



EFSPi-SFdS B&S
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Integrating Biomarkers in Clinical Trials: an overview



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NON-RESPONDERS AND TOXIC RESPONDERS



Treat with
alternative
drug or dose

RESPONDERS AND PATIENTS NOT
PREDISPOSED TO TOXICITY



Treat with
conventional
drug or dose

Rebecca Henrichs

Ref: Piquette-Miller & Grant, Clin Pharmacol Ther 2007

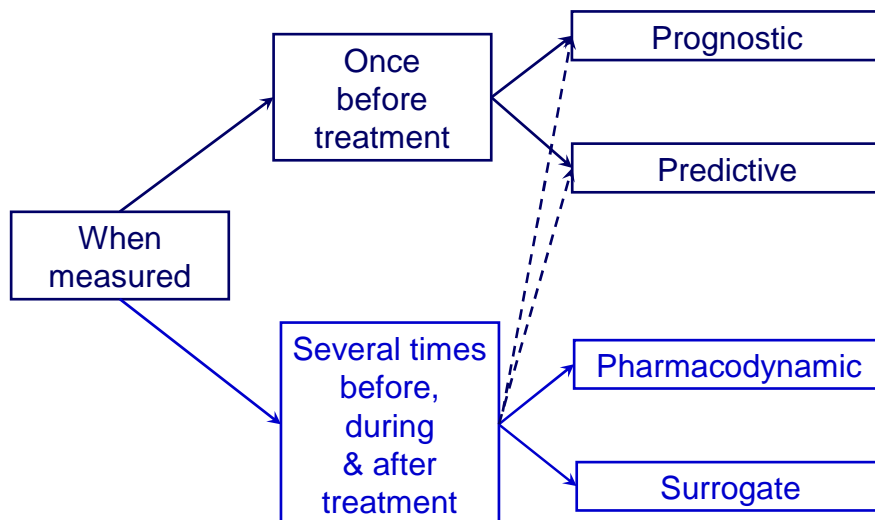
TYPES OF BIOMARKERS (1)

“A characteristic that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention.”

- **Prognostic** biomarkers, which affect the outcome of patients in terms of a clinical endpoint
- **Predictive** biomarkers, which affect the effect of a specific treatment on a clinical endpoint
- **Surrogate** biomarkers, which may replace a clinical endpoint in clinical trials carried out to evaluate the effect of a specific treatment

Ref: Buyse & Michiels, in Kelly & Halabi, Eds: Oncology Clinical Trials 2010

TYPES OF BIOMARKERS (2)



BIOMARKER-BASED TRIAL DESIGNS

| <u>Trial phase</u> | <u>Effect of treatment</u> | <u>Type of biomarker</u> | <u>Effect of biomarker</u> |
|--------------------|----------------------------|--------------------------|----------------------------|
| <i>II</i> | <i>Known</i> | <i>Prognostic</i> | <i>Known</i> |
| <i>III</i> | <i>Unknown</i> | <i>Predictive</i> | <i>Unknown</i> |

↳ Trial design

↳ Examples

Ref for this presentation: Buyse, Michiels et al, Expert Rev Mol Diag (to appear).

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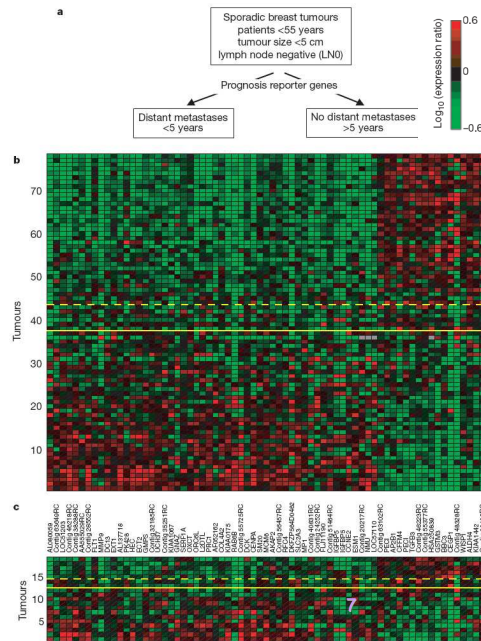
↳ Trial designs
Retrospective series

↳ Examples
*Gene signatures
(Mammaprint™,
OncotypeDX®)*

MAMMAPRINT® DEVELOPMENT

- Training set: 78 pts, 34 with distant metastasis at 5 years
- Gene expression levels ranked by correlation coefficient with metastatic status at 5 years
- 70 genes with highest correlations = « molecular signature »

Ref: van't Veer, Nature 2002



EXTERNAL VALIDATION OF MAMMAPRINT®

Validation study 1

- N=295 breast cancers from one single center
- Potential bias: inclusion of 61 pts of the training set
- Accuracy of MammaPrint for distant relapse at 5-years:
 - Se (correctly classifying pts who relapsed) = 93% (CI_{95%} 81% to 99%)
 - Sp (correctly classifying pts who did not) = 53% (CI_{95%} 44% to 61%)

Validation study 2

- N=307 breast cancers from 5 European centers
- Accuracy of MammaPrint for distant relapse at 5-years:
 - Se = 90% (CI_{95%} 78% to 95%)
 - Sp = 42% (CI_{95%} 36% to 48%)

