

Design Elements of Clinical Trials Involving Biomarkers

Canadian Cancer Trials Group

New Investigator Clinical Trials Course

Bingshu E. Chen, Ph.D. Queen's University

Learning Objectives

At the end of the lecture the participants will be able to:

- 1. Distinguish the difference between prognostic and predictive biomarker
- 2. Understand three types of biomarker related clinical trial designs: biomarker enrichment design, biomarker stratify design, biomarker adaptive design.
- 3. Get basic idea on how to identify cut-point for a continuous biomarker.



Outline

- Prognostic and predictive biomarkers
- Design of Clinical Trials that involves biomarker
 - ➤ Biomarker enriched designs
 - ➢ Biomarker stratified designs
 - ➤ Biomarker adaptive designs
- Cut point issues for continuous biomarkers



Classification of Biomarkers in Clinical Trials

▶ Prognostic biomarker: A measurement that is associated with clinical outcome in the absence of therapy or with standard therapy.

▶ Predictive biomarker: Biological characteristics of patients measured at baseline, that helps identify patients who are likely or not likely to benefit from a therapy.



	Is the biomarker predictive?	
Is the biomarker prognostic	No	Yes
No	Neither prognostic nor predictive	Predictive but not prognostic
Yes	Prognostic but not predictive	Both prognostic and predictive



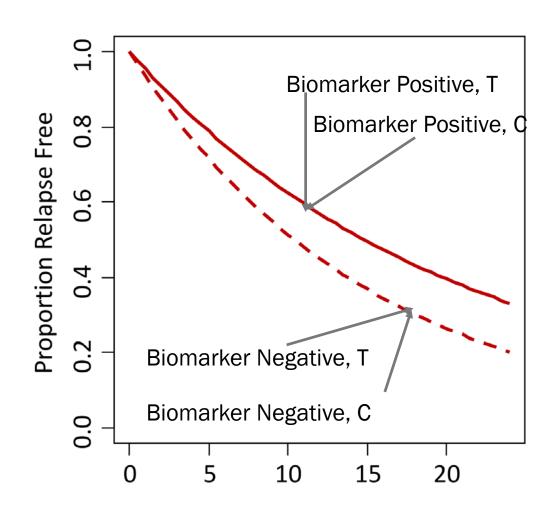
In statistical term: Interaction effect between treatment
 Z and a biomarker W for response variable Y

$$(Y|Z,W) \sim \beta_0 + \beta_1 Z + \beta_2 W + \beta_3 ZW$$

- \triangleright Neither prognostic nor predictive: $\beta_2 = 0$, $\beta_3 = 0$
- Prognostic but not predictive: $\beta_2 \neq 0$, $\beta_3 = 0$
- ightharpoonup Predictive but not prognostic: $β_2 = 0$, $β_3 ≠ 0$
- ► Both predictive and prognostic: $\beta_2 \neq 0$, $\beta_3 \neq 0$

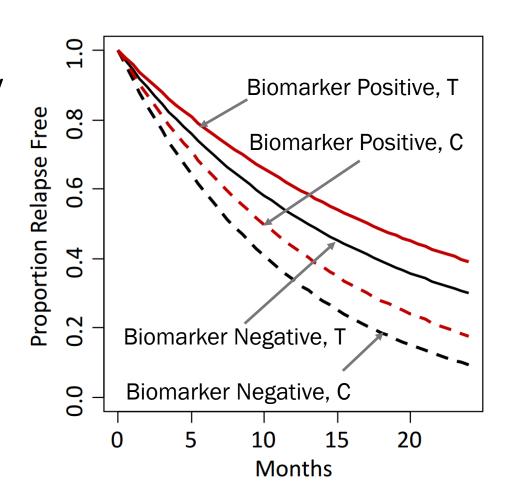


- Examples of biomarker
- ▶ Prognostic
- ➤ But no predictive
- No treatment effect
 - ➤T: Treatment arm
 - ➤ C: Control arm



