Model checking - overview

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- Internal validation
 - posterior predictive checking
 - cross-validation predictive checking

Chapter 6

- 6.1 The place of model checking in applied Bayesian statistics
- 6.2 Do the inferences from the model make sense?
- 6.3 Posterior predictive checking
- 6.4 Graphical posterior predictive checks
 - this can be skimmed, see instead the paper Gabry et al. (2019). Visualization in Bayesian workflow https://doi.org/10.1111/rssa.12378
- 6.5 Model checking for the educational testing example

Model checking

- demo6_1: Posterior predictive checking light speed
- demo6_2: Posterior predictive checking sequential dependence
- demo6_3: Posterior predictive checking poor test statistic
- https://avehtari.github.io/BDA_R_demos/demos_rstan/brms_demo.html

Simon Newcomb's light of speed experiment in 1882

Newcomb measured (n = 66) the time required for light to travel from his laboratory on the Potomac River to a mirror at the base of the Washington Monument and back, a total distance of 7422 meters.

- Newcomb's speed of light measurements
 - model $y \sim \text{normal}(\mu, \sigma)$ with prior $(\mu, \log \sigma) \propto 1$

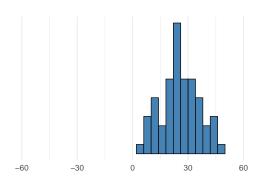
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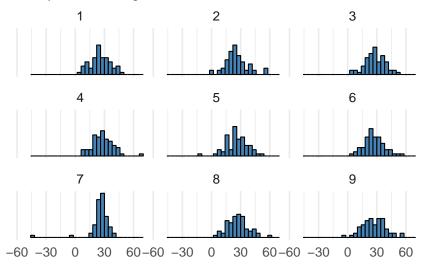
Replicates vs. future observation

Predictive ỹ is the next not yet observed possible observation.
 y^{rep} refers to replicating the whole experiment (potentially with same values of x) and obtaining as many replicated observations as in the original data.

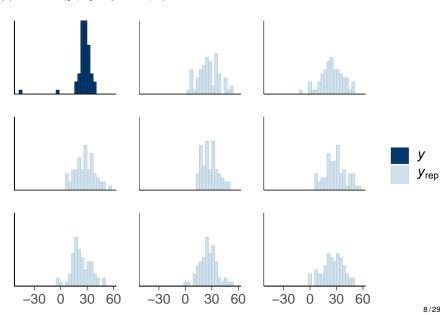
Generate several replicated datasets y^{rep}

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- Compare to the original dataset

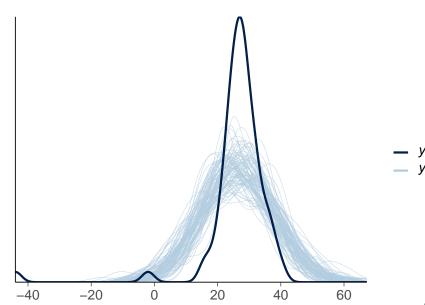
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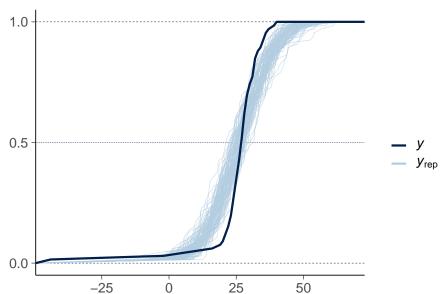
Posterior predictive checking – bayesplot ppc_hist(y, yrep[1:8,])



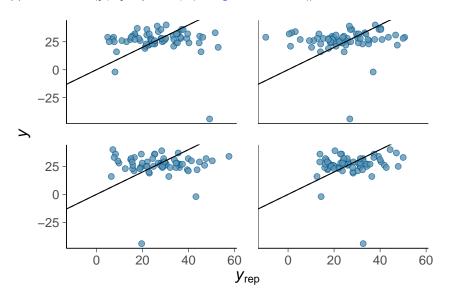
ppc_dens_overlay(y, yrep[1:100,])



ppc_ecdf_overlay(y, yrep[1:100,])



ppc_scatter(y, yrep[1:4,]) + geom_abline()



