

Three Methods for Phase I/II Clinical Trials, with Application to Allogeneic Stem Cell Transplantation

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Workshop on Clinical Trial Endpoints for Acute Graft-vs-Host Disease after Allogeneic Hematopoietic Stem Cell Transplantation

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Financial Conflicts of Interest

- None

Standard “3+3” Phase I Designs for Oncology

- Objective: Identify the maximum tolerated dose (MTD)
- MTD defined by algorithm: *Implicitly* either 17% or 33% grades 3-5 AE
- But the incidence of grade 3 AEs far exceeds 17-33% for BMT patients, so this design is rarely applicable for this population of patients
- Well known to have inferior properties compared to Bayesian adaptive designs

Three Phase I and Phase I-II Designs

| Treatment Optimized | Outcome | Decision Criterion | Example |
|--|-----------------------------------|------------------------------|---|
| Dose | Bivariate binary (phase I-II) | Efficacy-toxicity trade-offs | GVHD prophylaxis, anergized cells post allotx, etc. |
| Dose and Schedule | Time to toxicity (phase I) | Pr(toxicity by day t^*) | Azacitidine post allotx |
| Doses of two agents ($dose_1$, $dose_2$) | Bivariate ordinal (phase I-II) | Utility of outcome | Bladder cancer |

All methods are

Bayesian : Model parameters are considered to be RANDOM quantities

Sequentially Outcome Adaptive :

Choose a treatment

(dose, dose-schedule, dose pair) →

Treat a cohort of patients →

Observe the patients' outcomes

Repeat until a stopping rule says “**Stop**”

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Dose-Finding Based On Efficacy-Toxicity Trade-Offs

(Thall and Cook, 2004; Thall, Cook and Estey, 2006)

Patient Outcome = {Efficacy, Toxicity}

- each a binary indicator

$$\pi_E(x) = \Pr(\text{Efficacy at dose} = x)$$

$$\pi_T(x) = \Pr(\text{Toxicity at dose} = x)$$

MD must specify:

- A Lower Limit on $\pi_E(x)$ (minimum response of interest)
- An Upper Limit on $\pi_T(x)$ (maximum acceptable toxicity)
- Three or more equally desirable (π_E, π_T) targets...

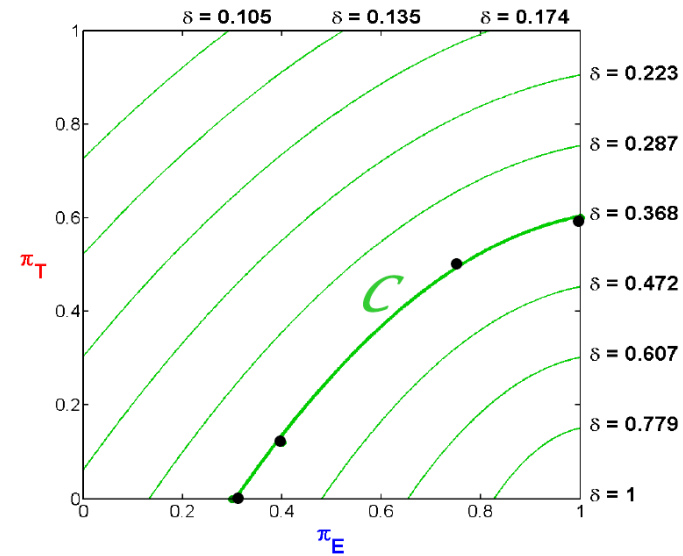
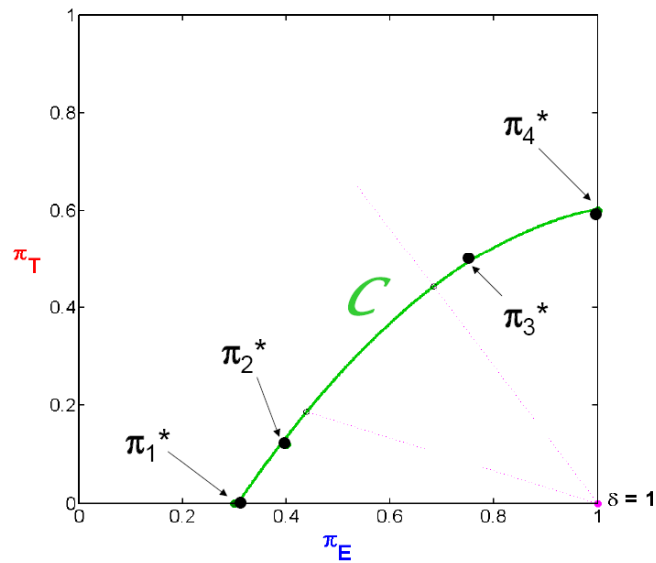
Two Dose Acceptability Criteria



