

Adaptive biomarker-based design applied to an early phase trial in Oncology

26th Feb 2026 – EFSPI Adaptive Design in Oncology Webinar

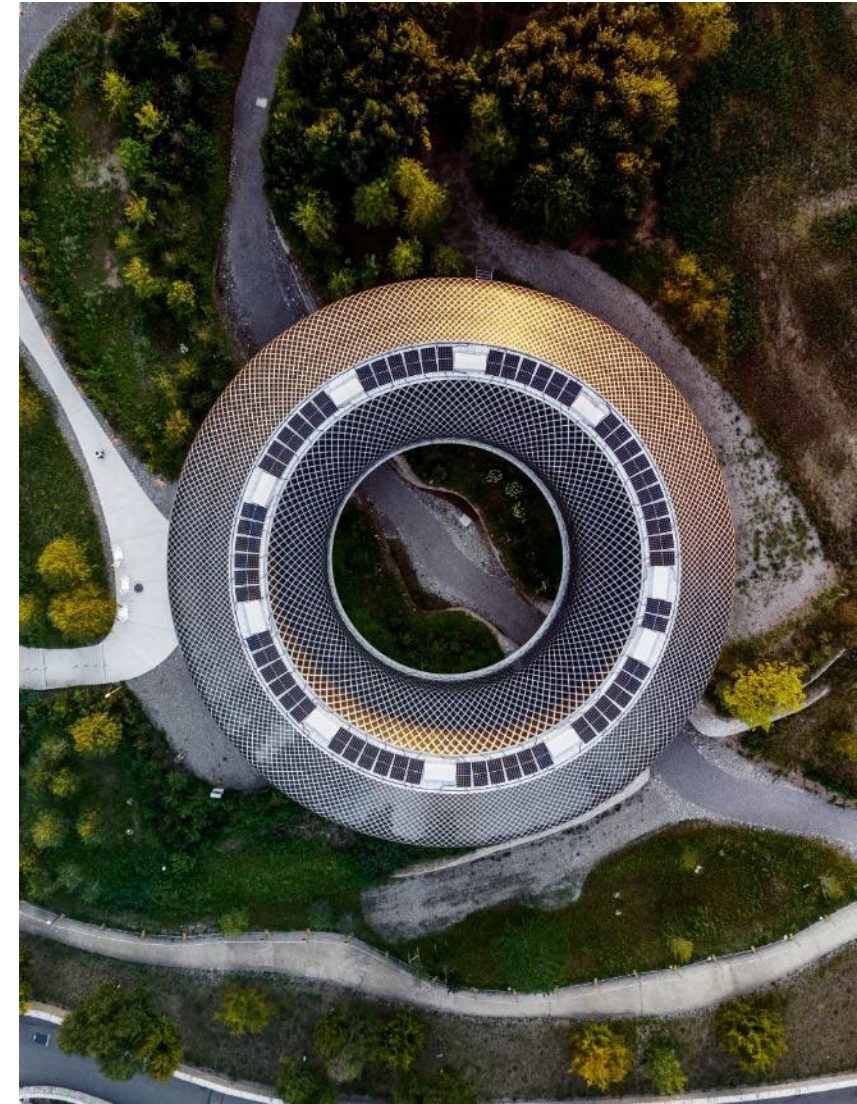
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Disclaimer and acknowledgments

The views expressed here are solely mine and do not represent my employer, organization, or any affiliated entity.