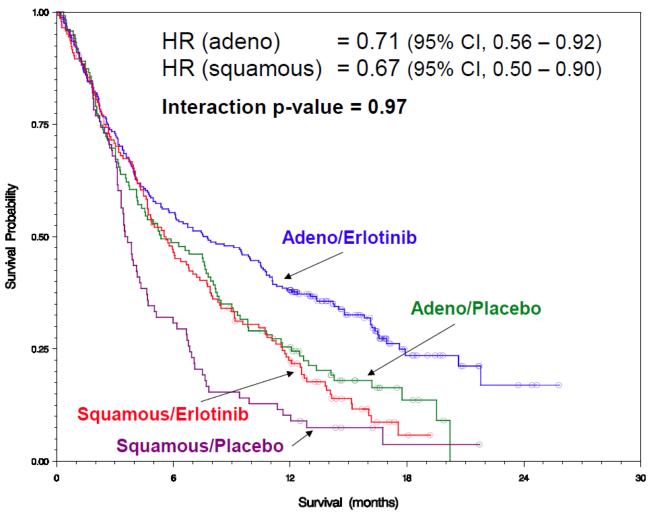


- Examples of biomarker
- ▶ Prognostic
- ➤ But no predictive
- ➤ Treatment benefit equally
 - >T: Treatment arm
 - ➤ C: Control arm





BR.21: Histology is Prognostic but not Predictive

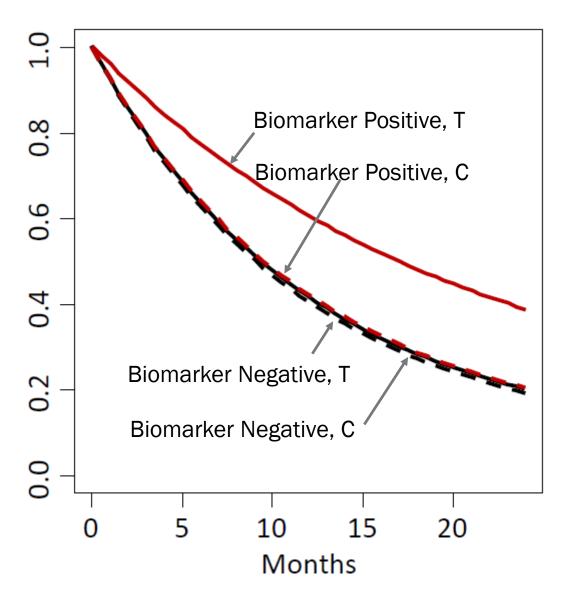


Clark GM. Mol Oncol 2008; 1:406-12



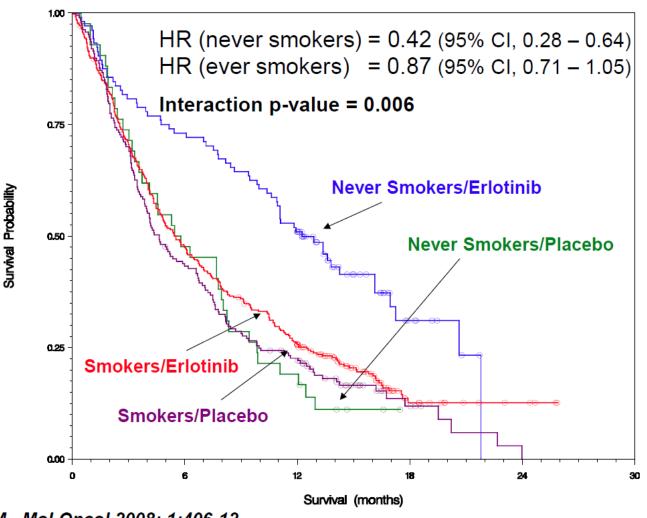
- Examples of biomarker
 - **→** Predictive
 - ➤ But no prognostic
 - Treatment benefit only the biomarker positive group but not the biomarker negative group

