

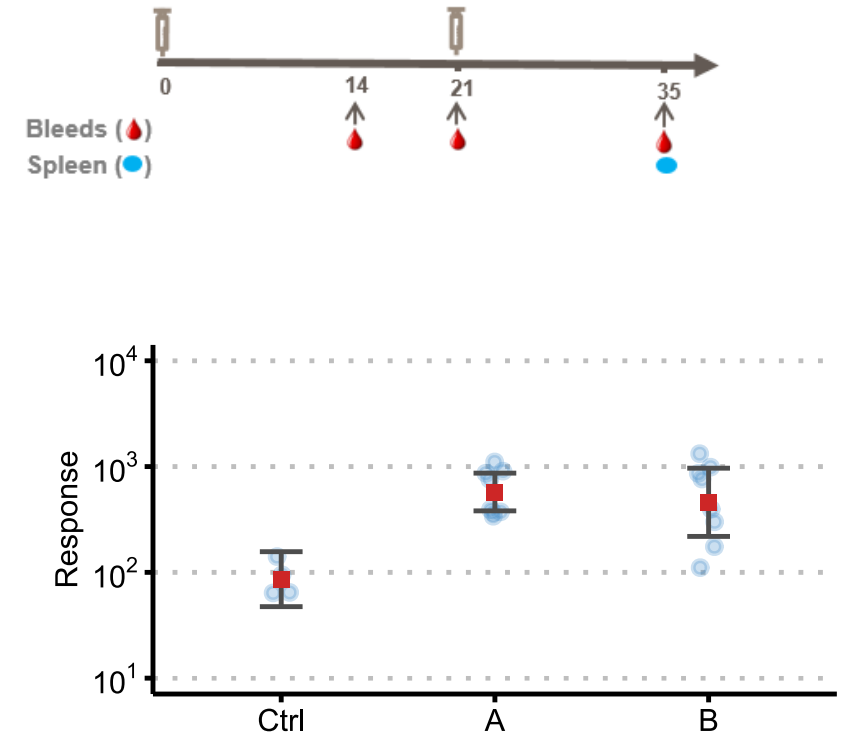


Longitudinal Analysis of *In Vivo* mRNA Expression Data Using Bayesian P-Splines

Hakem Ben Addi, Steve Lenhard, Emiliano Chiarot, Laura Lessen, Yamina Bennasser, Sonia Budroni & Cédric Taverne

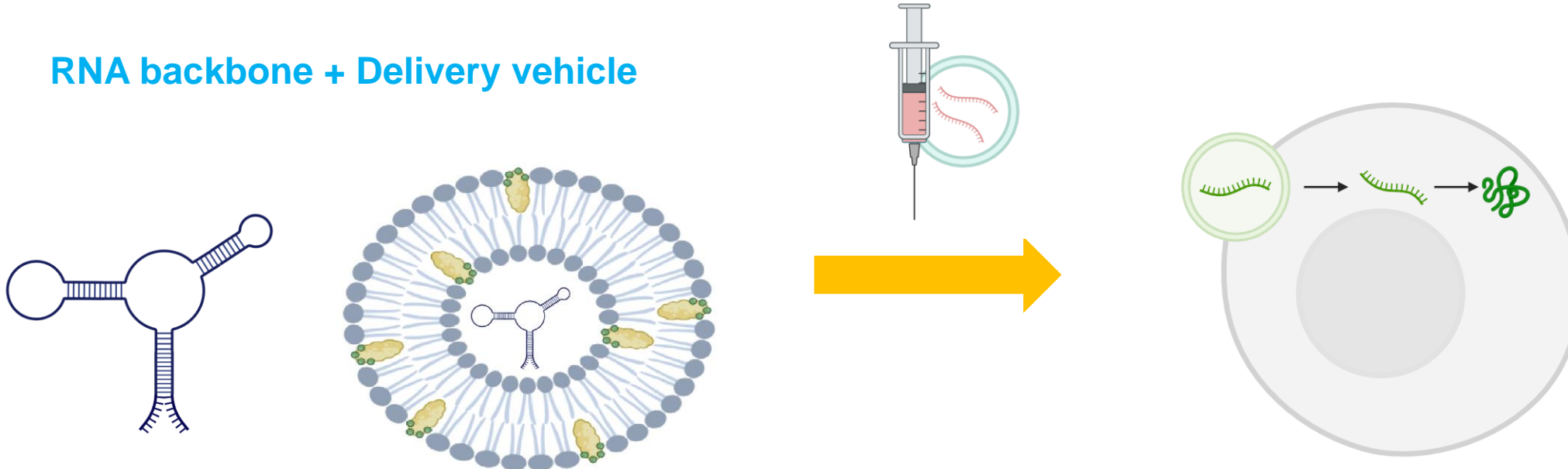
Vaccines in the Preclinical Research Setup

- Vaccine immunogenicity
= Ability to induce an immune response
- Mainly assessed in small animal models
on limited sample sizes (≤ 10 / group)
- Inbred mice (Balb/c, C57BL/6)
- Responses: Antigen-specific antibodies in sera, cellular
responses (T cells,...) in the spleen, bacterial load...



