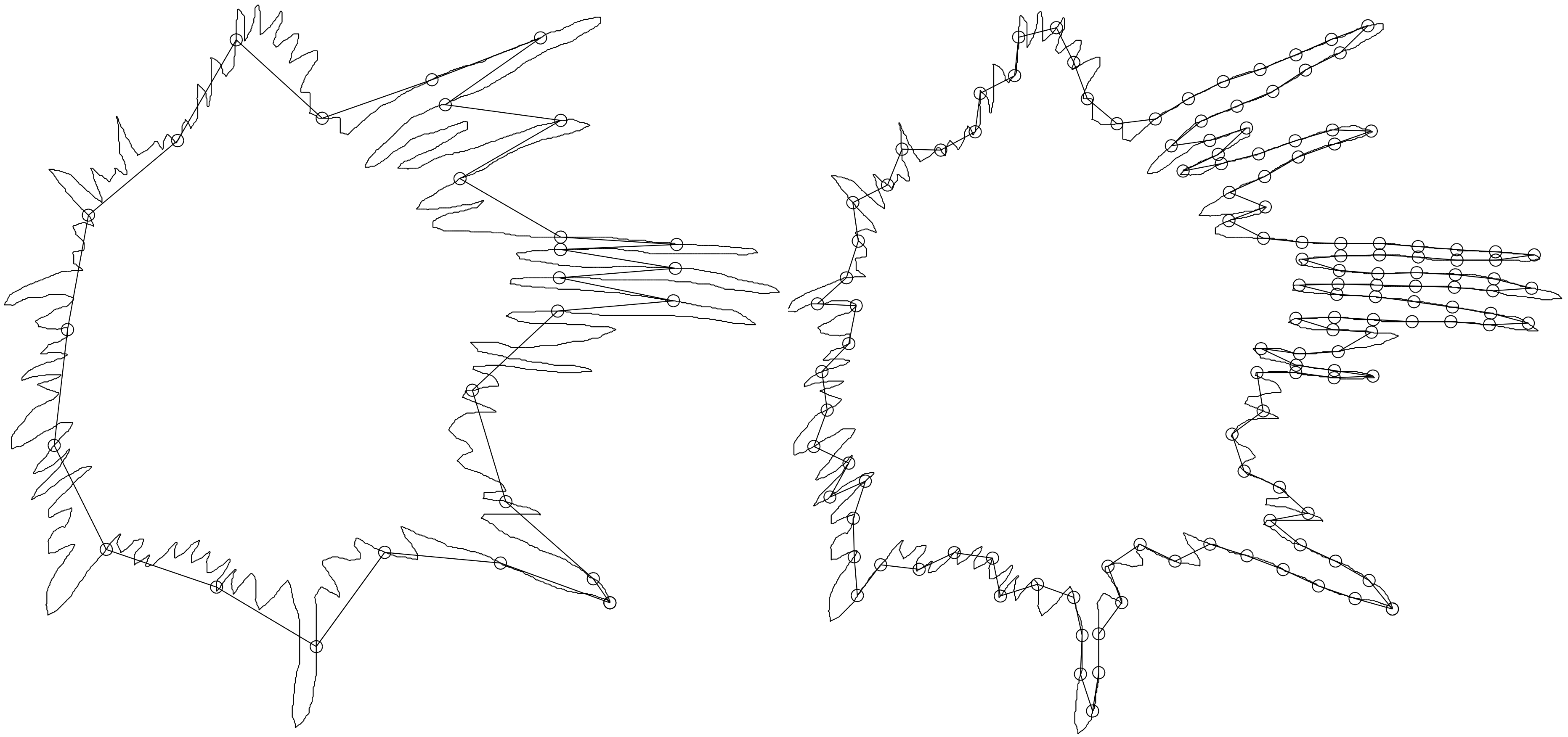
The Ruler Method

Let u be the length measured with a ruler of size s

$$u = c\,\frac{1}{s^d} \qquad\qquad D = 1 + d$$

$$\log(u) = \log(c) + d\,\log(1/s)$$

The Ruler Method Applied to a 2D Contour

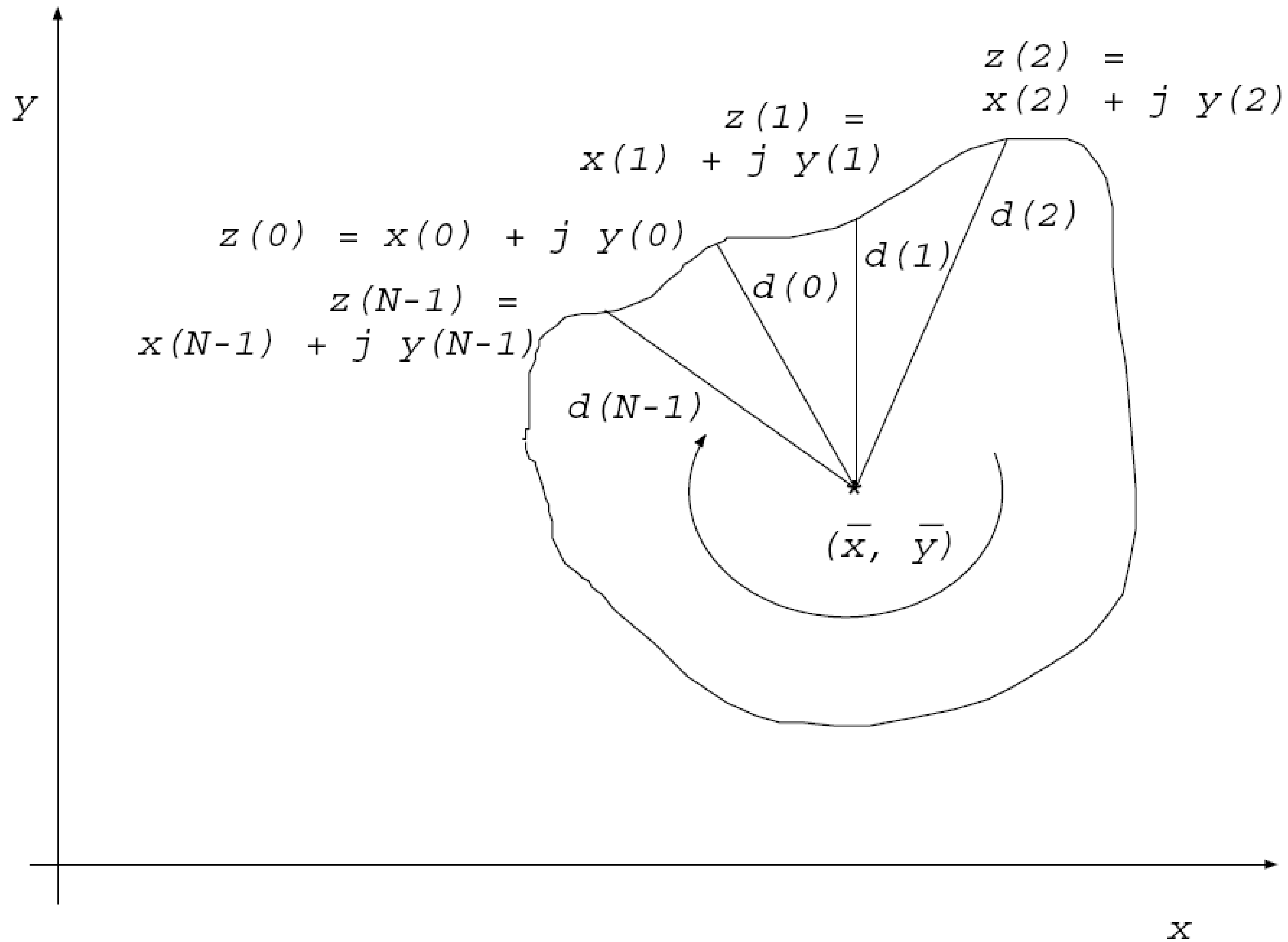


1D Signature of a 2D Contour

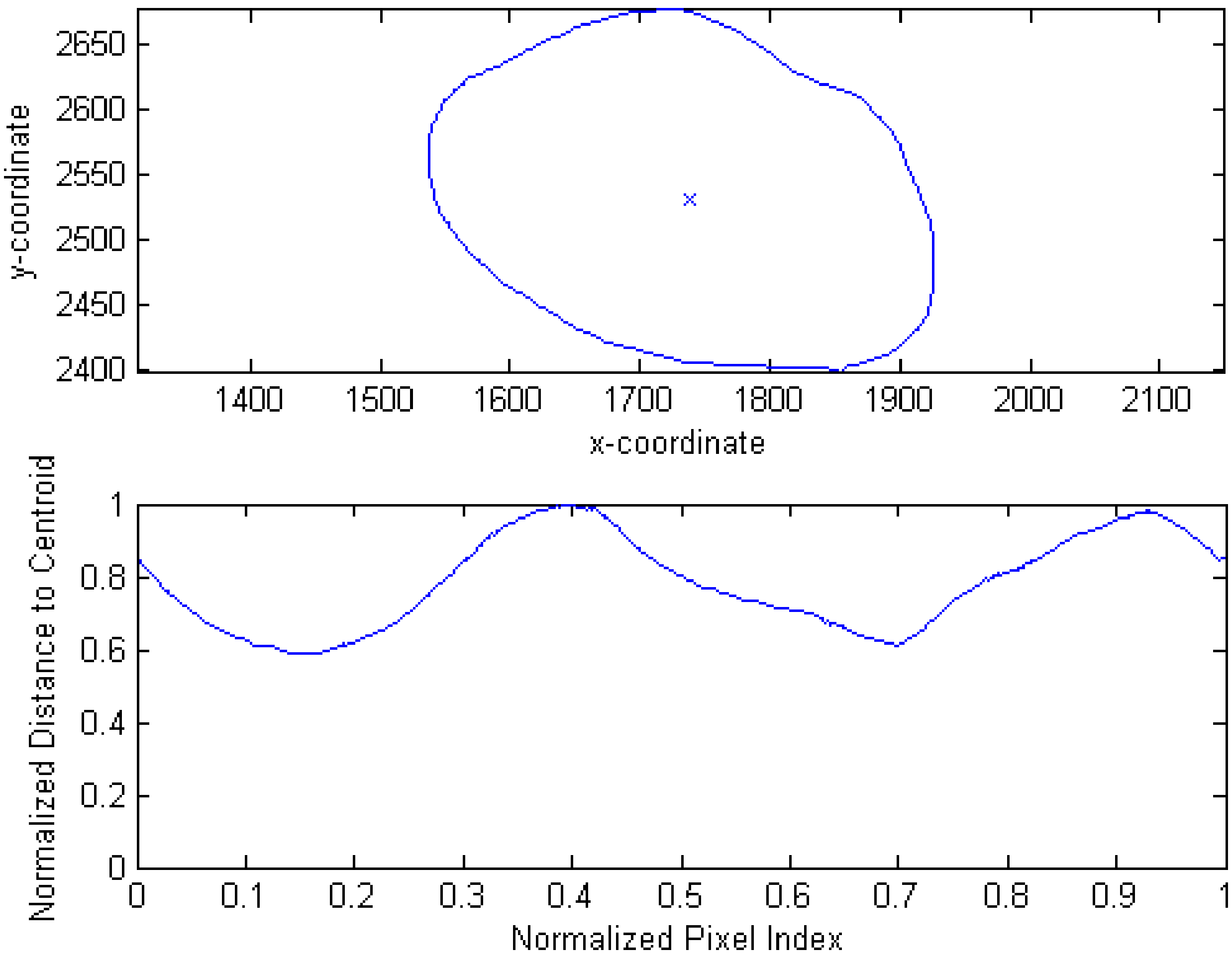
A 2D contour may be converted to a 1D signature using the distance of each contour point to the centroid (x_0, y_0)

