Using Hamiltonian Monte-Carlo to design longitudinal studies with discrete outcomes accounting for parameter and model uncertainties

Florence Loingeville, Jérémy Seurat, Thu Thuy Nguyen, Marie-Karelle Riviere, France Mentré

IAME, UMR 1137 INSERM - University Paris Diderot, Paris, France

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Infection • Antimicrobials • Modelling • Evolution

Integrated DEsign and AnaLysis
of small population group trials

Contents

Designs in pharmacometrics

- Last decades: several methods/software for **maximum likelihood estimation** of population parameters from **longitudinal data** using **nonlinear mixed effect models** (NLMEM)

- Problem beforehand: **choice of "population" design**
    - To obtain precise estimates / adequate power
      - number of individuals?
      - number of sampling times/individual?
      - allocation of sampling times?
      - other design variables (doses, etc.)

    - **Clinical trial simulation (CTS)**: time consuming

    - Asymptotic theory: **expected Fisher Information Matrix** [1] (FIM)

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[1] Mentré et al. *Biometrika*, 1997.

Fisher Information Matrix in NLMEM

- **Analytical expression for FIM in NLMEM**
  - Current approach in PFIM [2] and other design software programs [3]:
    first order linearisation of model around the expectation of random effects (FO)
    - Only for continuous data
    - Performs well but has limitations in case of complex nonlinear models and/or large variability

- **FIM for discrete longitudinal data**:
  - Methods based on approximations [4], [5]
  - We propose new approaches for computation of FIM
    - Monte Carlo - Adaptive Gaussian Quadrature (MC-AGQ) [6]
    - Monte Carlo - Hamiltonian Monte Carlo (MC-HMC) [7]

    These approaches:
    - Without model linearisation
    - Evaluated and compared to CTS and Laplace approx. on 4 longitudinal data types: continuous, binary, count, time to event

[2] PFIM group, www.pfim.biostat.fr.

[3] Nyberg et al. *Br J Clin Pharmacol*, 2014.

[4] Waite and Woods. *Biometrika*, 2015.

[5] Ogungbenro and Aarons. *J Pharmacokinet Pharmacodyn*, 2011.

[6] Ueckert and Mentré. *Comput Stat Data Anal*, 2016.

[7] Riviere, Ueckert and Mentré. *Biostatistics*, 2016.

Parameter and model uncertainty in designs

- **Optimal design depends on knowledge on model and parameters**
  - Local planification: given the model m and parameter values Ψ_m^*
  - Widely used criterion: D-optimality [8]

- **Alternative: Robust designs**
  - Taking into account uncertainty on parameters
  - Across a set of candidate models (Example in dose-response study proposed [9], [10] and implemented in MCP-MOD [11])

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[8] Atkinson, Donev and Tobias. *Optimum experimental designs, with SAS*, 2009.

[9] Bretz, Pinheiro and Branson. *Biometrics*, 2005.

[10] Pinheiro et al. *Stat Med*, 2014.

[11] Bornkamp et al. cran.r-project.org/web/packages/MCPMod/index.html, 2008.

NLMEM: Notations

For continuous data:
$$y_i = f(g(\mu, b_i, z_i, \beta), \xi_i) + \epsilon_i$$

For discrete data:
$$p(y_i|b_i) = \prod_{j=1}^{n_i} h(y_{ij}, g(\mu, b_i, z_i, \beta), \xi_i)$$

with

$y_i = (y_{i1}, \ldots, y_{in_i})^T$ response for individual i ($i = 1, \ldots, N$)

f, h structural model

ξ_i elementary design for subject i

$\theta_i = g(\mu, b_i, z_i, \beta)$ individual parameters vector

μ vector of fixed effects

b_i vector of random effects for individual i, $b_i \sim \mathcal{N}(0, \Omega)$

z_i vector of covariates

β vector of covariate effects

ϵ_i vector of residual errors, $\epsilon_i \sim \mathcal{N}(0, \Sigma)$ and Σ diagonal matrix

Ψ: Population parameters $\{\mu, \Omega, \Sigma, \beta\}$

MC-HMC method to compute the FIM in NLMEM

Population FIM for one group design: $\mathcal{M}(\Psi, \Xi) = N \times \mathcal{M}(\Psi, \xi)$

Population design $\Xi = \{\xi, N\}$ with identical elementary design ξ in all N subjects

Elementary FIM: $\mathcal{M}(\psi, \xi) = E_y \left(\frac{\partial \log(L(y, \psi))}{\partial \psi} \frac{\partial \log(L(y, \psi))}{\partial \psi}^T \right)$

$$\mathcal{M}(\psi, \xi)_{k,l} = E_y \left(\underbrace{\frac{\partial \log(L(y, \psi))}{\partial \psi_k} \frac{\partial \log(L(y, \psi))}{\partial \psi_l}^T}_{D_{k,l}} \right)$$

Monte Carlo - MC

After calculation... $D_{k,l} \Longleftrightarrow$

$$\int_{b_1} \frac{\partial \big(\log(p(y|b_1, \psi) p(b_1|\psi)) \big)}{\partial \psi_k} \underbrace{\frac{p(y|b_1, \psi) p(b_1|\psi)}{\int p(y|b, \psi) p(b|\psi) db}}_{\substack{\text{conditional density} \\ \text{of } b \text{ given } y}} db_1 \cdot \int_{b_2} \frac{\partial \big(\log(p(y|b_2, \psi) p(b_2|\psi)) \big)}{\partial \psi_l} \underbrace{\frac{p(y|b_2, \psi) p(b_2|\psi)}{\int p(y|b, \psi) p(b|\psi) db}}_{\substack{\text{conditional density} \\ \text{of } b \text{ given } y}} db_2$$

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[7] Riviere, Ueckert and Mentré. *Biostatistics*, 2016.

[12] Stan Development Team. Stan: A C++ Library for Probability and Sampling.

[13] Riviere and Mentré. https://cran.r-project.org/web/packages/MIXFIM/index.html, 2015.

$$\mathcal{M}(\psi,\xi) = E_y\left(\frac{\partial \log(L(y,\psi))}{\partial \psi}\frac{\partial \log(L(y,\psi))}{\partial \psi}^T\right)$$

$$\mathcal{M}(\psi,\xi)_{k,l} = E_y\left(\underbrace{\frac{\partial \log(L(y,\psi))}{\partial \psi_k}\frac{\partial \log(L(y,\psi))}{\partial \psi_l}^T}_{D_{k,l}}\right)$$

Monte Carlo - MC

After calculation... $D_{k,l} \Longleftrightarrow$
$E_b\left(\frac{\partial(\log(p(y|b,\psi)p(b|\psi)))}{\partial \psi_k}\Big|Y\right).E_b\left(\frac{\partial(\log(p(y|b,\psi)p(b|\psi)))}{\partial \psi_l}\Big|Y\right)$

Markov Chains Hamiltonian Monte Carlo (MC-HMC)

⇒ **Two integrals to compute: w.r.t. *y* and w.r.t. *b***

Use of **MC** and **Hamiltonian Monte Carlo (HMC) (in Stan** [12]) [7], implemented in R package MIXFIM [13]

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[7] Riviere, Ueckert and Mentré. *Biostatistics*, 2016.

[12] Stan Development Team. Stan: A C++ Library for Probability and Sampling.

[13] Riviere and Mentré. https://cran.r-project.org/web/packages/MIXFIM/index.html, 2015.

Robust FIM, assuming a distribution $p(\Psi)$ on the parameters

$$\mathscr{M}_R(\Xi) = E_\Psi(\mathscr{M}(\Psi, \Xi))$$

$$\mathscr{M}_R(\Xi) = E_\Psi(\mathscr{M}(\Psi, \Xi)) = E_\Psi\left(E_y(\underbrace{\frac{\partial \log(L(y,\psi))}{\partial \psi_k} \frac{\partial \log(L(y,\psi))}{\partial \psi_l}^T}_{D_{k,l}})\right) = E_{\Psi,y}(D_{k,l})$$

- two integrals **w.r.t. y** and **w.r.t. b** for evaluation of $\mathscr{M}(\Psi, \Xi)$
- one supplementary integral **w.r.t. Ψ** for evaluation of $\mathscr{M}_R(\Xi)$
- Evaluation by **MC-HMC** using Stan (drawing jointly Ψ and y by MC)

Application to robust designs for repeated count data

- Example: Daily count of events that we want to prevent [7]
- Poisson model for repeated count response

$$P(y = k|b) = \frac{\lambda^k exp(-\lambda)}{k!}$$
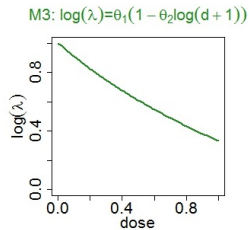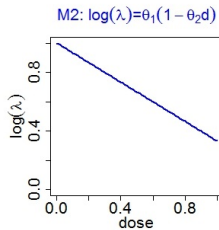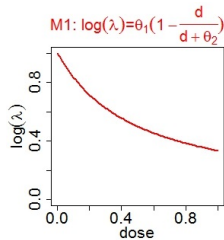
- Each patient observed at 3 dose levels (one placebo) during x days
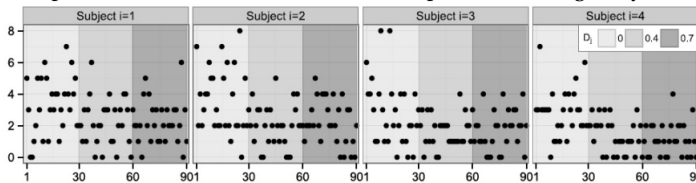
- Several candidate models for the link between $\log(\lambda)$ and dose
- λ: mean number of events / day

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[7] Riviere, Ueckert and Mentré. *Biostatistics*, 2016.

Five models of effect of dose on decreasing Poisson parameter
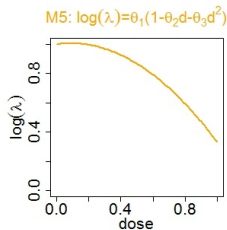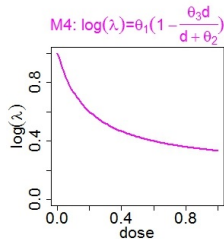
$$\theta_p = \mu_p exp(b_p); \, b_p \sim \mathcal{N}(0, \omega_p^2)$$

Constraints

	Count example
N	60 subjects
n_{rep}	10 replications
n	3 doses
Choice of doses	$d_1 = 0$ (placebo) d_2, d_3 from 0.1 to 1 ($step = 0.1$, no repetition)

a priori parameter values / parameter distributions:

	μ_1^*	μ_2^*	ψ_m^* μ_3^*	ω_1^*	ω_2^*	μ_1	$p_m(\psi_m)$ $\boldsymbol{\mu_2}$	μ_3	ω_1	$\boldsymbol{\omega_2}$
M_1	1.00	0.50		0.30	0.30	1.00	$\mathscr{LN}(-0.89, 0.63)$		0.30	$\mathscr{LN}(-1.50, 0.77)$
M_2	1.00	0.67		0.30	0.30	1.00	$\mathscr{LN}(-0.60, 0.63)$		0.30	$\mathscr{LN}(-1.50, 0.77)$
M_3	1.00	0.96		0.30	0.30	1.00	$\mathscr{LN}(-0.24, 0.63)$		0.30	$\mathscr{LN}(-1.50, 0.77)$
M_4	1.00	0.20	0.80	0.30	0.30	1.00	$\mathscr{LN}(-1.81, 0.63)$	0.80	0.30	$\mathscr{LN}(-1.50, 0.77)$
M_5	1.00	0.80	0.13	0.30	0.30	1.00	$\mathscr{LN}(-0.60, 0.63)$	0.13	0.30	$\mathscr{LN}(-1.50, 0.77)$

Optimality criteria

Parameters \ Model	Given model m	Set of candidate models $m = 1, \ldots, M$
Given parameter values ψ_m^*	**D-optimality** [8] $$\Phi_{D,m}(\Xi) = \det(\mathcal{M}(\Psi_m^*, \Xi))^{1/P_m}$$	**Compound-D optimality** [8,14,15] $$\Phi_{CD}(\Xi) = \prod_{m=1}^{M} \Phi_{D,m}(\Xi)^{w_m}$$
a priori distribution on parameters $p_m(\psi_m)$	**DE-optimality** [8] $$\Phi_{DE,m}(\Xi) = \det(\mathcal{M}_R(\Xi))^{1/P_m}$$	**Compound-DE optimality** $$\Phi_{CDE}(\Xi) = \prod_{m=1}^{M} \Phi_{DE,m}(\Xi)^{w_m}$$

- P_m: number of population parameters of model m
- w_m: weight quantifying the balance between the M models, $\sum_m w_m = 1$

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[8] Atkinson, Donev and Tobias. *Optimum experimental designs, with SAS*, 2009.

[14] Atkinson et al. *J Stat Plan Inference*, 2008.

