

Challenges of underdosing control in dose-escalation studies for DNA-based gene therapies

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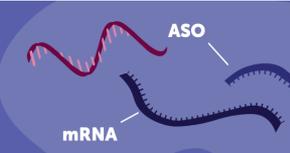
Gene therapy is characterized by inducing significant changes in host genetics

Challenges and opportunities for developing novel gene therapies for rare disease



One type of gene therapy is **gene addition**, which adds in a working gene that has the instructions for the cell to make more of a desired protein. A vector is often used to deliver the working gene to the cell's nucleus. This gene will live in the nucleus which gives a greater chance of being a permanent change and is only given one time.

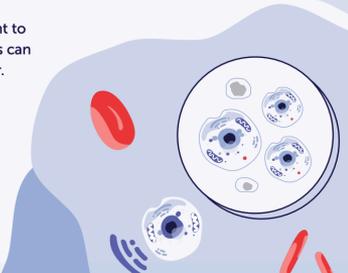
RNA Therapy is the use of shorter sequences of genetic material in RNA format to treat or prevent a disease. There are many different types of RNA therapy because there are so many types of RNA sequences and sizes that can affect cell functions. Some of these types include mRNA, ASOs, miRNA, Ribosomal RNA, siRNA and tRNA. These therapies often involve **gene silencing**, which silences a gene to stop it from creating a toxic protein. Receiving repeat doses is common for these types of therapies because they do not permanently change any of our DNA.



Gene Editing is a type of gene therapy that corrects pieces of DNA by changing or deleting the information **within** the affected individual's gene rather than adding a new gene like gene addition. Gene editing uses technology that is highly precise to make these types of changes.

Cell Therapy is the transfer of a specific cell type(s) into a patient to treat or prevent disease. Depending on the cell therapy, the cells can come from either the affected individual or an unaffected donor.

Gene-Modified Cell Therapy is a combination of gene and cell therapy. It first removes a person's own cells from the body. Certain cell types are then treated by adding a working gene or modifying the affected one. The modified or treated cells are then returned to the person.



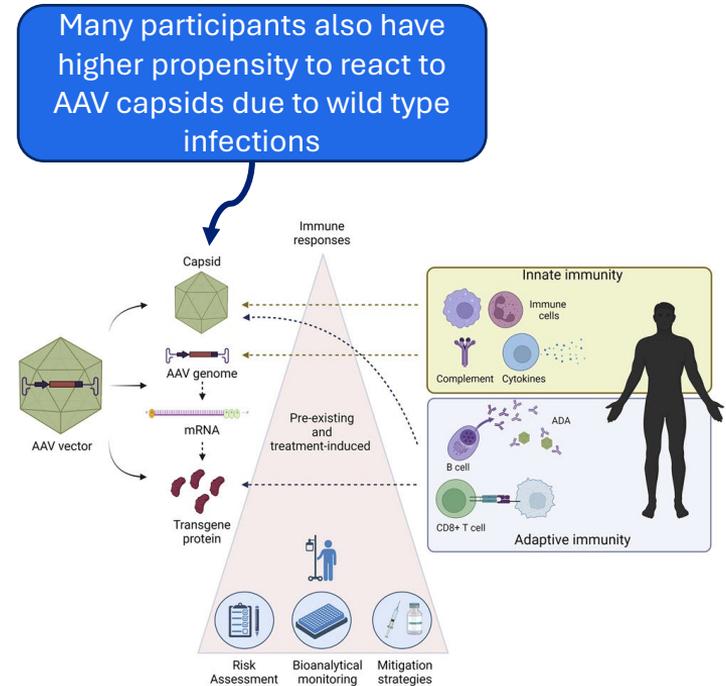
Human gene therapy seeks to **modify or manipulate** the expression of a gene or to alter the biological properties of living cells for therapeutic use.

DNA-based therapies, such as **gene editing** or **gene addition**, are challenging since they **permanently change** cellular genetics where therapies can be given **only one time**.

Immunogenicity can prevent patients from receiving future gene therapies from the same platform

After treatment, many patients will **develop antibodies** targeting various components of the gene therapy delivery system.

Immunogenicity can **reduce efficacy** of the intended activity of the transgene product, while also **increasing the potential for serious and severe adverse events**.



Yang et al. Molecular Therapy. 2022

Regulatory perspective for design of gene therapy clinical trials from published guidelines

- The dose exploration strategy during clinical phase can be difficult to ascertain prior to conducting clinical trials.
 - Identifying the MTD during early phase trials should not be ruled out since there is considerable risk of treating patients with subtherapeutic dose.
 - Regulatory agencies agree that due to the extended activity of CGT products, re-dosing is not an acceptable risk.
- Early phase I dose escalation studies can opt to not having a control arm due to ethical considerations. However, this does not mean that future registrational trials are always single arm trials.

Considerations for the Design of Early-Phase Clinical Trials of Cellular and Gene Therapy Products

Guidance for Industry

There is a lot of uncertainty!

Addressing underdosing risk can be challenging from a data perspective



- Treatment is targeted as well as systemic, where the desired product is produced in the liver and then circulated throughout the body.
- Gene therapies are developed to target rare and orphan diseases.



Clinically relevant efficacy outcomes might not be available during the escalation phase



Limited number of participants to be recruited into large cohorts.

