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August 2014
Volume 272, Issue 2

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Original Research
Breast Imaging**Identification of Intrinsic Imaging Phenotypes for Breast Cancer Tumors:
Preliminary Associations with Gene Expression Profiles**

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Address correspondence to D.K. (e-mail: Despina.Kontos@uphs.upenn.edu).DOI: <http://dx.doi.org/10.1148/radiol.14131375>

Abstract Full Text Figures References Supplemental Materials Cited by PDF

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PODCAST

Intrinsic Imaging Phenotypes in Breast Cancer Tumors[Listen to this Discussion](#) [Duration: 10:06]**Moderator:** Deborah Levine, MD, Senior Deputy Editor of *Radiology***Guest:** Ahmed Bilal Ashraf, PhD, Department of Radiology, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pa**Article Discussed:** Identification of intrinsic imaging phenotypes for breast cancer tumors: preliminary associations with gene expression profiles. *Ashraf AB, Daye D, Gavenonis S, et al. Radiology 2014;272(2):374-384.*

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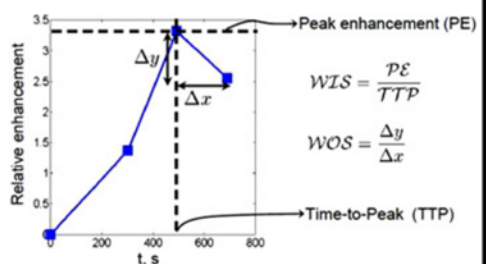
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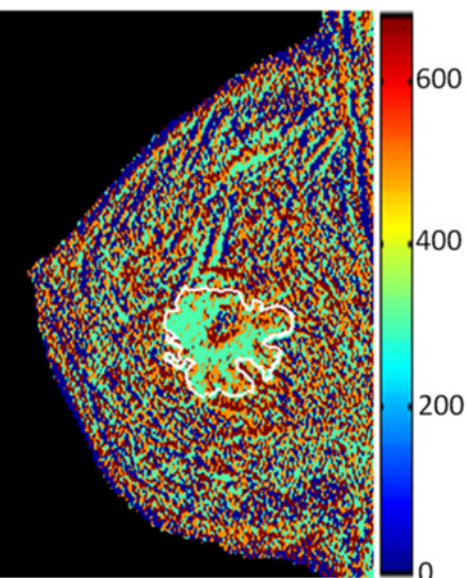
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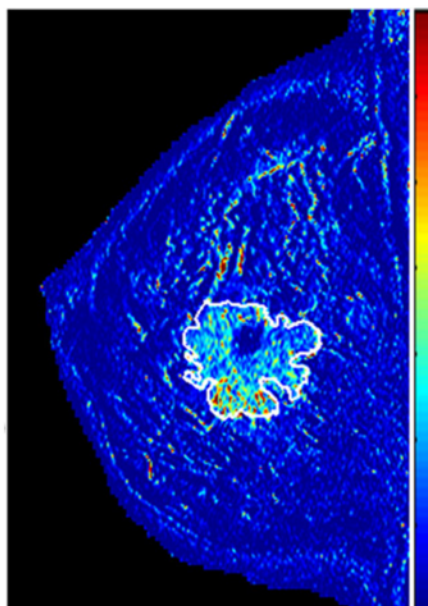
SUPPLEMENTAL FIGURES



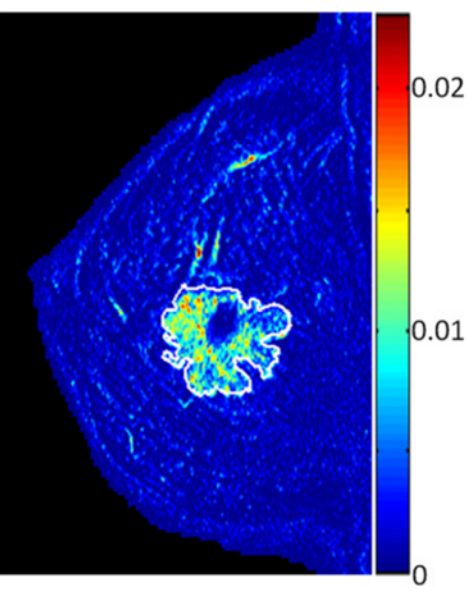
a.



b.



c.



d.

