Metrics for Quantifying and Comparing Markers Used for Treatment Selection

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A LIFE OF SCIENCE

Many Roles for Biomarkers

- surrogate outcomes
- early diagnosis of disease (EDRN)
- prognosis
- treatment selection (predictive) (prescriptive)

A Motivating Example

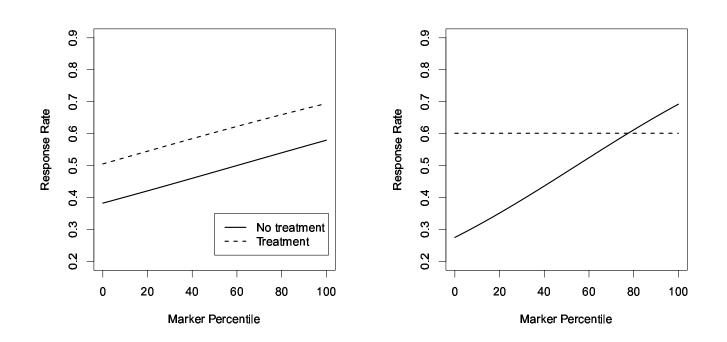
- most women with ER+ breast cancer are treated with chemotherapy but likely only a subset benefit
- Oncotype DX is an RT-PCR assay on 21 genes: 16 cancer related, 5 reference
- Oncotype DX useful for guiding the decision to have chemotherapy
- MammaPrint is another candidate marker

Not Targeted Therapy

A Common Approach to Evaluating a Treatment Selection Marker

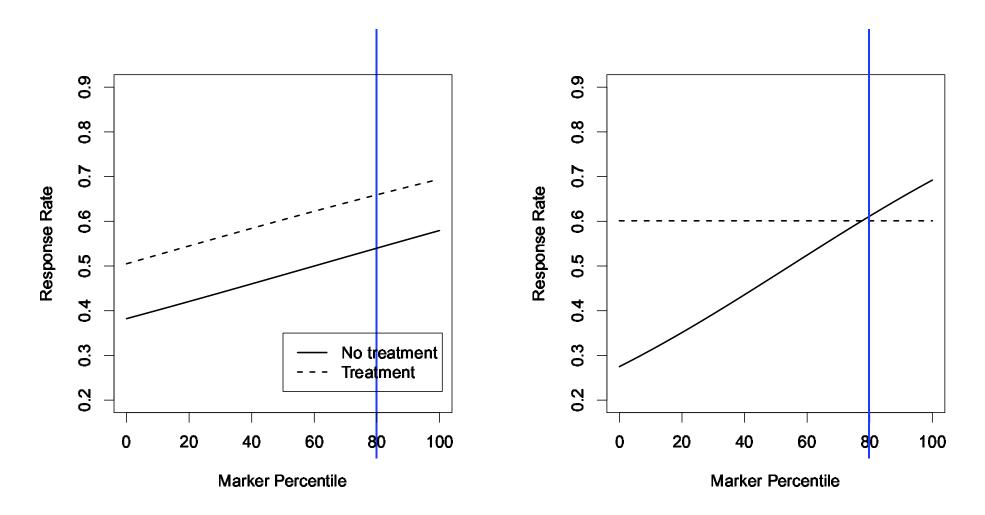
- is the marker predictive of response among subjects treated?
- not adequate

Marker equally prognostic on both treatments Marker not prognostic on treatment but useful for treatment selection



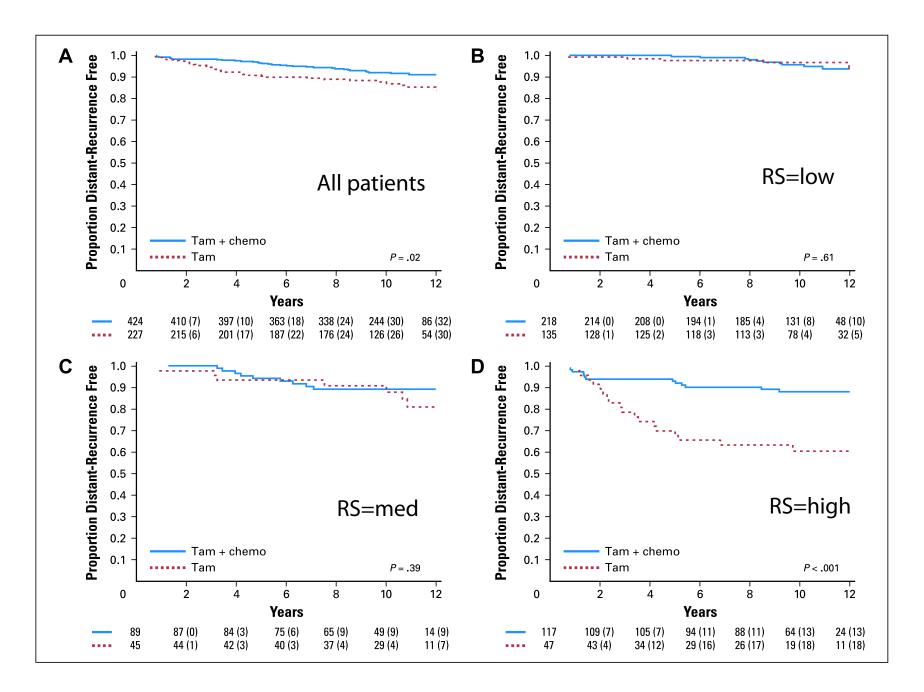
A Common approach to Evaluating a Treatment Selection Marker