[15] Nguyen et al. *Pharm Stat*, 2016.

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Design optimisation: robustness on model

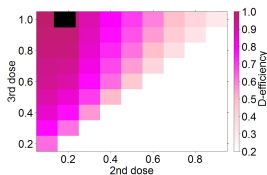|	Count example
Evaluation of FIM for all 45 possible designs	5000 MC 200 HMC
Combinatorial optimisation For each model	D-criterion on FIM
Over 5 models	Compound D-criterion (averaging for uncertainty on models)

Results: Robust design w.r.t model
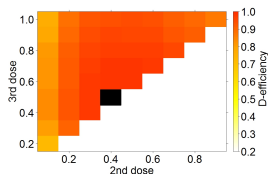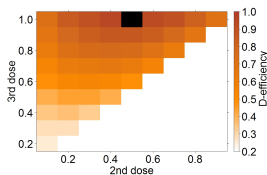

Optimal doses: $\xi_{D,1} = \{0, \mathbf{0.4, 0.5}\}$.
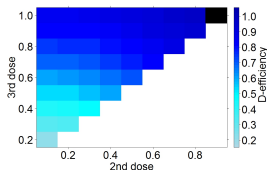
Optimal doses: $\xi_{D,2} = \{0, \mathbf{0.9, 1}\}$.
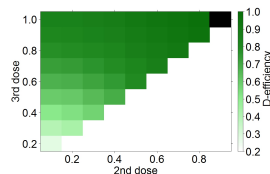
Optimal doses: $\xi_{D,3} = \{0, \mathbf{0.9, 1}\}$.

Optimal doses: $\xi_{D,4} = \{0, \mathbf{0.2, 1}\}$.

Optimal doses: $\xi_{D,5} = \{0, \mathbf{0.5, 1}\}$.

1. Full Emax
2. Linear
3. Log-Linear
4. Emax
5. Quadratic
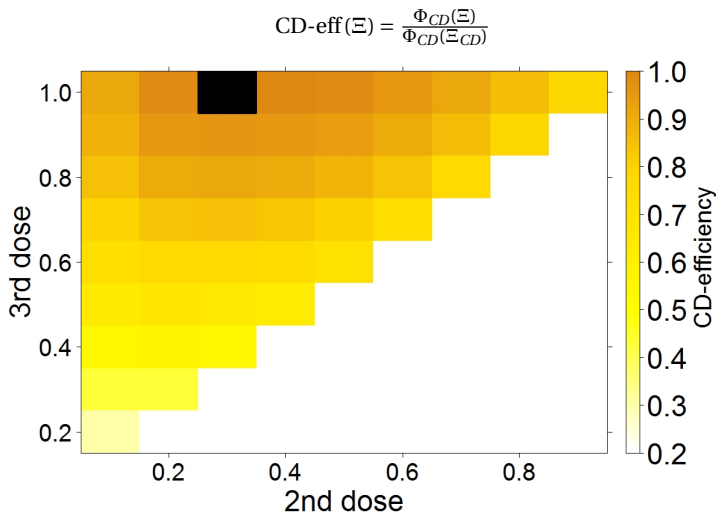
$$\text{D-eff}(\Xi) = \frac{\Phi_D(\Xi)}{\Phi_D(\Xi_D)}$$

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Results: Robust design w.r.t model

	M_1 Full Emax	M_2 Linear	M_3 Log-linear	M_4 Emax	M_5 Quadratic
$\Xi_{D,1}$ $\{N = 60, \xi = (0, 0.4, 0.5)\}$	100%	60.8%	68.9%	50.3%	27.7%
$\Xi_{D,2}$ $\{N = 60, \xi = (0, 0.9, 1)\}$	87.0%	100%	100%	30.8%	67.2%
$\Xi_{D,3}$ $\{N = 60, \xi = (0, 0.9, 1)\}$	87.0%	100%	100%	30.8%	67.2%
$\Xi_{D,4}$ $\{N = 60, \xi = (0, 0.2, 1)\}$	88.4%	85.7%	85.4%	100%	85.6%
$\Xi_{D,5}$ $\{N = 60, \xi = (0, 0.5, 1)\}$	94.6%	89.9%	91.7%	69.9%	100%

- Important loss of efficiency in some scenarios where the model is not correctly pre-specified

Compound D-optimal design: $\xi_{CD} = (0, \mathbf{0.3}, \mathbf{1})$.

$$\text{CD-eff}(\Xi) = \frac{\Phi_{CD}(\Xi)}{\Phi_{CD}(\Xi_{CD})}$$

Results: Robust design w.r.t model

	M_1 Full Emax	M_2 Linear	M_3 Log-linear	M_4 Emax	M_5 Quadratic
$\Xi_{D,1}$ $\{N=60, \xi=(0, 0.4, 0.5)\}$	100%	60.8%	68.9%	50.3%	27.7%
$\Xi_{D,2}$ $\{N=60, \xi=(0, 0.9, 1)\}$	87.0%	100%	100%	30.8%	67.2%
$\Xi_{D,3}$ $\{N=60, \xi=(0, 0.9, 1)\}$	87.0%	100%	100%	30.8%	67.2%
$\Xi_{D,4}$ $\{N=60, \xi=(0, 0.2, 1)\}$	88.4%	85.7%	85.4%	100%	85.6%
$\Xi_{D,5}$ $\{N=60, \xi=(0, 0.5, 1)\}$	94.6%	89.9%	91.7%	69.9%	100%
Ξ_{CD} $\{N=60, \xi=(0, 0.3, 1)\}$	94.1%	88.1%	88.5%	79.7%	93.1%

- Good performance of the compound D-optimal design

Design optimisation: robustness on parameters and model

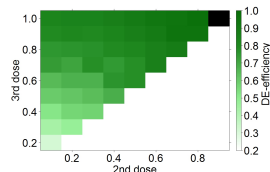|	Count example
Evaluation of FIM for all 45 possible designs	5000 MC 200 HMC
For each model	DE-criterion on FIM
Combinatorial optimisation	
Over 5 models	Compound DE-criterion (averaging for uncertainty on models)

Results: robust optimal design w.r.t. parameters for each model
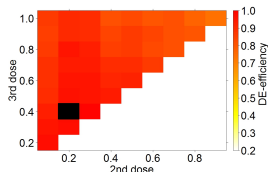
Optimal doses: $\xi_{DE,1}$ =(0, **0.2, 0.4**).
$\xi_{D,1}$ =(0, **0.4, 0.5**).
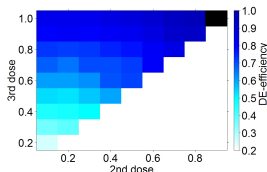
DE-eff($\xi_{D,1}$) = 94.1%

Optimal doses: $\xi_{DE,2}$ =(0, **0.9, 1**).
$\xi_{D,2}$ =(0, **0.9, 1**).

Optimal doses: $\xi_{DE,3}$ =(0, **0.9, 1**).
$\xi_{D,3}$ =(0, **0.9, 1**).
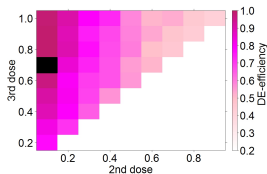
Optimal doses: $\xi_{DE,4}$ =(0, **0.1, 0.7**).
$\xi_{D,4}$ =(0, **0.2, 1**).

DE-eff($\xi_{D,4}$) = 84.6%
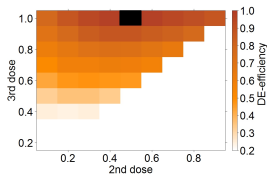
Optimal doses: $\xi_{DE,5}$ =(0, **0.5, 1**).
$\xi_{D,5}$ =(0, **0.5, 1**).

1. Full Emax
2. Linear
3. Log-Linear
4. Emax
5. Quadratic

$$\text{DE-eff}(\Xi) = \frac{\Phi_{DE}(\Xi)}{\Phi_{DE}(\Xi_{DE})}$$

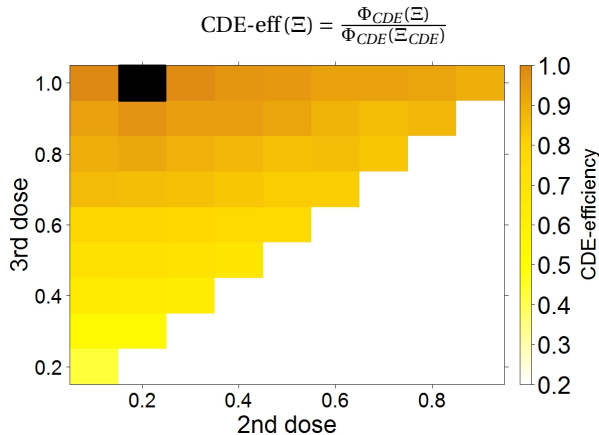# Results: robust optimal design w.r.t. parameters and model

	M_1 Full Emax	M_2 Linear	M_3 Log-linear	M_4 Emax	M_5 Quadratic
$\Xi_{DE,1}$ $\{N=60, \xi=(0,0.2,0.4)\}$	100%	49.9%	56.7%	77.5%	23.6%
$\Xi_{DE,2}$ $\{N=60, \xi=(0,0.9,1)\}$	73.3%	100%	100%	43.5%	87.1%
$\Xi_{DE,3}$ $\{N=60, \xi=(0,0.9,1)\}$	73.3%	100%	100%	43.5%	87.1%
$\Xi_{DE,4}$ $\{N=60, \xi=(0,0.1,0.7)\}$	89.1%	68.1%	73.9%	100%	51.4%
$\Xi_{DE,5}$ $\{N=60, \xi=(0,0.5,1)\}$	83.1%	87.8%	89.6%	58.5%	100%

Results: robust optimal design w.r.t. parameters and model

Compound DE-optimal design: $\xi_{CDE} = (0, \mathbf{0.2}, \mathbf{1})$.
Compound D-optimal design: $\xi_{CD} = (0, \mathbf{0.3}, \mathbf{1})$.

$$\text{CDE-eff}(\Xi) = \frac{\Phi_{CDE}(\Xi)}{\Phi_{CDE}(\Xi_{CDE})}$$

Results: robust optimal design w.r.t. parameters and model

	M_1 Full Emax	M_2 Linear	M_3 Log-linear	M_4 Emax	M_5 Quadratic
$\Xi_{DE,1}$ $\{N = 60, \xi = (0, 0.2, 0.4)\}$	100%	49.9%	56.7%	77.5%	23.6%
$\Xi_{DE,2}$ $\{N = 60, \xi = (0, 0.9, 1)\}$	73.3%	100%	100%	43.5%	87.1%
$\Xi_{DE,3}$ $\{N = 60, \xi = (0, 0.9, 1)\}$	73.3%	100%	100%	43.5%	87.1%
$\Xi_{DE,4}$ $\{N = 60, \xi = (0, 0.1, 0.7)\}$	89.1%	68.1%	73.9%	100%	51.4%
$\Xi_{DE,5}$ $\{N = 60, \xi = (0, 0.5, 1)\}$	83.1%	87.8%	89.6%	58.5%	100%
Ξ_{CDE} $\{N = 60, \xi = (0, 0.2, 1)\}$	90.9%	83.8%	83.9%	84.6%	82.8%

- Efficiency greater than 80% for all models

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Conclusion

- MC-HMC method for computation of FIM [7] enables applications to design optimisation for count data
- Extension of this method to propose robust optimal designs accounting for uncertainty w.r.t. parameters and/or models

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[7] Riviere, Ueckert and Mentré. *Biostatistics*, 2016.