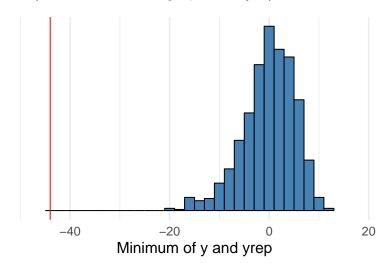
Posterior predictive checking with test statistic

- Replicated data sets y^{rep}
- Test quantity (or discrepancy measure) $T(y, \theta)$
 - summary quantity for the observed data $T(y, \theta)$
 - summary quantity for a replicated data $T(y^{rep}, \theta)$
 - can be easier to compare summary quantities than data sets

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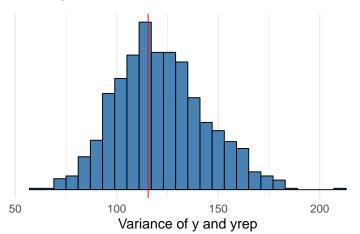
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 - · e.g. variance for normal model



Posterior predictive checking

Posterior predictive p-value

$$p = \Pr(T(y^{\text{rep}}, \theta) \ge T(y, \theta)|y)$$
$$= \int \int I_{T(y^{\text{rep}}, \theta) \ge T(y, \theta)} p(y^{\text{rep}}|\theta) p(\theta|y) dy^{\text{rep}} d\theta$$

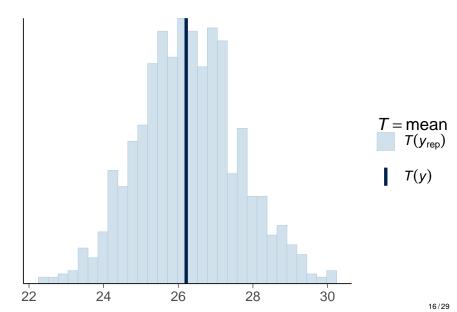
where I is an indicator function

• having $(y^{\text{rep }(s)}, \theta^{(s)})$ from the posterior predictive distribution, easy to compute

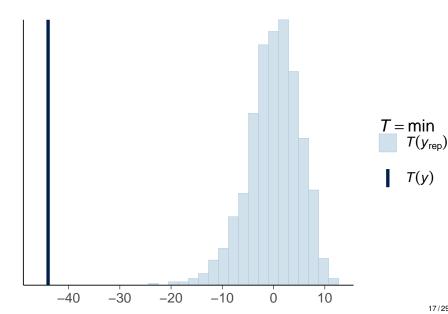
$$T(y^{\text{rep}(s)}, \theta^{(s)}) \ge T(y, \theta^{(s)}), \quad s = 1, \dots, S$$

- Posterior predictive p-value (ppp-value) estimates whether difference between the model and data could arise by chance
- Not commonly used, as
 - not calibrated in case of non-ancillary statistic
 - the distribution of test statistic has more information

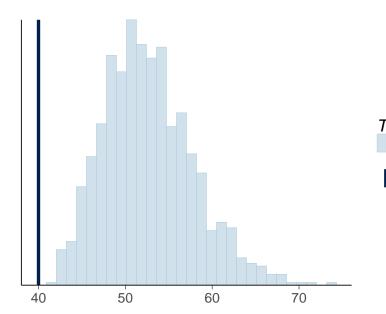
 ${\tt ppc_stat}({\tt y}, {\tt yrep}),$ the default statistic "mean" is usually bad



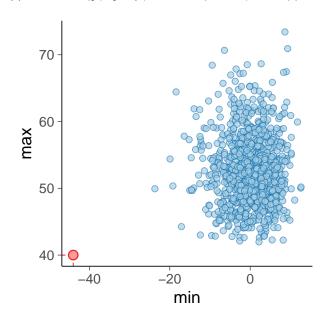
ppc_stat(y, yrep, stat="min")



ppc_stat(y, yrep, stat="max")



ppc_stat2d(y, yrep, stat=c("min", "max"))



