Enrichment Designs for the Development of Personalized Medicines

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Identifying Target Populations

In recent years, clinical trials with more complex objectives, confirming treatment effects in sub-populations and/or in the overall populations, have raised more and more attention.

- The knowledge on the genetic basis of many diseases is increasing rapidly and therapies are developed that target underlying molecular mechanisms.
- Patients' responses are predicted to targeted treatments based on genetic features or other biomarkers.

Objective: Identify subgroups (based on biomarkers) where the treatment has a positive benefit risk balance.

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• Overall treatment effect

$$\theta_{F} = \lambda \theta_{S} + (1 - \lambda) \theta_{S^{c}}$$

where λ is the prevalence of subgroup *S*.

- Test the null hypotheses $H_F : \theta_F \leq 0$ and $H_S : \theta_S \leq 0$.
- If θ_{S^c} ≪ θ_S and the prevalence of the subgroup is small, the power to reject H_F is low.

Enrichment and Stratification Design

Enrichment Design: Randomize only patients of subgroup S (say Biomarker +). Patients of the complement S^C are excluded from the trial (Biomarker –).

Stratification Design: Include Biomarker + and Biomarker – patients. Stratify randomization by biomarker status.

- With both designs one can test *H*_S, i.e., for a treatment effect in the subpopulation.
- With the stratification design one can test in addition H_F .
- With equal overall sample size *n*, the enrichment design has a larger number of biomarker+ patients.

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Testing Problem

- Parallel group comparison of the means of normal distributions.
- Total sample size *n* is chosen to detect an effect size Δ with a two sample one-sided *z*-test with α = 0.025 and power of about 90%.

Enrichment Design:

• Test *H_S* with a z-test.

Stratification Design:

- Test *H_S* with a *z*-test
- Test H_F with a stratified z-test
- Correct for multiplicity with the Hochberg test.

To Enrich or not to Enrich?

- The power to reject any hypothesis depends on the effect sizes $\Theta = (\theta_S, \theta_{S^c})$
- Assume we suspect that θ_{S^c} ≤ θ_S but believe that θ_{S^c} > θ_S is not plausible.
- Then, the enrichment design (recruiting only patients in *S*) always leads to the highest power:
 - If $\theta_{S^c} = \theta_S$ the enrichment design has the larger power than the stratification design using a multiple testing procedure.
 - If $\theta_{S^c} < \theta_S$ the enrichment design has larger power.

Thus, is enrichment always preferable?

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Different Gains, different Costs...

The argument results from an oversimplification. The Power to reject any null hypotheses is not the only criteria.

- The stratification design tests the full population H_F : θ_F ≤ 0, demonstrating that the treatment works "on average".
- The enrichment design tests a limited null hypothesis H_S : θ_S ≤ 0 leading to a limited indication.
- Ethical problem if patients that may benefit are excluded.
- Enrichment maybe costly (e.g. due to longer patient recruitment, ...).

To account for these aspects we may use an approach based on utility functions.

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The utility function approach

A sponsor view:

Rejection of	Gain	
H _F	G_F	G < G (for example $G = (G)$
H_S only	G_S	$G_S \ge G_F$ (ioi example, $G_S = \lambda G_F$)
none	0	

 $U_{C}(\Theta) = G_{F}P_{\Theta}(\text{reject } H_{F}) + G_{S}P_{\Theta}(\text{reject only}H_{S})$

A public health view:

		Rejection of	Gain
+	+	H_F	G_F
+	+	H_S only	G_S
+	0	H_F	G_S
+	0	H_S only	G_S
0	0	H_S, H_F	0
0	0	None	0

 $\begin{aligned} U_{P}(\Theta) &= G_{F} \mathbf{1}_{\{\theta_{S}, \theta_{S^{c}} > 0\}} P_{\Theta}(\text{reject } H_{F}) + G_{S} \mathbf{1}_{\{\theta_{S}, \theta_{S^{c}} > 0\}} P_{\Theta}(\text{reject only } H_{S}) + \\ G_{S} \mathbf{1}_{\{\theta_{S} > 0, \theta_{S^{c}} \leq 0\}} P_{\Theta}(\text{reject } H_{F}) + G_{S} \mathbf{1}_{\{\theta_{S} > 0, \theta_{S^{c}} \leq 0\}} P_{\Theta}(\text{reject only } H_{S}) \end{aligned}$

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A public health view:

θ_{S}	$\theta_{\mathcal{S}^c}$	Rejection of	Gain
+	+	H _F	G _F
+	+	H _S only	G_S
+	0	H _F	G_S
+	0	H _S only	G_S
0	0	H_S, H_F	0
0	0	None	0

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Bayesian expected Utility

If $G_S = G_F = 1$ then $U_C = U_P$ is equal to the power of rejecting any hypothesis.

