

MODULE 3

ESTIMATION AND INFERENCE

ESTIMATION OVERVIEW

- Maximum likelihood has been the go-to estimator for multilevel models for many years
- MCMC is becoming increasingly popular because of its flexibility in estimating complex MLMs
- Recent methodological innovations (e.g., dynamic SEMs, intensive repeated measures) primarily leverage MCMC

OUTLINE

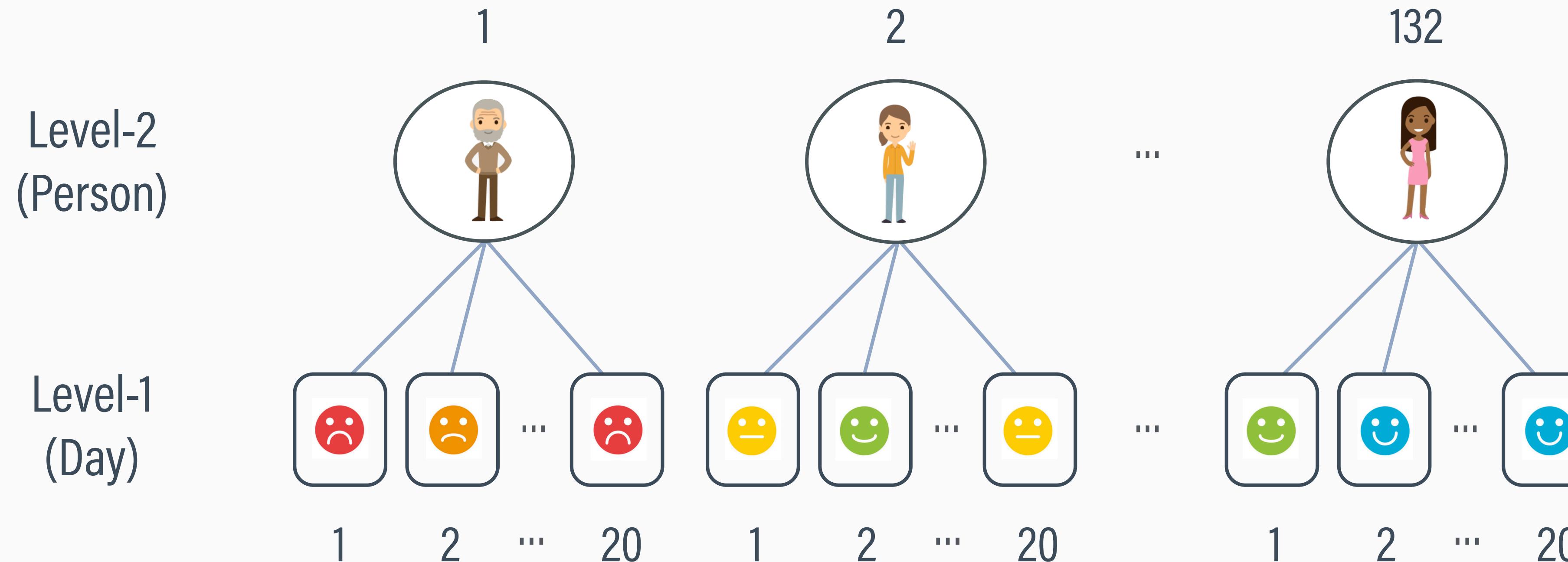
- 1 Analysis Example
- 2 Frequentist vs. Bayesian Statistical Paradigms
- 3 Maximum Likelihood Estimation
- 4 MCMC Estimation
- 5 MCMC Diagnostics
- 6 Checking MLM Assumptions

OUTLINE

- 1 Analysis Example
- 2 Frequentist vs. Bayesian Statistical Paradigms
- 3 Maximum Likelihood Estimation
- 4 MCMC Estimation
- 5 MCMC Diagnostics
- 6 Checking MLM Assumptions

DAILY DIARY APPLICATION

- $n_j = 20$ daily positive affect and sleep assessments nested within $J = 132$ chronic pain patients ($N = 2680$ data records)