Efficacy Cop



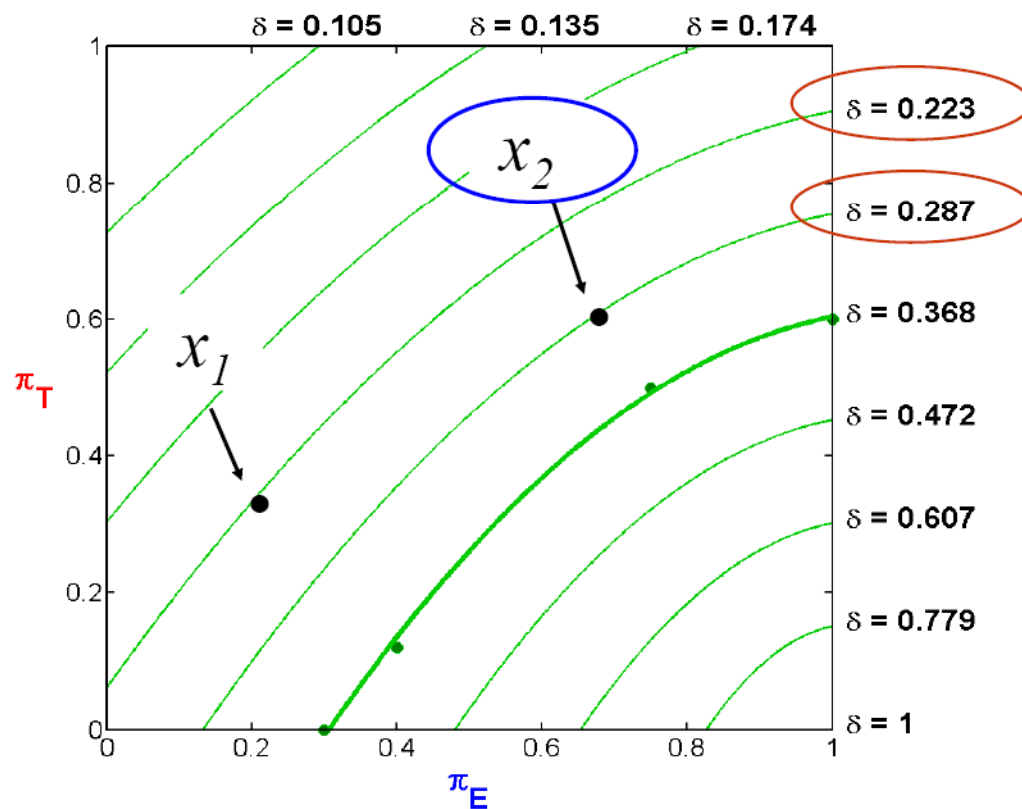
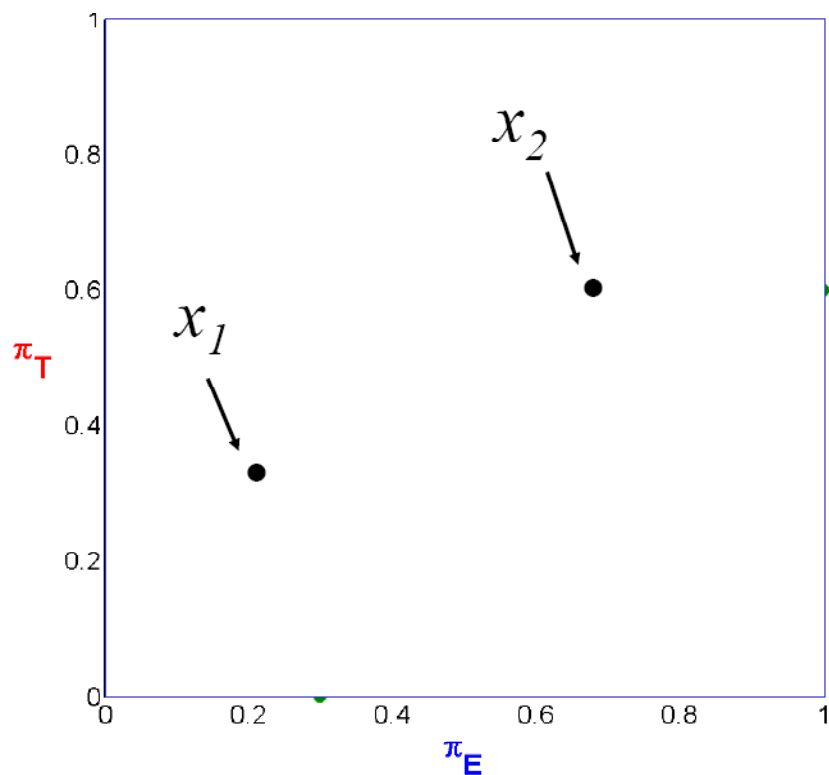
Toxicity Cop



Target pairs are used to construct an **Efficacy-Toxicity** Trade-off Contour...

and a family of Contours each with desirability, δ , for the (π_E, π_T) pair

Which of these two π pairs is more desirable?



Trial Conduct

- 1) The physician chooses the **starting dose**
- 2) A dose is **Acceptable** if either
 - a) it has acceptable π_E & π_T or
 - b) it is the lowest untried dose and has acceptable π_T
- 3) **Treat each cohort at the current most desirable dose**
 - a) The dose chosen for the next cohort may be *higher than, the same as, or lower than* the current dose
 - b) *After de-escalation due to excessive toxicity or low efficacy*, if subsequent outcomes at a lower dose are sufficiently safe and efficacious, then *the algorithm may re-escalate*
- 4) Do not skip untried doses
- 5) No dose acceptable → **Stop the trial**
- 6) **At the end, select the most desirable dose**

