

Meta-Analysis of Clinical Dose Response and Its Application

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Introduction

- **Numerous statistical methods for estimating dose response**
 - MCP-MOD, NDLM, Bayesian model averaging
 - Derived to be optimal under some conditions

Introduction

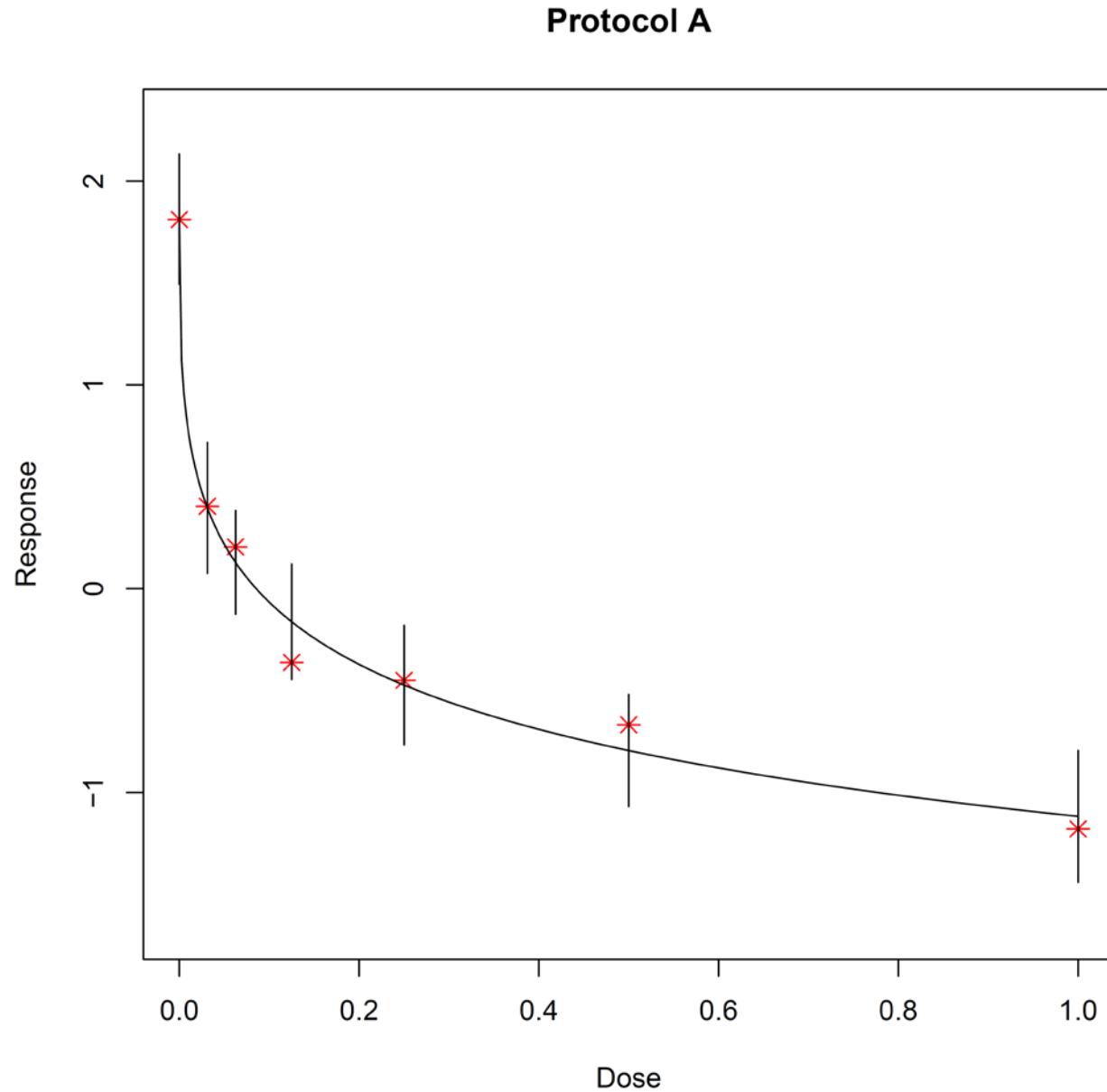
- **What are the relevant conditions?**
 - Meta-analysis of 225 compounds supports the Emax model from clinical pharmacology
- **Bayesian model-based dose response**
 - Empirically-based prior distribution combining dose response meta-data and compound-specific information
 - Brief example illustrating software to implement this approach and the potential for large improvements