DATA STRUCTURE

- Data in stacked or long format
- Each level-2 unit (person) has multiple rows, one per level-1 (daily) observation
- The i subscript indexes level-1 observations, and j indexes level-2 units

| Row | i | j | PAFFECT _{ij} | SLEEP _{ij} |
|------|-----|-----|-----------------------|---------------------|
| 1 | 1 | 1 | 7.3 | 5.6 |
| 2 | 2 | 1 | 2.5 | 4.3 |
| ... | ... | 1 | ... | ... |
| 20 | 20 | 1 | 6.3 | 7.3 |
| 21 | 1 | 2 | 4.0 | 3.9 |
| 22 | 2 | 2 | 4.0 | 7.1 |
| ... | ... | 2 | ... | ... |
| 40 | 20 | 2 | 4.4 | 3.5 |
| ... | ... | ... | ... | ... |
| 2621 | 1 | 132 | 3.3 | 5.4 |
| 2622 | 2 | 132 | 4.8 | 3.5 |
| ... | ... | 132 | ... | ... |
| 2640 | 20 | 132 | 4.8 | 7.9 |

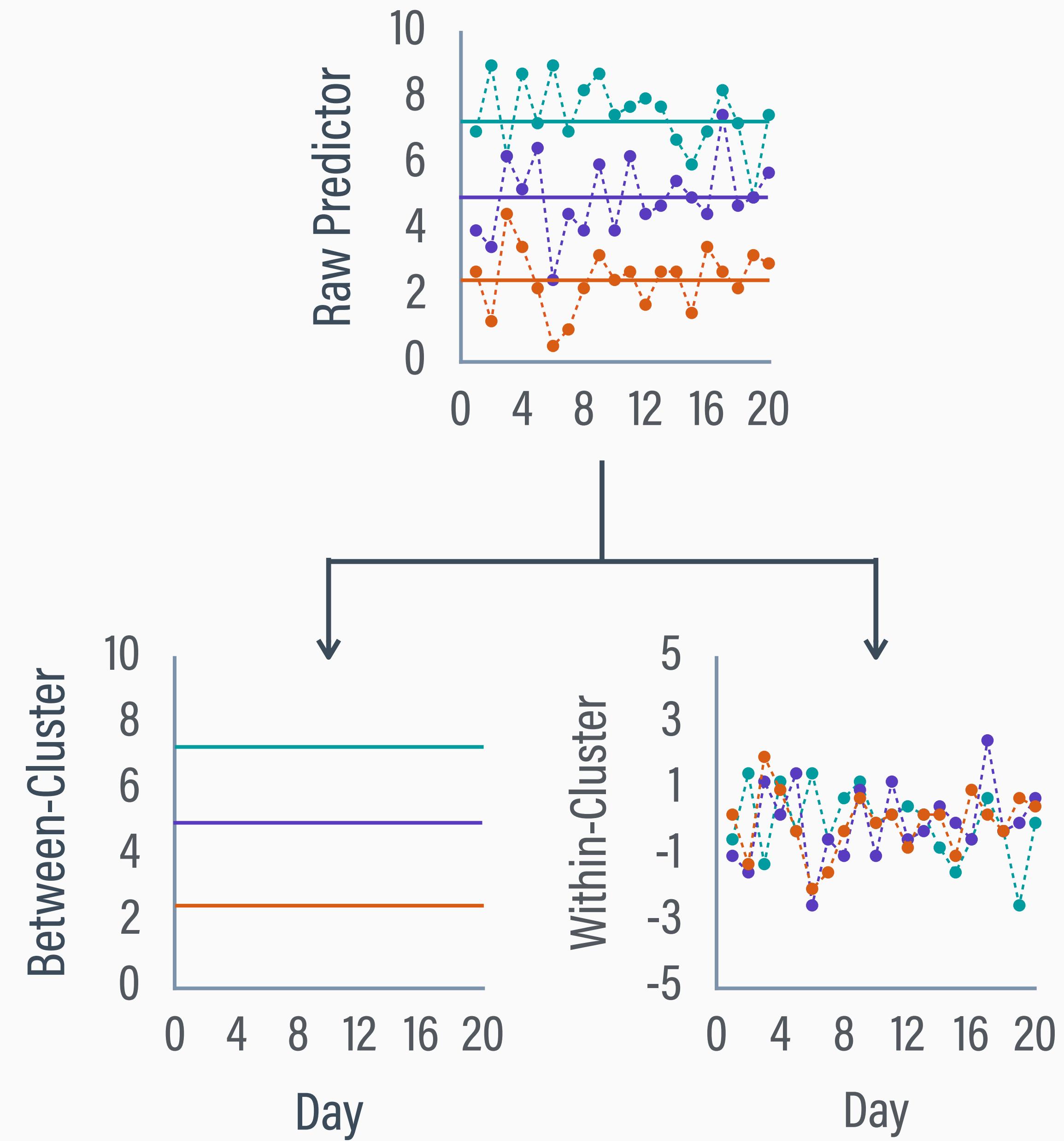
DISAGGREGATED PREDICTOR

- Disaggregation centers each daily score around its level-2 person mean

$$\text{sleep}^b_j = \mu_j(\text{sleep})$$

$$\text{sleep}^w_{ij} = \text{sleep}_{ij} - \mu_j(\text{sleep})$$

- sleep^w contains only intraindividual (level-1) variation, and sleep^b reflects only person (level-2) mean differences