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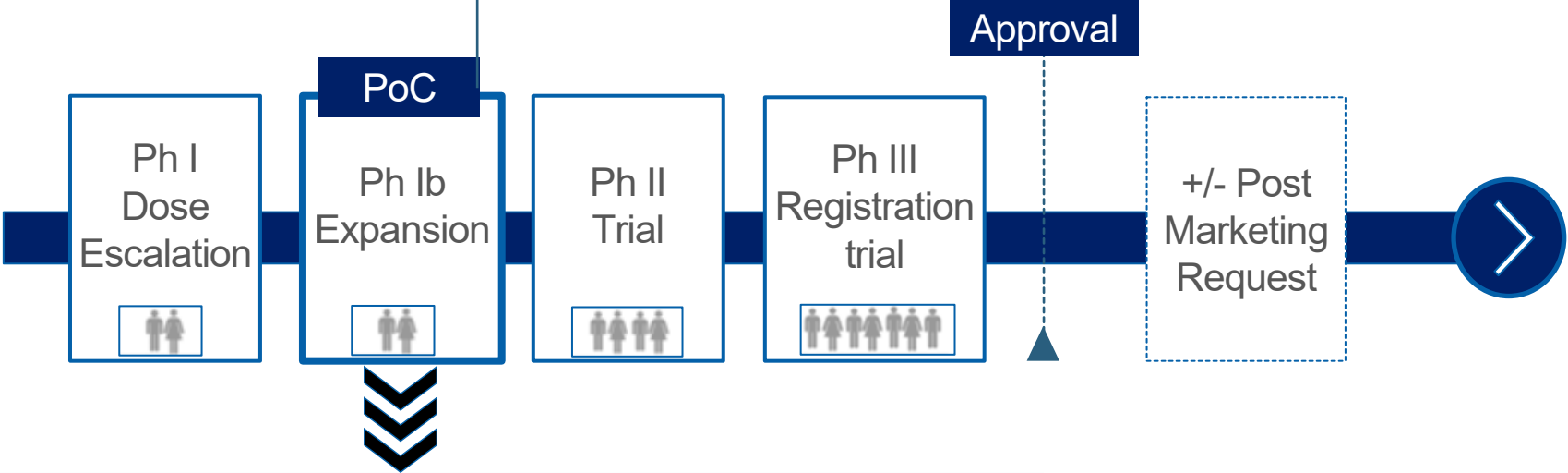
The results reported herein are part of a collaboration between Servier, Saryga, and the MRC Biostatistics Unit.



Motivation

Goal: Quickly establish that the drug is worth pursuing further, on the overall indication or in a biomarker subgroup

“Traditional” development journey



Putative biomarker (BMK) predictive of treatment responses

- Measured on a continuous scale
- No predefined cutoff for BMK+ patients

➔ Enrich on BMK + or not ?

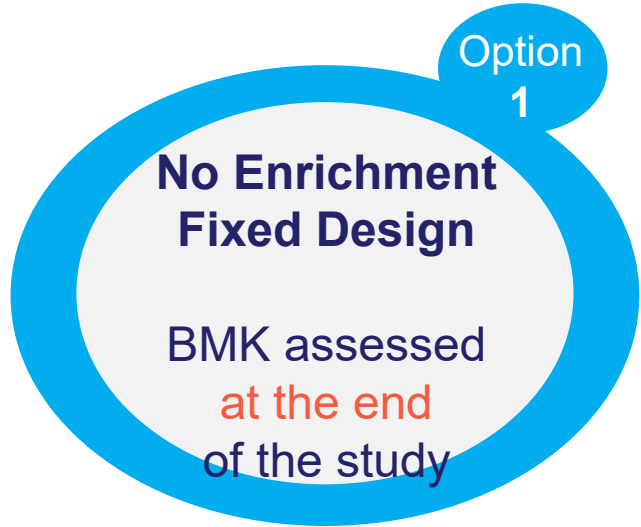


No, lack of evidence in patients to support BMK hypothesis

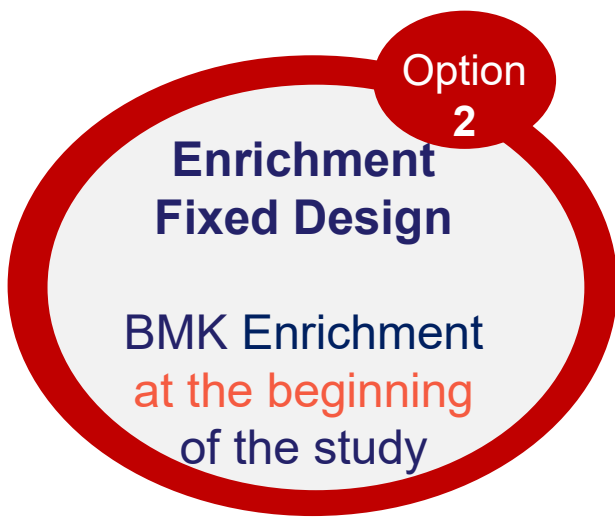
Yes, to avoid the risk of missing an efficacy signal