 $T = (\min, \max)$

- O T(y)
- $T(y_{rep})$

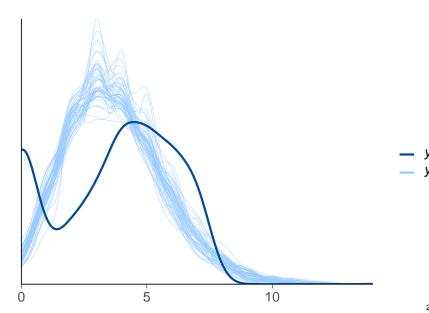
Posterior predictive checking - Stan code

demo demos_rstan/ppc/poisson-ppc.Rmd

```
data {
  int<lower=1> N;
  int<lower=0> y[N];
parameters {
  real<lower=0> lambda;
model {
  lambda ~ exponential(0.2);
 v ~ poisson(lambda);
generated quantities {
  real log_lik[N];
  int y_rep[N];
  for (n in 1:N) {
    y_rep[n] = poisson_rng(lambda);
    log_lik[n] = poisson_lpmf(y[n] | lambda);
```

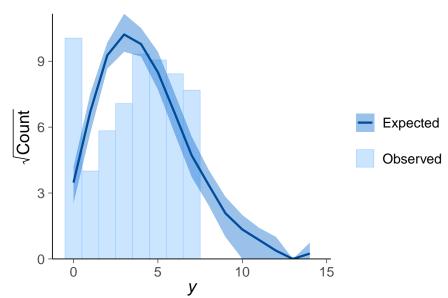
PPC for count data - Poisson model

ppc_dens_overlay(y, yrep[1:50,])



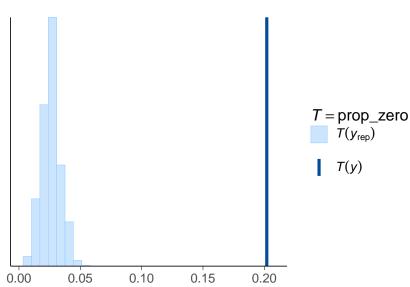
PPC for count data - Poisson model

ppc_rootogram(y, yrep)



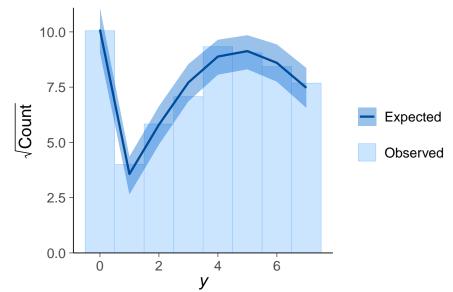
PPC for count data - Poisson model

```
prop_zero <- function(x) mean(x == 0)
ppc_stat(y, yrep, stat = "prop_zero")</pre>
```



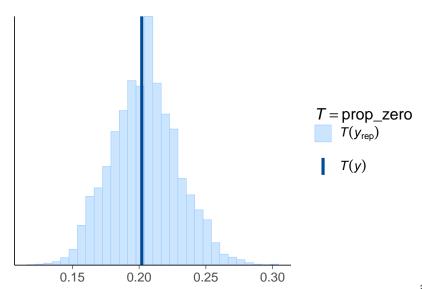
PPC for count data - hurdle truncated Poisson model

ppc_rootogram(y, yrep2)



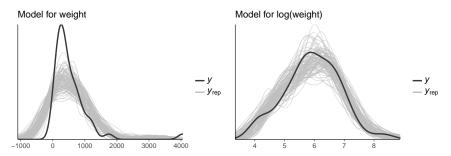
PPC for count data - hurdle truncated Poisson model

```
prop_zero <- function(x) mean(x == ∅)
ppc_stat(y, yrep2, stat = "prop_zero")</pre>
```



Posterior predictive checking: Mesquite bushes

Positive target: normal vs log-normal model

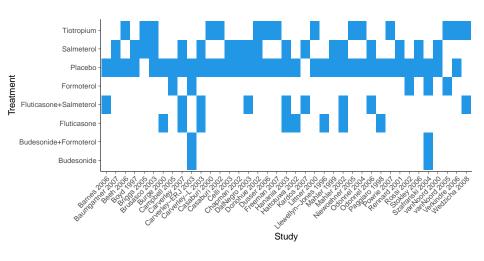


Predicting the yields of mesquite bushes.