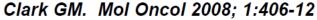






BR.21: Smoking is Predictive but not Prognostic







Different type of design with biomarkers

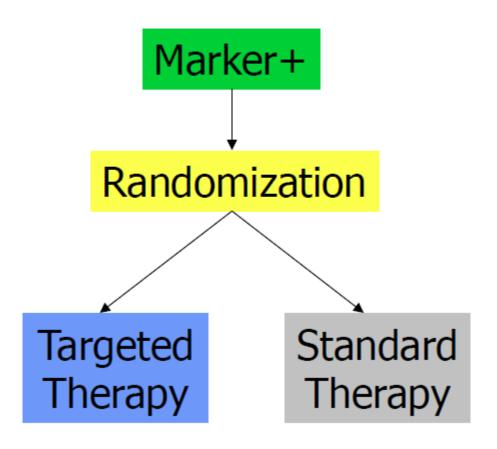
Biomarker enriched designs

➤ Biomarker stratified designs

➤ Biomarker adaptive design



Biomarker enriched designs (Targeted designs)





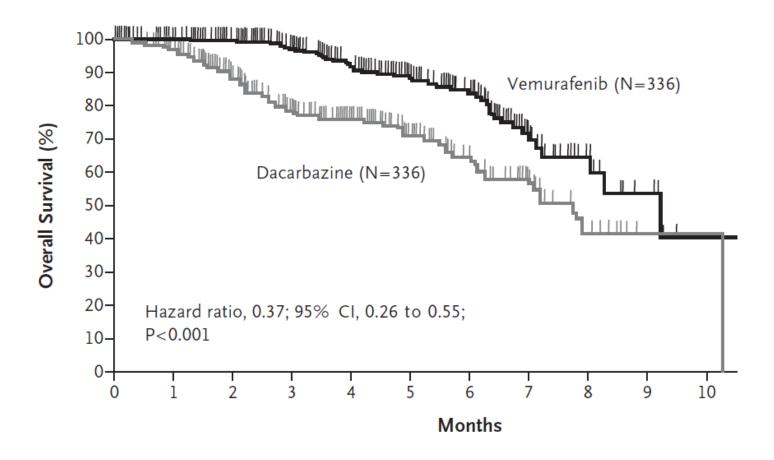
- To use biomarker enrichment designs, we need
 - ➤ Validated diagnostic test to identify Marker positive and Marker negative patients
 - Strong biological evidence that Marker negative patients will not benefit from the Target Therapy
 - ➤ Only Marker positive patients will be randomized to Target Therapy and Standard Therapy groups



- Examples of biomarker enriched designs
 - Trastuzumab (Herceptin) for HER2 positive breast cancer patients (Shak S. Overview of the trastuzumab (Herceptin) anti-HER2 monoclonal antibody clinical program in HER2-overexpressing metastatic breast cancer. Herceptin Multinational Investigator Study Group. Semin Oncol 1999;26:71-7.)
 - ➤ Vemurafenib for BRAF V600E mutation melanoma patients (Chapman PB, Hauschild A, Robert C, et al. Improved survival with vemurafenib in melanoma with BRAF V600E mutation. N Engl J Med 2011;364:2507-16.)



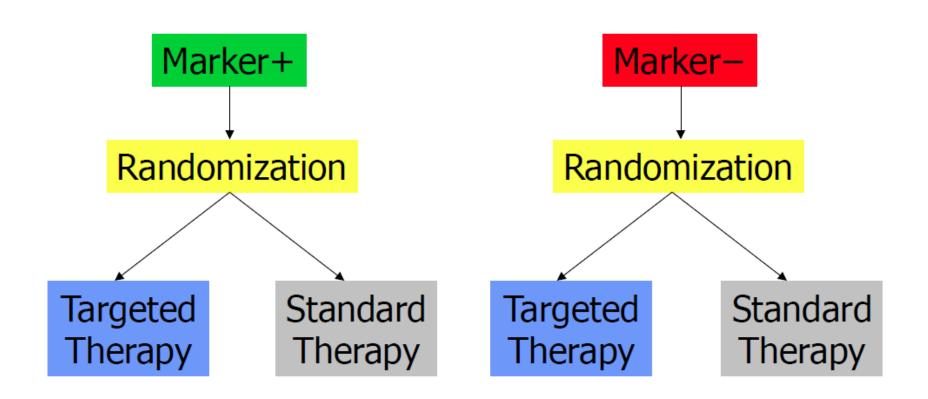
Overall survival from Vemurafenib trail for melanoma patients with BRAF mutation