PoC = Proof of Concept

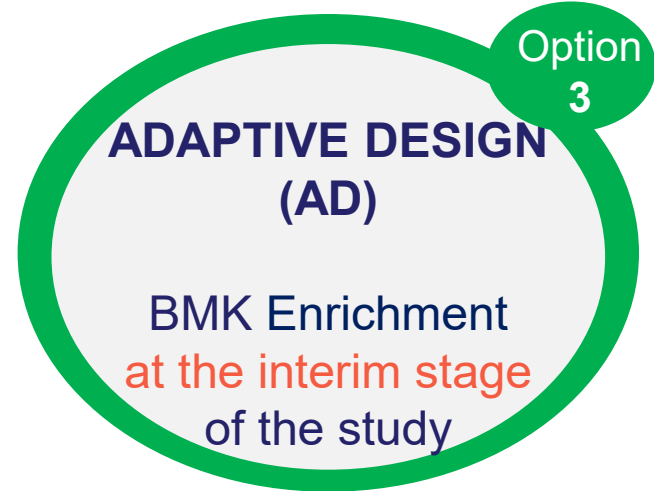
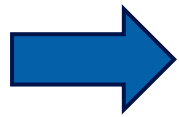
Don't Miss a Signal



- Risk of **missing a signal** when treatment benefit is limited to a **small BMK+ subgroup**



- Risk of **missing a signal** when the **cutoff** of the BMK is **not well established**
- Cannot establish that the **BMK-neg patients** do not respond
- **Longer recruitment** duration

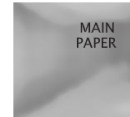


- AD offers **more power** than the non-AD for **detecting an effect** in a BMK+ subgroup

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Approaches to evaluation of treatment effect in randomized clinical trials with genomic subset^{†,§}



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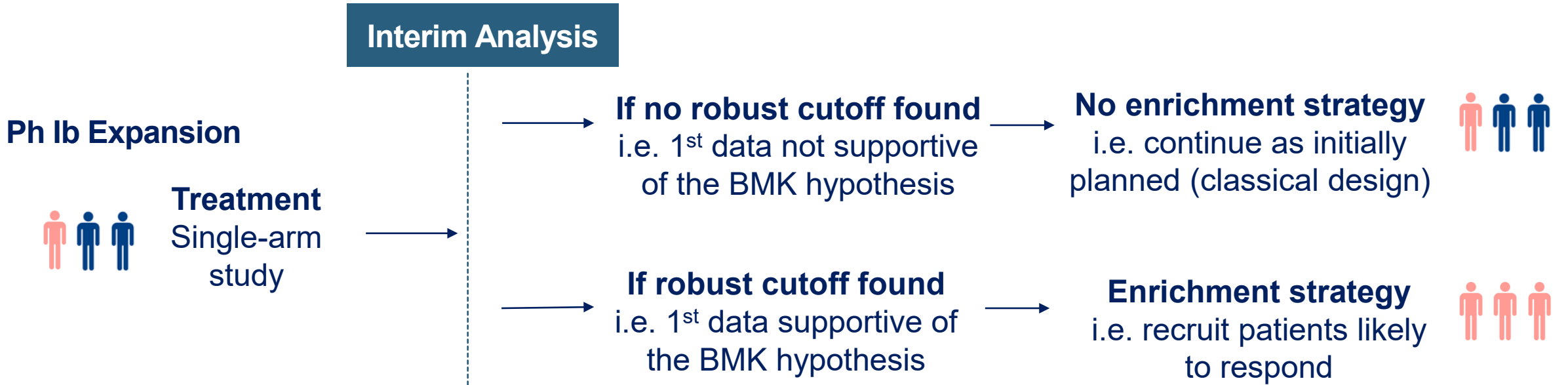