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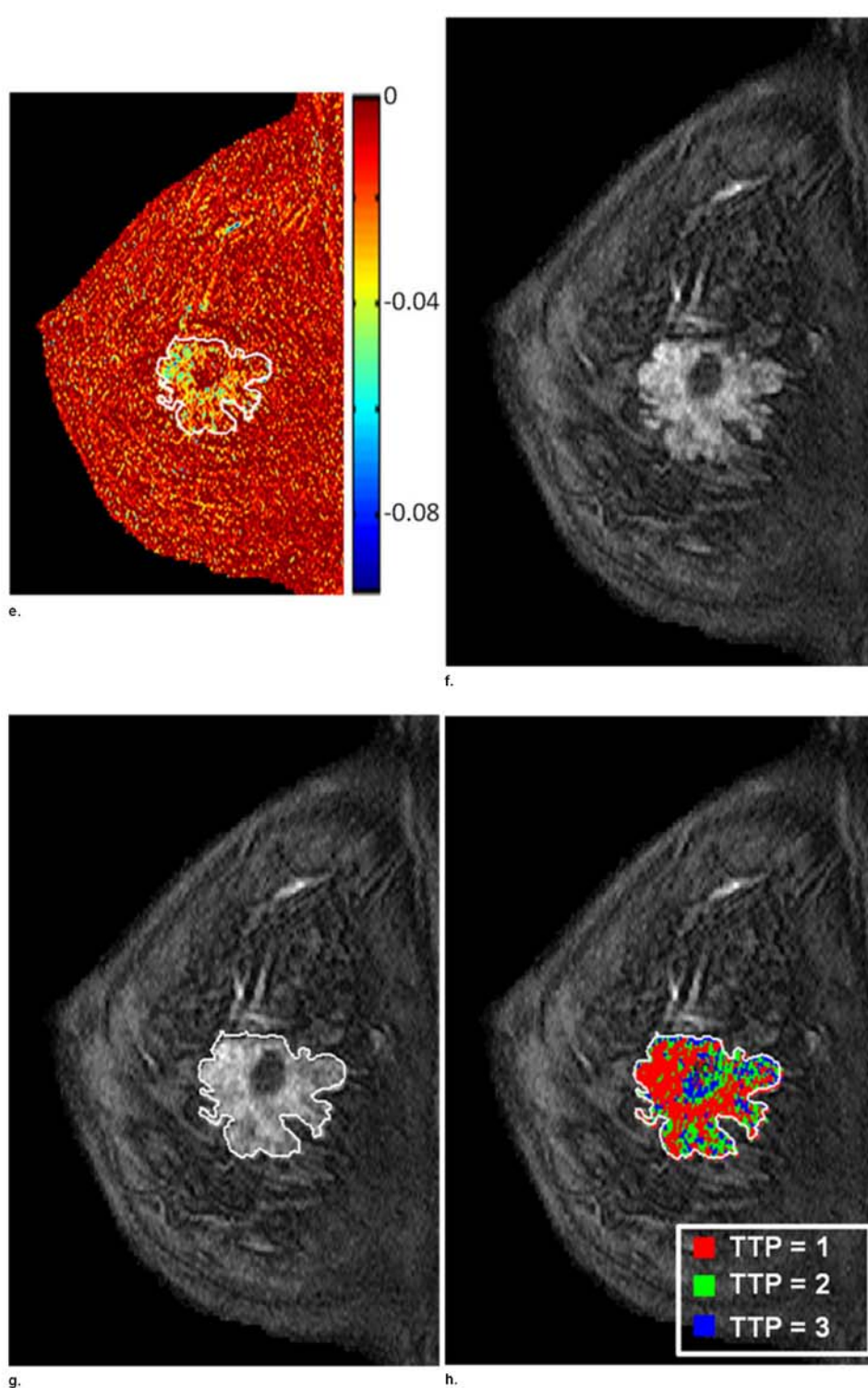


Figure E1:

Extraction of heterogeneity kinetic statistic features. (a) Kinetic curve of relative enhancement for a single pixel. (b–e) Pixel-wise maps of TTP (b), peak enhancement (c), wash-in slope (d), and washout slope (e). (f) First postcontrast image. (g) Image shows segmented lesion. (h) Image shows partitioning of tumor pixels based on their TTP value: Set 1 pixels (red) represent tumor areas with rapid uptake having peak enhancement at the first postcontrast time point (TTP = 1); set 2 pixels (green) have peak enhancement at the second time point (TTP = 2); and set 3 pixels (blue) have slow peak enhancement at the third time point (TTP = 3).