Gelman, Hill & Vehtari (2020): Regression and Other Stories, Chapter 11.

Meta-analysis

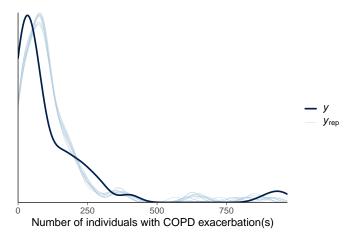
Pharmacologic treatments for chronic obstructive pulmonary disease



Posterior predictive checking

Pharmacologic treatments for chronic obstructive pulmonary disease

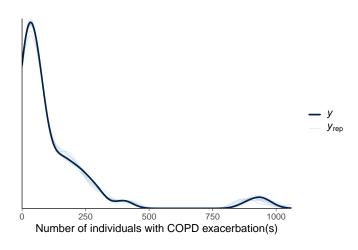
Pooled over studies, separate for treatments



Posterior predictive checking

Pharmacologic treatments for chronic obstructive pulmonary disease

Hirerachical for studies, hierarchical for treatments

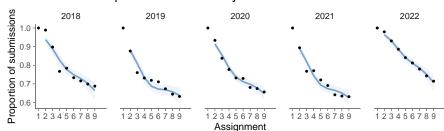


Student retention

Latent hierarchical linear + spline

```
nstudents | trials(nstudents1) ~
  s(assignment, k=4) + (assignment | year),
  family=binomial()
```

Latent functions + posterior uncertainty

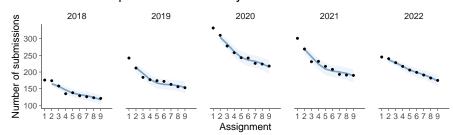


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Student retention

1. Latent hierarchical linear model

```
nstudents | trials(nstudents1) ~
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```

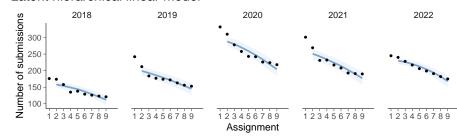
2. Latent spline + hierarchical linear model

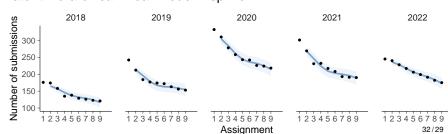
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```

Student retention – Posterior predictive distributions

with tidybayes

Latent hierarchical linear model

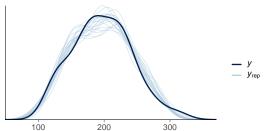


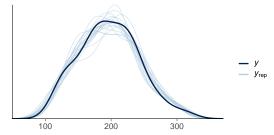


Student retention – Marginal PPC (brms)

pp_check(fit, ndraws=100)

Latent hierarchical linear model

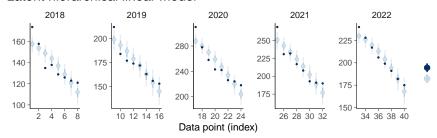


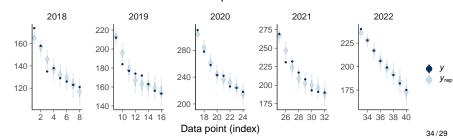


Student retention – Posterior predictive intervals (brms)

pp_check(fit, type = "intervals_grouped", group="year")

Latent hierarchical linear model

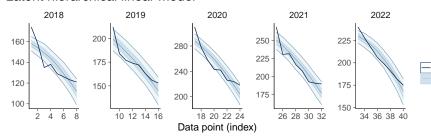


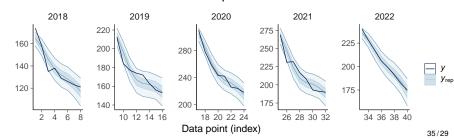


Student retention – Posterior predictive ribbon (brms)

pp_check(fit, type = "ribbon_grouped", group="year")

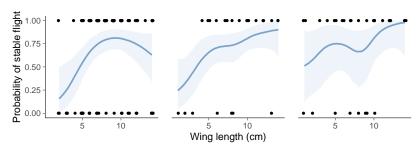
Latent hierarchical linear model





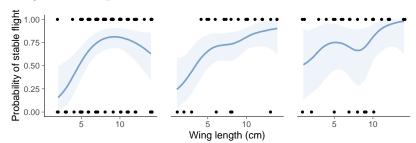
PPC for binary target – Helicopters (brms)

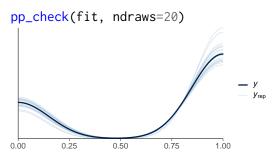
```
stable_flight ~ s(wing_length) + s(wing_length, by = nclips),
family = bernoulli()
```



PPC for binary target - Helicopters (brms) stable_flight ~ s(wing_length) + s(wing_length, by = nclips),

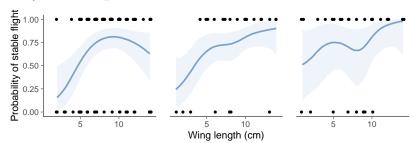
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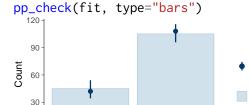


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family = bernoulli()
```