Many uncertainties at this early stage

Uncertainties about :

- The predictive value of the BMK
- The cutoff value of the BMK used to identify patients in the BMK+ subgroup
- The proportion of patients who are in the BMK+ subgroup
- The magnitude of the treatment effect in patients BMK+ and BMK-

Our design proposal



Evaluation of the

- **Predictive value** of the biomarker of interest
- **Robust biomarker cutoff** that will guide the next recruitments

Assuming:

- **No prognostic value** of the BMK of interest (as cannot be verified in a single-arm study)
- **Intermediate clinical endpoint** with a reasonable correlation relationship with the clinical endpoint
- **Preliminary analytical validation of the bioassay** used to measure the BMK of interest

Criterion to find a robust cut-off

Comparison of **3 approaches** to find a robust cut-off: 'cut-off' or 'no cut-off' based on the following rules:

- **Naïve**: at least 15% of responses in at least pp% of the population;
- **Naïve with step function**: find cut-off by fitting a step function^(*) and then see whether there are at least 15% of responses in at least pp% of the population with this cut-off value;
- **Probability based**: find cut-off by fitting a step function^(*), check if there are at least pp% of the population above the cut-off value and declare to find cutoff if $P(p_1 - p_0 > \text{diff}_{\text{thr}}) > p_{\text{thr}}$, where p_0 is the response rate in the BMK- subgroup and p_1 is the response rate in the BMK+ subgroup

(*) Same principle (fit a step function) of (**) but with Ordinary Least Squares instead of a Bayesian model (due to convergence issues with the Bayesian model with a small sample size).

Assuming to not have much prior information on the BMK-response shape of the curve and to avoid the issue of misspecified model.

No other method has been used to compare this approach. The aim was initially to assess the feasibility of an adaptive enrichment design at PhI stage.

(**) Article

A Bayesian model to estimate the cutoff and the clinical utility of a biomarker assay

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Criterion to find a robust cut-off

- Evaluation under two scenarios:
 - non-predictive with high response rate scenario (**NPHR**) where $p_1=p_0=0.15$
 - predictive with high response rate scenario (**PHR**) where $p_1=0.25$ and $p_0=0.05$
- **Gain:** the difference between the probability of declaring to find a cutoff under the alternative and the null scenarios

➤ **Chosen approach:**

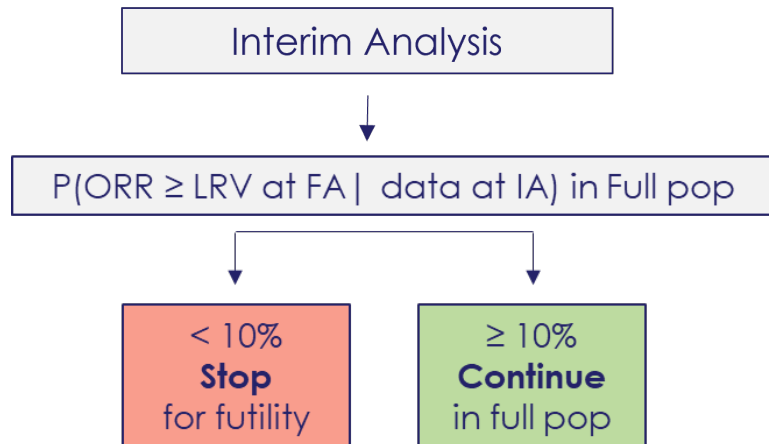
If **80%** certain that there is **10%** of difference in response rate between the 2 groups in at least **10%** of the population.