Addressing underdosing risk can be challenging from a data perspective



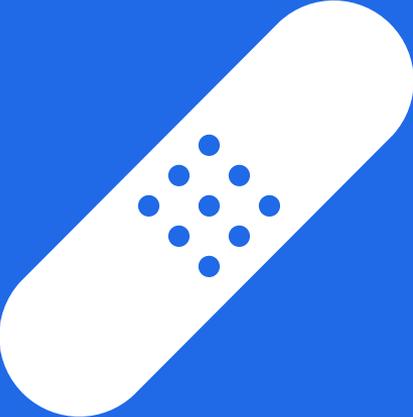
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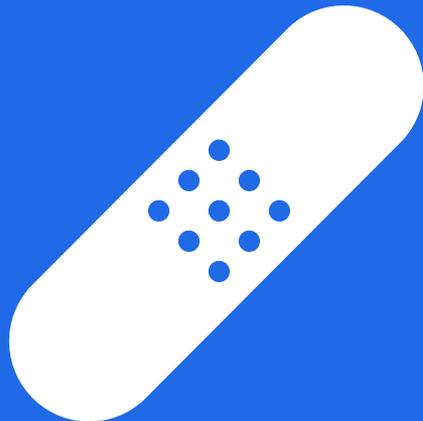
Continuous PD markers (concentration/activity of the protein in circulation) can be used to guide dose escalation.

Utilizing acceleration strategies or relying more on model-based designs.



Objectives: How can we design clinical trials using **continuous markers to** identify the correct dose to move forward while limiting participant **exposure to suboptimal dose ranges?**

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Using simulated scenarios we will evaluate:

- The operating characteristics of existing approaches for this scenario
- Evaluate whether additional rule-based or model-assisted components can be used to simplify designs.
- Evaluate whether acceleration strategies can be used to avoid underdosing while still recommending the correct dose to further develop.

Hypothetical clinical trial scenario for simulation

We assume a hypothetical clinical trial where we are evaluating a DNA-based gene therapy for a rare disease.

N per cohort = 3
1-dose level skipping allowed

Dose 4:
 $60 (\times 10^{10} \text{vg/kg})$

The concentration of the transgene protein circulating in plasma can be available during dose escalation, which gives us a continuous PD marker, denoted as W_i

Dose 3:
 $45 (\times 10^{10} \text{vg/kg})$

We will evaluate toxicity by the presence/absence of dose-limit toxicities, denoted as $Y_i = \{0,1\}$

Dose 2:
 $30 (\times 10^{10} \text{vg/kg})$

Stopping criteria:

- If no dose can be obtained due to toxicity of futility (design-specific)
 - If the decision is to escalate to a toxic dose or to de-escalate to a futile dose, we will choose to stay at the current dose for an additional cohort.
- Total sample size reaches 30
- 3 cohorts have been dosed at a given dose level

Dose 1:
 $15 (\times 10^{10} \text{vg/kg})$

Hypothetical clinical trial scenario for simulation (cont.)

We assume a hypothetical clinical trial where we are evaluating a DNA-based gene therapy for a rare disease.

The concentration of the transgene protein circulating in plasma can be available during dose escalation, which gives us a continuous PD marker, denoted as W_i

$$W \sim \text{LogNormal}(\mu_{log}, \sigma_{log}^2)$$

$\mu_{log}, \sigma_{log}^2$ computed from pre-specified mean as well as coefficient of variation of 0.5. Prior knowledge indicates that the maximum possible value for the biomarker is 200

We will evaluate toxicity by the presence/absence of dose-limit toxicities, denoted as $Y_i = \{0,1\}$

$$Y \sim \text{Bernoulli}(p(x))$$

$p(x)$ is the pre-specified DLT probability per dose level.

Summary of evaluated designs

A non-exhaustive list chosen primarily on ease of available software for implementation

Implementation of the modeling component of these designs can be easily accessible through the crmPack package, developed by industry professionals



Considered designs	Efficacy Outcome	Toxicity Outcome	Escalation/De-escalation Rules
Bekele and Shen 2005 (BS)	Model-based, using the joint modeling using the latent variable parameterization of probit regression by Albert and Chib		Next dose is assigned based on assessment of safety and futility with the highest posterior probability in the target range
Yeung and Jaki 2015 (YJ)	Model-based, using a log-log model for efficacy outcomes.	Model-based, using the two-parameter logistic regression model	Based on assessment of safety as well as a gain function.
Checkerboard – (CB)	Model-based, using the joint modeling using the latent variable parameterization of probit regression by Albert and Chib		Keyboard approach with a pre-specified decision table based on posterior densities
Customized design combining BOIN with modeling continuous outcomes	Model-based, allowing for borrowing between doses.	BOIN based	Next dose is assigned based on a modification of BOIN decision rules.

Approaches to perform dose escalation using binary toxicity and continuous efficacy responses

CRM Designs modeling the dose-response relationship

Bekele and Shen 2005

Jointly models toxicity and efficacy using a probit model with the Albert and Chib parameterization.

$$\begin{aligned} \text{Probit}[p(x)] &= \beta_{Z_1} + \beta_{Z_2} \log\left(\frac{x}{x^*}\right) + \epsilon \\ w(x) &\sim N(f(x), \sigma_w^2) \\ f(x) &= \beta_{W_i} \\ \beta_{W_i} - \beta_{W_{i-1}} &\sim N(0, (x_i - x_{i-1})\sigma_{\beta_w}^2) \end{aligned}$$

Acceptable doses are selected based on the following criteria:

For a given dose k , target toxicity probability π_t , minimum sample size m , and minimum efficacy level W_{min}

$$\begin{aligned} P(\beta_{W,k} > W_{min}^*) &> \delta_1 \\ P(p(x) < \pi_t | \text{Data}, n_k \geq m) &> \delta_2 \end{aligned}$$

Or

$$\Pr(p(x)_{k-1} < \pi_t | \text{data}, n_k < m, n_{k-1} \geq m) > \delta_3$$

The acceptable dose with the highest probability of efficacy in the target range is chosen.

Yeung and Jaki et al. 2015

Separately models the toxicity and efficacy

$$\Pr(Y = 1) = \frac{\exp(\phi_1 + \phi_2 \log(x))}{1 + \exp(\phi_1 + \phi_2 \log(x))}$$

$$W_i = \theta_1 + \theta_2 \log(\log(x))$$

Decision rules based on the dose that generates the maximum gain that is not toxic.