Example



Example: Lipitor to lower LDL-c (continuous endpoint)



The Emax model in pharmacology



Dose Response Model: Emax

$$Response = E0 + \frac{Emax * Dose^\lambda}{ED50^\lambda + Dose^\lambda}$$

- **E0 = response under placebo treatment**
- **Emax = maximum difference with PBO**
- **ED50 = dose producing half the maximum response**
- **The power parameter determines the steepness of the curve**

Meta-analyses of dose response



Compound sampling frame

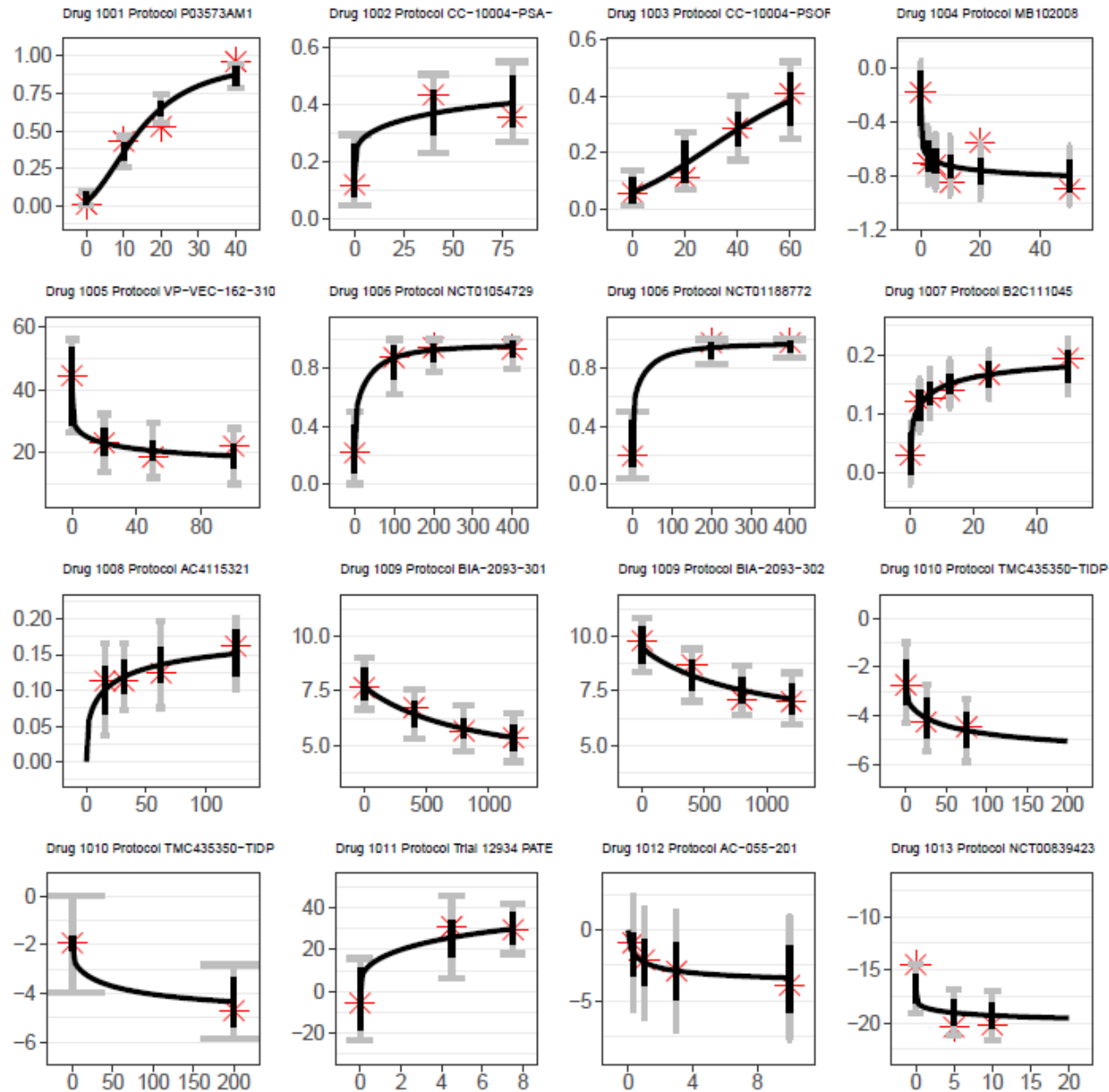
- Approximately 225 compounds
 - Pfizer compounds 1998-2017
 - FDA approved compounds 2009-2017
 - Includes small molecule and biologics. Excludes oncology and vaccines
- Study criteria (315 studies)
 - Phase 2 studies. Phase 3 studies included if they had ≥ 2 doses and the Phase 2 endpoint was collected