Approach	pp%	diff _{thr}	p _{thr}	False positives under NPHR _{q1}	True Positives under PHR _{q1}	Gain: True - False Positives
'Naive'	10	-	-	0.74	0.83	0.10
	20	-	-	0.73	0.83	0.11
	30	-	-	0.74	0.82	0.09
'Naive with step function'	10	-	-	0.41	0.65	0.23
	20	-	-	0.35	0.56	0.20
	30	-	-	0.27	0.37	0.11
'Probability based'	10	0.1	0.7	0.29	0.55	0.26
			0.8	0.24	0.50	0.26
			0.9	0.14	0.37	0.23
		0.15	0.7	0.24	0.50	0.26
			0.8	0.16	0.40	0.24
			0.9	0.10	0.28	0.18
	20	0.2	0.7	0.19	0.42	0.22
			0.8	0.13	0.33	0.20
			0.9	0.07	0.21	0.14
		0.15	0.7	0.23	0.45	0.23
			0.8	0.19	0.41	0.22
			0.9	0.13	0.32	0.19
	30	0.2	0.7	0.19	0.42	0.24
			0.8	0.13	0.33	0.19
			0.9	0.08	0.25	0.18
		0.1	0.7	0.13	0.33	0.20
			0.8	0.10	0.27	0.17
			0.9	0.06	0.18	0.12
30	0.1	0.7	0.14	0.31	0.17	
		0.8	0.13	0.29	0.15	
		0.9	0.09	0.23	0.14	
	0.15	0.7	0.13	0.28	0.16	
		0.8	0.10	0.24	0.14	
		0.9	0.05	0.15	0.10	
0.2	0.7	0.10	0.23	0.13		
	0.8	0.06	0.18	0.12		
	0.9	0.04	0.12	0.08		

Original design

- The primary outcome of the trial is the overall response rate (ORR)

Decision rules at Interim analysis (IA)



Decision rules at final analysis (FA)

No Go: $\Pr(\text{ORR} \geq \text{Target Value (TV)} \mid \text{data at FA}) \leq 10\%$
Go: $\Pr(\text{ORR} \geq \text{Low Reference Value (LRV)} \mid \text{data at FA}) \geq 80\%$
Consider: Not a Go or a No Go

