# Genetic Variants Improve Breast Cancer Risk Prediction on Mammograms

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## **Personalized Medicine**



#### **EHR and informatics tools**

#### Individualized risk





#### **Discoveries in genetics**

# **Related Work**

• Gail Model (http://www.cancer.gov/bcrisktool/)

Risk Calculator							
(Click a question number for a brief explanation, or read all explana	tions.)						
<ol> <li>Does the woman have a medical history of any breast cancer or of ductal carcinoma in situ (DCIS) or lobular carcinoma in situ (LCIS)?</li> </ol>	Select -						
<ol> <li>What is the woman's age? This tool only calculates risk for women 35 years of age or older.</li> </ol>	Select -						
<ol> <li>What was the woman's age at the time of her first <u>menstrual</u> period?</li> </ol>	Select •						
4. What was the woman's age at the time of her first live birth of a child?	Select -						
<ol> <li>How many of the woman's first-degree relatives - mother, sisters, daughters - have had breast cancer?</li> </ol>	Select -						
<u>6</u> . Has the woman ever had a breast <u>biopsy</u> ?	Select -						
<u>6a</u> . How many breast biopsies (positive or negative) has the woman had?	Select -						
<u>6b</u> . Has the woman had at least one breast biopsy with atypical hyperplasia?	Select -						
7. What is the woman's race/ethnicity? Select	•						
7a. What is the sub race/ethnicity? Select	•						
	Calculate Risk >						

- 7 SNPs + Gail model: AUC-ROC  $0.607 \rightarrow 0.632$ 
  - Gail, M.H., Value of adding singlenucleotide polymorphism genotypes to a breast cancer risk model. J Natl Cancer Inst, 2009. 101(13): p. 959-63.
- 10 SNPs + Gail model: AUC-ROC 0.580 → 0.618
  - Wacholder, S., et al., Performance of common genetic variants in breastcancer risk models. N Engl J Med, 2010. 362(11): p. 986-93.

#### Assess 10-year or lifetime risk of breast cancer

## **Combine SNPs with Mammograms**



#### Assess breast cancer risk at mammogram

# **Subjects**

- From PMRP at Marshfield Clinic
- Cases: a confirmed diagnosis of breast cancer obtained from the institutional cancer registry
- Controls: absence from the cancer registry and no breast cancer diagnosis in EHR
- Age matching
- Include both invasive breast cancer and DCIS
- Sample size: 404 cases / 399 controls

## **Inclusion Criterion**

mammogram

#### plasma



biopsy



Within 12 months

#### **Controls are false positives!**

**Can genetics help eliminate false positives?** 

## **Genetic Variants**

				•••	
SNPs	Chr	Minor Allele	Source	In Gail (2009)	In Wacholder et al (2010)
rs11249433	1	С	Thomas et al. 2009		×
rs4666451	2	А	Easton et al. 2007		
rs13387042	2	G	Stacey et al. 2007,Thomas et al. 2009	×	×
rs1045485	2	С	Cox et al. 2007	×	×
rs17468277	2	Т	Odefrey et al. 2010		
rs4973768	3	Т	Ahmed et al. 2009	÷	
rs10941679	5	G	Stacey et al. 2008, Thomas et al. 2009		×
rs981782	5	G	Easton et al. 2007		
rs30099	5	Т	Easton et al. 2007		
rs889312	5	С	Easton et al. 2007	×	×
rs2180341	6	G	Gold et al. 2008		
rs2046210	6	Т	Zheng et al. 2009		
rs13281615	8	G	Easton et al. 2007	×	×
rs2981582	10	Т	Easton et al. 2007, Hunter et al. 2007	×	×
rs3817198	11	С	Easton et al. 2007, Thomas et al. 2009	×	×
rs2107425	11	Т	Easton et al. 2007	÷	
rs6220	12	G	Kelemen et al. 2008, Biong et al. 2010		
rs999737	14	Т	Thomas et al. 2009		×
rs3803662	16	Т	Easton et al. 2007, Stacey et al. 2007	×	×
rs8051542	16	Т	Easton et al. 2007		
rs12443621	16	G	Easton et al. 2007	÷	
rs6504950	17	А	Ahmed et al. 2009		
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## **Mammogram Features**



