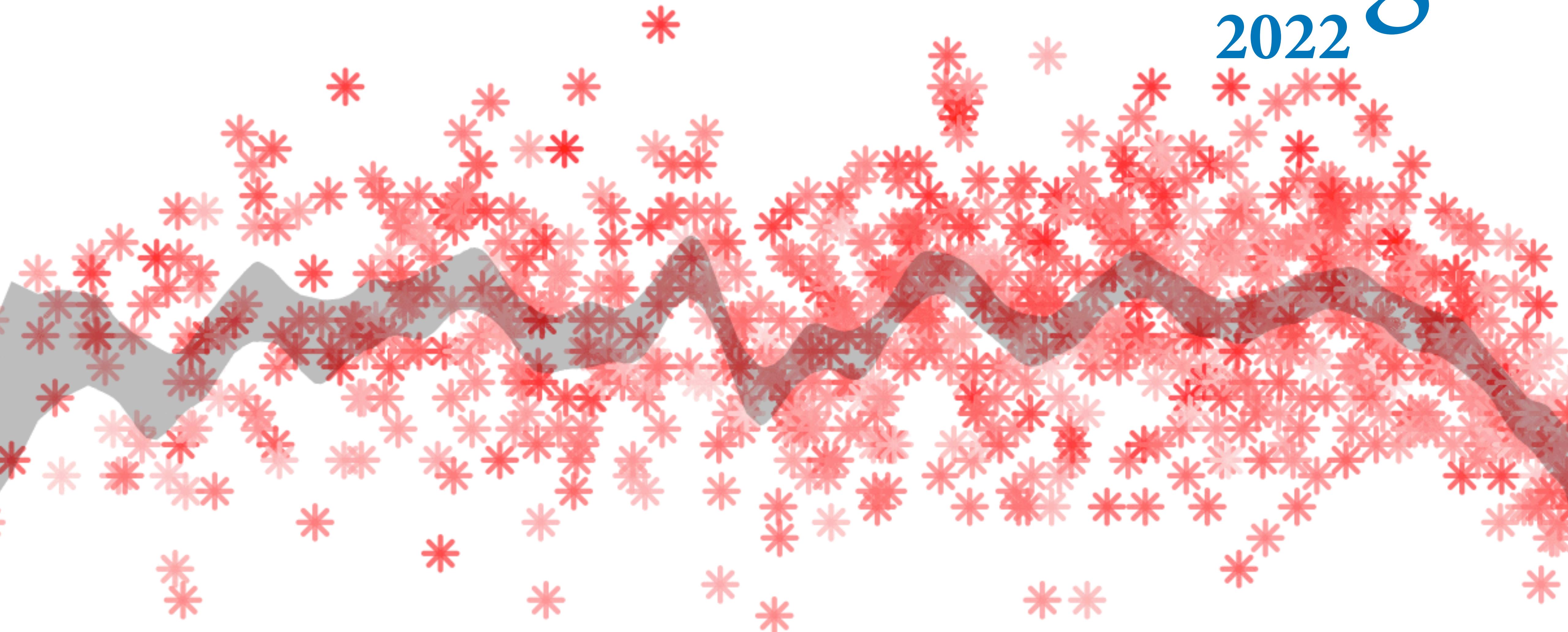


# Statistical Rethinking

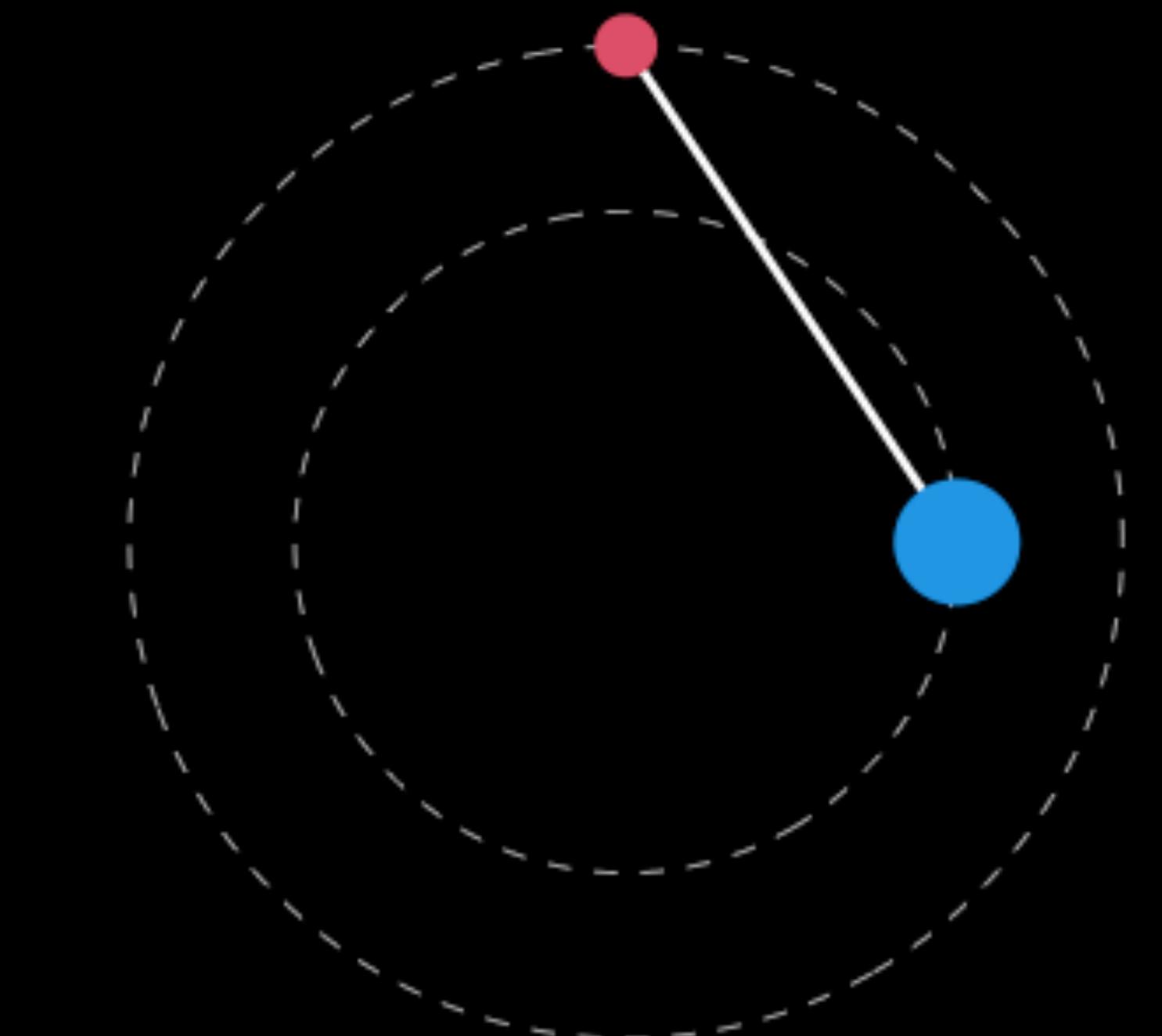
2022



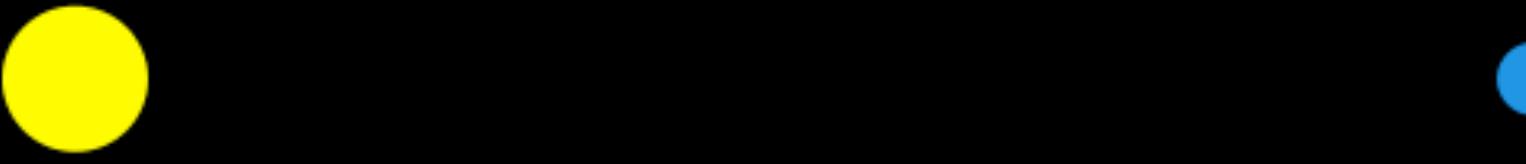
07: Fitting Over and Under



Mikołaj Kopernik (1473–1543)



# Copernican Model



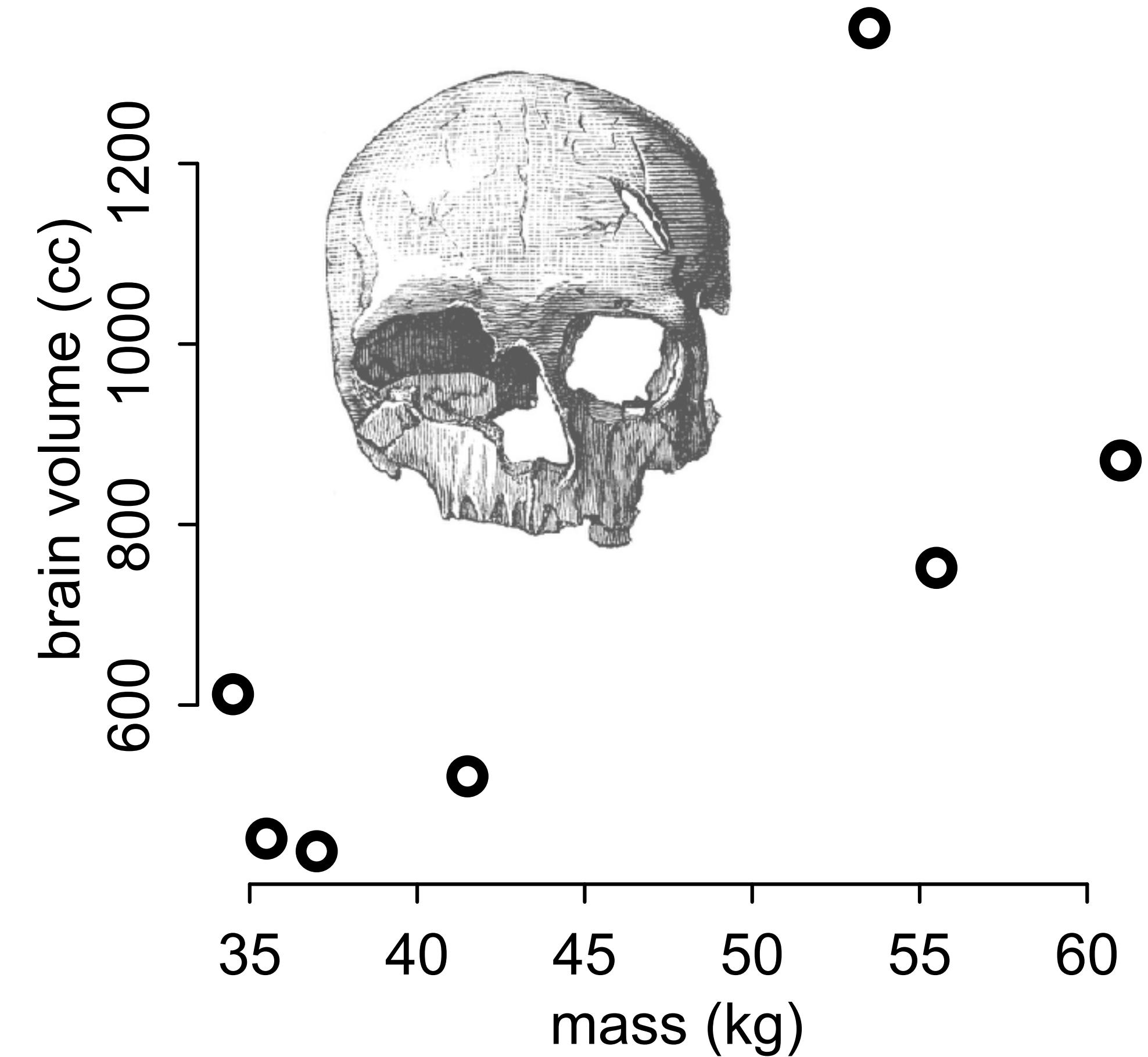
# Problems of Prediction

What function describes these points?  
(fitting, compression)

What function explains these points?  
(causal inference)

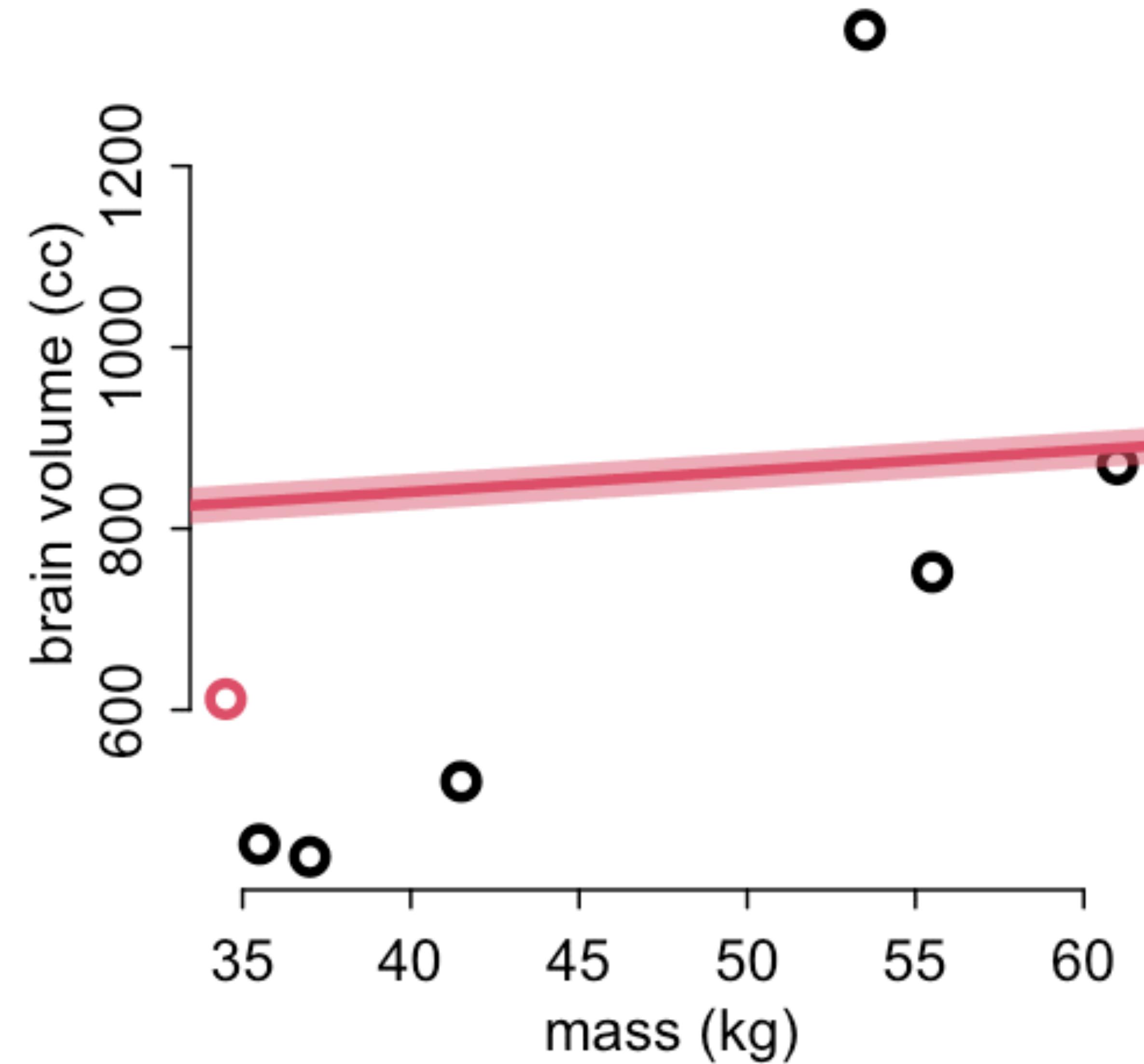
What would happen if we changed a point's mass? (intervention)

What is the next observation from the same process? (prediction)



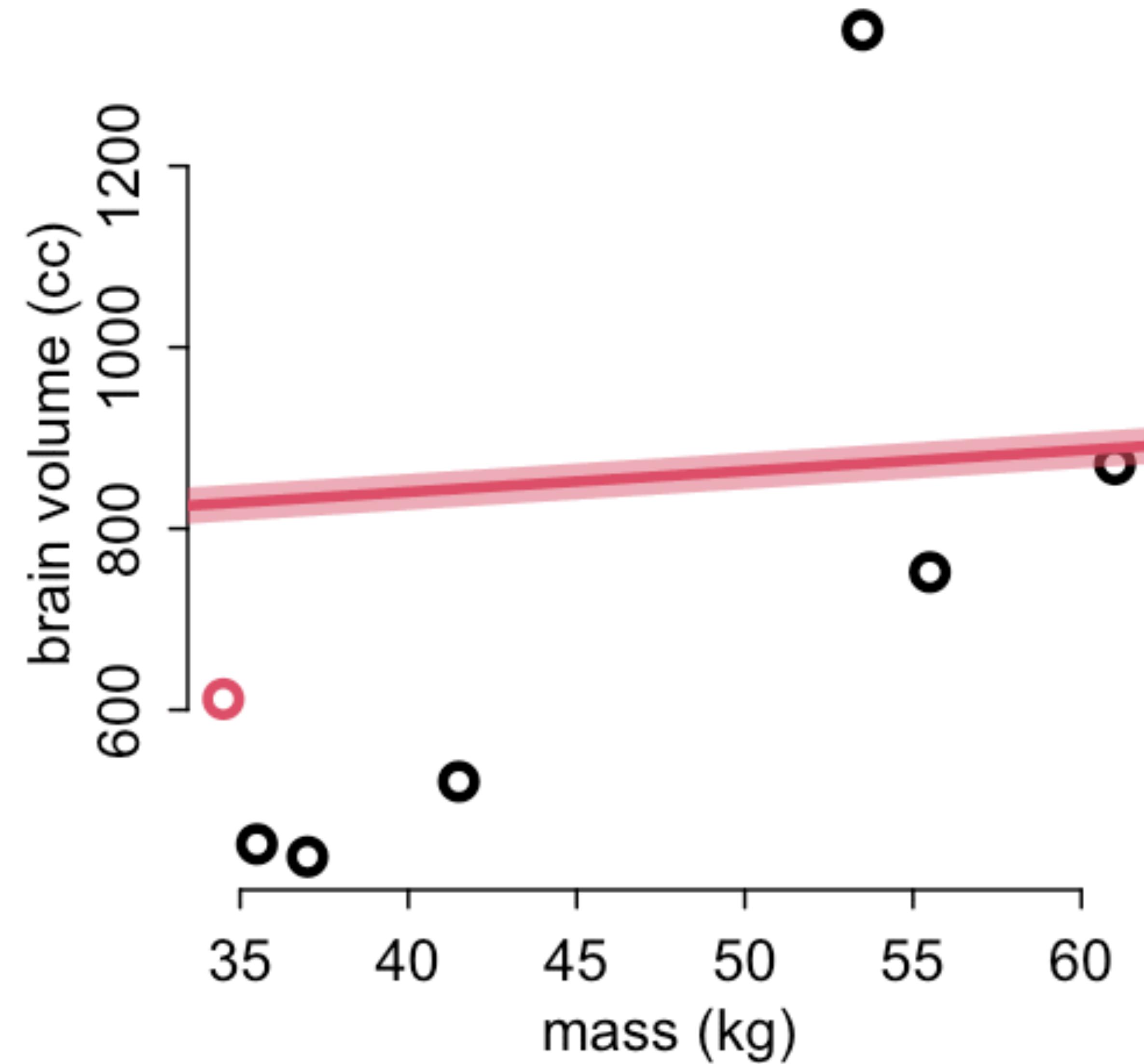
# Leave-one-out cross-validation

- (1) Drop one point
- (2) Fit line to remaining
- (3) Predict dropped point
- (4) Repeat (1) with next point
- (5) Score is error on dropped



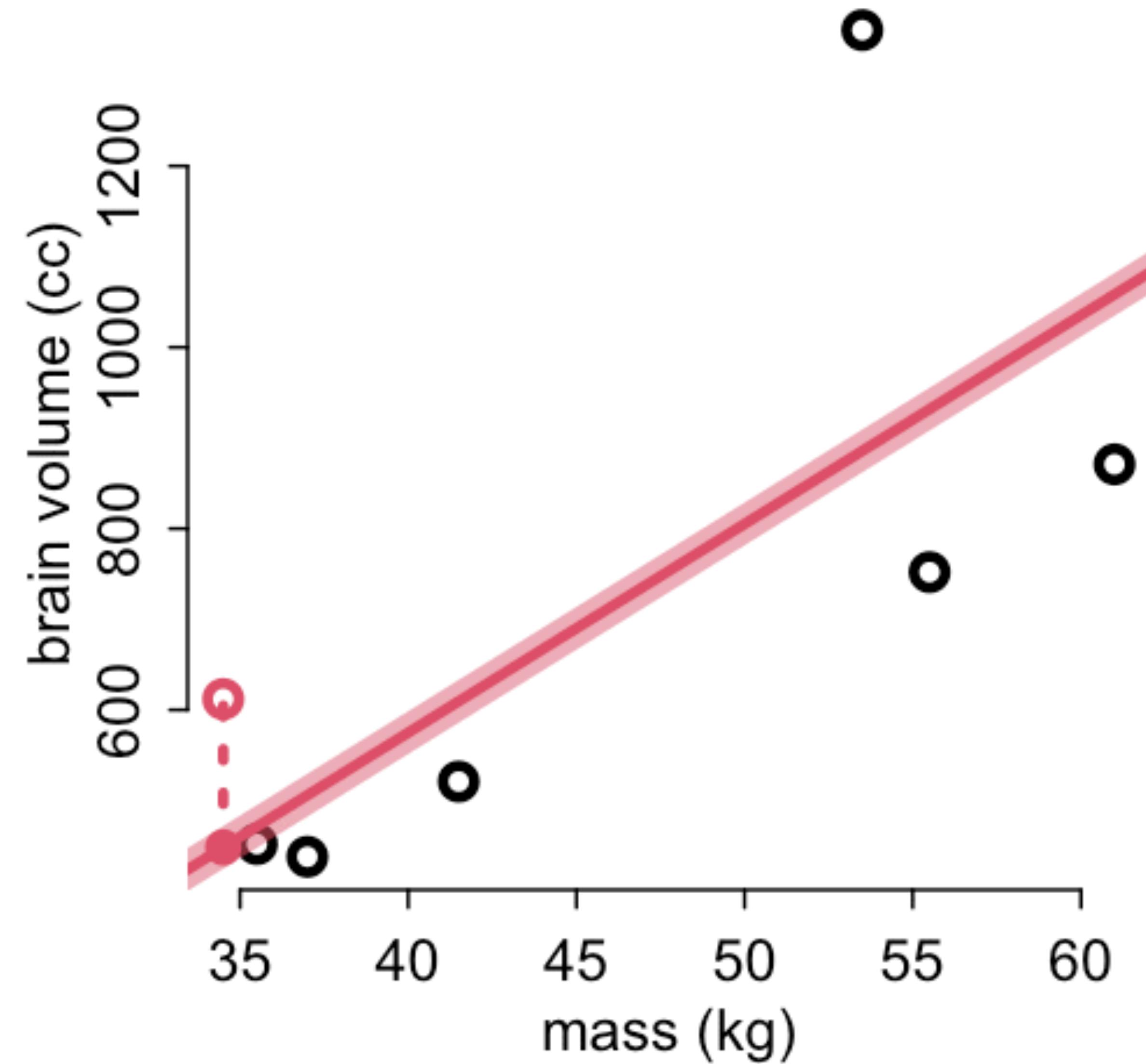
# Leave-one-out cross-validation

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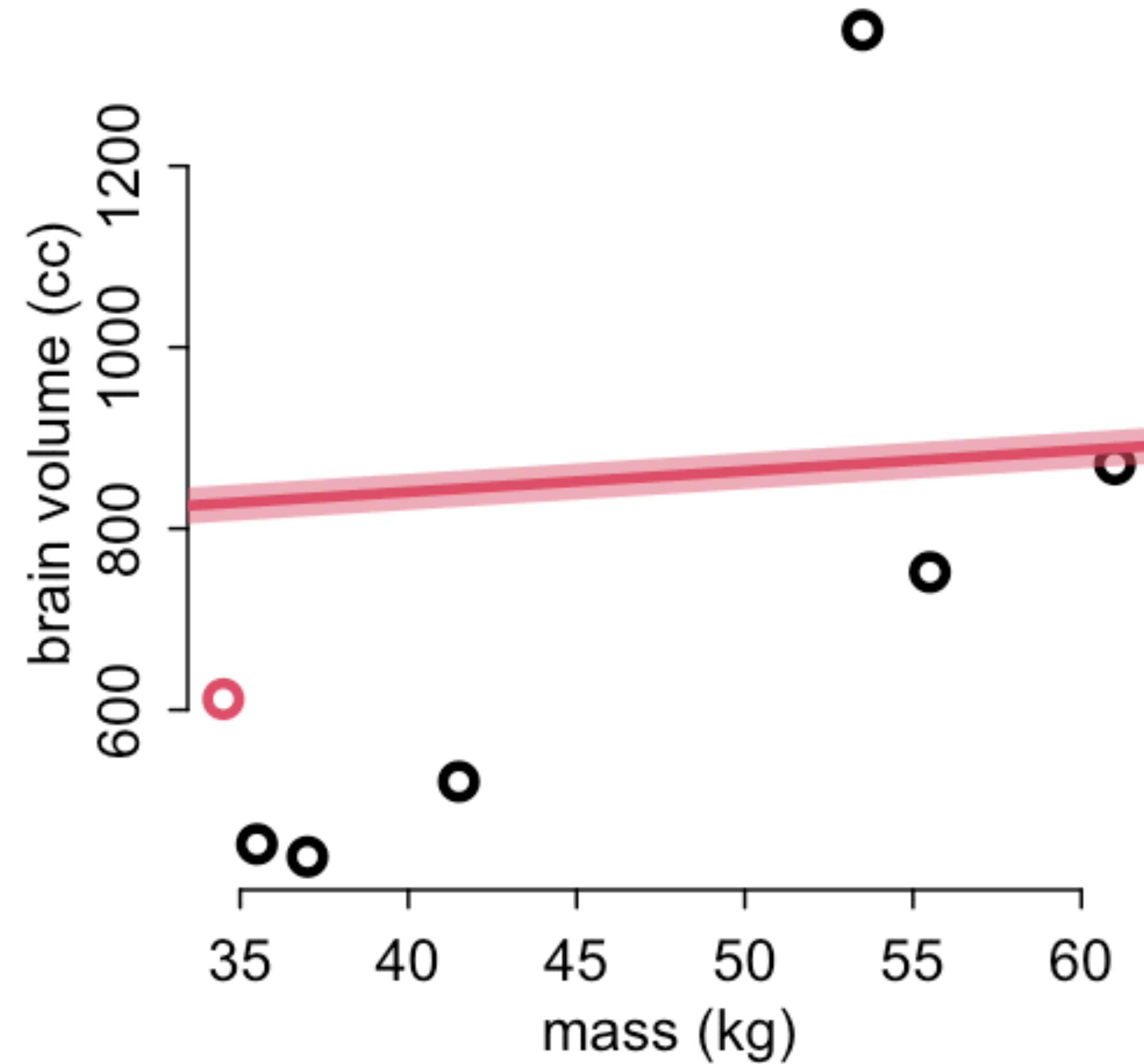
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- (5) Score is error on dropped



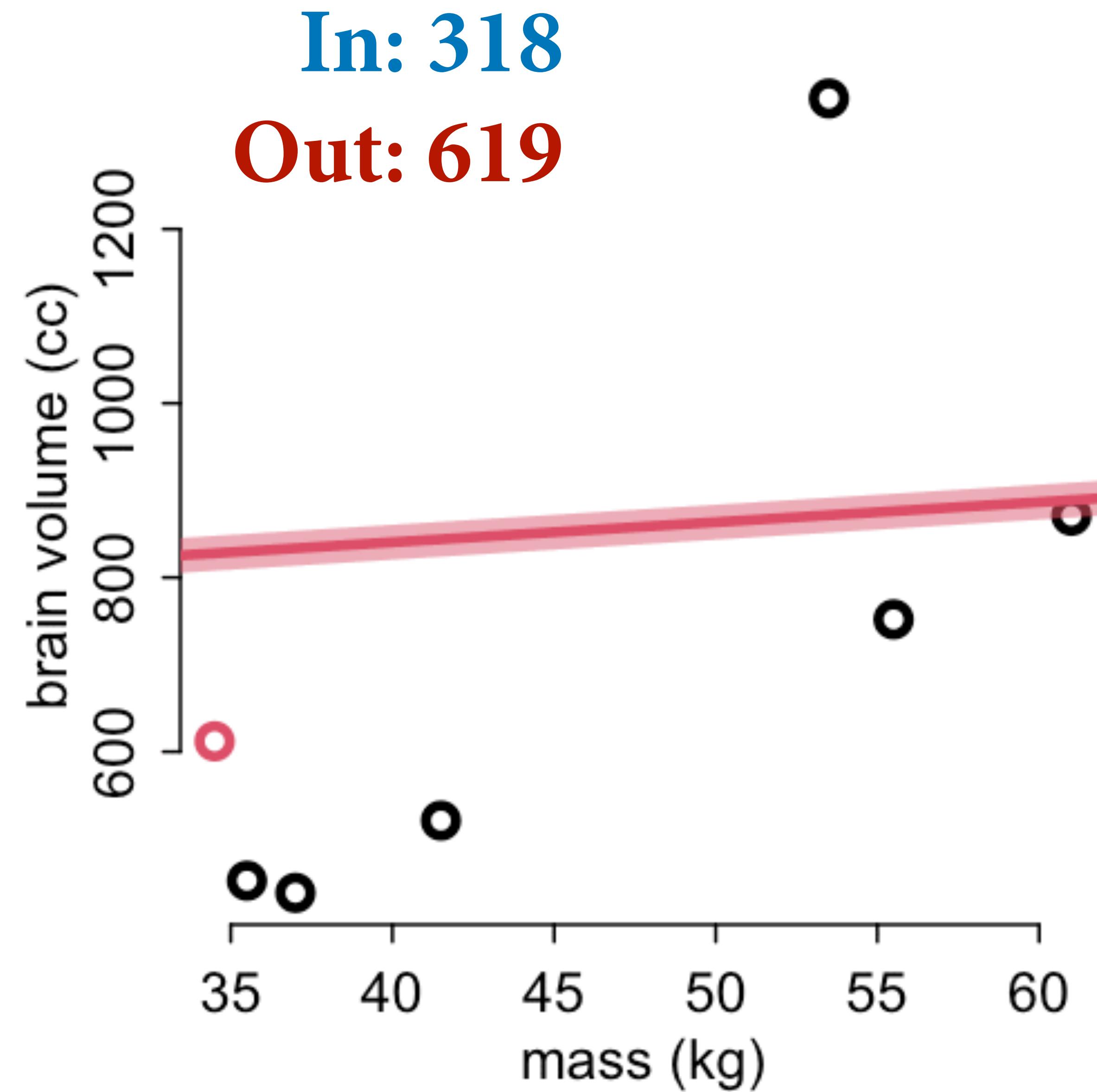
# Leave-one-out cross-validation

- (1) Drop one point
- (2) Fit line to remaining
- (3) Predict dropped point
- (4) Repeat (1) with next point
- (5) Score is error on dropped



## Leave-one-out cross-validation

- (1) Drop one point
- (2) Fit line to remaining
- (3) Predict dropped point
- (4) Repeat (1) with next point
- (5) Score is error on dropped

