On the Feasibility of Phase II/III Studies in Oncology

Werner Brannath, MUW, Vienna

Uli Burger, Hoffmann-La Roche, Basel Maximo Carreras, Hoffmann-La Roche, Basel

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Scope of the presentation

- Dose finding in oncology
- Surrogates in oncolcogy and their problems
- Proposals and limitations for seamless phase II/III designs
- Comparison of different methods
- Summary

Dose finding in oncology

- Classical paradigm:
 - Dose defined in Phase I based on safety endpoints only (e.g. 3 plus 3 designs or CRM designs)
 - Chose highest dose with acceptable safety profile (MTD - maximal tolerated dose)
 - Explore in phase II if MTD is active
 - Proof in phase III that it is more active than standard
- Classical paradigm today often outdated
 - Not all new treatments are cytotoxics, i.e., highest dose not always solely most effective dose.
 - In this case MTD usually not well defined
 - ⇒ Breakdown of classical paradigm
 - ⇒ Other dose finding steps are needed
 - Efficacy plays a major role already for dose finding

Dose finding in oncology based on efficacy

- Potential endpoints are
 - response rate (RR; e.g. 50% reduction in tumor size)
 - ▶ progression-free survival (PFS; e.g. time till ≥ 25% increase in tumor size) or
 - overall survival (OS).
- RR and PFS usually viewed as surrogate for OS.
- OS only clinically relevant endpoint
- Level of surrogacy of RR and PFS for OS usually unknown.

Dose finding in oncology - Problems

- All three endpoints statistically insensitive, leading to large and time consuming phase II dose finding trials.
- ▶ One-sided $\alpha = \beta = 0.2$
 - RR: Test 10% difference in RR ⇒ about 280 patients
 - ▶ PFS: Test 25% reduction in HR in PFS ⇒ 137 events
- Solutions:
 - Using of more sensitive biomarkers
 - Use of adaptive design allowing larger phase II dose finding parts while still maintaining overall size of the program
 - ⇒ How should such designs look like?

Surrogates in oncology – Problems

- When using a surrogate for phase II we face:
 - How to describe the relationship between RR and OS?
 - What difference in RR do we need to observe to believe in a difference in OS?
- Example:
 - Usual thinking is that a difference in PFS or OS is induced by a difference in response.
 - When this would be true, most oncology treatments would not be sufficiently effective. Necessary response rate difference is above 30% under standard assumptions to yield meaningful difference in PFS solely caused by difference in RR.
 - Effect on PFS or OS is usually composite, increases response rate and effects survival within each response category.

Surrogates in oncology – Problems

- Surrogate model for RR for an experimental treatment E versus a standard treatment S can be described as
 - Cytotoxic effect: Increase in RR by $\Delta = \theta_E \theta_S$
 - Cytostatic effect: Prolongation in OS within responder and non-responder subgroups
- If the effect of E on OS is working only through the response category, then RR is a perfect surrogate.
- But usually: Effect of E on OS is partially an effect working through change in response category and change in OS within category.

Surrogates in oncology - Model

 $S_g(t)$ survival function, $\lambda_g(t)$ hazard function in groups g=E or S,

With $S_{g,R}(t)$, $\lambda_{g,R}(t)$ and $S_{g,N}(t)$, $\lambda_{g,N}(t)$ for responder (R) and non-responder (N):

$$\lambda_g(t) = \theta_g \, \lambda_{g,R}(t) + (1 - \theta_g) \, \lambda_{g,N}(t)$$

Assuming proportional hazards: $\lambda_{S,N}(t) = \lambda(t)$ and $\lambda_{S,R}(t) = r \lambda(t)$, $\lambda_{E,N}(t) = c\lambda(t)$, $\lambda_{E,R}(t) = cr\lambda(t)$,

$$\implies \mathsf{HR}_{E/S} = \frac{\lambda_E(t)}{\lambda_S(t)} = c \cdot \left\{ 1 - \frac{(1-r)(\theta_E - \theta_S)}{1 - (1-r)\theta_S} \right\}$$

Surrogates in oncology – Examples

• $\theta_S = 20\%$ (RR in S); r = 0.50 (HR R/N).

$$\theta_{E}=\theta_{S}+$$
 10% $=$ 30% and $c=\lambda_{E,R}(t)/\lambda_{S,R}(t)\sim$ 1,

$$\Rightarrow$$
 HR_{E/S} = 0.95

(Capecitabine 1st line CRC monotherapy, true rate \sim 0.93?)