$$d = [(x - x_0)^2 + (y - y_0)^2]^{1/2}$$

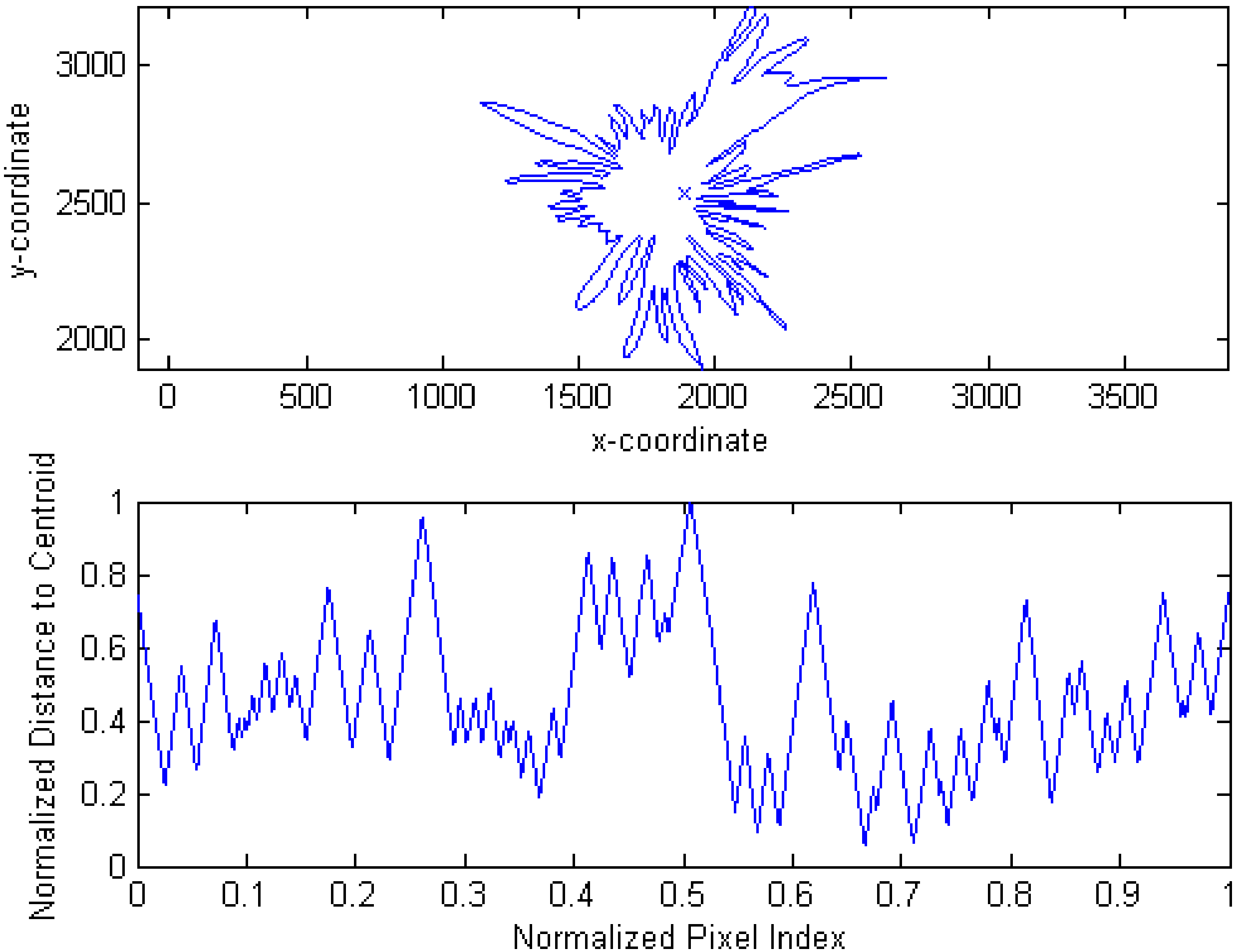
1D Signature of a 2D Contour



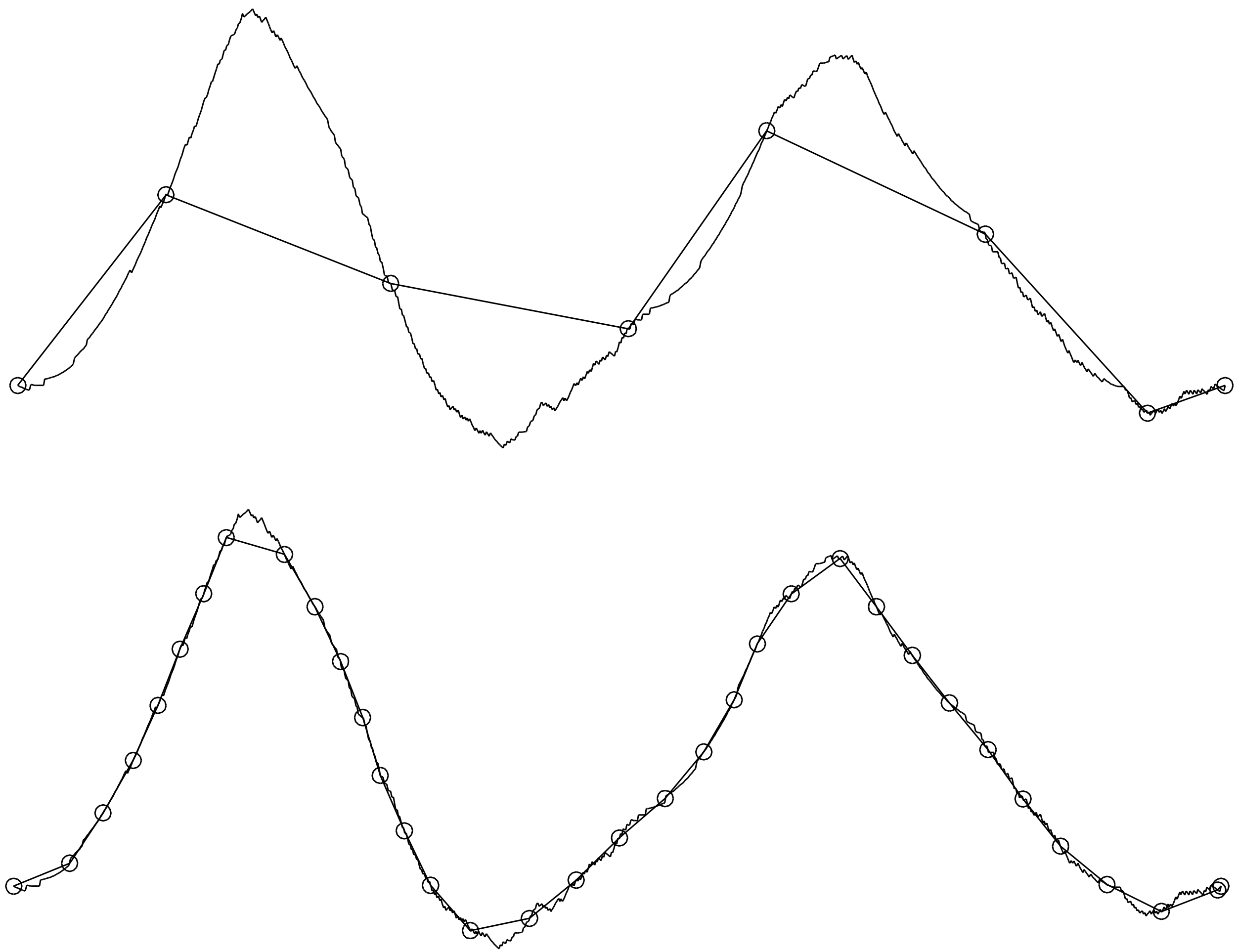
1D Signature of a Benign Mass



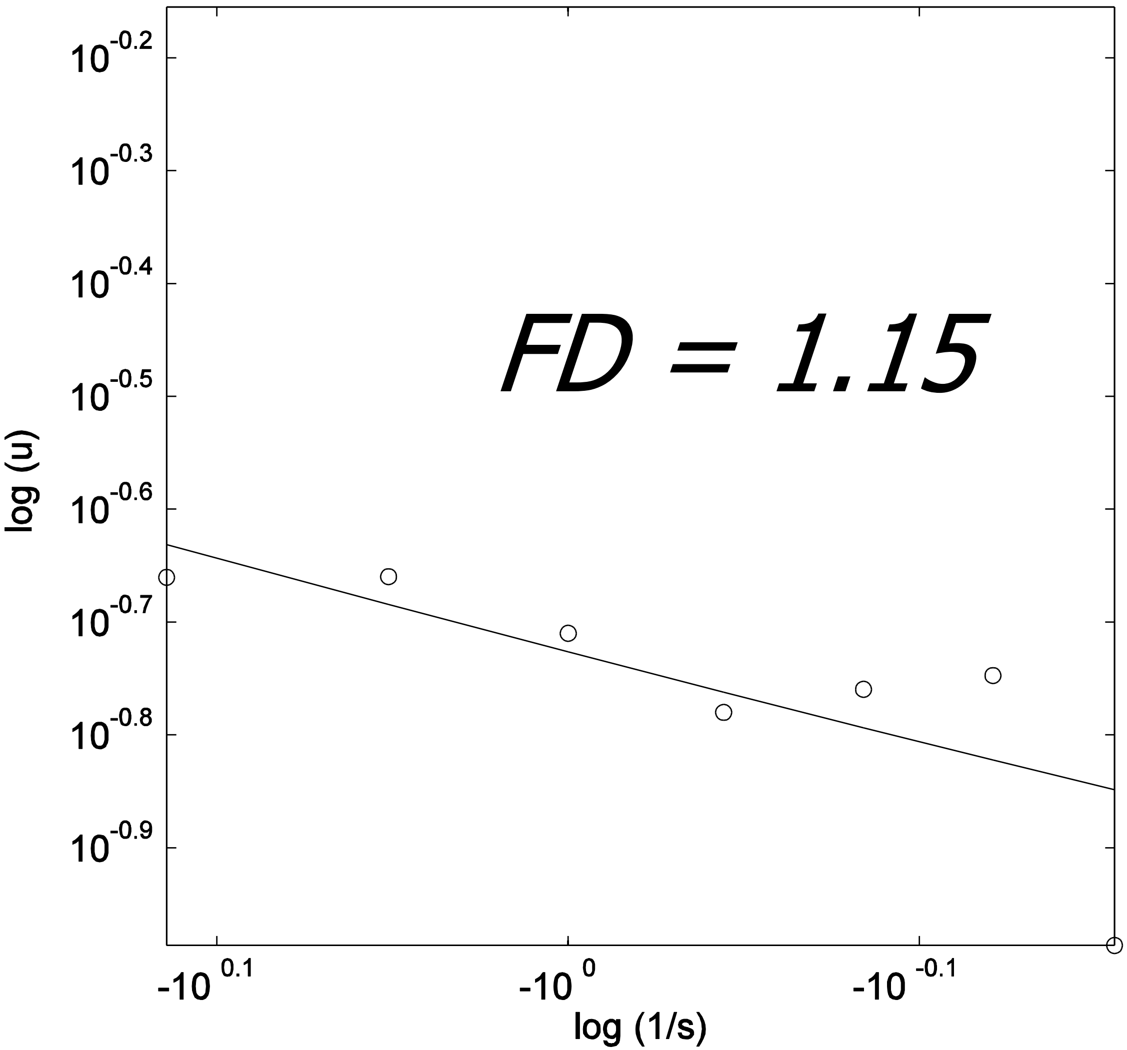
1D Signature of a Malignant Tumor



The Ruler Method Applied to a 1D Signature of a 2D Contour



The Ruler Method Applied to a 1D Signature of a 2D Contour



Fractional Brownian Motion

$$var[V(t_2) - V(t_1)] \propto |t_2 - t_1|^{2H}$$

Hurst exponent $0 < H < 1$

For a self-affine process in the *n*-dimensional Euclidean space

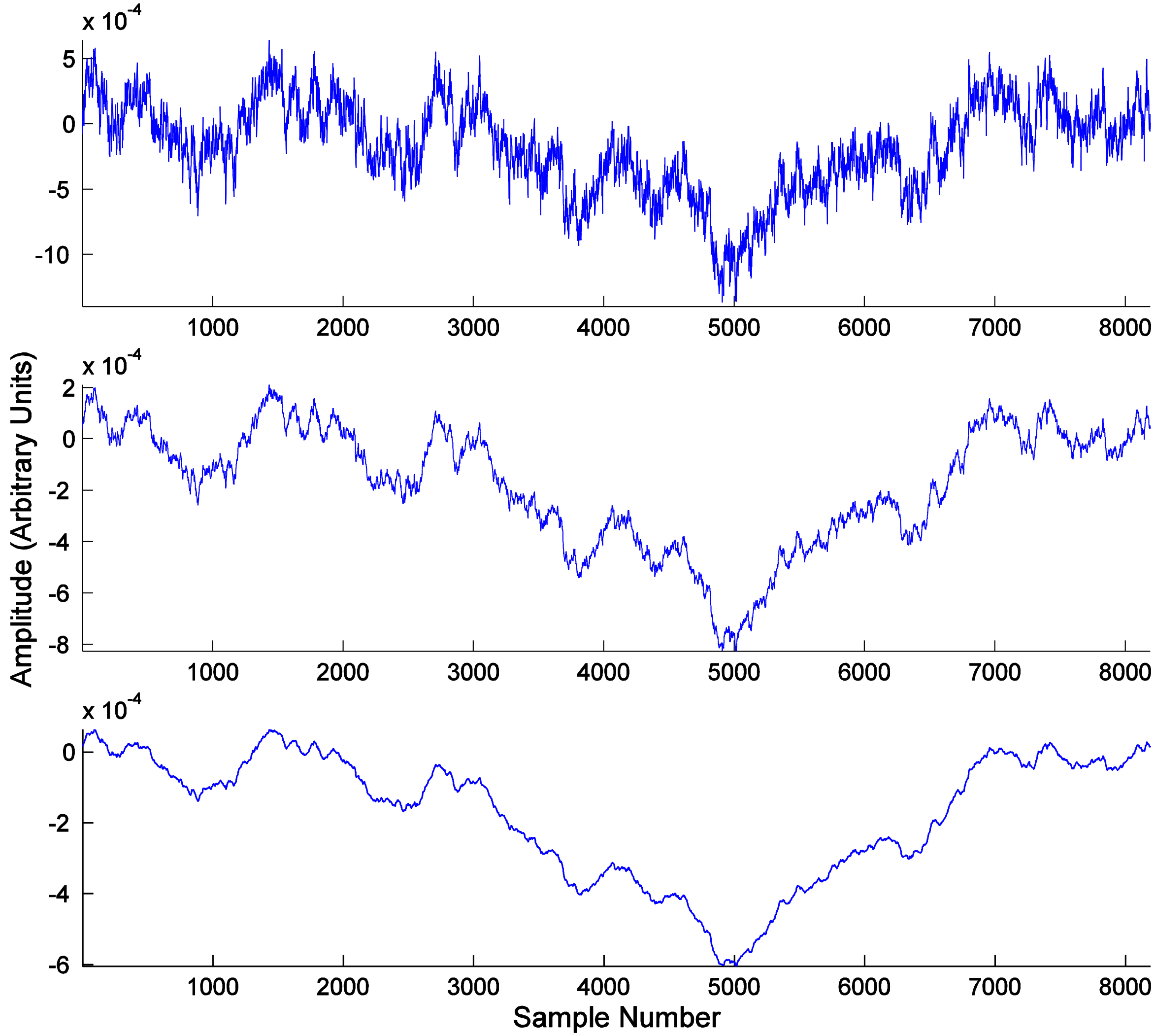
$D + H = n + 1$

Fractional Brownian Motion