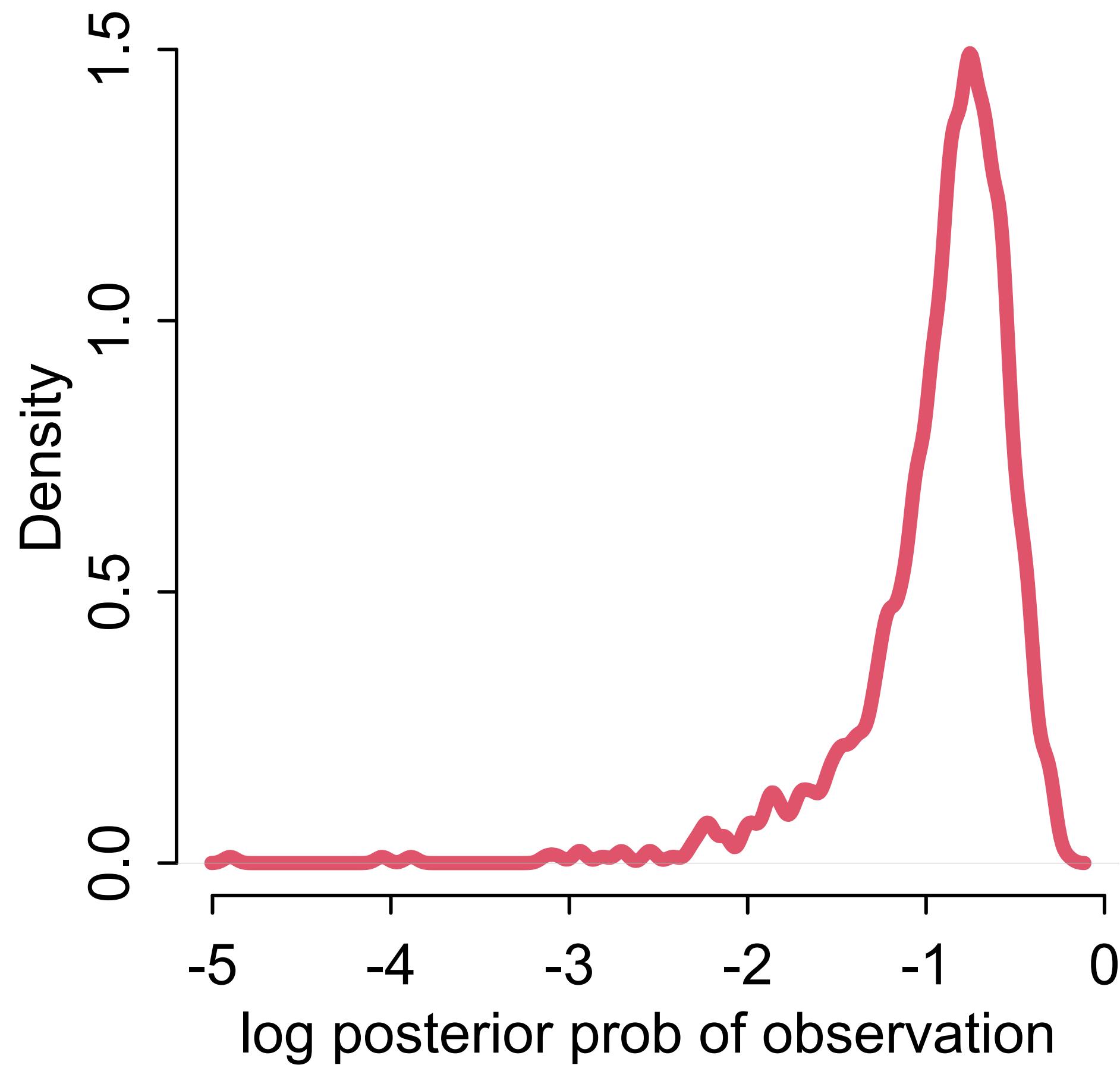


# Bayesian Cross-Validation

We use the entire posterior, not just a point prediction

Cross-validation score is:

$$\text{lppd}_{\text{CV}} = \sum_{i=1}^N \frac{1}{S} \sum_{s=1}^S \log \Pr(y_i | \theta_{-i,s})$$



# Bayesian Cross-Validation

$$\text{lppd}_{\text{CV}} = \sum_{i=1}^N \frac{1}{S} \sum_{s=1}^S \overline{\log \Pr(y_i | \theta_{-i,s})}$$

*log pointwise  
predictive density*

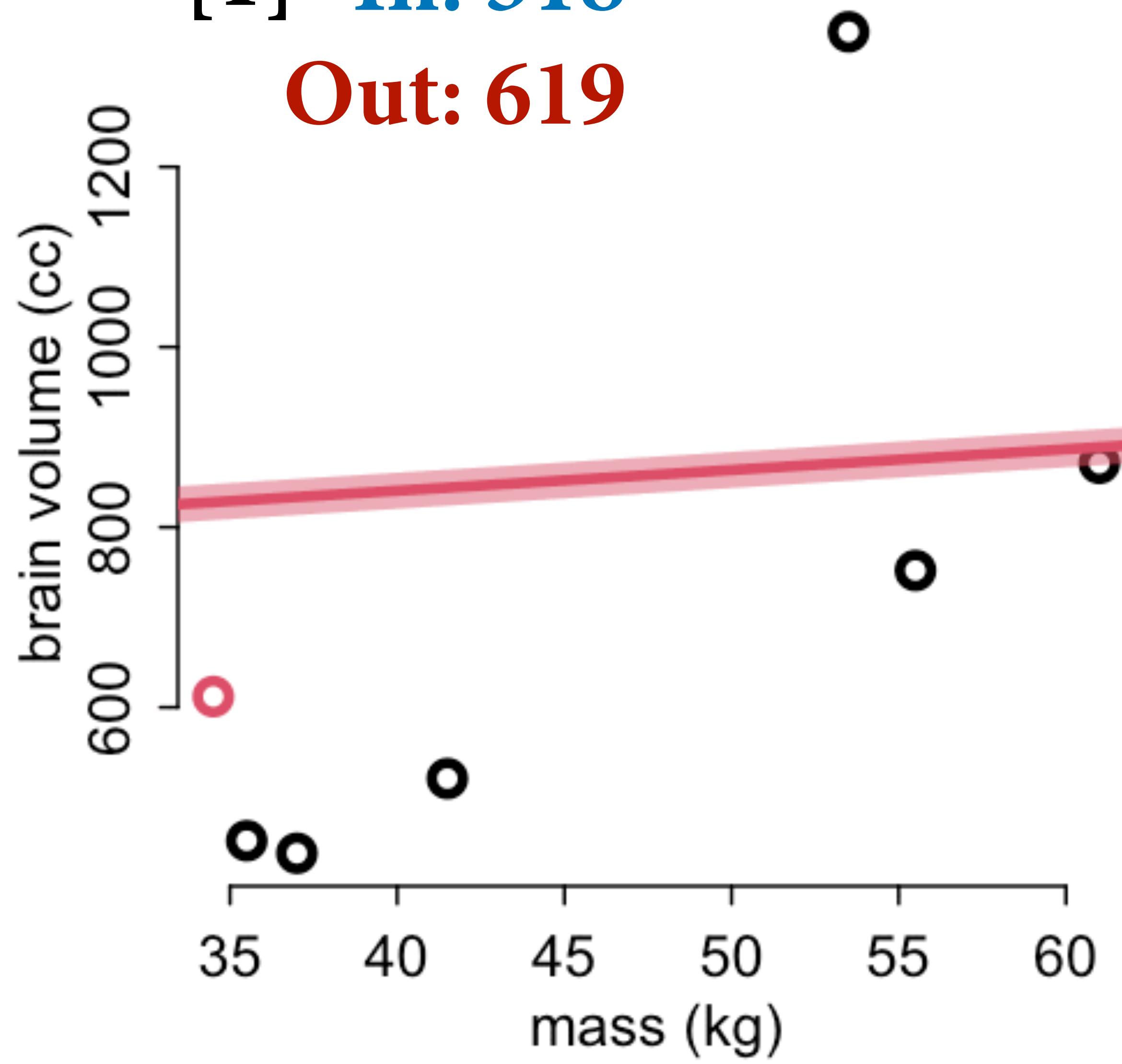
*N data points*

*S samples  
from posterior*

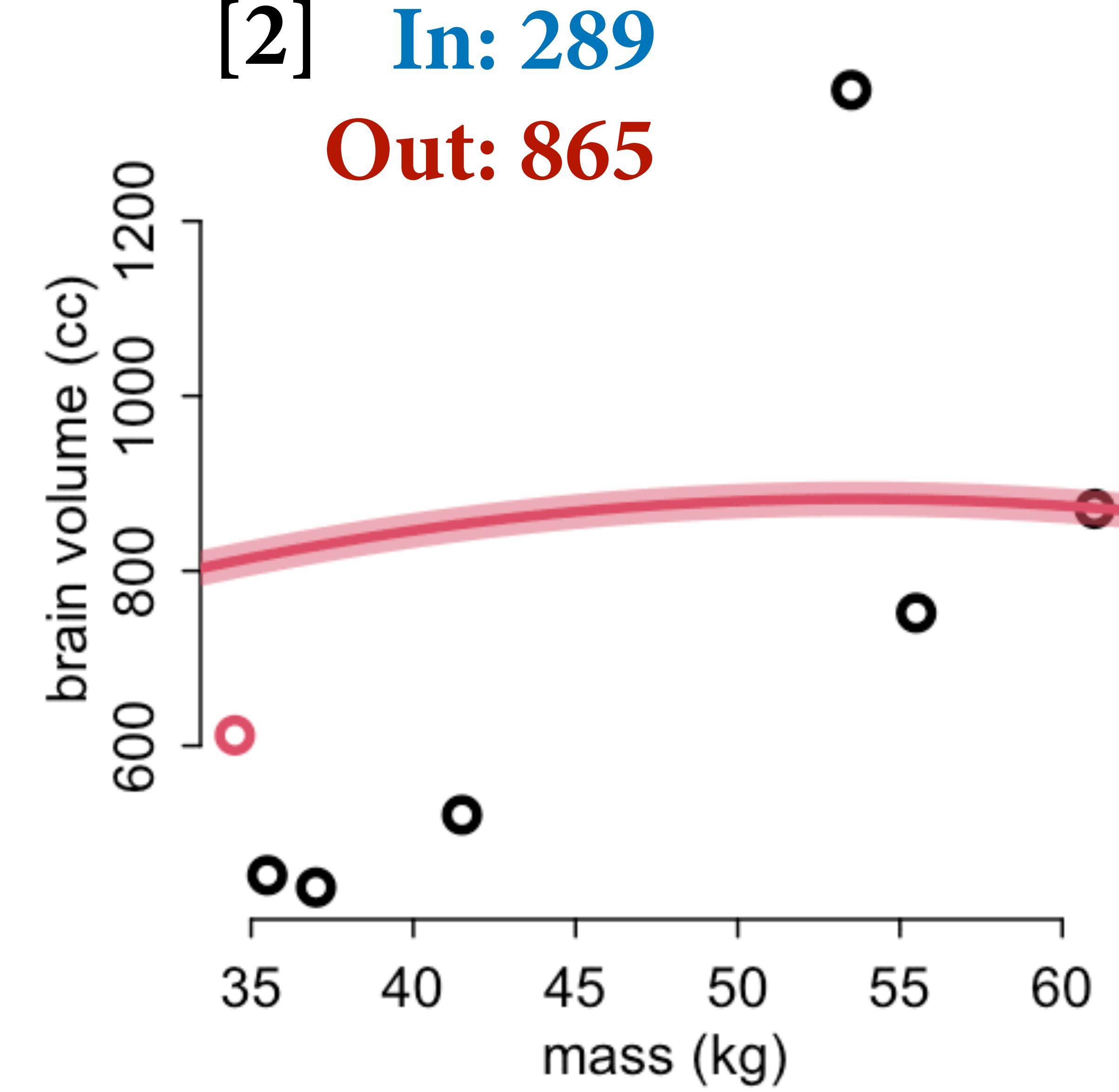
*average log probability  
for point i*

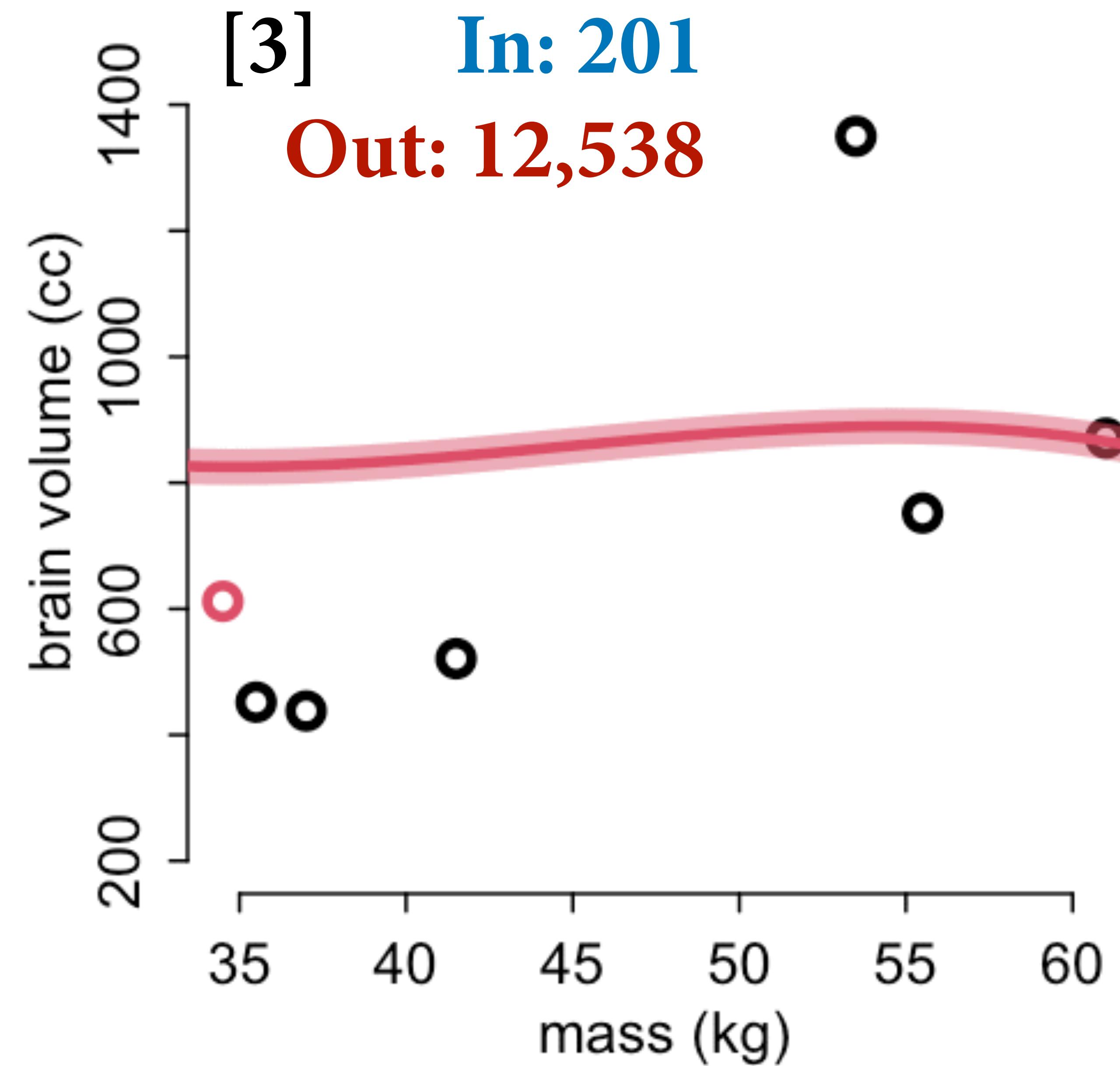
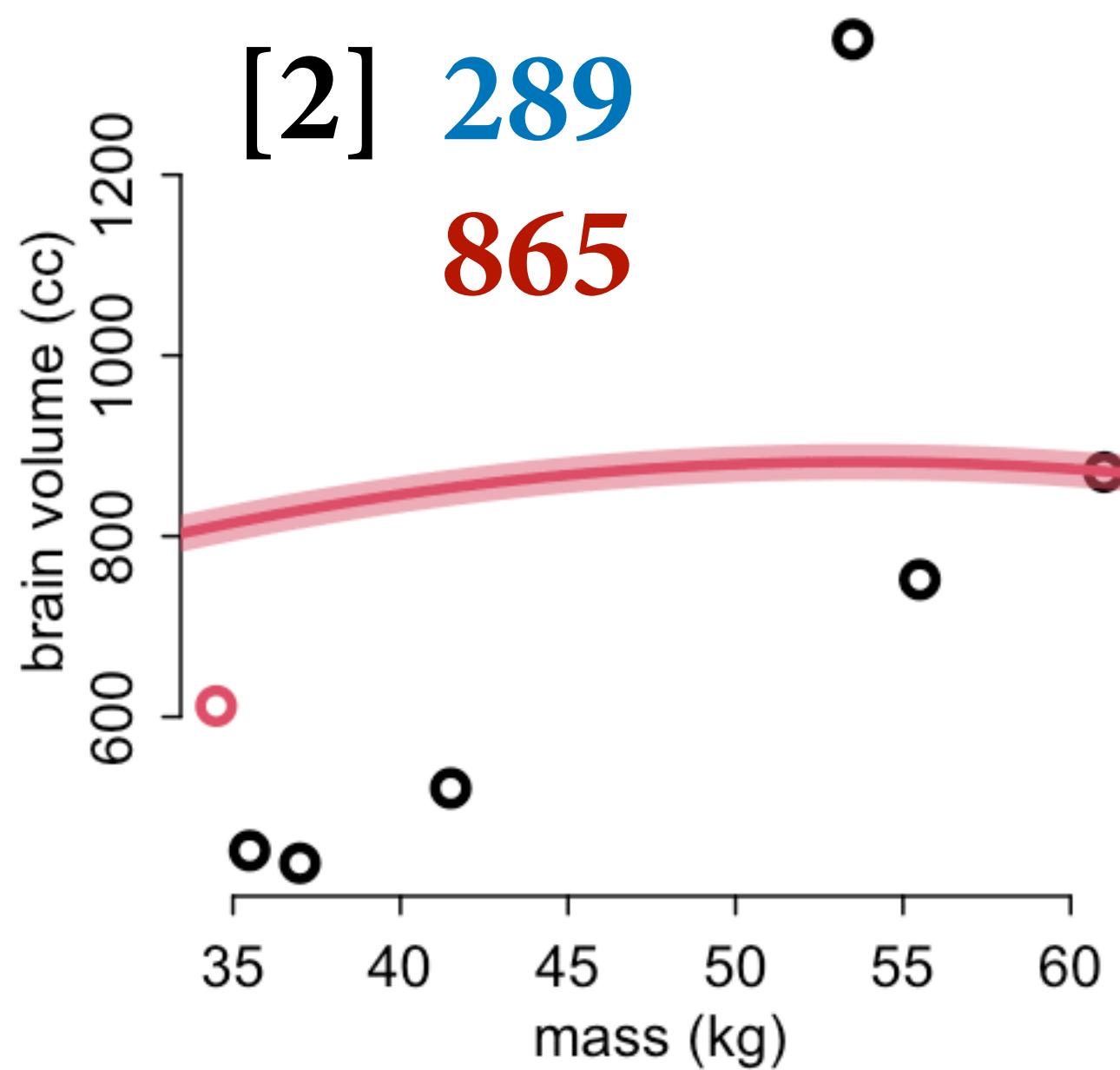
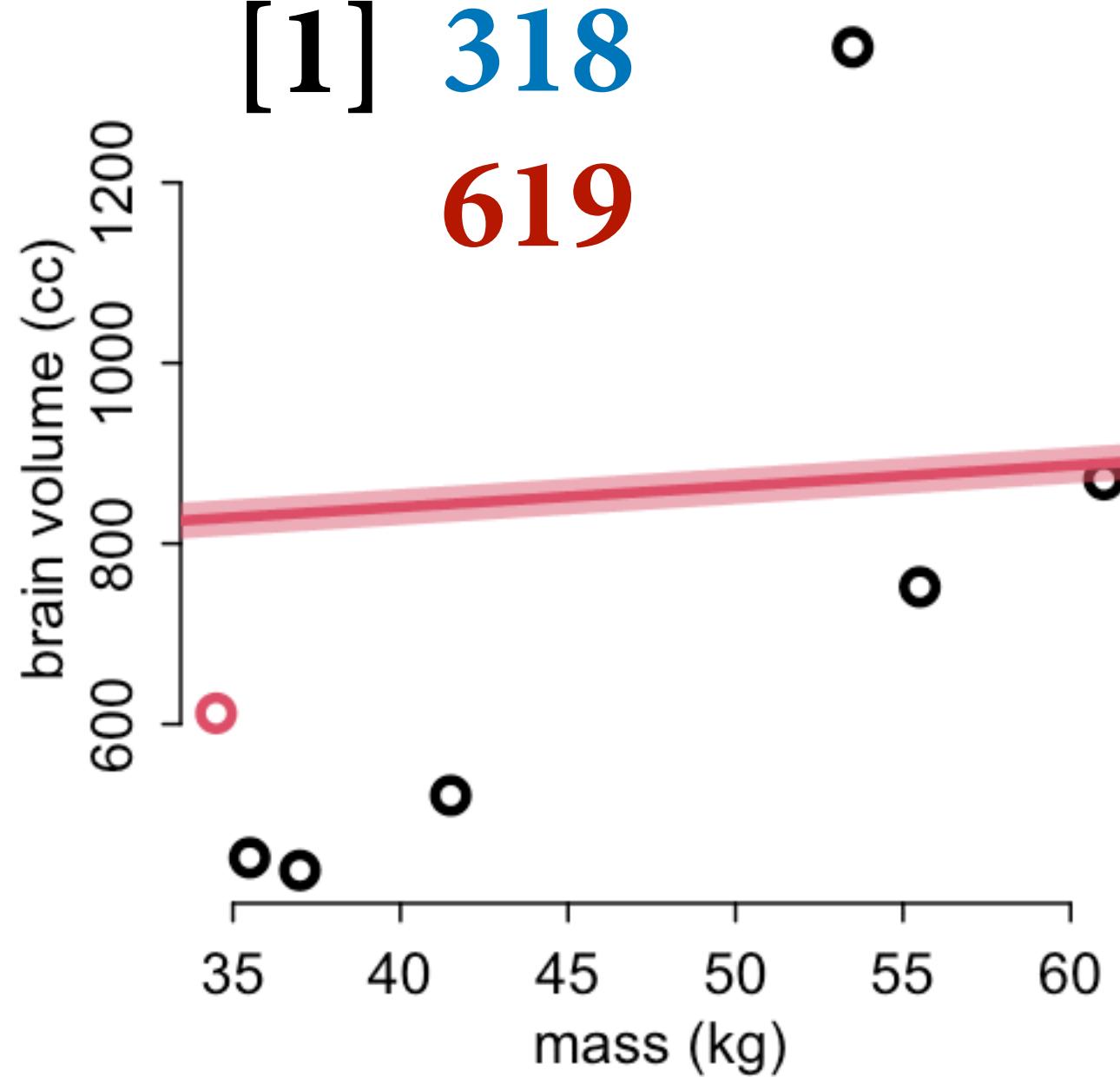
*log probability of each point i,  
computed with posterior that  
omits point i*