## **BI-RADS Category**



#### **Baseline clinical assessment**

## **Bayesian Network**



Elizabeth S. Burnside. Bayesian networks : Computer-assisted diagnosis support in radiology. *Academic Radiology*, Volume 12, Issue 4, April 2005, Pages 422–430.

## Models

- TAN (tree augmented naive Bayes)
  - Genetic model: use the 22 SNPs only
  - Breast imaging model: use the 49 imaging features
  - Combined model: use both SNPs and imaging features
- **Baseline clinical assessment**: use the BI-RADS scores from radiologists
- ROC, PR (precision-recall) analysis
- 10-fold cross validation

### **ROC and PR Curves**



AUC-ROC: 0.693 (breast imaging model)  $\rightarrow$  0.731 (combined model) (P=0.02)

Significant improvement in high recall region (recall > 0.8)

## Interaction

	SNP-Name	Associated Gene	BI-RADS Feature with Highest CMI	CMI 95% C.I.
Í	rs1045485	CASP8	calcification shape: pleomorphic	0.0141 (0.006,0.030)
1	rs17468277	CASP8	calcification shape: pleomorphic	0.0141 (0.005,0.032)
**	rs2180341	RNP146	calcification shape: dystrophic	0.0115 (0.006,0:021)
	rs2981582	FGFR2	calcification distribution: diffuse	0.0112 (0.006,0.021)
	rs4666451		mass shape: oval	0.0100 (0.004,0.017)
	rs11249433		special case: focal asymmetry	0.0095 (0.003,0.024)
	rs12443621	TNRC9/TOX3	calcification shape: dystrophic	0.0091 (0.004,0.020)
	rs13281615		calcification shape: dystrophic	0.0087 (0.002,0.023)
	rs3803662	TNRC9/TOX3	calcification distribution: linear	0.0086 (0.002,0.024)
	rs2107425	H19	mass shape: round	0.0080 (0.003,0.017)
	rs889312	MAP3K1	breast composition: extreme	0.0078 (0.001,0.019)
	rs981782	HCN1/MRPS30	breast composition: fat	0.0076 (0.004,0.015)
	rs8051542	TNRC9/TOX3	calcification distribution: linear	0.0076 (0.002,0.021)
	rs3817198	LSP1	calcification shape: punctate	0.0075 (0.002,0.022)
	rs13387042		breast composition: extreme	0.0069 (0.003,0.011)
	rs999737	RAD51L1	calcification distribution: linear	0.0069 (0.001,0.021)
	rs30099		calcification shape: amorphous	0.0063 (0.000,0.018)
	rs4973768	SLC4A7	calcification shape: amorphous	0.0058 (0.003,0.010)
	rs6504950	STXBP4	mass shape: lobular	0.0058 (0.001,0.019)
	rs2046210	C6orf97	associated finding: architectural distortion	0.0053 (0.001,0.018)
	rs6220	IGF-1	calcification shape: amorphous	0.0050 (0.001,0.014)
	rs10941679	HCN1/MRPS30	mass shape: oval	0.0048 (0.000,0.014)

#### **CASP8 and Pleomorphic Calcification Shape**

GWAS OR = 0.88 Our OR = 0.86

CASP8 has decreased risk of ductal tumors (MacPherson et al. 2004, Frank et al. 2005)



pleomorphic calcification shape

# Conclusion

- The first exploration of combining genetic variants and mammography features
- Statistically significant improvement
- Limitations
  - Small sample size
  - Extraction of mammography features
- Ongoing work
  - More SNPs from COGS (Michailidou et al. 2013)

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