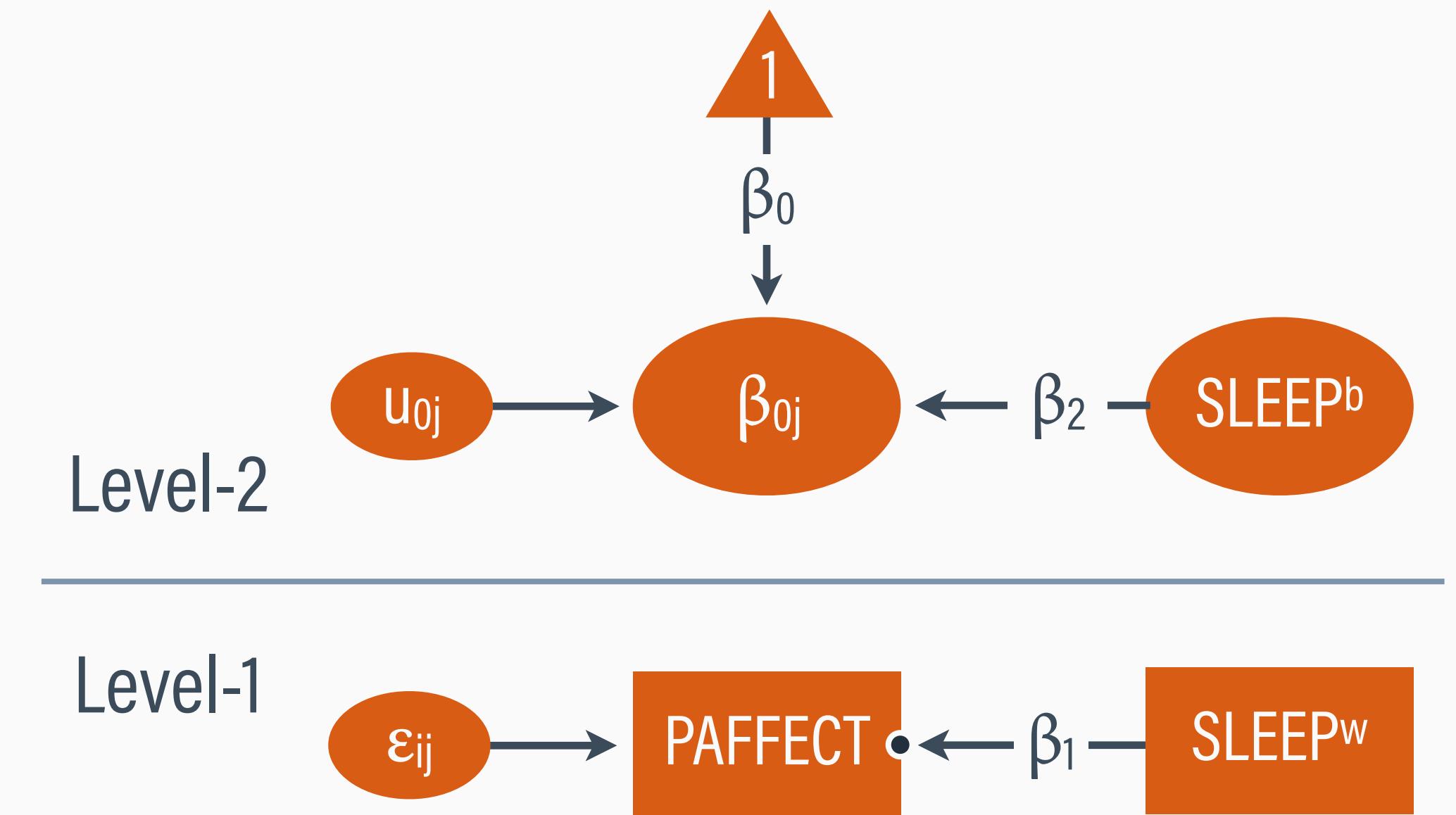


ANALYSIS MODEL

- Model featuring sleep disaggregated into unique level-1 and level-2 predictors

$$PAFFECT_{ij} = \beta_0 + \beta_1(SLEEP_{ij}^W) + \beta_2(SLEEP_j^B) + u_{0j} + \varepsilon_{ij}$$

- Person-average sleep quality predicts person-average positive mood (β_2), and within-person fluctuations in daily sleep predict within-person fluctuations in daily affect (β_1)



• = random intercept (β_{0j})

BLIMP STUDIO SCRIPT 3.1

DATA: PainDiary.dat;

VARIABLES: Person Day PosAffect NegAffect Pain WorkGoal LifeGoal SleepQual Female Education
Employment MarStatus NumDiagnose ActivityLevel PainAccept Catastrophize Stress Anxiety;

CLUSTERID: Person;

CENTER:

grandmean = SleepQual.mean; # defines the fixed (average) intercept as the grand mean

groupmean = SleepQual; # cwc with level-2 latent group means

MODEL: PosAffect ~ intercept SleepQual SleepQual.mean | intercept; # .mean invokes latent means

BURN: 10000;

ITERATIONS: 10000;

SEED: 90291;

RBLIMP SCRIPT 3 (MODEL 1)

```
model1 <- rblimp(  
  data = PainDiary,  
  clusterid = 'Person',  
  center = 'grandmean = SleepQual.mean; groupmean = SleepQual',  
  model = 'PosAffect ~ intercept SleepQual SleepQual.mean | intercept',  
  seed = 90291,  
  burn = 10000,  
  iter = 10000)  
  
output(model1)
```