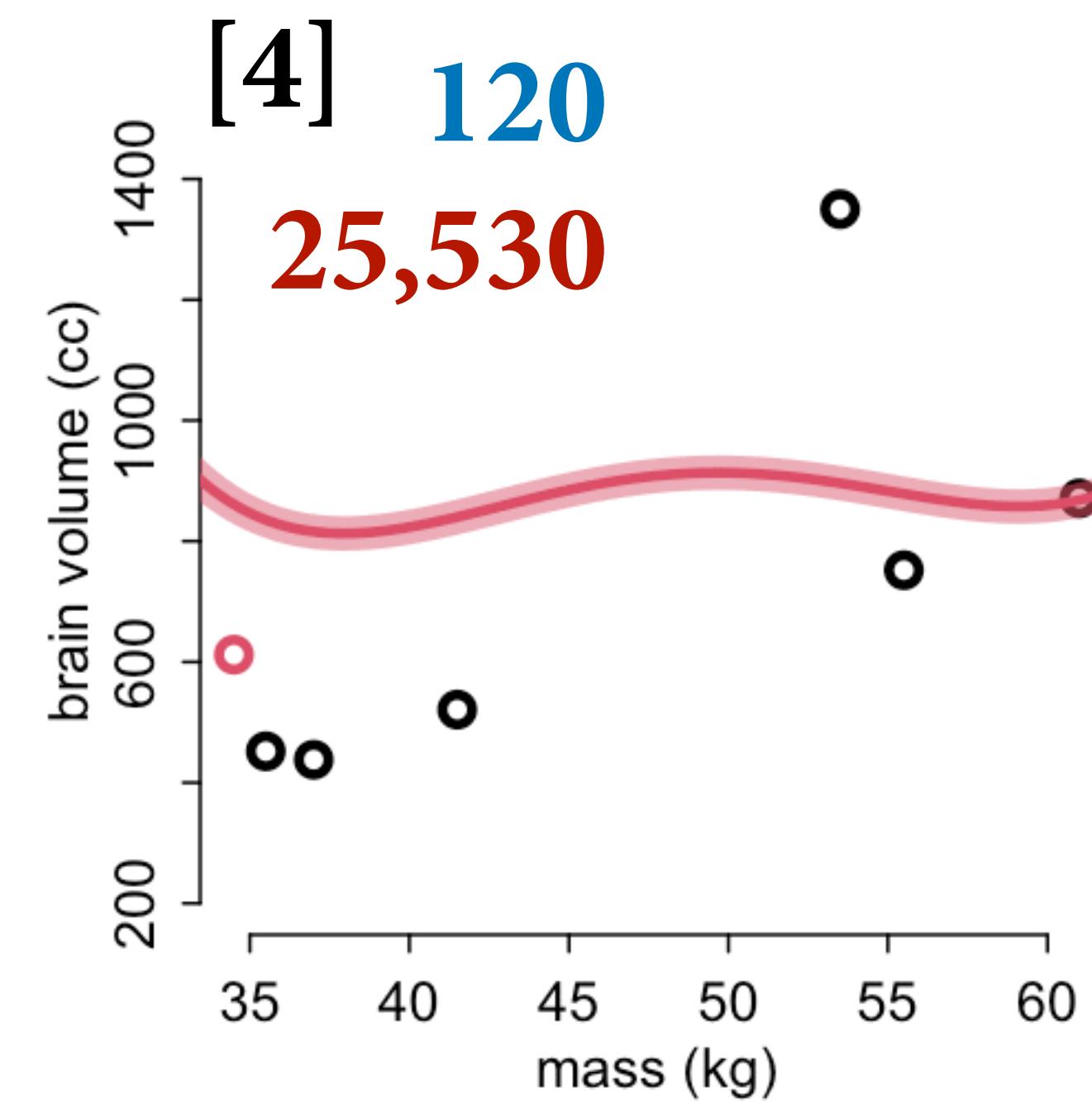
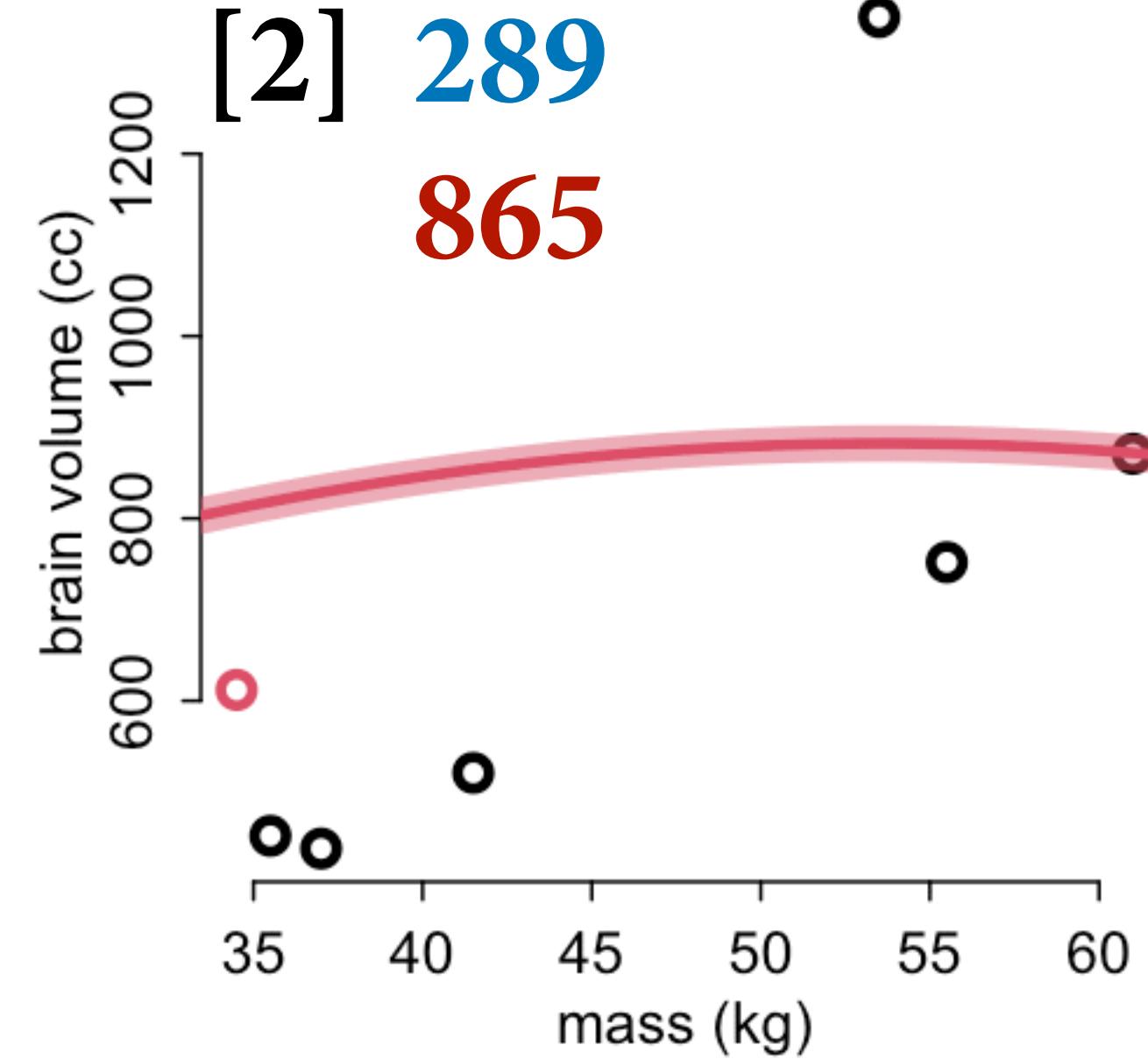
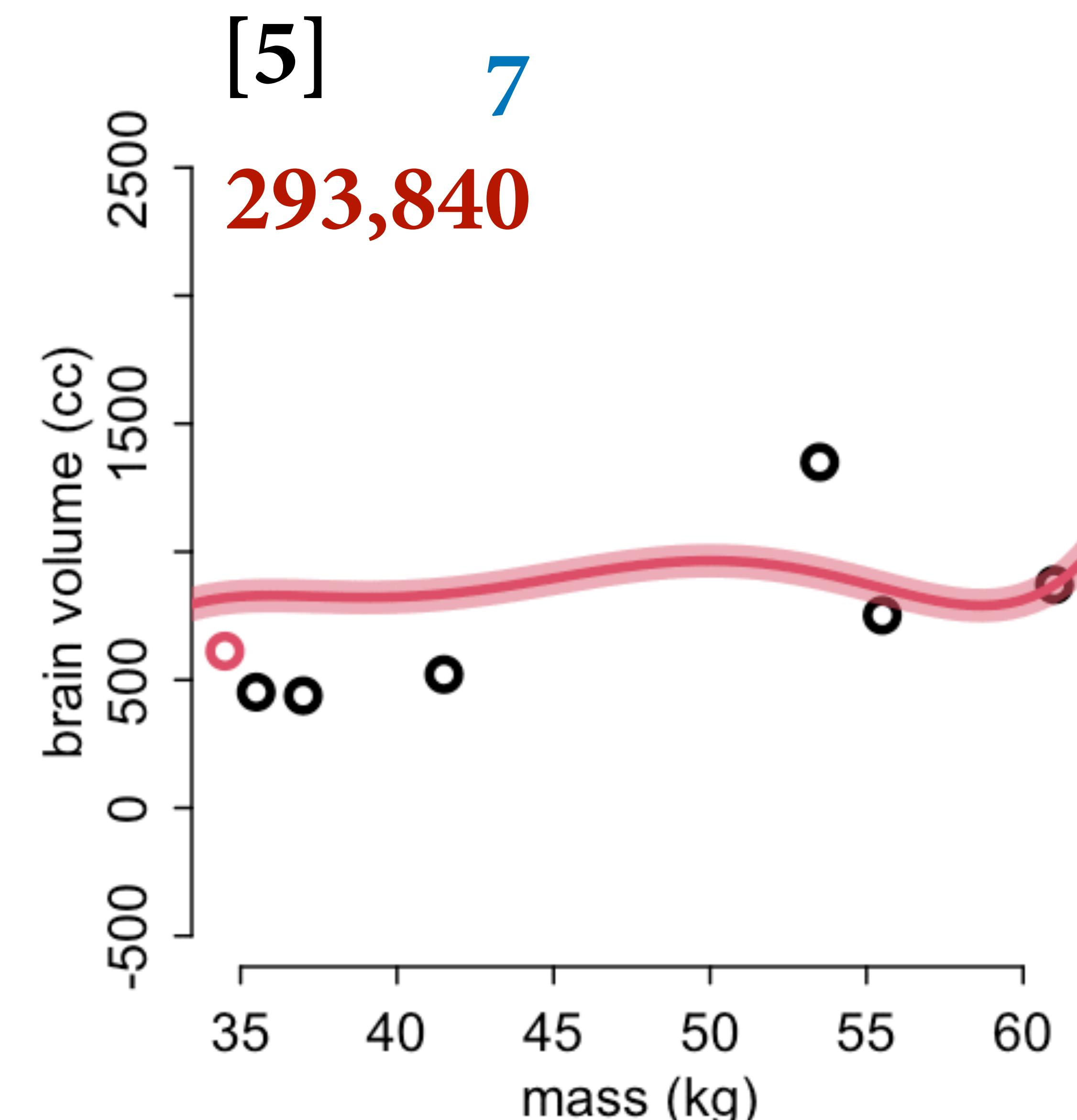
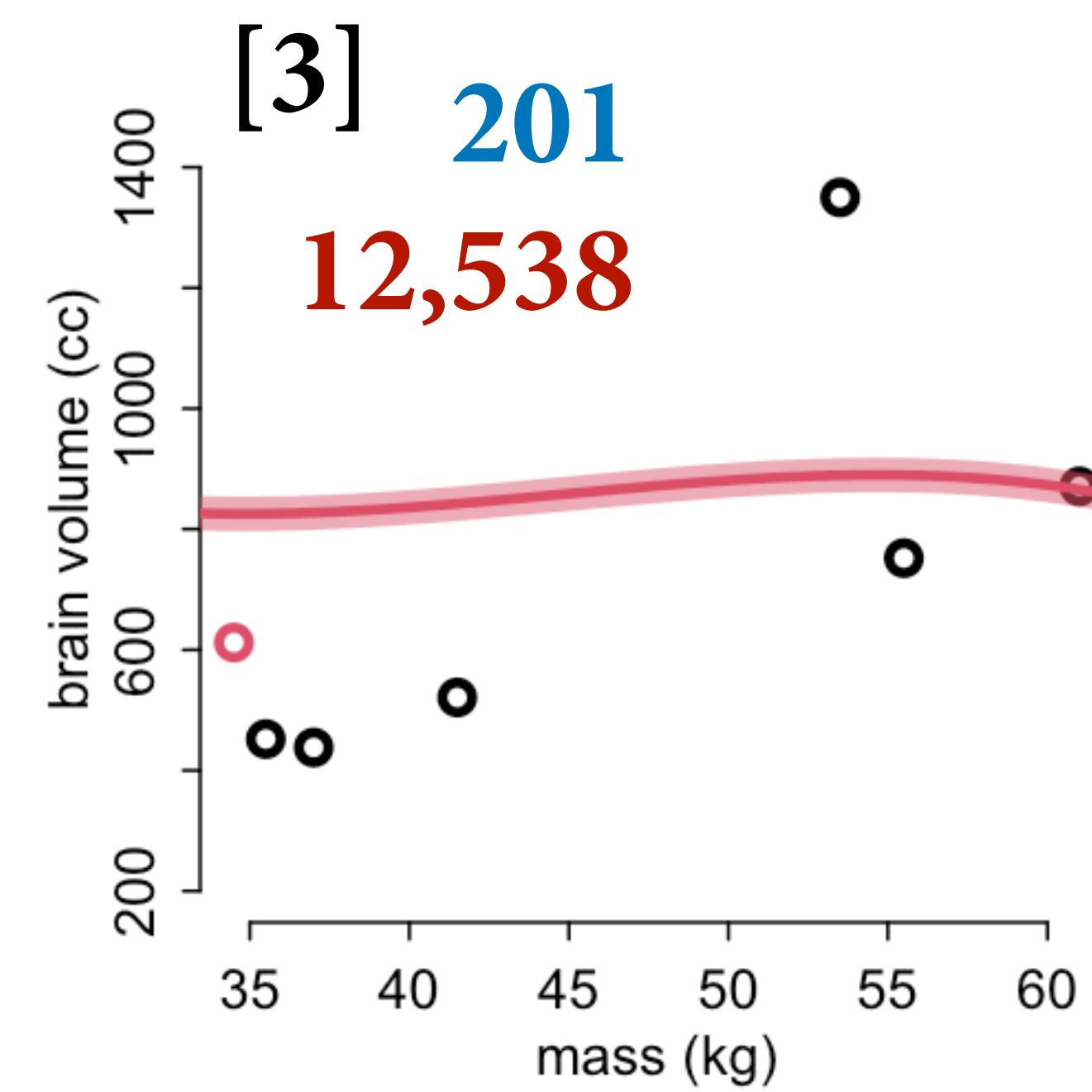
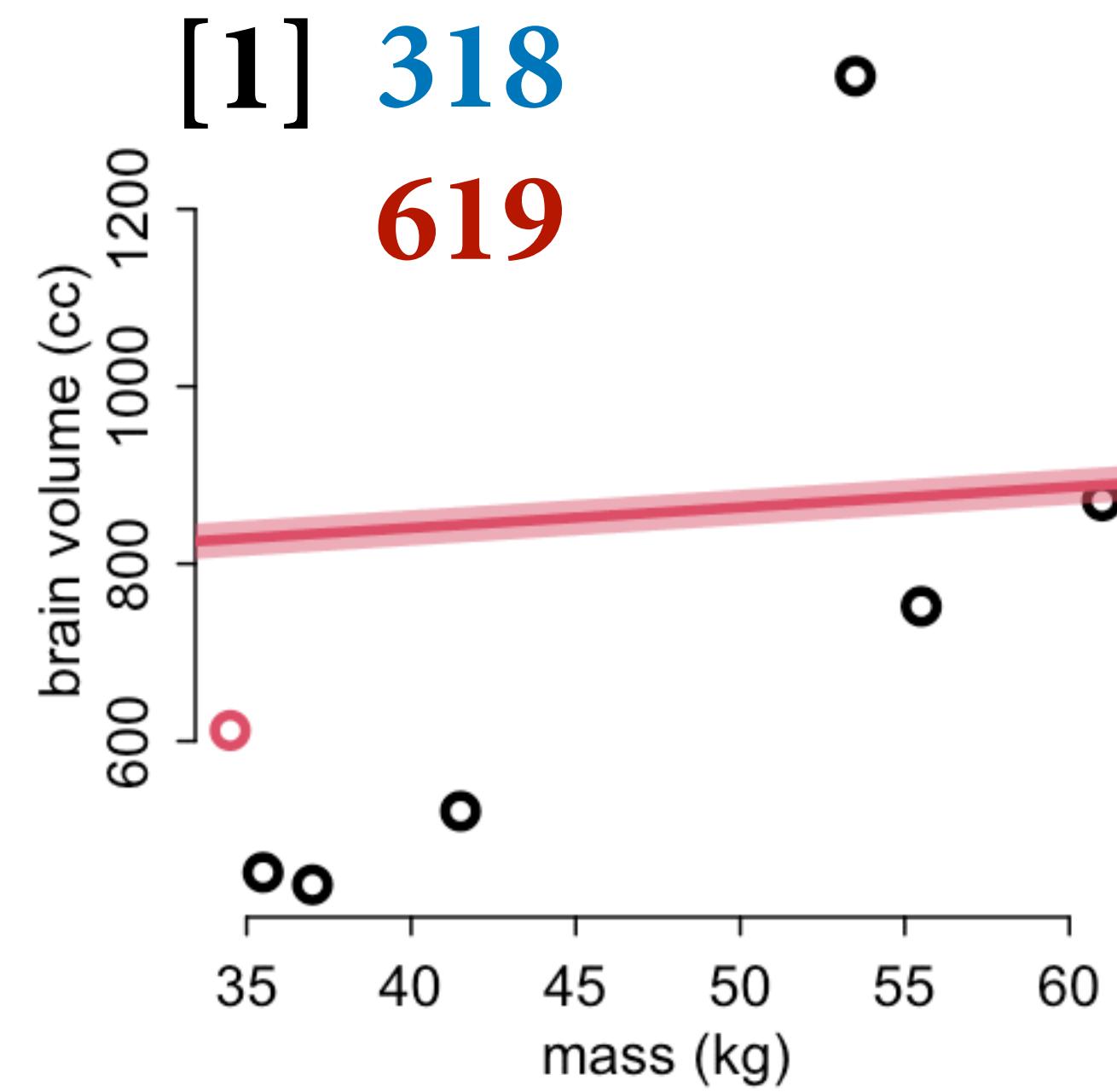
[1] In: 318  
Out: 619



[2] In: 289  
Out: 865





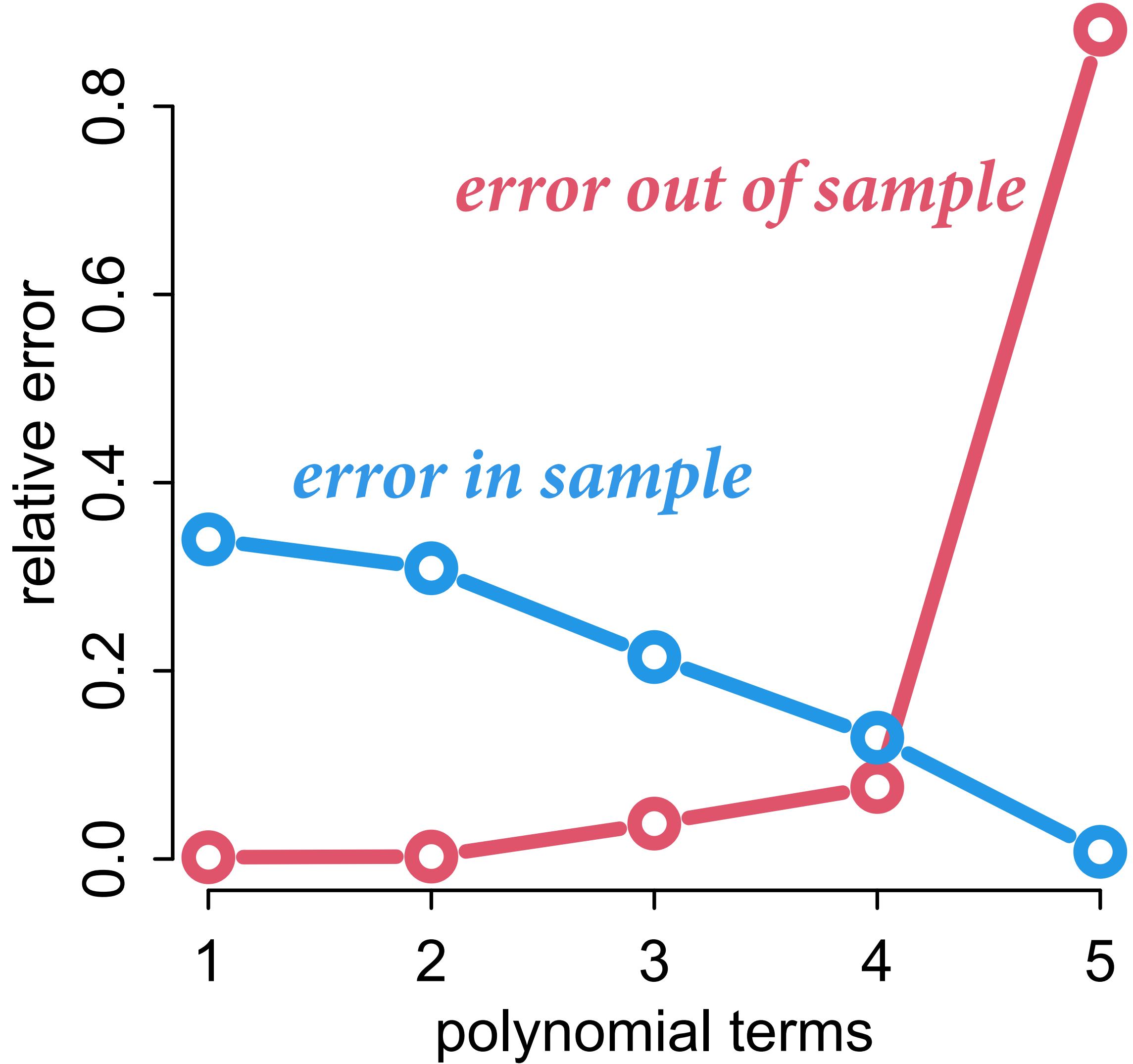


# Cross-validation

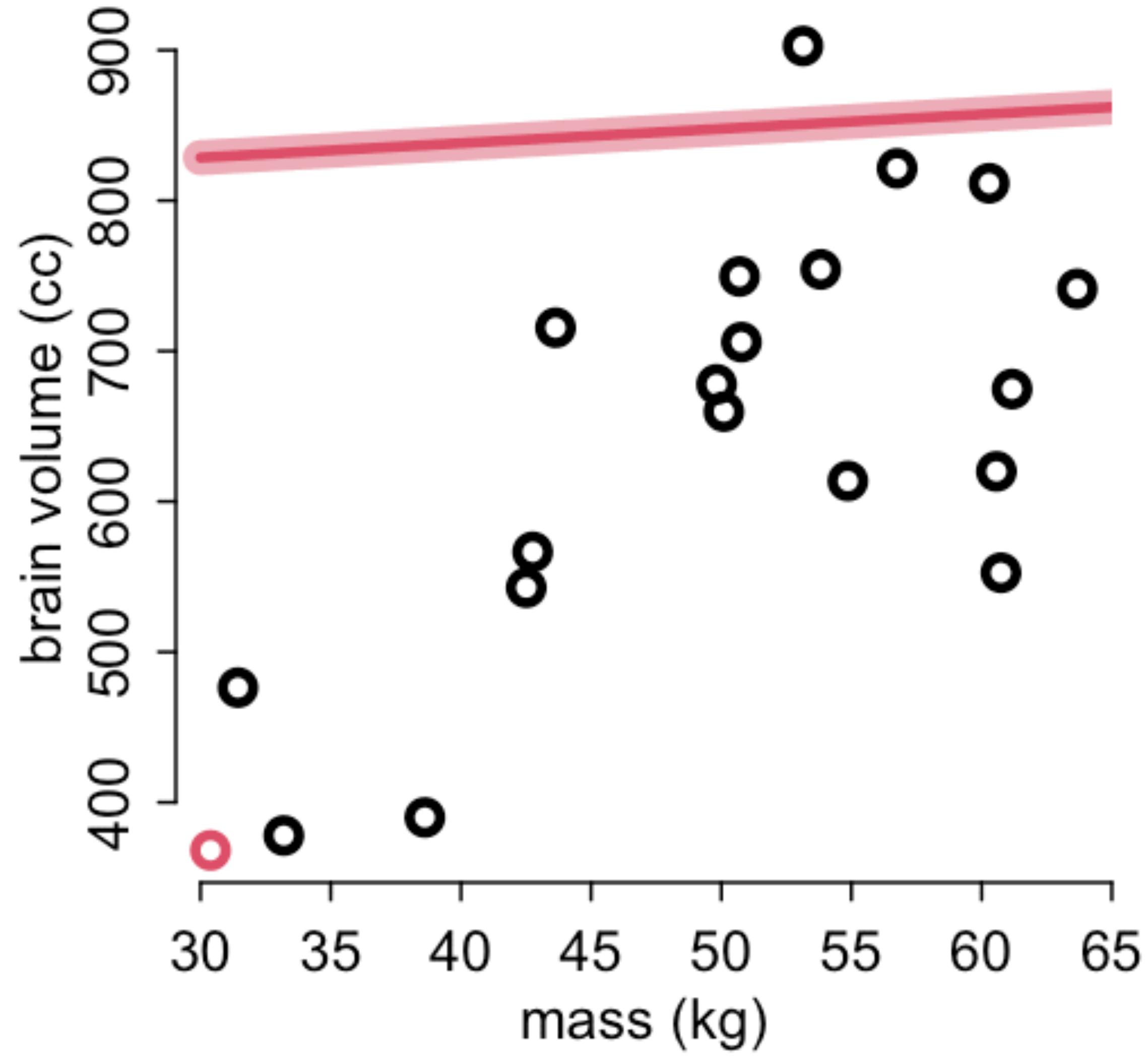
For simple models, increasing parameters improves fit to sample

But may reduce accuracy of predictions out of sample

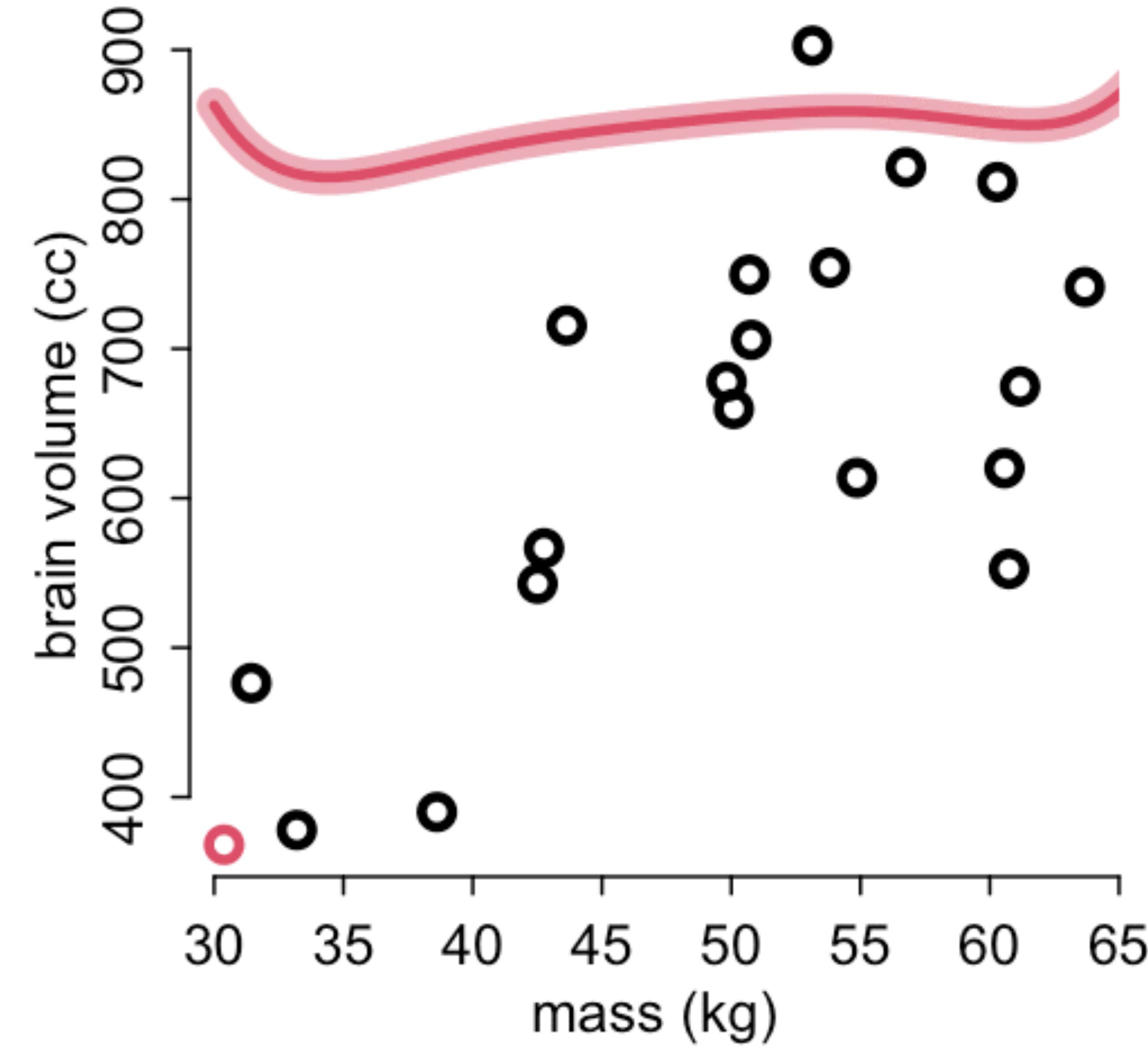
Most accurate model trades off flexibility with overfitting



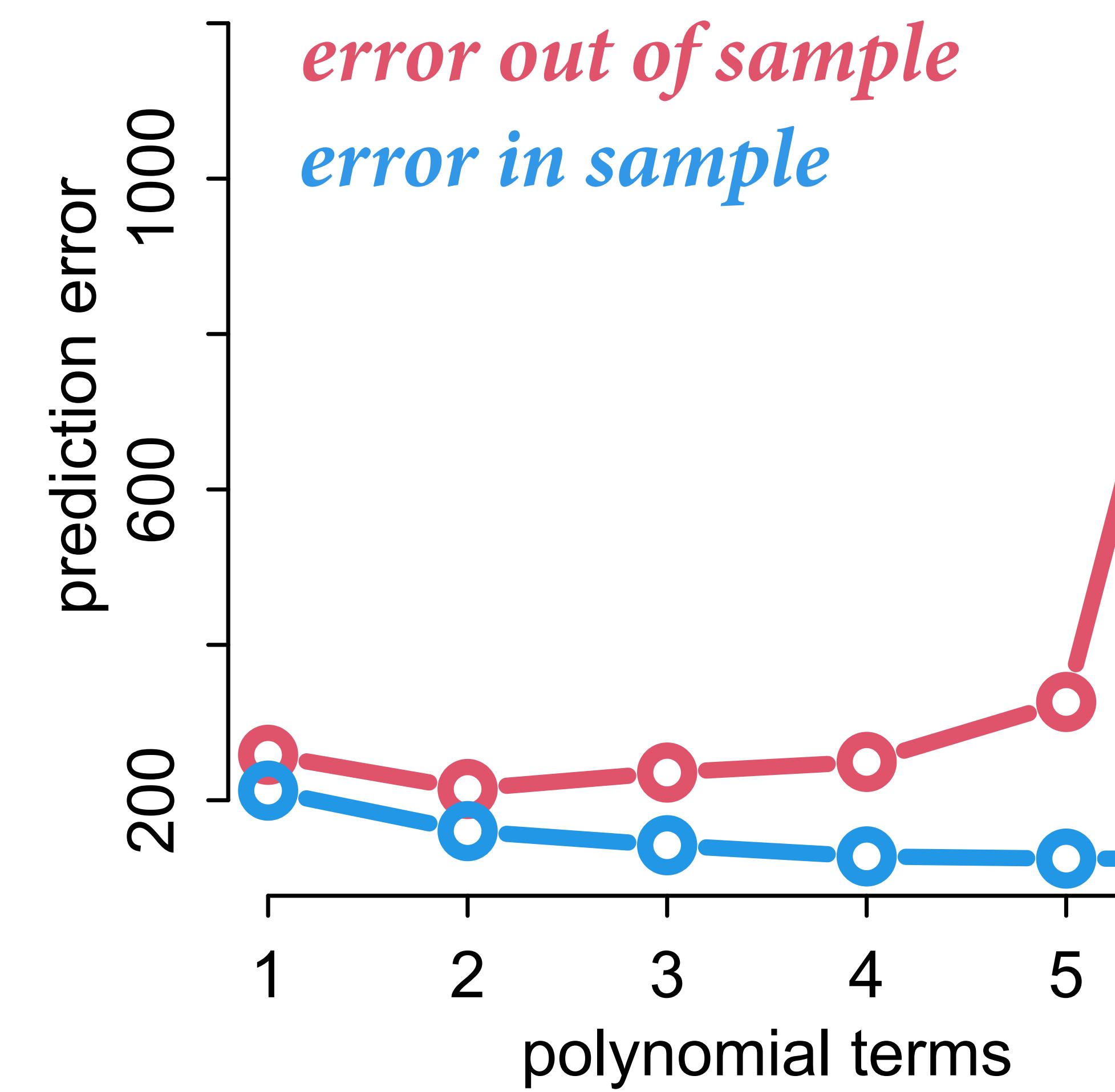
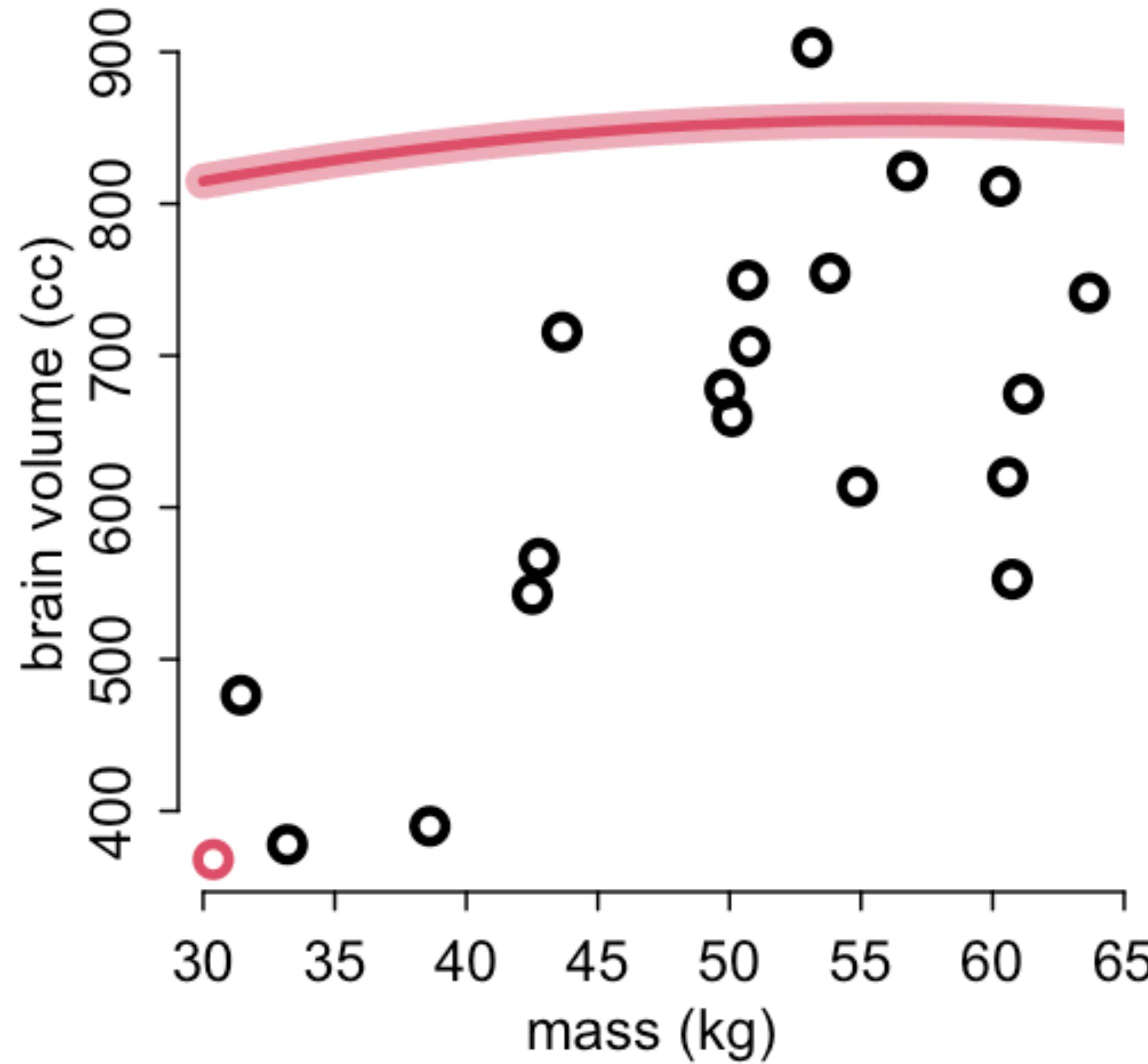
1st degree polynomial