- is treatment effective among marker positive patients?
- not adequate for evaluating the marker

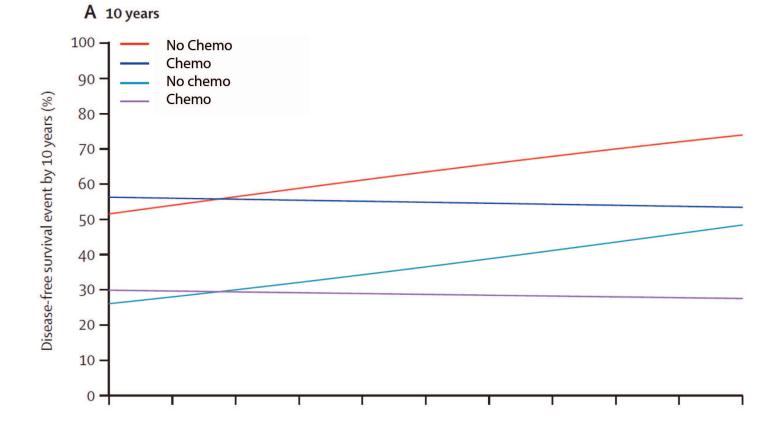


History of Onco*type* DX

- developed as a *prognostic* marker for women not receiving chemotherapy (Paik 2004)
- evaluated as a treatment selection marker
 - for node negative breast cancer (Paik et al 2006)
 - for node positive breast cancer (Albain et al 2010)



Breast Cancer Intergroup Study (Albain et al 2010) Node Positive Breast cancer



The Paradigm

- biospecimens collected prospectively before treatment in a RCT
- retrospectively blinded evaluation of stored specimens
- PRoBE design for prognostic biomarkers extended to address treatment (Pepe et al *JNCI* 2008)

Simulated Data for Illustration

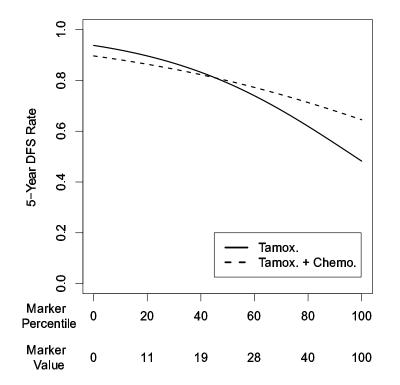
- Randomized trial with 3,000 participants
- Comparing no treatment (T = 0) vs. treatment (T = 1)
- 1,500 subjects each arm
- Response is 5-year disease-free survival (R)
- Chemotherapy is marginally effective:

$$P(R = 1 | T = 1) = 79\%$$
 vs $P(R = 0 | T = 0) = 76\%$

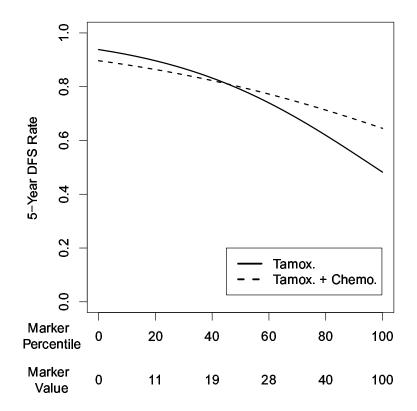
- Two markers measured at baseline on all trial participants:
 - $-Y_1$ has performance similar to Onco*type* DX
 - $-Y_2$ has better performance