RNA Vaccines: Expression and timing

RNA backbone + Delivery vehicle



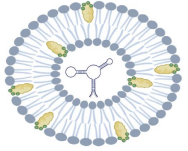
Challenges

- **Low expression level**
- (Innate immune sensing)

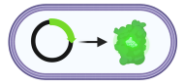
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In Vivo tracking of particles by BioLuminescent Imaging (BLI)

mRNA coding for bioluminescent Luciferase
+ substrate



OR

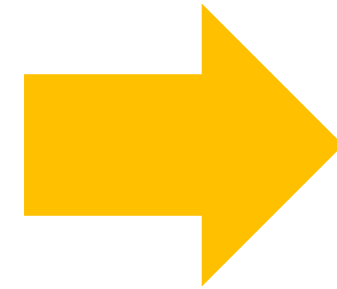
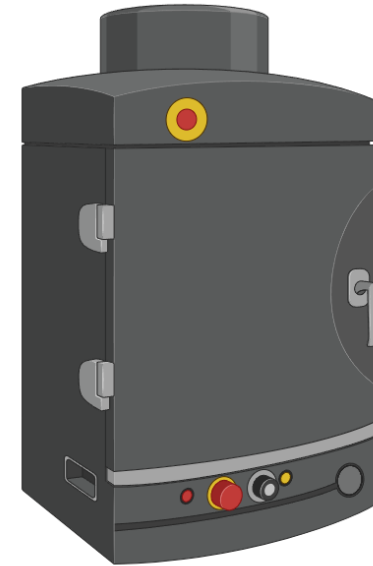
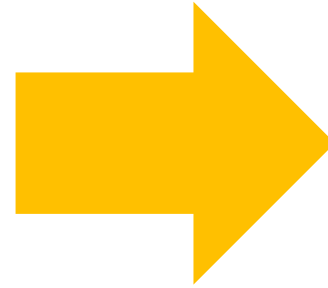


Bioluminescent engineered bacteria



In Vivo Imaging system

(acquisition of light signal)

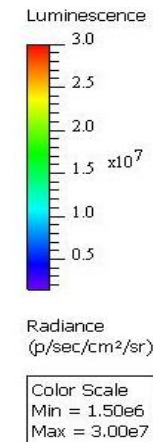
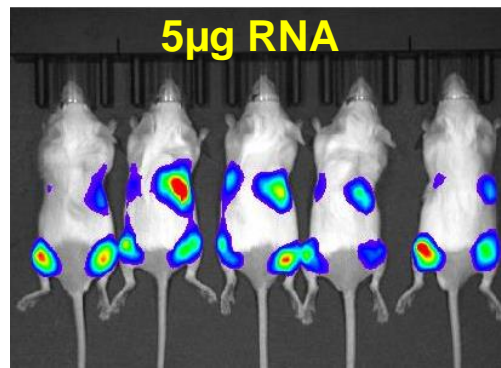
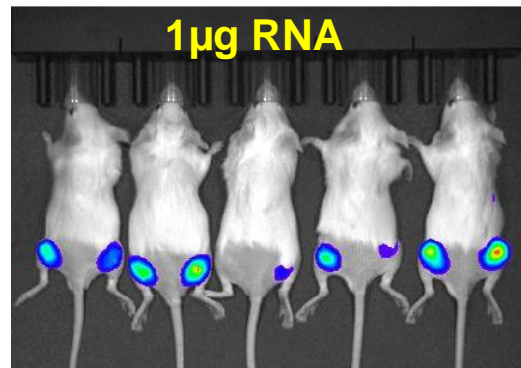
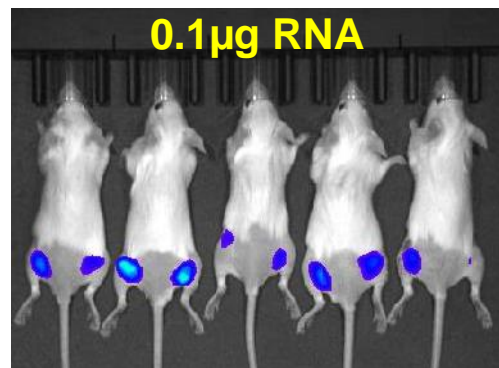


Data

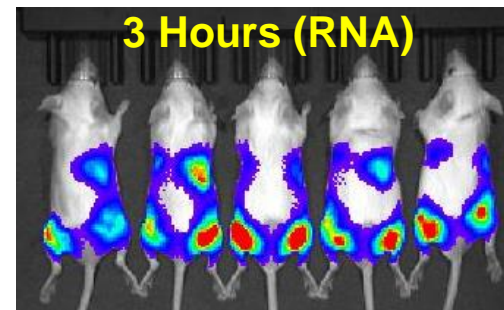
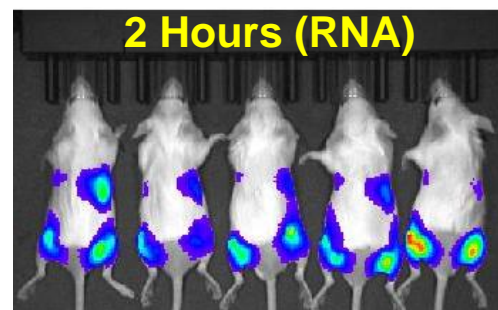
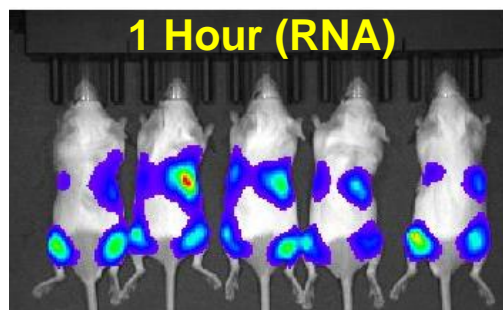
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In Vivo BioLuminescent Imaging (BLI)

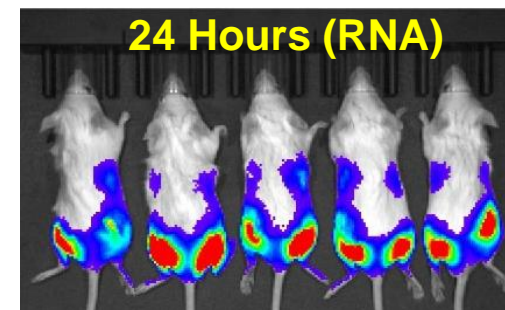
Proportionality of response signal to “treatment”