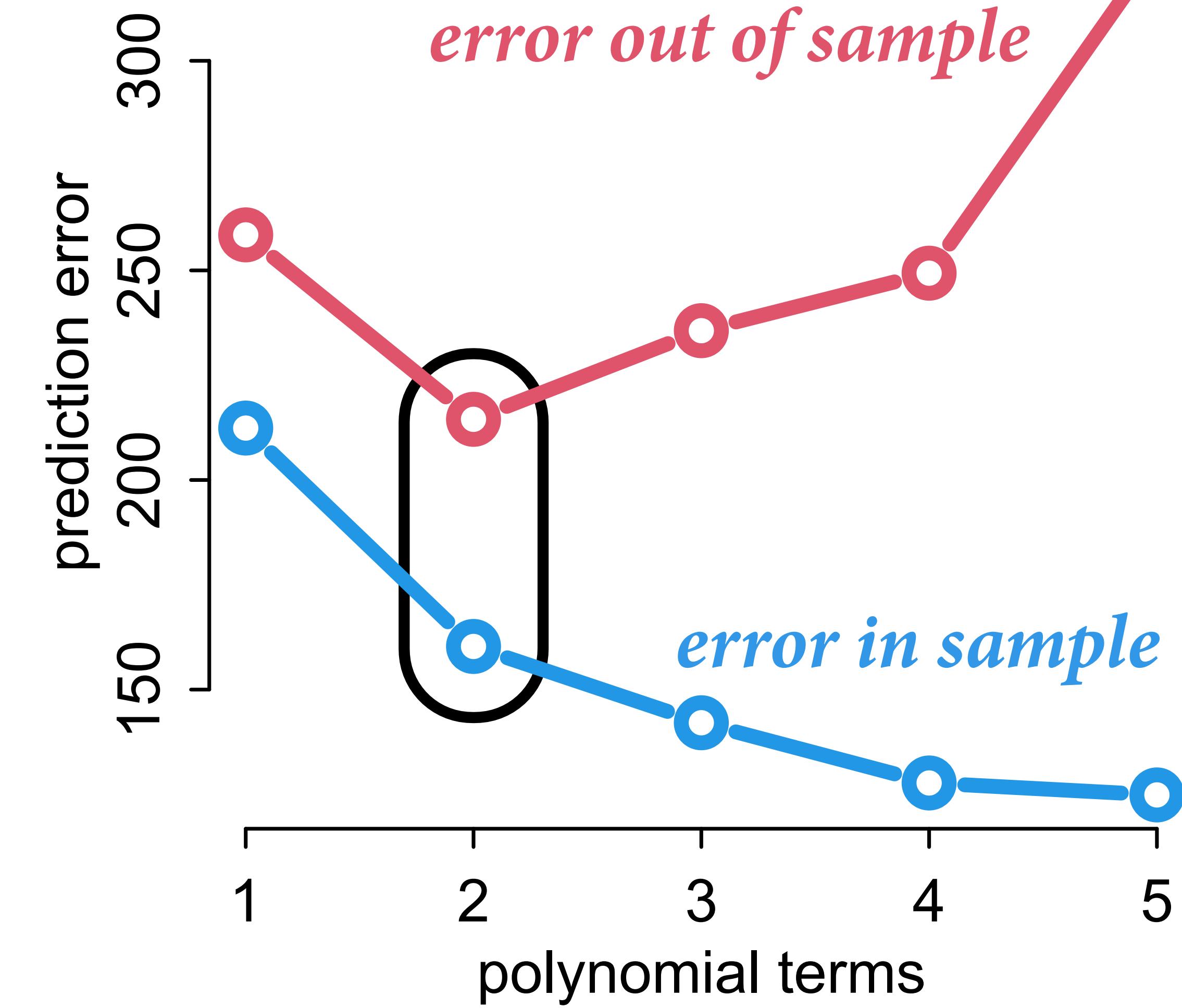
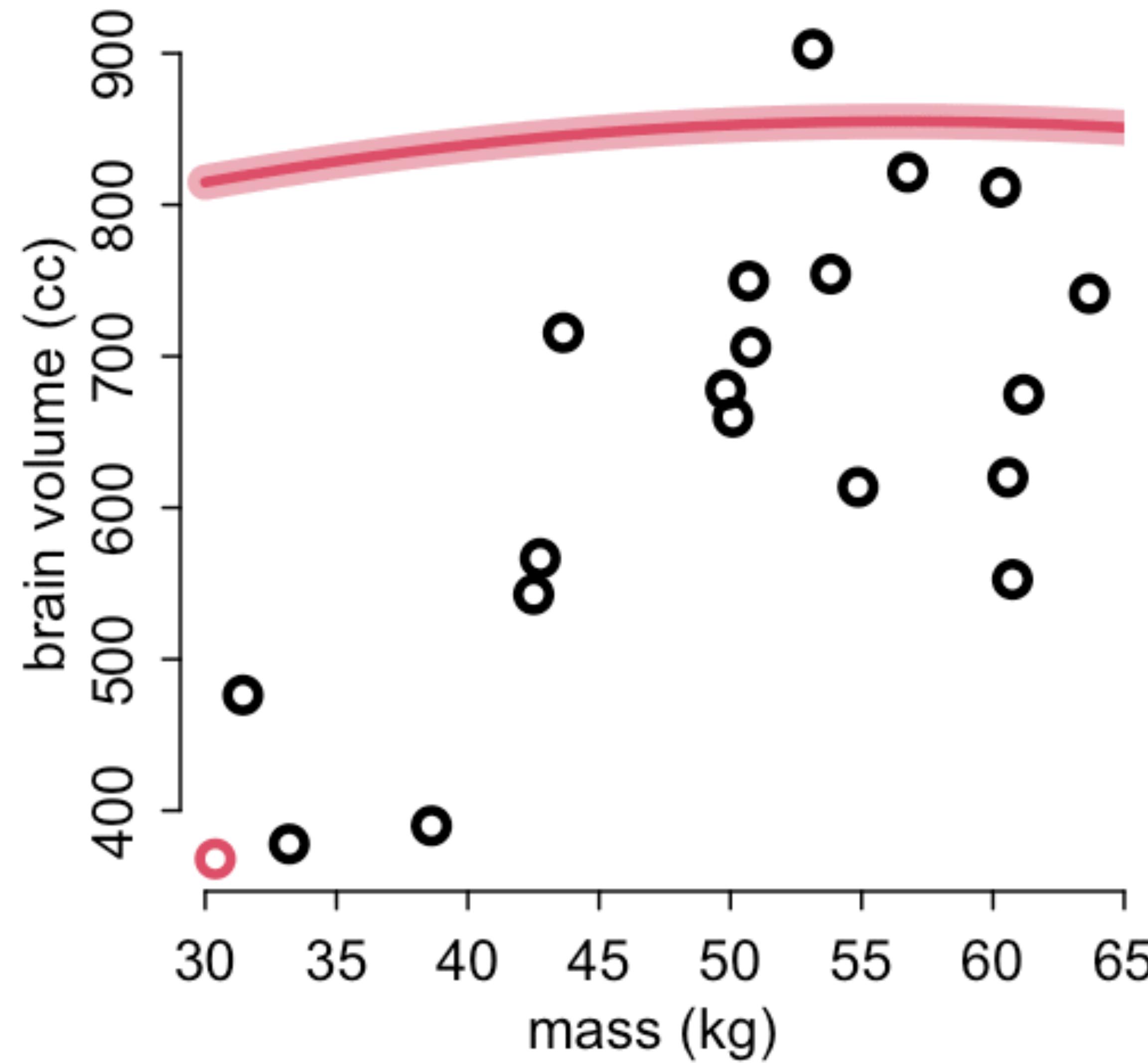
6th degree polynomial



## 2nd degree polynomial



## 2nd degree polynomial



# Regularization

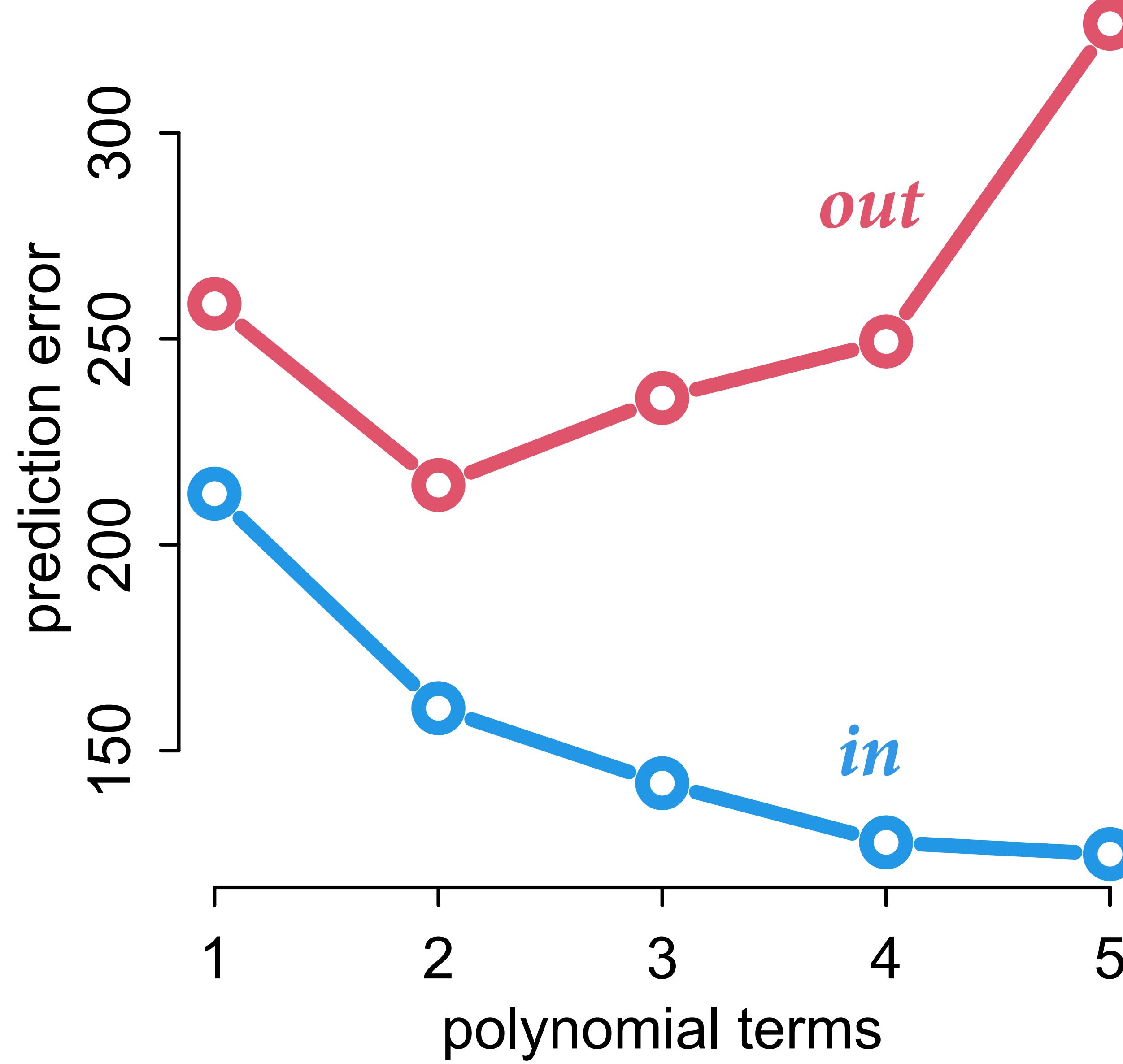
Overfitting depends upon the priors

Skeptical priors have tighter variance, reduce flexibility

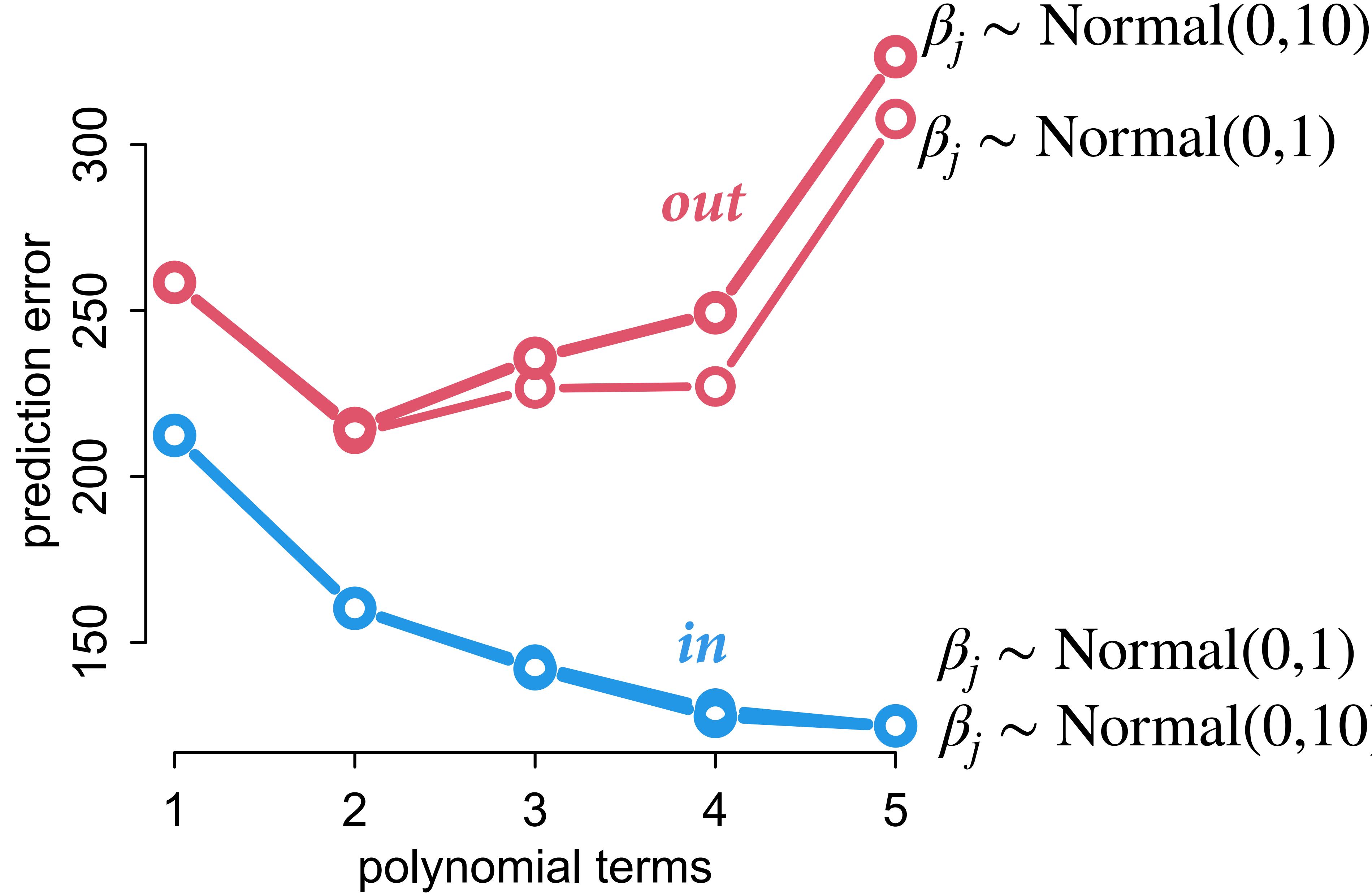
***Regularization***: Function finds regular features of process

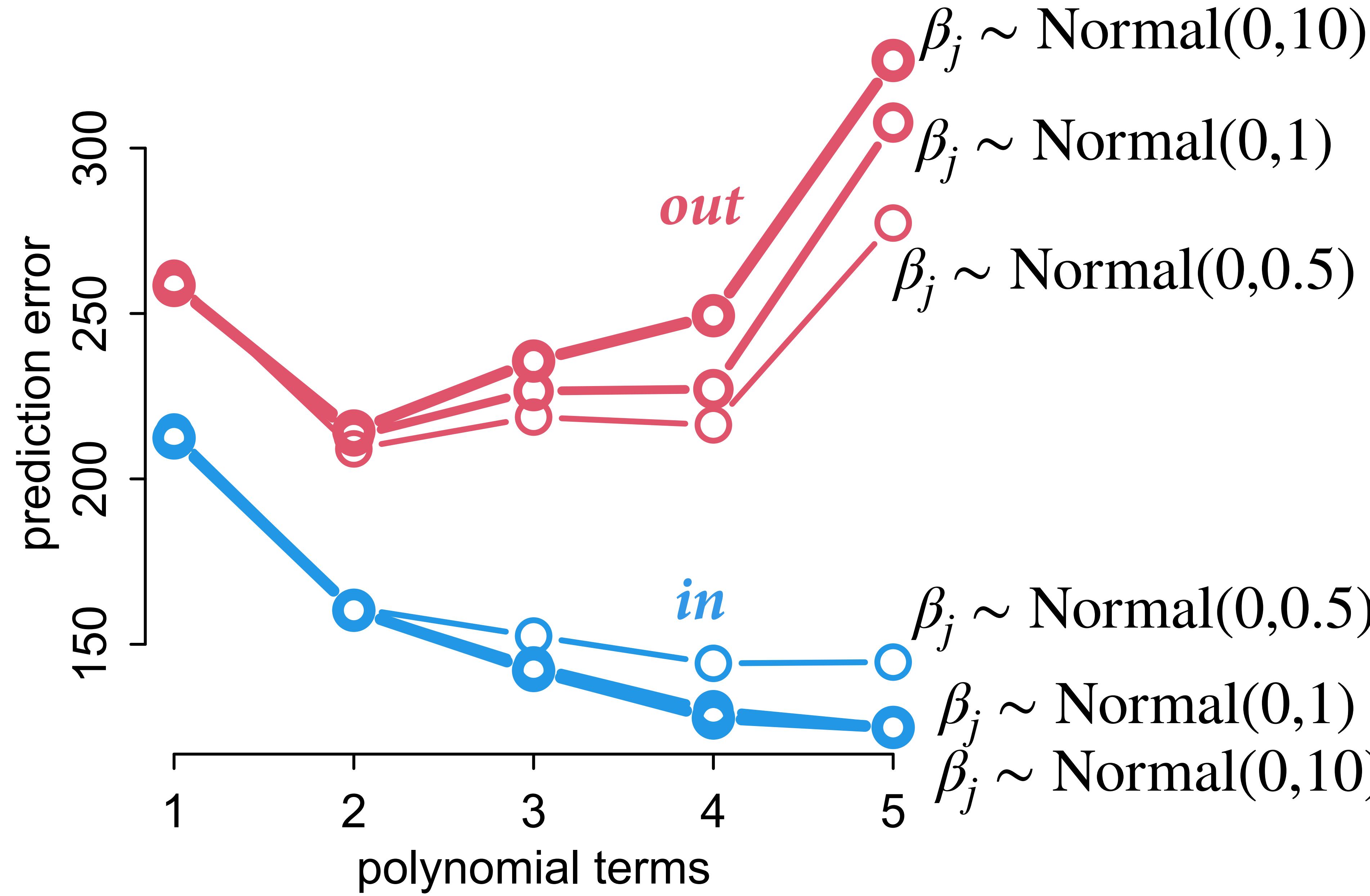
Good priors are often tighter than you think!

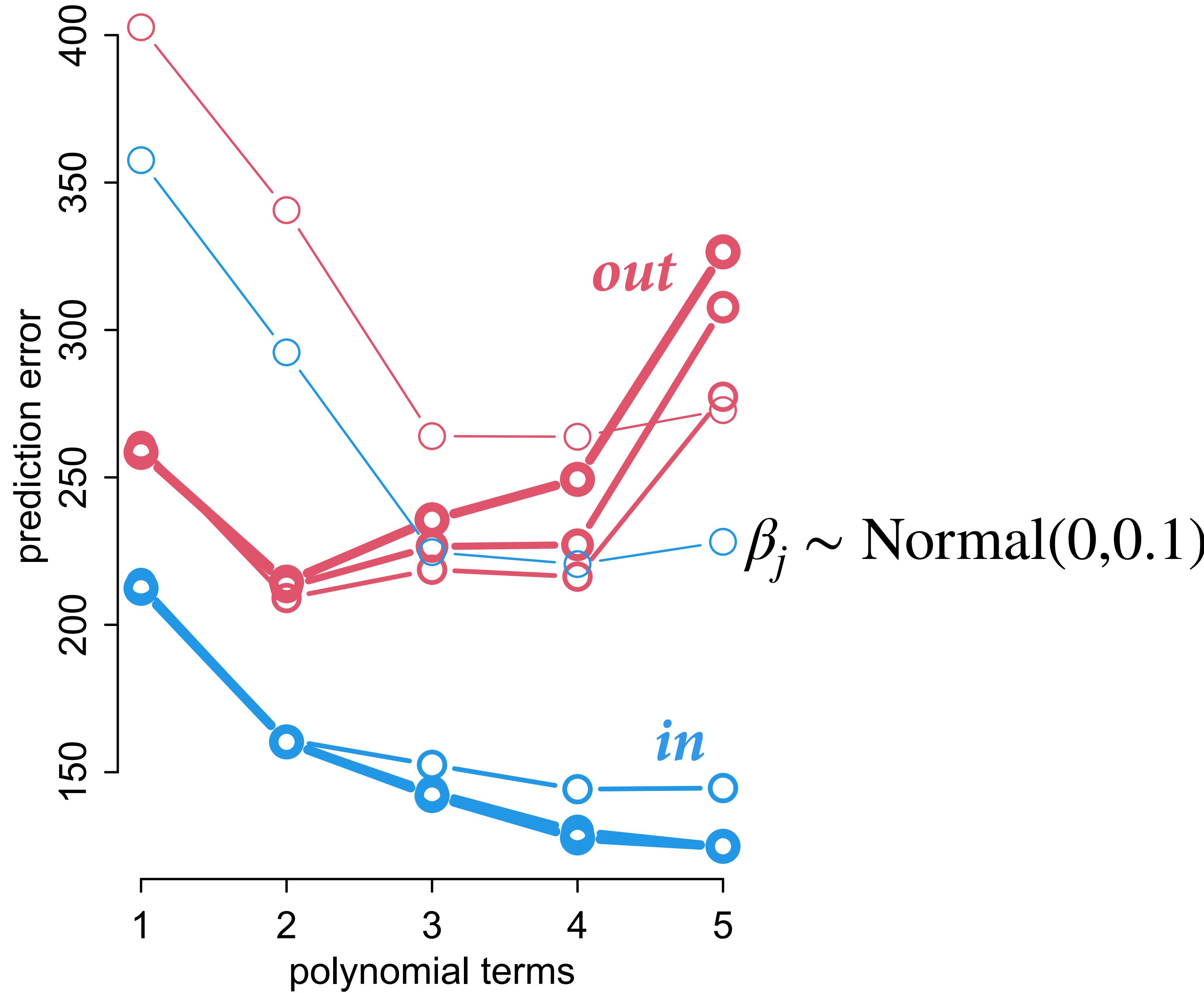




$$\mu_i = \alpha + \sum_{j=1}^m \beta_j x_i^j$$
$$\beta_j \sim \text{Normal}(0, 10)$$







# Regularizing priors

How to choose width of prior?

For causal inference, use science

For pure prediction, can tune the prior using cross-validation

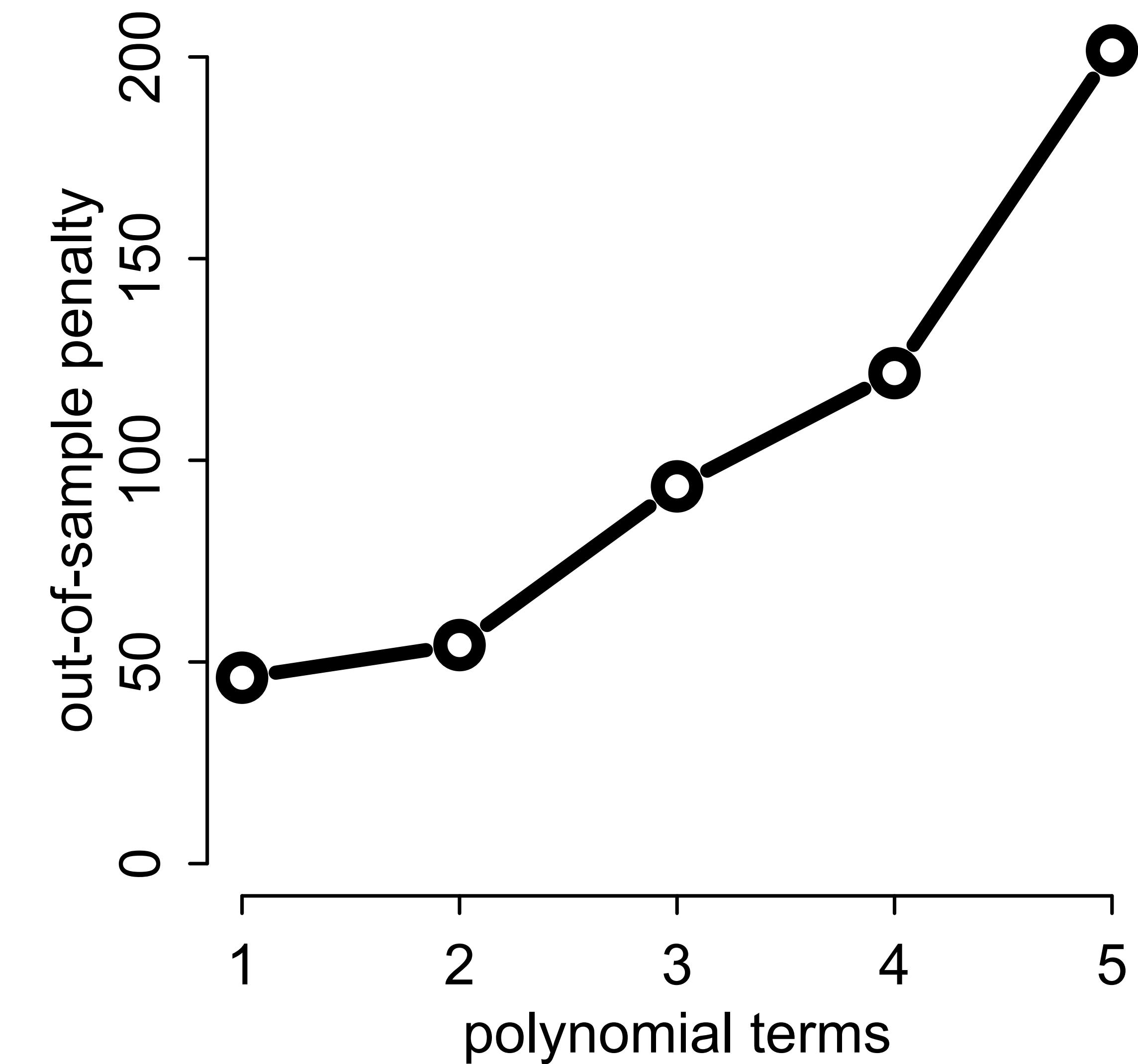
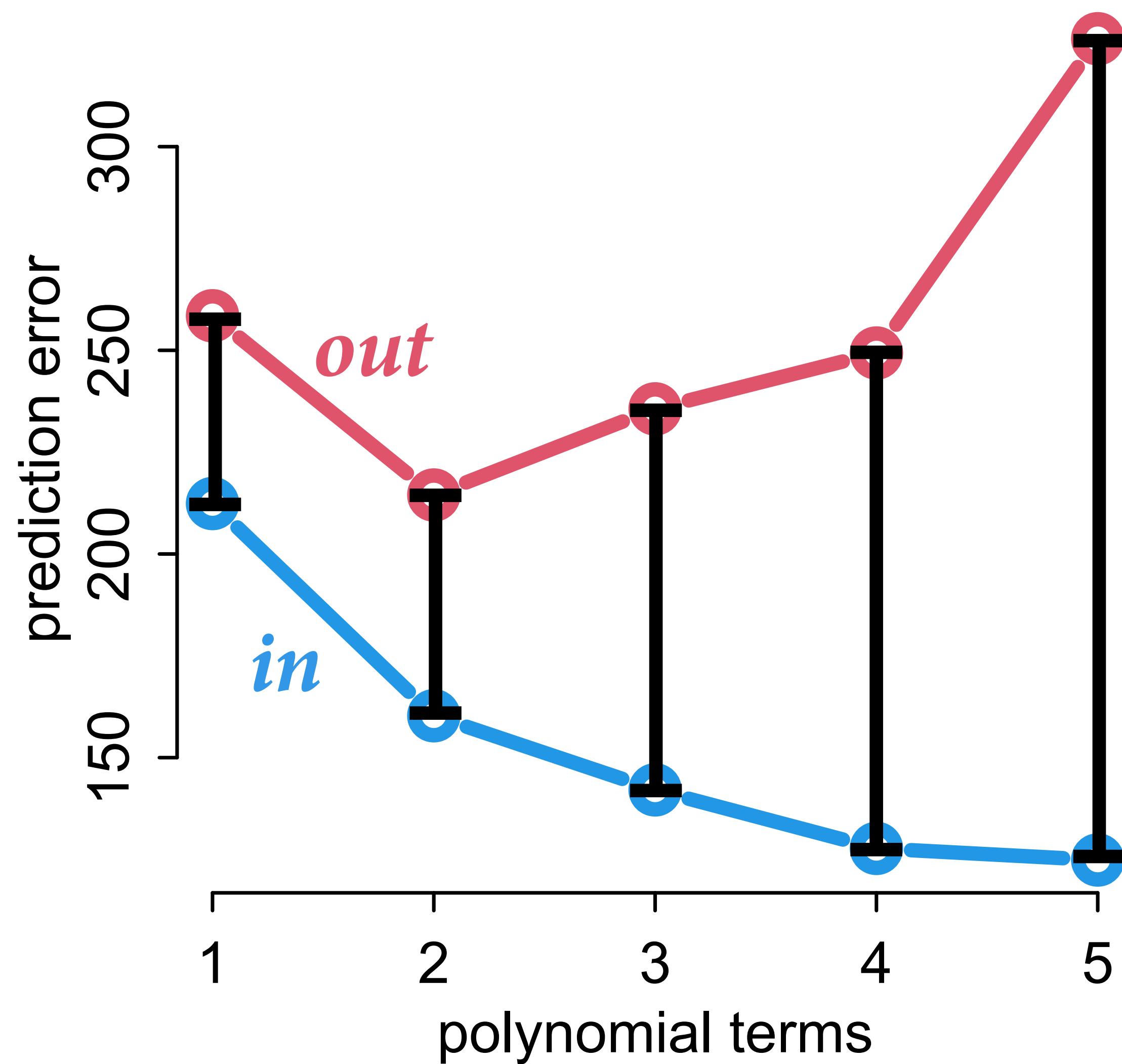
Many tasks are a mix of inference and prediction

No need to be perfect, just better



**PAUSE**

# Prediction penalty



# Penalty prediction

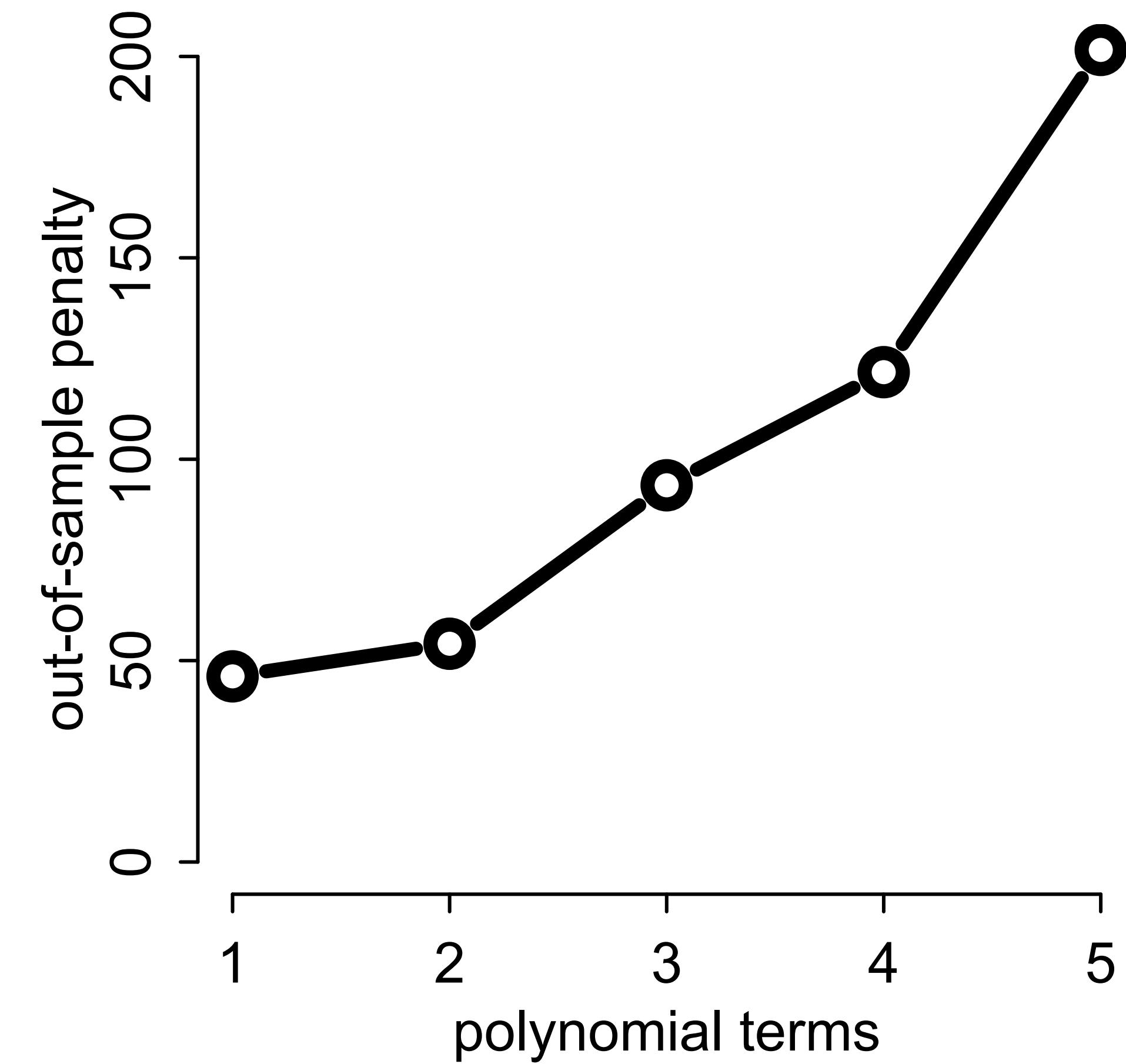
For  $N$  points, cross-validation  
requires fitting  $N$  models

What if you could compute the  
penalty from a single model fit?