 y_{rep}



0.5

1.0

1.5

-0.5

0.0

PPC for binary target - Helicopters (brms) stable_flight ~ s(wing_length) + s(wing_length, by = nclips), family = bernoulli() Probability of stable flight .00 0.75 0.50 0.25 10 5 10 10 Wing length (cm) pp_check(fit, type="bars_grouped") 0 60 Count

40 20

-0.5

0.0 0.5 1.0 1.5 -0.5

0.0 0.5 1.0 1.5 -0.5

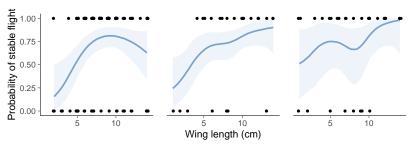
0.5 1.0

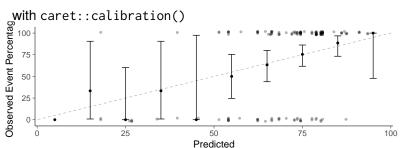
0.0

 y_{rep}

PPC for binary target - Helicopters (brms) stable_flight ~ s(wing_length) + s(wing_length, by = nclips),

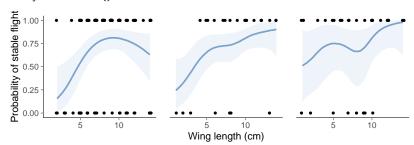
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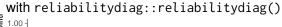


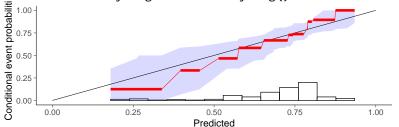


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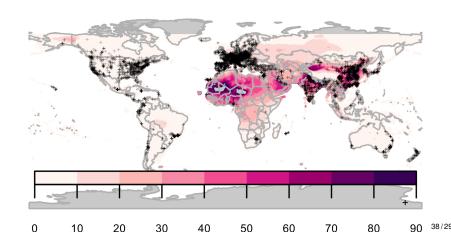




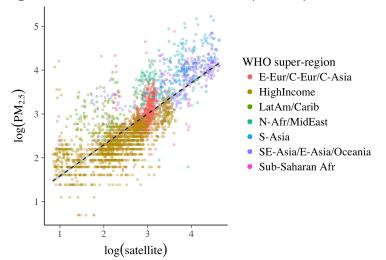


- Example from Jonah Gabry, Daniel Simpson, Aki Vehtari,
 Michael Betancourt, and Andrew Gelman (2019). Visualization in Bayesian workflow. https://doi.org/10.1111/rssa.12378
- Estimation of human exposure to air pollution from particulate matter measuring less than 2.5 microns in diameter (PM_{2.5})
 - Exposure to PM_{2.5} is linked to a number of poor health outcomes and a recent report estimated that PM_{2.5} is responsible for three million deaths worldwide each year (Shaddick et al., 2017)
 - In order to estimate the public health effect of ambient PM_{2.5}, we need a good estimate of the PM_{2.5} concentration at the same spatial resolution as our population estimates.