Example

- Repeated binary data
  2 treatment groups : Control *vs.* Treated

- Logistic models to describe the
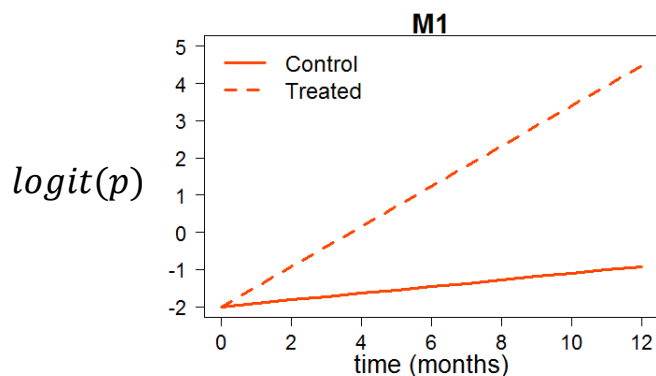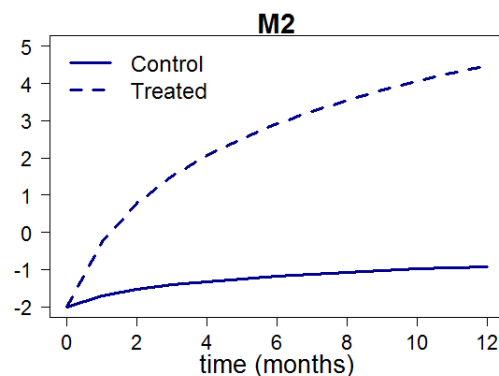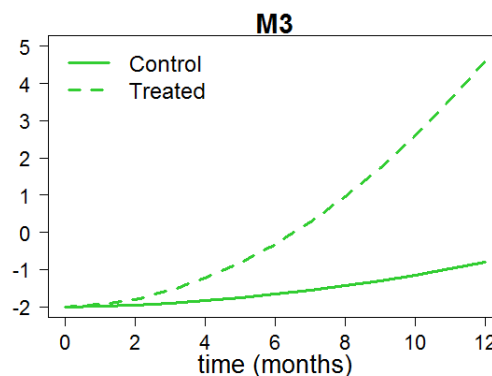 probability p of response y over time

24: Lestini G., Ueckert S. and Mentré F., PODE, Sweden, 2016

$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)t$$

Linear[24]

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Example

- Repeated binary data

  2 treatment groups : Control *vs.* Treated

- Logistic models to describe the

  probability p of response y over time

$logit(p)$

M1 — Control, Treated — Linear
$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)t$$

M2 — Control, Treated — Loglinear
$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)\log(t + 1)$$

M3 — Control, Treated — Quadratic
$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)t^2$$

M4 — Control, Treated — Sigmoid Emax
$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)t^3/(\theta_3^{3} + t^3)$$
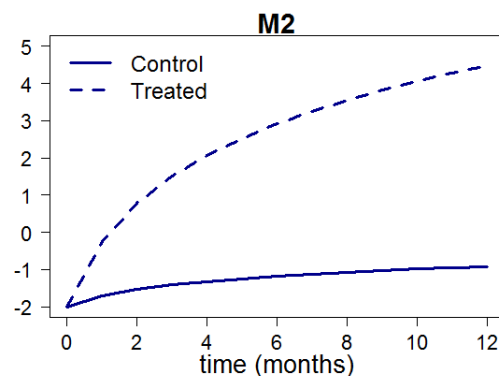
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- ▪ **Example**

  - Constraints

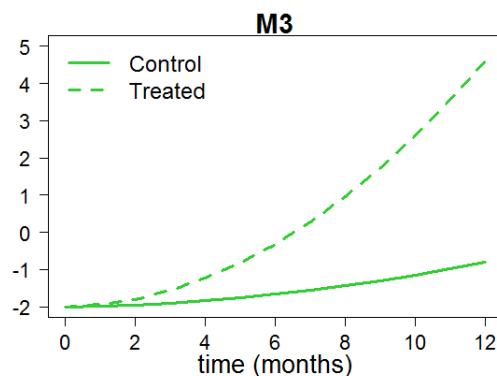| Number of individuals	N = 100 (50 per treatment group)
Number of samples	n = 4 by individual (from 0 to 12 months)
Sampling times $\xi=(t_1,t_2,t_3,t_4)$	t_1 = 0, t_4 = 12 months (fixed) **t_2, t_3 optimized among 11 possible times from 1 to 11**

M1 — Linear
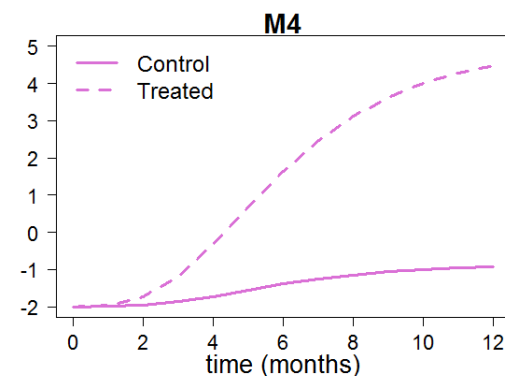$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)t$$

M2 — Loglinear
$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)\log(t + 1)$$

M3 — Quadratic
$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)t^2$$

M4 — Sigmoid Emax
$$logit(p) = \theta_1 + \theta_2(1 + \beta \times 1_T)t^3/(\theta_3{}^3 + t^3)$$

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Optimality criteria

Parameters of interest	Given model m	Set of candidate models $m = 1,…,M$
All the population parameters	D-optimality [8] $$\Phi_{D,m} = Det(\mathcal{M}(\psi^*, \Xi))^{\frac{1}{P_m}}$$	**CD-optimality [8,14,15]** $$\Phi_{CD} = \prod_{m=1}^{M} \Phi_{D,m}{}^{w_m}$$

P_m : number of parameters

$$\sum_{m=1}^{M} w_m = 1$$

$$w_1 = w_2 = w_3 = w_4 = 1/4$$

8: Atkinson AC. Donev A. and Tobias R., Optimum experimental designs, with SAS, 2009

14: Atkinson AC. et *al.*, J Stat Plan inference, 2008

15: Nguyen TT. et *al.*, Pharm Stat, 2016

Parameters of interest	Given model m	Set of candidate models $m = 1,…,M$
All the population parameters	**D-optimality** [8] $$\Phi_{\mathrm{D},m} = Det(\mathcal{M}(\psi^*, \Xi))^{\frac{1}{P_m}}$$	**CD-optimality** [8,14,15] $$\Phi_{\mathrm{CD}} = \prod_{m=1}^{M} \Phi_{\mathrm{D,m}}{}^{w_m}$$
Subset of parameters of interest (treatment effect)	**D_S-optimality** [8] $$\Phi_{\mathrm{DS},m} = \left(\frac{Det(\mathcal{M}(\psi^*, \Xi))}{Det(\mathcal{M}_t(\psi^*, \Xi))} \right)^{\frac{1}{S_m}}$$	**CD$_S$-optimality** $$\Phi_{\mathrm{CDS}} = \prod_{m=1}^{M} \Phi_{\mathrm{DS,m}}{}^{w_m}$$

P_m : number of parameters
S_m : number of parameters of interest
$\mathcal{M}_t$: truncated FIM (without information on parameters of interest)

$$\sum_{m=1}^{M} w_m = 1$$

$$w_1 = w_2 = w_3 = w_4 = 1/4$$

8: Atkinson AC. Donev A. and Tobias R., Optimum experimental designs, with SAS, 2009   15: Nguyen TT. et *al*., Pharm Stat, 2016
14: Atkinson AC. et *al*., J Stat Plan inference, 2008

Parameters of interest	Given model m	Set of candidate models $m = 1,\dots,M$
All the population parameters	D-optimality [8] $$\Phi_{D,m} = Det(\mathcal{M}(\psi^*,\Xi))^{\frac{1}{P_m}}$$	**CD-optimality** [8,14,15] $$\Phi_{CD} = \prod_{m=1}^{M} \Phi_{D,m}{}^{w_m}$$
Subset of parameters of interest (treatment effect)	D_S-optimality [8] $$\Phi_{D_S,m} = \left(\frac{Det(\mathcal{M}(\psi^*,\Xi))}{Det(\mathcal{M}_t(\psi^*,\Xi))} \right)^{\frac{1}{S_m}}$$	**CD_S-optimality** $$\Phi_{CD_S} = \prod_{m=1}^{M} \Phi_{D_S,m}{}^{w_m}$$
Compromise	DD_S-optimality [8,16] $$\Phi_{DD_S,m} = \left(Det(\mathcal{M}_t(\psi^*,\Xi)) \right)^{\frac{1-\alpha_m}{P_m - S_m}} \left(\frac{Det(\mathcal{M}(\psi^*,\Xi))}{Det(\mathcal{M}_t(\psi^*,\Xi))} \right)^{\frac{\alpha_m}{S_m}}$$	**CDD_S-optimality** $$\Phi_{CDD_S} = \prod_{m=1}^{M} \Phi_{DD_S,m}{}^{w_m}$$

P_m : number of parameters
S_m : number of parameters of interest
$\mathcal{M}_t$: truncated FIM (without information on parameters of interest)
α_m: interest for S, $0 \leq \alpha \leq 1$

$$\sum_{m=1}^{M} w_m = 1$$

$$w_1 = w_2 = w_3 = w_4 = 1/4$$

8: Atkinson AC. Donev A. and Tobias R., Optimum experimental designs, with SAS, 2009
14: Atkinson AC. et *al*., J Stat Plan inference, 2008
15: Nguyen TT. et *al*., Pharm Stat, 2016
16: Atkinson AC. and Bogacka B., Technometrics, 1997

Design optimization accounting for model uncertainty

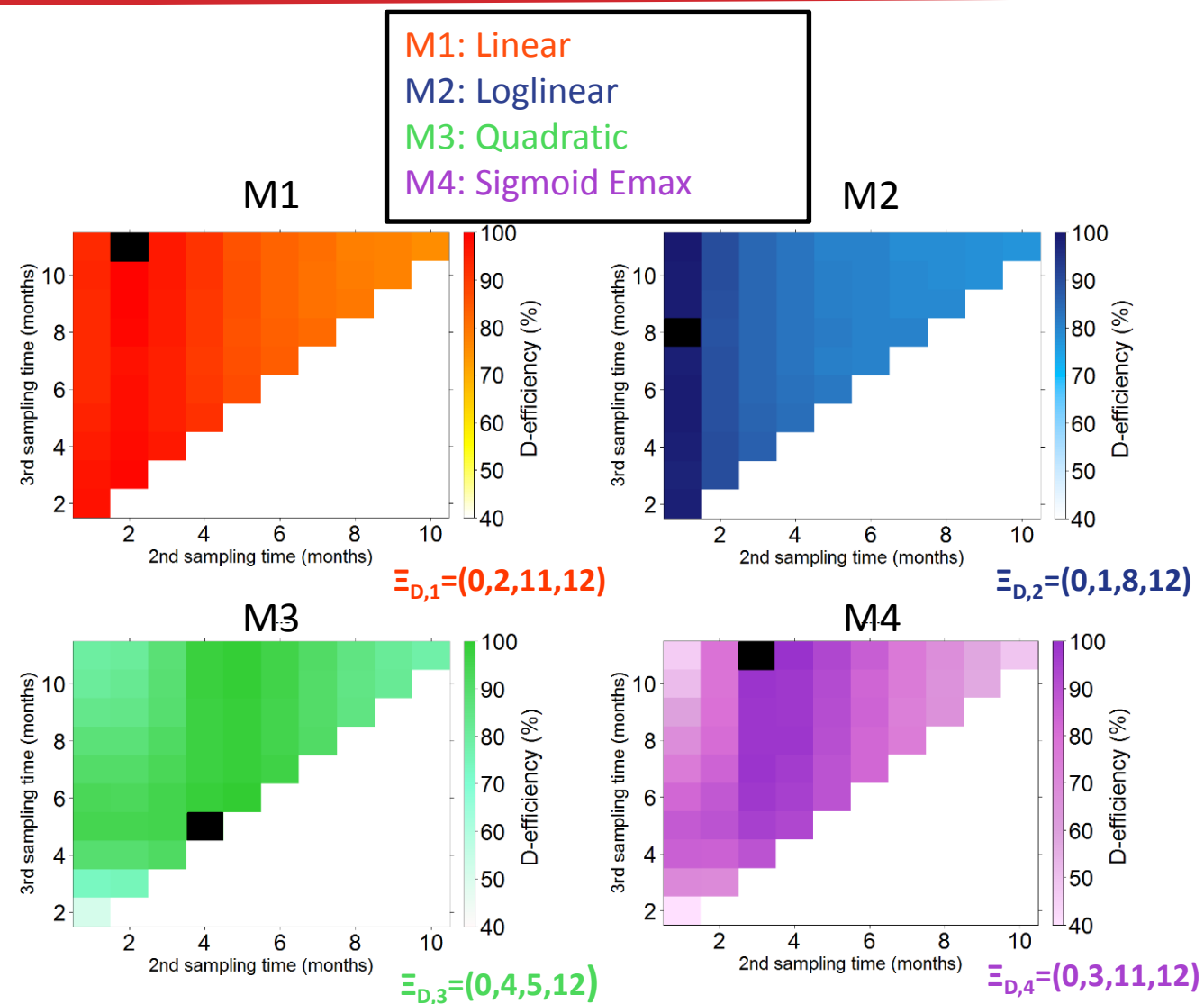|		Binary example
Combinatorial optimisation	Evaluation of FIM by MC/HMC [7] for all 55 possible designs ξ	5000 MC 200 HMC
	For each model	D-, D_S- and DD_S-criteria
	Averaging over 4 models	Compound D-, D_S- and DD_S-criteria

- **Choice of α_m in $\Phi_{DD_S,m}$ for each model**

  - $\Phi_{DD_S,m}$ computed for values of α between 0 and 1 with a step of 0.05

  - α_m chosen to maximize [D-eff × D_S-eff]

- **Predictions from FIM**

  - Relative standard errors (RSE) for population parameters of each model

  - Power of the Wald test to detect a significant effect β (with each model [17] and average)