Good news! You can:

Importance sampling (PSIS)

Information criteria (WAIC)

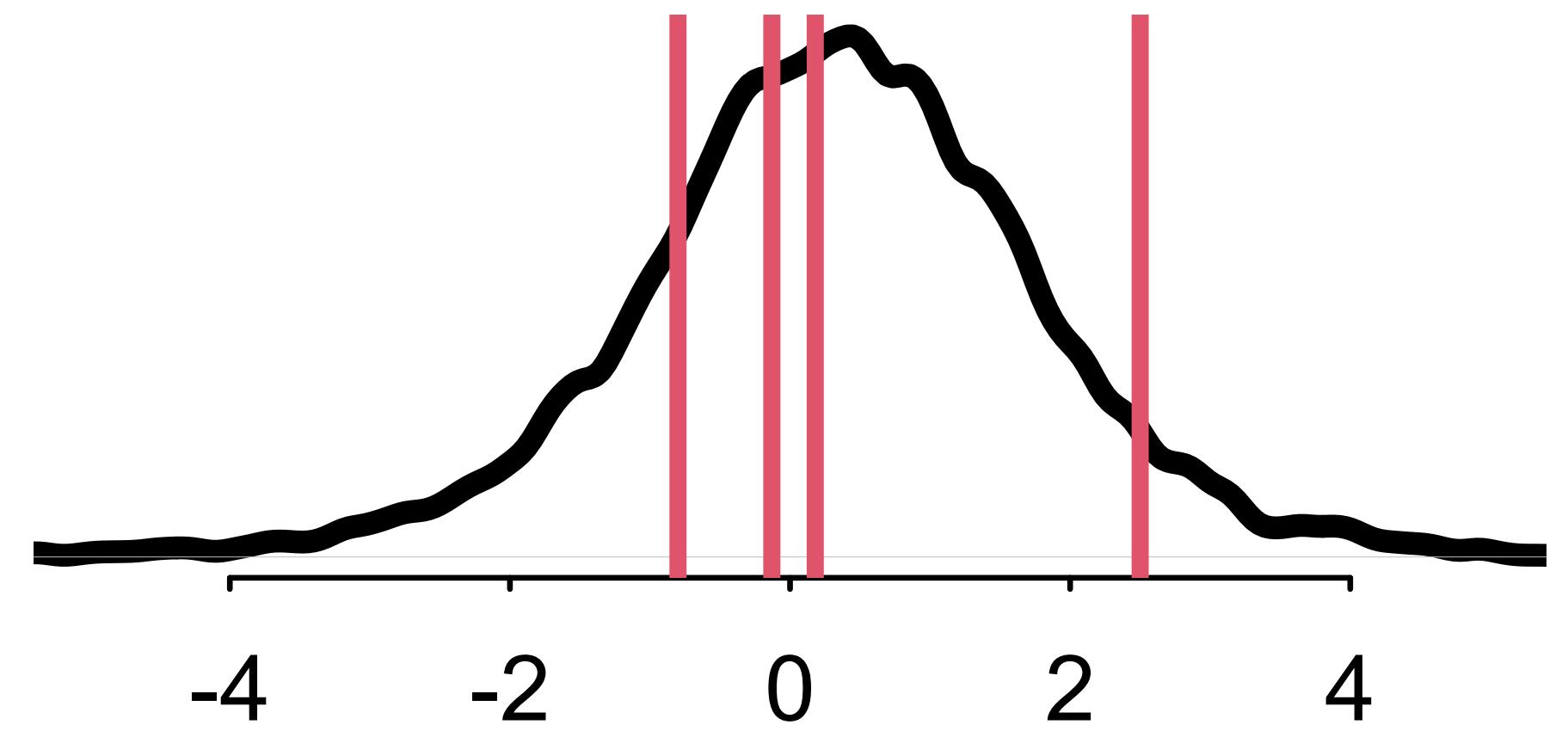


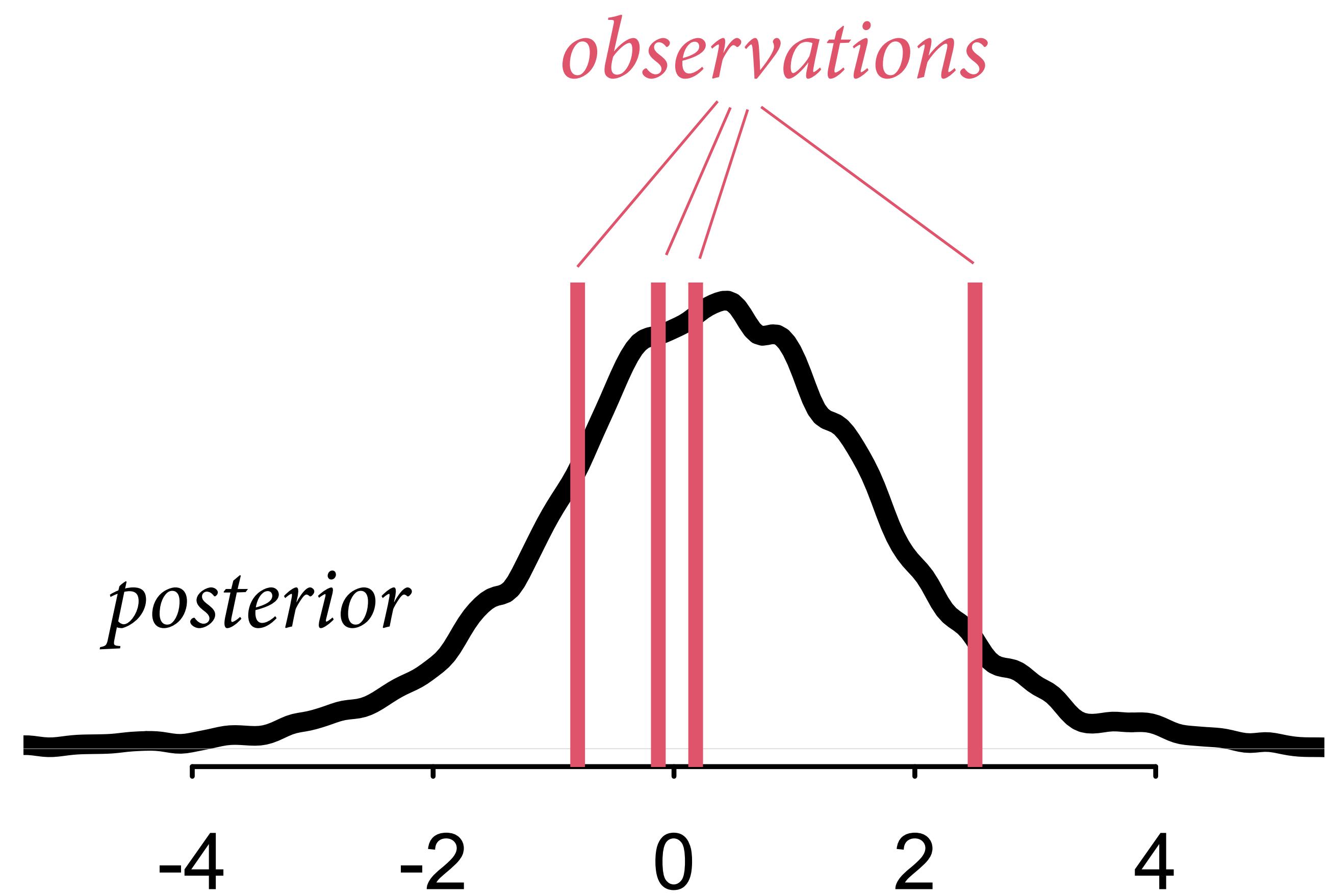
# Importance Sampling

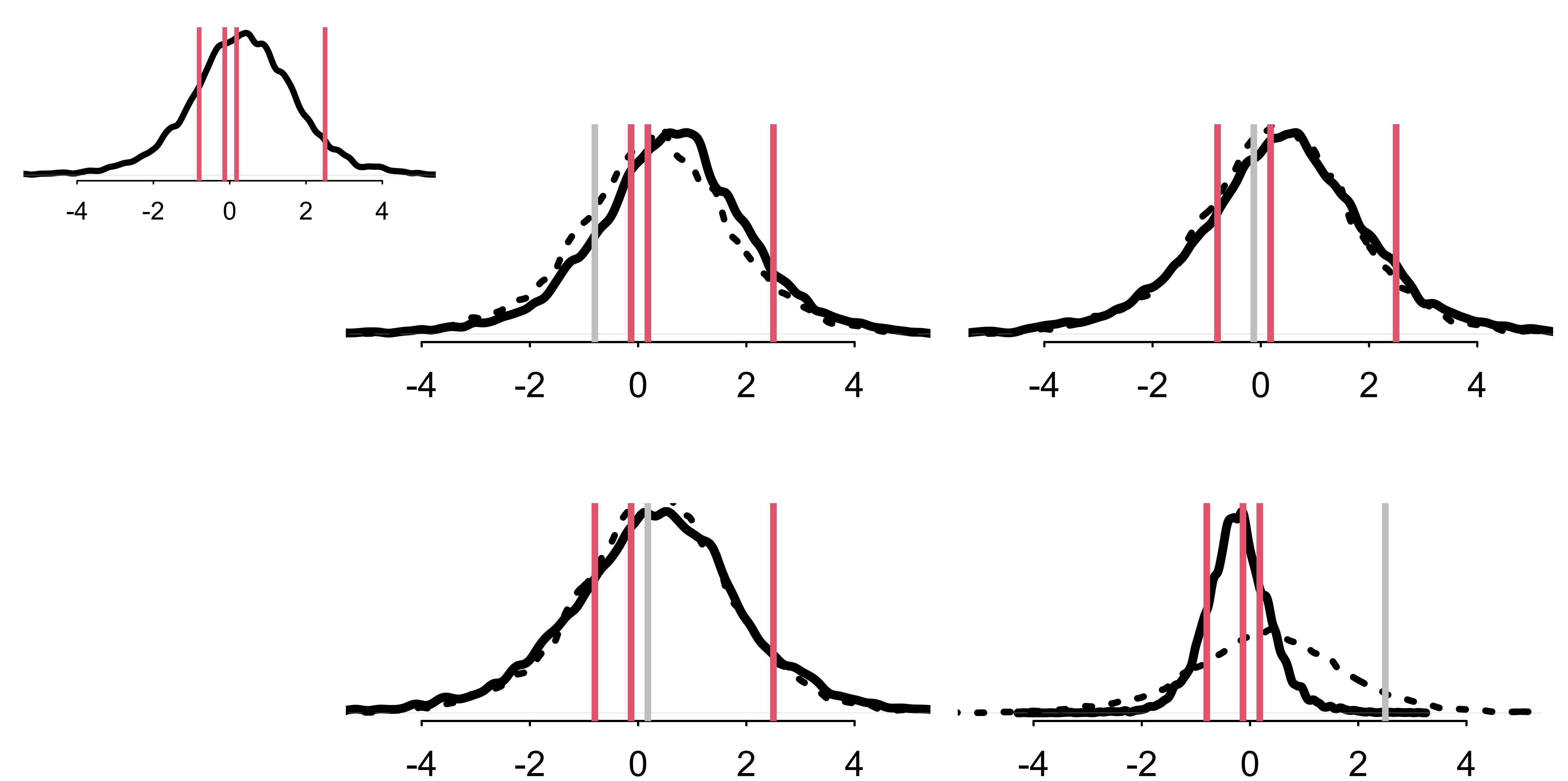
Importance sampling: Use a single posterior distribution for  $N$  points to sample from each posterior for  $N-1$  points

Key idea: Point with **low** probability has a strong influence on posterior distribution

Can use pointwise probabilities to reweight samples from posterior







# Smooth Importance Sampling

Importance sampling tends to be unreliable, has high variance

Pareto-smoothed importance sampling (PSIS) more stable (lower variance)

Useful diagnostics

Identifies important (high leverage) points (“outliers”)



Prof Aki Vehtari (Helsinki),  
smooth estimator

# Akaike information criterion

[ah-ka-ee-kay]

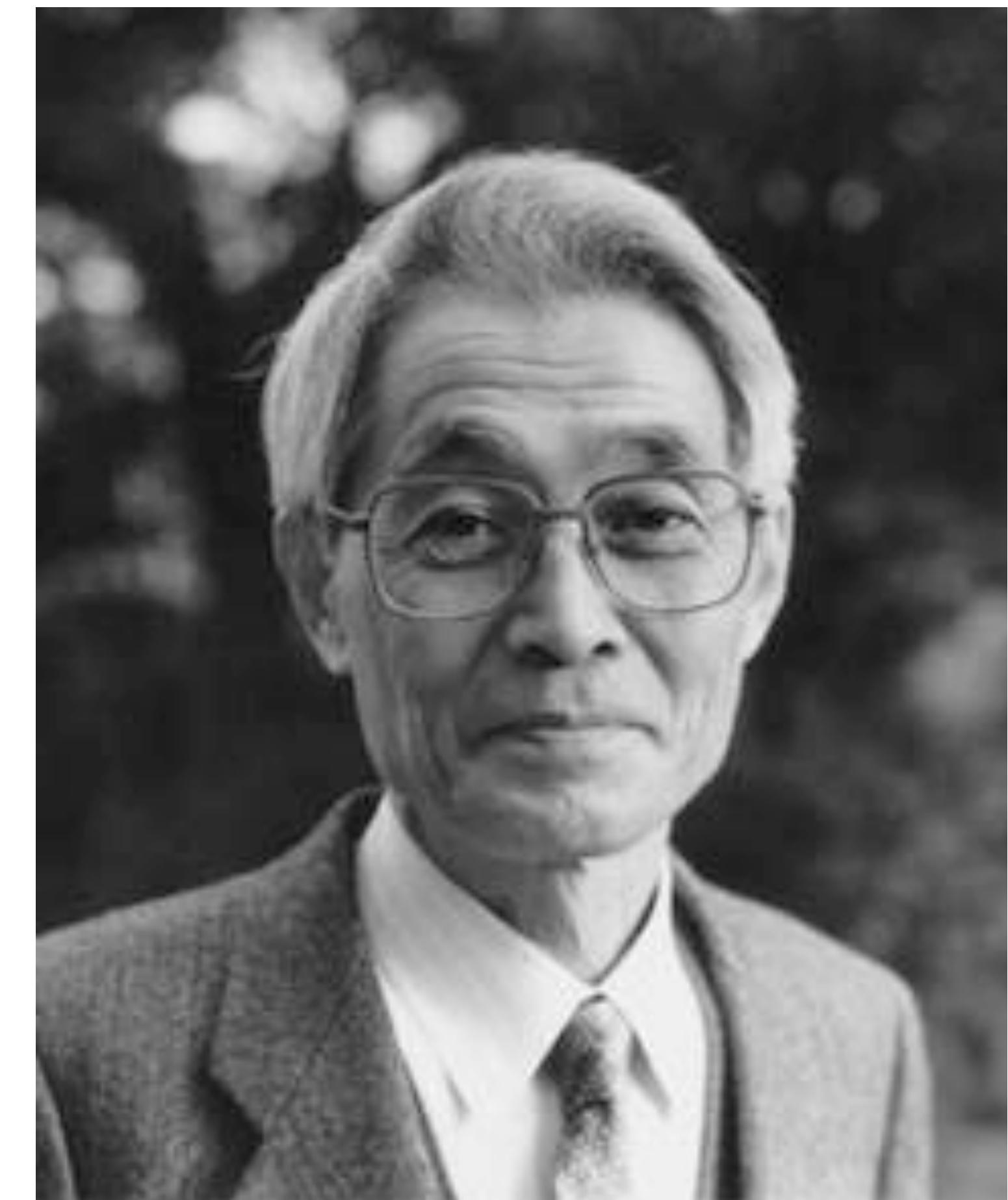
Estimate information-theoretic  
measure of predictive accuracy  
(K-L Distance)

For flat priors and large samples:

$$\text{AIC} = (-2) \times \text{lppd} + 2k$$

*log pointwise  
predictive density*

*number of  
parameters*



Hirotugu Akaike (1927–2009)

赤池弘次

# Widely Applicable IC

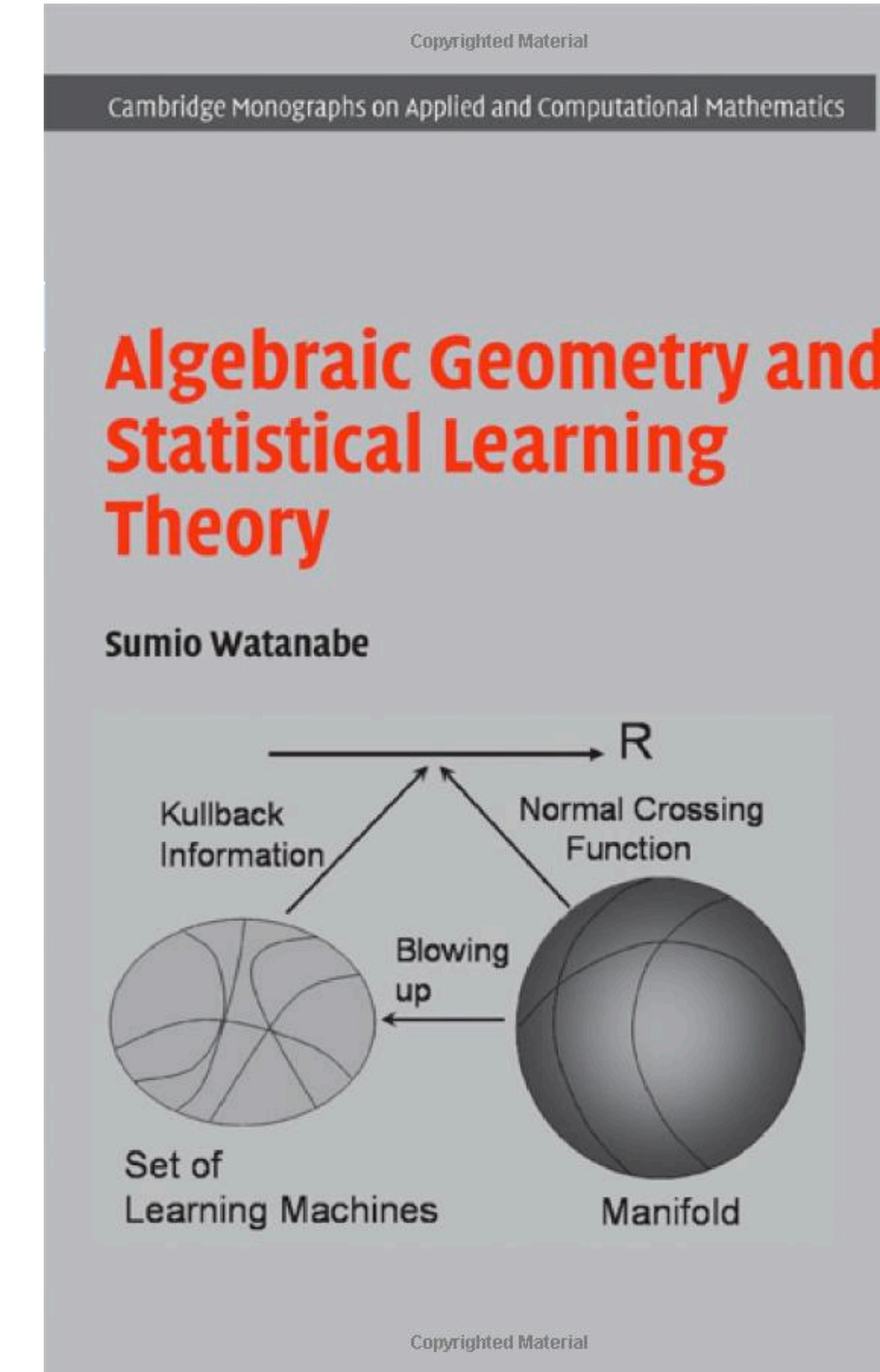
AIC of historical interest now

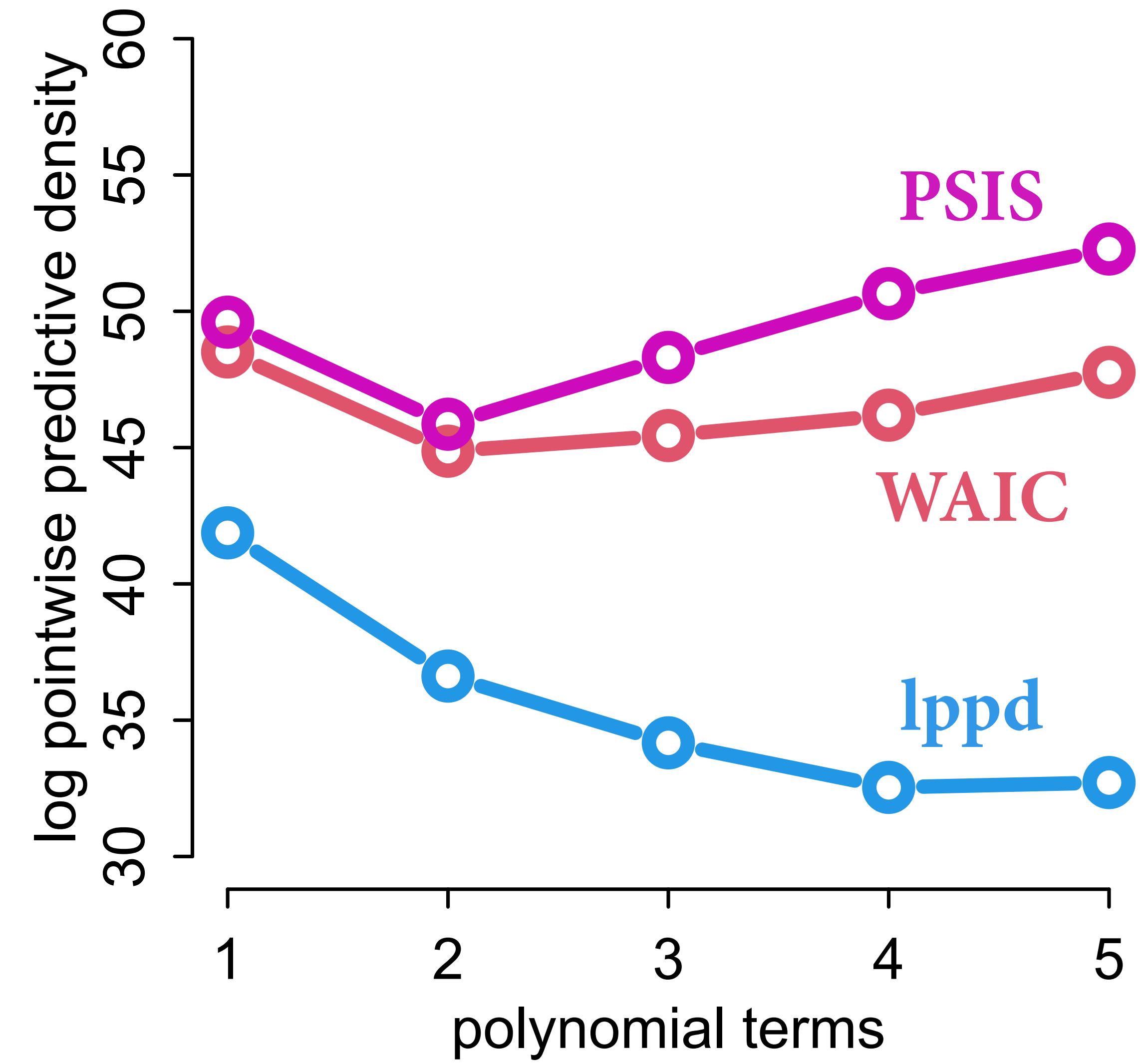
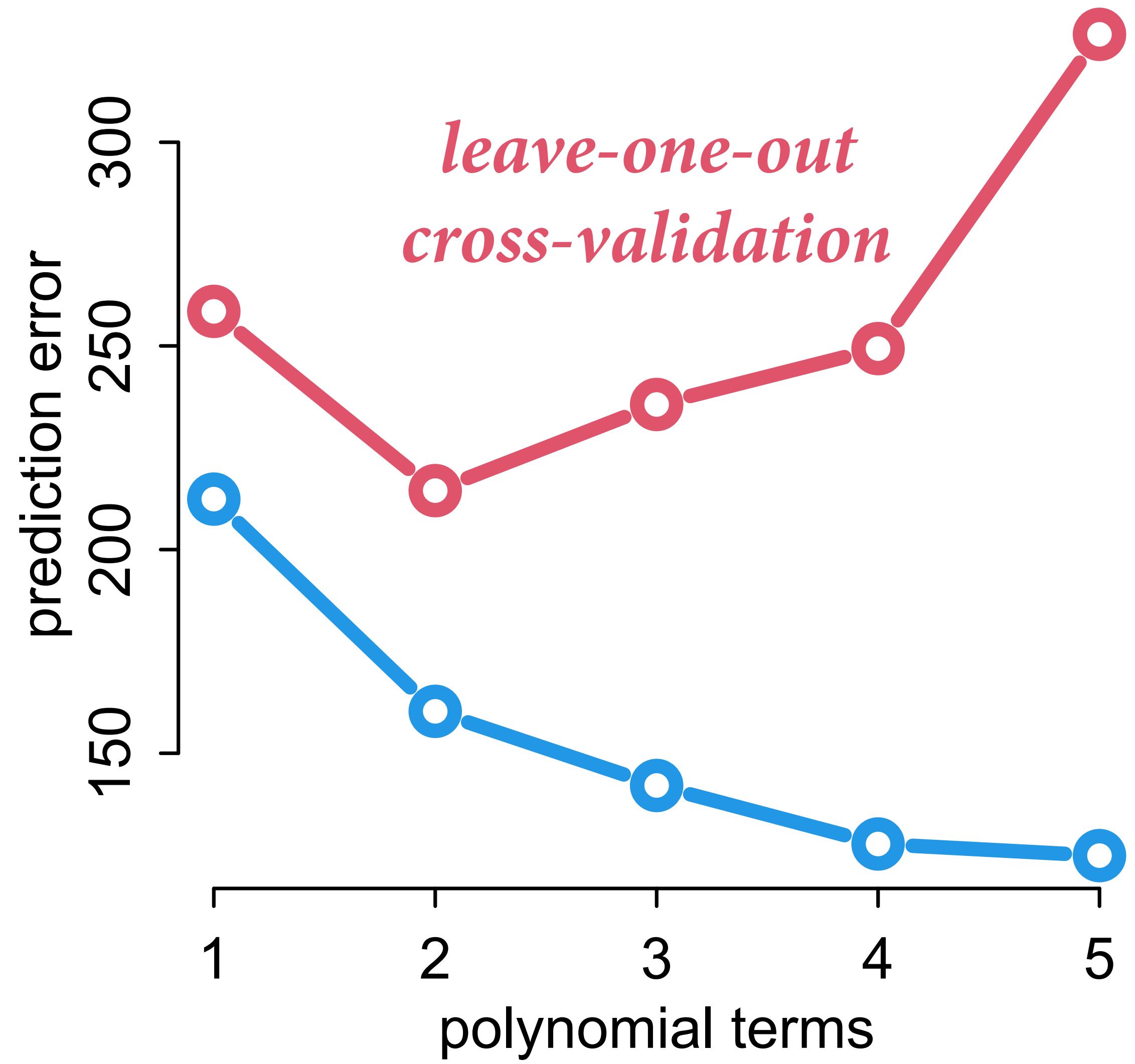
Widely Applicable Information Criterion (WAIC)

Sumio Watanabe (渡辺澄夫) 2010

$$\text{WAIC}(y, \Theta) = -2 \left( \text{lppd} - \underbrace{\sum_i \text{var}_\Theta \log p(y_i | \Theta)}_{\text{penalty term}} \right)$$

