Quantitative and Semantic MRI–Based Phenotypes of Breast Cancer in the Multi-Institutional National Cancer Institute Cancer Imaging Archive Dataset

TCGA Breast Phenotype Research Group

TCIA: The Cancer Imaging Archive

TCGA: The Cancer Genome Atlas

Presented for the TCIA Breast Group by:
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University of Texas MD Anderson Cancer Center

TCGA Breast Phenotype Research Group

Radiologists:
- Elizabeth Morris – MSKCC
- Ermelinda Bonaccio – Roswell
- Kathleen Brandt – Mayo
- Elizabeth Burnside – U Wisconsin Madison
- Basak Dogan – MD Anderson
- Marie Ganott – Magee
- Jose Net – U Miami
- Elizabeth Sutton – MSKCC
- Gary Whitman – MD Anderson
- Margarita Zuley – U Pittsburgh
- H. Carisa Le-Petross – MD Anderson

NCI:
- Carl Jaffe
- John Freymann
- Marie Ganott
- Erich Huang
- Justin Kirby
- Brenda Fevrier-Sullivan

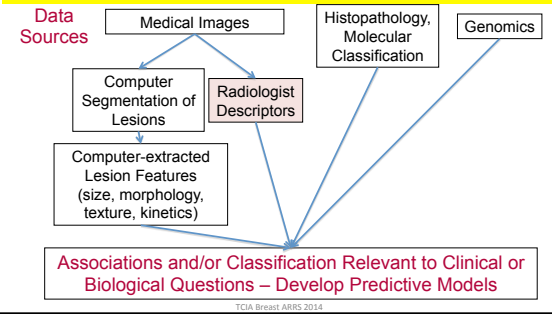
Quantitative Image Analysis and Computational Researchers:
- Maryellen Giger – U of Chicago
- Hui Li – U of Chicago

TCGA Breast Phenotype Research Group

- **Breast Image Feature Scoring Project**
  - aimed at developing and testing a BIRADS-inspired Breast Feature Key for correlative analysis with the other TCGA data types (genetics, pathology, clinical)
- **Mapping of Breast Image-based Phenotypes to Histopathology and Genomics**
  - seeks to advance and relate quantitative, computer-extracted tumor and parenchymal characteristics from breast images to clinical outcomes (diagnosis, staging, and response to therapy), histopathology, and genomics.

Aim of Imaging Genomics

Asks questions about the relationships between features "seen" in medical images and the biology of cancer



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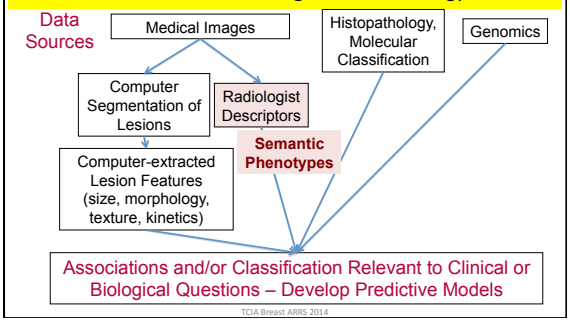