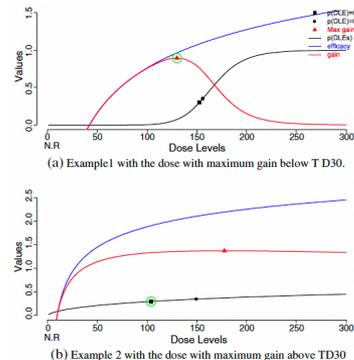


Figure 1. Dose-limiting event, efficacy and gain curve examples.

- Estimates the dose that has the highest mean posterior probability closest to the target DLT rate.
- Computes the dose that maximizes the gain function.
- $$G(j) = \frac{\theta_1 + \theta_2 \log(\log(x))}{1 + \exp(\phi_1 + \phi_2 \log(x))}$$
- Selects the smaller of the two doses

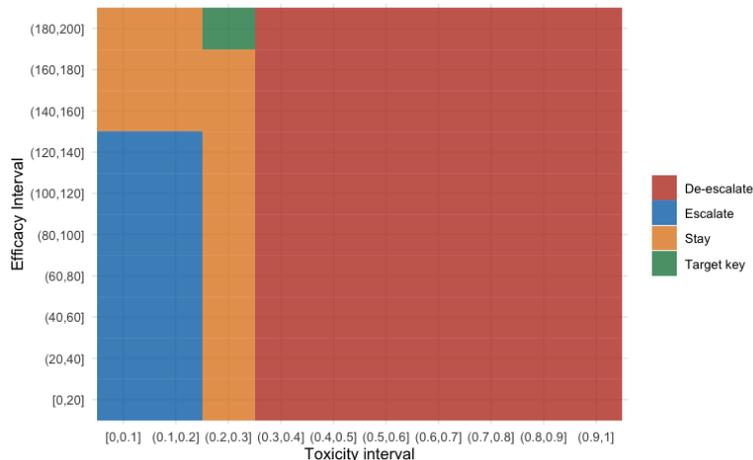
Approaches to perform dose escalation using binary toxicity and continuous efficacy responses (cont.)

Designs utilizing simpler decision rules for escalation and de-escalation purposes

Checkerboard (Yi and Yuan 2020)

Utilizes the joint modeling approach as specified in Bekele and Shen.

”Keys” (similar to Keyboard/mTPI-2 design) are defined apriori, including the **target key**. Decisions are made based on which key is the ”strongest” key, or the key with the highest posterior density for each toxicity/efficacy dimension.



Custom BOIN

Modeling is only performed for the efficacy endpoint.

$$W | \beta_w, \sigma_w^2 \sim N(X * \beta_w, \sigma_w^2 * I)$$

where X_{ij} indicates the assignment of patient i to dose j .

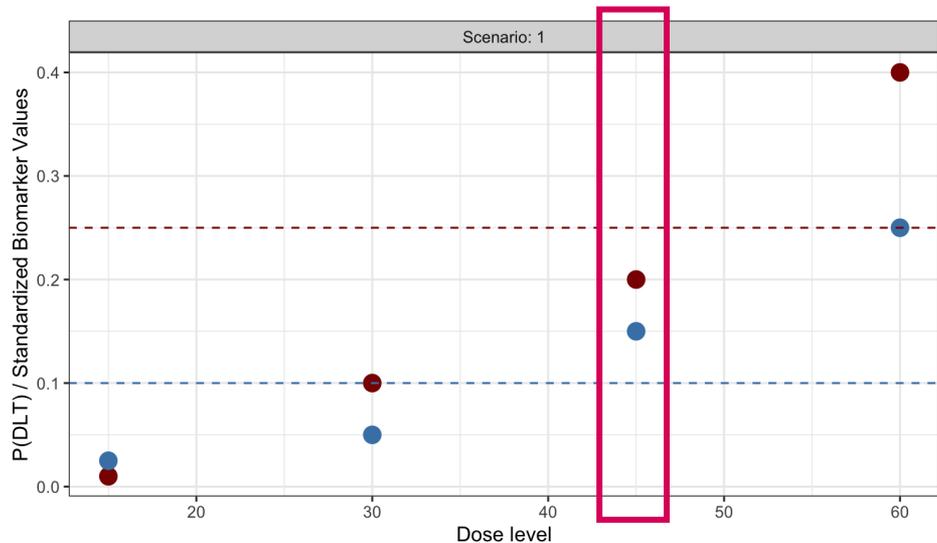
$$\beta_{w_j} - \beta_{w_{j-1}} \sim N(0, \sigma_{\beta_w}^2)$$

This model is similar to the BS and Checkerboard approaches, however without estimating the correlation between efficacy and toxicity.

We then combine this with BOIN decision rules for safety, based on target probability of 0.3 (since our cohort size is 3).

Decision Table	DLT rate $\leq \lambda_e$	$\lambda_e \leq$ DLT rate $\leq \lambda_d$	DLT rate $\geq \lambda_d$
$\Pr(W \geq W_{min} Data) \geq 0.5$	Escalate	Stay	De-escalate
$\Pr(W \geq W_{min} Data) \leq 0.5$	Escalate	Escalate	De-escalate