Very similar to PSIS score, but no automatic diagnostics





WAIC,PSIS,CV measure  
overfitting

Regularization manages  
overfitting

None directly address  
causal inference

All important to  
understanding how  
statistical inference works

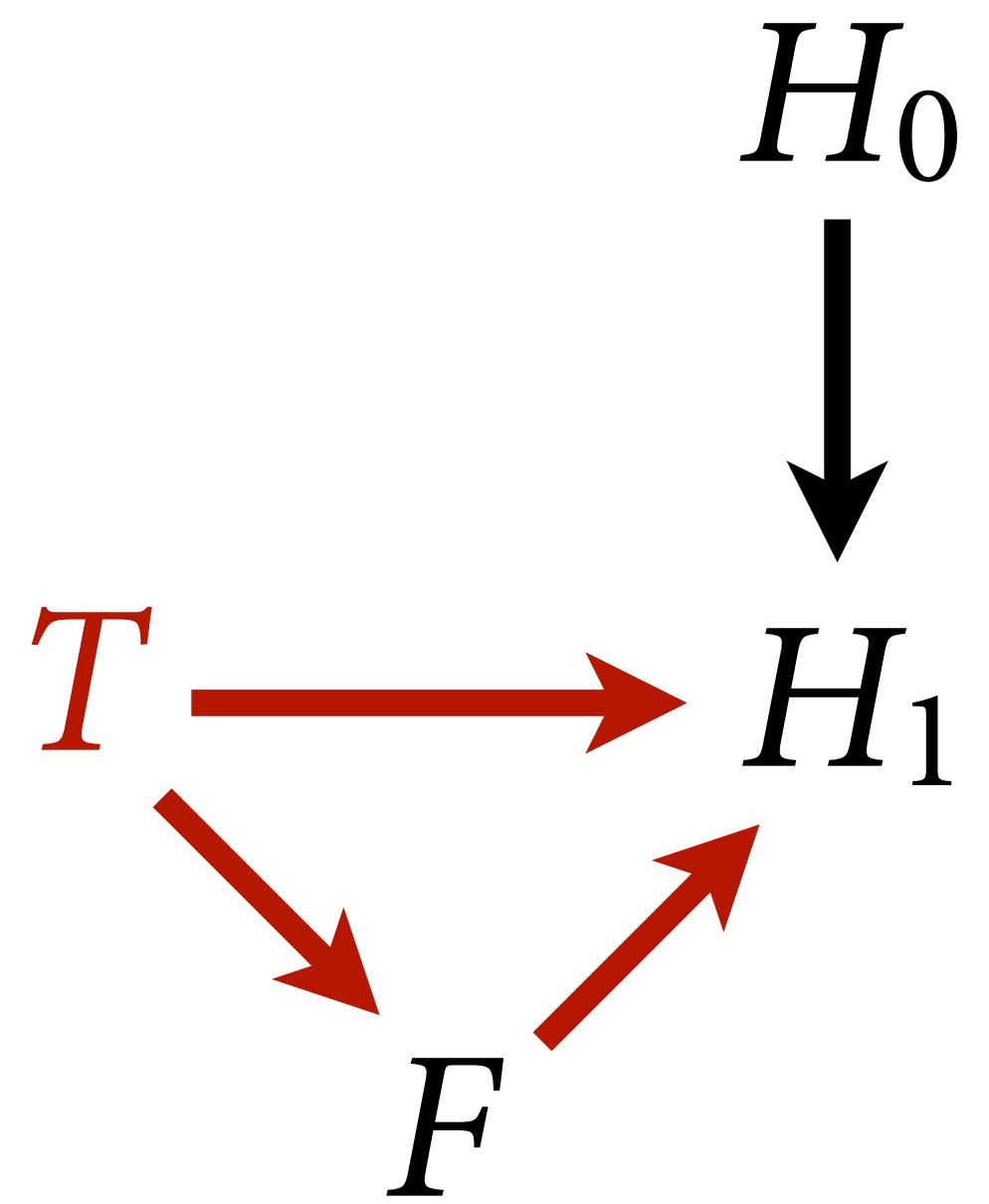


# Model Mis-selection

Do not use predictive criteria (WAIC, PSIS, CV) to choose a causal estimate

Predictive criteria actually prefer confounds & colliders

Example: Plant growth experiment

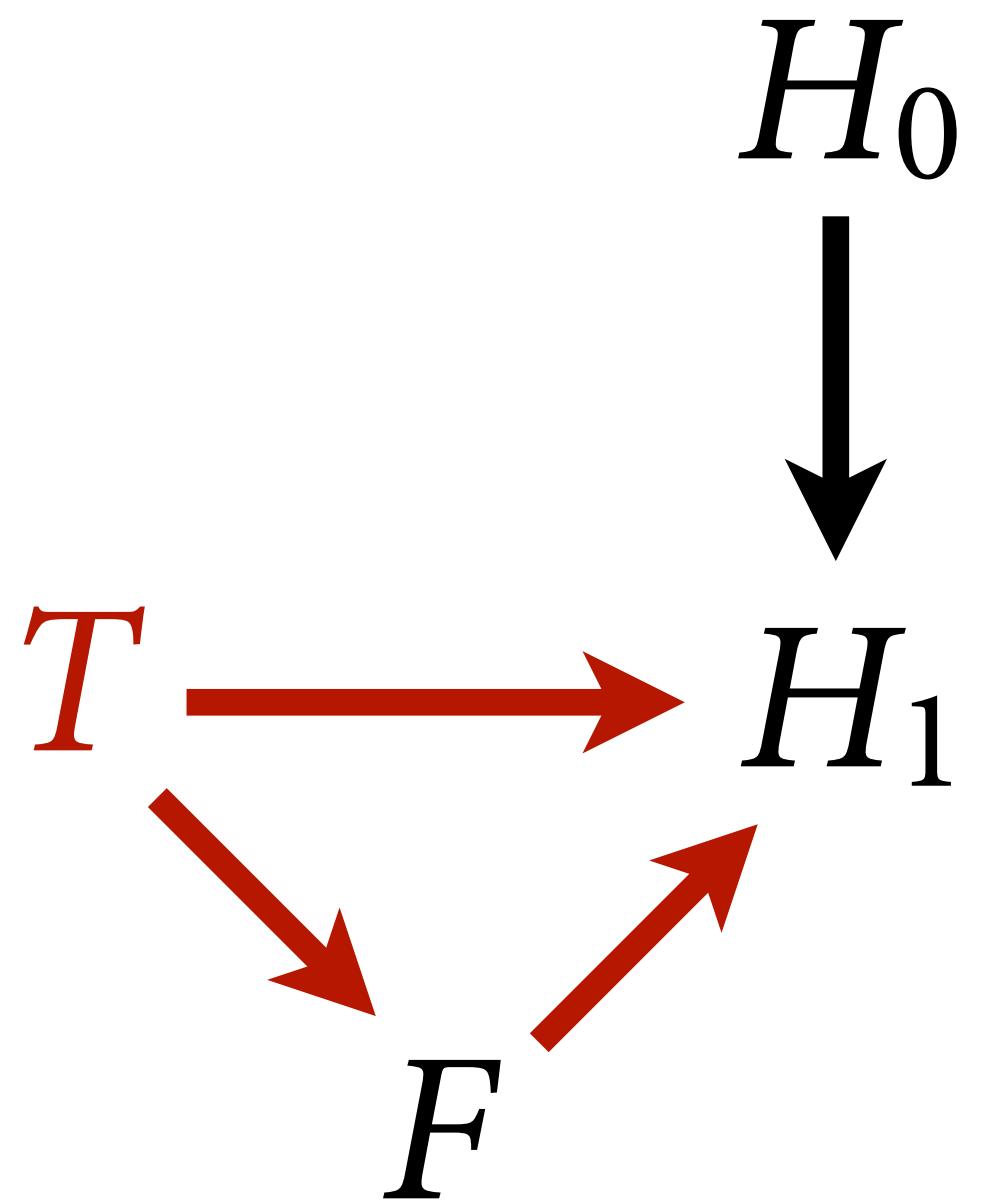


$$H_1 \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = H_0 \times p_i$$

$$p_i = \alpha + \beta_T T_i + \beta_F F_i$$

*Wrong adjustment set  
for total causal effect of  
treatment (blocks  
mediating path)*



$$H_1 \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = H_0 \times p_i$$

$$p_i = \alpha + \beta_T T_i$$

*Correct adjustment set for  
total causal effect of  
treatment*

$$H_1 \sim \text{Normal}(\mu_i, \sigma)$$

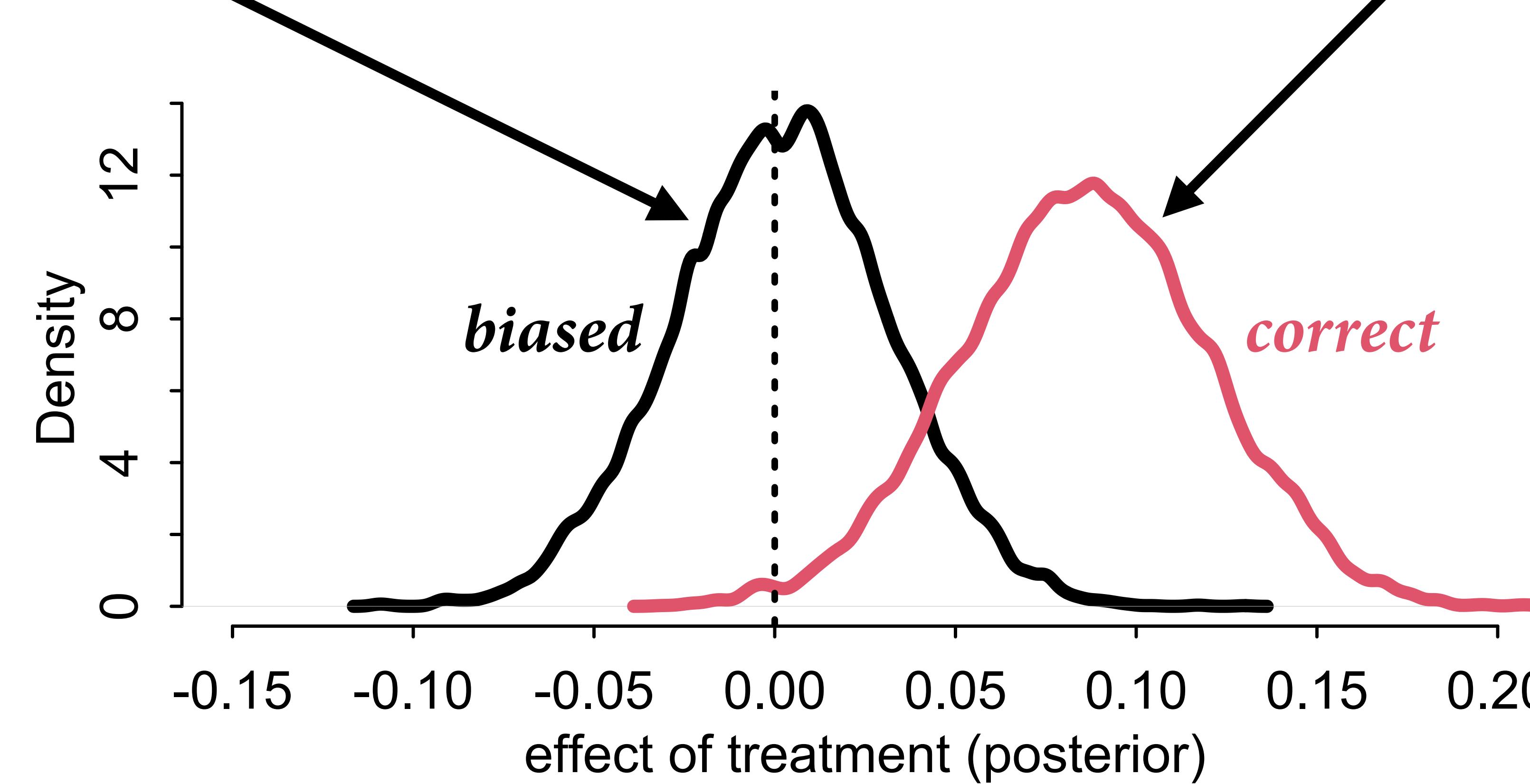
$$\mu_i = H_0 \times p_i$$

$$p_i = \alpha + \beta_T T_i + \beta_F F_i$$

$$H_1 \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = H_0 \times p_i$$

$$p_i = \alpha + \beta_T T_i$$



$$H_1 \sim \text{Normal}(\mu_i, \sigma)$$

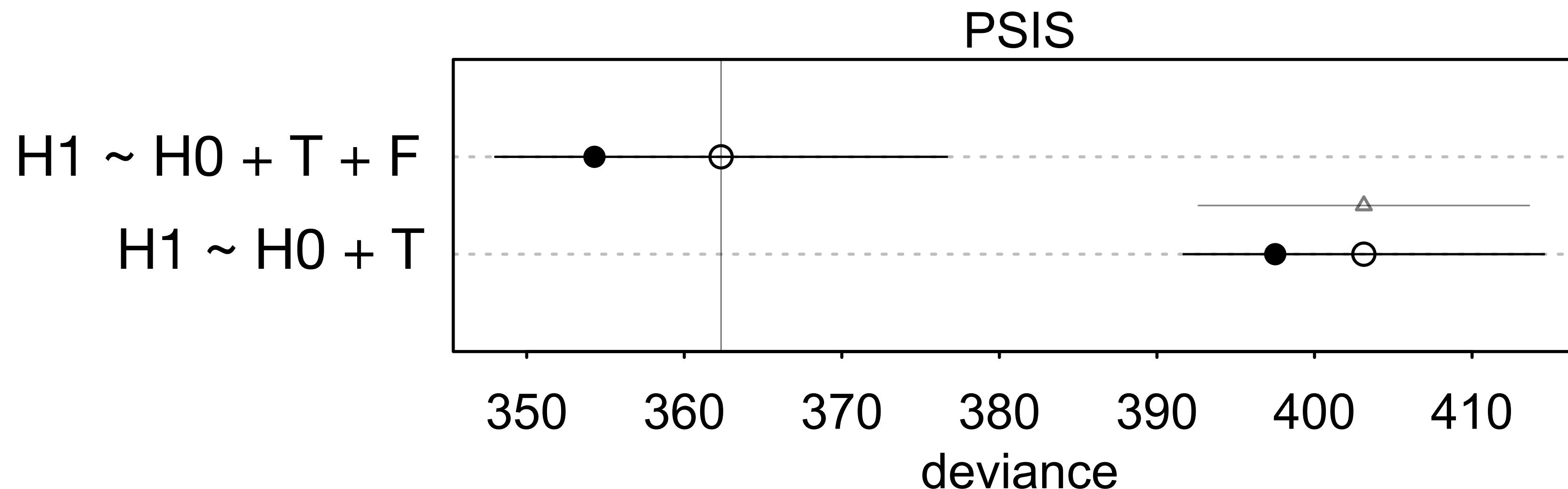
$$\mu_i = H_0 \times p_i$$

$$p_i = \alpha + \beta_T T_i + \beta_F F_i$$

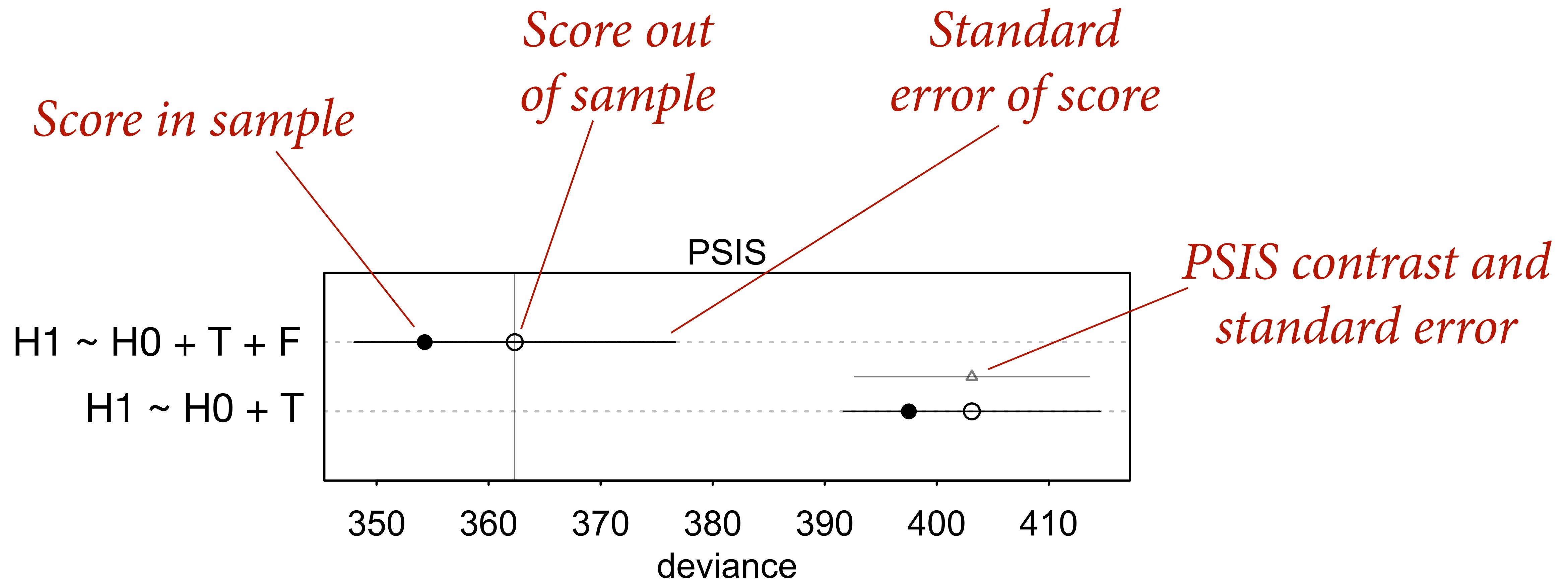
$$H_1 \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = H_0 \times p_i$$

$$p_i = \alpha + \beta_T T_i$$

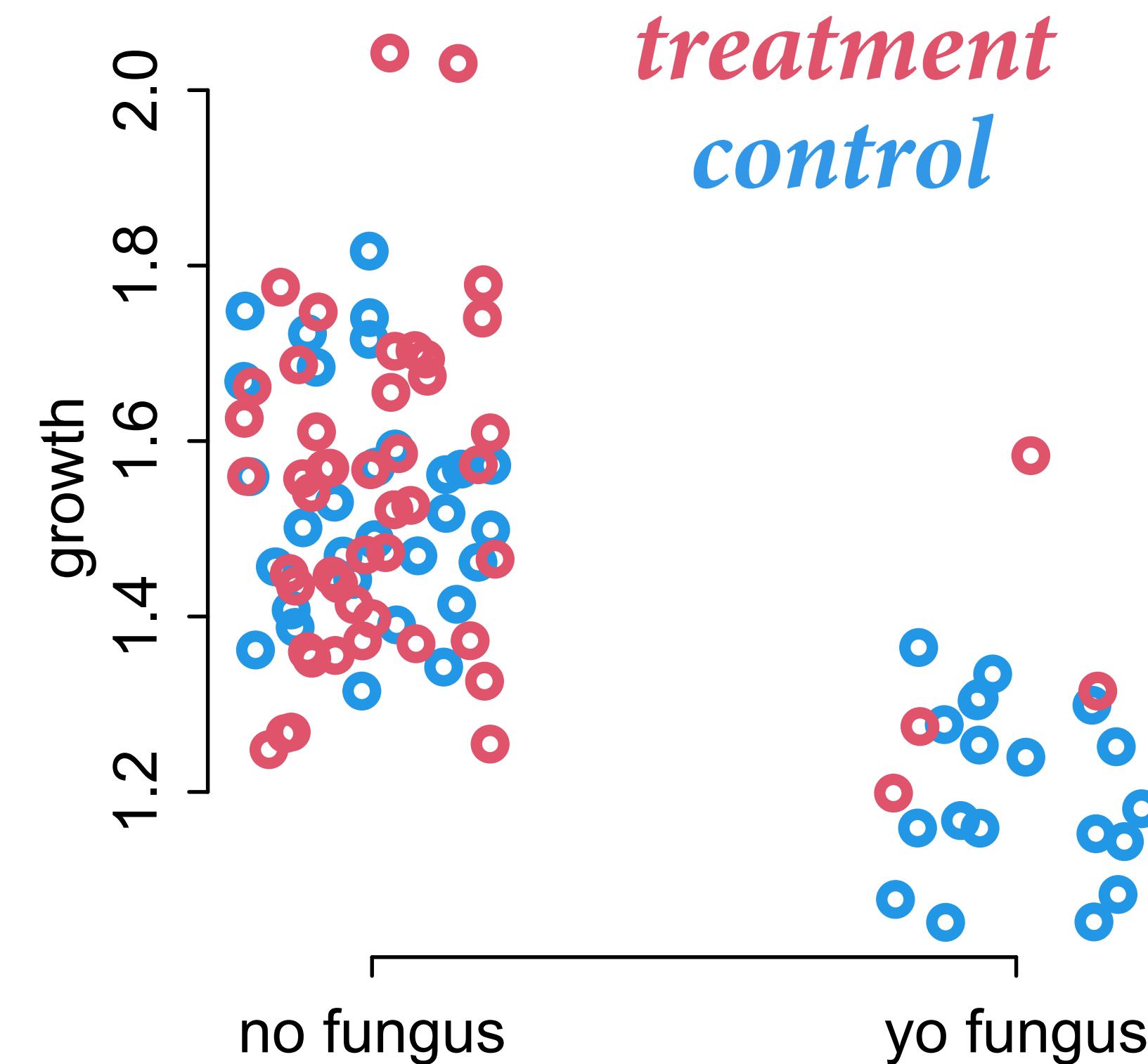
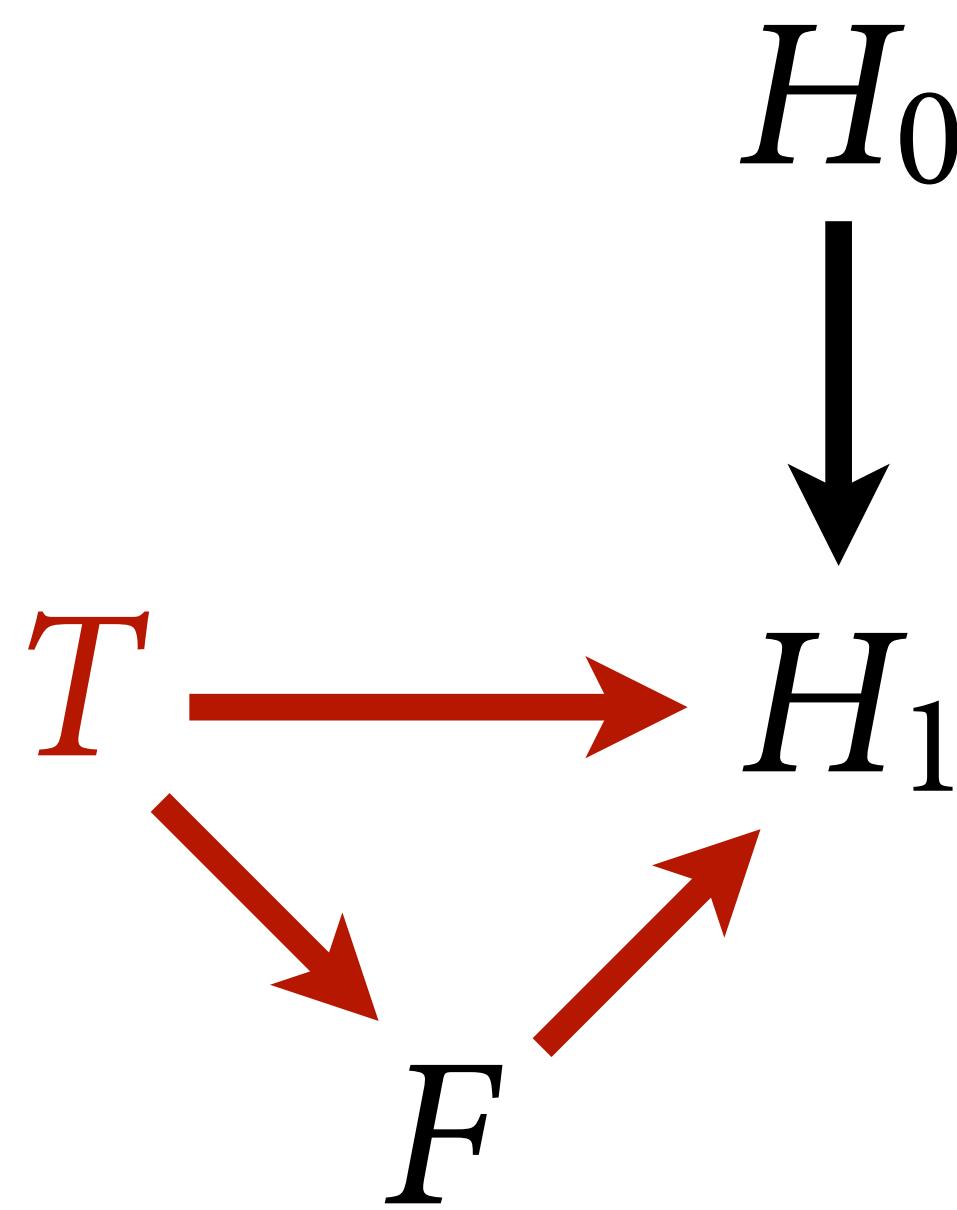


*Wrong model wins at prediction*

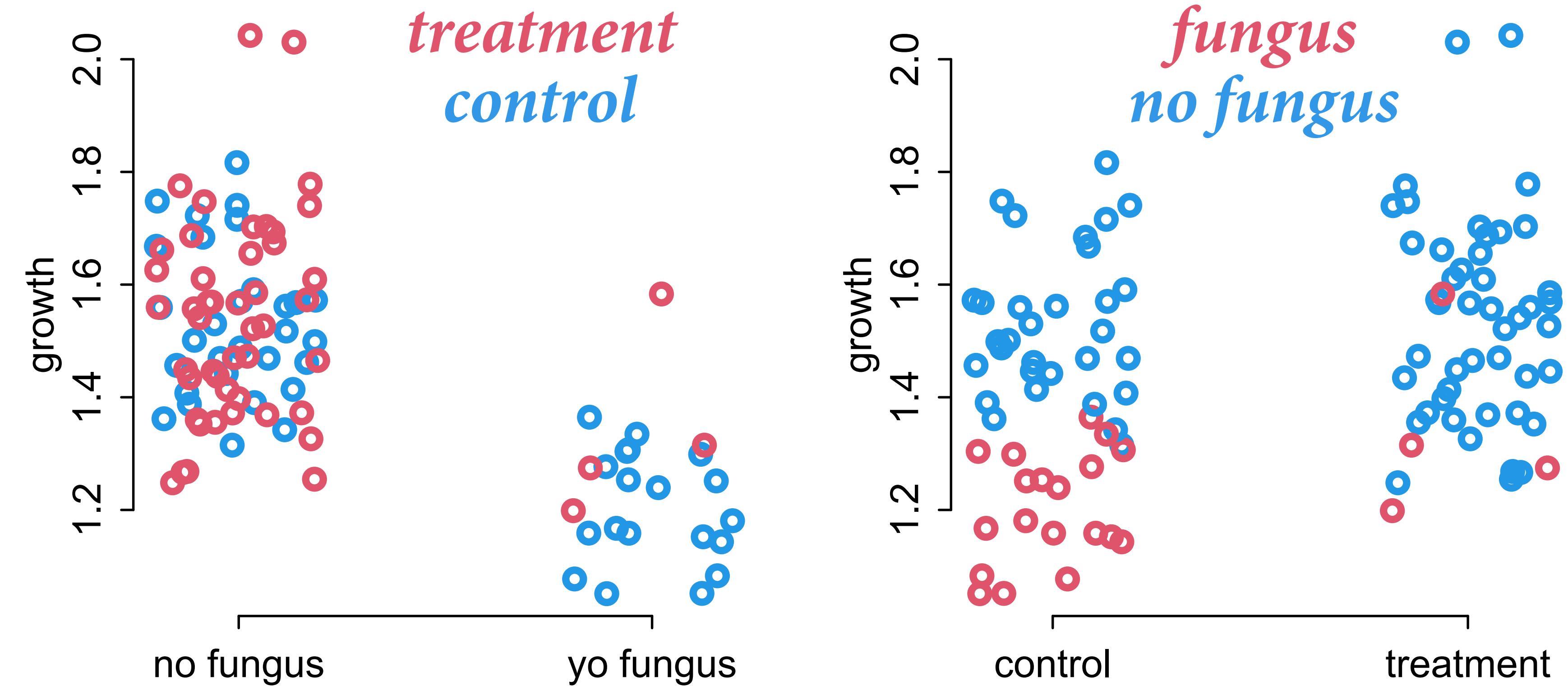
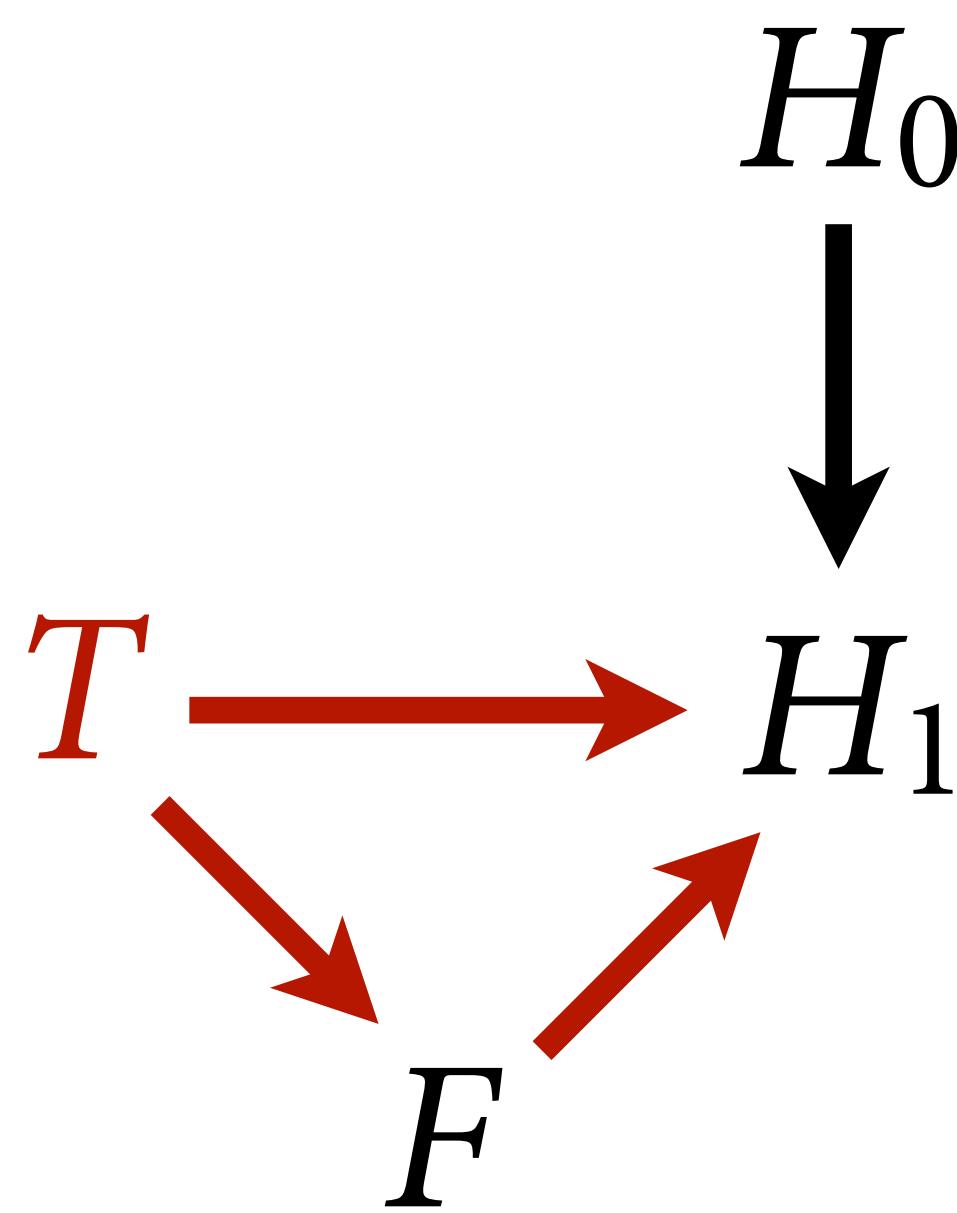