Ref: Van de Vijver, NEJM 2002; Buyse, JNCI 2006; Michiels, BJC 2007

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↳ Trial designs

Retrospective analyses of randomized phase III trials

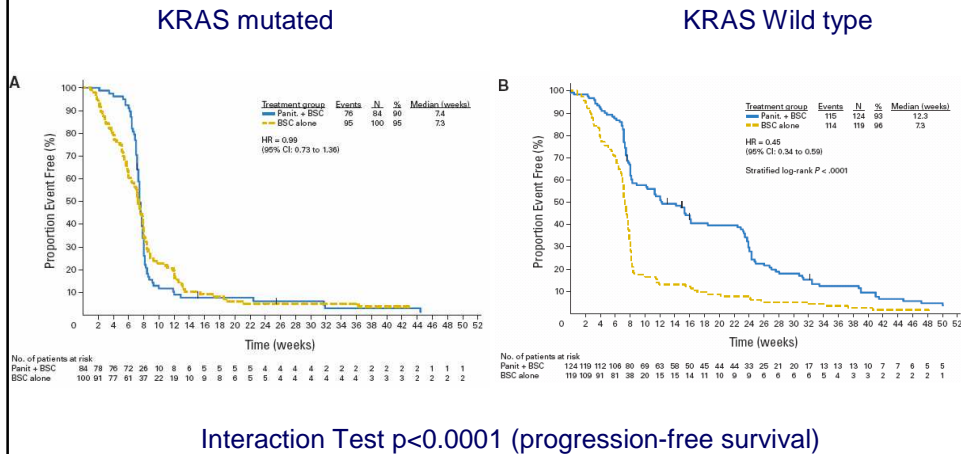
↳ Examples

- *KRAS mutations in CRC*
- *EGFR mutations in NSCLC*

LACK OF RESPONSE OF MUTANT KRAS TUMORS: 1ST EVIDENCE IN SMALL RETROSPECTIVE SERIES

| Reference | Responses among <i>KRAS</i> mutant | Responses among <i>KRAS</i> wild-type |
|--------------------|---------------------------------------|--|
| Lièvre 2006 | 0/13 | 11/17 (65%) |
| Di Fiore 2007 | 0/16 | 12/43 (28%) |
| Khambata-Ford 2007 | 3/30 | 24/50 (48%) |
| Benvenuti 2007 | 1/16 | 10/32 (31%) |
| Frattini 2007 | 1/10 | 9/17 (53%) |
| De Roock 2008 | 0/42 | 27/66 (41%) |
| Lièvre 2008 | 0/36 | 34/78 (44%) |
| Amado 2008 | 0/84 | 21/124 (17%) |

RETROSPECTIVE ANALYSIS OF PHASE III TRIALS



Interaction Test $p < 0.0001$ (progression-free survival)

Ref: Amado, JCO 2008

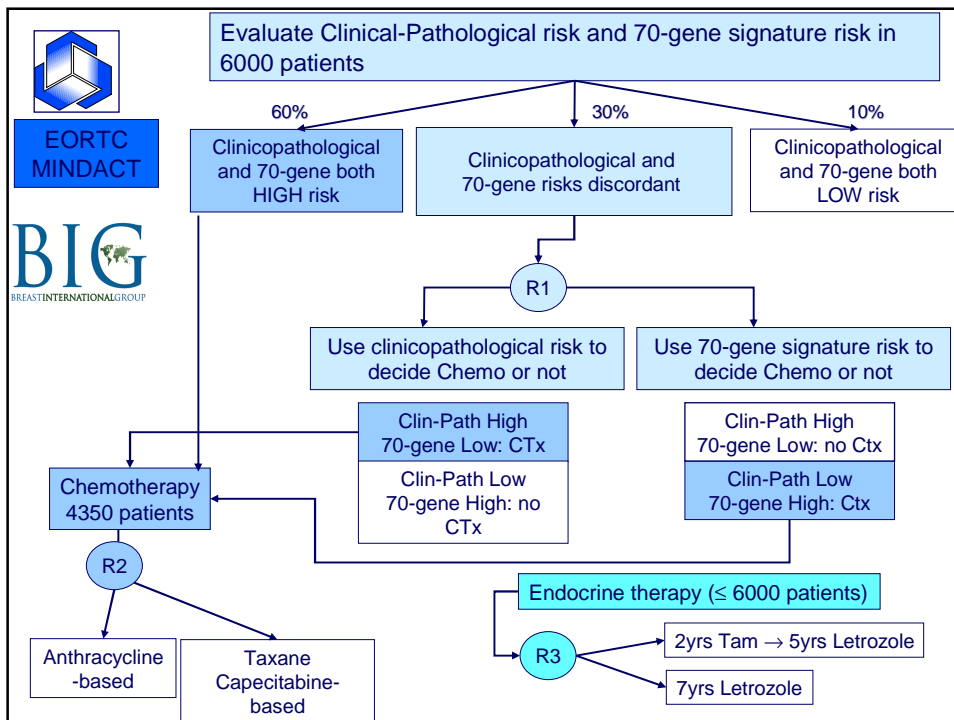
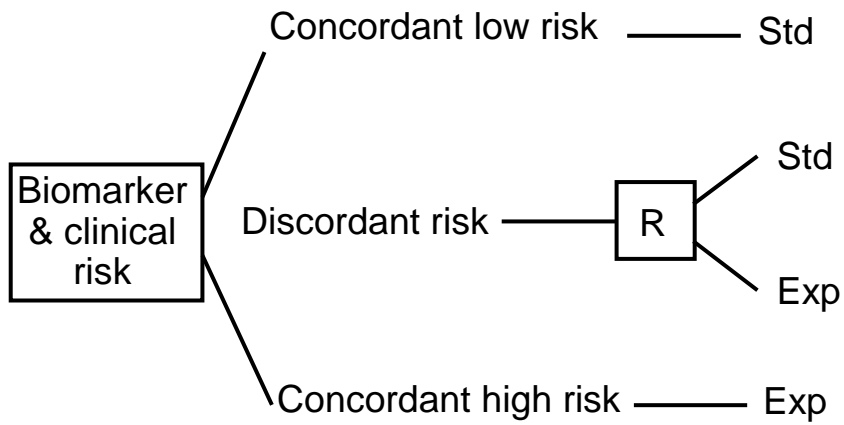
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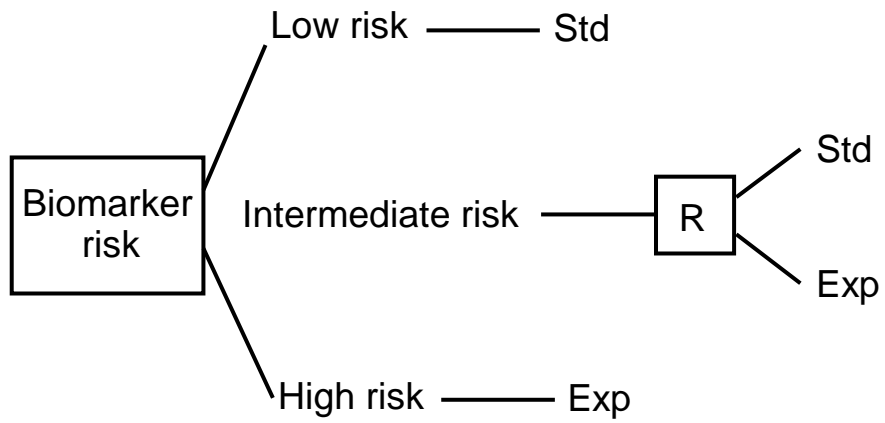
↳ Trial designs
« *Clinical utility* » trials