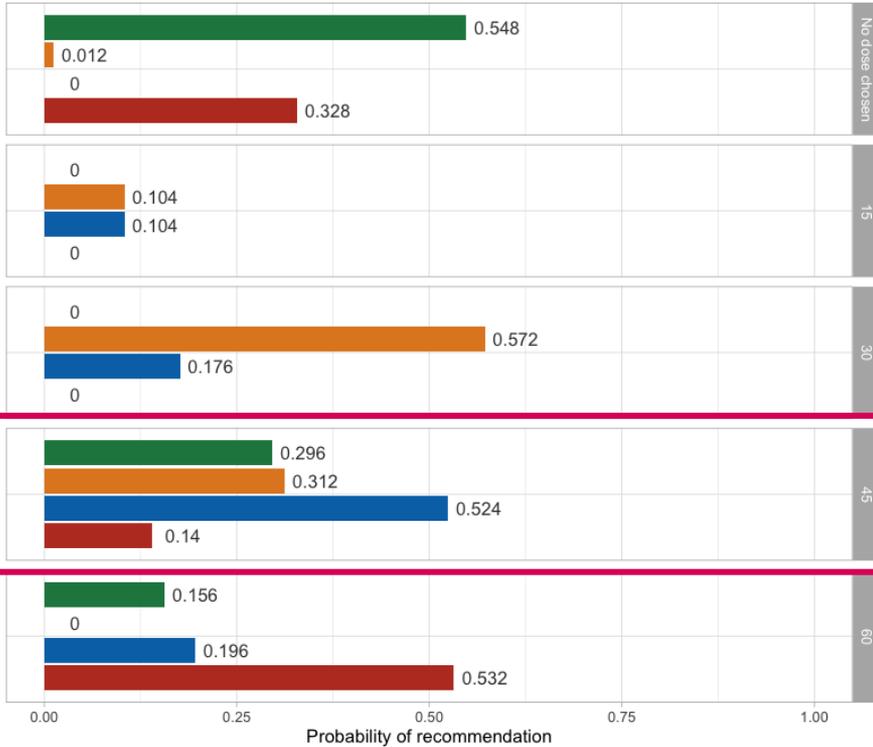
A "typical" scenario with monotonically increasing efficacy and toxicity



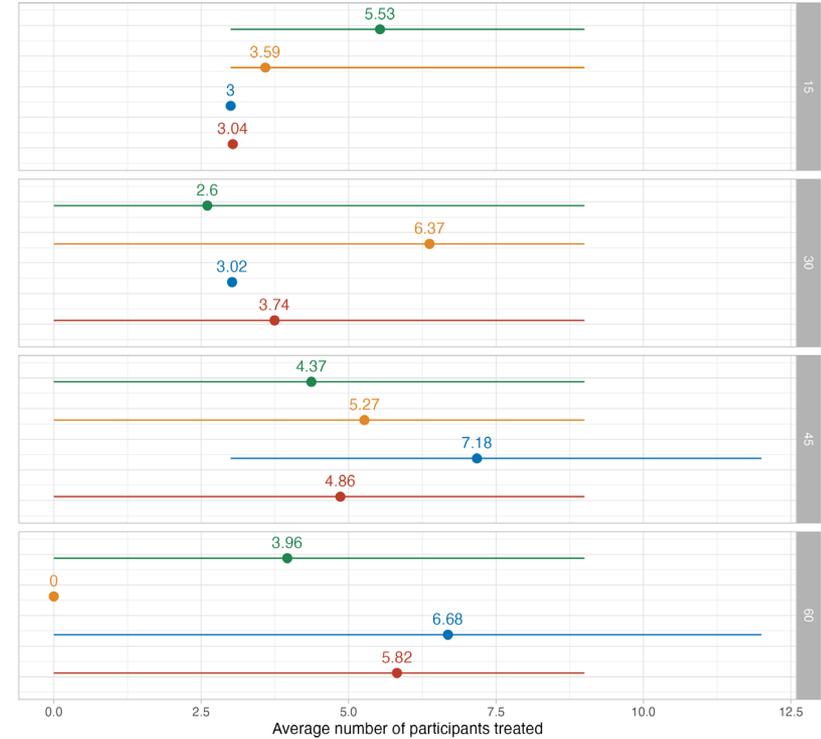
Red dashed lines represent target toxicity 0.25
Blue dashed lines represent minimum efficacy of 10% maximum value

In this scenario, doses 1 and 2 are sub-optimal and below the pre-defined minimum threshold. Dose 4 is the toxic dose ($\text{Pr}(DLT) = 0.4$). **Dose 3 is the optimal biological dose (OBD)**

BOIN is more likely to identify the correct OBD, while also limiting participant exposure to subtherapeutic dose.



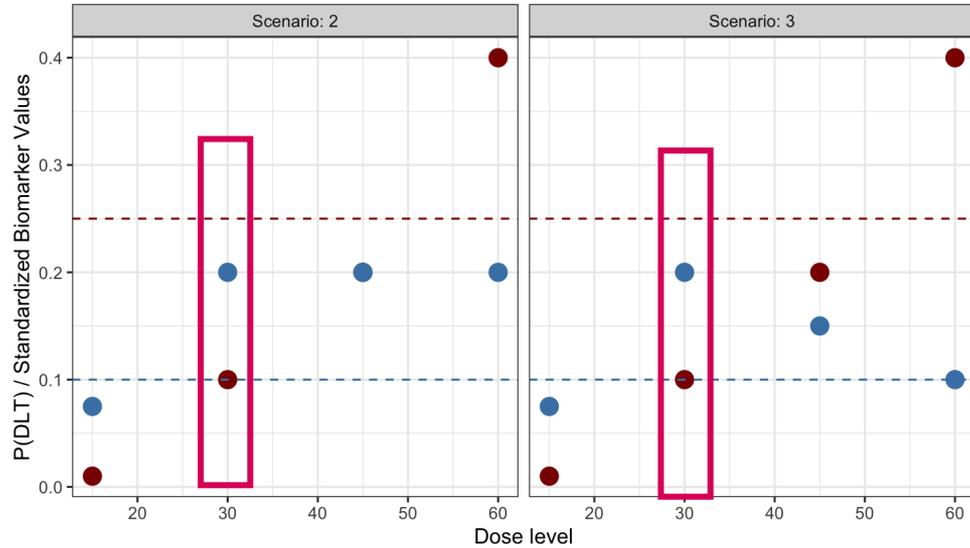
Evaluated approach ■ Checkerboard ■ Custom BOIN-based ■ YJ - Separate Models ■ BS - Joint Models