Design Characteristics

- Data types
 - 63% were continuous endpoints
 - 37% were binary endpoints
- Dosing
 - Dosing summarized by total daily dosing in the meta-analyses (a few adjustments required)

FDA Approved Compounds



Detecting Model Deviations (Goodness of fit)



Model checking

- How much power do we have to detect clinically important deviations from the model?
 - Several approaches to assess model adequacy have been explored
 - The most concerning deviation is a loss of efficacy at the higher doses

Conclusions

- How much power do we have to detect non-monotone deviations from the model?
 - The proportion of compounds with clinically important (non-monotone) deviations from the model is roughly (1/100, 1/10)
 - Two likely non-monotone dose response curves identified.



Quantitative Trends in the model parameters

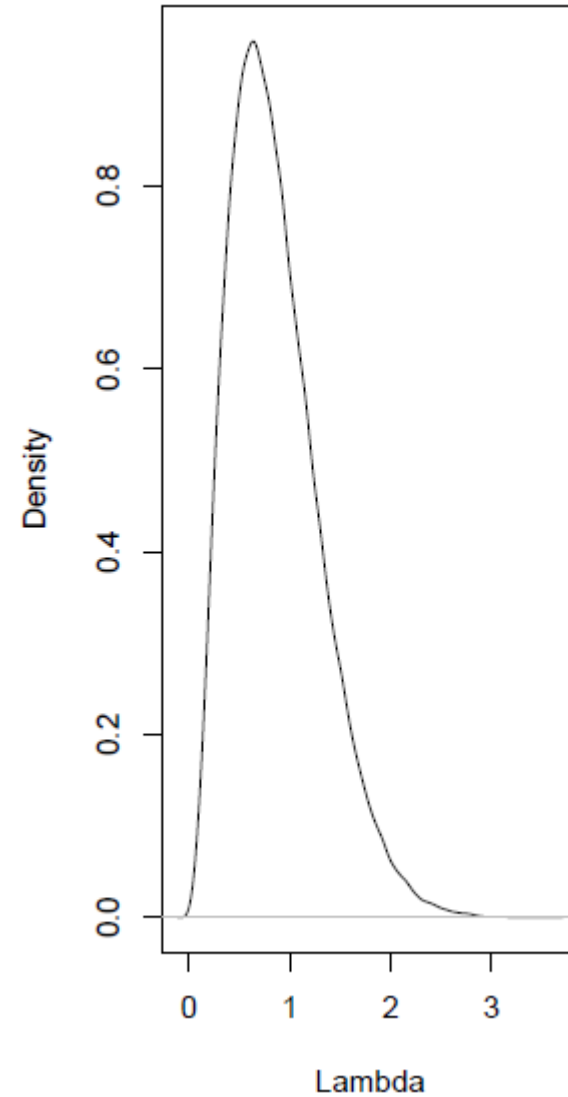
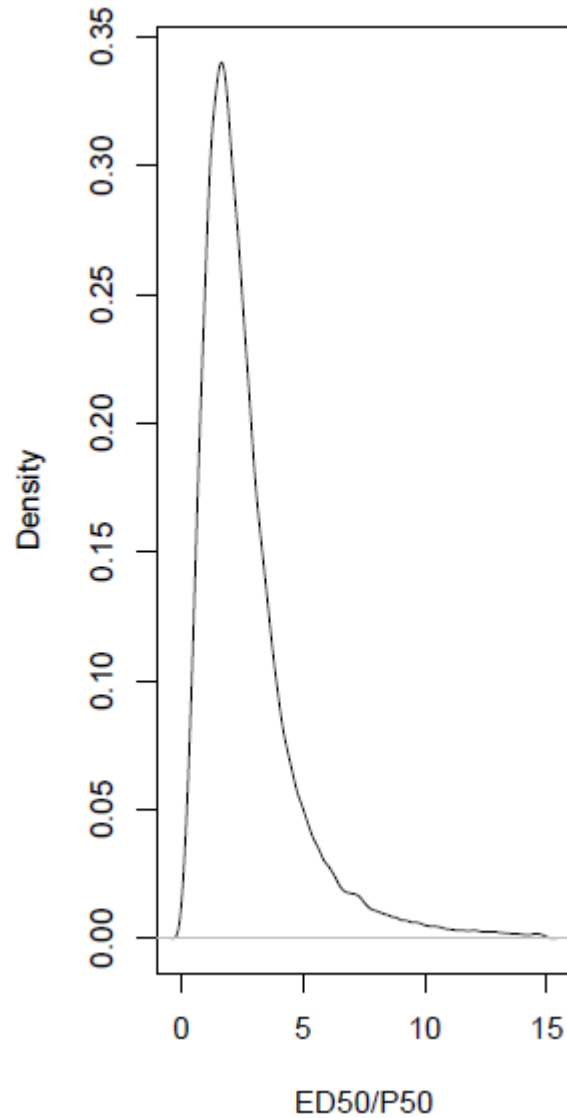


Bayesian Hierarchical Model

- Diffuse, but proper prior distributions were specified for the E_0 , E_{max} and residual standard deviation
- The Hill parameters, λ and the, ED_{50} , have hierarchical distributions
- An Emax model on the logit scale was used for binary data, and then back-transformed