Hurst exponent = 0.2
model FD = 1.8
estimated FD = 1.807

Hurst exponent = 0.5
model FD = 1.5
estimated FD = 1.5076

Hurst exponent = 0.8
model FD = 1.2
estimated FD = 1.2081

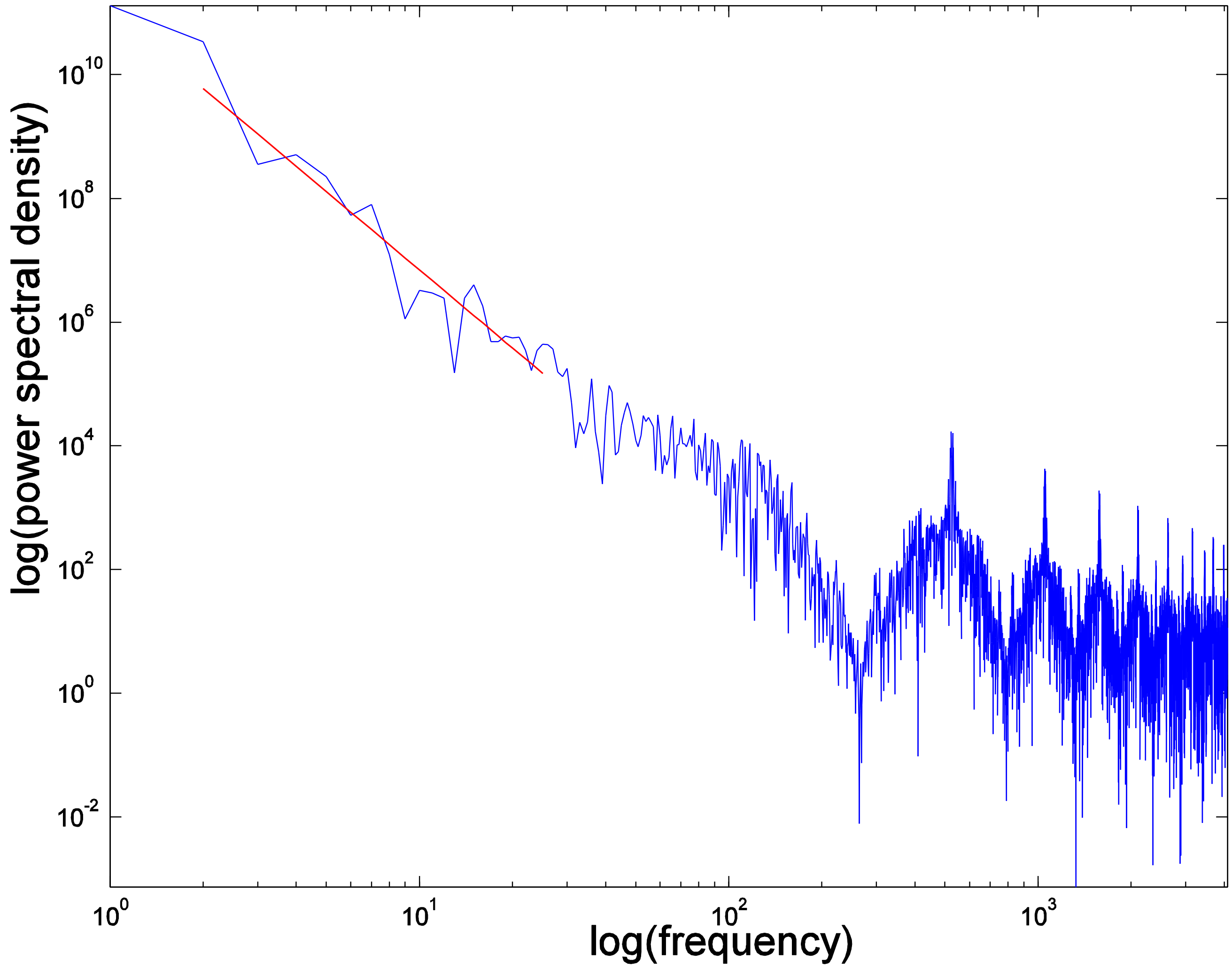


FD via Spectral Analysis of Signatures of Contours

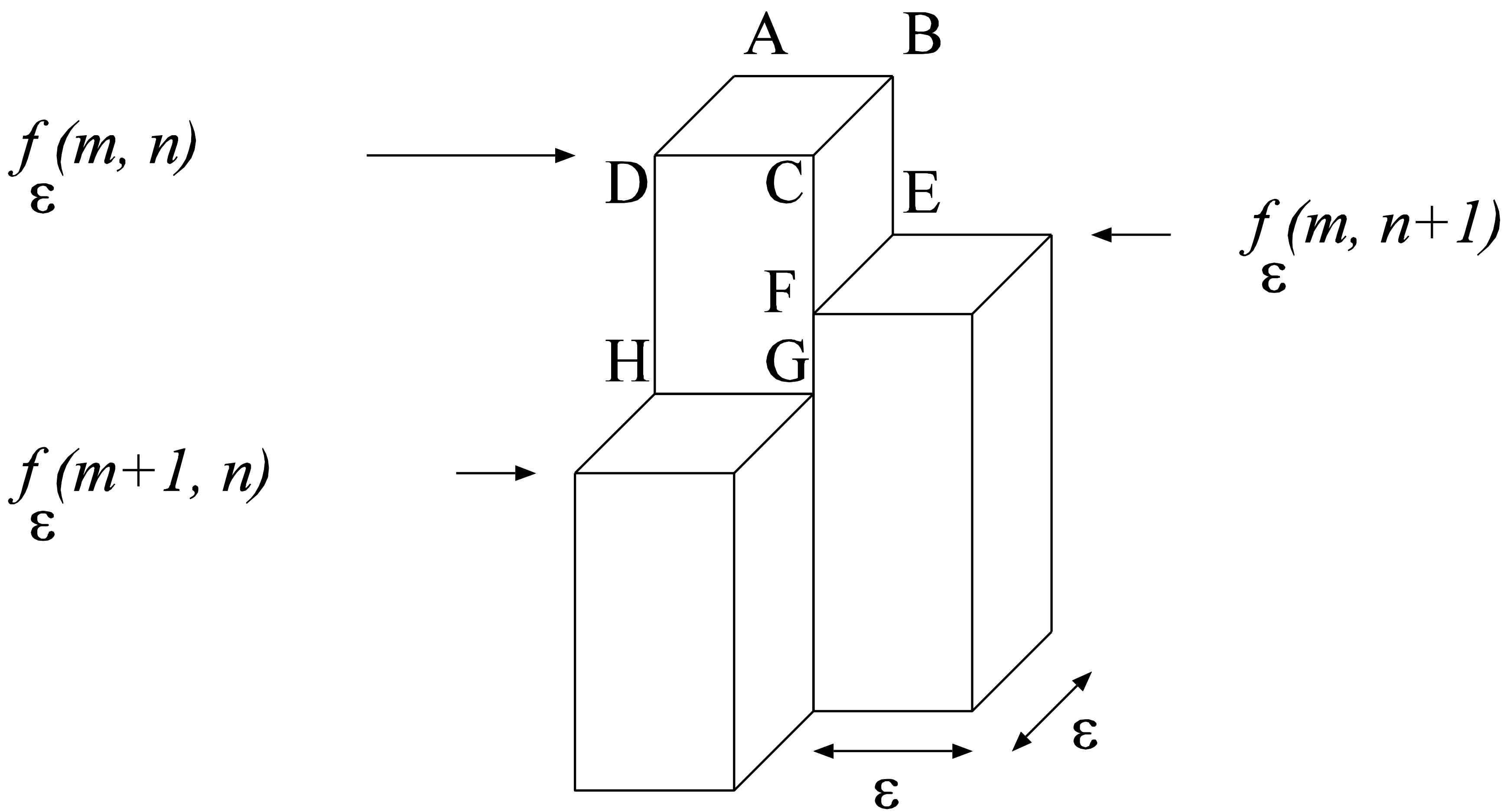
$$S_V(f) \propto \frac{1}{f^{\beta}}$$

$$D = \frac{5 - \beta}{2}$$

FD via Spectral Analysis of Signatures of Contours



Fractal Analysis of Grayscale Images: Blanket Method



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Fractal Analysis of Grayscale Images: Blanket Method

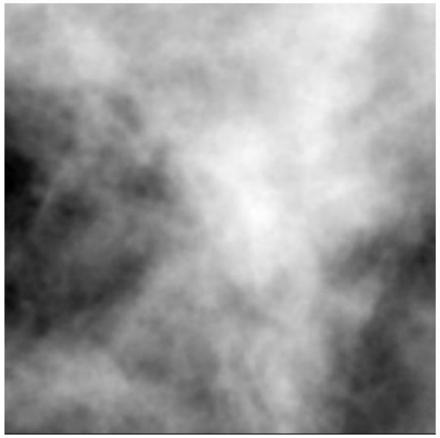