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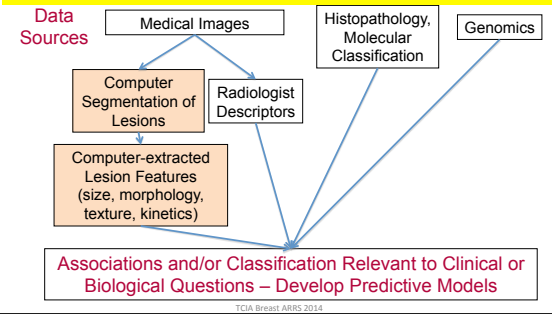
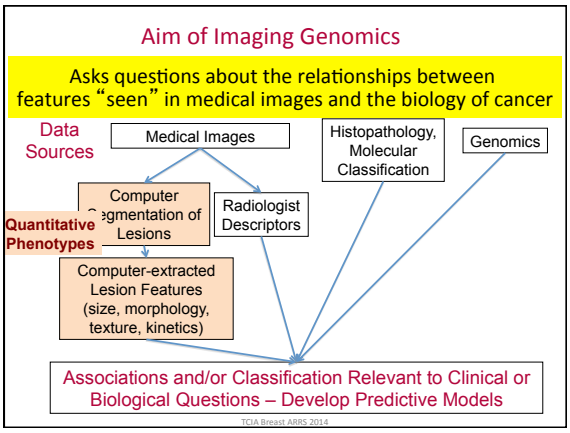
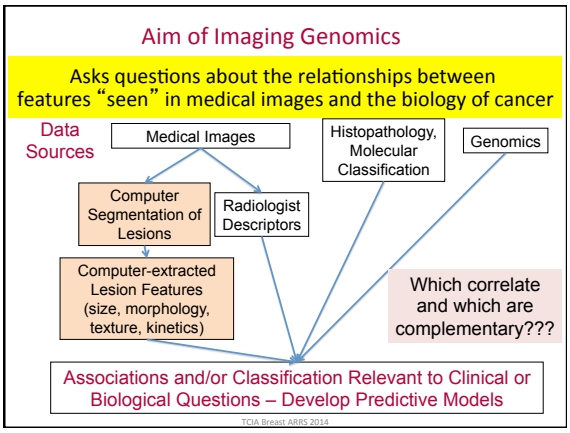
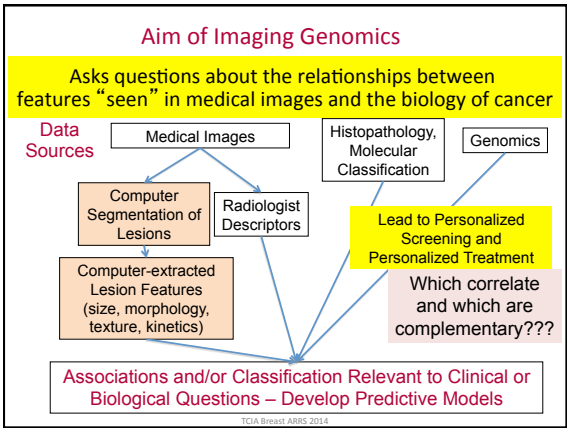








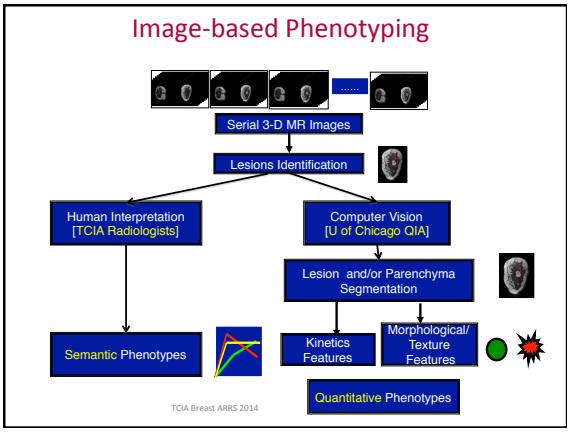


Image-Based Phenotyping Semantic Descriptors

TCGA Breast Imaging Scoring Visual Guide v8

Based on
TCGA BI-RADS PowerPoint
Elizabeth Morris, M.D.
Memorial Sloan-Kettering Cancer Center

Each case is read by three of the TCIA radiologists

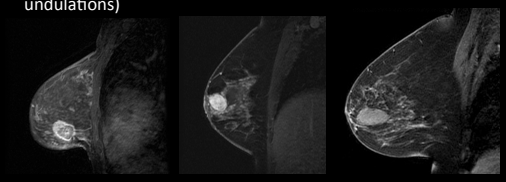
2.2 Mass Observations - Shape

- Round-Oval
- Irregular

2.2 Mass Observations - Shape

Option: Round - Oval (Includes Lobulated)

- A mass that is elliptical or egg-shaped (may include 2 or 3 undulations)



OVAL rim enhancing mass *Invasive ductal carcinoma*

OVAL heterogeneous enhancement *Phyllodes tumor*

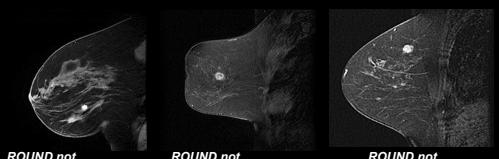
OVAL homogeneous enhancement *Fibroadenoma*