Kinetic of response signal

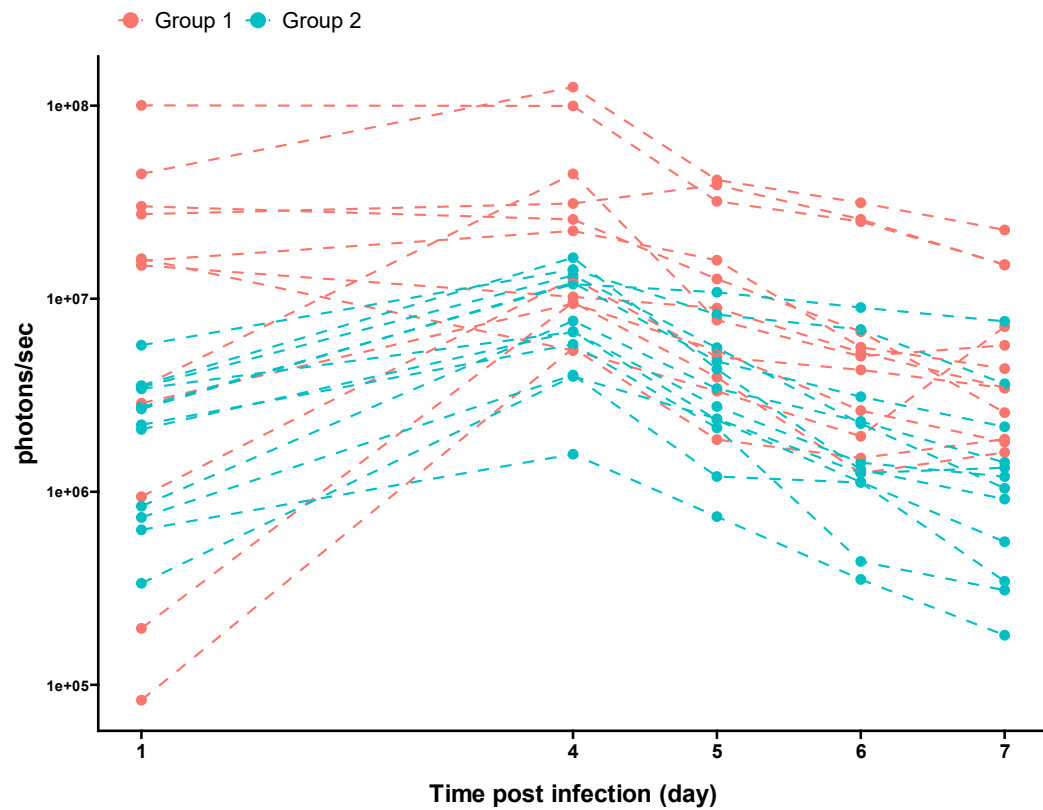


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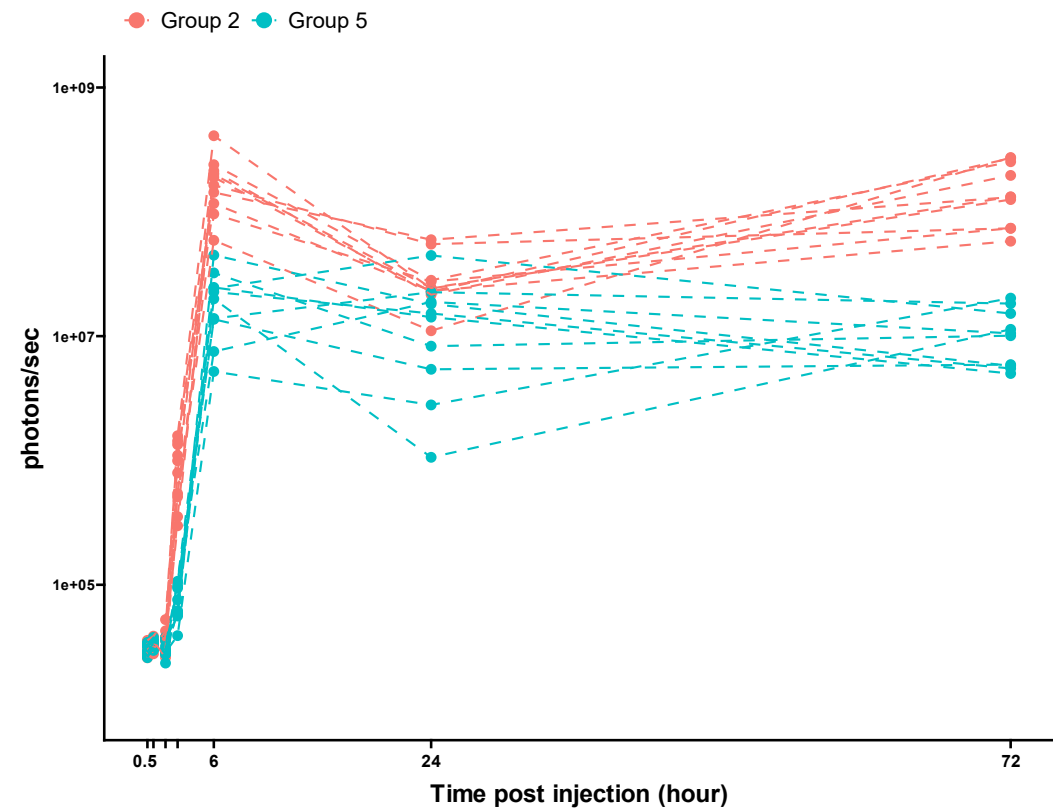