↳ Examples
MINDACT and TAILORx in early breast cancer

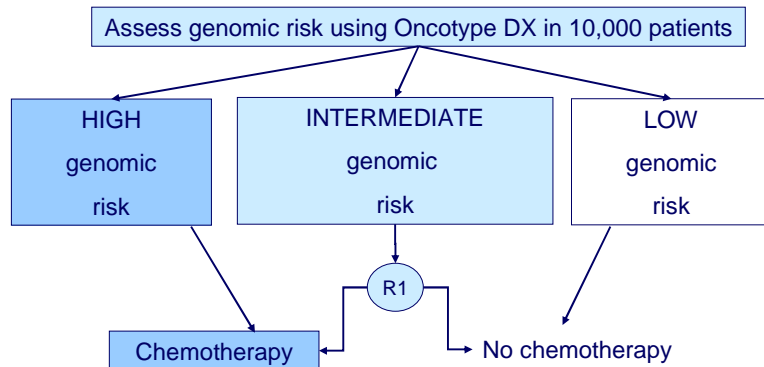
DISCORDANT RISK RANDOMIZED DESIGN



INTERMEDIATE RISK RANDOMIZED DESIGN



THE TAILOR-X TRIAL



ISSUES WITH CLINICAL UTILITY TRIALS

- Very large sample sizes are required (pragmatic trials)
- Unclear what hypothesis is being tested (treatment effect known)
- Prognostic biomarkers less useful to choose treatment than predictive biomarkers (hence emphasis from now on will be on predictive biomarkers)

Ref: Bogaerts, Nature Clin Pract 2006

BIOMARKER-BASED TRIAL DESIGNS

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↳ Trial designs

- *Cross-over designs*
- *Bayesian*

↳ Examples

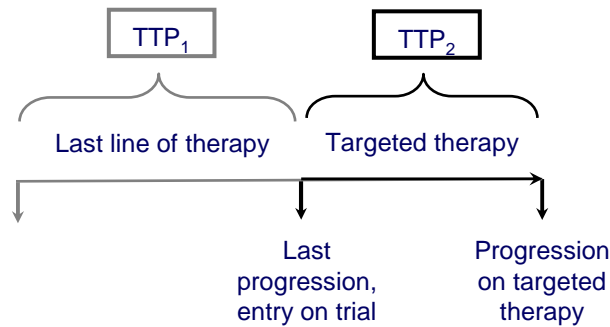
- *Molecular profiling*
- *BATTLE in NSCLC*

TRIAL OF MOLECULAR PROFILING

At least two prior lines of therapy for advanced disease, no further therapy available

Molecular profiling of tumor biopsy by IHC, FISH or micro-array to identify target

Targeted agents were all approved agents (cytotoxics or biologicals)



Ref: Von Hoff, AACR 100th Annual Meeting, Denver, CO, April 18-22, 2009

TRIAL OF MOLECULAR PROFILING

Define the "Time To Progression Ratio" as

$$TTPR = TTP_2 / TTP_1$$

The natural history of most advanced tumors suggests that $TTPR < 1$ (patients tend to progress faster on successive lines of treatment)

Trial designed to test the hypothesis that at least 15% of the patients have $TTPR > 1.3$

Ref: Mick, *Contr ClinTrials* 2000

TRIAL OF MOLECULAR PROFILING

Proportion of patients with TTPR > 1.3:

18 / 66 (27%, 95% C.I. 17% - 38%, $P = 0.007$)

| | |
|------------|--------------|
| Breast | 8 / 18 (44%) |
| Colorectal | 4 / 11 (36%) |
| Ovarian | 1 / 5 (20%) |
| Others | 5 / 32 (16%) |

Among the 18 patients with TTPR > 1.3, none would have received same drug through physician's choice

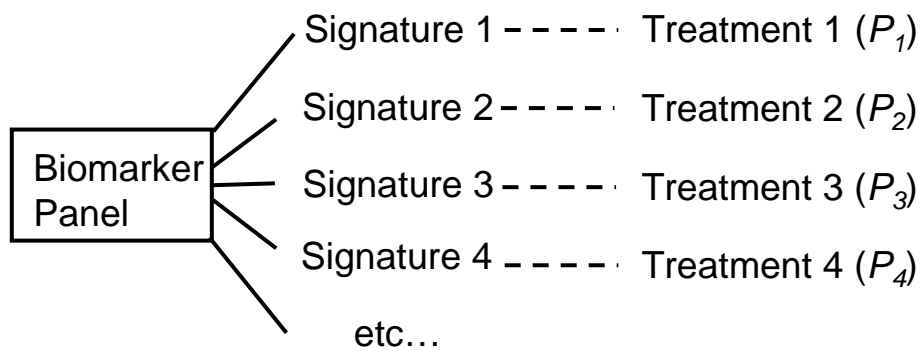
Ref: Von Hoff, AACR 100th Annual Meeting, Denver, CO, April 18-22, 2009.