$$A(\varepsilon) = \sum_{m=0}^{N-2} \sum_{n=0}^{N-2} \{ \varepsilon^2 + \varepsilon [| f_\varepsilon(m,n) - f_\varepsilon(m,n+1)| + | f_\varepsilon(m,n) - f_\varepsilon(m+1,n)|] \}$$

$$D = 2 - \frac{\Delta \log[A(\varepsilon)]}{\Delta \log[\varepsilon]}$$

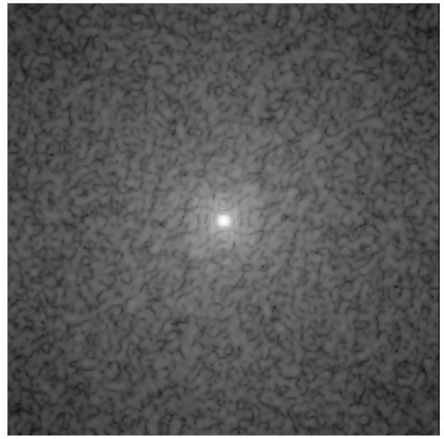
Fractal Analysis of Grayscale Images: Spectral Method

1. Compute the 2D Fourier transform of the image
2. Compute the 2D PSD
3. Transform the 2D PSD into a 1D PSD by radial averaging
4. Fit a straight line to a selected range of frequencies of the 1D PSD on a log−log scale
5. Determine the slope β of the best-fitting straight line