*Wrong model wins at prediction*

# Why does the wrong model win at prediction?



# Why does the wrong model win at prediction?



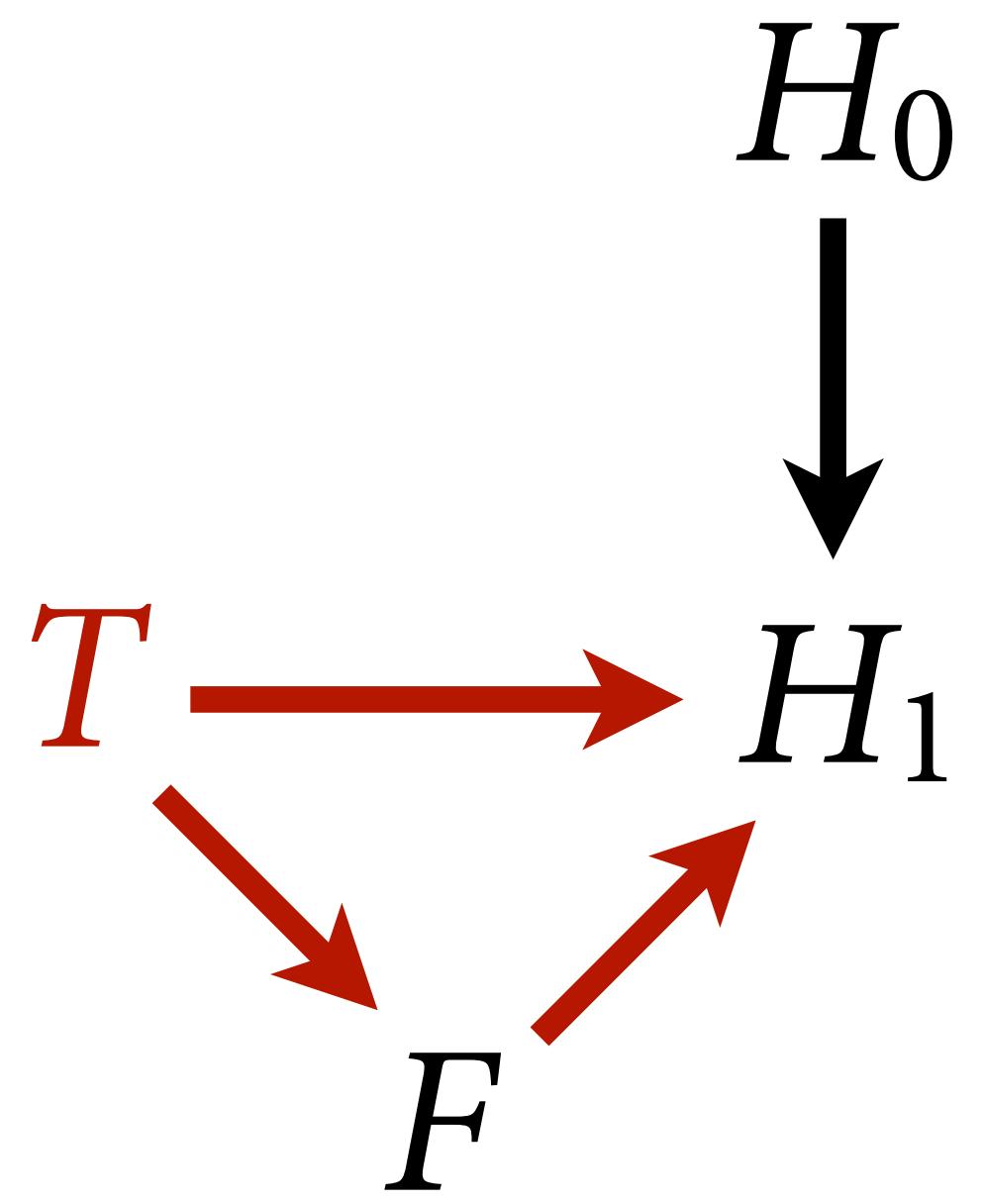
*Fungus is in fact a better predictor than treatment*

# Model Mis-selection

Do not use predictive criteria (WAIC, PSIS, CV) to choose a causal estimate

However, many analyses are mixes of inferential and predictive chores

Still need help finding good functional descriptions while avoiding overfitting



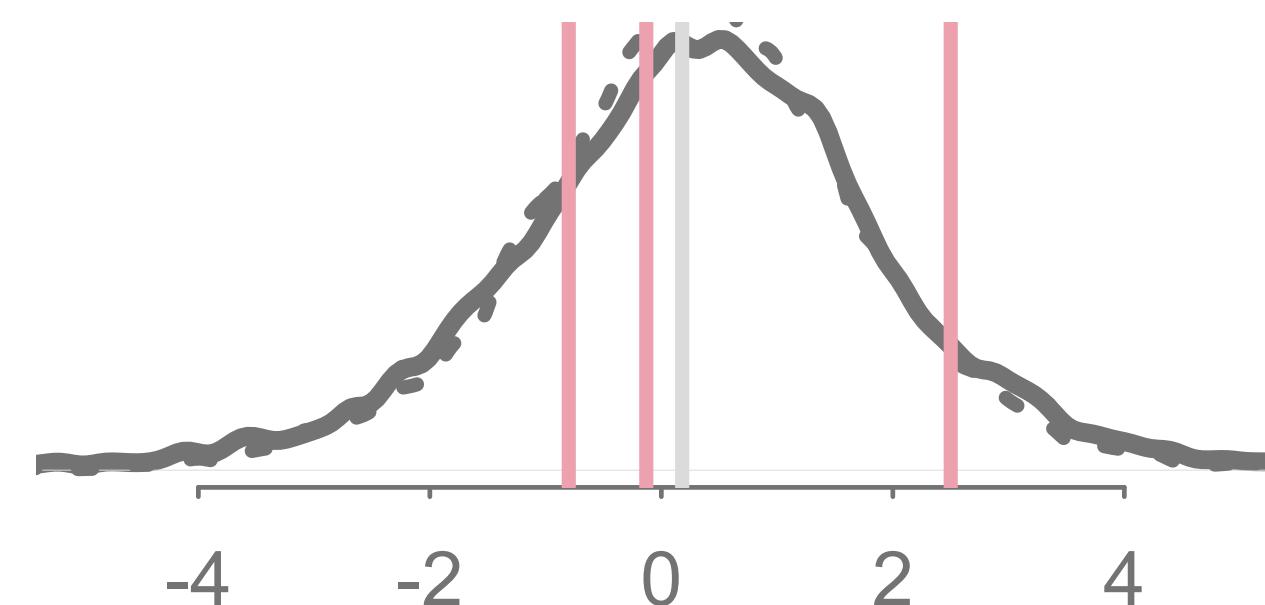
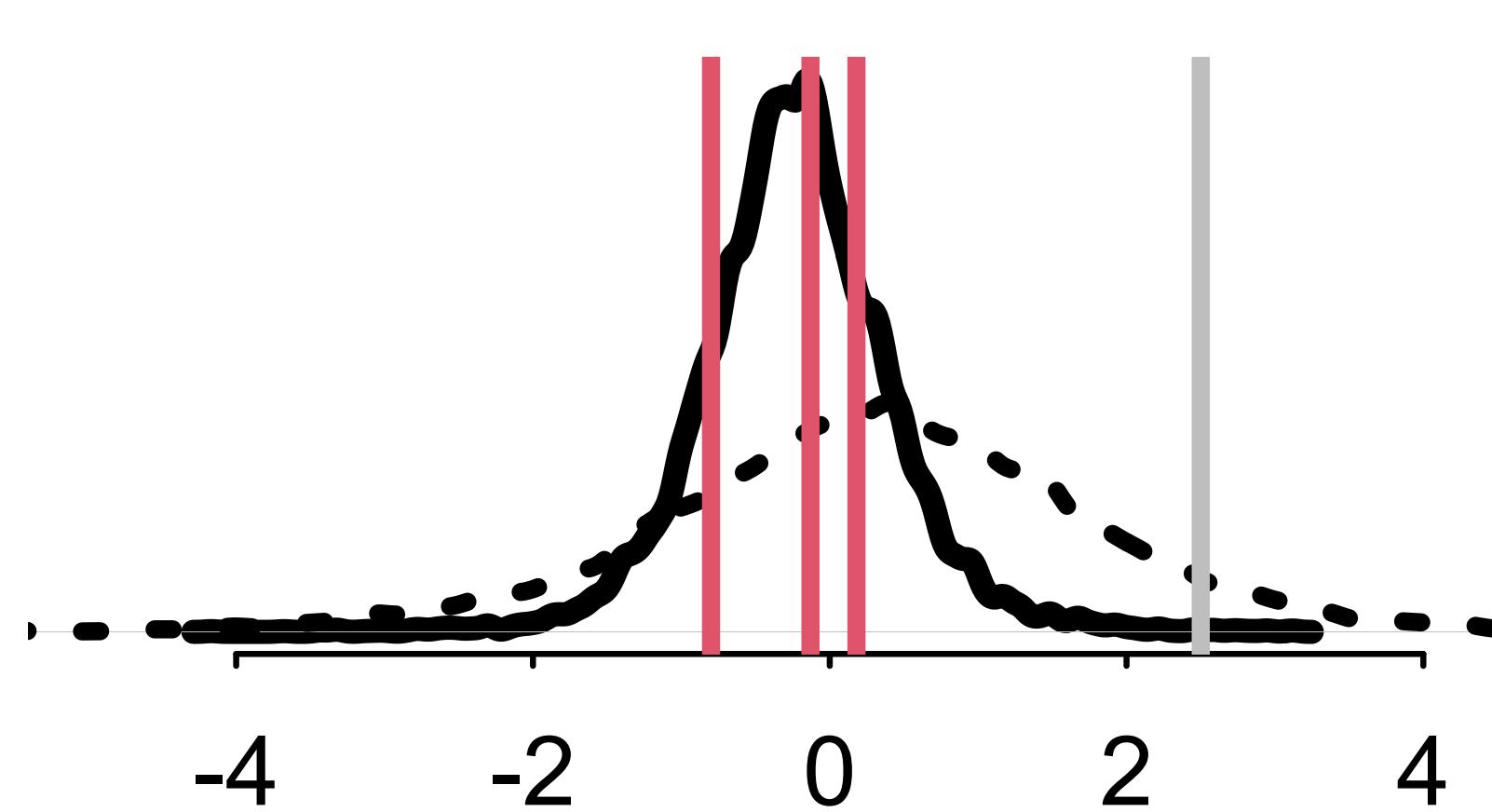
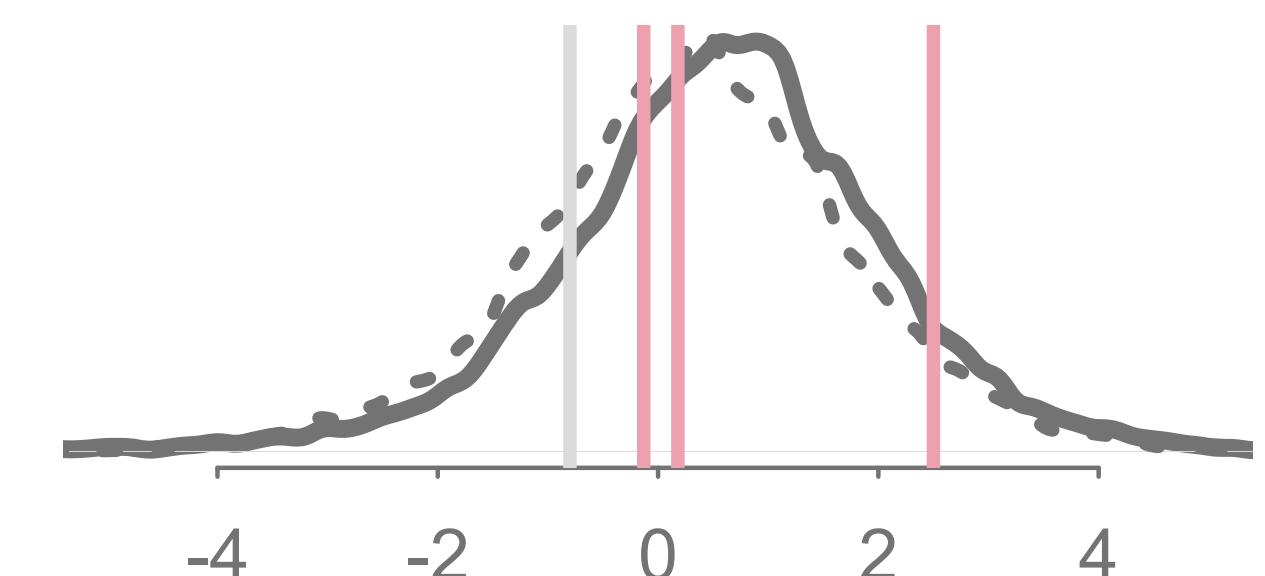
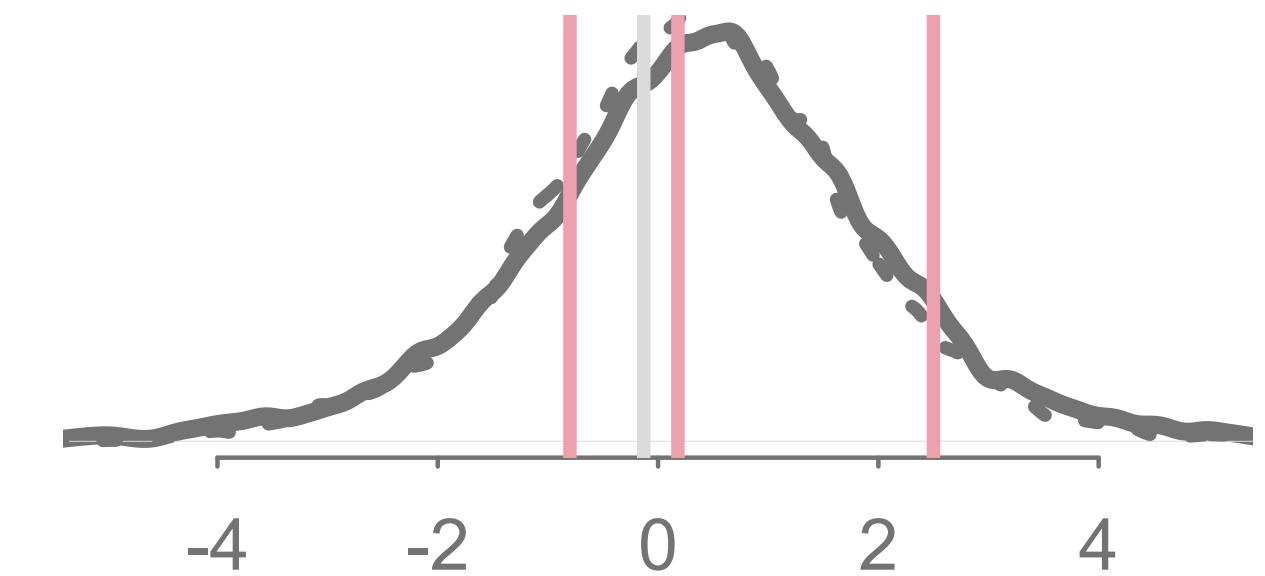
# Outliers & Robust Regression

Some points are more influential than others

“Outliers”: Observations in the tails of predictive distribution

Outliers indicate predictions are possibly overconfident, unreliable

The model doesn’t expect enough variation



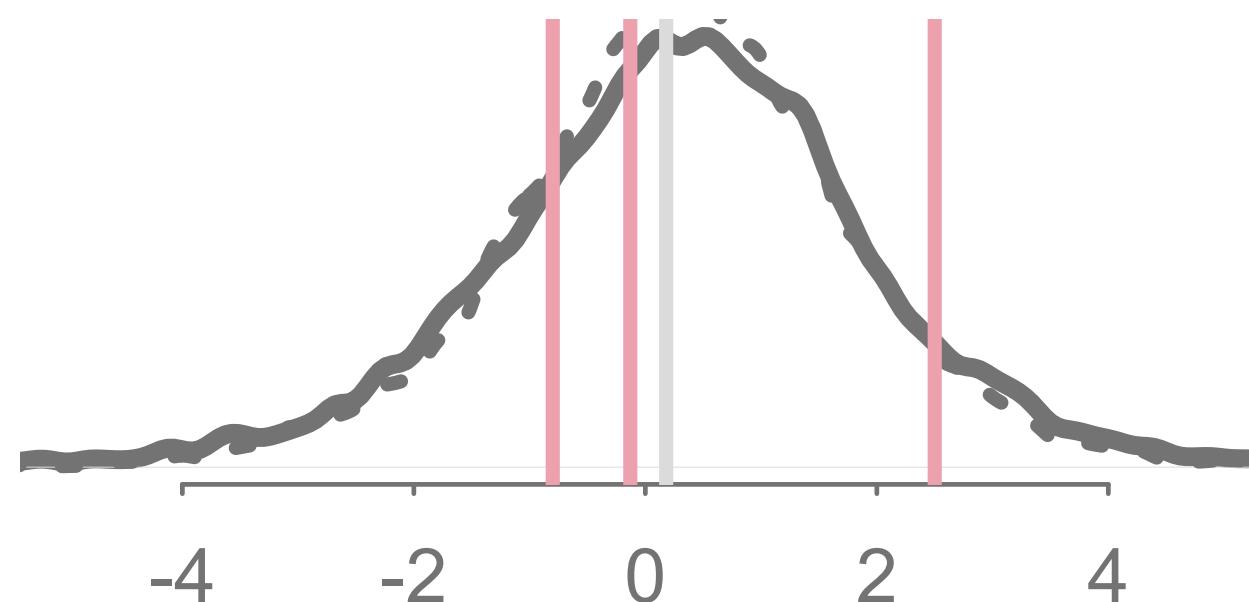
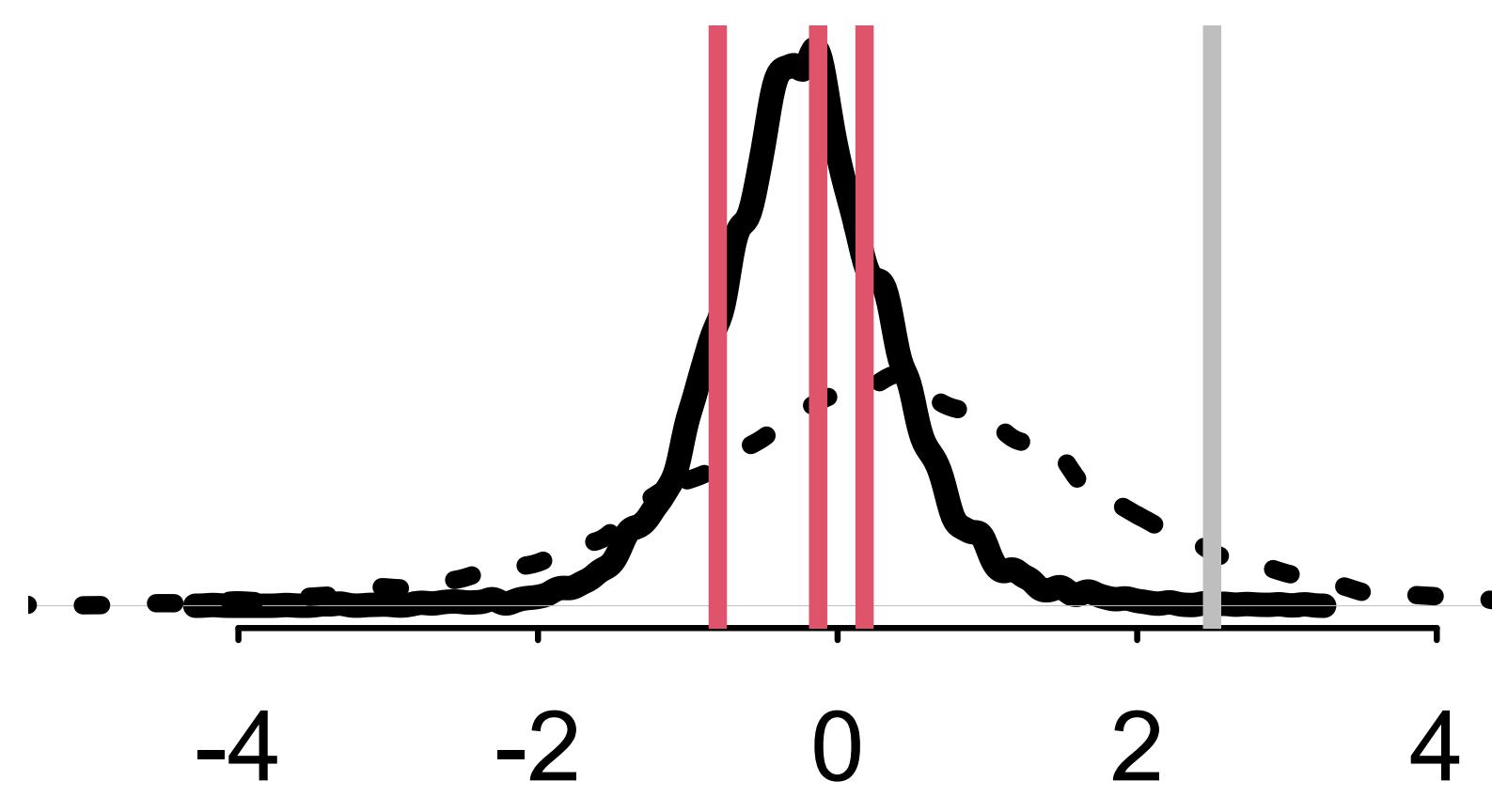
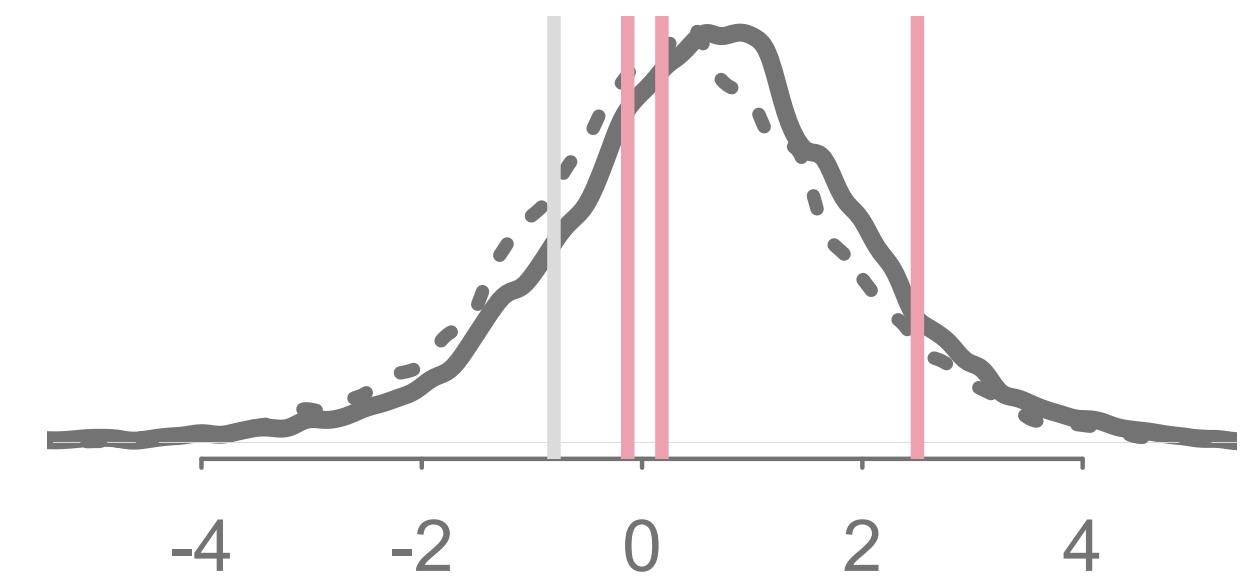
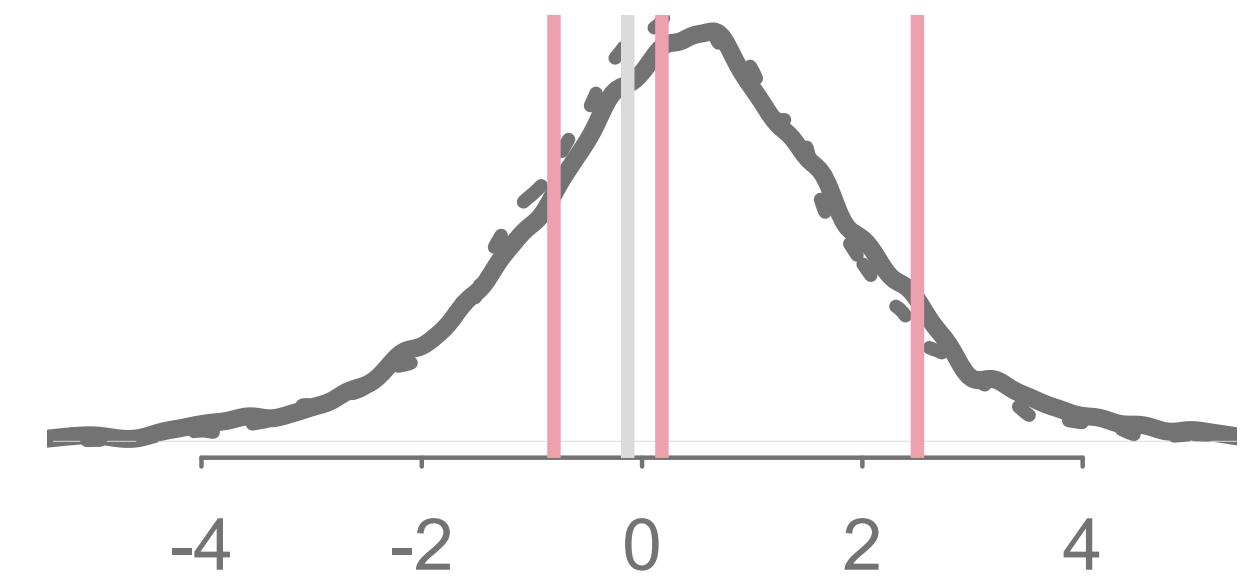
# Outliers & Robust Regression

Dropping outliers is bad: Just ignores the problem; predictions are still bad!

It's the model that's wrong, not the data

First, quantify influence of each point

Second, use a mixture model (robust regression)