ISSUES WITH TRIAL OF MOLECULAR PROFILING

- Only 66 patients of 106 could have molecular profiling
- Non-randomized trial, hence no evidence that physician's choice would have yielded inferior results
- Is TTPR > 1.3 a relevant endpoint?
- Cross-over design inefficient if low correlation between TTP₁ and TTP₂

Ref: Von Hoff, AACR 100th Annual Meeting, Denver, CO, April 18-22, 2009.

BAYESIAN ADAPTIVE PHASE II DESIGN
(PUTATIVE BIOMARKER)



P_i : probability of allocating treatment i

BATTLE (Biomarker-based Approaches of Targeted
Therapy for Lung Cancer Elimination)

- Evaluate targeted therapy agent(s) with different biomarker profiles
- Stage IV recurrent non-small cell lung cancer with endpoint: 8-week disease-free survival (DFS) rate

Ref: Lee, Clin Trials 2008; Kim, AACR 2010

BATTLE CHARACTERISTICS (1)

- Treat more patients in promising groups according to each pt's biomarker profile
- Start with equal randomization but switch to « adaptive » randomization after 20 pts in each treatment arm
- Early stopping for lack of efficacy in a biomarker × treatment group
- Provide an accurate estimate of true DFS in each of the biomarker × treatment groups
- Borrow strength from patients treated with same agent but different biomarker profile

BATTLE CHARACTERISTICS (2)

Four Molecular Pathways Targeted in NSCLC: BATTLE Program

Enrollment into BATTLE Umbrella Protocol

Biomarker Profile and Adaptive Randomization

| MG | Biomarker | | | | | Frequency |
|----|-----------|--------------------|-------------------|----------------------|--|-----------|
| | EGFR | K-ras and/or B-raf | VEGF and/or VEGFR | RXR and/or cyclin D1 | | |
| 1 | + | x | x | x | | 0.15 |
| 2 | - | + | x | x | | 0.2 |
| 3 | - | - | + | x | | 0.3 |
| 4 | - | - | - | + | | 0.25 |
| 5 | - | - | - | - | | 0.1 |

Erlotinib

Sorafenib

Vandetanib

Erlotinib + Bexarotene

ISSUES WITH BATTLE DESIGN

- Needs prior information to form and rank biomarker groups
- Needs prior distribution for treatment effects
- Choice of adaptive randomization (when to start, what allocation ratio)
- Ethics of adaptive randomization
- Need fast outcome assessment
- Missing or incomplete biomarker profile (with inadequate amount of tissue)
- No power gain as compared to equal randomization

Ref: Lee, Clin Trials 2008

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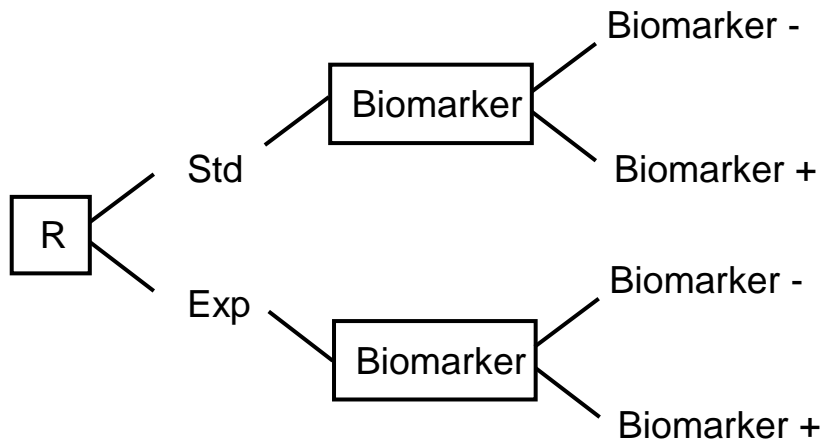
↳ Trial designs