  - Number of subjects needed (NSN) to obtain a $\pi_{average}$ of 80%

$$\pi_{average} = \sum_{m=1}^{M} w_m \, \pi_m$$

7: Riviere M-K. Ueckert S. and Mentré F., Biostatistics, 2016
17: Retout S. *et al.*, Stat Med, 2007

M1: Linear
M2: Loglinear
M3: Quadratic
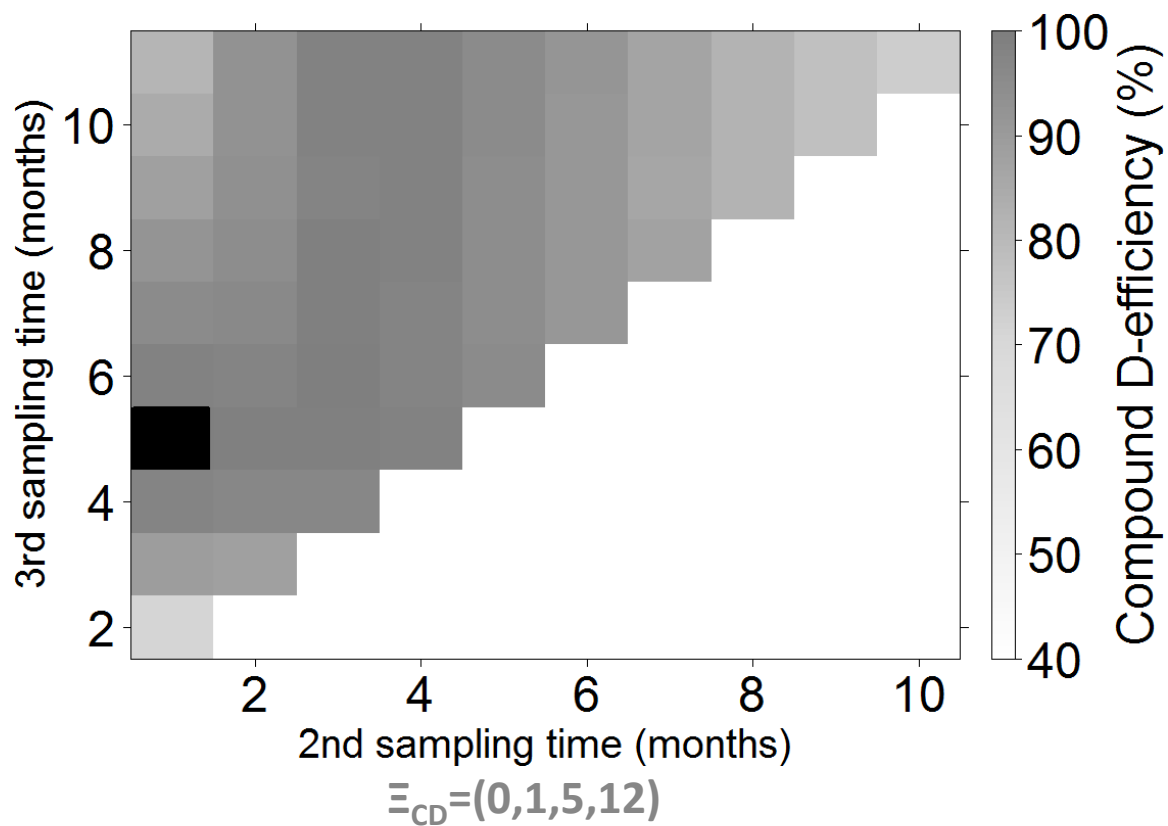M4: Sigmoid Emax

D-efficiency

D-optimal design for a pre-specified model \ Final model	M1 Linear	M2 Loglinear	M3 Quadratic	M4 Sigmoid Emax
$\Xi_{D,1}=(0,2,11,12)$	100%	89.8%	81.2%	79.1%
$\Xi_{D,2}=(0,1,8,12)$	93.2%	100%	87.5%	68.0%
$\Xi_{D,3}=(0,4,5,12)$	91.6%	83.4%	100%	93.1%
$\Xi_{D,4}=(0,3,11,12)$	96.3%	85.2%	88.4%	100%

$$\text{D-eff}(\Xi) = \frac{\Phi_D(\Xi)}{\Phi_D(\Xi_D)}$$

Ξ_D : D-optimal design

CD-efficiencies

D-efficiency

Final model / D-optimal design for a pre-specified model	M1 Linear	M2 Loglinear	M3 Quadratic	M4 Sigmoid Emax
$\Xi_{D,1}=(0,2,11,12)$	100%	89.8%	81.2%	79.1%
$\Xi_{D,2}=(0,1,8,12)$	93.2%	100%	87.5%	68.0%
$\Xi_{D,3}=(0,4,5,12)$	91.6%	83.4%	100%	93.1%
$\Xi_{D,4}=(0,3,11,12)$	96.3%	85.2%	88.4%	100%
$\Xi_{CD}=(0,1,5,12)$	94.0%	98.9%	95.1%	86.9%

$\Xi_{CD}=(0,1,5,12)$

$$\text{CD-eff}(\Xi)= \frac{\Phi_{CD}(\Xi)}{\Phi_{CD}(\Xi_{CD})}$$

Ξ_D : CD-optimal design

D$_S$-efficiencies for each model

M1: Linear
M2: Loglinear
M3: Quadratic
M4: Sigmoid Emax

D$_S$-efficiency

	M1 Linear	M2 Loglinear	M3 Quadratic	M4 Sigmoid Emax
$\Xi_{Ds,1}=(0,2,11,12)$	100%	80.6%	**43.4%**	59.5%
$\Xi_{Ds,2}=(0,1,11,12)$	75.1%	100%	**38.9%**	60.0%
$\Xi_{Ds,3}=(0,5,11,12)$	77.4%	60.0%	100%	89%
$\Xi_{Ds,4}=(0,6,7,12)$	72.0%	60.2%	82.3%	100%

Final model / D$_S$-optimal design for a pre-specified model

$\Xi_{Ds,1}=(0,2,11,12)$

$\Xi_{Ds,2}=(0,1,11,12)$

$\Xi_{Ds,3}=(0,5,11,12)$

$\Xi_{D,4}=(0,6,7,12)$

$$D_S-\text{eff}(\Xi)=\frac{\Phi_{Ds}(\Xi)}{\Phi_{Ds}(\Xi_{Ds})}$$

Ξ_{Ds} : D$_S$-optimal design

$\Xi_{D,1}=(0,2,11,12)$

$\Xi_{D,2}=(0,1,8,12)$

$\Xi_{D,3}=(0,4,5,12)$

$\Xi_{D,4}=(0,3,11,12)$

$$\Xi_{CDs}=(0,5,11,12)$$

$\Xi_{CD}=(0,1,5,12)$

$$\text{CDs−eff}(\Xi)= \frac{\Phi_{CDs}(\Xi)}{\Phi_{CDs}(\Xi_{CDs})}$$

Ξ_{CDs} : CDs-optimal design

D$_S$-efficiency

D$_S$-optimal design for a pre-specified model \ Final model	M1 Linear	M2 Loglinear	M3 Quadratic	M4 Sigmoid Emax
$\Xi_{Ds,1}=(0,2,11,12)$	100%	80.6%	**43.4%**	59.5%
$\Xi_{Ds,2}=(0,1,11,12)$	75.1%	100%	**38.9%**	60.0%
$\Xi_{Ds,3}=(0,5,11,12)$	77.4%	60.0%	100%	89%
$\Xi_{Ds,4}=(0,6,7,12)$	72.0%	60.2%	82.3%	100%
$\Xi_{CDs}=(0,5,11,12)$	**77.4%**	**63.7%**	**100%**	**89%**

M1: Linear
M2: Loglinear
M3: Quadratic
M4: Sigmoid Emax

M1: Linear
M2: Loglinear
M3: Quadratic
M4: Sigmoid Emax

$\longleftrightarrow$ α_m values maximizing [D-eff × D_S−eff]
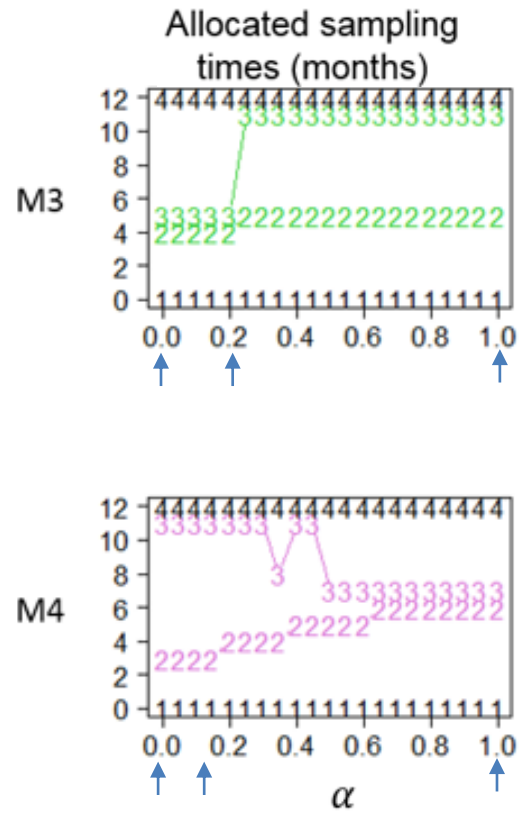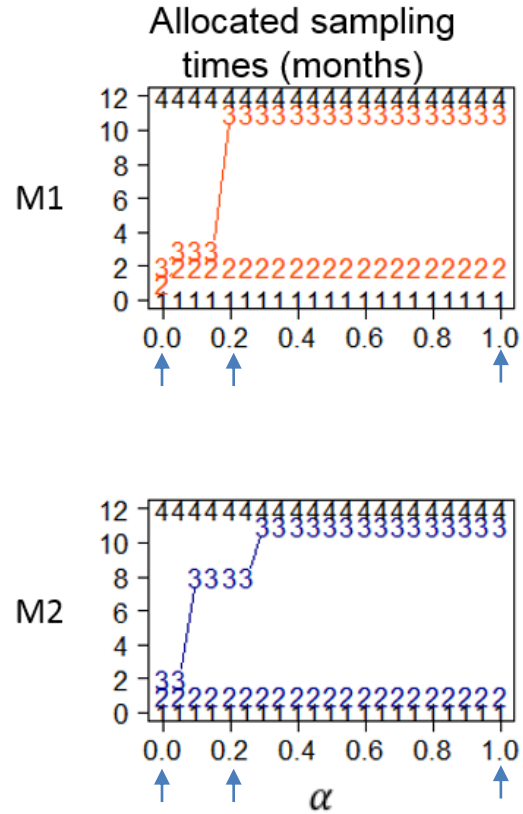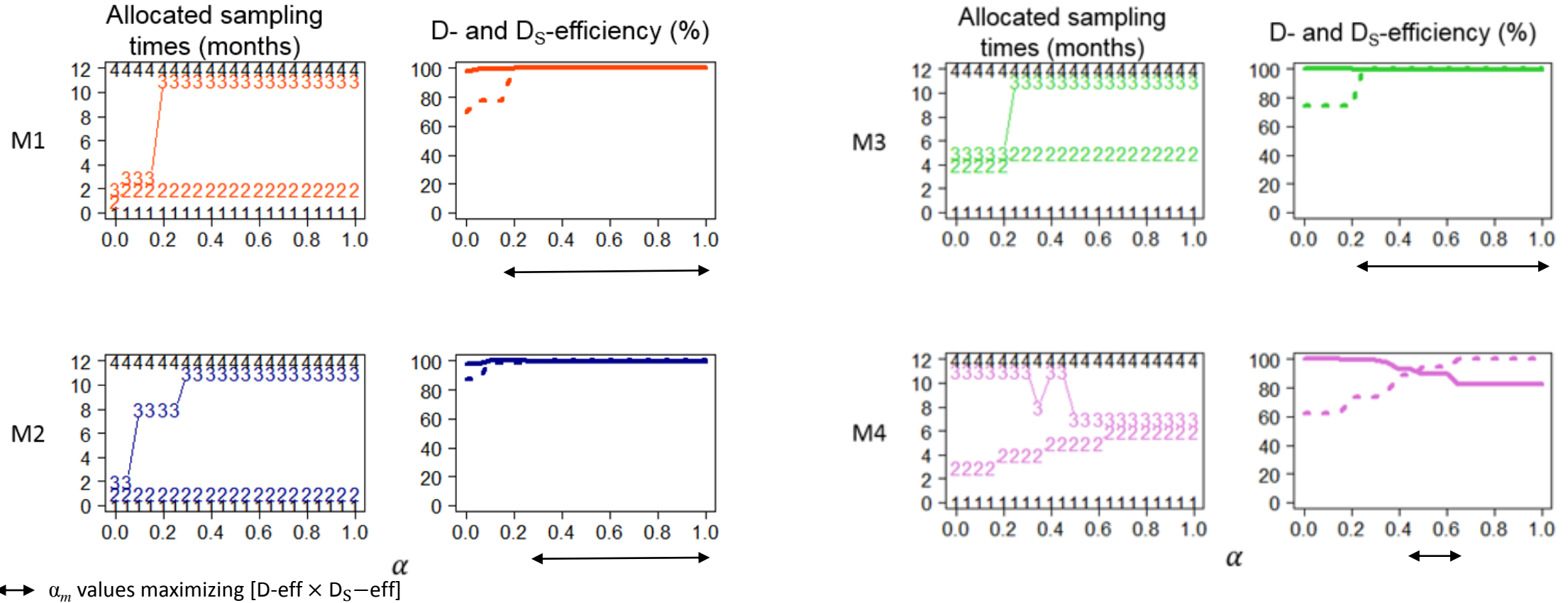
$\Longrightarrow$ DD_S- and CDD_S-optimality computed with α = 0.6