Pentostatin for Graft-Versus-Host Disease

Patients with steroid-refractory GVHD after allotx
from an HLA-matched donor

Doses : $x = .25, .50, .75, \text{ or } 1.00 \text{ mg/m}^2$

$N_{\max} = 36$, cohort size = 3

First cohort treated at $.25 \text{ mg/m}^2$

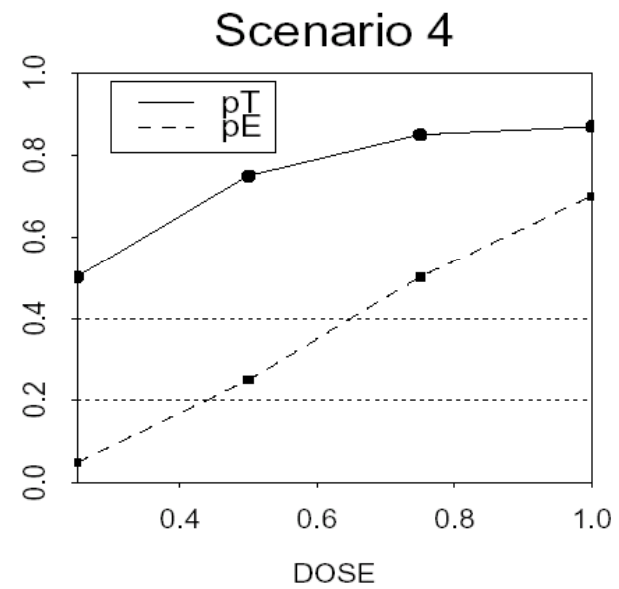
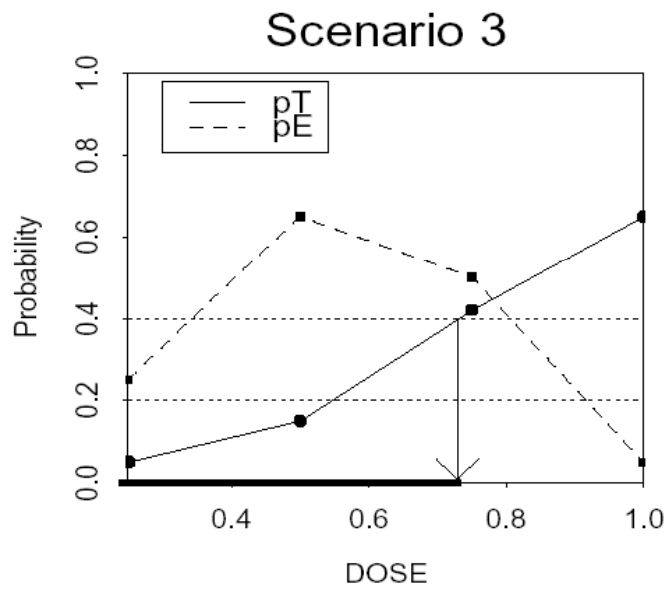
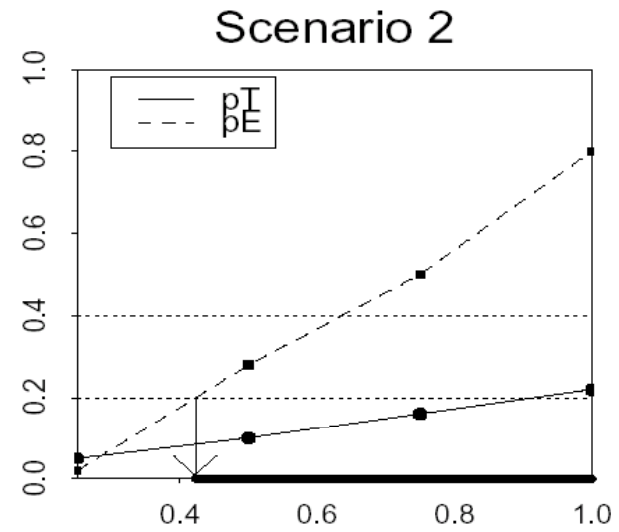
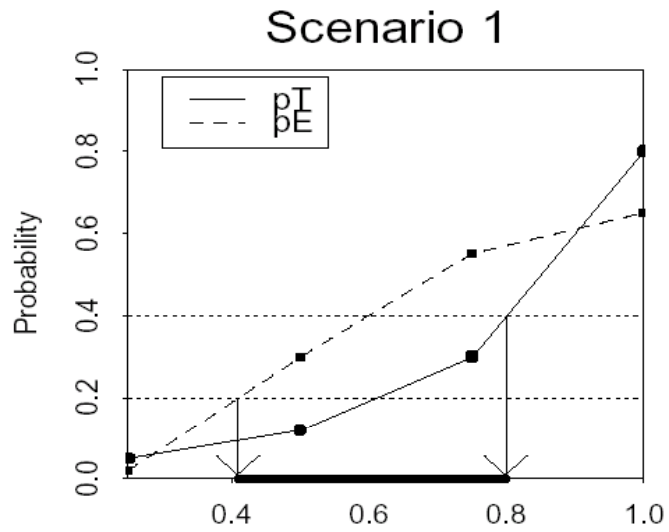
Toxicity = {Infection unresolved by antibiotics, or
death, within 2 weeks}