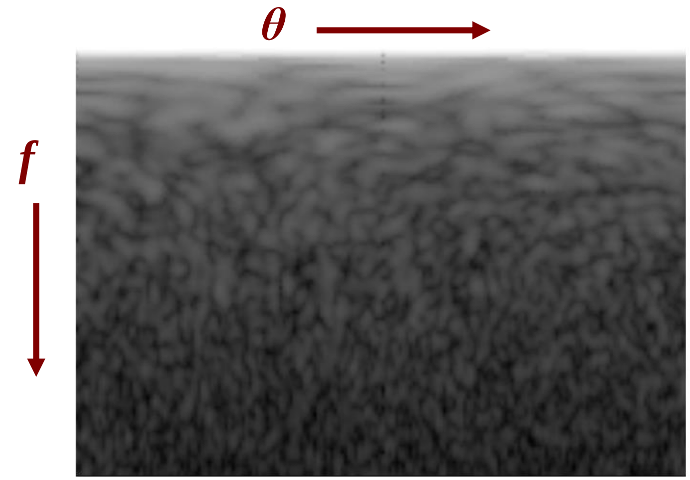
$$FD = \frac{8 - \beta}{2}$$



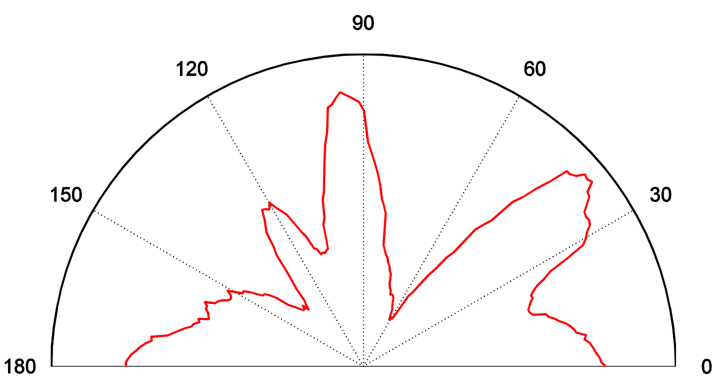
ROI, $s(x, y)$



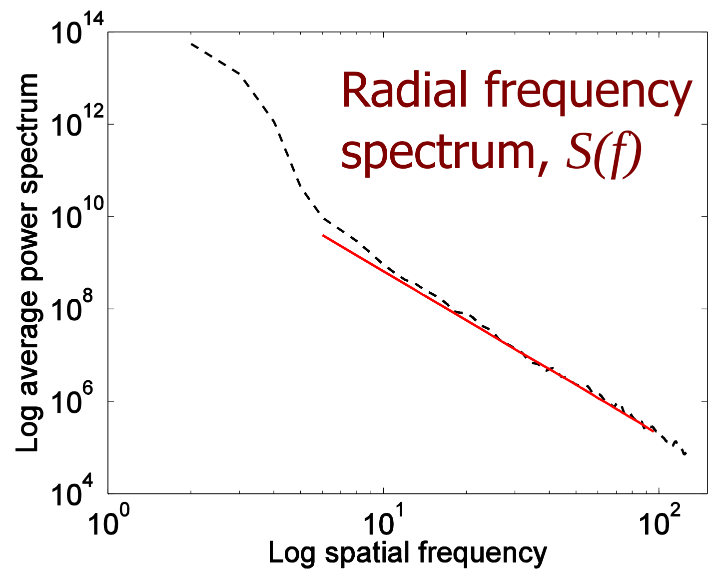
Fourier power spectrum, $S(u, v)$



Power spectrum in polar coordinates, $S(f, \theta)$

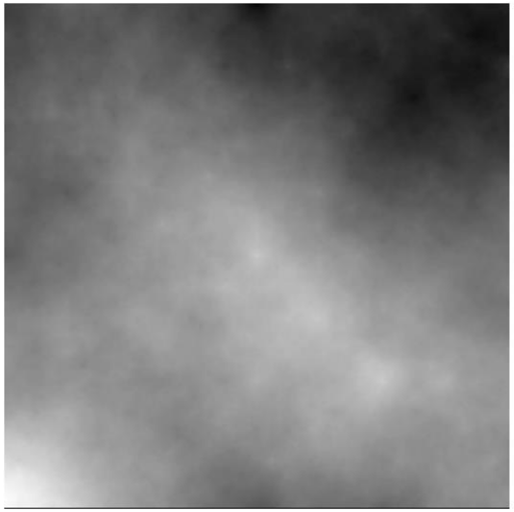


Angular spread of power, $S(\theta)$

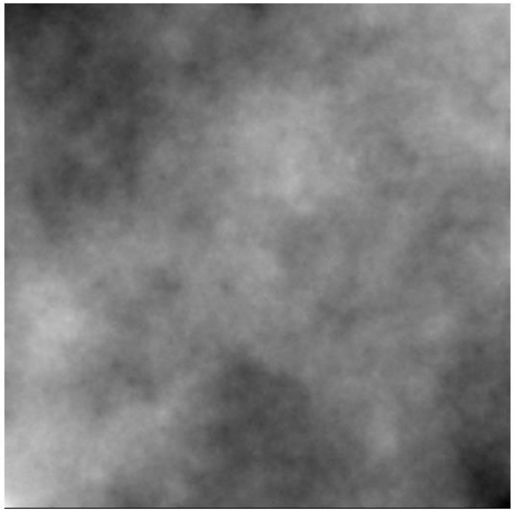


Radial frequency spectrum, $S(f)$

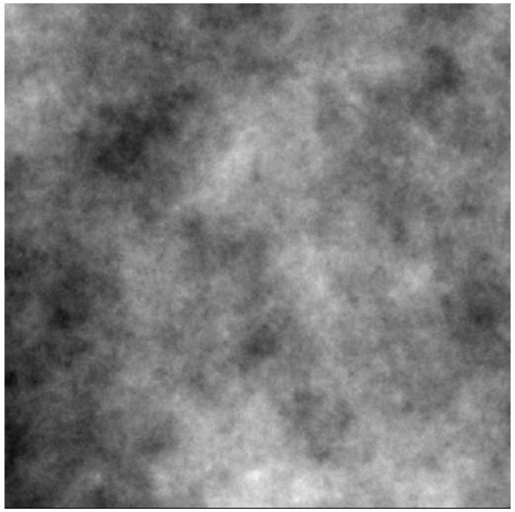
Fractal Analysis of Grayscale Images: Example



Model FD = 2.20
Blanket FD = 2.50
PSA FD = 2.66



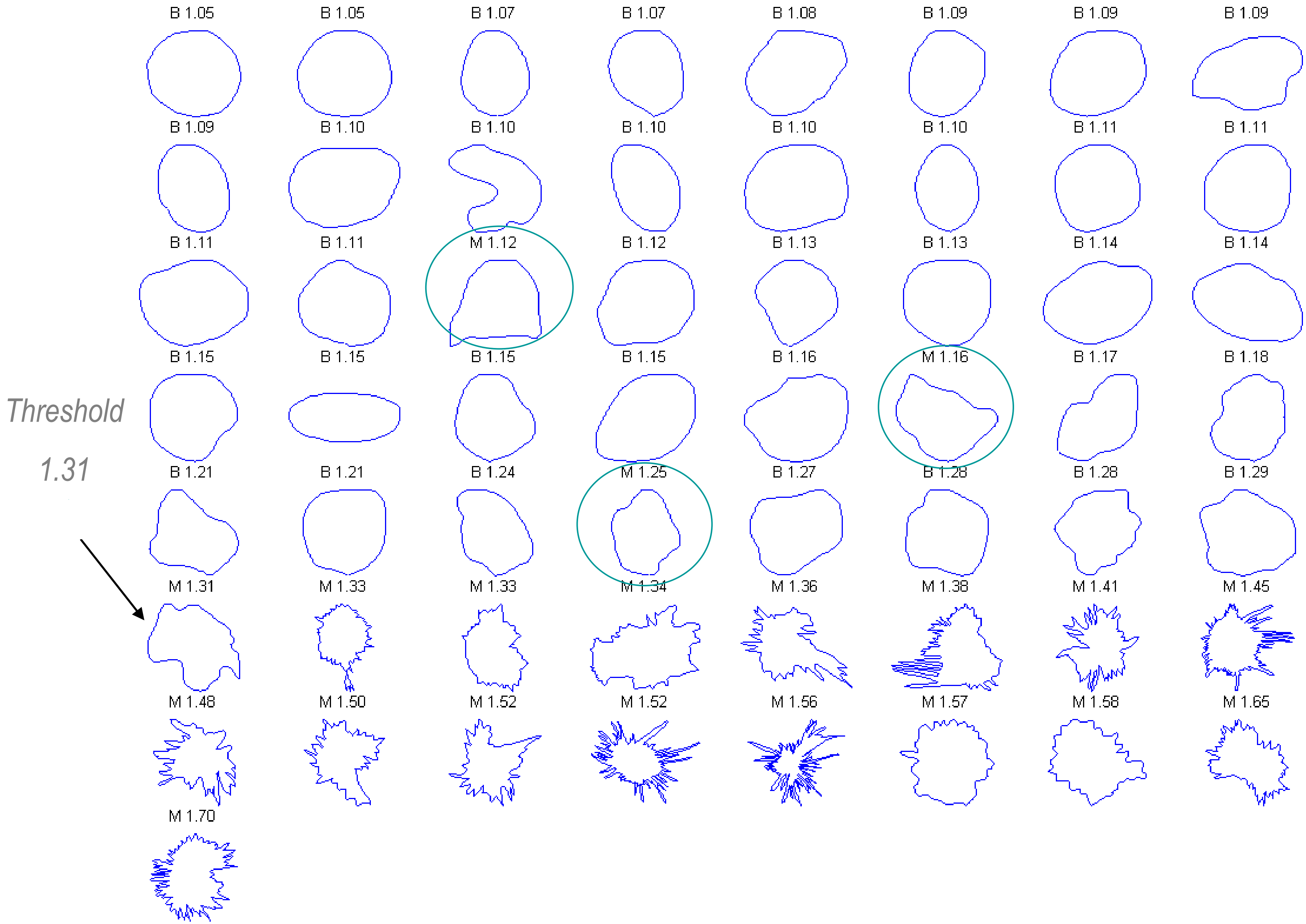
Model FD = 2.40
Blanket FD = 2.57
PSA FD = 2.67