Biomarker stratified designs





- To use biomarker stratified designs, we need
 - ➤ Validated diagnostic test to identify Marker positive and Marker negative patients
 - ➤ Marker negative patients may have benefit from the Target Therapy
 - ➤ Both Marker positive and negative patients will be randomized to Target Therapy and Standard Therapy groups



- Challenges for analyzing data from biomarker stratified designs
 - The statistical analysis plan have to be pre-specified
 - ➤ Multiple study populations could inflate type I error rates (have to control overall alpha < 0.05)
 - ➤ Scenario A: If treatment is more like to be effective in biomarker positive group
 - ➤ Scenario B: If there is limited confident in the predictive biomarker



- Test I: Sequential approach
 - ➤ Step 1: Test treatment effect in the biomarker positive group with alpha = 0.05
 - ➤ If significant, then stop!
 - ➤ If negative, go to step 2

➤ Step 2: Test treatment effect in the biomarker negative group with alpha = 0.05

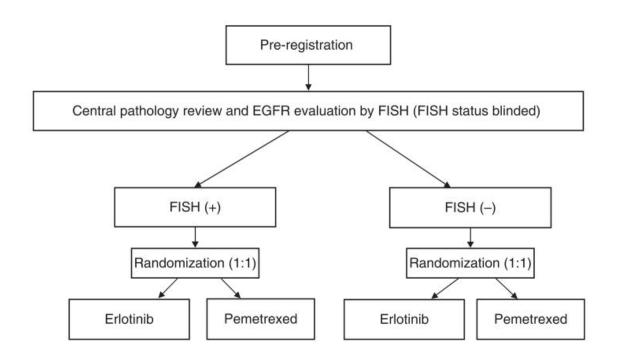
- Test II: Fall-back approach
 - Step 1: Test treatment effect in the overall population with alpha = 0.03 (a reduced significant level)
 - ➤ If significant, then stop!
 - ➤ If negative, go to step 2

➤ Step 2: Test treatment effect in the biomarker positive population with the remaining (unused) significant level alpha = 0.02

Simon R, Wang SJ. Pharmacogenomics J 2006;6:166-73.



Example of biomarker stratified design



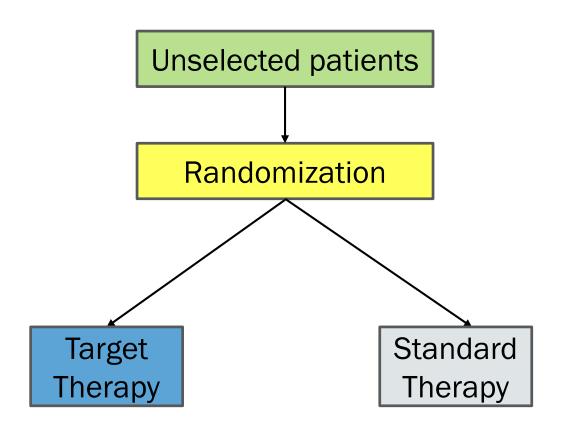
Mandrekar SJ, Sargent DJ. Clinical Trials 2010;7:567-73. Marker Validation for Erlotinib in Lung Cancer



- Using archived tumour specimens to conduct prospectiveretrospective analysis of a randomized phase III trial to identify predictive biomarker
 - This requires archived specimens be available on most patients
 - > The Statistical analysis plan have to be developed beforehand
 - > Example:
 - ➤ CO.17 with K-RAS mutation