Proposed Descriptive: Marker by Treatment Predictiveness Curves

• response rate as a function of marker percentile and treatment

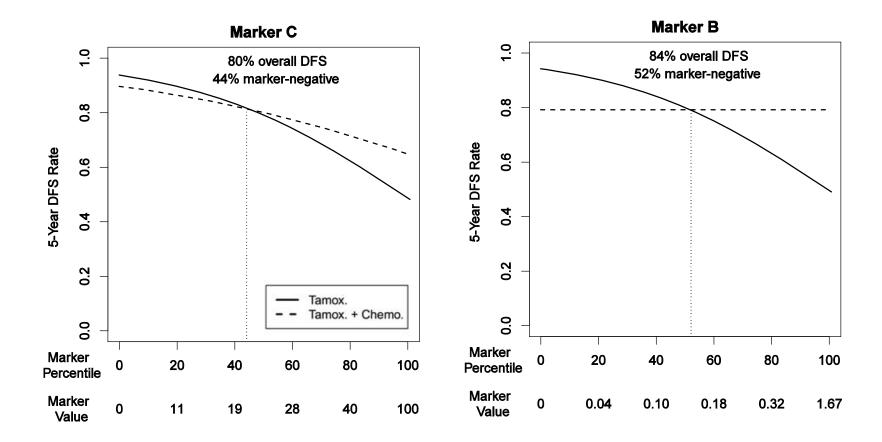


• similar to plots in Paik et al (2006) and Albain et al (2010)



- useful for guiding individual treatment decisions
- percentile scale shows % patients that opt to forego chemotherapy

• useful for comparing markers



Estimation

- P(R = 1 | T, Y) versus F(Y) T = 0, 1
- extension of predictiveness curves for prognostic markers P(R = 1|Y) versus F(Y)
- Huang, Pepe, Feng (*Biometrics* 2007) combine fitted risk model $P_{\hat{\theta}}(R = 1|Y)$ with empirical $\hat{F}(Y)$ using cohort data

More Estimation (Huang and Pepe)

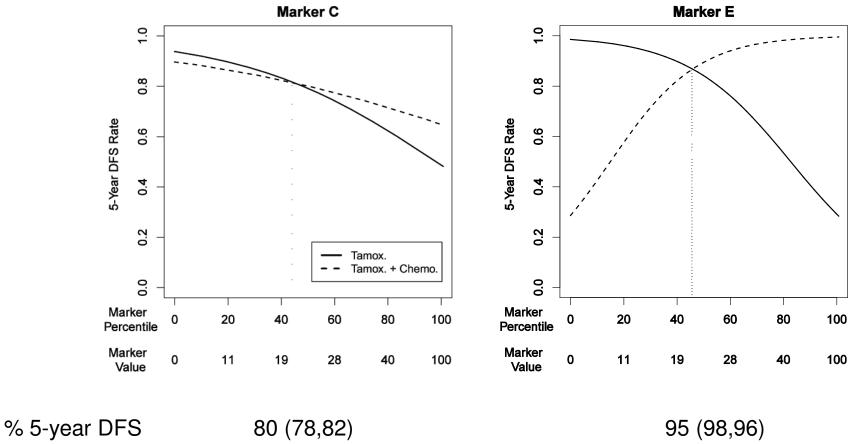
- nested case-control data
 - select on the basis of R = 1 and R = 0 for measuring Y
 - relevant also for Treatment Selection Markers
- semiparametric efficient estimation (*Biometrika* 2009)
- nonparametric estimation (*Statistics in Medicine* 2010)

Estimation Accommodating Covariates

- how does the marker perform in subpopulations?
 e.g. node+ versus node- patients
 e.g. younger versus older patients
- covariate specific predictiveness curves (JRSS C 2010)
- accommodates matching controls (R = 0) to cases (R = 1) in regards to covariates (and treatment)

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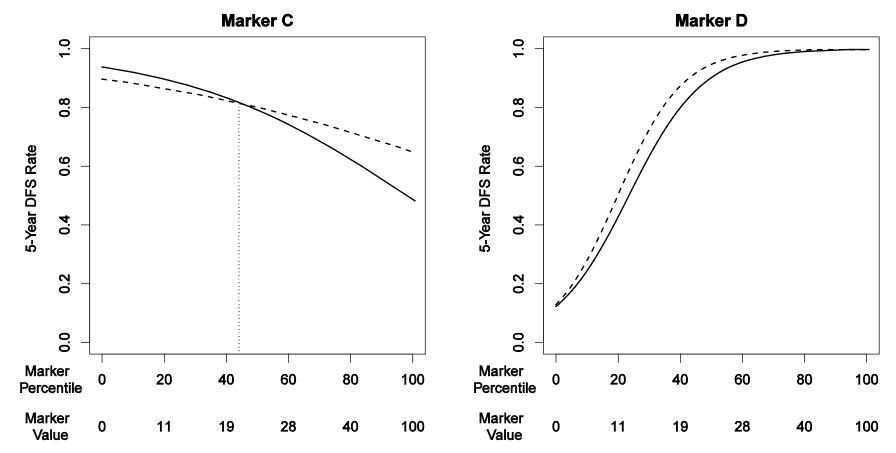
- $\widehat{P}[\text{response}|\text{use of marker}] = \int max(\widehat{PC}_{T=1}(v), \widehat{PC}_{T=0}(v))dv$
- for comparing markers
- for discovery work



- using marker
 - CI and inference using the bootstrap (for now)
 - p-value < 0.001

Interactions

- are not sufficient
- interactions do not *quantify* performance



• same interactions but different performance possible

Combining Markers

- multiple markers may be available
 - Onco*type* DX is a combination of 21 markers
 - combine MammaPrint and Oncotype DX together
- add marker to existing clinical information
 - age, nodal status, . . .