Efficacy = { ≥ 1 grade drop in GVHD severity,
within 2 weeks}

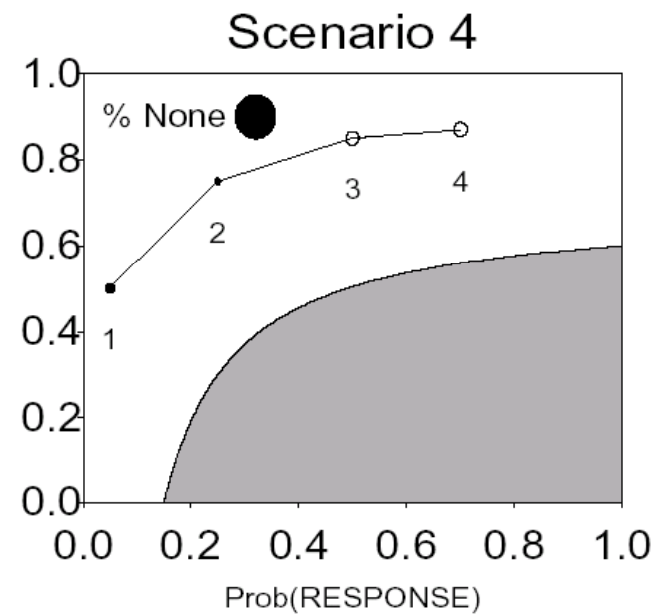
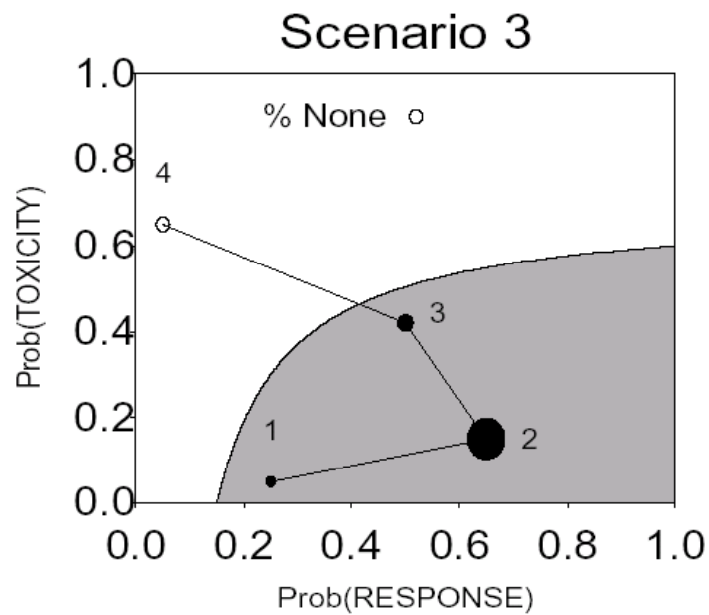
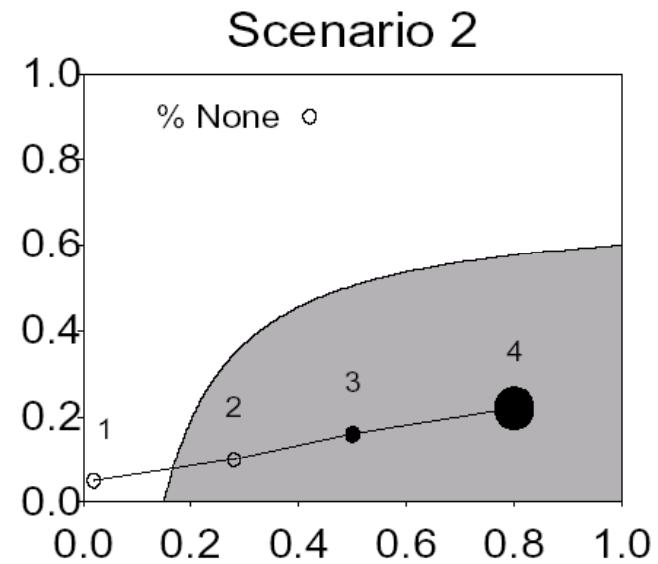
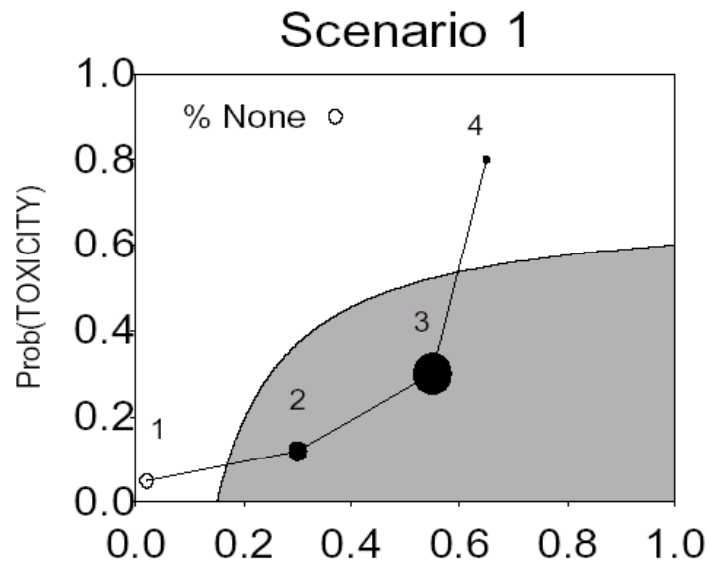
.40 = Upper Limit on $\pi_T(x)$

.20 = Lower Limit on $\pi_E(x)$

Simulation Scenarios for the Pentostatin Trial



Dose Selection Probabilities



Conclusions

The *Trade-Off-Based Algorithm* reliably

- 1) Finds Safe Doses having High **Efficacy**
- 2) **Stops** if no dose is acceptable

Implementation is Hard Work, but a free computer program is available!

Three Phase I and Phase I-II Designs

| Treatment Optimized | Outcome | Decision Criterion | Example |
|---|---------------------------------------|-------------------------------|---|
| Dose | Bivariate binary (phase I-II) | Efficacy-toxicity trade-offs | GVHD prophylaxis, anergized cells post allotx, etc. |
| Dose and Schedule | Time to toxicity (phase I) | Pr(toxicity by day t*) | Azacitidine post allotx |
| Doses of two agents (dose ₁ , dose ₂) | Bivariate ordinal (phase I-II) | Utility of outcome | Bladder cancer |