Proposed BMK-based design

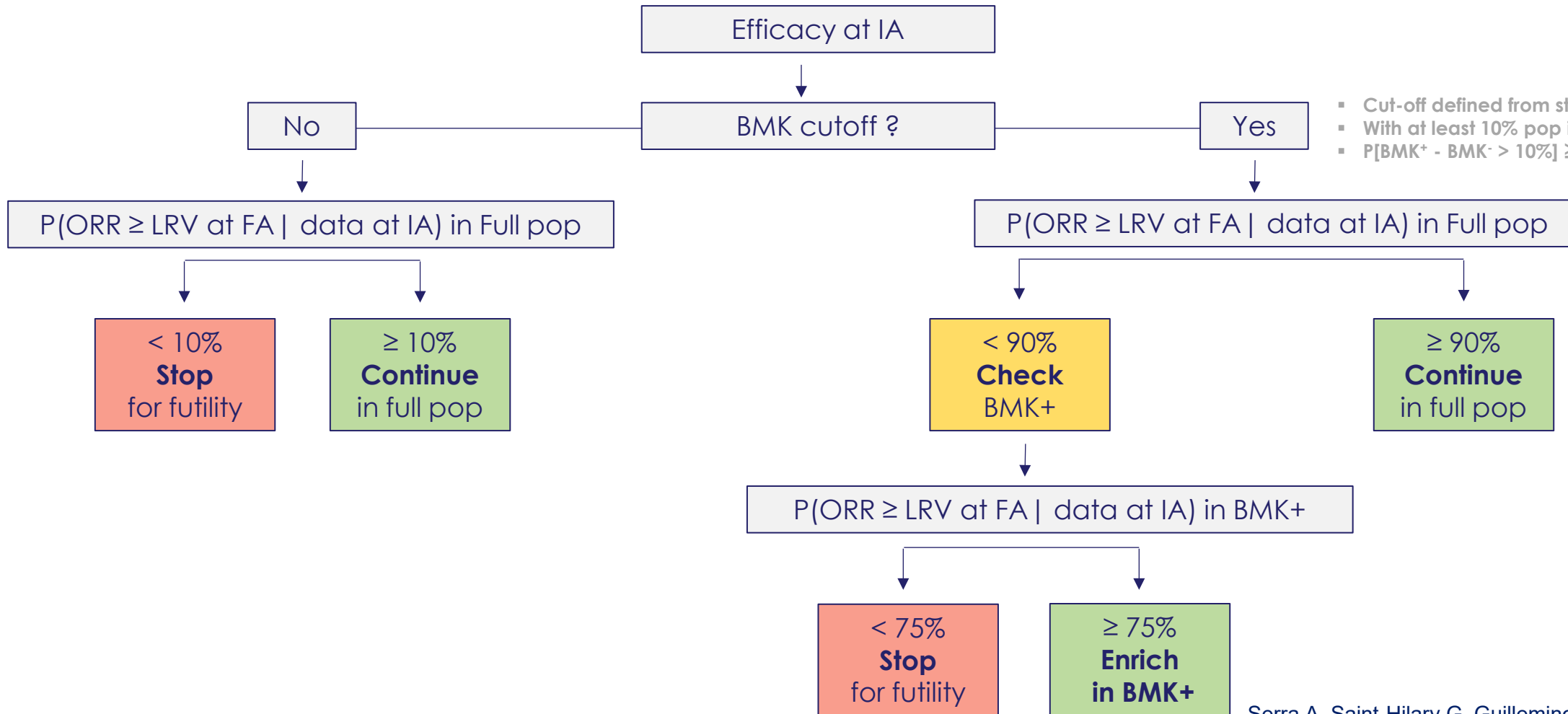
Decision rules at final analysis (FA)

No Go: $\Pr(\text{ORR} \geq \text{Target Value (TV)} \mid \text{data at FA}) \leq 10\%$

Go: $\Pr(\text{ORR} \geq \text{Low Reference Value (LRV)} \mid \text{data at FA}) \geq 80\%$

Consider: Not a Go or a No Go

Decision rules at Interim analysis (IA)