- *Randomize-all*
- *Interaction*
- *Biomarker-strategy*

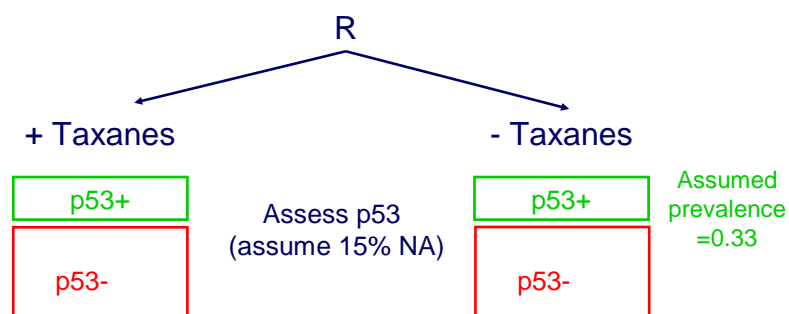
↳ Examples

- *P53 in ABC*
 - *MARVEL in NCSLC*
 - *ERCC1 in NSCLC*
-

RANDOMIZE-ALL DESIGN



EORTC 10994 ("P53") TRIAL IN ADVANCED BREAST CANCER



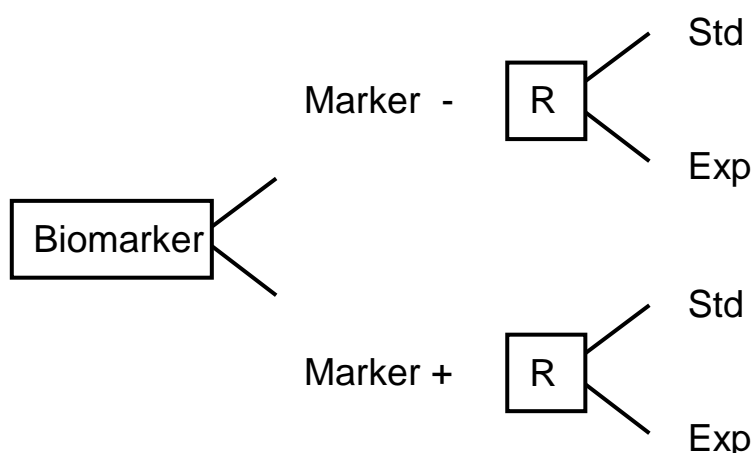
- Powered for detecting a larger effect in p53+ subgroup
- Overall: 80% power of detecting a HR=1.25 at $\alpha=0.02$
- Also planned to test for interaction
- Anticipated 5.5 yr accrual, analyses 2.5 yrs after last entry

ISSUES WITH RANDOMIZE-ALL DESIGN

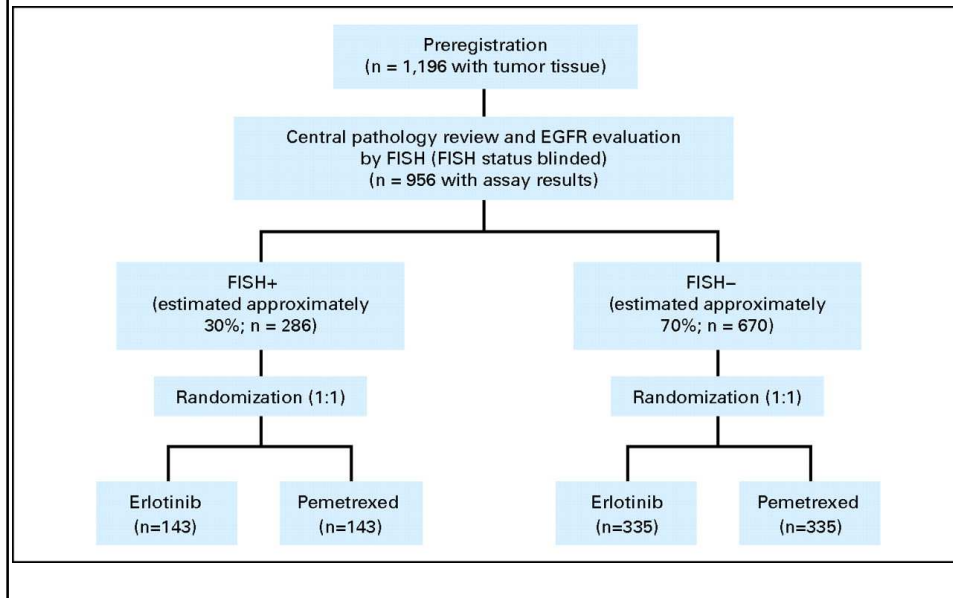
- Randomize-all design not efficient if
 - there is a strong biological rationale for no or little treatment effect in the biomarker - subgroup
 - the prevalence of biomarker + is low
 - the positive predictive value of the assay is high (> 0.90)

Ref: Maitournam, Stat Med 2005; Simon, CCR 2006; Simon, CCR 2008; George, CCR 2008; Hoering, CCR 2008