Diversity of response profiles

Bacterial infection study 1



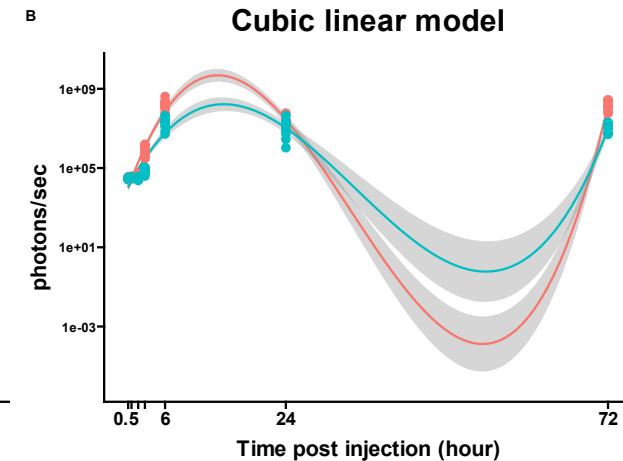
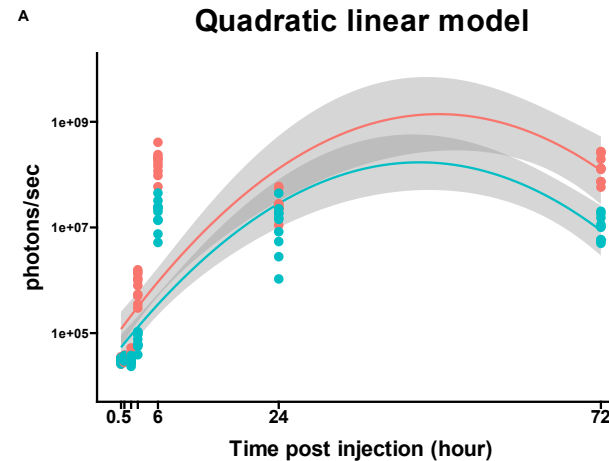
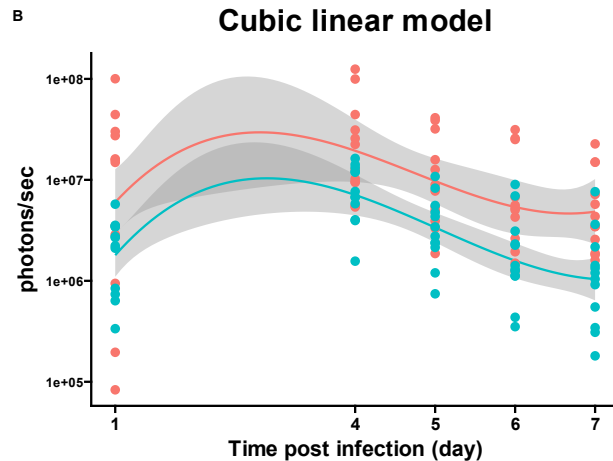
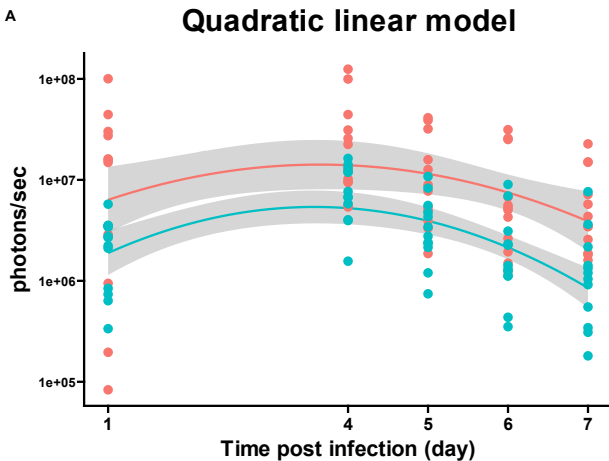
RNA vaccine study



Fitting Models

Bacterial infection study 1

RNA vaccine study



Increase polynomial order?

$$y_i = \beta_0 + \beta_1 x + \beta_2 x^2 + \beta_3 x^3 + \dots + \beta_k x^k + \epsilon_i$$

Devise a mathematical model for each response profile?

Generalized Additive Models (GAM)

smooth functions \leftarrow

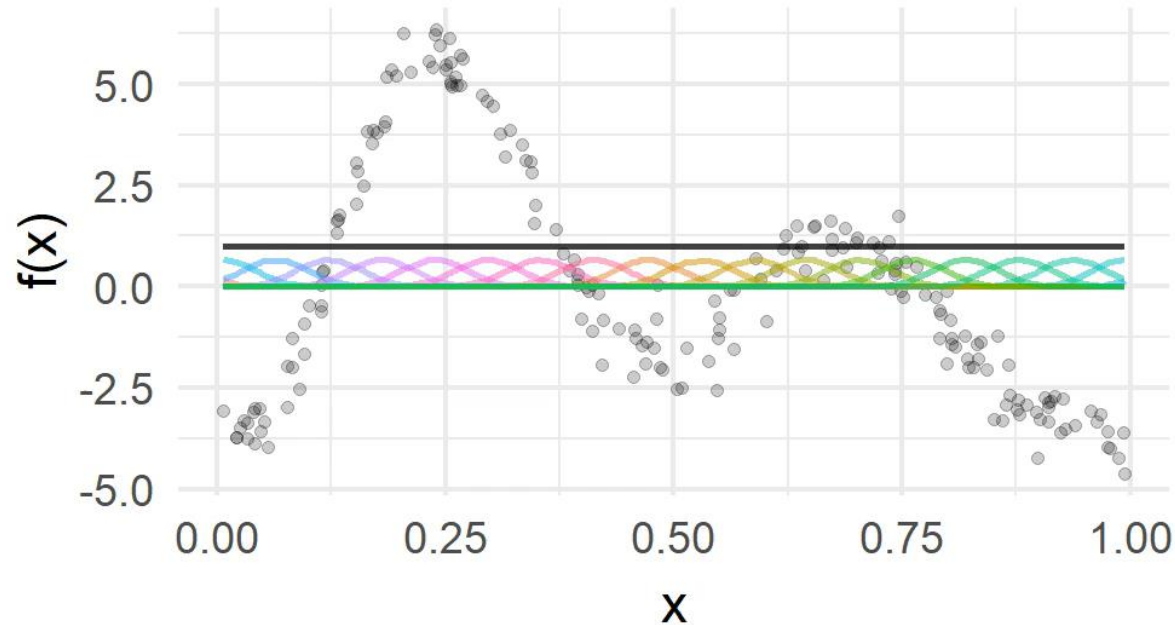
$$g(y_i) = \beta_0 + \sum_j s_j(x_{ji}) + \epsilon_i$$