Biomarker adaptive design



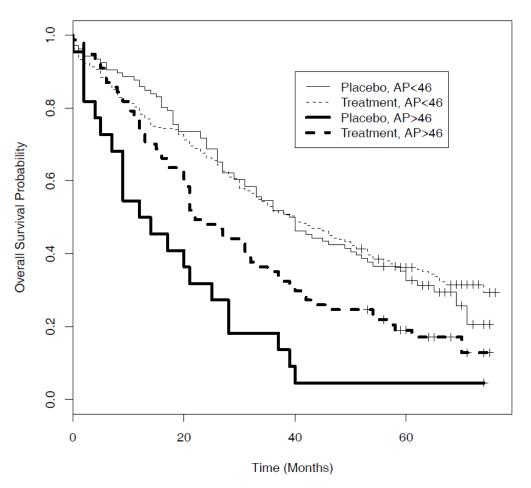
Jiang, W. and Simon, R. (2007) JNCI 1036-1043



- To use biomarker adaptive designs, we need
 - Tumour specimen to be collected from all patients at study entry
 - ➤ Value of the biomarker is NOT used as an eligibility criteria
 - ➤ Allow phase III trial without pre-specify the cut-point for biomarker
 - >Statistical inferences for treatment effects:
 - ➤ Jiang, W. and Simon, R. (2007). JNCI 1036-1043
 - ➤ Chen, B. E., Jiang, W. and Tu, D. (2014). Computational Statistics and Data Analysis. 324-334.

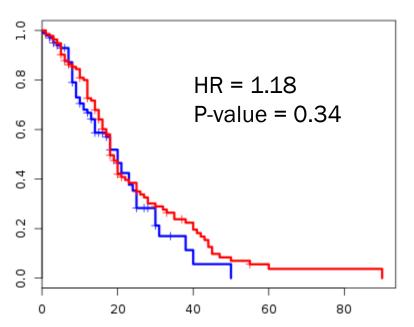


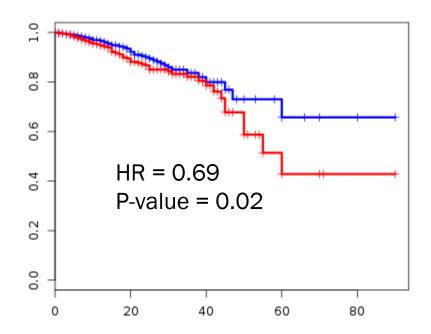
• Example of biomarker adaptive design for prostate cancer with serum prostatic acid phosphatase (AP) biomarker.





➤ An example of ki67 biomarker for breast cancer patients (Demo data)





Interaction p-value: 0.03

http://statapps.tk/biomarker interaction/

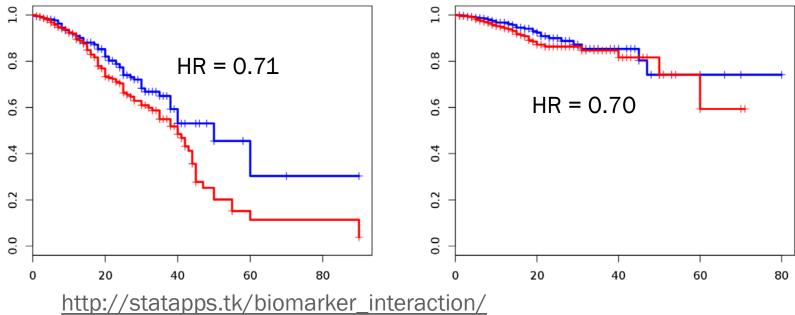


Continuous biomarker

Many biomarkers are continuous variables.

