

Adaptive Enrichment Design to Address Emerging Uncertainty Regarding Optimal Target Population - Case Study

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Background

Triple Negative Breast Cancer (TNBC): high unmet medical need

- Absence of ER, PR and HER-2 gene ⇒ reduced or voided benefit from drug targeting these biomarkers
- Poor outcome: rapid progression, short time to relapse^a



pCR: pathological complete response; EFS: event-free survival; DFS: disease-free survival; OS: overall survival; PFS: progression-free survival.^a Dent et al. 2007

^a https://www.esmo.org/Press-Office/Press-Releases/IMpassion130-atezolizumab-nab-pac-triple-negative-breast-cancer-Schmid

Roche



Original neoadjuvant TNBC Design

- Pathological complete response (pCR): binary endpoint
- All-comer: no pre-specified formal testing for PD-L1+



Background

Emerging Goals for neoadjuvant TNBC study

- Current AC design MIGHT not lead to ITT label even with positive read-out AND
- Efficacy in PDL1+ not formally tested

⇒ Optimize chance of success and timeline for timely patient's access & Minimize exposing patients to futile treatment

Challenges in extrapolating from 1L to neo-adj. TNBC

- PD-L1 predictive value: inconsistency across treatment lines observed in other indications
- Different entpoints: PFS vs pCR
- ⇒ Fixed (re)design options at high risk of misspecification



Neo-adjuvant Trial - Adaptive Design

F = ITT population, **S** = PDL1+ subpopulation, **C** = PDL1- subpopulation



Analysis at end of Stage 1 conducted by independent statisticians and reviewed by iDMC, following above prespecified algorithm.

Type-I Error - Sources of Inflation

- Roche
- Stage 2 and final target population driven by stage 1 outcomes
 - No direct pooling of data BUT: $p_2^h \perp p_1^h$ under $H_0^{h_a}$
 - p-value combination (inverse weighted normal approach)^b

$$p_{1,2}^{h} = 1 - \Phi\{w_1 \times \Phi^{-1}(1 - p_1^{h}) + w_2 \times \Phi^{-1}(1 - p_2^{h})\}$$

- Early look at data for efficacy claim at stage 1: α_1 , α_2 specified via $(Z_1^h, Z_{1,2}^h) \sim N\left(\mu = \begin{pmatrix} 0\\ 0 \end{pmatrix}, \Sigma = \begin{pmatrix} 1 & w_1\\ w_1 & 1 \end{pmatrix}\right)$ under H_0^h
- Multiplicity in target populations: **F** and **S**
 - Sime's closed test procedured: exploit **positivity** in correlation between **F** and **S**

^a $h \in \{F, S, F \cap S\}$. ^b Wassmer & Brannath 2016. ^c E.g. $w_1^2 = \frac{N_1}{N_1 + N_2}$, $w_2^2 = \frac{N_2}{N_1 + N_2}$. ^d $p^{F \cap S} = \min\{2 \times \min(p^F, p^S), \max(p^F, p^S)\}$



• Frequency of making "correct" IA decision across key scenarios.

E.g. Frequency of Decision at IA - Threshold: Δ_S =0.14, Δ_C =0.11

(Results for illustration only)

Subgroup S credential	Δ_S	Δ _C	Stop		Continue & Target Population		
			Efficacy	Futility	S only	F only	F & S
Very Strong	0.20	0.04	0.34	0.16	0.38	0.05	0.07
Dismal	0.00	0.00	0.013	0.74	0.11	0.13	0.01

Fine-tuning Criteria for Adaptive Design

- Frequency of making "correct" IA decision across key scenarios.
- Overall power: more relevant if decision made at trial onset or when investment at stage 1 matters.
- Go (conditional) power i.e. Prob. of Success conditional on GO: more relevant if not concerned by wasting stage 1 investment





Why NOT Conditional Power as Decision Criteria?

- At IA "precise" estimate for each hypothesis not easy due to rejection of their intersection $H_0^{F \cap S}$ as gate keeper.
 - For Sime: $p^{F \cap S} = \min\{2 \times \min(p^F, p^S), \max(p^F, p^S)\}$ ⇒ reject $H_0^{F \cap S}$ at α-level iff at least one p-value ≤ 0.5 × α
 OR both p-values ≤ α
- Not straight-forward for clinician to give input
- → More complex decision tree & simulation needed for optimal thresholds e.g. TAPPAS trial^{*}
- Might be warranted for sample size re-estimation

* An adaptive population enrichment phase III trial of TRC105 and pazopanib versus pazopanib alone in patients with advanced angiosarcoma (TAPPAS trial)

Minimum Detectable Difference



- i.e. solution to $\hat{\Delta}_{MDD}/SE(\hat{\Delta}_{MDD}) = Z_{\alpha}$ (one-sided)
- Binary outcome: $SE(\widehat{\Delta})$ depends on both \hat{p}_{con} , \hat{p}_{trt}
- \Rightarrow fix \hat{p}_{con} , solve for \hat{p}_{trt}
- Rejection of H_0^F (resp. H_0^S) depends on both p-values through rejection of $H_0^{F \cap S}$ in closed test procedure \Rightarrow E.g. at Stage 1

Significance level	$m{H_0^S}$ not rejected at $lpha_1$	$m{H_0^S}$ rejected at $lpha_1$
for $\widehat{\varDelta}^F_{MDD}$	$lpha_1/2$ (higher MDD)	α_1

 Different choice for target populations at stage 2 ⇒ various sets of MDDs

Operational and Regulatory Challenges

- Stage 1 enrollment already concluded before amendment → need to minimize accrual gap if stage 2 initiated
 - Timely protocol / SAP / iDMC amendment and gain alignment from iDMC / Regulators
 - Keep sites motivated during enrollment break
- Acceptance by Regulators
 - FDA: minimal questions and swift approval
 - EMA: all statistical details mandated in protocol NOT SAP*

* Reflection Paper on Methodological Issues in Confirmatory Clinical Trials Planned with an Adaptive Design



CONCLUSION

- Adaptive design = "rescue strategy" for ad-hoc mid-trial adaptation if original design is challenged
 - Update trial based on its own data → mimimize mispecification risk
 - Established and straight forward theory (at least for binary endpoint) to maintain study's integrity
- Operational and regulatory challenges expected
 - Cross-functional discussions: stats, science, ops and reg ...
 - Sponsor & iDMC / Regulators interactions
- Prospective design of an adaptive enrichment trial would be preferable in general.

Reference



- Gernot Wassmer and Werner Brannath. Group Sequential and Confirmatory Adaptive Designs in Clinical Trials.
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