Evaluated approach ● Checkerboard ● Custom BOIN-based ● YJ - Separate Models ● BS - Joint Models

Bars represent 95% quantiles

Scenarios with non-monotonic efficacy



Red dashed lines represent target toxicity 0.25
Blue dashed lines represent minimum efficacy of 10% maximum value

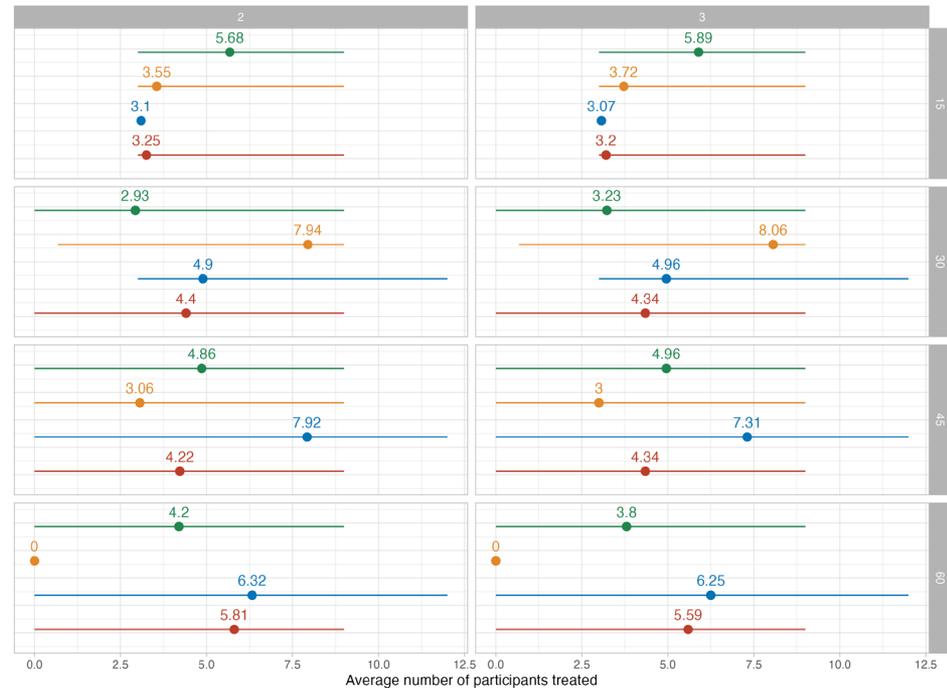
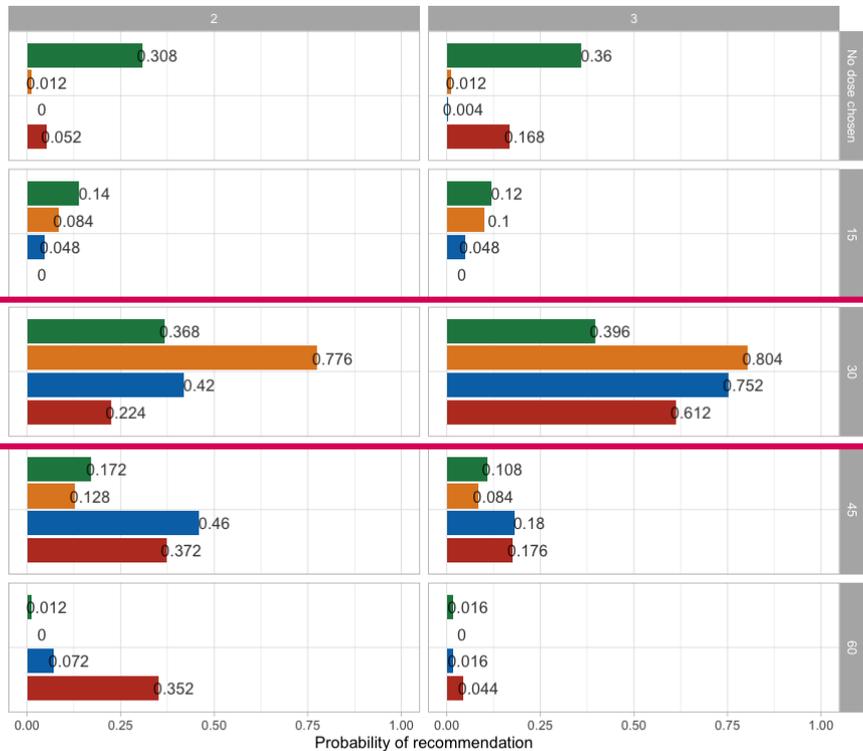
Scenario 2: Efficacy plateaus at dose 2 after 20% of maximum efficacy has been reached

Scenario 3: Efficacy decreases after dose 2 after 20% of maximum efficacy has been reached.