E. Morris

2.2 Mass Observations - Shape

Option: Round - Oval

- A mass that is spherical, ball-shaped, circular, or globular



ROUND not circumscribed homogeneous enhancement *Invasive ductal carcinoma*

ROUND not circumscribed rim enhancement *Invasive ductal carcinoma*

ROUND not circumscribed heterogeneous enhancement *Fibroadenoma*

E. Morris

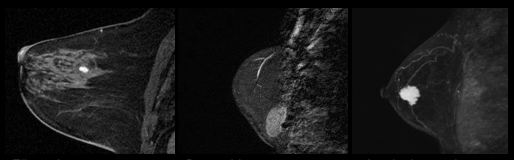
2.3 Mass Observations - Internal Enhancement

- Homogeneous
- Heterogeneous

2.3 Mass Observations - Internal Enhancement

Option: Homogenous

- There is confluent uniform enhancement of the mass.



Fibroadenoma

Desmoid tumor

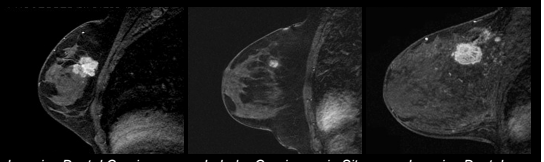
Atypical vascular lesion

E. Morris

2.3 Mass Observations - Internal Enhancement

Option: Heterogenous

- Non-uniform enhancement with variable signal intensity



Invasive Ductal Carcinoma

Lobular Carcinoma in Situ

Invasive Ductal Carcinoma

E. Morris

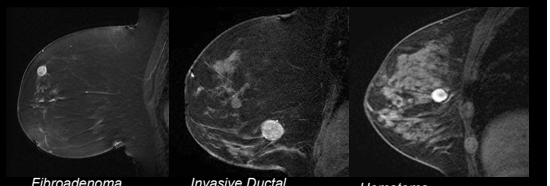
2.7 Mass Observations - Margin

- Circumscribed
- Not Circumscribed - Spiculated
- Not Circumscribed - Irregular

2.7 Mass Observations - Margin

Option: Circumscribed

- Sharply demarcated with an abrupt transition between lesion and surrounding tissue. For MRI, the entire margin must be well-defined for a mass to qualify as circumscribed.



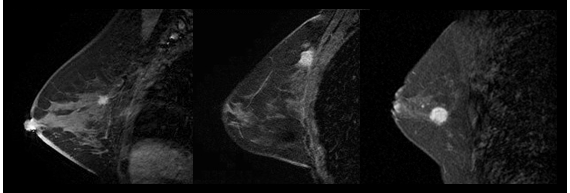
Fibroadenoma Postcontrast | *Invasive Ductal Carcinoma* | *Hematoma*

E. Morris

2.7 Mass Observations - Margin

Option: Not circumscribed - irregular

- composed of edges either round or jagged but not spiculated. Implies suspicious finding.



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2.7 Mass Observations - Margin

Option: Not circumscribed spiculated

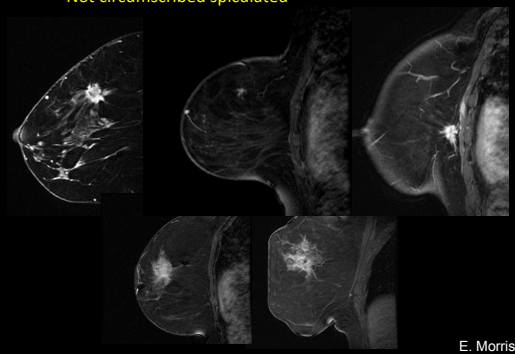

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Image-based Phenotyping

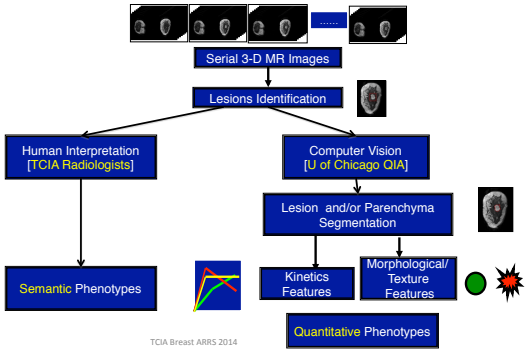


Image-Based Phenotyping Quantitative Descriptors

Quantitative Image Analysis Workstation for High-Throughput Image-based Phenotyping in the Assessment of Breast Lesions on Magnetic Resonance Imaging

from **Giger lab**

Maryellen Giger, Ph.D.