Consider a prior π on $\Theta = (\theta_S, \theta_{S^c})$. Then the expected utilities are

$$U_{\pi,C} = E_{\pi}(U_C(\Theta)), \quad U_{\pi,P} = E_{\pi}(U_P(\Theta))$$

We use the simple prior

$$P\{\Theta = (\Delta, \Delta)\} = \pi$$
$$P\{\Theta = (\Delta, 0)\} = (1 - \pi)$$

setting $G_F = 1$.

Utility for different Priors and Gains G_S Prevalence $\lambda = 0.3$

$$G_S = 1$$



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Utility for different Priors and Gains G_S Prevalence $\lambda = 0.3$

$$G_{\rm S} = 0.5$$



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Fixed Overall Sample Size: n

Sample size Stage 1:

F: n₁=r*n S: λ*n₁



Interim Analysis Planning of Second Stage Subgroup Selection

• First stage data is used to choose the second stage population

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Example:

Decision based on the interim p-value \mathbf{p}_{sc} of the Complement $\mathsf{S}^{\texttt{C}}$

Introducing a "stopping-for-futility"-boundary α_C for S^c

Interim Analysis Planning of Second Stage Subgroup Selection

• First stage data is used to choose the second stage population



- First stage data is used to choose the second stage population
- Efficacy is demonstrated with Stage 1 and 2 data



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The Adaptive Closed Test

• To control the family wise error rate apply the closure principle using adaptive combination tests at level α for

$$H_S$$
, H_F , $H_{FS} = H_S \cap H_F$.

(Bauer and Kieser, 1999, Hommel, 2001)

• Reject $H_j, j \in \{S, F\}$ if H_{FS} and H_j are rejected at local level α .

- Compute stage wise p-values
 - First stage elementary p-values p_S, p_F
 - Second stage elementary p-values q_S, q_F (computed from second stage data only)
- Define a combination function *C*(*p*, *q*) and critical value *c* such that for independent and uniformly distributed p-values

 $P(C(p,q) \leq c) = \alpha.$

• Reject H_S if

 $C(p_S,q_S) \leq c$

• If the trial continues in F, reject H_F if

 $C(p_F, q_F) \leq c,$

otherwise retain H_F .

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Test of the intersection hypothesis $H_F \cap H_S$

• First stage p-value for $H_F \cap H_S$ with Simes test:

 $p_{FS} = \min[\max(p_F, p_S), 2\min(p_F, p_S)]$

- Second stage p-value for $H_F \cap H_S$
 - If both populations are continued with Simes test:

 $q_{FS} = \min[\max(q_F, q_S), 2\min(q_F, q_S)]$

• If only *H_S* is selected:

 $q_{FS} = q_S$

• Final Analysis: Reject H_{FS} if

 $C(p_{FS}, q_{FS}) \leq c$

(I) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1))

Test of the intersection hypothesis $H_F \cap H_S$

• First stage p-value for $H_F \cap H_S$ with Simes test:

 $p_{FS} = \min[\max(p_F, p_S), 2\min(p_F, p_S)]$

- Second stage p-value for $H_F \cap H_S$
 - If both populations are continued with Simes test:

 $q_{FS} = \min[\max(q_F, q_S), 2\min(q_F, q_S)]$

• If only *H_S* is selected:

 $q_{FS} = q_S$

• Final Analysis: Reject H_{FS} if

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(I) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1)) < ((1))

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• First stage p-value for $H_F \cap H_S$ with Simes test:

 $p_{FS} = \min[\max(p_F, p_S), 2\min(p_F, p_S)]$

- Second stage p-value for $H_F \cap H_S$
 - If both populations are continued with Simes test:

 $q_{FS} = \min[\max(q_F, q_S), 2\min(q_F, q_S)]$

• If only *H*_S is selected:

 $q_{FS} = q_S$

Final Analysis: Reject H_{FS} if

 $C(p_{FS}, q_{FS}) \leq c$

The Adaptive Closed Test

Adaptive Closed Test

- Reject $H_i, i \in \{F, S\}$ if
 - $C(p_{FS}, q_{FS}) \leq c$ and
 - $C(\boldsymbol{\rho}_i, \boldsymbol{q}_i) \leq c.$
 - The population selection rule may depend on the interim data and external data in any way.
 - The selection rule needs not to be specified in detail.
 - Sample sizes may be adapted based on unblinded interim data
 - The familywise error rate is controlled in the strong sense.