DD$_S$-efficiencies for each model ($\alpha = 0.6$)

M1

M2

M1: Linear
M2: Loglinear
M3: Quadratic
M4: Sigmoid Emax
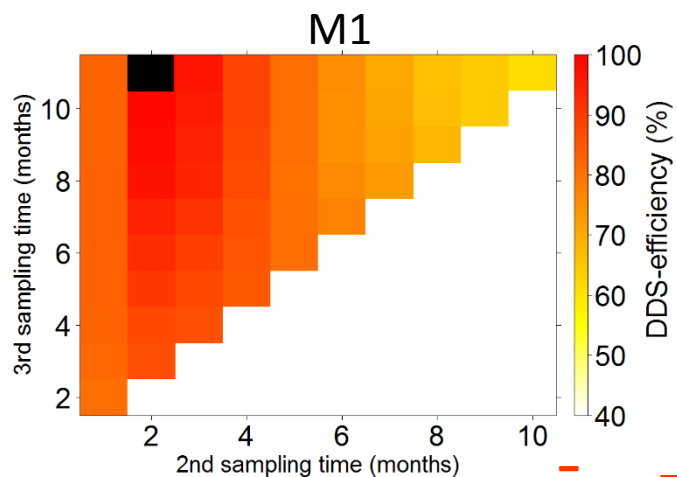
$\Xi_{DDs,1}=(0,2,11,12)$
$\Xi_{D,1}=(0,2,11,12)$, DD$_S$−eff($\Xi_{D,1}$) = 100%
$\Xi_{Ds,1}=(0,2,11,12)$, DD$_S$−eff($\Xi_{Ds,1}$) = 100%
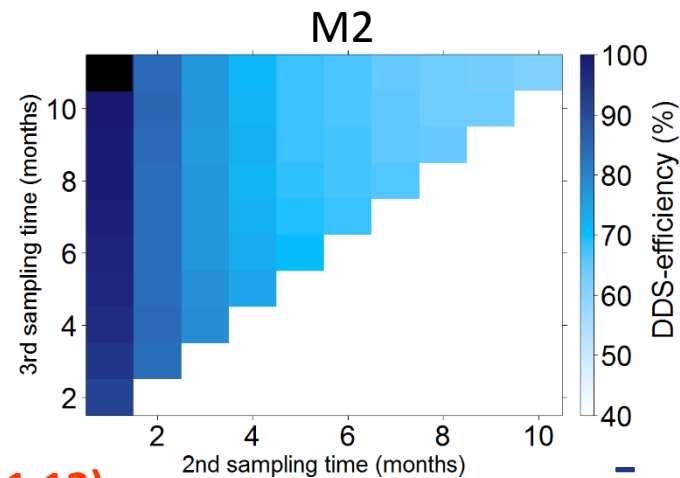
$\Xi_{DDs,2}=(0,1,11,12)$
$\Xi_{D,2}=(0,1,8,12)$, DD$_S$−eff($\Xi_{D,2}$)= 99.3%
$\Xi_{Ds,2}=(0,1,11,12)$, DD$_S$−eff($\Xi_{Ds,2}$) = 100%

M3

M4

$$DD_S-eff(\Xi)= \frac{\Phi_{DDs}(\Xi)}{\Phi_{DDs}(\Xi_{DDs})}$$

Ξ_{DDs} : DDs-optimal design
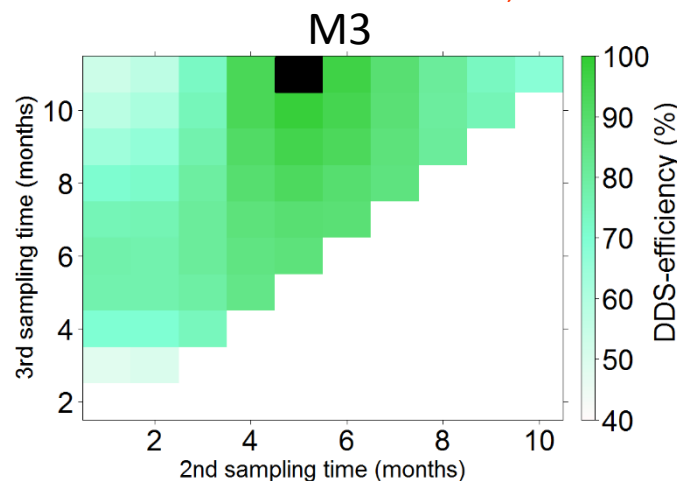
$\Xi_{DDs,3}=(0,5,11,12)$
$\Xi_{D,3}=(0,4,5,12)$, DD$_S$−eff($\Xi_{D,3}$)= 84.7%
$\Xi_{Ds,3}=(0,5,11,12)$, DD$_S$−eff($\Xi_{Ds,3}$) = 100%
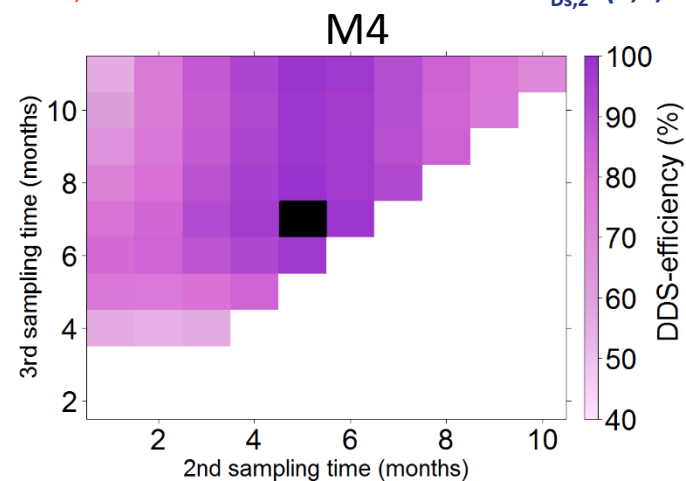
$\Xi_{DDs,4}=(0,5,7,12)$
$\Xi_{D,4}=(0,3,11,12)$, DD$_S$−eff($\Xi_{D,4}$)= 86.8%
$\Xi_{Ds,4}=(0,6,7,12)$, DD$_S$−eff($\Xi_{Ds,4}$)= 98.5%

CDD$_S$-efficiencies ($\alpha = 0.6$)

$\Xi_{CDDs}=(0,4,11,12)$

Final model DDs-optimal design for a pre-specified model	M1 Linear	M2 Loglinear	M3 Quadratic	M4 Sigmoid Emax
$\Xi_{DDs,1}=(0,2,11,12)$	100%	84.5%	**57.2%**	75.6%
$\Xi_{DDs,2}=(0,1,11,12)$	82.5%	100%	**53.4%**	**56.9%**
$\Xi_{DDs,3}=(0,5,11,12)$	81.0%	68.3%	100%	99.4%
$\Xi_{DDs,4}=(0,5,7,12)$	80.7%	69.2%	88.8%	100%
$\Xi_{CDDs}=(0,4,11,12)$	88.4%	71.5%	93.9%	93.7%
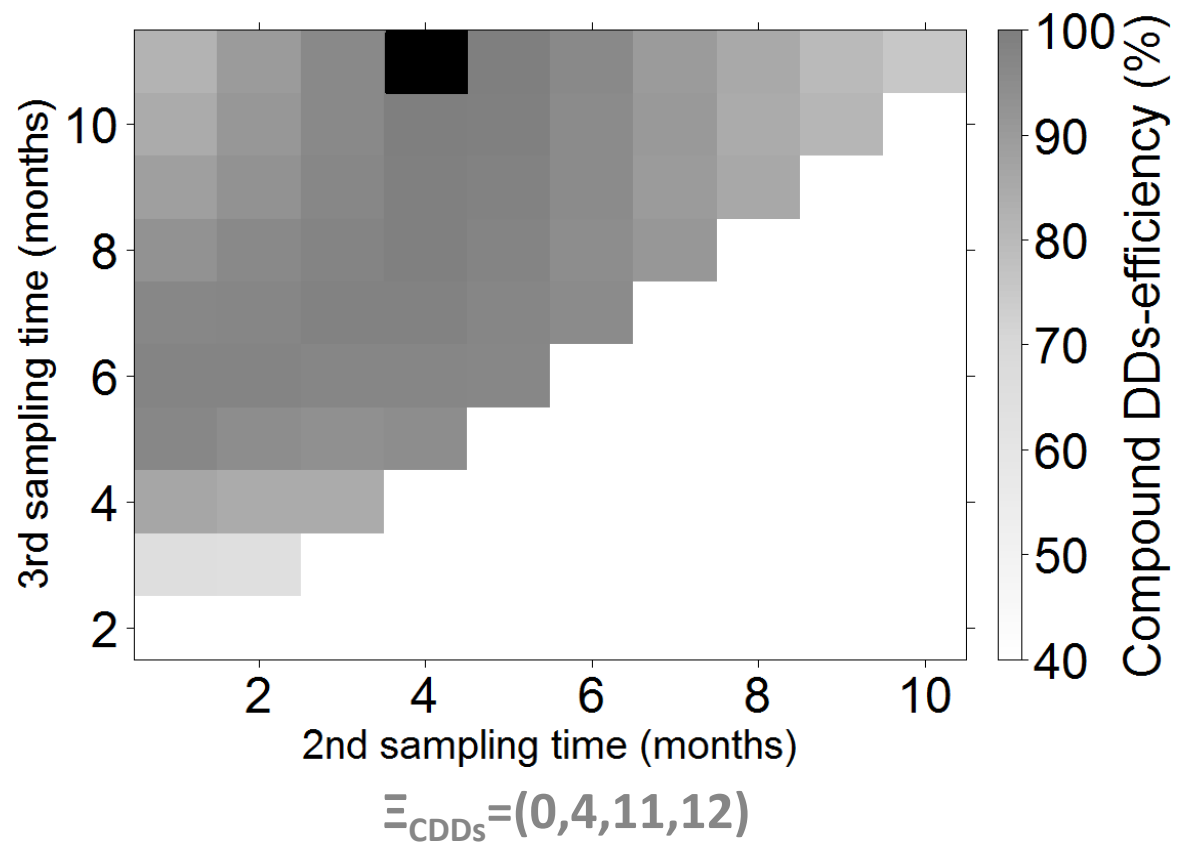
$$CDD_S-eff(\Xi)= \frac{\Phi_{CDDs}(\Xi)}{\Phi_{CDDs}(\Xi_{CDDs})}$$