Optimizing Dose and Schedule Based On Time to Toxicity

Braun, Thall, Nguyen, deLima *Clinical Trials*, 2007

Goal: Optimize (**Dose, Schedule**)
based on **Time to Toxicity**

Vidaza[®] (azacitidine) given post allotx in AML pts

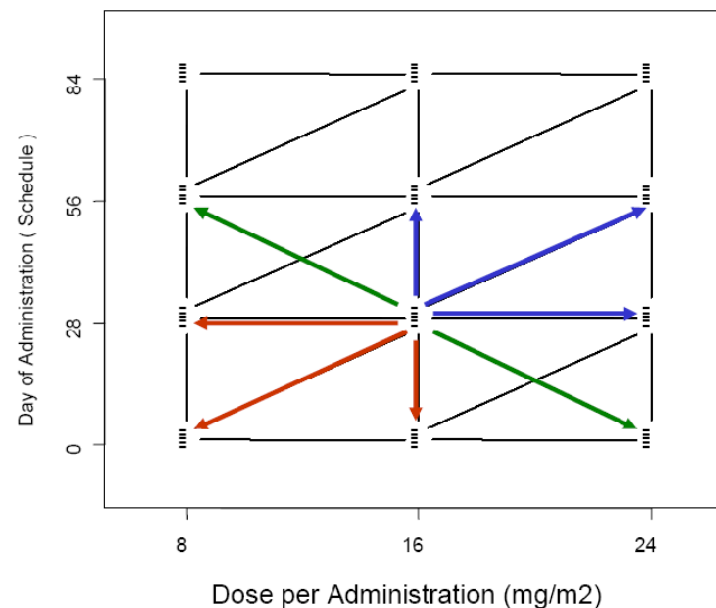
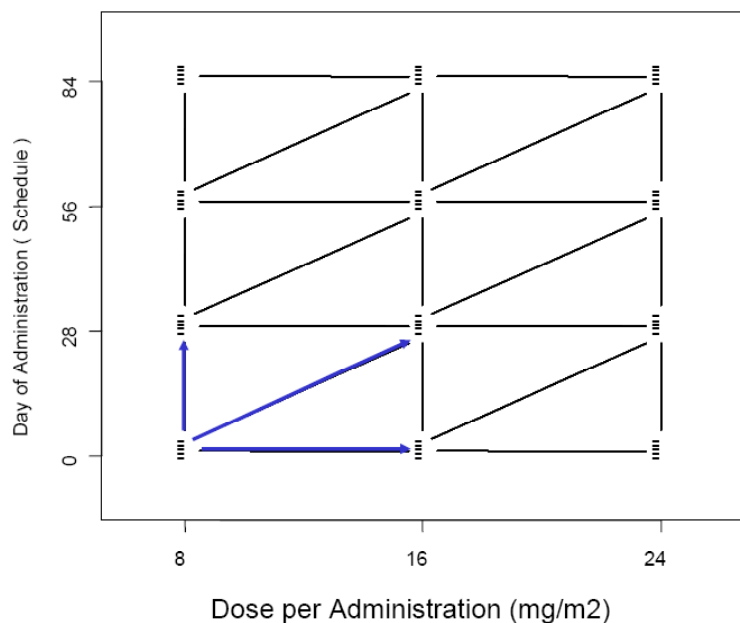
- Dose-toxicity profile of Vidaza[®] unknown
- Cumulative toxicity of repeated administration (multiple 28-day cycles) unknown

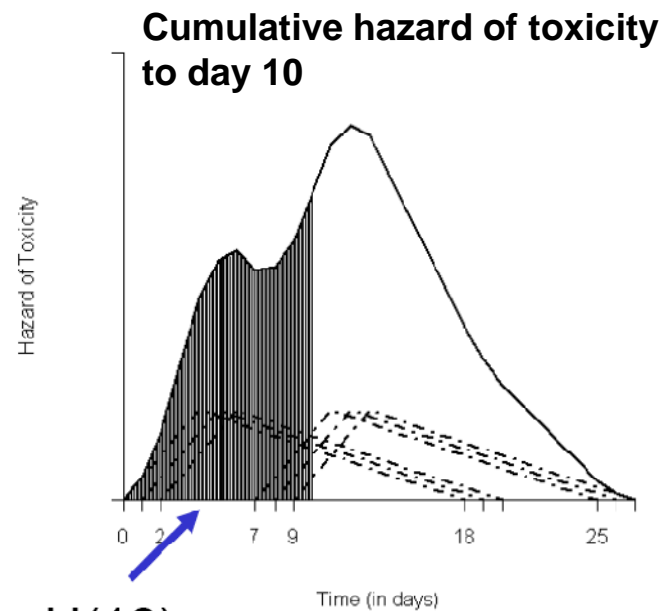
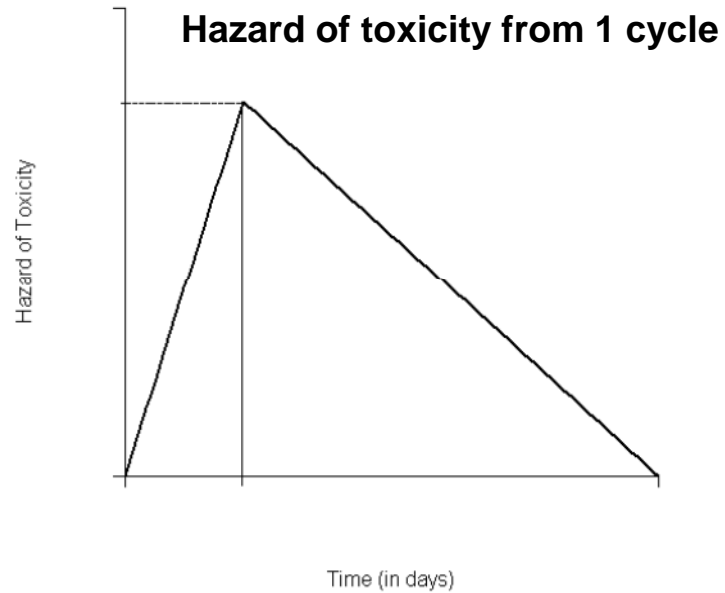
Patient Outcome

- $T = \text{Time from the start of treatment to toxicity}$
- Usual “time-to-event” data, as in a survival time analysis. A patient’s outcome consists of
 - a) *Time to toxicity* if it occurred, or *Time to last follow up* if toxicity has *not* occurred
 - b) An *indicator* of whether toxicity has occurred
- Why is “time-to-event” better than a binary outcome?
Using a usual binary (Yes / No) indicator of
[“Toxicity” within 28 days from the start of therapy]
 - A patient with toxicity at day 27 is scored “Yes”
 - A patient with toxicity at day 29 is scored “No”
 - A patient followed for only 25 days w/o toxicity is inevaluable and **cannot be scored**