It is critical to establish a validate cut-point for biomarker

Example of using median Ki-67 as cut-point gives total different results

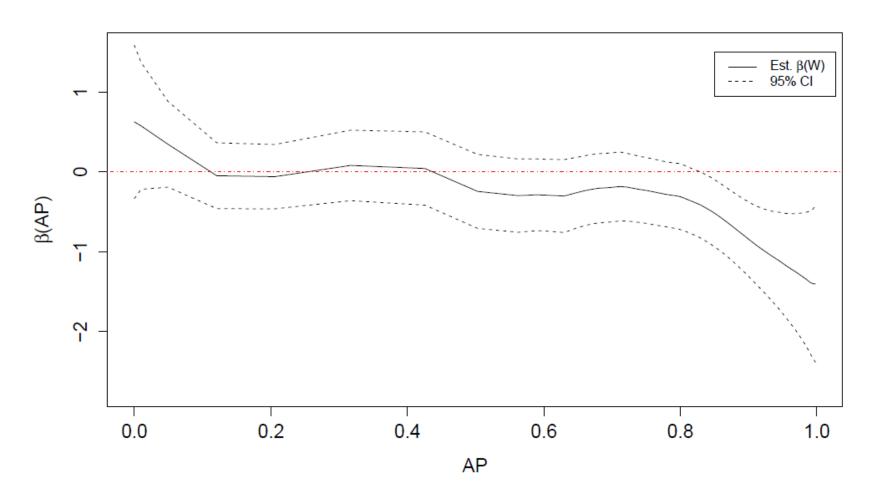






Continuous biomarker

Treat biomarker as a continuous variables



Liu, Jiang and Chen (2015): Statistics in Medicine



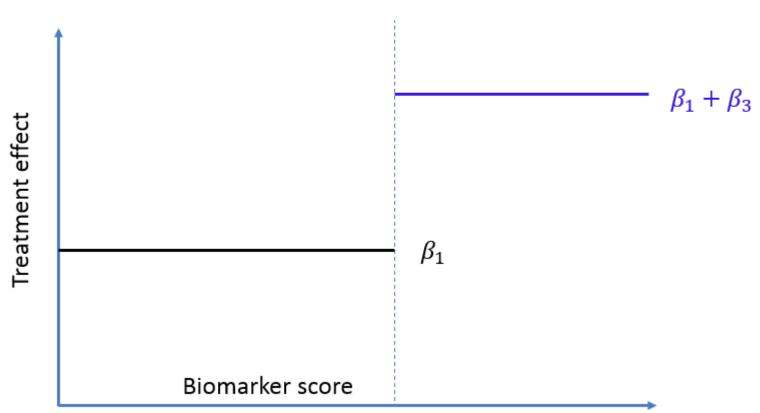
Continuous biomarker

- Actionable predictive biomarker? Clinically useful vs Statistically significance
- ➤Idea situation: exists an obvious threshold (or a cut point)
- Clinically useful situation: exists a potential threshold
- Clinically not useful situation: a moderate but statistically significant linear relationship



≻Idea

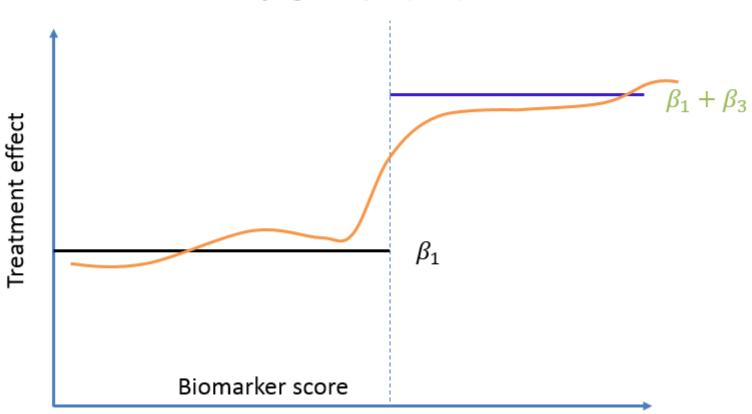
$$\beta_0 + \{\beta_1 + \beta_3 I(W \ge c)\}Z$$