BLIMP OUTPUT

= level-2 estimate

= level-1 estimate

Outcome Variable: PosAffect

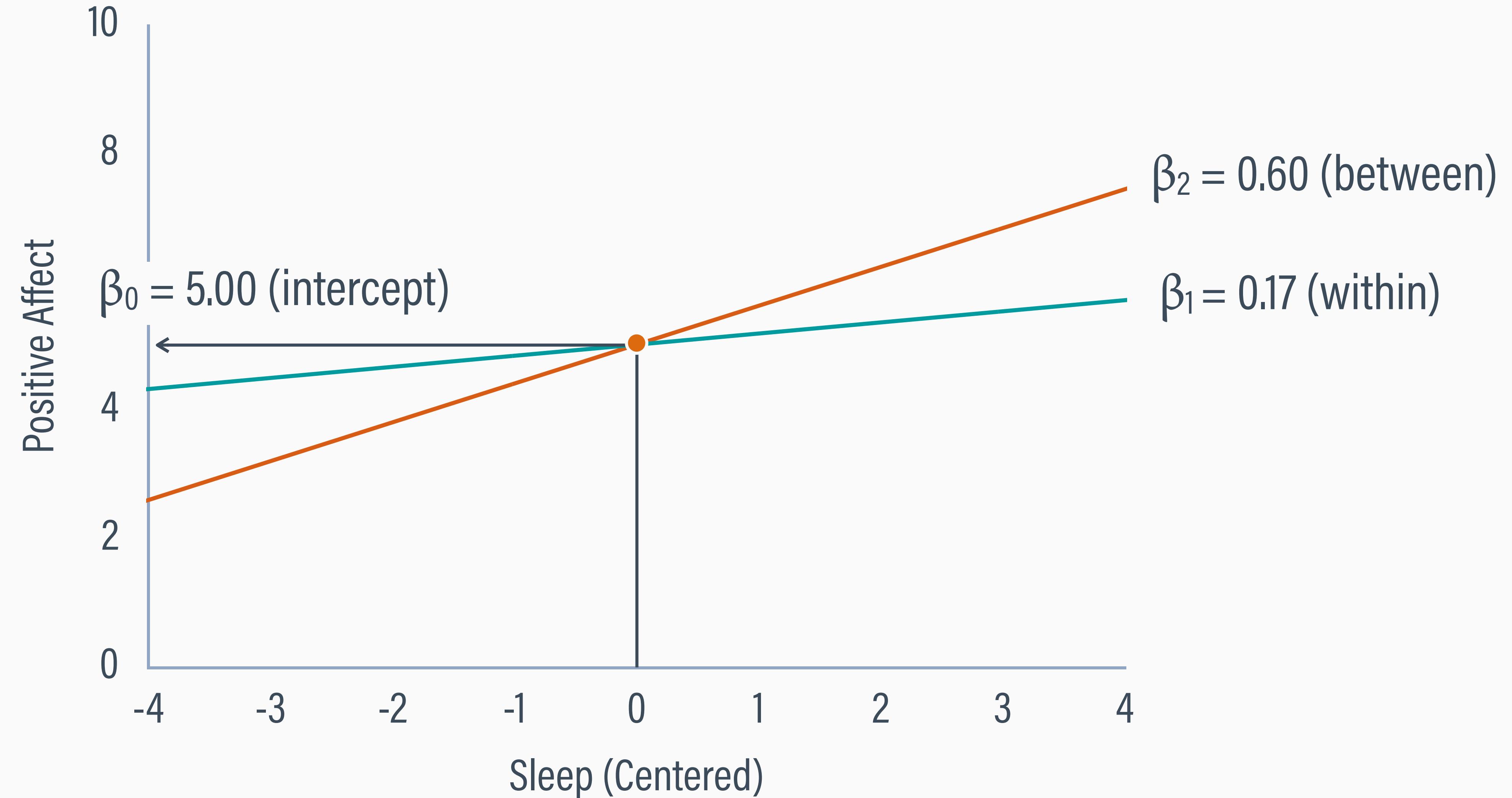
Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|-------------------------------|--------------|--------|-------|-------|----------|--------|----------|
| <hr/> | | | | | | | |
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.839 | 0.246 | 1.436 | 2.399 | --- | --- | 5051.168 |
| Residual Var. | 1.307 | 0.037 | 1.238 | 1.380 | --- | --- | 8227.580 |
| <hr/> | | | | | | | |
| Coefficients: | | | | | | | |
| Intercept | 4.997 | 0.133 | 4.761 | 5.277 | 1423.604 | 0.000 | 154.295 |
| SleepQual | 0.173 | 0.013 | 0.147 | 0.199 | 174.595 | 0.000 | 9302.345 |
| SleepQual.mean[Person] | 0.598 | 0.094 | 0.416 | 0.788 | 40.936 | 0.000 | 161.345 |
| <hr/> | | | | | | | |
| Standard Deviations: | | | | | | | |
| L2 : SD(Intercept) | 1.356 | 0.090 | 1.198 | 1.549 | --- | --- | 5041.908 |
| Residual SD | 1.143 | 0.016 | 1.113 | 1.175 | --- | --- | 8223.888 |
| <hr/> | | | | | | | |
| Standardized Coefficients: | | | | | | | |
| SleepQual | 0.151 | 0.013 | 0.127 | 0.176 | 142.389 | 0.000 | 1996.211 |
| SleepQual.mean[Person] | 0.412 | 0.055 | 0.297 | 0.513 | 55.809 | 0.000 | 169.087 |
| <hr/> | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.193 | 0.044 | 0.112 | 0.286 | --- | --- | 175.664 |
| by Level-2 Random Intercepts | 0.471 | 0.042 | 0.392 | 0.555 | --- | --- | 414.230 |
| by Level-1 Residual Variation | 0.334 | 0.027 | 0.280 | 0.387 | --- | --- | 511.829 |

FIXED EFFECT INTERPRETATIONS

- $\beta_0 = 5.00$ is the positive affect grand mean (because both predictors are centered)
- $\beta_1 = 0.17$ is the expected affect difference between two daily sleep scores from the same person that differ by one point
- $\beta_2 = 0.60$ is the expected affect difference between two individuals whose average sleep ratings differ by one point