INTERACTION (BIOMARKER-STRATIFIED) RANDOMIZED DESIGN



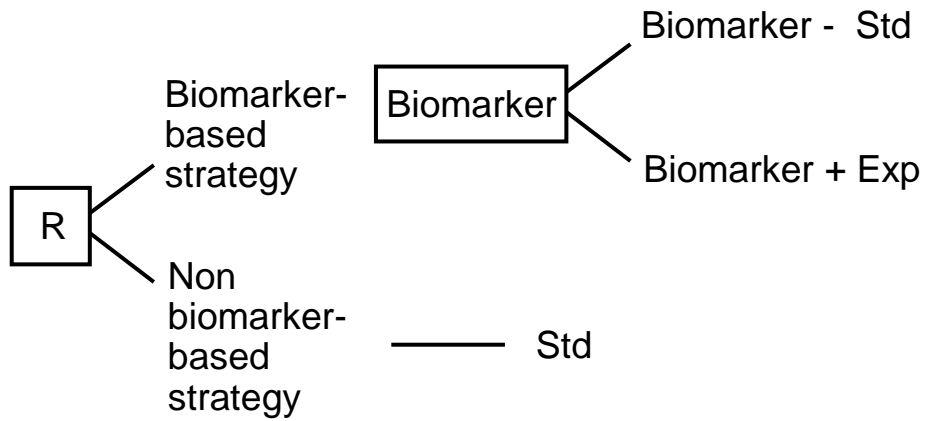
MARVEL TRIAL IN NSCLC



ISSUES WITH INTERACTION DESIGNS

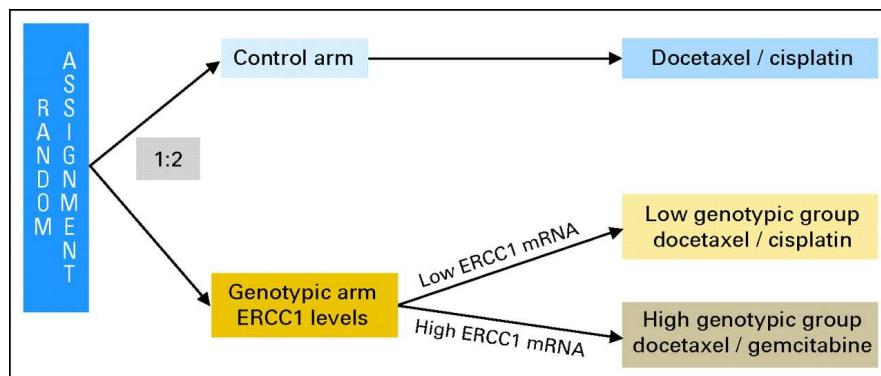
- Biomarker often unknown or poorly defined (e.g. EGFR mutations in NSCLC, *KRAS* mutations in colorectal cancer) for prospective stratification
- The power of the “interaction test” is very low, hence huge sample sizes are required and/or a very sensitive endpoint (e.g. PSA, tumor measurements or functional imaging)

BIOMARKER-BASED STRATEGY DESIGN WITH STANDARD CONTROL



Ref: Sargent, JCO 2005

SPANISH ERCC1 TRIAL



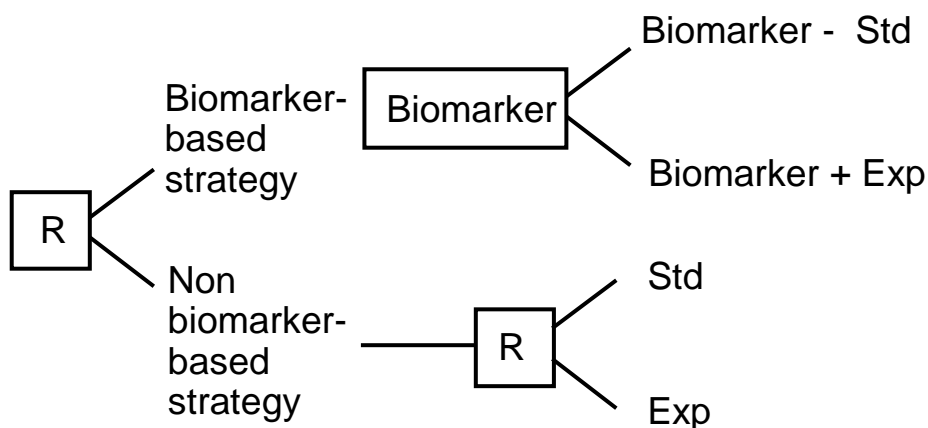
Ref: Cobo, JCO 2007

ISSUES WITH BIOMARKER-BASED STRATEGY WITH STANDARD CONTROL

- Low statistical power, especially if prevalence of biomarker is low, since in that case few patients benefit from the marker-based treatment optimization
- Confounding between predictive effect of biomarker and effect of experimental therapy

Ref: Mandrekar, JCO 2009; Freidlin, JNCI 2010; Hoering, CCR 2008; Young, Clin Trials 2010; Lee, Clin Trials 2010; Michiels, Stat Med (in

BIOMARKER-BASED STRATEGY DESIGN WITH RANDOMIZED CONTROL



ISSUES WITH BIOMARKER-BASED STRATEGY WITH RANDOMIZED CONTROL

- Very low statistical power, since random strategy will lead to correct treatment for many patients
- Randomization ratio must reflect biomarker prevalence, often unknown in advance

Ref: Mandrekar, JCO 2009; Freidlin, JNCI 2010; Hoering, CCR 2008; Young, Clin Trials 2010; Lee, Clin Trials 2010

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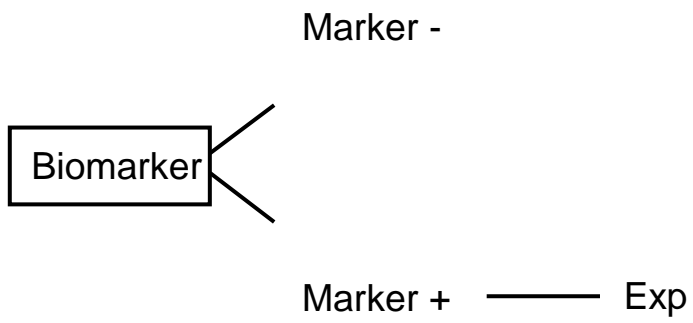
↳ Trial designs