- The ED50 requires special consideration
 - An initial prediction (explicit or implicit) of the ED_{50} is required when designing the first dose finding study. Denote it by P_{50}
 - When it is not recorded, the mid-point between the lowest two non-PBO doses in the first Phase 2 is a reasonable approximation
 - Modelling is performed on the $\log(ED50/P50)$

Predictive Distribution for your next compound



- Summaries

- The ED_{50} has high probability (approx 90%) to be in $(P_{50}/10, 10P_{50})$
- The λ has high probability (approx 90%) to be in $(1/2, 2)$

Applying the Results of the Meta-analyses



Planning a dose response study

- POC study is on-going. Results from the POC study will be available at the time of final planning
- Preliminary planning assumes the POC study is successful

Prior distribution (R package clinDR)

```
e0mu<-qlogis(0.2)
```

```
e0sd<-2
```

```
emaxmu<-qlogis(0.6)-qlogis(0.2)
```

```
emaxsd<-2
```

```
p50<-20
```

```
prior<-prior.control(epmu=e0mu,epsd=e0sd,emaxmu=emaxmu,  
emaxsd=emaxsd, p50=p50, edDF = 5, binary=TRUE)
```

Initial proposed design:

```
doselev<-c(0,10,25,50)
```

```
n<-c(150,150,150,150)
```