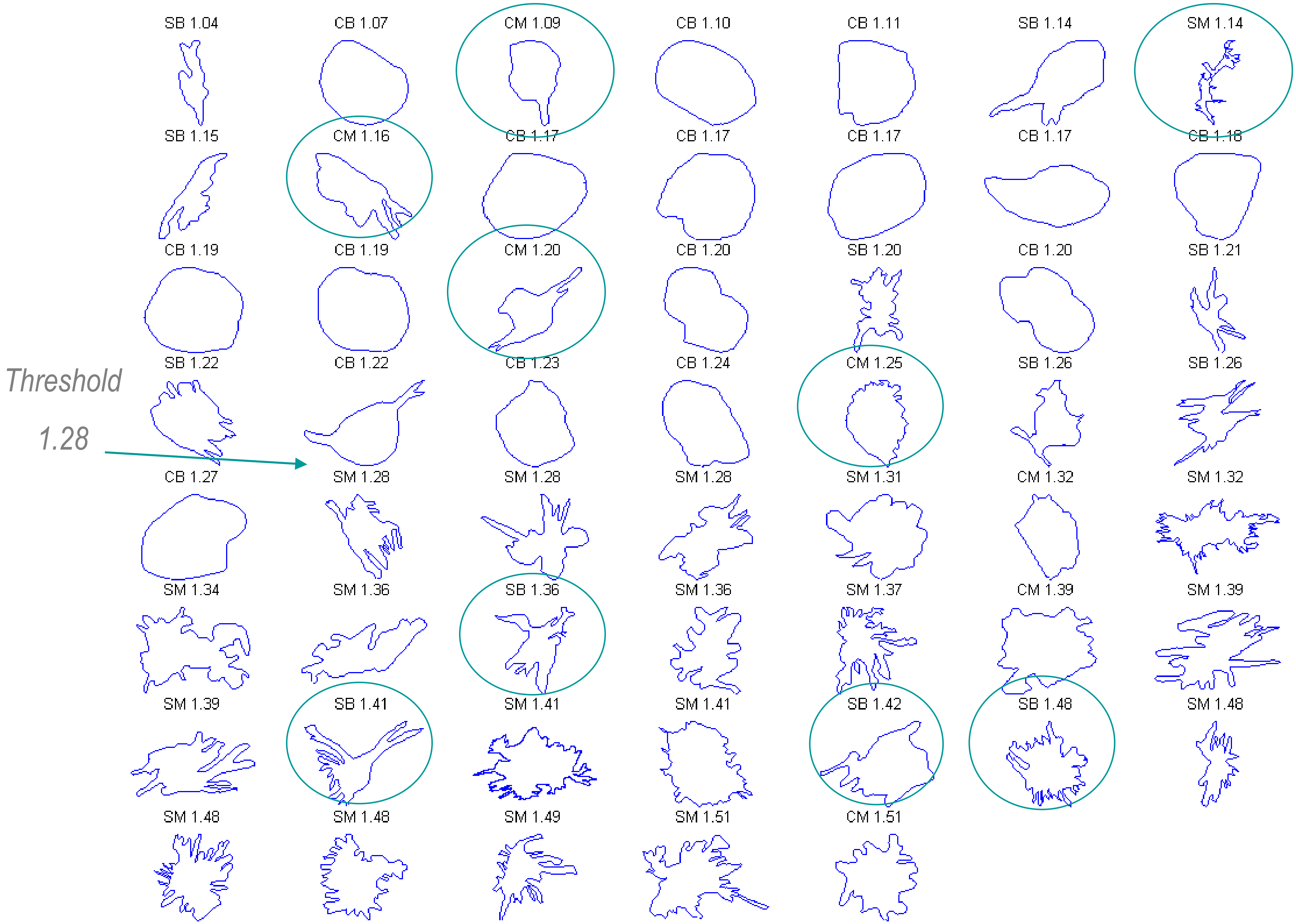


Model FD = 2.60
Blanket FD = 2.70
PSA FD = 2.68

Experiments with Contours of Breast Masses in Mammograms

- Dataset # 1:
  - 57 contours: 37 benign, 20 malignant
- Dataset # 2:
  - 54 contours: 28 benign, 26 malignant
    - 16 CB: circumscribed benign
    - 12 SB: spiculated benign
    - 7 CM: circumscribed malignant
    - 19 SM: spiculated malignant


Threshold
1.31
B 1.05
B 1.05
B 1.07
B 1.07
B 1.08
B 1.09
B 1.09
B 1.09
B 1.09
B 1.10
B 1.10
B 1.10
B 1.10
B 1.10
B 1.11
B 1.11
B 1.11
B 1.11
M 1.12
B 1.12
B 1.13
B 1.13
B 1.14
B 1.14
B 1.15
B 1.15
B 1.15
B 1.15
B 1.16
M 1.16
B 1.17
B 1.18
B 1.21
B 1.21
B 1.24
M 1.25
B 1.27
B 1.28
B 1.28
B 1.29
M 1.31
M 1.33
M 1.33
M 1.34
M 1.36
M 1.38
M 1.41
M 1.45
M 1.48
M 1.50
M 1.52
M 1.52
M 1.56
M 1.57
M 1.58
M 1.65
M 1.70



SB 1.04
CB 1.07
CM 1.09
CB 1.10
CB 1.11
SB 1.14
SM 1.14
SB 1.15
CM 1.16
CB 1.17
CB 1.17
CB 1.17
CB 1.17
CB 1.18
CB 1.19
CB 1.19
CM 1.20
CB 1.20
SB 1.20
CB 1.20
SB 1.21
Threshold
1.28
SB 1.22
CB 1.22
CB 1.23
CB 1.24
CM 1.25
SB 1.26
SB 1.26
CB 1.27
SM 1.28
SM 1.28
SM 1.28
SM 1.31
CM 1.32
SM 1.32
SM 1.34
SM 1.36
SB 1.36
SM 1.36
SM 1.37
CM 1.39
SM 1.39
SM 1.39
SB 1.41
SM 1.41
SM 1.41
SB 1.42
SB 1.48
SM 1.48
SM 1.48
SM 1.48
SM 1.49
SM 1.51
CM 1.51

Classification of Masses

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Dataset # 1

- Fractal dimension
  - Benign: 1.14 ± 0.06
  - Malignant: 1.43 ± 0.16
- Classification accuracy
  - 54/57 = 94.7%

Dataset # 2

- Fractal dimension
  - Benign: 1.21 ± 0.10
  - Malignant: 1.35 ± 0.12
- Classification accuracy
  - 45/54 = 83.3%

with the ruler method and 1D signatures of the contours

Pattern Classification

- Leave-one-out method

- Receiver operating characteristics (ROC)

  - Sensitivity = True-positive fraction
  - Specificity = 1 – False-positive fraction
  - Classification accuracy: area under the ROC curve (*AUC*)

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Results of Classification *AUC* with Fractal Dimension

Method	Dataset 1	Dataset 2	Both
2D box counting	0.90	0.75	0.84
1D box counting	0.89	0.80	0.88
2D ruler	0.94	0.81	0.88
1D ruler	0.91	0.80	0.89

Comparative Analysis with Shape Factors: Compactness

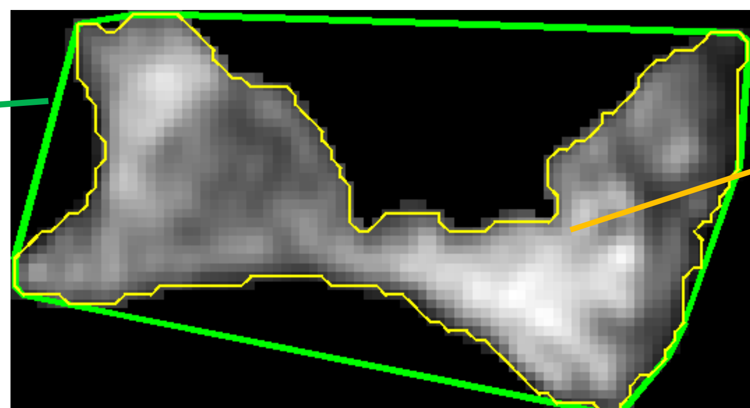
- Compactness C based on area A and perimeter P