"weighting" \rightarrow

base functions \rightarrow

$$s(x) = \sum_k^K \beta_k b_k(x)$$

with $\epsilon_i \sim N(0, \sigma^2)$



Adapted from: [Introduction to Generalized Additive Models with R and mgcv](#) – YouTube channel [Bottom of the Heap](#) by Gavin Simpson, University of Regina - Canada

“Smoothing” parameters estimation

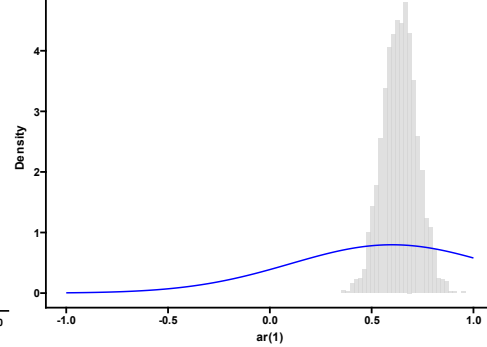
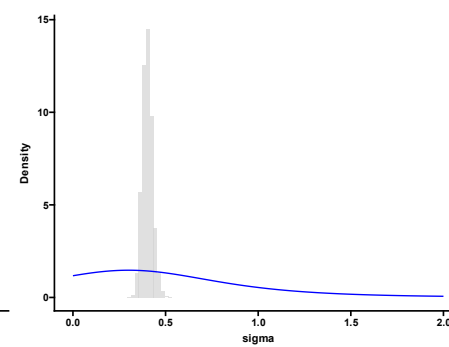
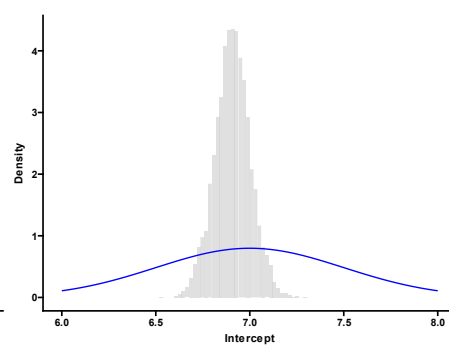
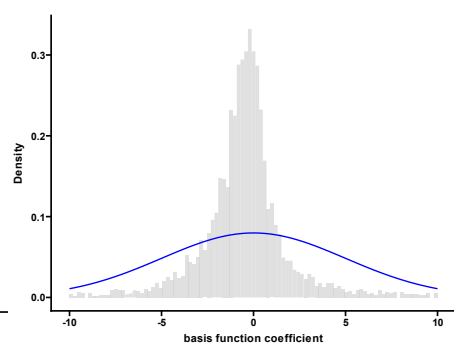
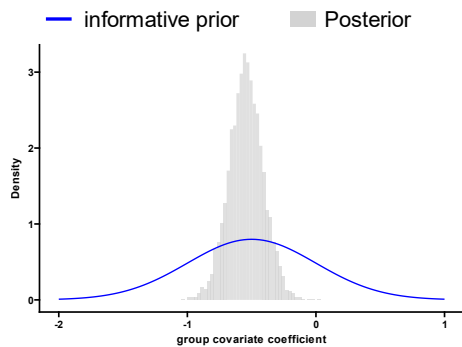
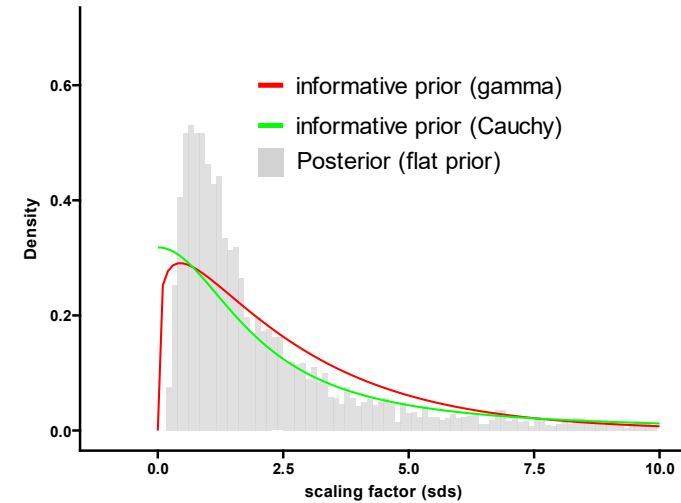
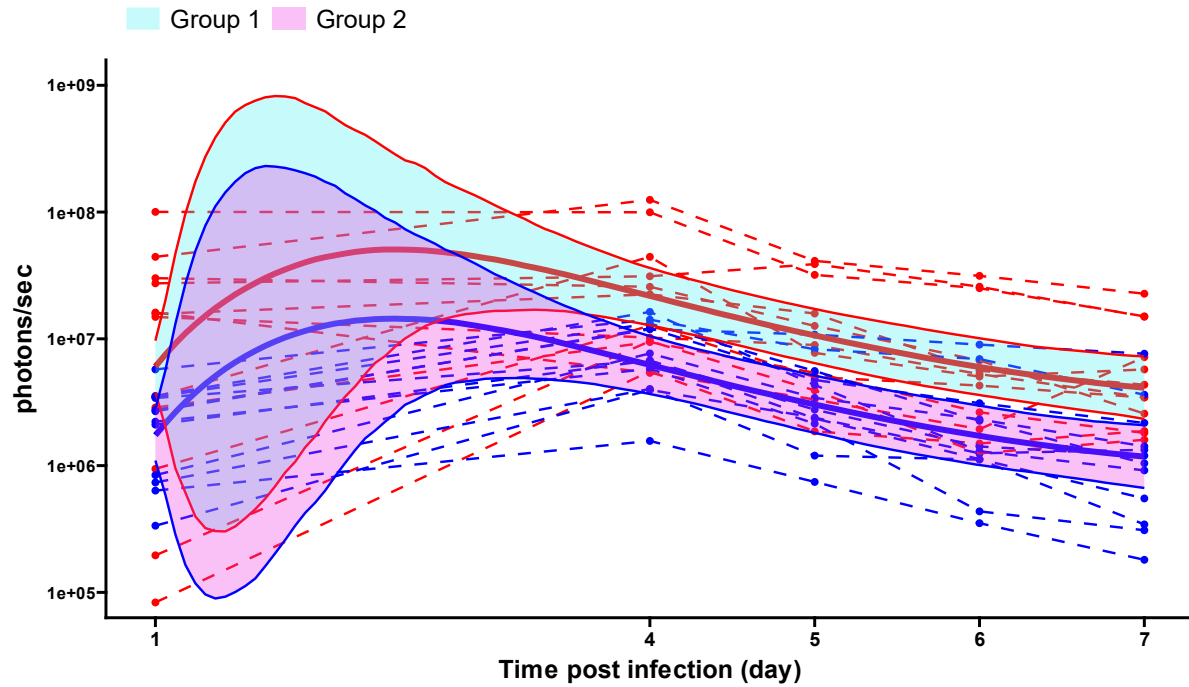
$$\mathcal{L}_p(\beta, \lambda) = \mathcal{L}(\beta) \exp(-\beta \mathcal{S}_\lambda \beta)$$