Ξ_{CDDs} : CDDs-optimal design

Number of subjects needed to reach an average power of 80 %

M1: Linear
M2: Loglinear
M3: Quadratic
M4: Sigmoid Emax

$\Xi_{CD}=(0,1,5,12)$

$\Xi_{CDDs}=(0,4,11,12)$

$NSN_{average}\ (\Xi_{CD}) = 200$

$NSN_{average}\ (\Xi_{CDDs}) = 188$
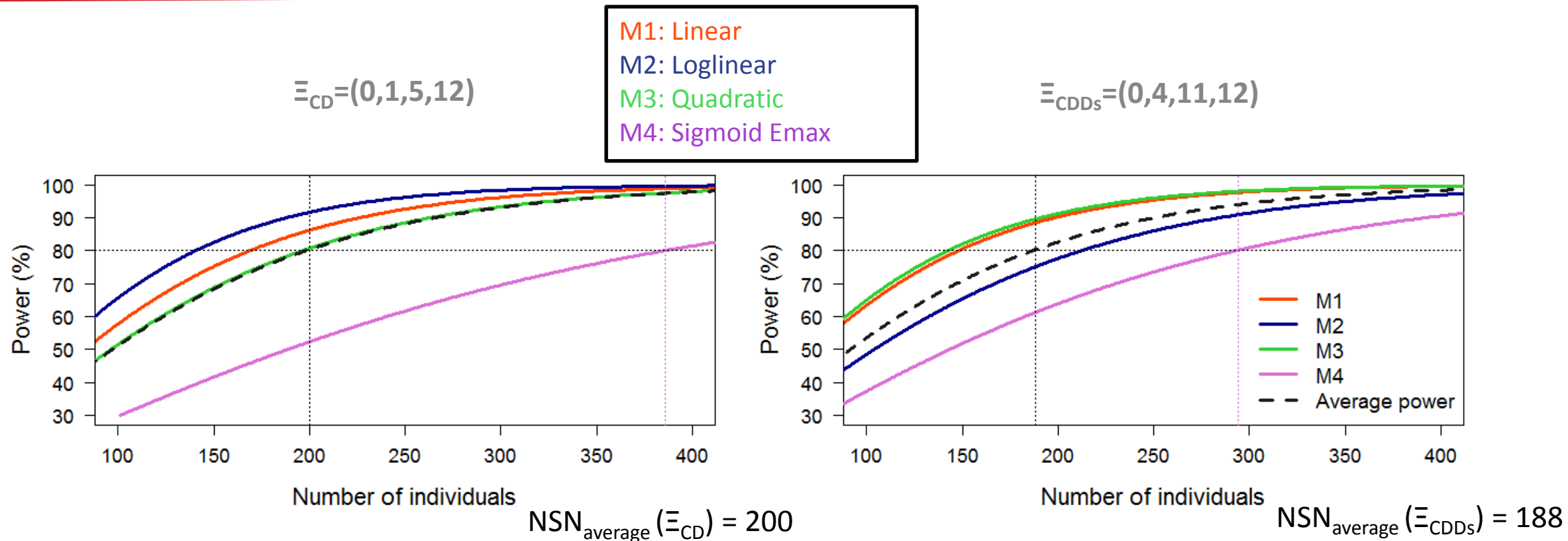
- Robust designs accounting for model uncertainty

- Balance between the parameters precision and the power of the Wald test

- Next steps:

  - To take into account the parameters uncertainty

  - To perform clinical trials simulations

- **Discussion**

  - MC-HMC method for computation of FIM [7] enables applications to design optimization for discrete data

  - Extension of this method to propose robust designs accounting for uncertainty w.r.t. parameters and/or models / balance between the parameters precision and the power of the Wald test

  - Computationally challenging, much slower than FO approach

- **Perspectives**

  - Implementation of an optimization algorithm: sparse grids – particle swarm optimization [18]

  - Replacement of MC by more efficient approach: quasi-random sampling [19]

  - Application to other type of data (continuous, time to event)

  - Use in model based adaptive design [20-22]/ model averaging [23]

7: Riviere M-K. Ueckert S. and Mentré F., Biostatistics, 2016
18: Shi Y., Zhang Z. and Wong W.K., BIRS Design Workshop, Canada, 2017
19: Ueckert S. and Mentré F., CM Statistics Conference, UK, 2015

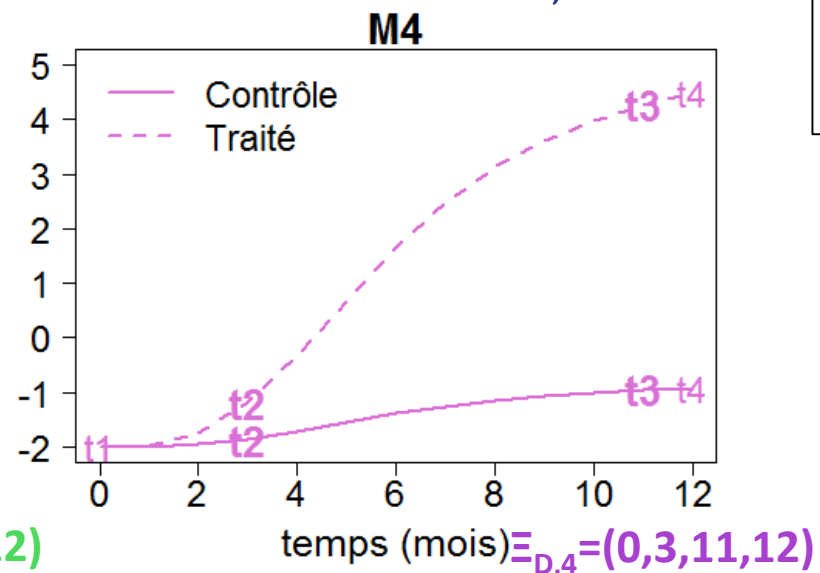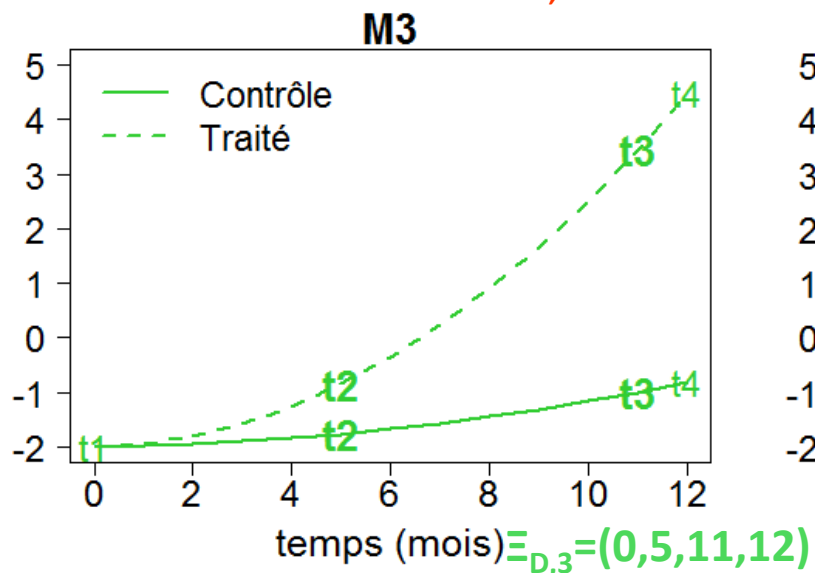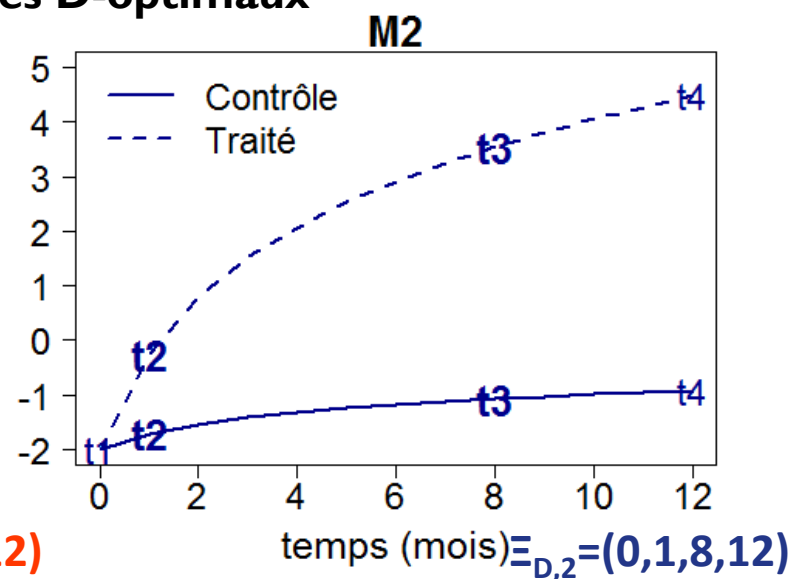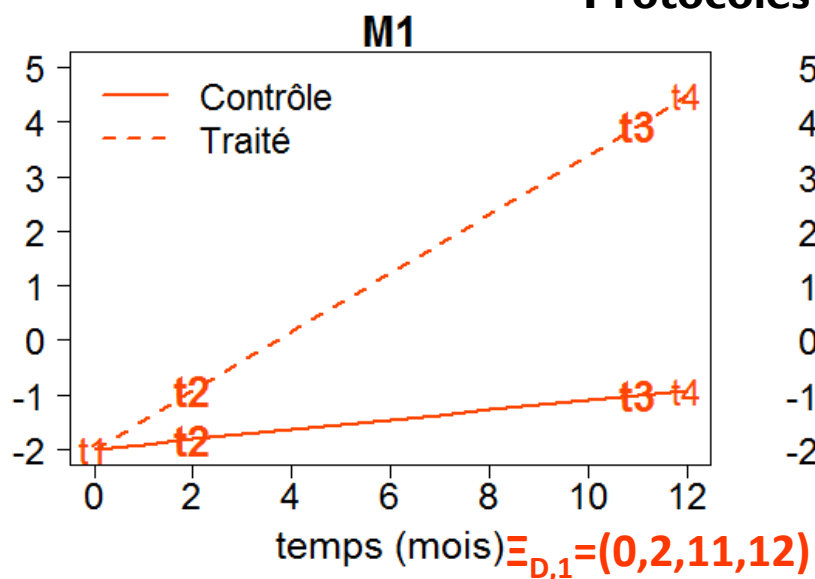20: Lestini G., Dumont C. and Mentré F., Pharm Res, 2015
21: Dumont C. *et al.,* Commun Stat Simul Comput, 2016
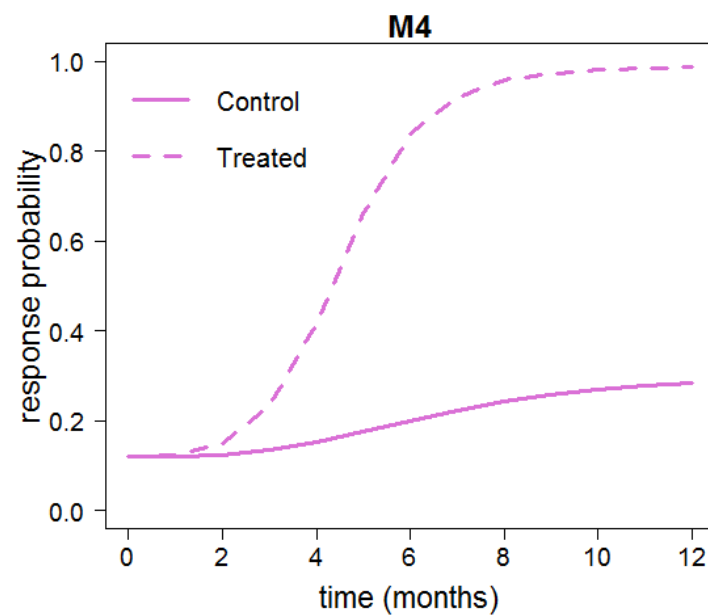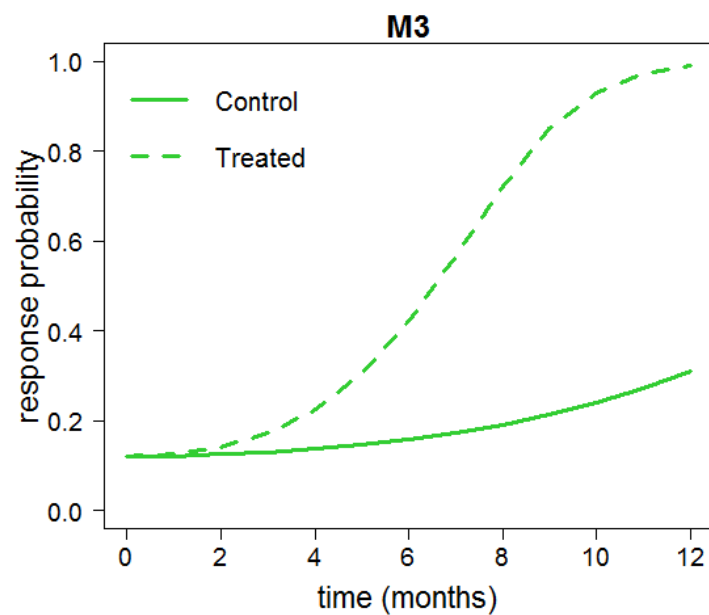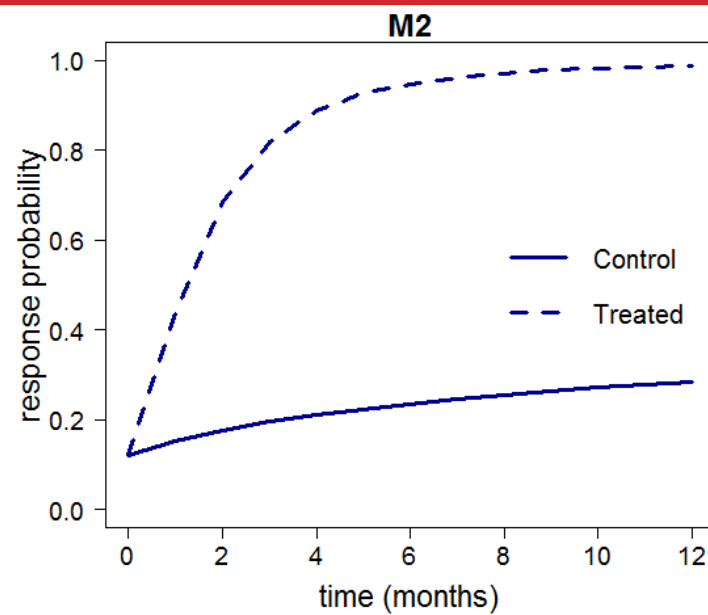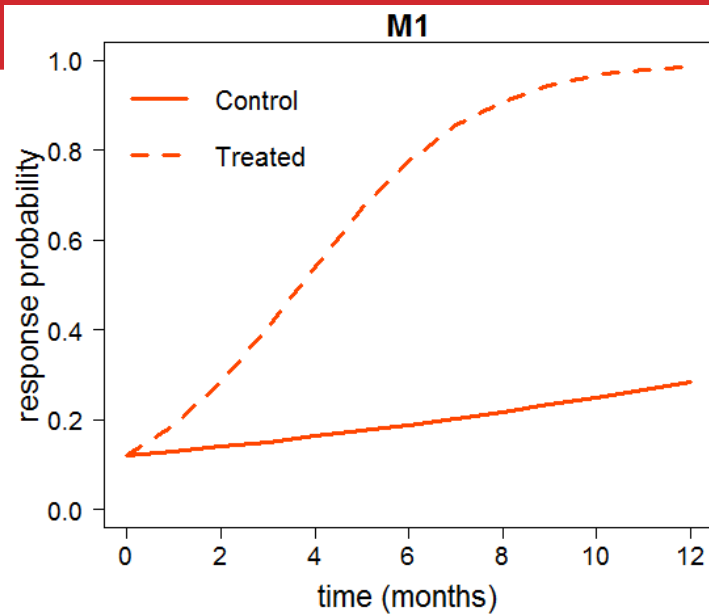22: Strömberg E.A. and Hooker A.C., JPKPD, 2017