$$C = 1 - \frac{4\pi A}{P^2}$$

Convex Deficiency

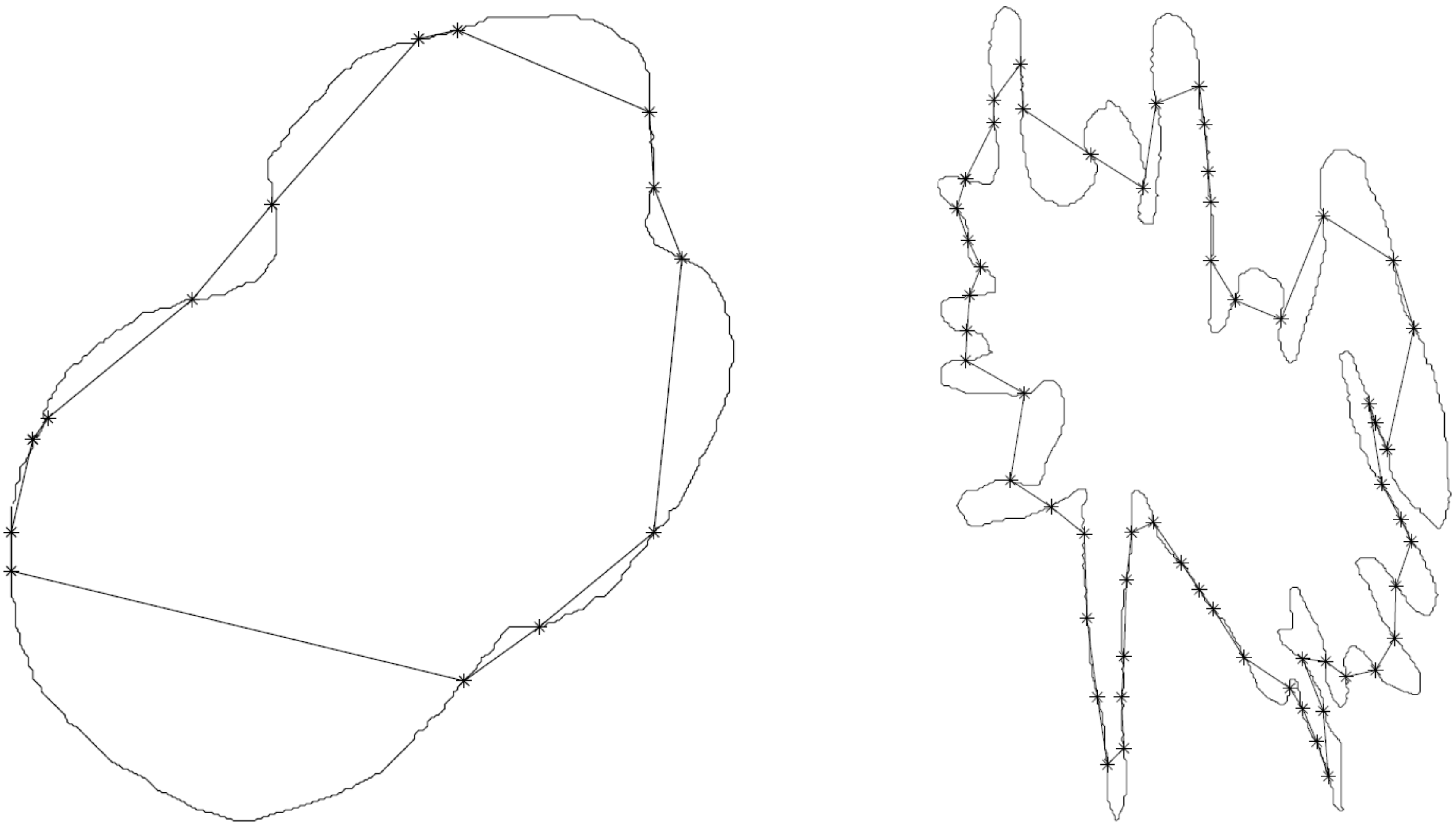
$$CD = (HA - OA) / HA$$

Convex Hull Area HA

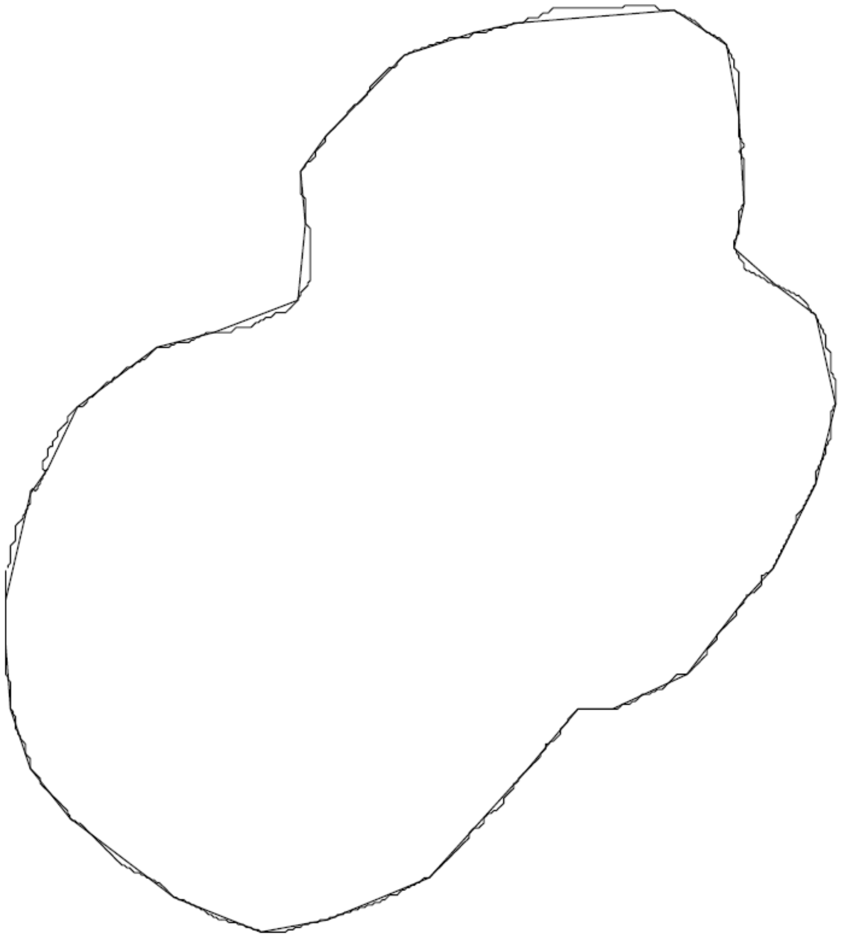


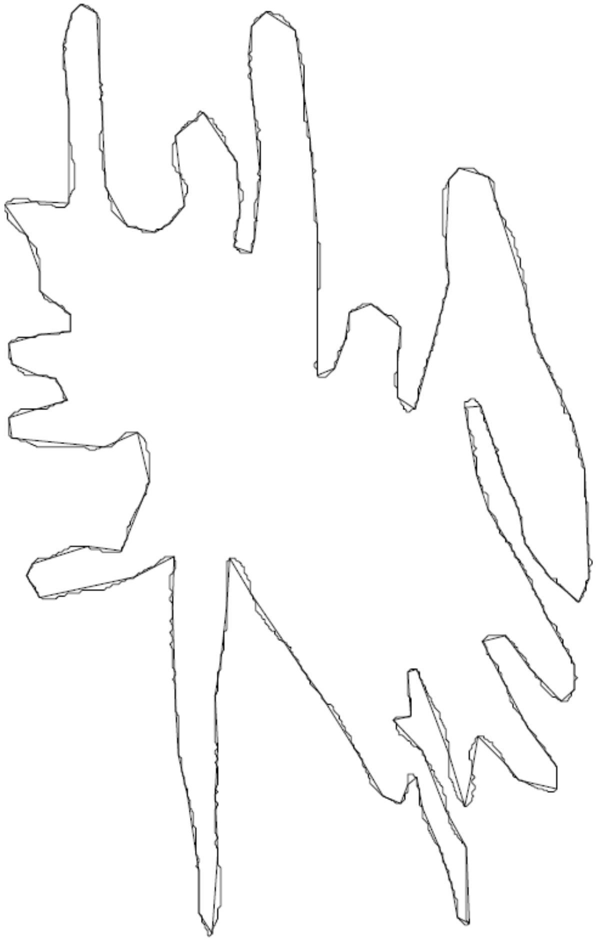
Object Area OA

Detection of Points of Inflexion: Benign (14) vs Malignant (58)



Polygonal Modeling: Benign (36) vs Malignant (146)





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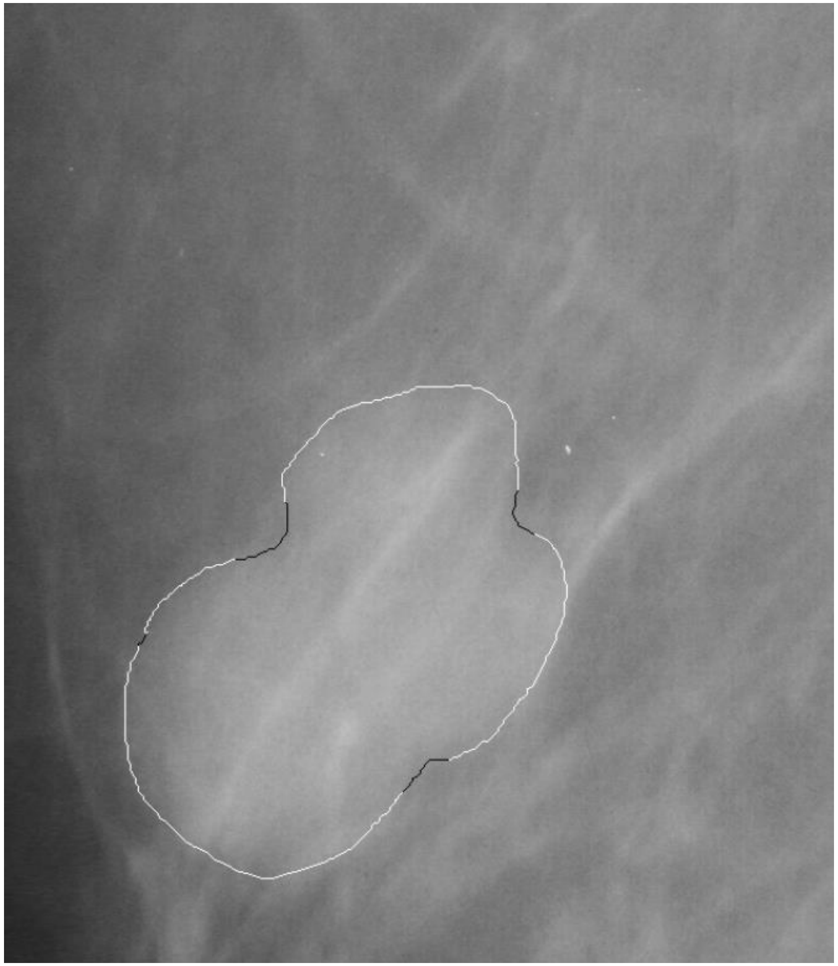
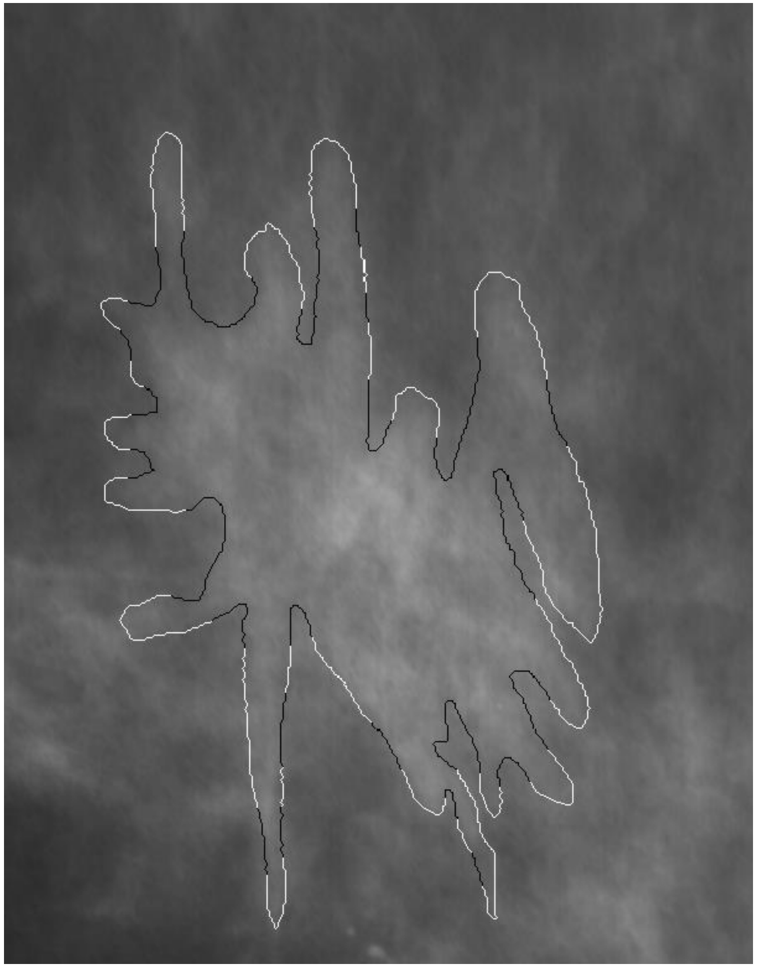
Fractional Concavity