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Adaptation Rule: Example

- Selection rule:
 - *p_{SC}*... the interim p-value for the z-test in the complement of the subpopulation.
 - α_C...selection threshold
 - Continue with F if $p_{SC} < \alpha_C$, otherwise enrich and continue with S only.
- Two types of adaptation: If the trial continues in the subpopulation only
 - Selection of hypothesis: H_F is dropped.
 - Reassessment of sample size: The sample size for H_S is increased.
- Combination Function: Inverse normal method (Lehmacher and Wassmer, 1999)

→ $r = 0, \alpha_{C} = 0$ Fixed Sample Trial in *S* only → $0 < r, \alpha_{C} < 1$ Adaptive Design integrating both phases → $r = 1, \alpha_{C} = 1$ Fixed Sample Trial in F

 $\pi = 0$



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 $\pi = 0.2$



< ≣ →

 $\pi = 0.4$







Utility $U_{\pi,C} = U_{\pi,P}$ for $G_S = 1$

 $\pi = 0.8$



Utility $U_{\pi,C} = U_{\pi,P}$ for $G_S = 1$

$$\pi = 1$$



Utility $U_{\pi,C}$ for $\mathbf{G_S} = .5$

$$\pi = 0$$



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Utility $U_{\pi,C}$ for $\mathbf{G}_{\mathbf{S}} = .5$

 $\pi = 0.2$



Utility $U_{\pi,C}$ for $\mathbf{G_S} = .5$





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Utility $U_{\pi,C}$ for $\mathbf{G_S} = .5$

 $\pi = 0.6$



Utility $U_{\pi,C}$ for $\mathbf{G}_{\mathbf{S}} = .5$

 $\pi = 0.8$



Utility $U_{\pi,C}$ for $\mathbf{G_S} = .5$

$$\pi = 1$$



Utility $U_{\pi,C}$ for $\mathbf{G}_{\mathbf{S}} = .3$

$$\pi = 0$$



Utility $U_{\pi,C}$ for $\mathbf{G}_{\mathbf{S}} = .3$

 $\pi = 0.2$



Utility $U_{\pi,C}$ for $\mathbf{G_S} = .3$

 $\pi = 0.4$



Utility $U_{\pi,C}$ for $\mathbf{G_S} = .3$

 $\pi = 0.6$



Utility $U_{\pi,C}$ for $\mathbf{G}_{\mathbf{S}} = .3$

 $\pi = 0.8$



Utility $U_{\pi,C}$ for $\mathbf{G}_{\mathbf{S}} = .3$

$$\pi = 1$$



Utility $U_{\pi,P}$ for $\mathbf{G_S} = .3$

$$\pi = 0$$



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Utility $U_{\pi,P}$ for $\mathbf{G}_{\mathbf{S}} = .3$

 $\pi = 0.2$



Utility $U_{\pi,P}$ for $\mathbf{G}_{\mathbf{S}} = .\mathbf{3}$

 $\pi = 0.4$



Utility $U_{\pi,P}$ for $\mathbf{G_S} = .3$

 $\pi = 0.6$



Utility $U_{\pi,P}$ for $\mathbf{G}_{\mathbf{S}} = .3$

 $\pi = 0.8$



Utility $U_{\pi,P}$ for $\mathbf{G}_{\mathbf{S}} = .3$

$$\pi = 1$$



Public View Utility Function

1 -0.9 -0.8 0.7 -0.6 -**∺** 0.5 -0.4 -0.3 -0.2 0.1 0 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1 gs

(A) PV: $\lambda = 0.3$

Martin Posch, Alexandra Graf, Franz Koenig (IMS)

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Sponsor View Utility Function

1 -0.9 -0.8 0.7 -0.6 -**∺** 0.5 -0.4 -0.3 -0.2 0.1 0 0.1 0.2 0.3 0.5 0.6 0.7 0.8 0.9 0 0.4 gs □ Adaptive ■ Enrichment

(D) SV: $\lambda = 0.3$

Stratification

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Public View Utility Function

1 -0.9 -0.8 0.7 -0.6 -**∺** 0.5 -0.4 -0.3 -0.2 0.1 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 0 gs

(C) PV: $\lambda = 0.5$

Martin Posch, Alexandra Graf, Franz Koenig (IMS)

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Sponsor View Utility Function

1 -0.9 -0.8 0.7 -0.6 -**∺** 0.5 -0.4 -0.3 -0.2 0.1 0 0.1 0.2 0.3 0.5 0.6 0.7 0.8 0.9 0 0.4 gs □ Adaptive ■ Enrichment

(F) SV: $\lambda = 0.5$

Stratification

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Summary and Limitations

- For enrichment designs investigating the power to reject any null hypothesis may not be sufficient.
- The optimized design depends critically on the prior.
- We investigated a very simple adaptation rule, that depended on the effect size of the complement of S only.
- Designs can be extended to optimize the conditional expected utility, taking into account also the effect size S.
- The loss resulting from false positive rejections of H_S and H_F is accounted for only through the multiple testing procedure but not included in the utility function.

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