- *Targeted (selection)*

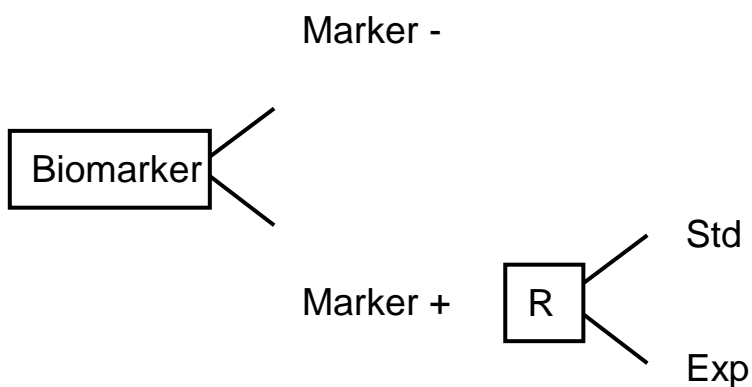
↳ Examples

- *Herceptin trials in ABC*
-

TARGETED (SELECTION) SINGLE-ARM DESIGN



TARGETED (SELECTION) RANDOMIZED DESIGN



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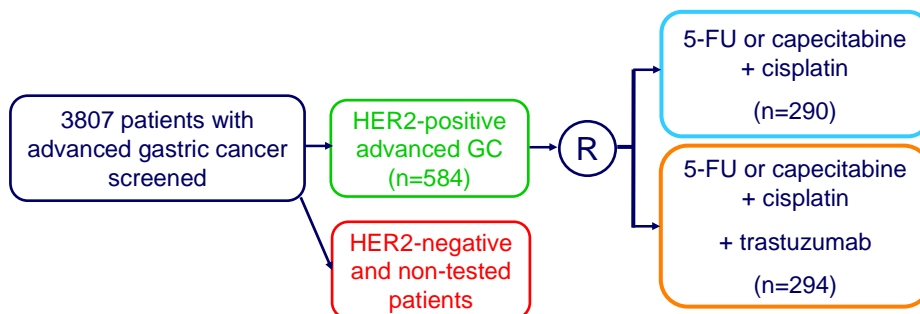
- *Targeted*

↳ Examples

- *TOGA in AGC*

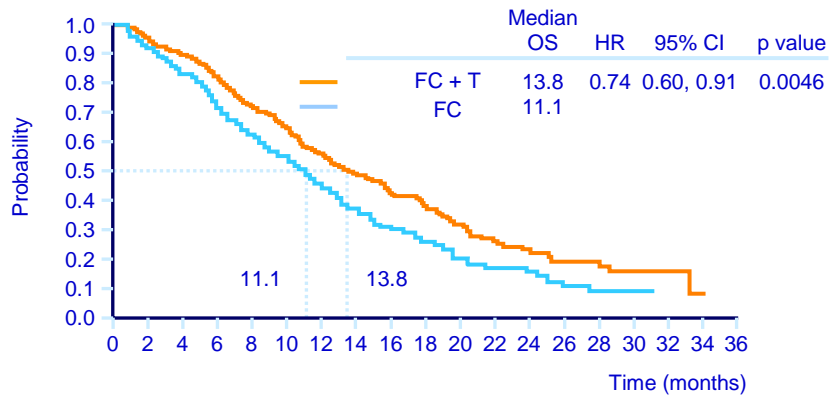
TOGA TRIAL DESIGN

Phase III, open-label international study



Ref: Bang, ASCO 2009; Abstract 4556

TOGA PRIMARY ENDPOINT: OS



| No. at risk | 0 | 2 | 4 | 6 | 8 | 10 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 |
|-------------|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|----|----|----|----|----|----|----|----|
| FC + T | 294 | 277 | 246 | 209 | 173 | 147 | 113 | 90 | 71 | 56 | 43 | 30 | 21 | 13 | 12 | 6 | 4 | 1 | 0 |
| FC | 290 | 266 | 223 | 185 | 143 | 117 | 90 | 64 | 47 | 32 | 24 | 16 | 14 | 7 | 6 | 5 | 0 | 0 | 0 |

CI, confidence interval; T, trastuzumab

ISSUES WITH TARGETED DESIGN

- Targeted design may be less efficient than randomize-all design if drug has at least some activity in biomarker - patients
- Effect in biomarker - patients may never be known (e.g. effect of adjuvant trastuzumab in patients with early breast cancer)
- Loss of opportunity for biomarker - patients
- In a randomize-all design, multiple candidate biomarkers can be tested

Ref: Maitournam, *Stat Med* 2005; Simon, *CCR* 2006; Simon, *CCR* 2008; George, *CCR* 2008; Hoering, *CCR* 2008; Michiels, *Stat Med* (in press)

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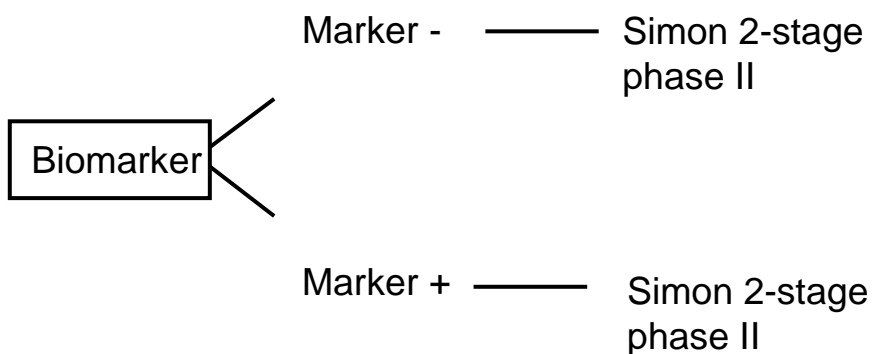
- *Adaptive parallel*
- *Tandem two-stage*

↳ Examples

- *FGFR1 inhibitor in BC*
- *saracatinib in PC*

ADAPTIVE PARALLEL

PUTATIVE BIOMARKER



Example : phase II trial of dovitinib in FGFR1-amplified and nonamplified HER2-negative metastatic breast cancer

Ref: Jones 2007; McShane 2009; André et al ASCO 2010

**TANDEM TWO-STAGE
(BIOMARKER NOT KNOWN AT ALL)**

- Simon 2-stage design in overall population
- End of stage 1:
 - if enough responses ⇨ continue in overall population
 - else ⇨ develop molecular predictor & only recruit patients predicted to be « responders »
- Example : phase II clinical trial of saracatinib as monotherapy in previously treated patients with metastatic pancreatic cancer