Clinically useful

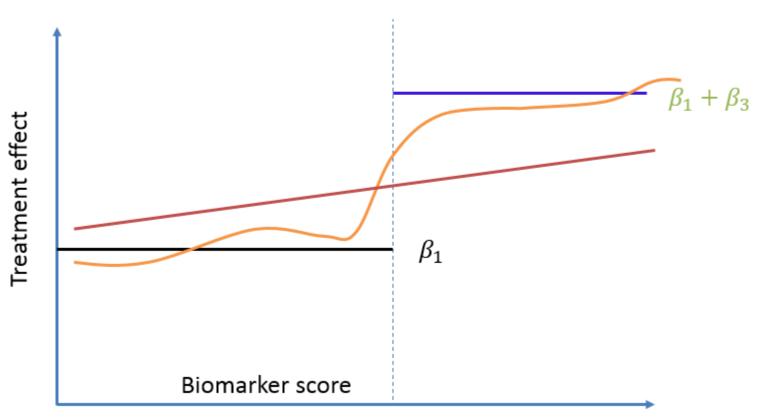
$$\beta_0 + \beta(W) Z$$





➤ Clinically not useful

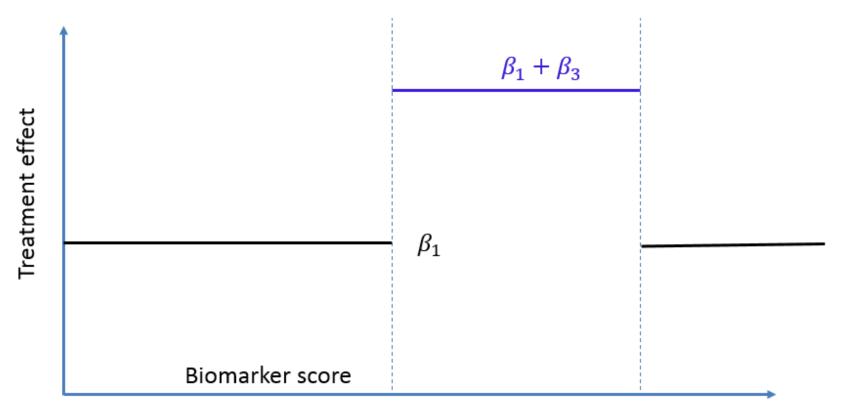
$$\beta_0 + (\beta_1 + \beta_3 W) Z$$





➤ General: multiple cut points

$$\beta_0 + \{\beta_1 + \beta_3 I(c_1 \le W \le c_2)\}Z$$





- >Statistical methods to estimate optimal cut-points
 - ➤ R package is now available for biomarker threshold models (the *bhm* package).
 - Source code from the Comprehensive R Archive Network (https://cran.Rproject.org/package=bhm). To install the package:

>install.packages("bhm")

Fang, T., Mackillop, W., Jiang, W., Hildesheim, A., Wacholder, S. and Chen, B. E. (2017). Computational Statistics and Data Analysis. 53-62.



bhm {bhm} R Documentation

Fitting Biomarker Threshold Models

Description

{bhm} is a R package for Biomarker Threshold Models. It uses either Hierarchical Bayes method or proflie likehood method (Chen, et al, 2014 and Tian, et al, 2016) to identify a cut-point (thershold parameter) for the biomarker in either generalized linear models or Cox proportional hazards model. The model is specified by giving a symbolic description of the linear predictor and a description of the distribution family.

Usage

```
bhm(x, ...)

## S3 method for class 'formula'
bhm(formula, family, data, control = list(...),...)

# use
# bhm(y ~ biomarker)
#
# to fit a prognostic model with biomarker term only
#
# use
#
# bhm(y ~ biomarker+treatment)
```



Summary

Predictive and prognostic biomarkers

Clinical trials design account for biomarkers

How to deal with continuous biomarkers