Both scenarios have toxicity monotonically increasing with dose 4 being the toxic dose ($\Pr(DLT) = 0.4$). **Dose 2 is the OBD.**



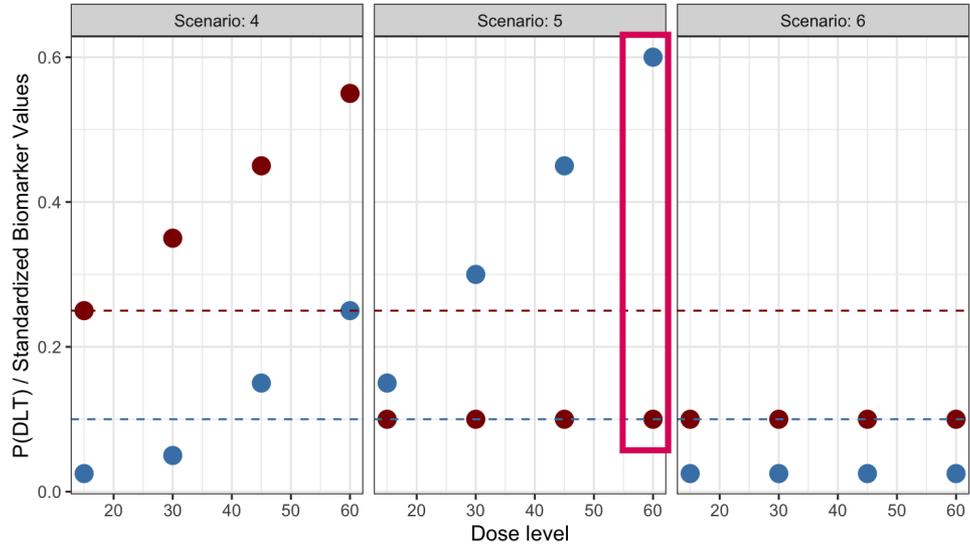
YJ design outperforms others when there exists plateau or decreasing efficacy with increasing dose.



Evaluated approach ● Checkerboard ● Custom BOIN-based ● YJ - Separate Models ● BS - Joint Models

Bars represent 95% quantiles

Scenarios with all toxic or subtherapeutic doses



Red dashed lines represent target toxicity 0.25
Blue dashed lines represent minimum efficacy of 10% maximum value

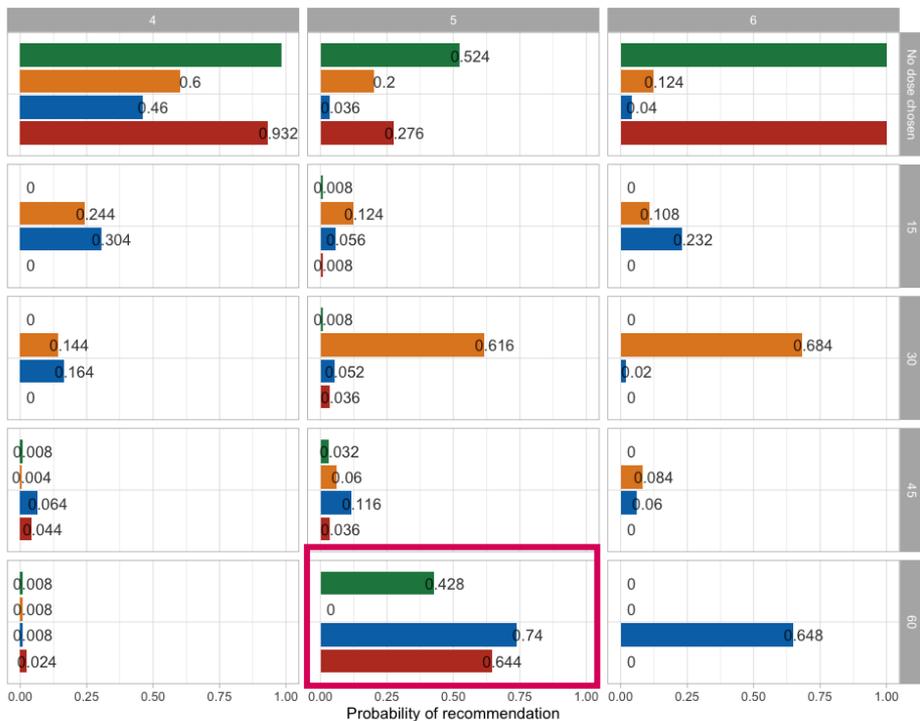
Scenario 4: There is a monotonically increasing efficacy, but all doses are toxic. **No dose is the OBD.**

Scenario 5: All doses are efficacious, and no doses are toxic. **Dose 4 (top dose) is the OBD.**

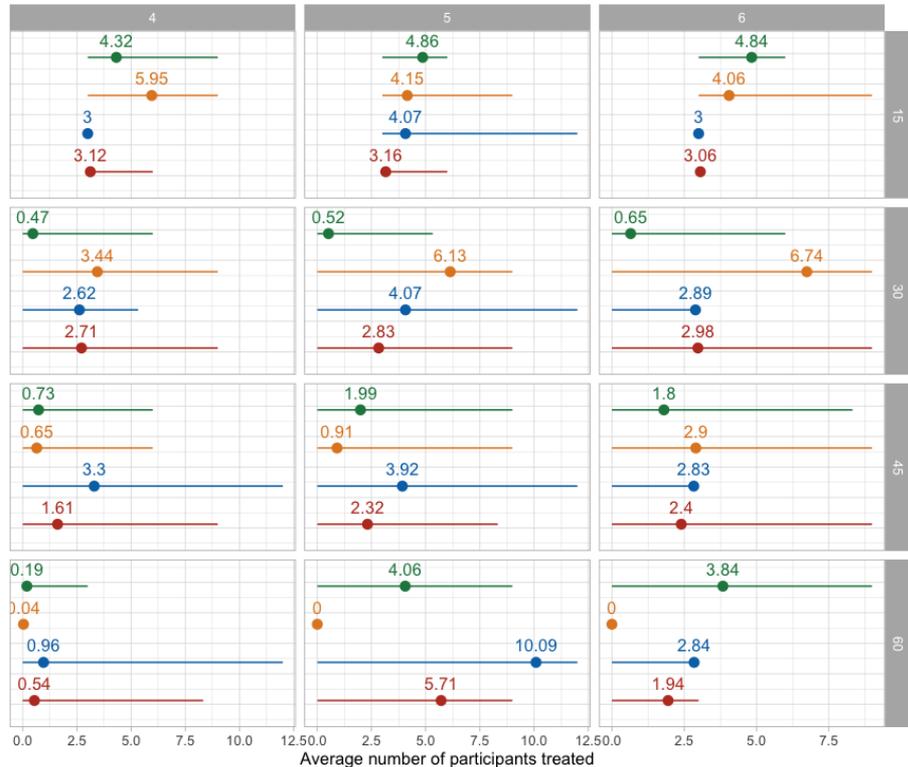
Scenario 6: All doses are subtherapeutic but are also not toxic ($\Pr(DLT) = 0.1$). **No dose is the OBD.**