Spiculation Index

- Each segment of the contour is treated as a spicule candidate with length S_i and angle θ_i

$$SI = \frac{\sum_{i=1}^{N} (1 + \cos\theta_i) S_i}{\sum_{i=1}^{N} S_i}$$

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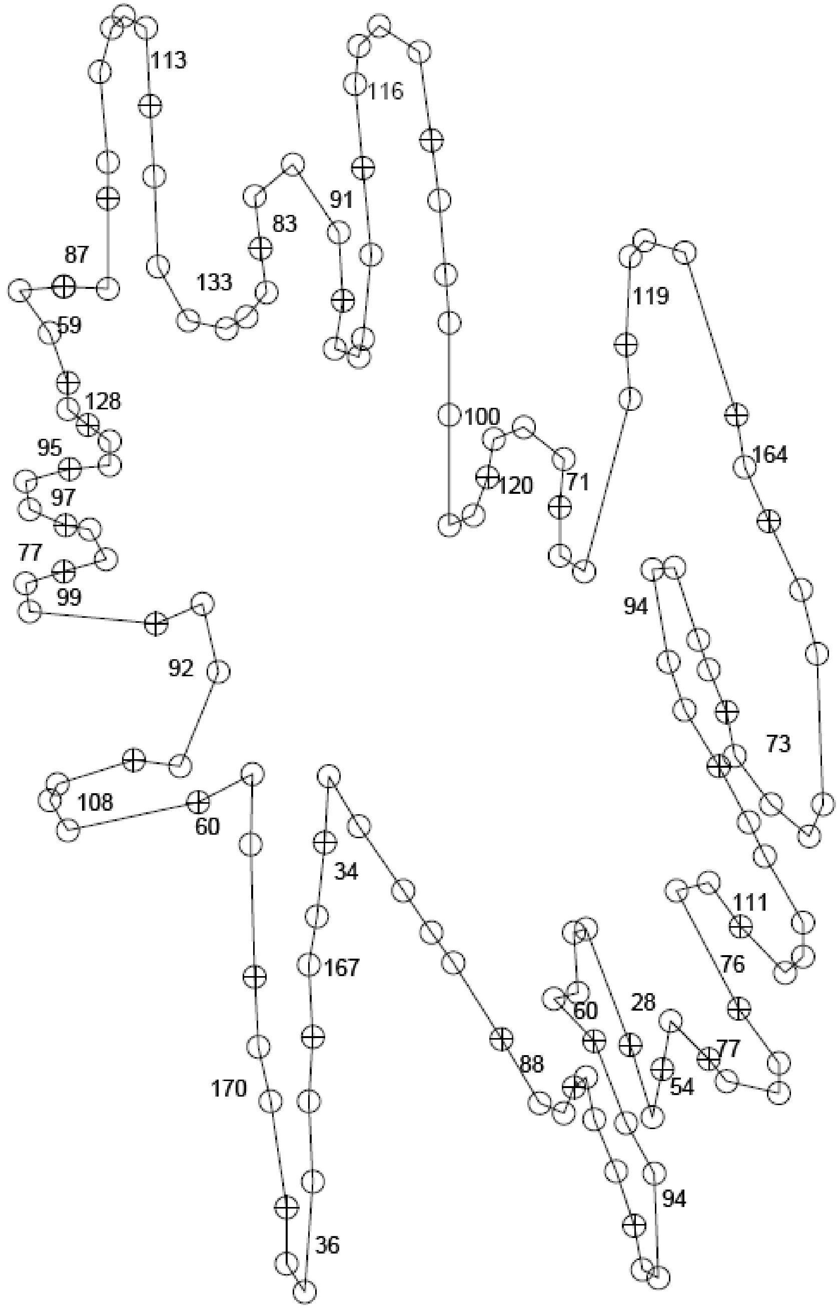
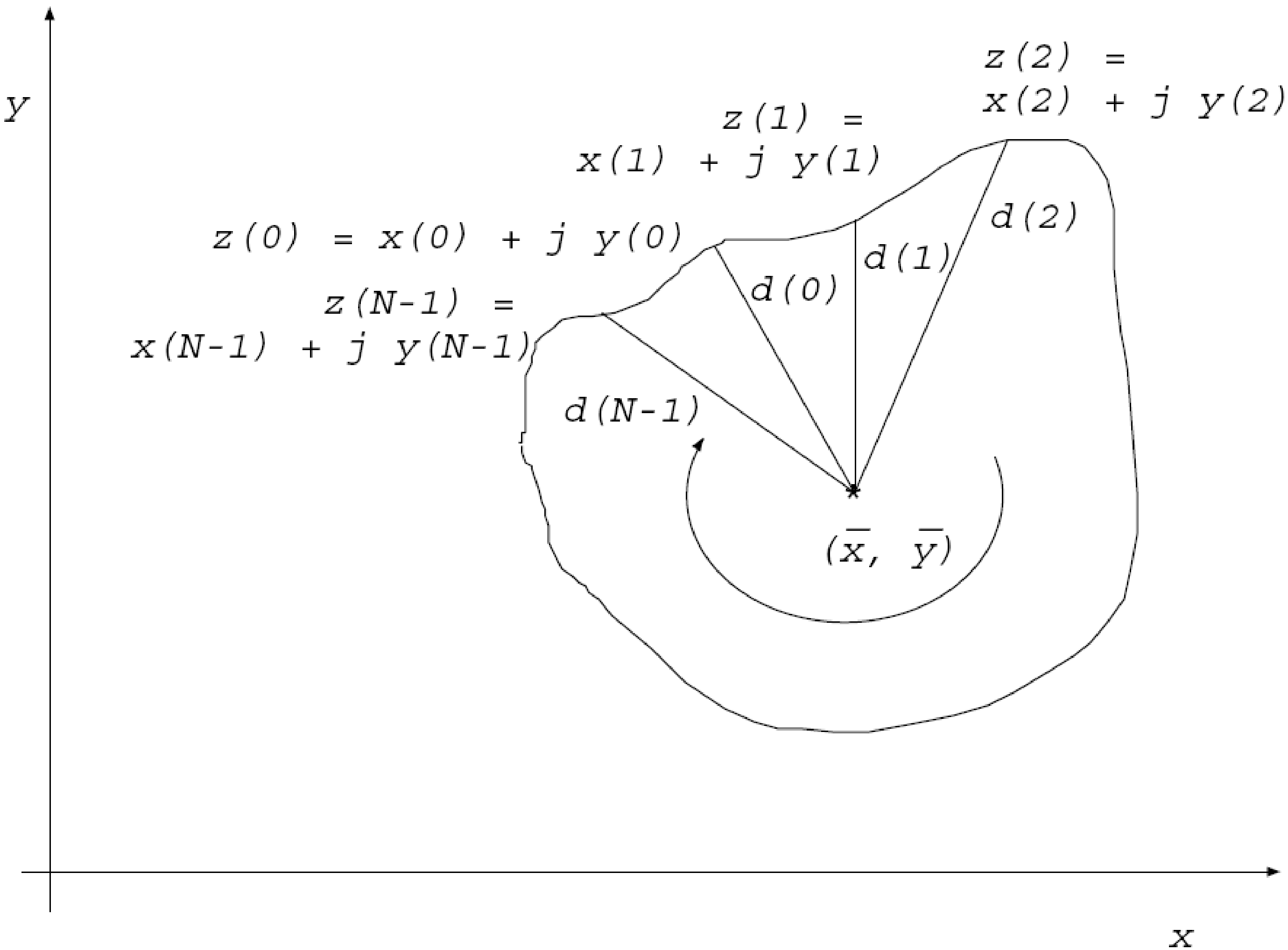


Fourier Descriptors using Coordinates of Contour Pixels



Fourier Descriptors

$$z(n) = x(n) + j\,y(n),\; n = 0, 1, 2, \ldots, N-1$$

$$Z(k) = \frac{1}{N} \sum_{n=0}^{N-1} z(n)\; \exp\left[-j\,\frac{2\pi}{N}\,nk\right]$$

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Fourier Factor from Normalized Fourier Descriptors

$$Z_o(k) = \begin{cases} 0, & k = 0; \\ \frac{Z(k)}{Z(1)}, & \text{otherwise} \end{cases}$$

$$ff = 1 - \frac{\Sigma_{k=-N/2+1}^{N/2} |Z_o(k)|/|k|}{\Sigma_{k=-N/2+1}^{N/2} |Z_o(k)|}$$

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Benign versus Malignant Classification Performance: AUC

❖ Fourier factor (FF)	0.77
❖ Compactness (C)	0.87
❖ Fractional concavity (Fcc)	0.88
❖ Fractal dimension (FD)	0.89
❖ Spiculation index (SI)	0.90
❖ [FD, Fcc]	0.93

with the two datasets combined (111 contours) and the ruler method on 1D signatures of the contours to compute FD

Additional Experiments Including FFDMs

Table 10.1 List of the nine shape factors and their individual AUC values for each dataset used in the present study.

Shape Factor	Dataset A	Dataset B	Dataset C
FD-ruler 1D	0.9419	0.8228	0.8794
FD-ruler 2D	0.9743	0.8448	0.9084
FD-box 1D	0.9230	0.8173	0.8752
FD-box 2D	0.9135	0.7761	0.8695
cf	0.9851	0.7967	0.9175
CD	0.9824	0.7308	0.9135
f_{cc}	0.9973	0.7527	0.8367
SI	0.9662	0.8118	0.8887
ff	0.9878	0.8173	0.9040

Table 10.2 List of the shape factors selected and the AUC values with various classifiers for the datasets used in the present study and combinations thereof. The rows indicated with an asterisk represent the features selected most often in the LOO procedure for each dataset listed. The set of selected features and the dimension of the feature vector (N_f) varies in each step of the LOO procedure (for each mass being tested). The initial set of features has a dimension of 9.

Feature Selection	Classifier	Dataset A	Dataset B	Dataset {A, B}	Dataset C	Dataset {A, B, C}
All features in Table 10.1	LDA	0.9797	0.7390	0.9117	0.8877	0.9267
	QDA	0.9797	0.7885	0.9154	0.8500	0.9084
	RBF	0.9919	0.7981	0.9348	0.9162	0.9309
Logistic regression	*	f_{cc}	FD-ruler 2D, FD-box 2D	f_{cc}, SI, CD	FD-ruler 1D, CD	FD-ruler 1D, f_{cc}
	LDA	0.9973	0.8448	0.9247	0.9243	0.9327
	QDA	0.9973	0.8393	0.9177	0.8982	0.9283
	RBF	0.9973	0.8599	0.9324	0.9264	0.9393
Stepwise regression	*	f_{cc}, SI	FD-ruler 2D, FD-box 2D	f_{cc}, SI, CD	FD-ruler 1D, cf, f_{cc}	FD-ruler 1D, cf, f_{cc}, SI, CD
	LDA	0.9919	0.8448	0.9247	0.9076	0.9297
	QDA	0.9920	0.8393	0.9177	0.8944	0.9044
	RBF	0.9973	0.8599	0.9324	0.9156	0.9362

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Conclusion

- Significant differences exist in the fractal dimension between contours of malignant tumors and benign masses
- Fractal dimension can serve as a useful feature in computer-aided diagnosis of breast cancer

Thank you!

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  Dr. Liang Shen, Dr. Naga Mudigonda,
  Dr. Nema El-Faramawy, Dr. Hilary Alto,
  Dr. Shantanu Banik, Dr. Faraz Oloumi,
  Lucas Frighetto-Pereira