penalty \leftarrow wiggleness \rightarrow

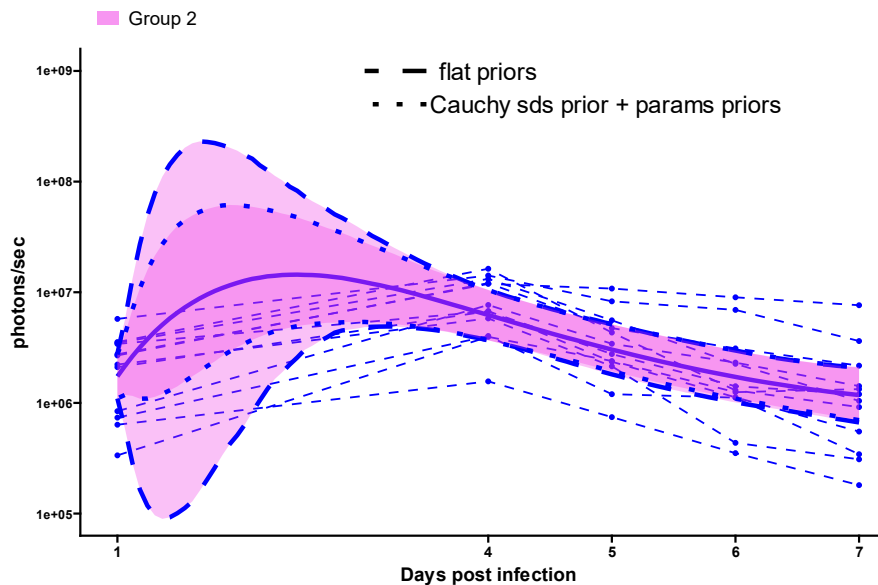
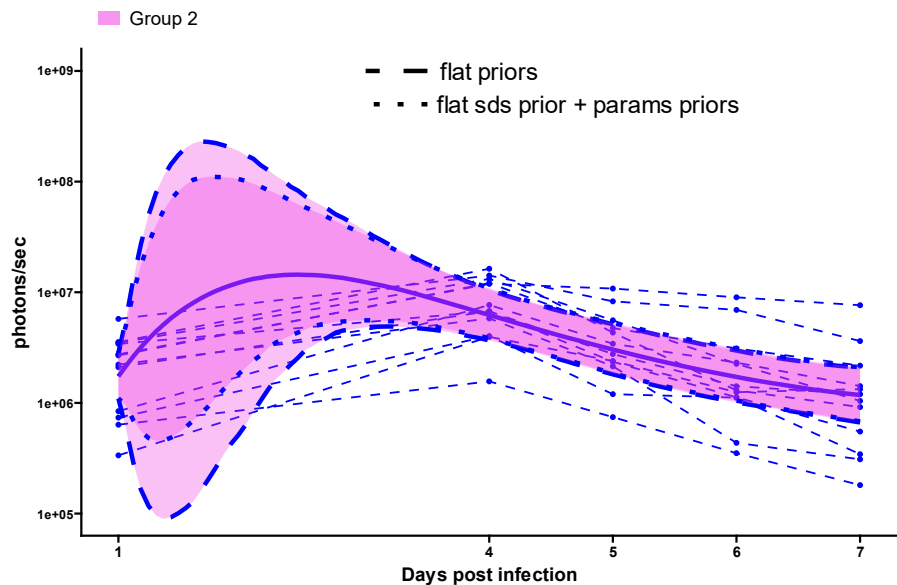
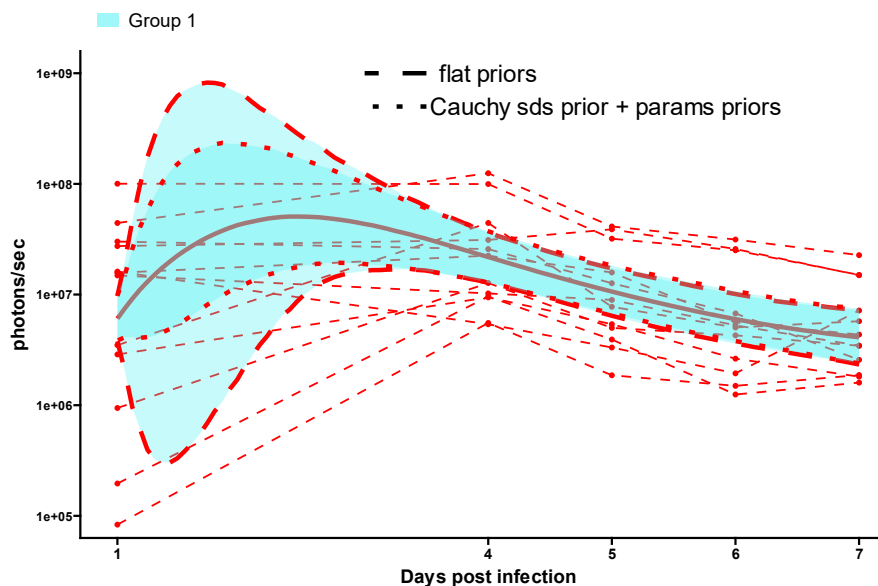
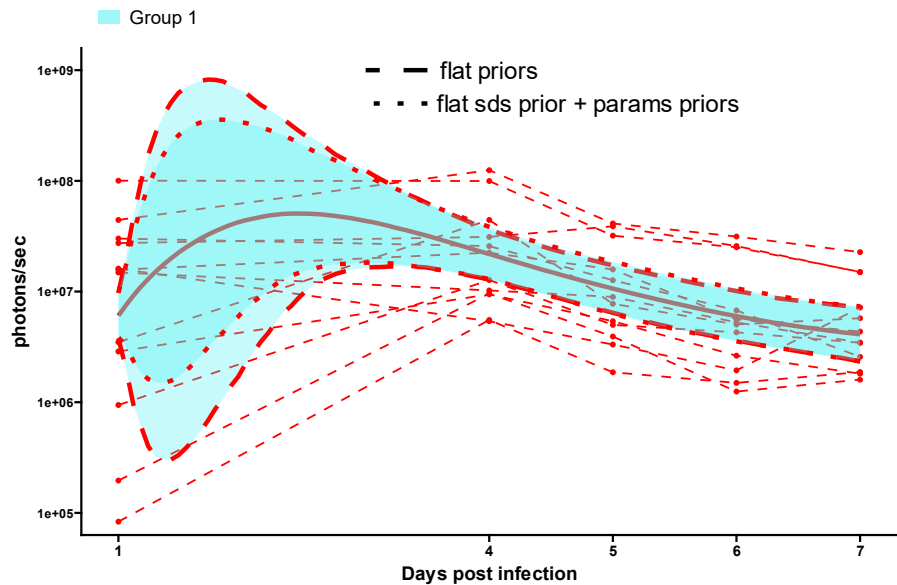