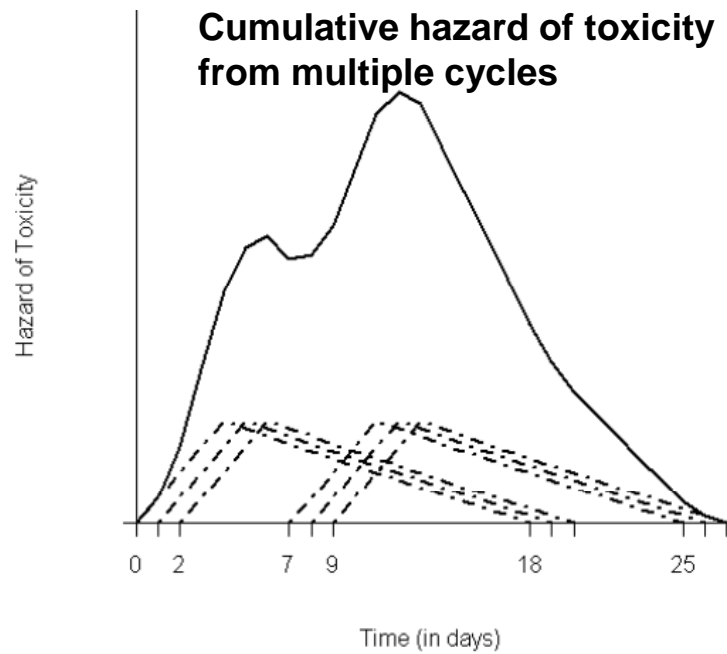
Trial Conduct

- 1) Treat 1st patient at the lowest (dose, schedule)
- 2) Using current **Time-to-Toxicity data**, treat each patient at the (dose, schedule) pair with **ptox** = $\Pr(\text{Toxicity by day } t^* \mid \text{dose, schedule})$ closest to the target max toxicity rate
- 3) Do not “skip” untried (dose, schedule) pairs
- 4) If no (dose, schedule) pair is acceptable \rightarrow Stop the trial





$H(10)$

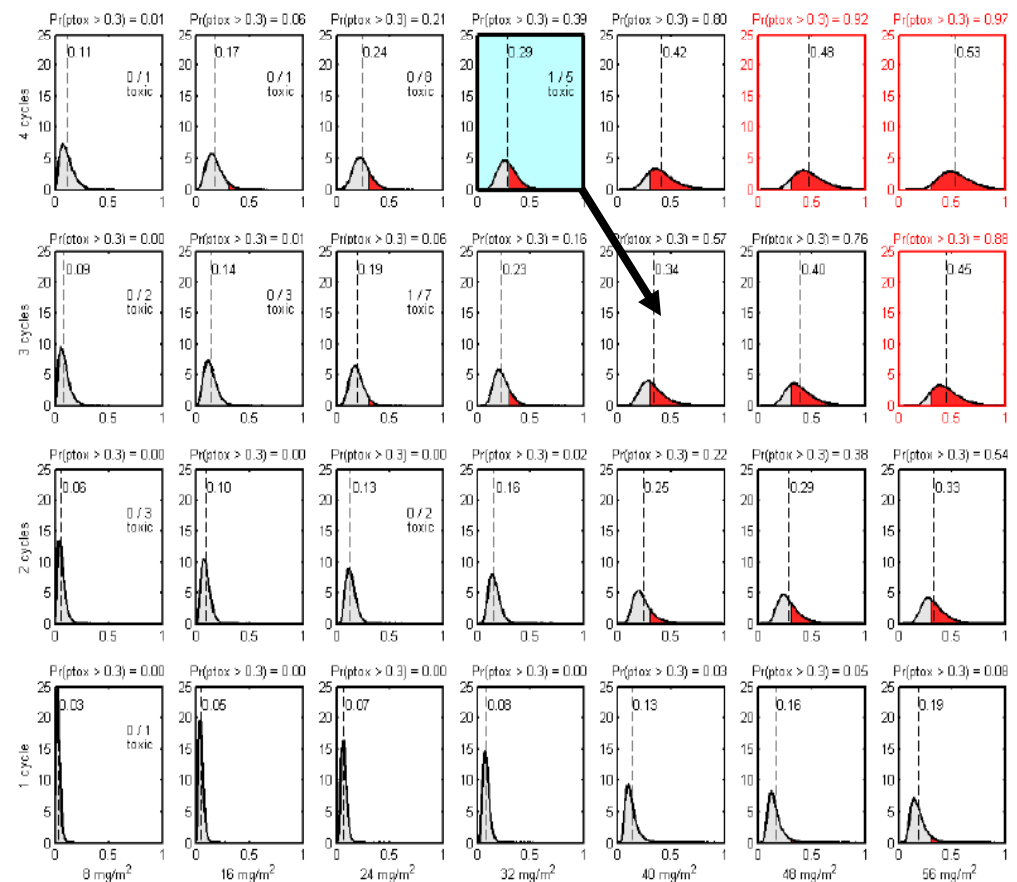


$$\text{Prob}(\text{Toxicity by day 10}) = 1 - e^{-H(10)}$$

What Actually Happened in the Vidaza[®] Trial?

- Treatment parameters
 - Vidaza doses 8, 16 or 24 mg/m² daily x 5 in each cycle
 - Given for 1, 2, 3 or 4 28-day cycles
- Definition of toxicity
 - Severe (NCI grade 3 or 4) kidney, liver, heart, lung or neural toxicity
 - Severe GVHD
 - Systemic infection not resolved by antibiotics within two weeks
 - Severe haematologic toxicity
- **ptox** = Pr(Toxicity by day 116 | dose, schedule) closest to the tox target 0.3
- Only 1 toxicity in 27 patients, so 4 more dose levels 32,40,48,56 added
- Optimal dose-schedule identified after 44 patients:
(40 mg/m² x 3 cycles)

After N=33 patients



Conclusions

The *Dose-Schedule Algorithm* reliably

- 1) Finds (Dose, Schedule) pairs having specified $\Pr(\text{Toxicity by day } t^*)$
- 2) **Stops** if no (Dose, Schedule) is acceptable

Implementation is Hard Work, but a free computer program is available!