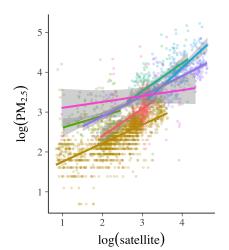
- Direct measurements of PM 2.5 from ground monitors at 2980 locations
- High-resolution satellite data of aerosol optical depth



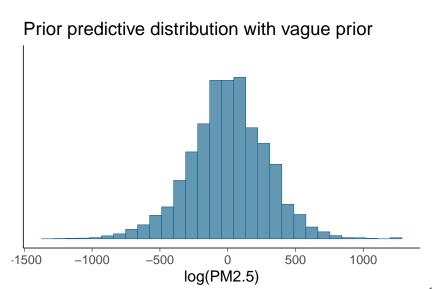
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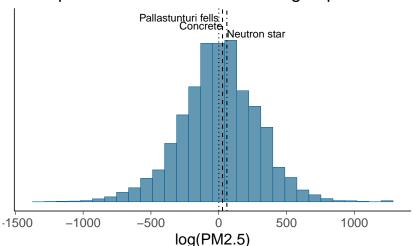


Prior predictive checking



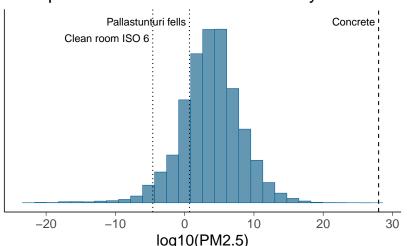
Prior predictive checking

Prior predictive distribution with vague prior



Prior predictive checking

Prior predictive distribution with weakly informative



Further reading and examples

- Gabry, Simpson, Vehtari, Betancourt, and Gelman (2019).
 Visualization in Bayesian workflow.
 https://doi.org/10.1111/rssa.12378.
- Graphical posterior predictive checks using the bayesplot package http://mc-stan.org/bayesplot/articles/graphical-ppcs.html
- brms demos https://avehtari.github.io/BDA_R_demos/demos_ rstan/brms_demo.html

 How much different choices in model structure and priors affect the results

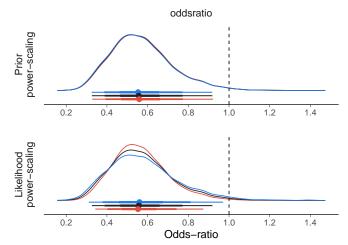
- How much different choices in model structure and priors affect the results
 - test different models and priors
 priorsense and adjustr packages use importance sampling
 for faster prior sensitivity analysis

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 - alternatively combine different models to one model
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 - e.g. *t* distribution contains Gaussian as a special case
 - robust models are good for testing sensitivity to "outliers"
 - e.g. t instead of Gaussian

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 - e.g. *t* distribution contains Gaussian as a special case
 - robust models are good for testing sensitivity to "outliers"
 - e.g. t instead of Gaussian
- Compare sensitivity of essential inference quantities
 - extreme quantiles are more sensitive than means and medians
 - extrapolation is more sensitive than interpolation

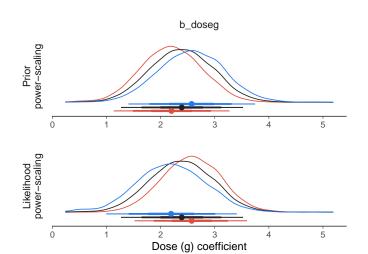
priorsense — prior and likelihood sensitivity analysis

- Power-scale prior and likelihood separately as $p(\theta)^{\alpha}$ and $p(y|\theta)^{\alpha}$
- Beta blockers randomized control-treatment experiment
 - no prior sensitivity
 - likelihood is informative



priorsense — prior and likelihood sensitivity analysis

- Power-scale prior and likelihood separately as $p(\theta)^{\alpha}$ and $p(y|\theta)^{\alpha}$
- Sorafenib Toxicity Binomial model meta analysis
 - prior-data conflict



priorsense — prior and likelihood sensitivity analysis

- Power-scale prior and likelihood separately as $p(\theta)^{\alpha}$ and $p(y|\theta)^{\alpha}$
- Sorafenib Toxicity Binomial model meta analysis
 - prior-data conflict
 - due to accidentally too narrow prior