How to Combine Markers?

• P(R = 1 | use of marker) is maximized by the rule

Treat(Y):
$$P(R = 1 | T = 1, Y) > P(R = 1 | T = 0, Y) \Rightarrow T = 1$$

otherwise $\Rightarrow T = 0$

Example

$$\begin{aligned} \mathsf{logit} P(R = 1 | T, Y) &= \alpha_0 + \alpha_1 T + \alpha_2 Y + \alpha_3 TY \\ P(R = 1 | T = 1, Y) > P(R = 1 | T = 0, Y) \\ \iff \alpha_1 + \alpha_3 Y > 0 \end{aligned}$$

- optimal marker combination = $\alpha_3 Y_2$
- interaction of Y and T

Cost-Benefit Analysis Framework

- treatment selection marker needed if treatment has positive and negative effects
- chemotherapy { positive effects: tumor response negative effects: toxicity
- how to put positive and negative effects on the same scale?
- composite outcome "any bad event"
 e.g., Onco*type* DX "disease free survival"
- more generally: assign costs and benefit values
- Expected benefit replaces Prob(R = 1)

Expected Benefit with Use of Marker (B)

C = cost of treatment

 C_1 = additional cost for those who respond in the absence of treatment

 B_0 = benefit for subjects that do not respond in the absence of treatment

$$B(Y) = P(R = 0 | T = 0, Y)B_0 - P(R = 1 | T = 0, Y)C_1 - C$$

When Costs and Benefits of Treatment do not Vary with *Y*

 $B(Y) = P(R = 0 | T = 0, Y)B_0 - P(R = 1 | T = 0, Y)C_1 - C$

- prognostic marker can serve as treatment selection marker if it is adequately prognostic
- prognostic score is the right function for combining markers
- Gail (*JNCI* 2009) used the Gail model for breast cancer risk as a treatment selection marker assuming uniform costs and benefits
- Oncotype DX is a prognostic score but costs and benefit of treatment may vary with components of it

Further Work

- 1. Visual displays for multiple markers
- 2. Evaluation of Incremental value
- 3. Extensions of the PRoBE design: selection of cases and controls; matching; sample size
- 4. Cost-Benefit Analysis Methods
- 5. Meta-analysis
- 6. Observational studies

Bibliography

Albain KS, Barlow WE, Shak S et al. Prognostic and predictive value of the 21-gene recurrence score assay in postmenopausal women with node-positive, oestrogen-receptor-positive breast cancer on chemotherapy: a retrospective analysis of a randomised clinical trial. Lancet Oncology 2010;11(1):55–65.

Gail MH. Value of Adding Single-Nucleotide Polymorphism Genotypes to a Breast Cancer Risk Model. J Natl Cancer Inst 2009;10(13):959–963.

Huang Y, Pepe MS. Assessing risk prediction models in case-control studies using semiparametric and nonparametric methods. Stat in Med 2010;29:1391–1410.

Huang Y, Pepe MS. Semiparametric methods for evaluating risk prediction markers in case-control studies. Biometrika 2009;96(4):991–997.

Huang Y, Pepe MS Semiparametric methods for evaluating the covariate-specific predictiveness of continuous markers in matched case-control studies. JRSS C Applied Statistics 2010;59:437–456.

Huang Y, Pepe MS, and Feng Z. Evaluating the predictiveness of a continuous marker. Biometrics 2007;63:1181–1188.

Paik S, Shak S, Tang G, Kim C, Baker J, et al. A multigene assay to predict recurrence of tamoxifen-treated, node-negative breast cancer. N Engl J Med. 2004;351:2817-2826.

Paik S, Tang G, Shak S, et al: Gene expression and benefit of chemotherapy in women with node-negative, estrogen receptor-positive breast cancer. J Clin Oncol 2006;24:3726–3734.

Pepe MS, Feng Z, Janes H, Bossuyt P and Potter J. Pivotal evaluation of the accuracy of a biomarker used for classification or prediction: Standards for study design. J Natl Cancer Inst 2008;100(20):1432–1438.