23: Buckland S.T., Burnham K.P. and Augustin N.H., Biometrics, 1997

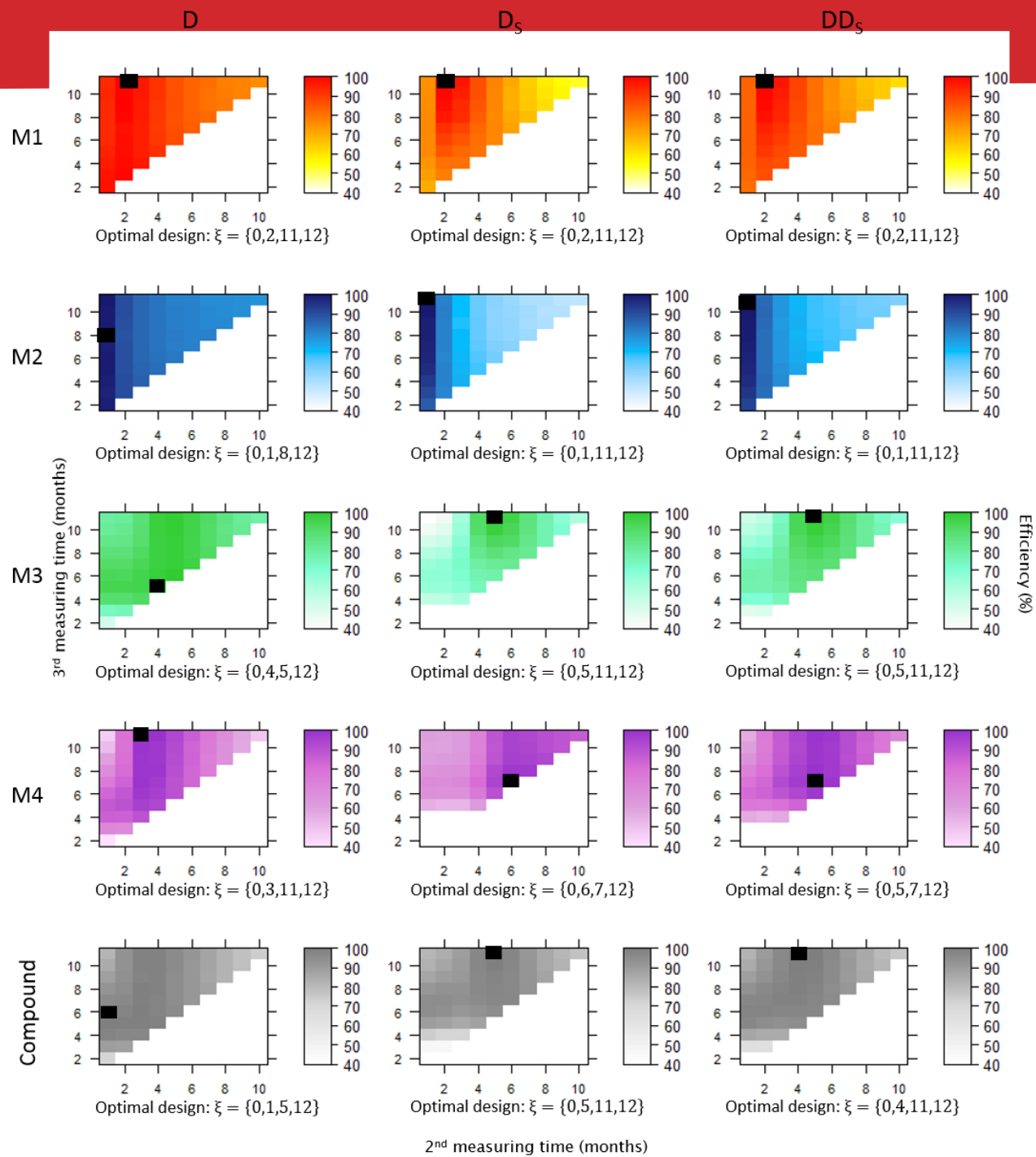# Thank you for your attention

Protocoles D-optimaux

D-efficacité

Protocole D-optimal du modèle *a priori* \ Modèle final	M1 Linéaire	M2 Loglinéaire	M3 Quadratique	M4 Emax sigmoïde
$\xi_{D,1}=(0,2,11,12)$	100 %	89,8 %	81,2 %	79,1 %
$\xi_{D,2}=(0,1,8,12)$	93,2 %	100 %	87,5 %	68,0 %
$\xi_{D,3}=(0,4,5,12)$	91,6 %	83,4 %	100 %	93,1 %
$\xi_{D,4}=(0,3,11,12)$	96,3 %	85,2 %	88,4 %	100 %
$\xi_{CD}=(0,1,5,12)$	94,0 %	98,9 %	95,1 %	86,9 %
$\xi_{CDDs}=(0,4,11,12)$	91,0 %	82,8 %	97,7 %	99,5 %

NSN pour une puissance de 80 % du test de Wald

	M1	M2	M3	M4
$\xi_{CD}=(0,1,5,12)$	170	142	198	386
$\xi_{CDDs}=(0,4,11,12)$	150	214	144	294

➡ Simulations d'essais cliniques avec le protocole CDD$_S$-optimal $\xi_{CDDs}=(0,4,11,12)$ et 294 patients

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D-efficacité : rapport de la D-optimalité d'un protocole **ξ** sur celle du protocole D-optimal $\xi_{D,m}$ du modèle m

- Clinical trial simulations (CTS) : For each candidate model, 500 datasets with a treatment effect (under H_1) and 500 without treatment effect (under H_0)
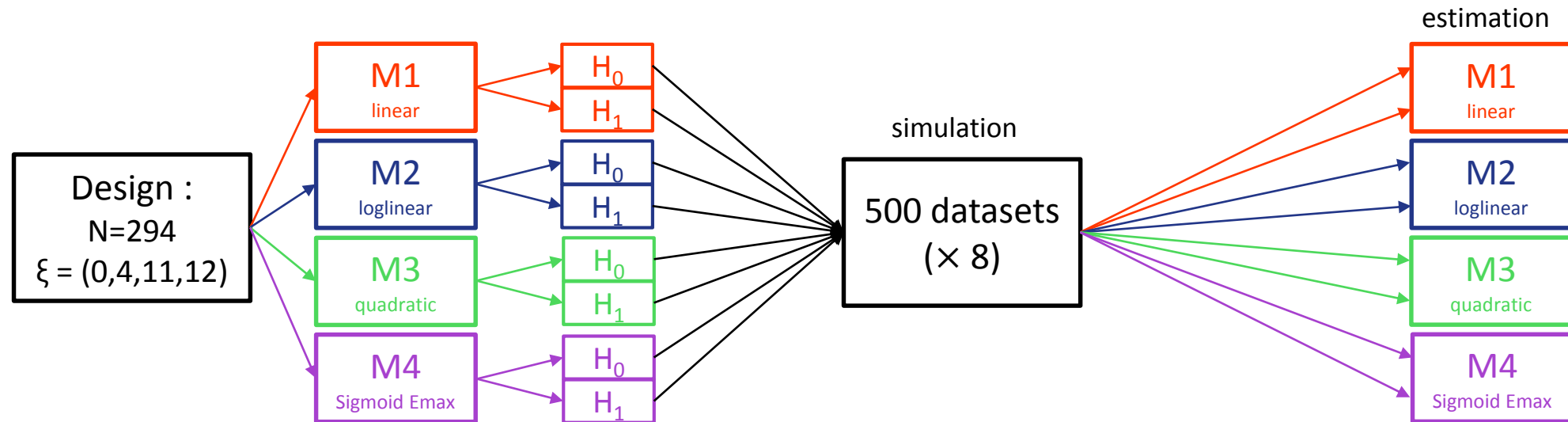
- Estimation of the parameters of each candidate model, by maximum likelihood (SAEM algorithm of MONOLIX 2016R1)

- Comparison between predictions by FIM and results with CTS

RSE : Relative Standard Error
Predicted RSE by computation of the **FIM**
Empirical RSE from the standard deviation of parameter estimations on **simulations**
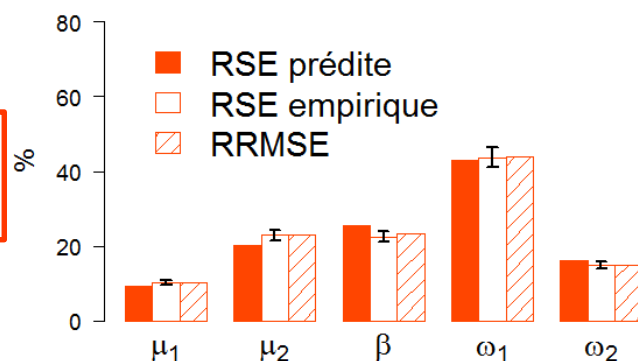RRMSE : Relative root mean square error
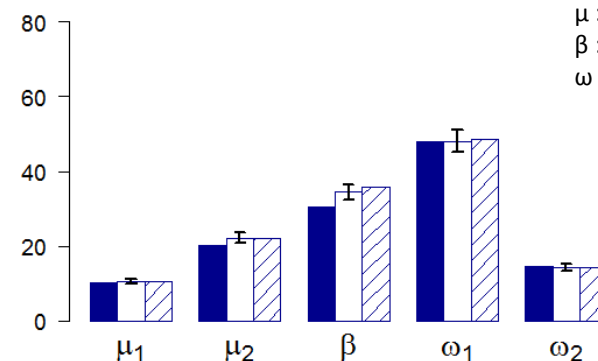
Parameters
μ : fixed effects
β : treatment covariate effect
ω : standard error of random effects (interindividual variability)