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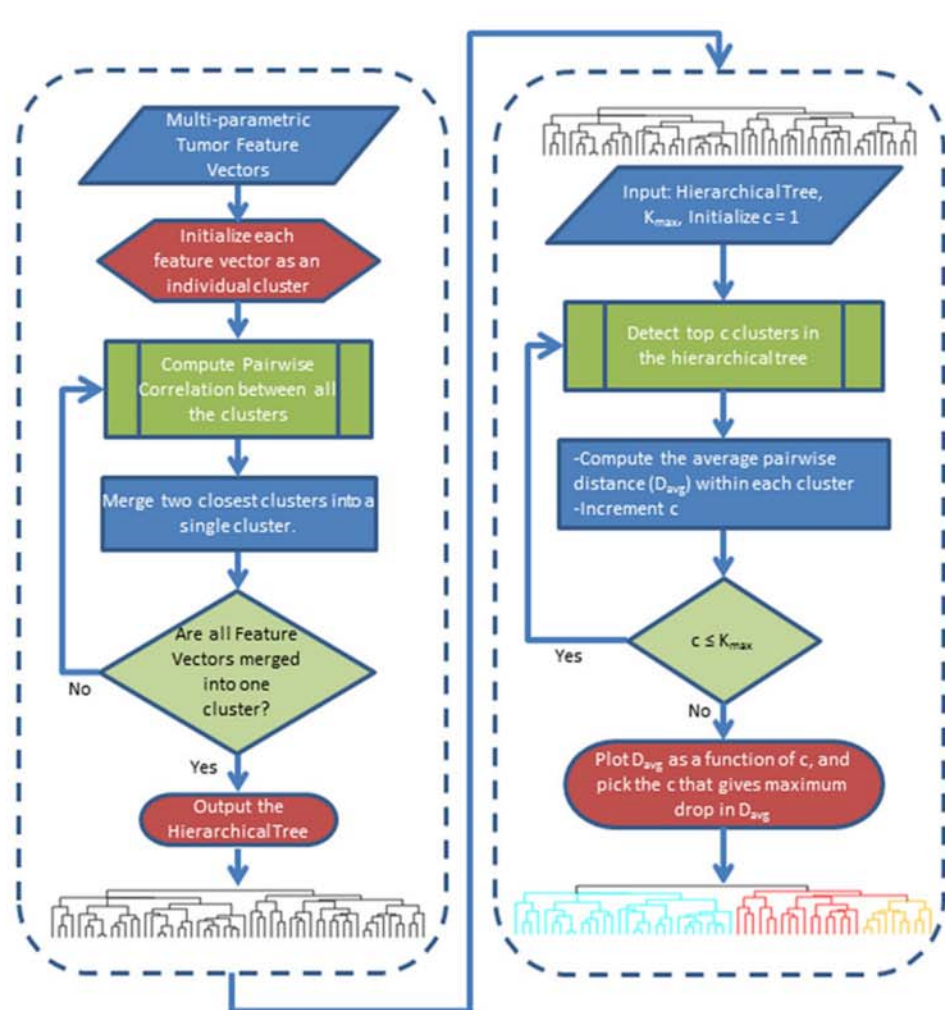


Figure E2:

Flowchart of the imaging phenotype discovery clustering algorithm. Stage 1: Steps for generating a hierarchical tree (ie, dendrogram) of tumors based on the extracted imaging features. Stage 2: Steps for determining the optimal number of distinct phenotypes (ie, clusters) hierarchical tree.