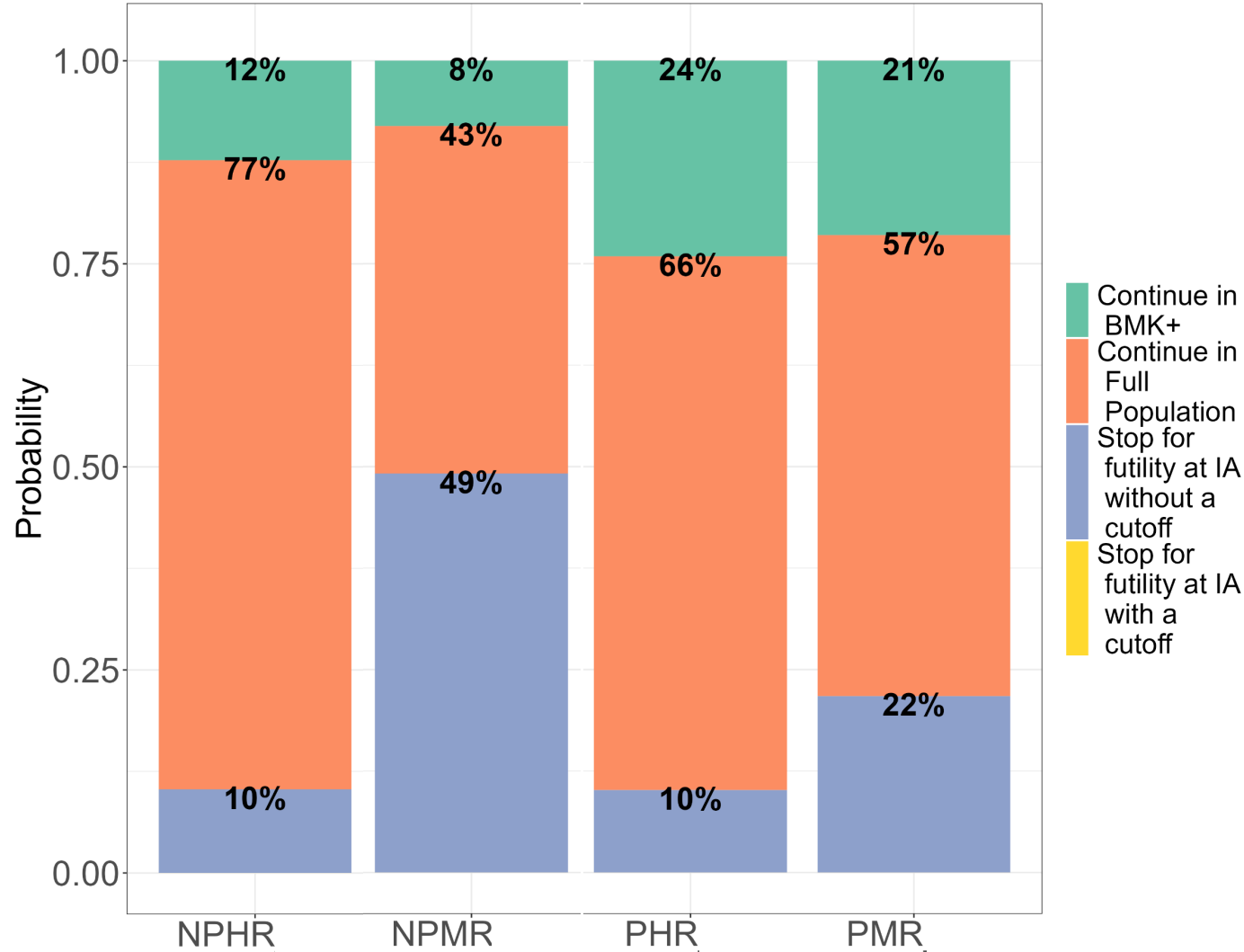
- Cut-off defined from step function
- With at least 10% pop in BMK+ subgroup
- $P[\text{BMK}^+ - \text{BMK}^- > 10\%] \geq 80\%$