Joint models are generally more conservative and does not recommend any doses to move forward in special scenarios



Evaluated approach ■ Checkerboard ■ Custom BOIN-based ■ YJ - Separate Models ■ BS - Joint Models



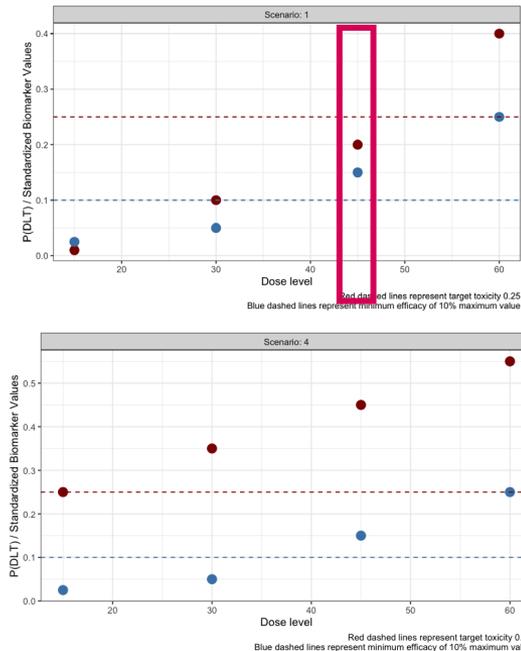
Evaluated approach ● Checkerboard ● Custom BOIN-based ● YJ - Separate Models ● BS - Joint Models

Bars represent 95% quantiles



Evaluating "accelerated titration" as a step for moving beyond subtherapeutic dose

Evaluated against scenarios 1 and 4



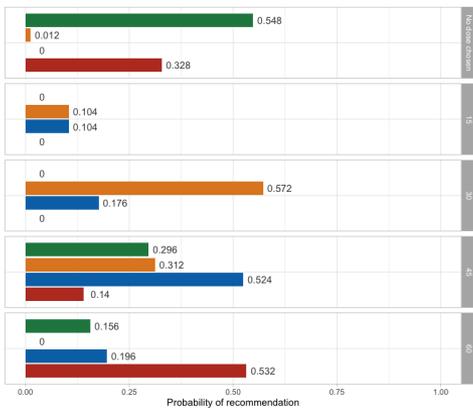
One participant is enrolled at the lowest dose. If that participant:

- Did not experience any DLT event or multiple toxicity events of grade II.
- Did not achieve the minimum efficacy threshold

Then the next participant will be dosed at a higher dose. The acceleration step will stop and cohorts of size 3 will be enrolled as specified when either:

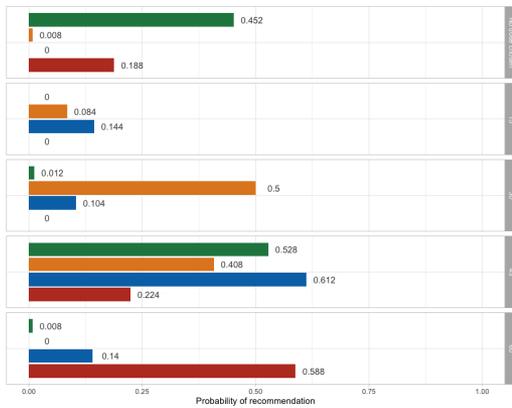
- Participants experienced a DLT event or 2 toxicity events of grade II
- If the minimum efficacy threshold has been reached.

Standard



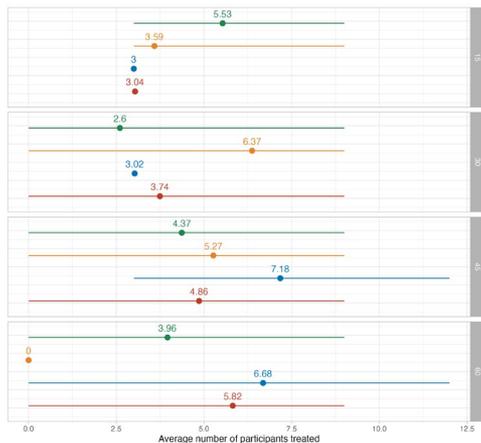
Evaluated approach: ■ Checkerboard ■ Custom BOIN-based ■ YJ - Separate Models ■ BS - Joint Models

With accelerated titration

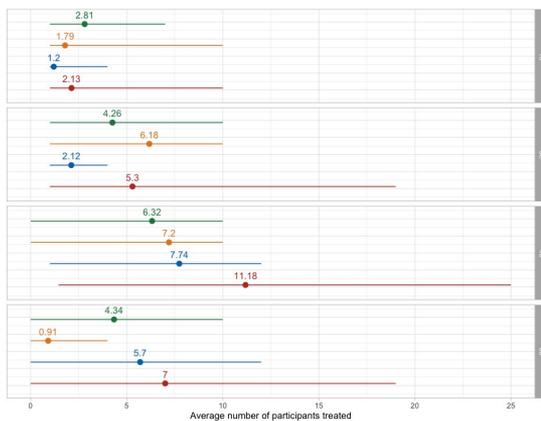


Evaluated approach: ■ Checkerboard ■ Custom BOIN-based ■ YJ - Separate Models ■ BS - Joint Models

Utilizing acceleration can assist in reducing sample size for subtherapeutic doses and increase the probability of recommending the correct dose