LEVEL-1 AND LEVEL-2 REGRESSIONS



RANDOM EFFECT INTERPRETATIONS

- $u_{0j} = \beta_{0j} - (\beta_0 + \beta_2(\text{sleep}_j^b))$
- $\text{var}(u_{0j}) = 1.84$ is the average squared distance between the level-2 affect means and their predicted values
- $\text{sd}(u_{0j}) = 1.36$ is the average distance between the level-2 affect means and their predicted values
- $\varepsilon_{ij} = \text{pffect}_{ij} - (\beta_{0j} + \beta_1(\text{sleep}_{ij}^w))$
- $\text{var}(\varepsilon_{ij}) = 1.31$ is the average squared distance between the level-1 affect observations and their predicted values
- $\text{sd}(\varepsilon_{ij}) = 1.14$ is the average distance between the level-1 affect observations and their predicted values

OUTLINE

- 1 Analysis Example
- 2 Frequentist vs. Bayesian Statistical Paradigms
- 3 Maximum Likelihood Estimation
- 4 MCMC Estimation
- 5 MCMC Diagnostics
- 6 Checking MLM Assumptions

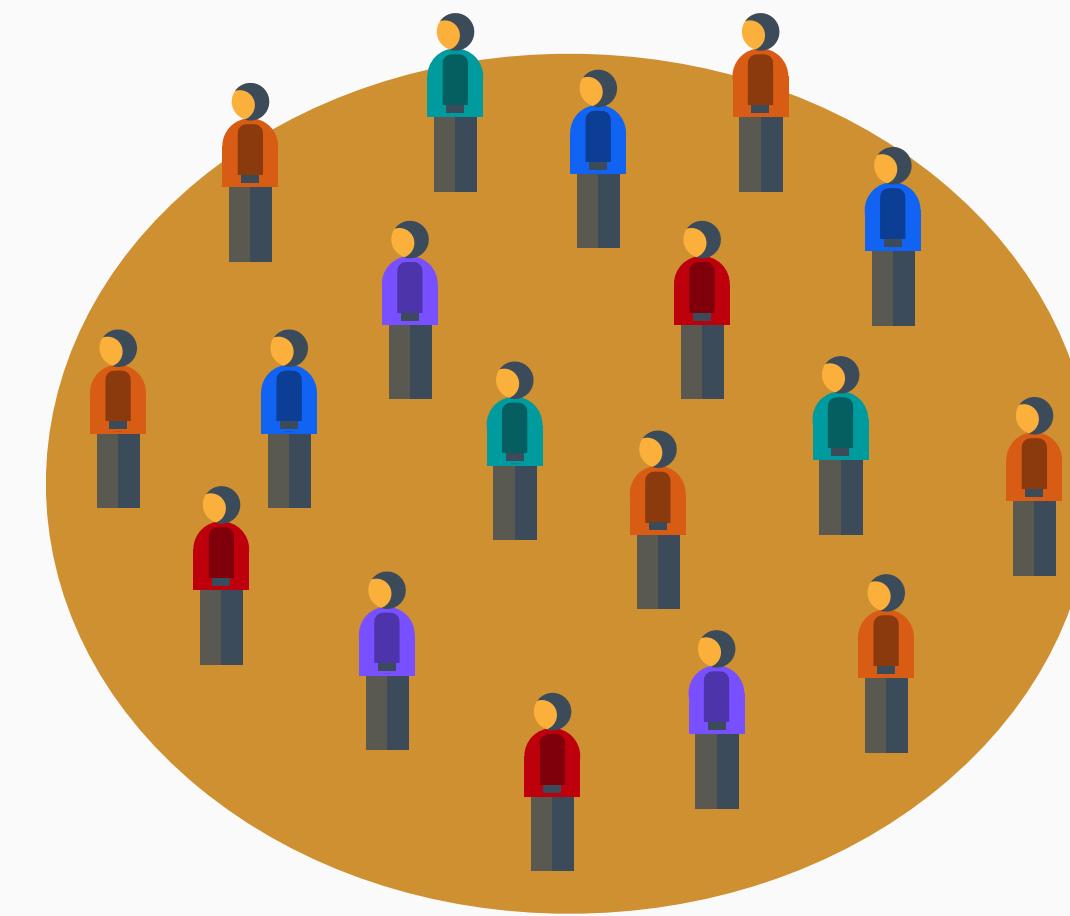
FREQUENTIST STATISTICAL PARADIGM

- The frequentist paradigm is defined by the idea that there is one population with unknown parameters (e.g., μ and σ)
- We imagine numerous hypothetical samples of size N from the population, each with its own unique estimates (e.g., \bar{X} and s)
- The population-level statistics (parameters) are locked in at a single set of values, whereas the sample-level statistics (estimates) vary across different data sets