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Optimizing the dose pair of a two-agent combination based on elicited utilities of (Toxicity, Efficacy) outcomes

Houede, Thall, Nguyen, Paoletti and Kramar. *Biometrics*, In press

Goal: Optimize (**Dose of 2 agents**)
based on **Toxicity** and **Efficacy**

Treatment of bladder cancer with a combination of chemotherapy (c) and a biologic (b) where optimal doses in combination are unknown

Dose-Combination (b_x, c_y) Matrix

| | | | | |
|------------|-------|-------------------|-------|-------|
| | (1,3) | (2,3) | (3,3) | (4,3) |
| ↑ c_y | (1,2) | (2,2) | (3,2) | (4,2) |
| | (1,1) | (2,1) | (3,1) | (4,1) |
| | | $b_x \rightarrow$ | | |

b_x = dose of biologic agent

c_y = dose of chemo agent

Patient Outcome is (Response, Toxicity)

Response

→

| | 0 = PD | 1 = SD | 2 = CR/PR | | |
|------------|--------|--------|-----------|--------|-------------|
| Toxicity ↓ | 0 | (0, 0) | (0, 1) | (0, 2) | — |
| | 1 | (1, 0) | (1, 1) | (1, 2) | — |
| | 2 | (2, 0) | (2, 1) | (2, 2) | (2, Ineval) |

Allows the possibility that Response may be inevaluable

Elicited Consensus Utilities

Response



PD

SD

CR/PR

Inevaluable

Toxicity



25

76

100

—

10

60

82

—

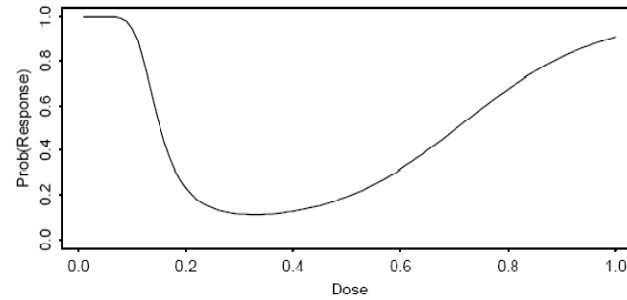
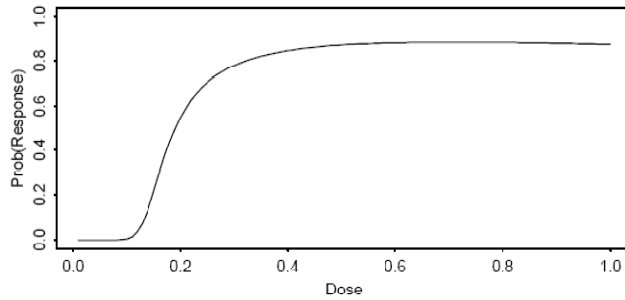
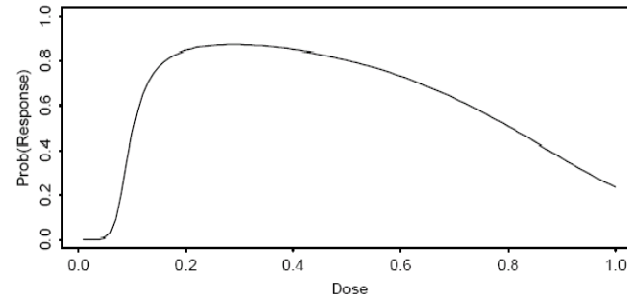
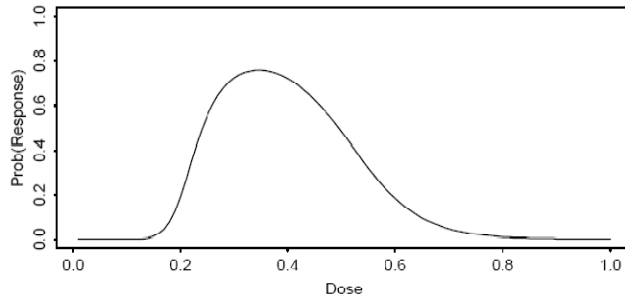
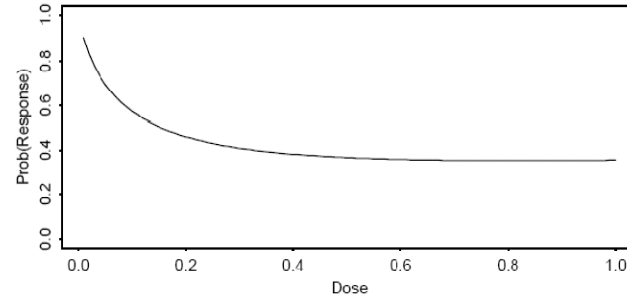
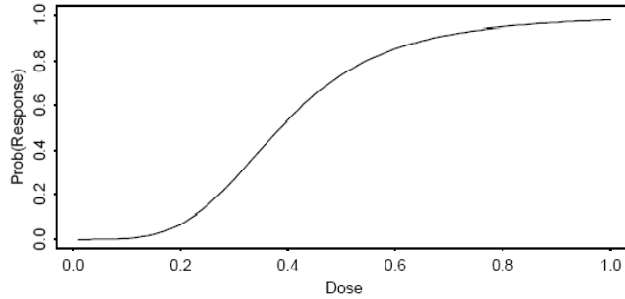
2