M1 linear
M2 loglinear
M3 quadratic
M4 Sigmoid Emax
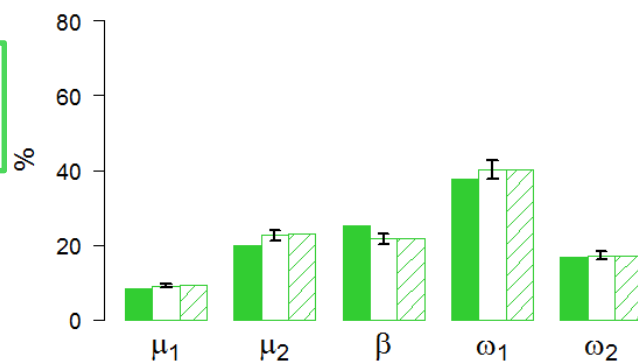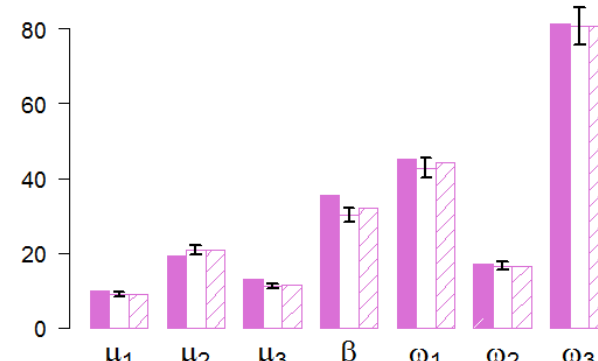
- RSE prédite
- RSE empirique
- RRMSE
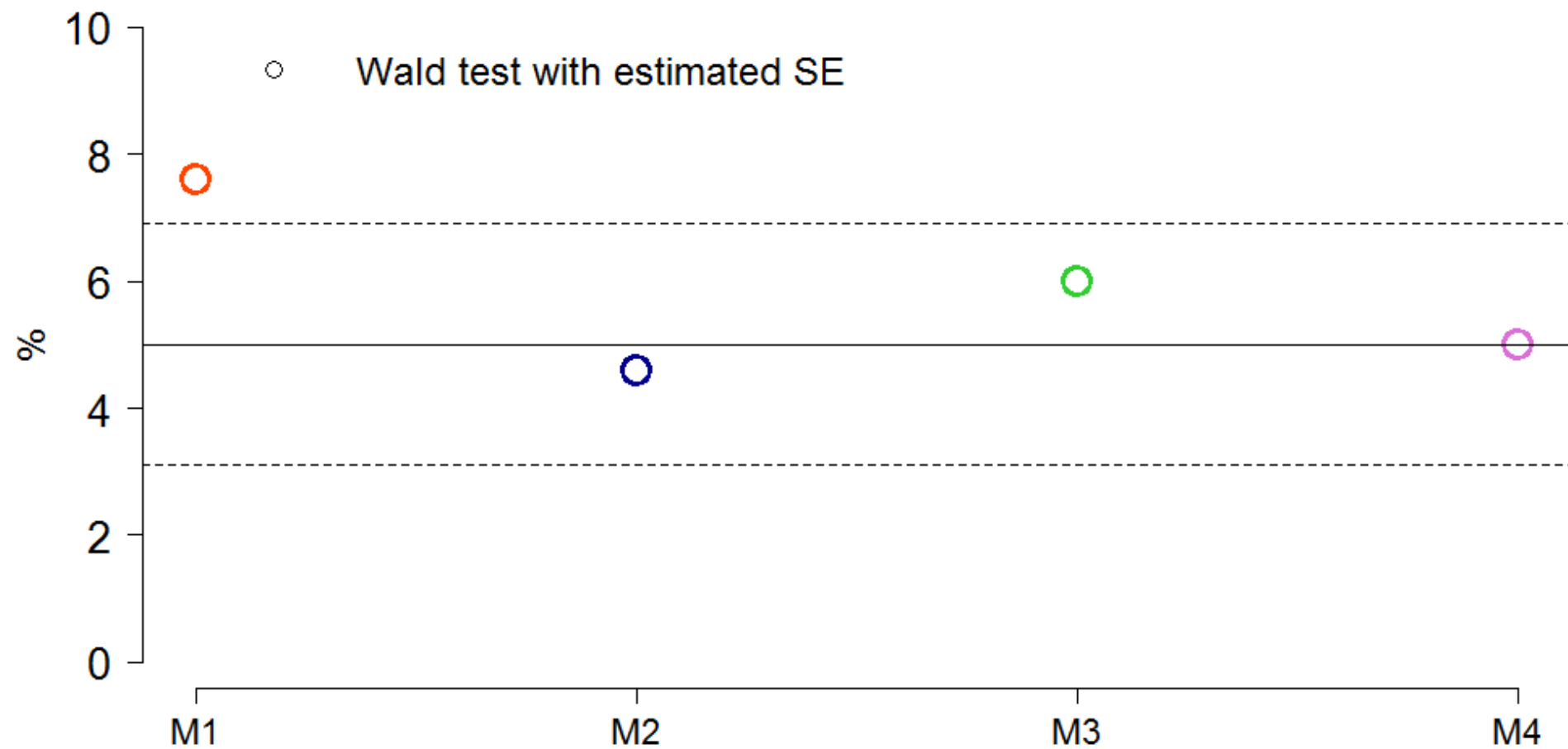
	FIM Predicted power (%)	CTS Observed power using estimated SE [CI_{95}] (%)
M1	97.7	99.8 [98.9;100]
M2	90.9	98.4 [96.9;99.3]
M3	97.8	99.6 [98.6;100]
M4	80.1	86.3 [83.0;89.2]

CTS Observed power = Proportion of significant Wald tests with a type I error of 5 %

Travaux de méthodologie : Développer une approche robuste et adaptative tenant compte de l'incertitude du modèle et des valeurs de paramètres

Planification de design prenant en compte l'incertitude du modèle et des paramètres

Incorporation de ces méthodes robustes dans la planification adaptative
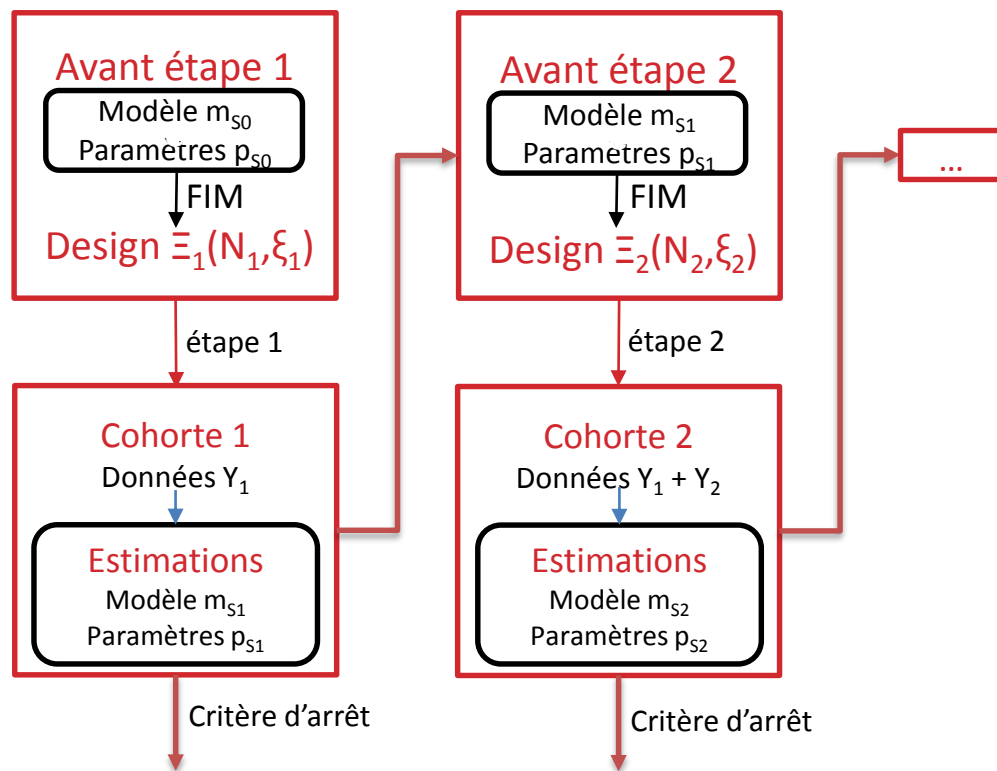
Schéma adaptatif **non** robuste

Travaux de méthodologie : Développer une approche robuste et adaptative tenant compte de l'incertitude du modèle et des valeurs de paramètres

Planification de design prenant en compte l'incertitude du modèle et des paramètres

Incorporation de ces méthodes robustes dans la planification adaptative

Schéma adaptatif **robuste**
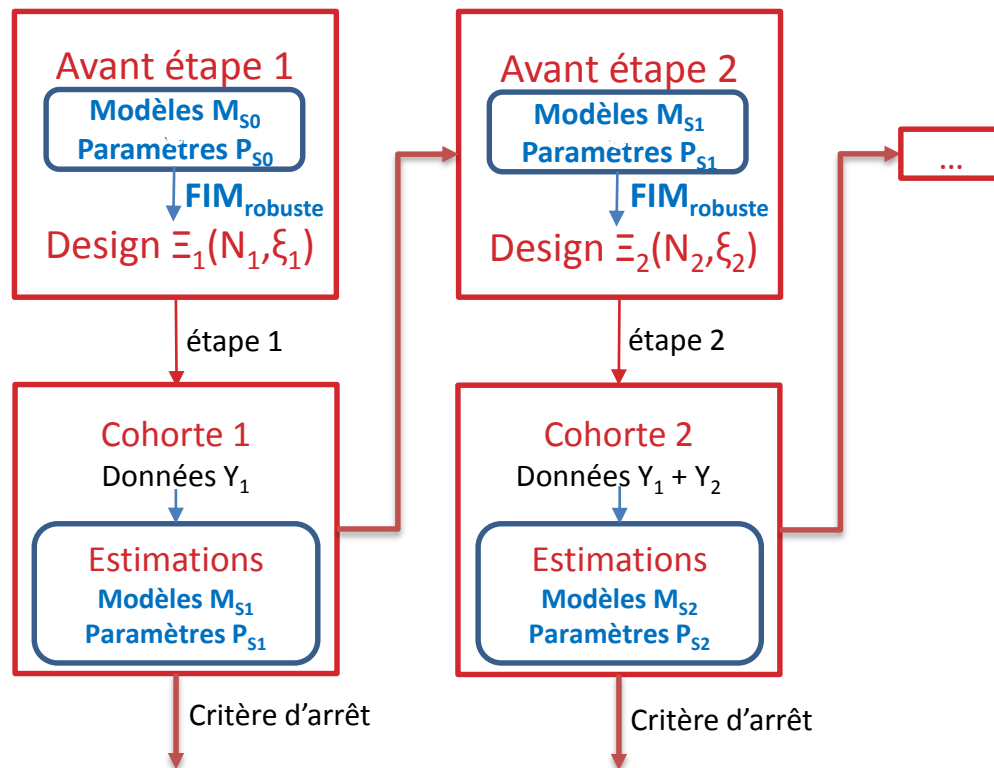
- **Extension du schéma de planification non robuste** [8]

  - Prise en compte de l'incertitude du modèle et des paramètres à chaque étape

  - Méthode de « model averaging » [9]

  - Influence du nombre d'étapes S et de la taille de chaque cohorte N_s

  - Étude des critères d'arrêt

  - Évaluation par CTS

8 : Lestini G. *et al.,* Pharm Res, 2015

9 : Buckland S.T. *et al.*, Biometrics, 1997

Predicted RSE (N=100)

Table A1. Predicted relative standard errors (%) of candidate models parameters

Model	RSE Optimal design	μ_1	μ_2	μ_3	β	ω_1^2	ω_2^2	ω_3^2
M1	$\Xi_{D,1} = (0,2,11,12)$	15	34	-	40	136	56	-
	$\Xi_{DS,1} = (0,2,11,12)$	15	34	-	40	136	56	-
	$\Xi_{DDS,1} = (0,2,11,12)$	15	34	-	40	136	56	-
	$\Xi_{CD} = (0,1,5,12)$	14	37	-	46	121	71	-
	$\Xi_{CDS} = (0,5,11,12)$	16	35	-	46	153	54	-
	$\Xi_{CDDS} = (0,4,11,12)$	16	35	-	43	147	55	-
M2	$\Xi_{D,2} = (0,1,8,12)$	15	34	-	42	139	56	-
	$\Xi_{DS,2} = (0,1,11,12)$	15	34	-	42	144	55	-
	$\Xi_{DDS,2} = (0,1,11,12)$	15	34	-	42	144	55	-
	$\Xi_{CD} = (0,1,5,12)$	15	35	-	42	139	58	-
	$\Xi_{CDS} = (0,5,11,12)$	18	35	-	54	169	49	-
	$\Xi_{CDDS} = (0,4,11,12)$	17	35	-	52	164	50	-
M3	$\Xi_{D,3} = (0,4,5,12)$	13	38	-	47	111	80	-
	$\Xi_{DS,3} = (0,5,11,12)$	15	34	-	41	135	58	-
	$\Xi_{DDS,3} = (0,5,11,12)$	15	34	-	41	135	58	-
	$\Xi_{CD} = (0,1,5,12)$	13	38	-	50	108	82	-
	$\Xi_{CDS} = (0,5,11,12)$	15	34	-	41	135	58	-
	$\Xi_{CDDS} = (0,4,11,12)$	15	34	-	43	130	57	-
M4	$\Xi_{D,4} = (0,3,11,12)$	16	32	24	66	140	59	269
	$\Xi_{DS,4} = (0,6,7,12)$	18	39	28	52	172	72	290
	$\Xi_{DDS,4} = (0,5,7,12)$	17	37	25	54	164	71	283
	$\Xi_{CD} = (0,1,5,12)$	14	38	31	70	120	89	266
	$\Xi_{CDS} = (0,5,11,12)$	18	34	22	55	169	58	283
	$\Xi_{CDDS} = (0,4,11,12)$	17	33	22	61	155	59	279