Building the priors for future studies

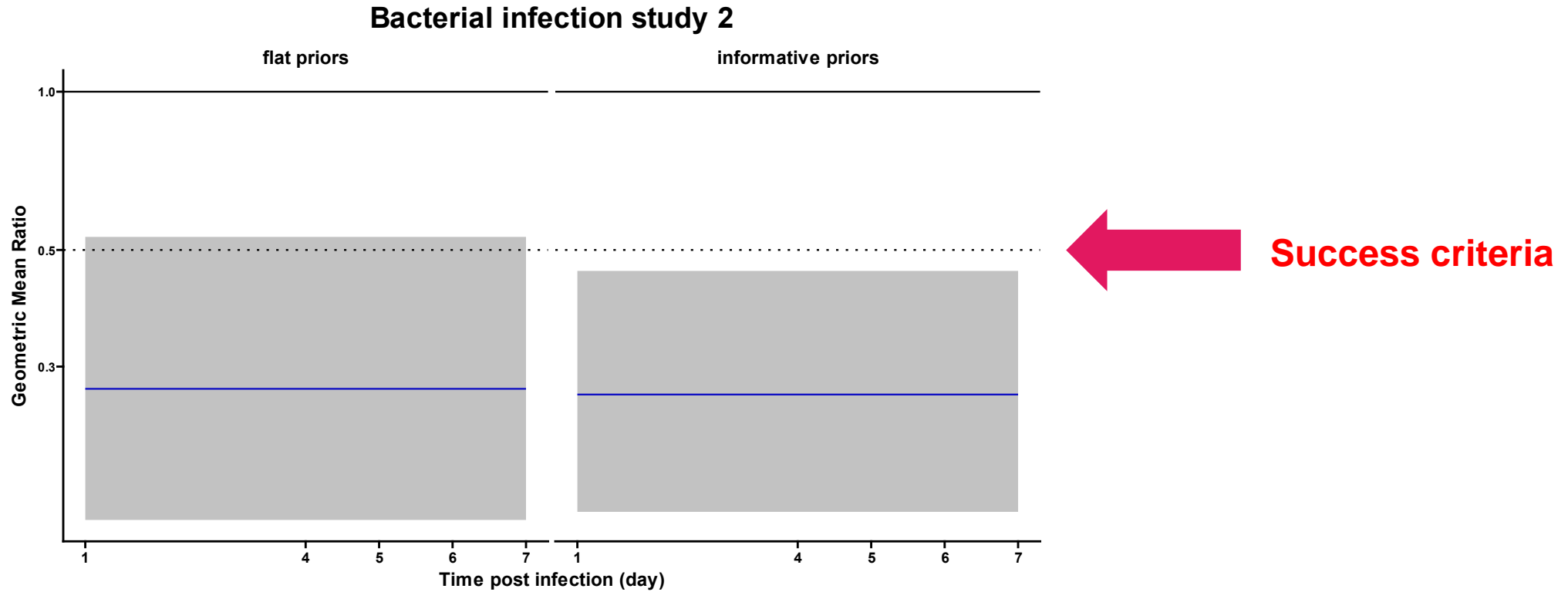
Bacterial infection study 1 (non-informative priors)