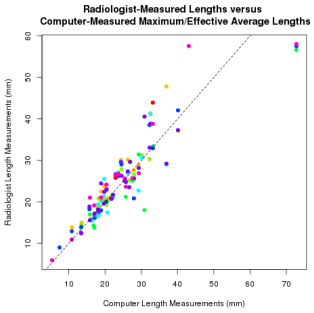
The University of Chicago

Preliminary Results

1. **Comparisons between radiologist-extracted semantic descriptors and computer-extracted quantitative features**
2. Initial relationships with clinical and histopathology data

TCIA Breast ARRS 2014

Radiologist vs. Computer Phenotype: Size



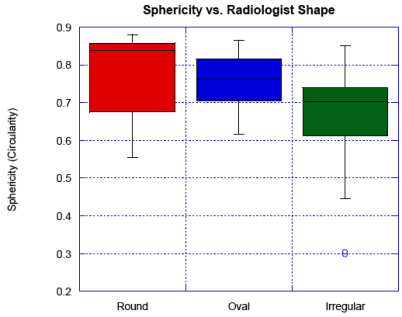
Assessment of the maximal lesion diameter on 61 cases

- interclass correlation of 0.865 (CI:0.717, 0.965) among radiologist raters
- a significant correlation of 0.95 between radiologist ratings and computer-extracted size.

Preliminary Results

TCIA Breast ARRS 2014

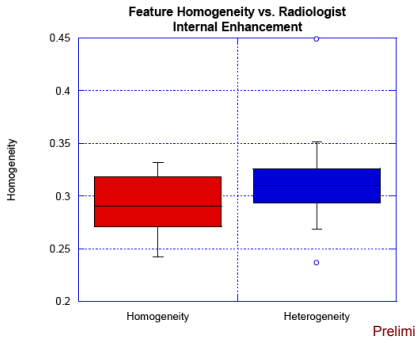
Radiologist vs. Computer Phenotype: Shape



Preliminary Results

TCIA Breast ARRS 2014

Radiologist vs. Computer Phenotype: Heterogeneity



Preliminary Results

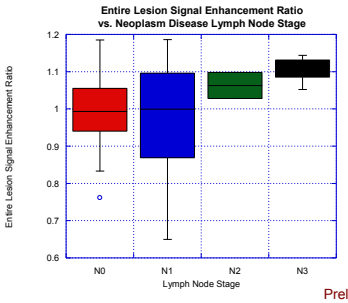
TCIA Breast ARRS 2014

Preliminary Results

1. Comparisons between radiologist-extracted semantic descriptors and computer-extracted quantitative features
2. **Initial relationships with clinical and histopathology data**

TCIA Breast ARRS 2014

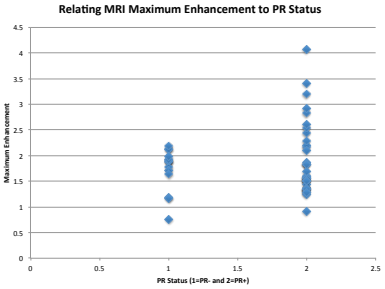
Computer Phenotype: Signal Enhancement vs. Lymph Node Status



Preliminary Results

TCIA Breast ARRS 2014

Computer Phenotype: Signal Enhancement vs. PR Status



Preliminary Results

TCIA Breast ARRS 2014

Summary & Conclusions - 1

While both qualitative and quantitative image-based phenotypes are expected to be useful in assessing changes in gene expression levels, correlation and agreement among these phenotypes is essential in understanding the phenotypic characterizations of breast cancers.

Summary & Conclusions - 2

- Relationships to pathology, molecular classification (HER2neu overexpression, progesterone receptor, and estrogen receptor status), and genetic findings continue to be investigated.
- Current database being analyzed includes 98 cases with MRIs, radiologist reads, computer analyses, clinical data, histopathology, genomics, and gene array outputs.

Thank You

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