Ref: Puztai, CCR 2007; Nallaparedy, ASCO GI 2010

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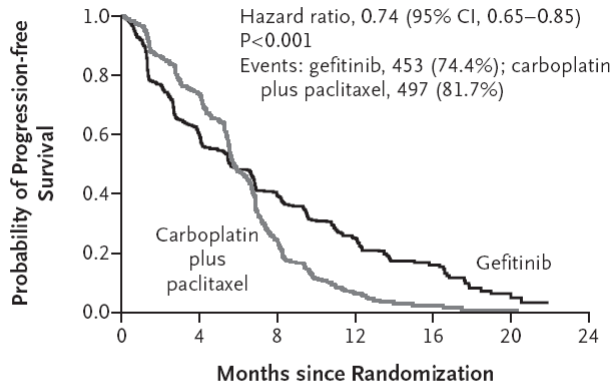
- *Enrichment*
- *Prospective subset*

↳ Examples

- *IPASS in NSCLC*
- *SATURN in NSCLC*

IPASS TRIAL ENRICHED FOR MUTATION + PATIENTS (ASIAN POPULATION)

Overall



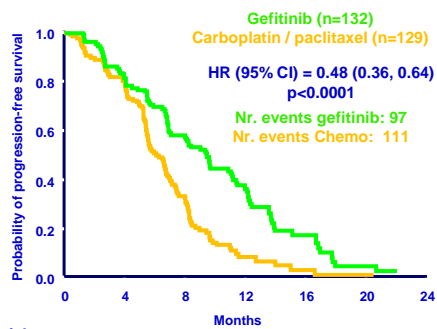
No. at Risk

| | | | | | | | |
|-----------------------------|-----|-----|-----|----|----|---|---|
| Gefitinib | 609 | 363 | 212 | 76 | 24 | 5 | 0 |
| Carboplatin plus paclitaxel | 608 | 412 | 118 | 22 | 3 | 1 | 0 |

Ref: Mok, NEJM 2009

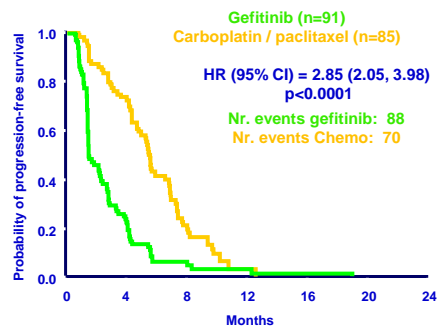
IPASS TRIAL ENRICHED FOR MUTATION + PATIENTS (ASIAN POPULATION)

EGFR mutation +



| | | | | | | | |
|-----------|-----|-----|----|----|----|---|---|
| At risk : | | | | | | | |
| Gefitinib | 132 | 108 | 71 | 31 | 11 | 3 | 0 |
| C/P | 129 | 103 | 37 | 7 | 2 | 1 | 0 |

EGFR mutation -



| | | | | | | | |
|-----------|----|----|----|---|---|---|---|
| At risk : | | | | | | | |
| Gefitinib | 91 | 21 | 4 | 2 | 1 | 0 | 0 |
| C/P | 85 | 58 | 14 | 1 | 0 | 0 | 0 |

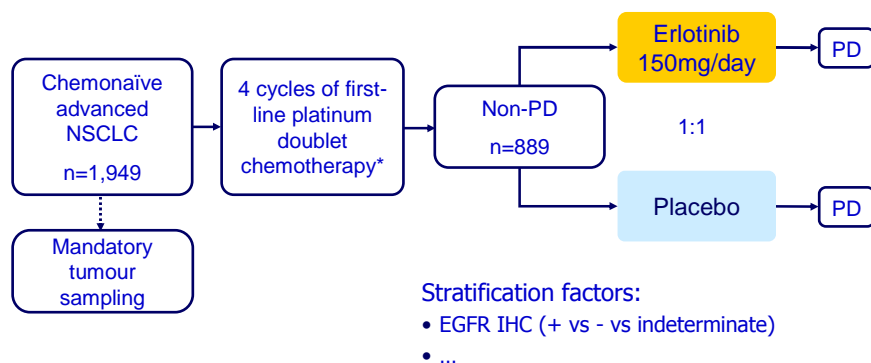
Ref: Mok, NEJM 2009

PROSPECTIVE SUBSET

- Simplest approach: split significance level:
 - $\alpha = \alpha_{\text{all}} + \alpha_{\text{biomarker+}}$
 - the new treatment is compared with the control in the overall population, ignoring the biomarker
 - if $p_{\text{all}} \leq \alpha_{\text{all}}$ claim effectiveness for all patients
 - if not, the new treatment is compared with the control in biomarker + patients only, and if $p_{\text{biomarker+}} \leq \alpha_{\text{biomarker+}}$ claim effectiveness for biomarker + patients only
- There are less conservative, yet properly controlled, ways of adjusting α for both (correlated) tests

Ref: Wang, *Pharm Stat* 2007; Jiang, *JNCI* 2007; Alosch, *Stat Med* 2009; Wang, *Biom J* 2009; Spiessens, *Contr Clin Trials* 2010

SATURN DESIGN



Co-primary endpoints:

- PFS in all patients
- PFS in patients with EGFR IHC+ tumours

SATURN OVERALL RESULTS

| | Erlotinib (n = 438) | Placebo (n = 451) | HR | <i>P</i> |
|-----------------|------------------------|------------------------|------|----------|
| PFS | (n = 437) | (n = 447) | | |
| PFS at 12 weeks | 53% | 40% | 0.71 | < .0001 |
| PFS at 24 weeks | 31% | 17% | | |
| Median PFS | 12.3 weeks | 11.1 weeks | | |
| Median OS | 12 months (n = 436) | 11 months (n = 445) | 0.81 | .0088 |

KEY QUESTIONS FOR DESIGN CHOICE

- What do we know reliably before the trial starts (in terms of treatment and biomarker effects)?
- What do we want to know reliably after the trial is done (i.e. is the trial for discovery or confirmation ?)
- What are the consequences of type I and type II errors in terms of biomarker usefulness?
- Will there be repeat trials?