FREQUENTIST FRAMEWORK

One population with unknown parameters β_0 , β_1 , and β_2

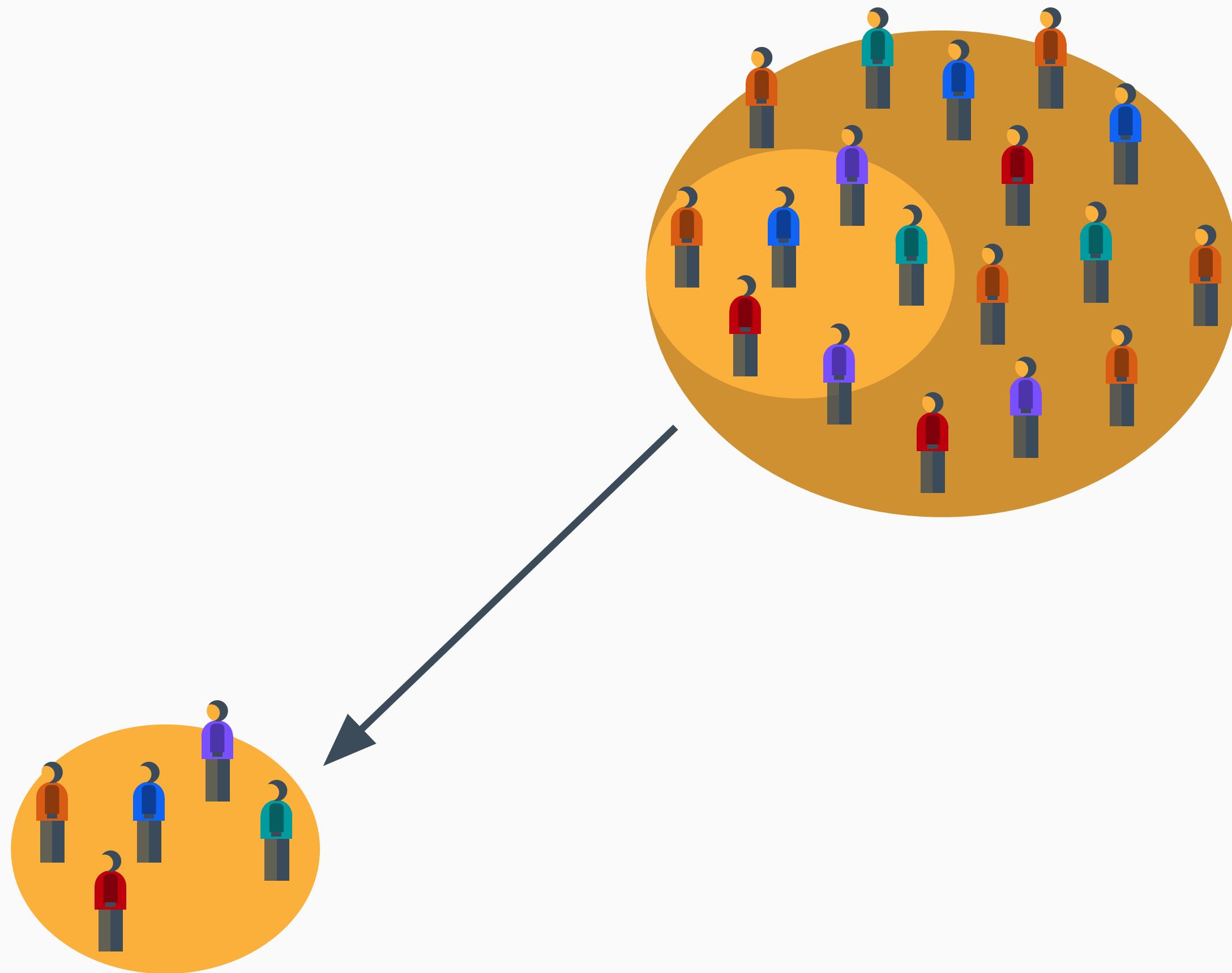
$$\boldsymbol{\beta} = (\beta_0, \beta_1, \beta_2)$$



FREQUENTIST FRAMEWORK

One population with unknown parameters. Estimates vary across different hypothetical samples.