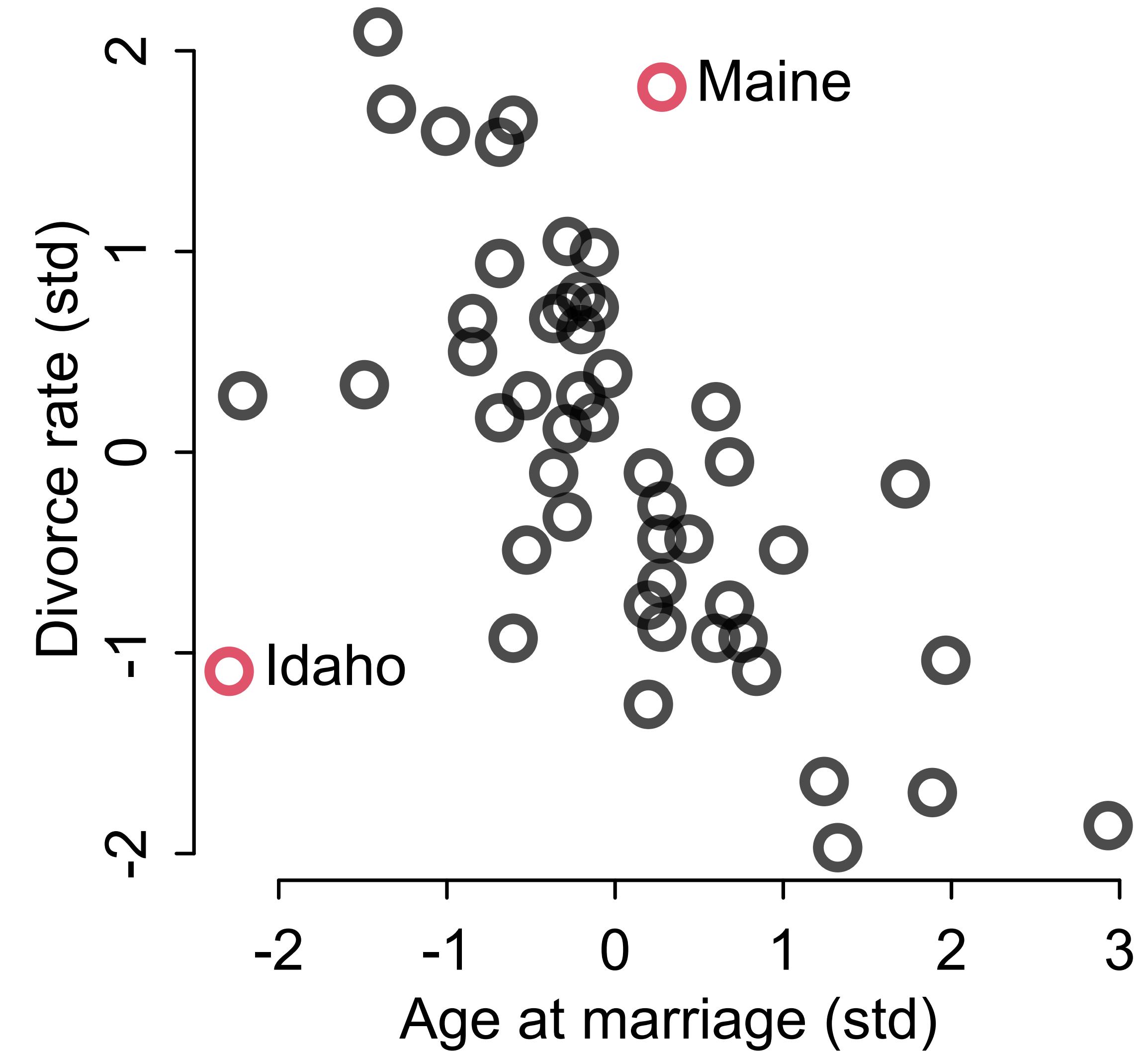
# Outliers & Robust Regression

Divorce rate example

Maine and Idaho both highly unusual

Maine: high divorce for trend

Idaho: low divorce for trend

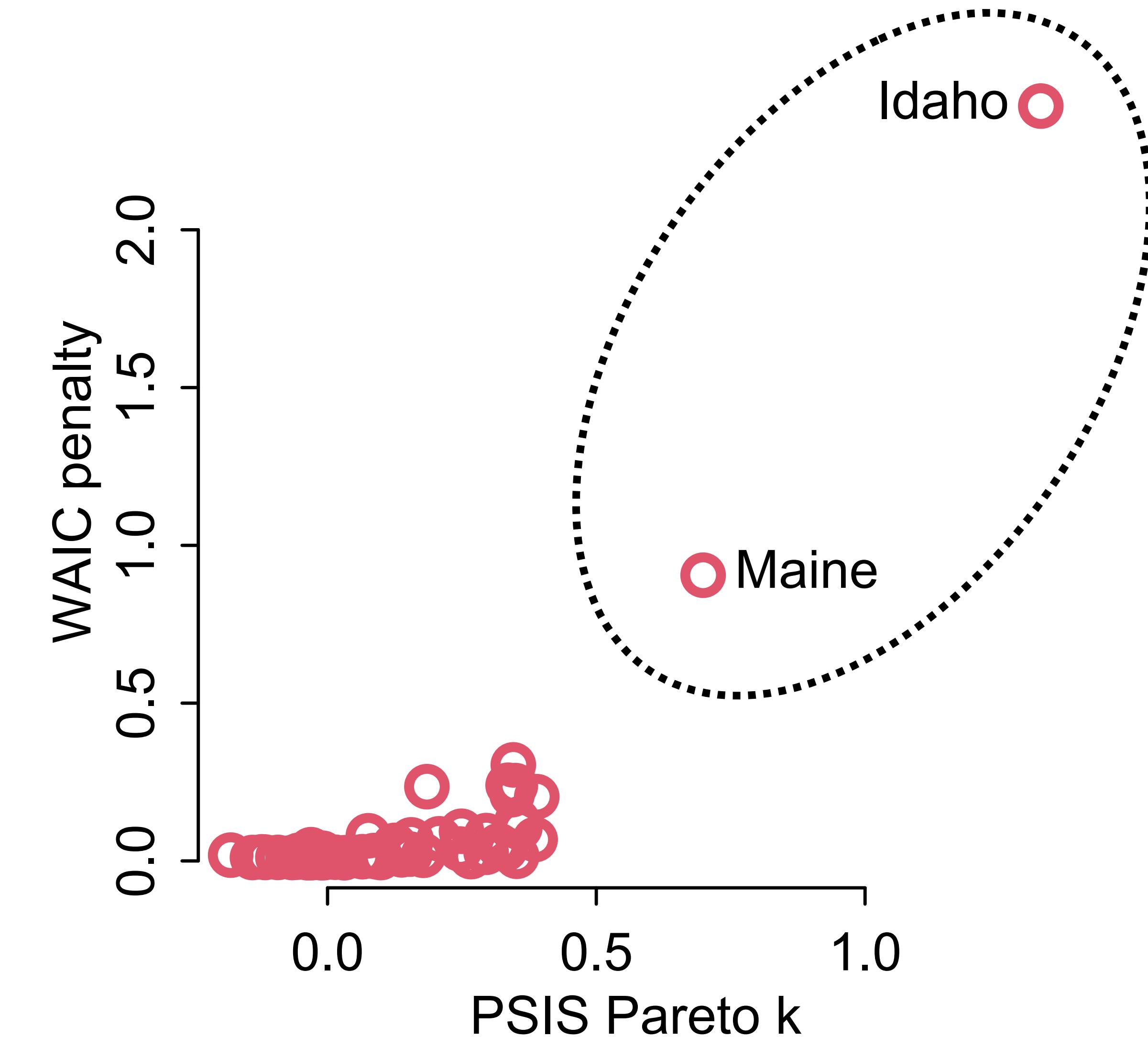


# Outliers & Robust Regression

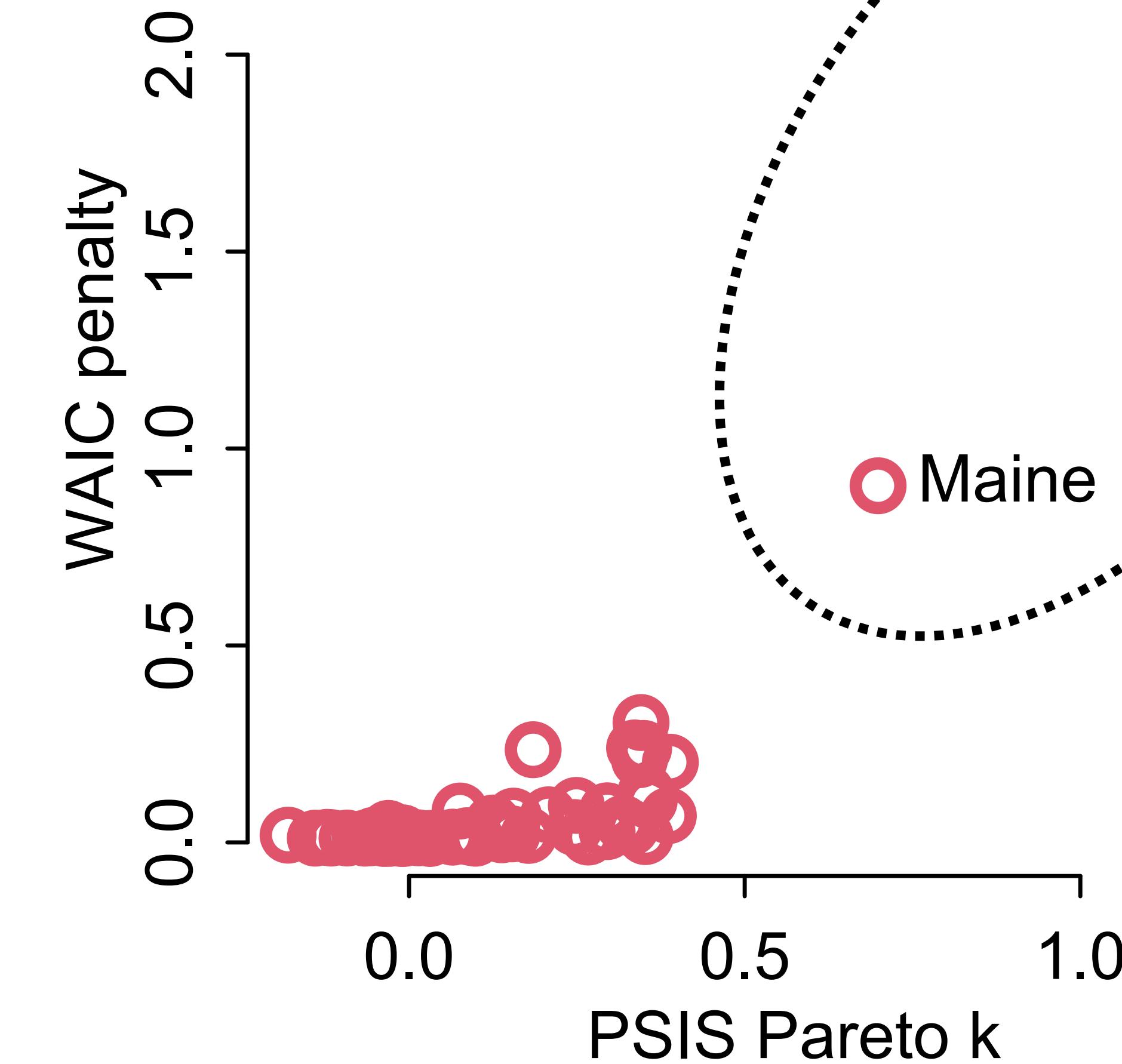
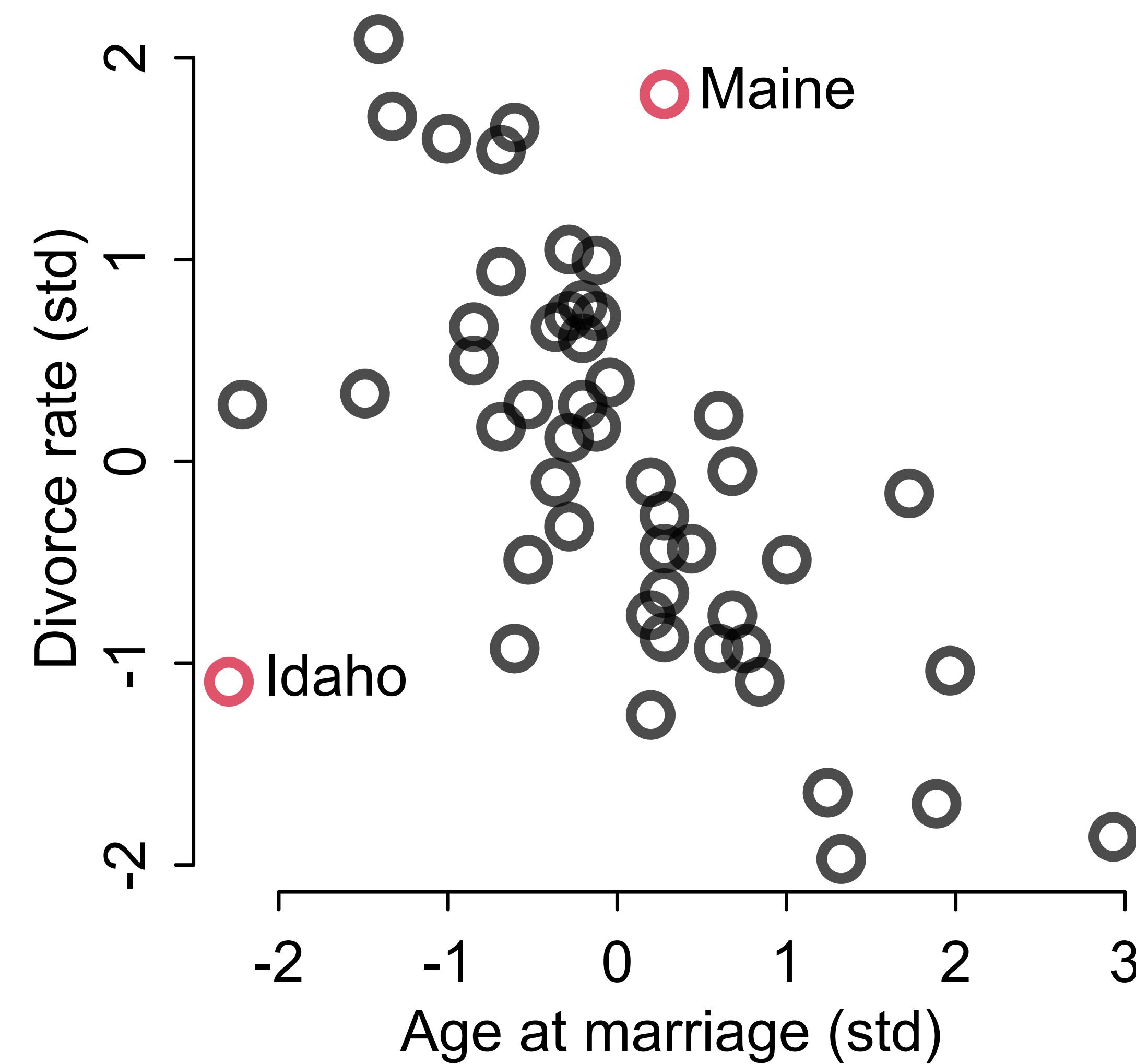
Quantify influence:

PSIS  $k$  statistic

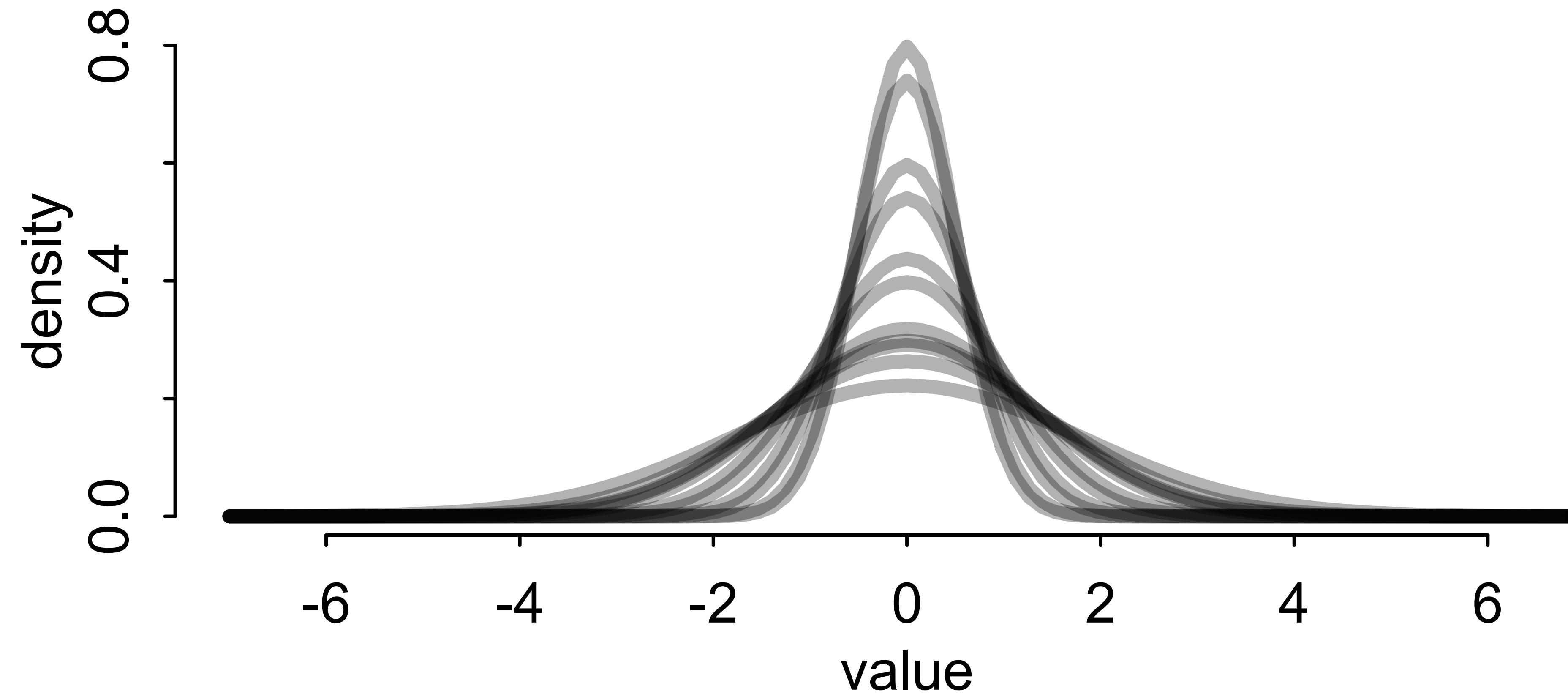
WAIC penalty term (“effective number of parameters”)



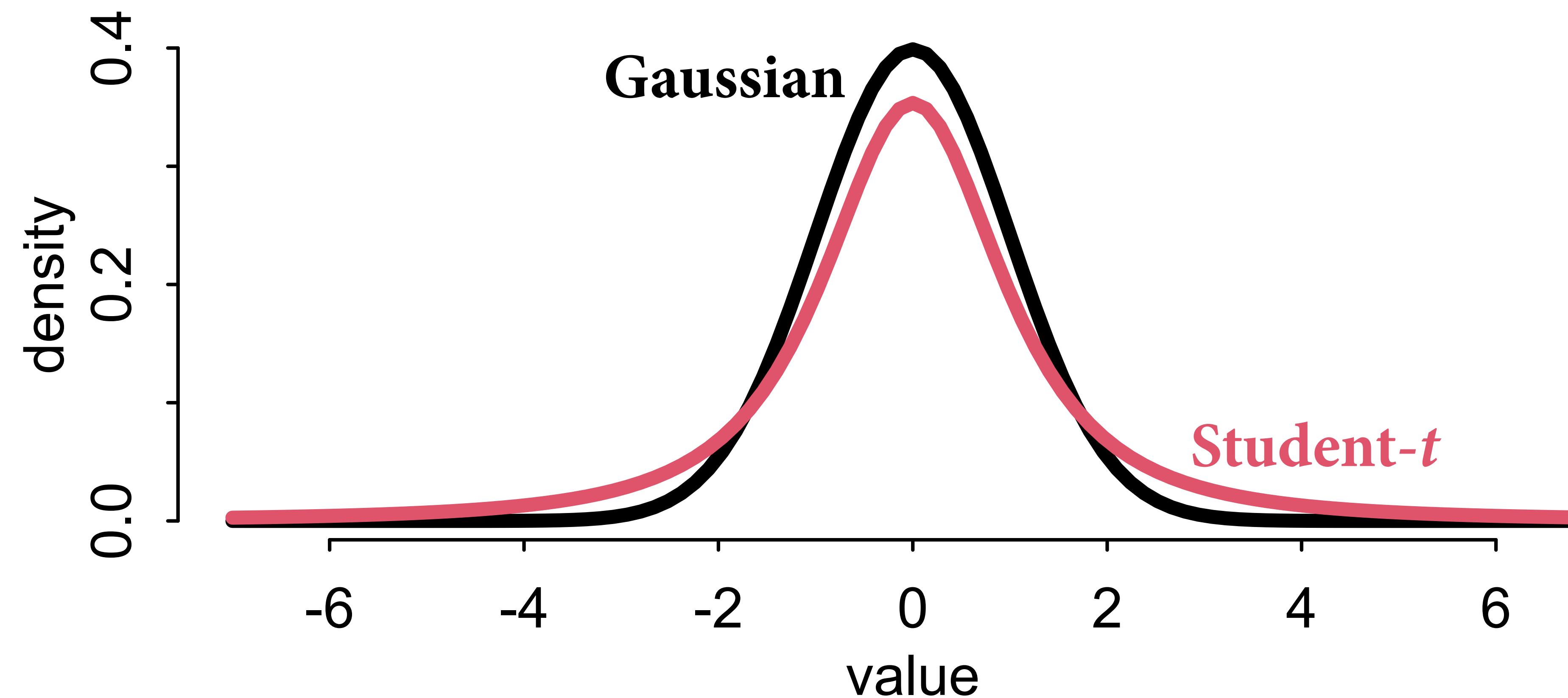
# Outliers & Robust Regression



# Mixing Gaussians



# Mixing Gaussians



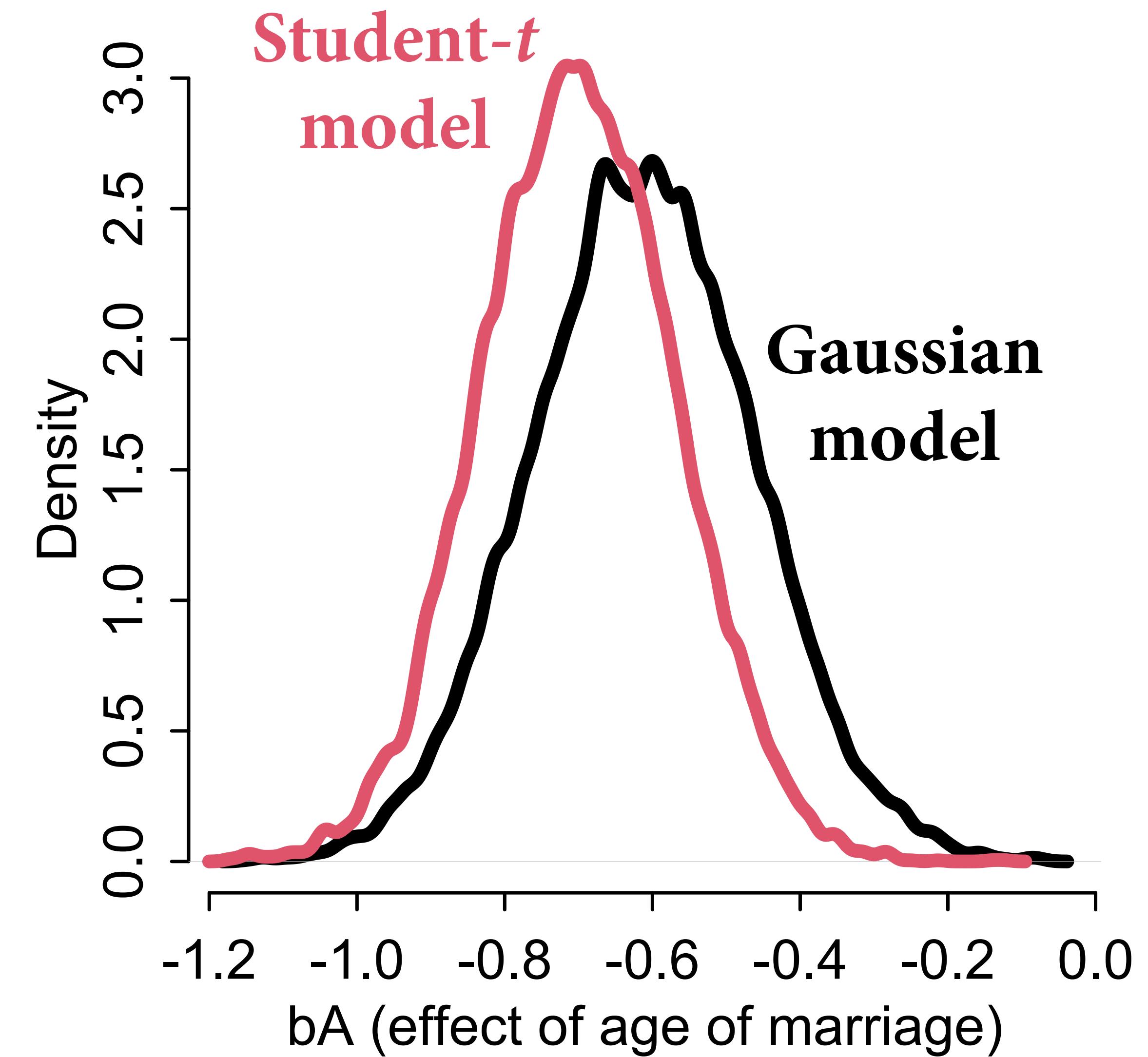
```
m5.3 <- quap(  
  alist(  
    D ~ dnorm( mu , sigma ) ,  
    mu <- a + bM*M + bA*A ,  
    a ~ dnorm( 0 , 0.2 ) ,  
    bM ~ dnorm( 0 , 0.5 ) ,  
    bA ~ dnorm( 0 , 0.5 ) ,  
    sigma ~ dexp( 1 )  
  ) , data = dat )  
  
m5.3t <- quap(  
  alist(  
    D ~ dstudent( 2 , mu , sigma ) ,  
    mu <- a + bM*M + bA*A ,  
    a ~ dnorm( 0 , 0.2 ) ,  
    bM ~ dnorm( 0 , 0.5 ) ,  
    bA ~ dnorm( 0 , 0.5 ) ,  
    sigma ~ dexp( 1 )  
  ) , data = dat )
```

```

m5.3 <- quap(
  alist(
    D ~ dnorm( mu , sigma ) ,
    mu <- a + bM*M + bA*A ,
    a ~ dnorm( 0 , 0.2 ) ,
    bM ~ dnorm( 0 , 0.5 ) ,
    bA ~ dnorm( 0 , 0.5 ) ,
    sigma ~ dexp( 1 )
  ) , data = dat )

m5.3t <- quap(
  alist(
    D ~ dstudent( 2 , mu , sigma ) ,
    mu <- a + bM*M + bA*A ,
    a ~ dnorm( 0 , 0.2 ) ,
    bM ~ dnorm( 0 , 0.5 ) ,
    bA ~ dnorm( 0 , 0.5 ) ,
    sigma ~ dexp( 1 )
  ) , data = dat )

```

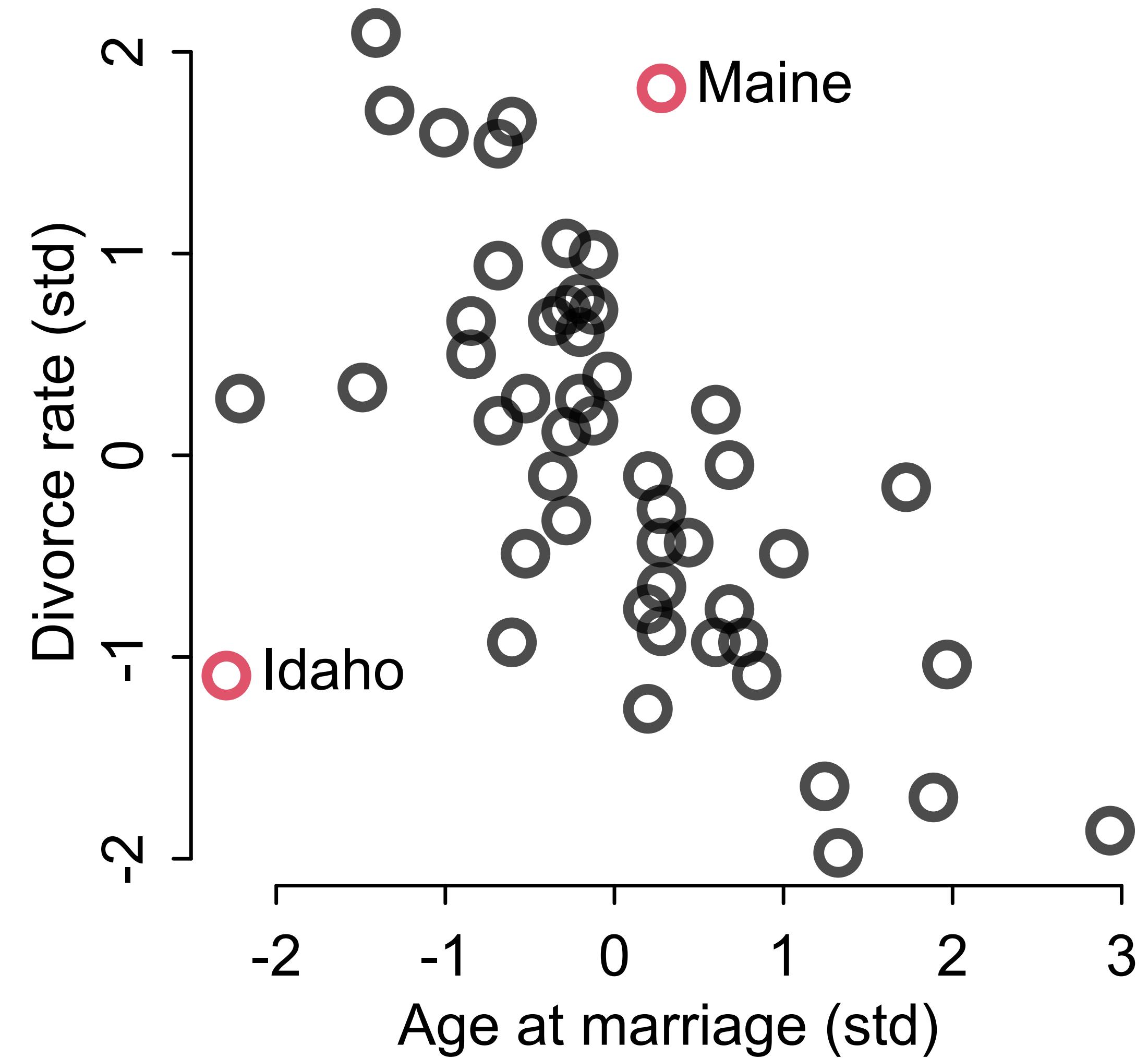


# Robust Regressions

Unobserved heterogeneity =>  
mixture of Gaussians

Thick tails means model is less  
surprised by extreme values

Less surprise, possibly better  
predictions if extreme values are  
rare



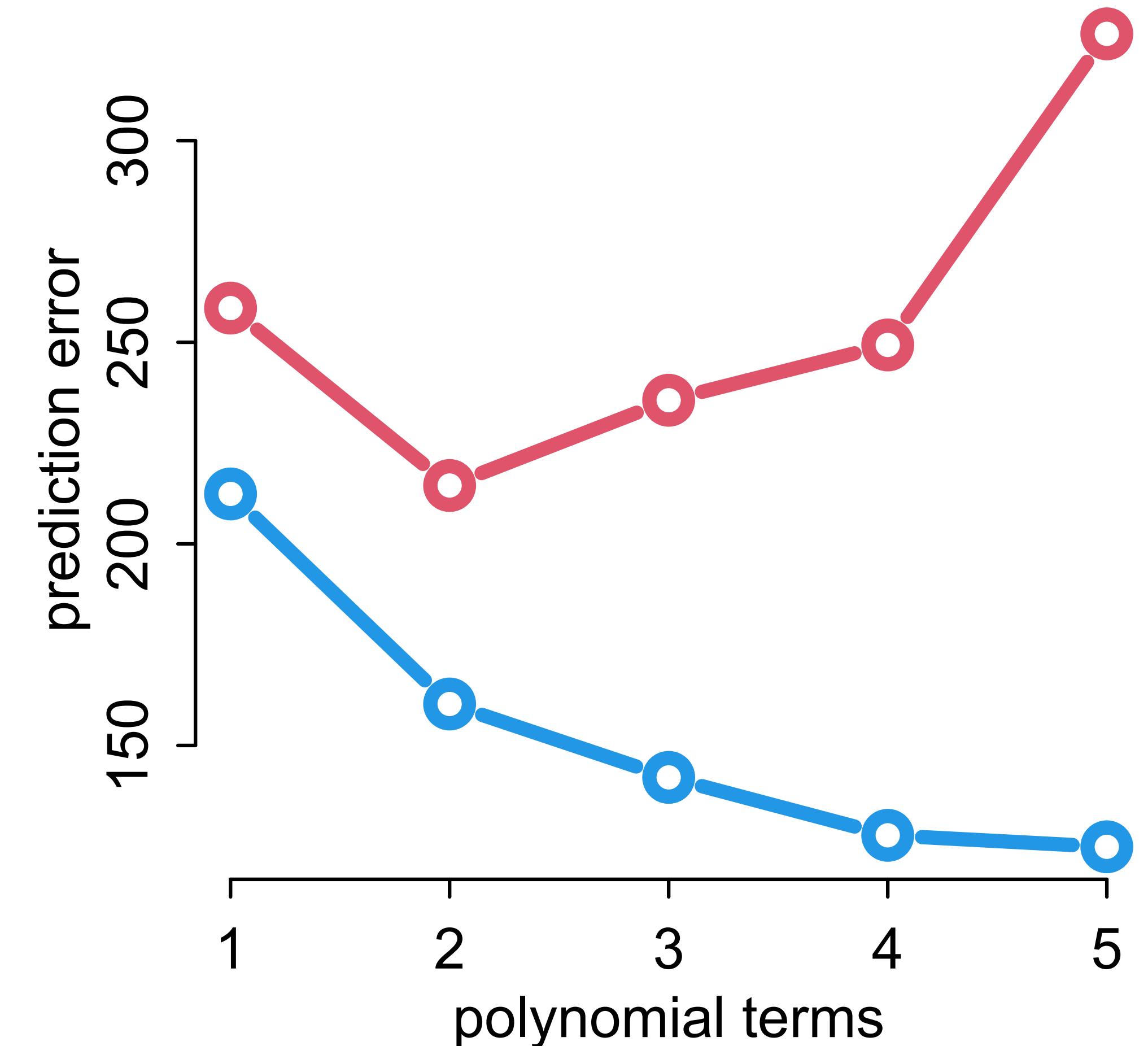
# Problems of Prediction

What is the next observation from the same process? (prediction)

Possible to make very good predictions without knowing causes

Optimizing prediction does not reliably reveal causes

Powerful tools (PSIS, regularization) for measuring and managing accuracy



# Course Schedule

Week 1	Bayesian inference	Chapters 1, 2, 3
Week 2	Linear models & Causal Inference	Chapter 4
Week 3	Causes, Confounds & Colliders	Chapters 5 & 6
Week 4	Overfitting / MCMC	Chapters 7, 8, 9
Week 5	Generalized Linear Models	Chapters 10, 11
Week 6	Integers & Other Monsters	Chapters 11 & 12
Week 7	Multilevel models I	Chapter 13
Week 8	Multilevel models II	Chapter 14
Week 9	Measurement & Missingness	Chapter 15
Week 10	Generalized Linear Madness	Chapter 16

[https://github.com/rmcelreath/stat\\_rethinking\\_2022](https://github.com/rmcelreath/stat_rethinking_2022)