• $\theta_S = 57\%$ (RR in S), r = 0.50 (HR R/N)

Cytotoxic effect and cytostatic effect:

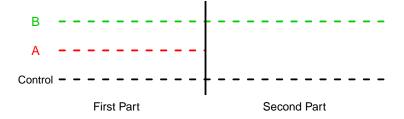
$$\theta_E = \theta_S + 24\% = 81\%$$
 and $c \sim 0.6$,

$$\Rightarrow$$
 HR_{E/S} = 0.50

(Rituximab-Chemo in NHL, observed HR =0.41)



Adaptive Designs with Treatment Selection



- First part: start with several treatment arms.
- Interim analysis (IA): select treatments, e.g., based on RR.
- Second part: continue recruitment only in selected arms.
- Final analysis: test treatment efficacy of the selected treatments from the data of both parts.

Testing efficacy of selected treatments

(BAUER & KIESER 1999, HOMMEL 2001, ...)

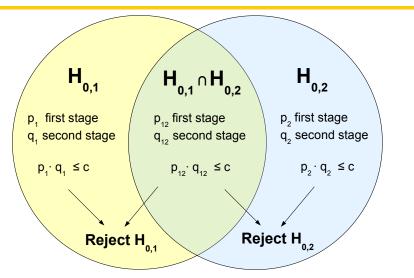
Testing strategy which combines two approaches:

- Closed Testing Principle to control the multiple type I error rate;
- Combination Test (Conditional Error Function Approach) to cope with the adaptations

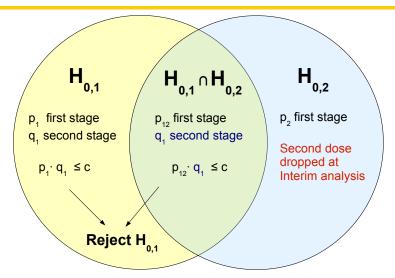
Methodology:

Use a combination test for each intersection hypothesis and apply the closed testing principle to these combination tests.

When selecting both treatments

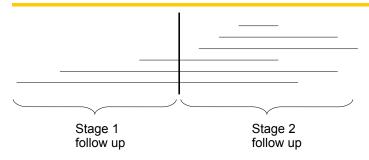


When selecting treatment 1 only



Combination test with follow-up wise stages

(Müller & Schäfer '01, Bauer & Posch '01, Wassmer '06, ..)



Stage 1: p_1 , p_2 , p_{12} from

log-rank tests, follow-up **till** time of IA, i.e., **right** censoring at time of IA

Stage 2: q_1 , q_2 , $q_{1,2}$ from

log-rank tests, follow-up **from** time of IA, i.e., **left** censoring at IA (or increments).

Combination test with follow-up wise stages

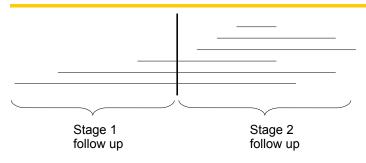
- Same type of stage-wise data splitting as in group sequential designs (Jennison and Turnbull, 2001).
- Gains power from both, cytotoxic and cytostatic effect.
- Strict type I error rate control only if IA-decisions depend solely on OS (Bauer & Posch '01),
- Reason: When using RR or PFS, first and second stage log-rank statistics may fail to be assym. independent.



No strict type I error rate control when treatment selection is based on RR or PFS!

Combination test with stratified log-rank test

(ZUBER ET AL. '06, BRANNATH ET AL. '08)



Stage 1: p_1 , p_2 , p_{12} from

stratified (e.g. for RR) log-rank tests, follow-up **till** time of IA,

Stage 2: q_1 , q_2 , $q_{1,2}$ from

stratified (e.g. for RR) log-rank tests follow-up **from** time of IA.

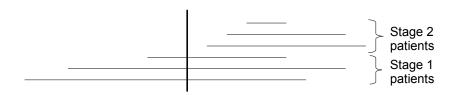
Combination test with stratified log-rank test

- Same type of stage-wise data splitting as in group sequential designs (Jennison and Turnbull, 2001).
- Strict type I error rate control when treatment selection is based on RR.
- Gains power only from cytostatic effect!
- Reason: We condition on RR. Stratified logrank test verifies (average) treatment effect only within each RR-group.



Strict type I error rate control for the price of a power loss!

Combination test with patient wise stages



Stage 1: p_1 , p_2 , p_{12} from

unstratified log-rank tests from patients recruited **before** the IA.

Stage 2: q_1 , q_2 , $q_{1,2}$ from

unstratified log-rank tests from patients recruited **after** the IA.