Building the studies: Bacterial infection study 2



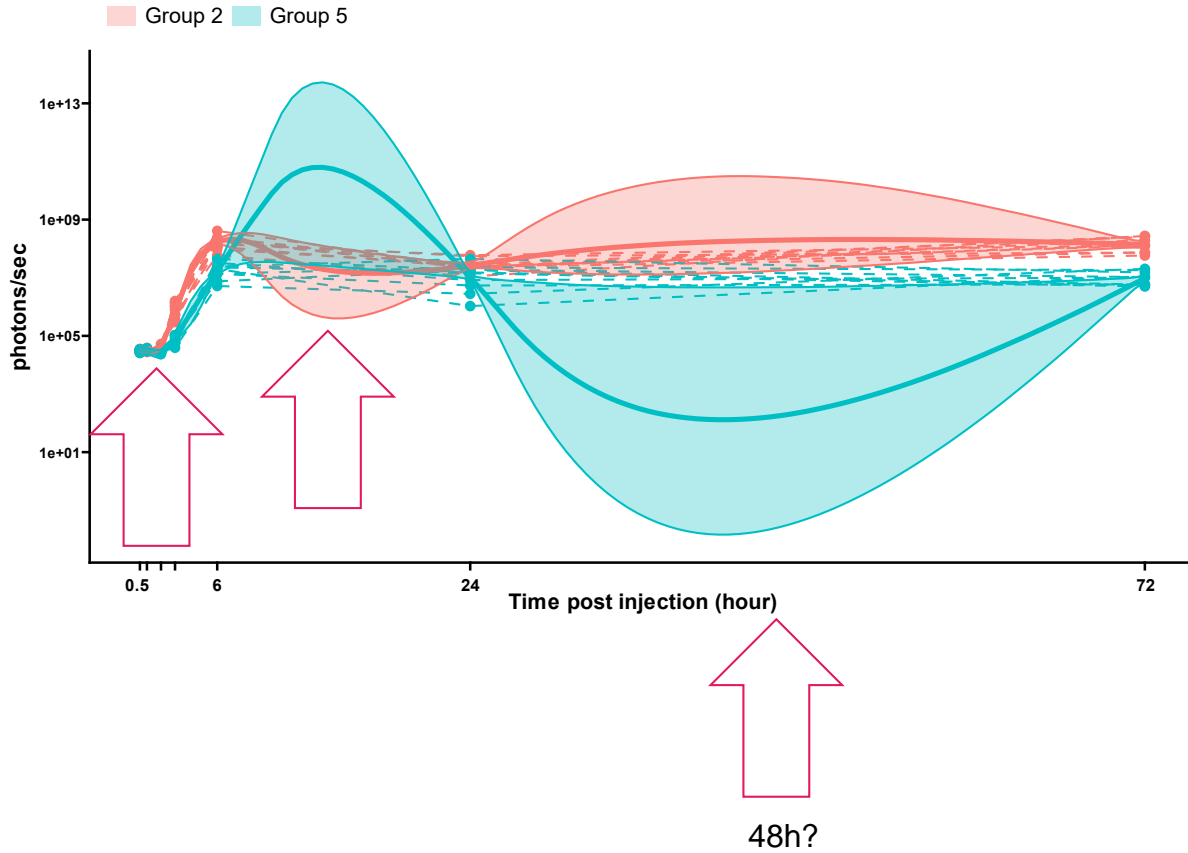
Building the studies (2)



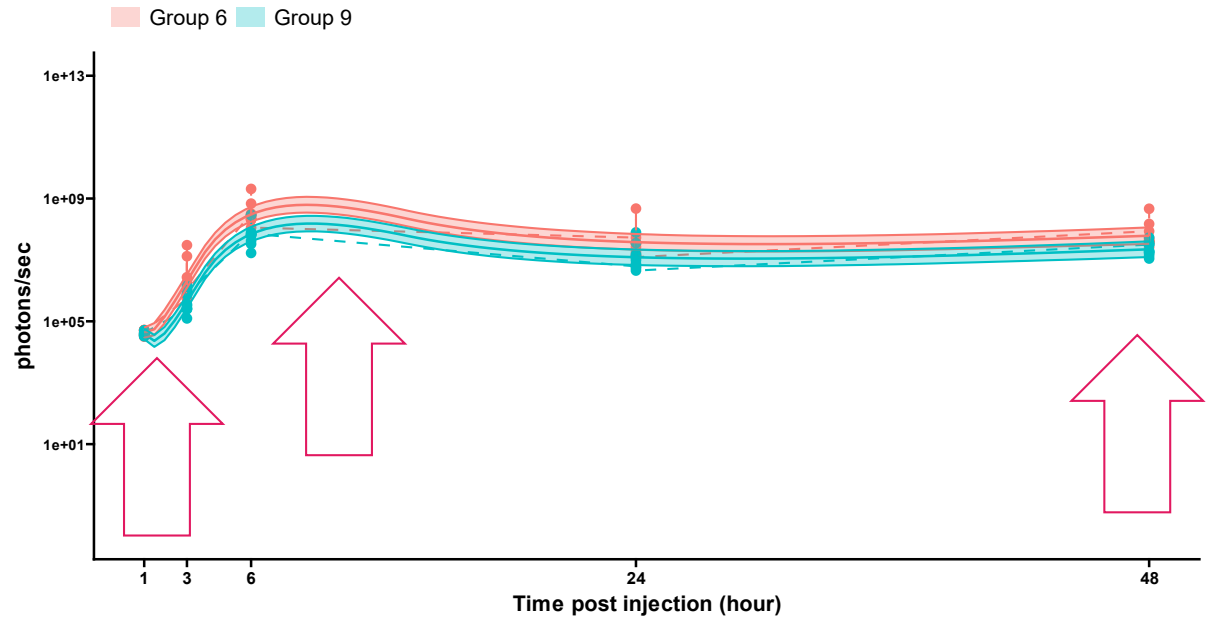
Conclusion impacted !

Impact of the study design

RNA vaccine study A



RNA vaccine study B



Appropriate time point measurements still critical

Concluding remarks

Advantages

- **Interpretability**
- **Flexibility and Automation**
- **Regularization**
- **Reduction of sample size (3Rs)**

Outstanding issues

- **Time points (study design) must be selected appropriately**
- **In-build autocorrelation specification not always available**

Thank you for your attention!

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- abduelhakem.x.ben-addi@gsk.com

Disclaimer

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3Rs statement - GSK is committed to the replacement, reduction, and refinement of animal studies (3Rs). Non-animal models and alternative technologies are part of our strategy and employed where possible. When animals are required, application of robust study design principles and peer review minimizes animal use, reduces harm, and improves benefit in studies.

GSK