40

52

0

Very Flexible Dose-Outcome Model



Trial Conduct

Choose each cohort's dose pair to

Maximize the Posterior Expected Utility

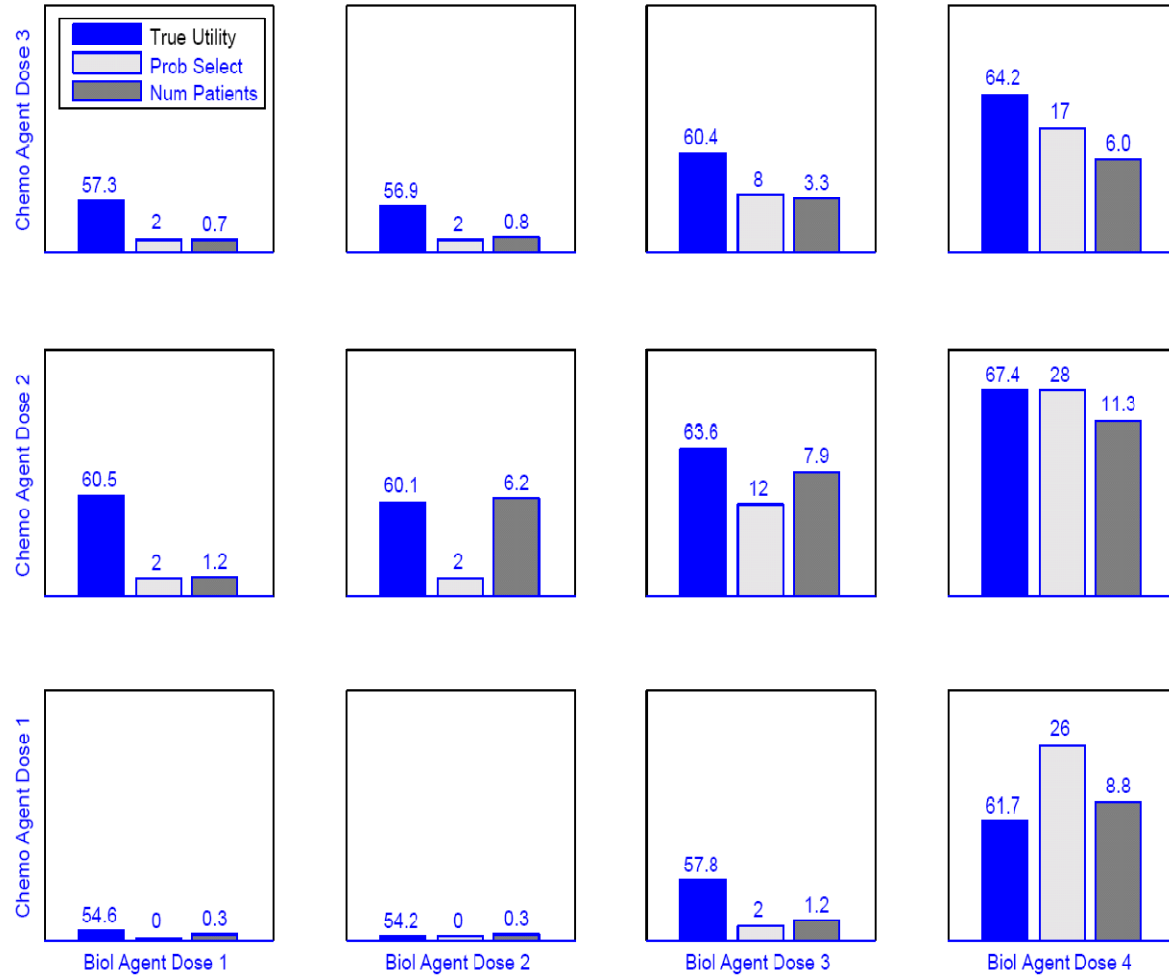
based on the data observed so far

Do Not Skip Untried Doses:

If (b_1, c_1) is the current dose pair, then escalation is allowed to as yet untried pairs (b_2, c_1) , (b_1, c_2) , or (b_2, c_2)

Stop the trial if all dose pairs are unacceptably toxic

Scenario 1



Application to Trials Monitoring GVHD

Toxicity =

0 if NO GVHD

1 if grade 1,2 GVHD

2 if grade 3,4 GVHD

or

0 if NO grade 3,4 GVHD

1 if grade 3,4 GVHD but **resolved** in <2 wks

2 if grade 3,4 GVHD **not resolved** in < 2 wks

Application to Trials Monitoring GVHD

Efficacy =

- 0 if dead, or alive but no response at day 100
- 1 if alive and engrafted with PR at day 100
- 2 if alive and engrafted with CR at day 100
(e.g. for CLL transplantation trials)

or

- 0 if dead, or no plt recovery in 100 days
- 1 if alive with $20 < \text{plt} < 50$ at day 100
- 2 if alive with $\text{plt} > 50$ by day 100
(e.g. for cord blood transplantation trials)

Extensive Computer Simulations Show
that the Utility-Based Dose-Finding
Method is

Very Reliable and Very Safe

Implementation is Hard Work, but a
free computer program is available!

Phase I and I/II Designs for GVHD Trials

| Design | Objective | Comments |
|-----------------------|---|---|
| 3+3 | MTD | Easy to do, poor properties, rarely applicable to BMT patients |
| Accelerated titration | MTD | Acceptable for relatively nontoxic agents, but rarely applicable (like 3+3) |
| CRM, mCRM | MTD | Stat-intensive, flexible for toxicity target, find dose based on toxicity |
| Time-To-Tox | Max tolerated dose and schedule combo | Stat-intensive, flexible for toxicity target, finds dose and schedule |
| Eff-Tox | Best dose based on toxicity and efficacy | Stat-intensive, optimizes efficacy and toxicity jointly |
| Doublet Studies | Best combo based on toxicity and efficacy | Stat-intensive, optimizes efficacy and toxicity jointly |

References

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Software at: <http://biostatistics.mdanderson.org/SoftwareDownload>