Combination test with patient wise stages

- Strict type I error rate control when treatment selection is based on PFS, RR, OS or any other information.
- ► Gains power from both, *cytotoxic* and *cytostatic* effect.
- First stage p-value can only be computed at end of trial and is not available at the IA
 - \Rightarrow early efficacy testing impossible (often anyhow not anticipated).

Combination test with patient wise stages

Design for first stage patients must be fixed and remain unaltered.

Consequently:

- Stage 1 patients must stay in trial and be treated and followed-up as pre-planned also when treatment arm is terminated.
- Patients of terminated treatment arm could be switched to selected treatment because only used for $H_{0.1} \cap H_{0.2}$.
- IA-decision should not influence follow-up time of stage 1 patients (e.g. avoid change of overall event/patient number by event/sample size reshuffling).
- Only a minor problem when proportion of censoring among first stage patients is small.

Simulation (10⁵ runs)

Two doses (E_1 , E_2) and standard treatment S, 305 patients per treatment group, uniform recruitment within 35 month.

exponential survival, no censoring

 $\lambda_{S,N} = 0.0462$ (hazard in S and NR),

 $HR_{R/N} = 0.7$ in S (hazard rate of RR vs. NR)

IA at 50% patients per arm; we select dose with higher RR.

Simulation (10⁵ runs)

Fisher's product test.

null hyp.:
$$\theta_S = \theta_{E_1} = \theta_{E_2} = 0.4, \ c_1 = c_2 = 1$$
 alternative 1: $\theta_S = \theta_{E_1} = \theta_{E_2} = 0.4, \ c_1 = c_2 = 0.8$ alternative 2: $\theta_S = 0.2, \ \theta_{E_1} = 0.3, \ \theta_{E_2} = 0.4, \ c_1 = 0.9, \ c_2 = 0.8$

STAGES	follow-up wise	follow-up wise	pat. wise
TEST	unstratified	stratified	(unstratified)
null hyp.	0.019	0.017	0.019
alternative 1	0.83	0.70	0.85
alternative 2	0.89	0.65	0.89

Further considerations

- What information should be used for IA-decision (RR only, RR and OS, RR and PFS and OS)? How to use this information? Answer requires modeling and extensive simulations
- When (at which proportion of patients) should the interim analysis be done?
- Comparison of Phase II/III design to separate phase II and phase III trials.
- Combination test with follow-up wise stages with p-values from a joint model of RR and OS.

Discussion

- ► There is no universally applicable method. All methods require specific additional assumptions or restrictions.
- Usual combination test (follow-up wise stages) with survival data and treatment selection based on surrogate endpoints may not control type I error rates.
- Stratification for IA-information (e.g. RR) allows control of type I error rate but will be inefficient.
- Combi. tests with patient wise stages, seems best and rigorously valid when follow-up times of stage 1 patients remain unaltered or are complete (at end of study).
- ▶ Phase II/III designs in oncology are an interesting option, but require modeling and extensive simulations.

Selected References

- Schäfer H., Müller H.-H. Modification of the sample size and the schedule of interim analyses in survival trials based on data inspections Statistics in Medicine 2001, 20:3741–3751
- Bauer B., Posch M. Modification of the sample size and the schedule of interim analyses in survival trials based on data inspections by H. Schäfer and H.-H. Müller, Statistics in Medicine 2001; 20: 3741-3751. Statistics in Medicine, 23:1333–1334
- Wassmer G. Planning and Analyzing Adaptive Group Sequential Survival Trials Biometrical Journal 2006, 48:714–729
- Brannath W., Zuber E., Branson M., Bretz F., Gallo P., Posch M., Racine-Poon A. Confirmatory adaptive designs with Bayesian decision tools for a targeted therapy in oncology. Statistics in Medicine 2009, 28:14451463.
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Simulation (10⁵ runs)

Inverse normal combination function with equal weights.

null hyp.:
$$\theta_S = \theta_{E_1} = \theta_{E_2} = 0.4, \ c_1 = c_2 = 1$$
 alternative 1: $\theta_S = \theta_{E_1} = \theta_{E_2} = 0.4, \ c_1 = c_2 = 0.8$ alternative 2: $\theta_S = 0.2, \ \theta_{E_1} = 0.3, \ \theta_{E_2} = 0.4, \ c_1 = 0.9, \ c_2 = 0.8$

STAGES	follow-up wise	follow-up wise	pat. wise
TEST	unstratified	stratified	(unstratified)
	0.017	0.022	0.018
alternative 1		0.75	0.85
alternative 2	0.89	0.71	0.85