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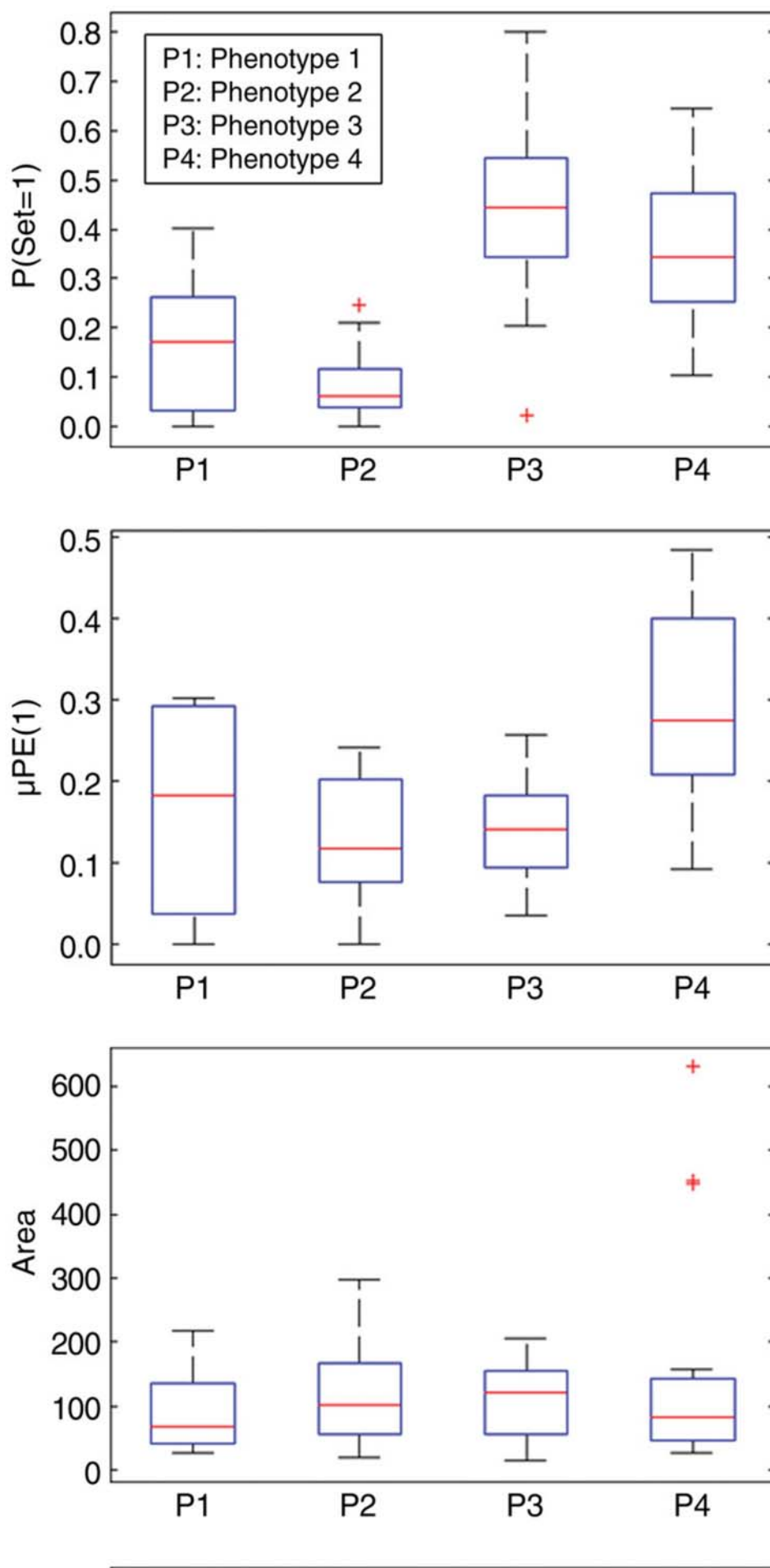


Figure E3:

Box plots of representative DCE MR imaging features for each of the four detected phenotypes (P1, P2, P3, P4). μ PE = maximum peak enhancement, $P(\text{Set} = 1)$ = proportion of pixels with TTP of 1. Red lines are medians, edges of boxes are 25th and 75th percentiles, and whiskers extend to the most extreme data points not considered as outliers (+).

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SUPPLEMENTAL TABLE

Table E1. Study Population Characteristics within Each of the Four Detected Phenotypes

Characteristic	Phenotype 1	Phenotype 2	Phenotype 3	Phenotype 4
No. of patients ($n = 56$)	7 (12)	18 (32)	15 (27)	16 (28)
Tumor type				
Ductal	6 (86)	16 (89)	15 (100)	15 (94)
Lobular	1 (14)	2 (11)	0 (0)	1 (6.2)
Tumor grade				
T1a	3 (43)	1 (5.6)	1 (6.7%)	2 (12)
T1b	3 (43)	2 (11)	8 (53)	6 (38)
T1c	1 (14)	14 (78)	4 (27)	5 (31)
T2	0 (0)	1 (5.6)	2 (13)	2 (12)
Tx	0 (0)	0 (0)	0 (0)	1 (6.2)
PR status				
Positive	6 (86)	17 (94)	13 (87)	14 (88)
Negative	1 (14)	1 (5.6)	2 (13)	2 (12)
Nodal status				
N0	7 (100)	17 (94)	14 (93)	15 (94)
N1	0 (0)	1 (5.6)	1 (6.7)	1 (6.2)
Patient ethnicity				
White	3 (43)	11 (61)	7 (47)	7 (44)
African American	1 (14)	1 (5.6)	2 (13)	3 (19)
Asian	0 (0)	1 (5.6)	0 (0)	0 (0)
Other	1 (14)	1 (5.6)	1 (6.7)	1 (6.2)
Unknown	2 (28)	4 (22.)	5 (33)	5 (31)
Patient age (y)				
Range	51–75	39–76	48–70	41–72
Mean	60.86	53.65	59.38	54.87
Tumor size				
Range	0.5–1.5	0.6–2.0	0.6–2.2	0.4–3.3
Mean \pm standard deviation	0.94 \pm 1.36	1.28 \pm 0.41	1.2 \pm 0.49	1.2 \pm 0.72

Note.—Numbers in parentheses are percentages.

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