Simulation setting

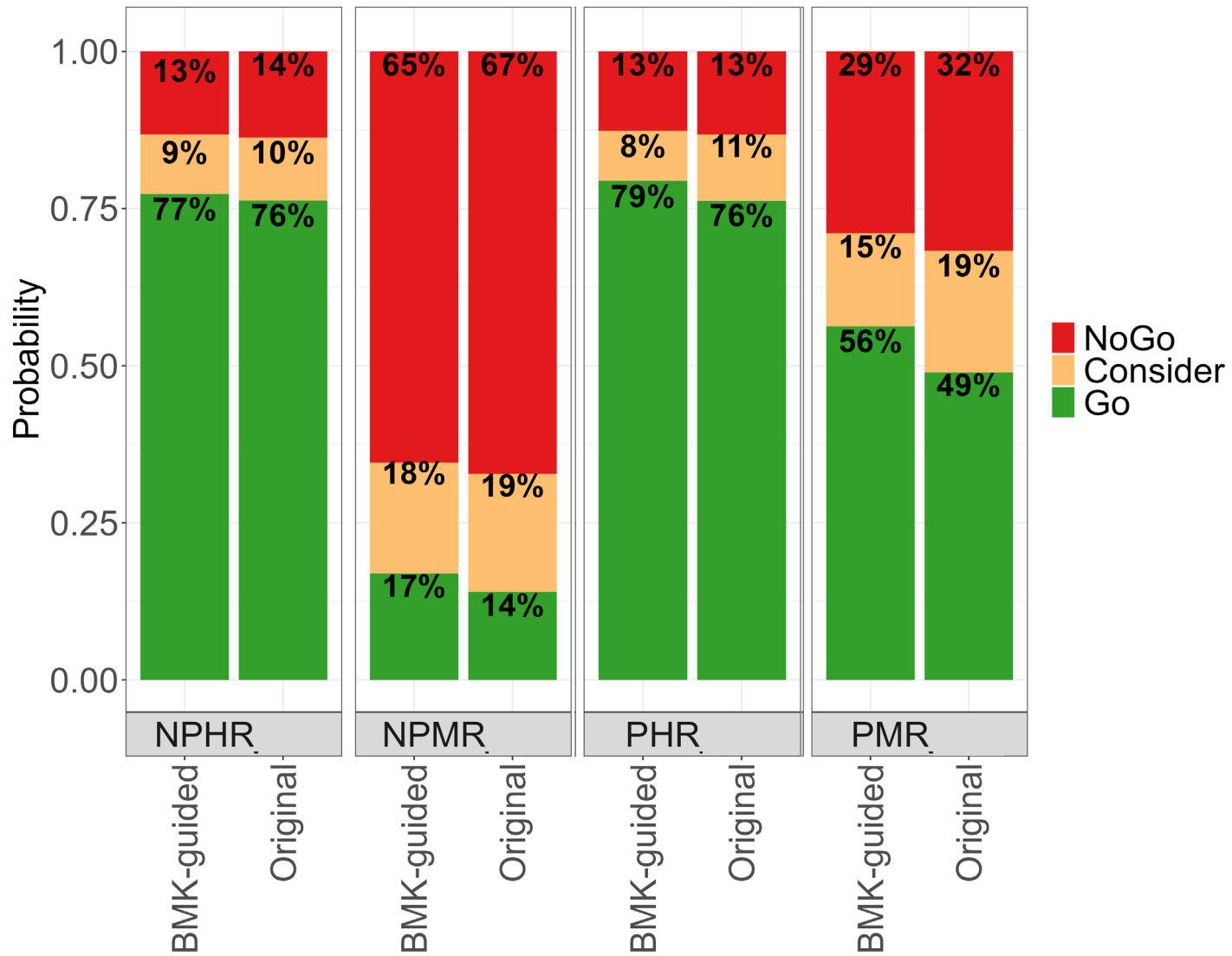
- Number of patients: N= 14 at the interim analysis (IA) and 27 at the final analysis (FA)
- BMK Normally distributed $\sim N(3.46, \sigma = 1.3)$ - *based on a Ph Ib expansion on a Servier project*
- One single cutoff – On/Off relationship between the BMK and the treatment response
- Several scenarios with different response rates above (p_1) and below (p_0) the true cutoff, different prevalence of BMK+ patients (q_+), different values of TV and LRV

Scenario	p_0	p_1	q_+	Overall p	TV/LRV
Non-Predictive High Response (NPHR)	15%	15%	50%	15%	15%/5%
Non-Predictive Medium Response (NPMR)	5%	5%	50%	5%	15%/5%
Predictive High Response (PHR)	5%	25%	50%	15%	15%/5%
Predictive Medium Response (PMR)	5%	15%	50%	10%	15%/5%

Numerical results – conditional decisions at IA



Numerical results – overall decisions at FA



Discussion

- The **proposed adaptive design** has been shown to **outperform** the **non-adaptive approach** with a **gain up to 60%** in the overall **probability to Go** compared to the classical design when there is a true biomarker cutoff
- **Limited false enrichment** when there is no true biomarker cutoff, and overall, the probability to Go/No Go is almost the same as per the classical design
- **Sensitivity analyses** have been performed considering **different variations of the trial setting** and different distributions of the biomarker. The proposed design has shown to **provide consistent results** across the considered settings
- The proposed **method** to declare the presence or absence of a **biomarker cutoff** at the time of the interim analysis seemed to **perform quite well** under all analysed scenarios, considering such a small sample size. Further work is needed to compare this approach to other classical approaches (e.g. Youden index, SIDES approach).

Thank you