Simulation population

```
e0<- qlogis(0.3)
emax<-qlogis(0.60)-qlogis(0.3)
ed50<-35
lambda<-1
pop<-c(log(ed50),lambda,emax,e0)
proplev<-plogis(emaxfun(doselev,pop))

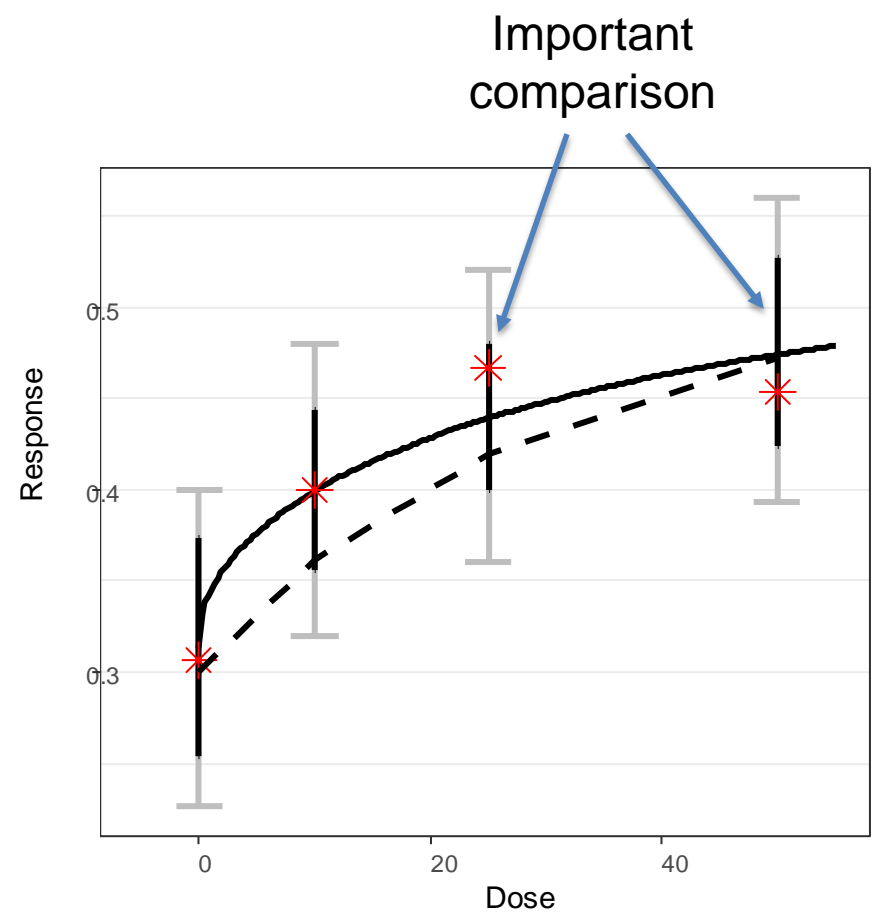
gen<-FixedMean(n,doselev,proplev,binary=TRUE,param=pop)
```

Execute Simulation

```
D1 <- emaxsimB(nsim=5000, gen, prior, seed=12357,binary=TRUE)
plot(D1[5000])
summary(D1)
```



Simulated sample: 5000



Output of summary

Coverage probabilities for nominal 0.95 intervals [Dose-PBO]:

Bayesian Dose response modeling posterior intervals:

10 25 50

0.982 0.970 0.957

Square Root Mean Squared Error [Dose-PBO]:

Bayesian dose response modeling (est=posterior mean) :

10 25 50

0.030 0.038 0.051

RMSE Pairwise comparisons: 0.054

Too large to be useful

Efficiency: 1.12-3.24

Key comparison of two highest doses

RMSE=0.021

Precise enough to be useful

Efficiency: 7.53



Concluding Remarks

- **Consistent with expectations from clinical pharmacology, our meta-data demonstrate a dose–response relationship that is well described by the Emax function for a high percentage of compounds**
- **For design and analysis we propose to use a Bayesian Emax model**
 - Graphical and quantitative assessments of goodness of fit are always performed
 - Exceptions only for compelling reasons, for example when there are toxicities/toleration issues combined with a non-specific endpoint (e.g. global assessment of change)