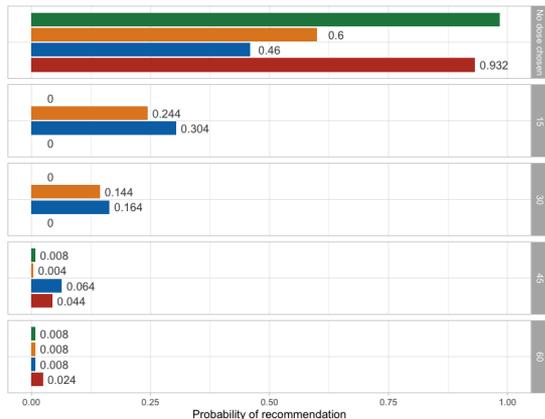


Evaluated approach: ● Checkerboard ● Custom BOIN-based ● YJ - Separate Models ● BS - Joint Models
Bars represent 95% quantiles

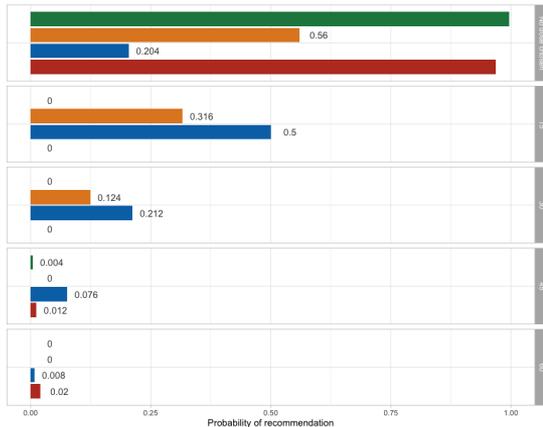


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Standard

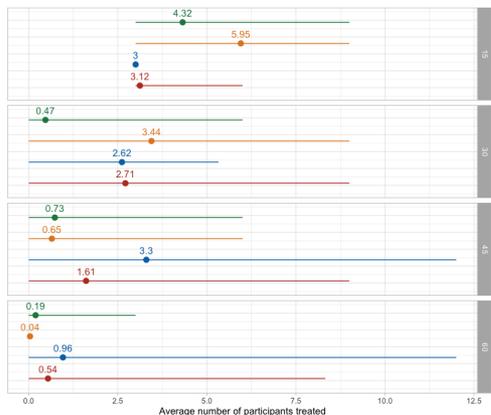


With accelerated titration



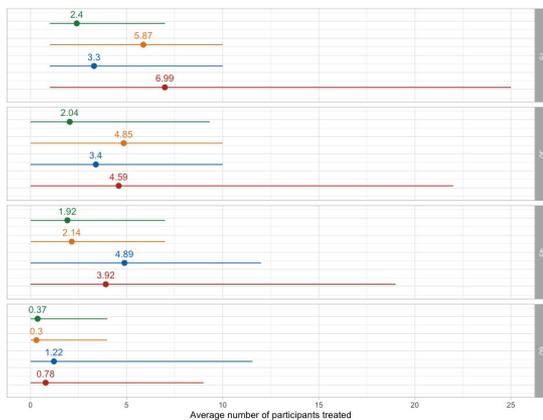
Acceleration strategy can inadvertently increased exposure to toxic doses

Evaluated approach: ■ Checkerboard ■ Custom BOIN-based ■ YJ - Separate Models ■ BS - Joint Models



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Evaluated approach: ● Checkerboard ● Custom BOIN-based ● YJ - Separate Models ● BS - Joint Models
Bars represent 95% quantiles

Summary of results

- Continuous efficacy outcomes means that the designs are never completely “model assisted”, meaning that the decision table cannot be pre-specified during the protocol/SAP drafting phase.
- Joint modeling approaches can be conservative, requiring generally more participants while also less likely to recommend a dose due to low sample sizes.
- Utilizing BOIN as the backbone for escalation can allow for rapid escalation but can run into issues if the majority of doses are toxic.
- Acceleration can be appropriate strategy to mitigate underdosing in dose escalation trials in gene therapies.

Challenges in implementing design strategies with continuous PD markers

- Choosing a threshold for the target PD/efficacy response can be challenging.
 - For the minimum activity level, the choice can be driven by the variability and level of what is considered normal activity of the PD marker.
 - There is not always clear evidence for which can be the **target** for PD levels, since there might not be a clear correlation between PD marker and efficacy outcomes.
- Due to low sample size, prior choice can have an outsized impact on the outcome of dose escalation process, especially for more challenging models.
 - The decision to elicit pessimistic or optimistic priors can alter the operating characteristics of the trial.
 - Evaluate and specify multiple types of priors and evaluate prior predictive distributions.

Thank you!

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Supplemental Information

Implementation Details

Prior specifications

For Bekele and Shen 2005, as well as for Checkerboard:

$$\beta_{Z_1}, \beta_{Z_2} \sim MVN \left(\begin{bmatrix} -1 \\ 0 \end{bmatrix}, \text{Diag}(2) \right)$$

$$\sigma_w^2 \sim IG(0.1, 0.1)$$

$$\rho \sim \text{Uniform}(0,1)$$

$$\beta_{W_0} = 0.3989$$

For Yeung et al. 2015, the prior for both efficacy and toxicity endpoints are based on the pseudo data approach (Whitehead et al.). For toxicity, we specified that the lowest dose and highest dose have DLT probabilities of 0.16 and 0.25 (respectively). For efficacy, we specified that the lowest dose and the highest dose have mean efficacy of 10% maximum efficacy, and 100% maximum efficacy, respectively.

For the custom BOIN approach, we used default priors as specified in the `crmPack` function for the EffFlexi model (<https://openpharma.github.io/crmPack/main/reference/EffFlexi-class.html>)