Supplementary slides

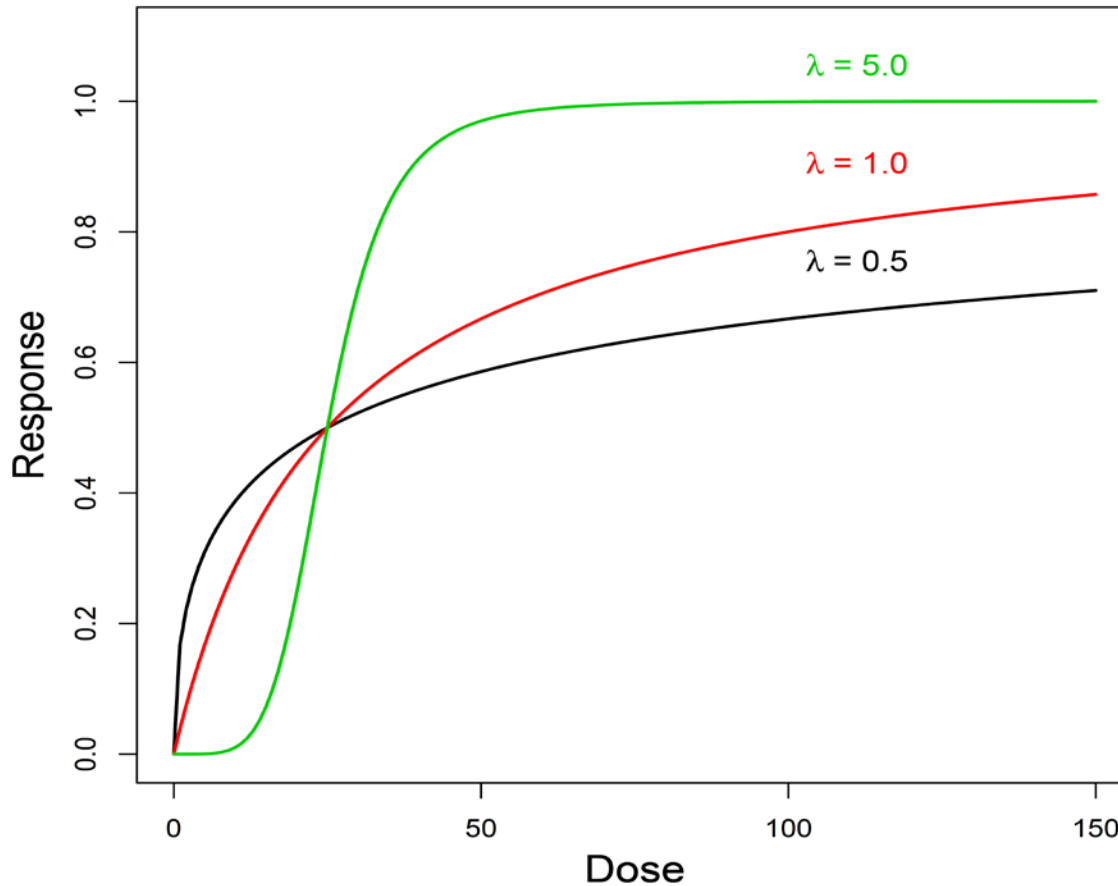


References

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- Wu, J., Banerjee, A., Jin, B. Menon, M. S., Martin, S. and Heatherington, A. (2017). **Clinical dose–response for a broad set of biological products: A model-based meta-analysis**. *Statistical Methods in Medical Research*. doi: 10.1177/0962280216684528.



Sigmoid Emax Model



- When $\lambda = 1$, $ED_{90} = 9 \cdot ED_{50}$
- When $\lambda = 0.5$, $ED_{90} = 81 \cdot ED_{50}$
- when $\lambda = 5.0$, $ED_{90} = 1.5 \cdot ED_{50}$

Prior density