$$\beta = (\beta_0, \beta_1, \beta_2)$$

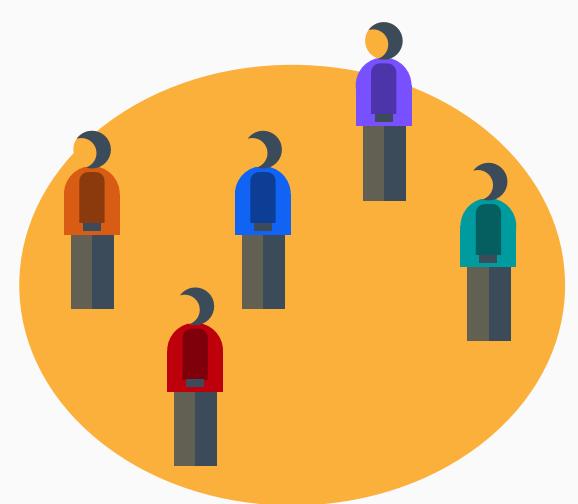
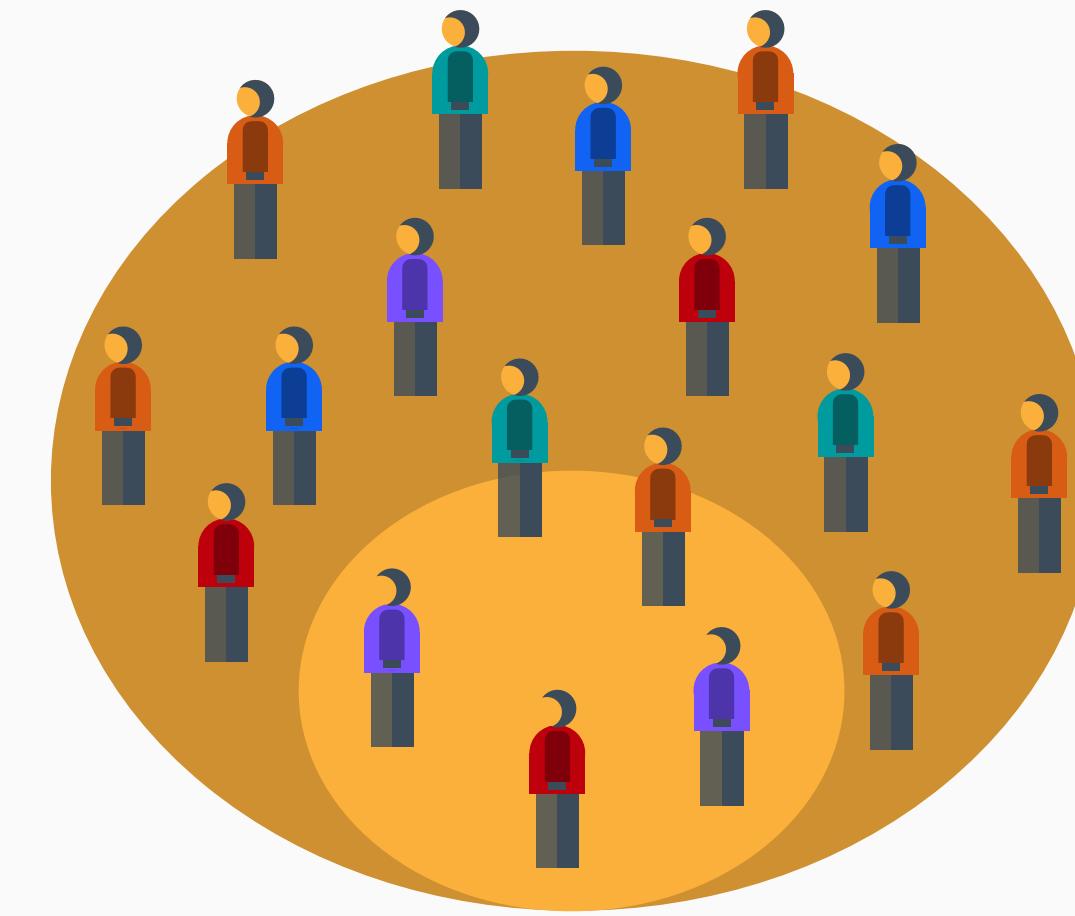


$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$

FREQUENTIST FRAMEWORK

One population with unknown parameters. Estimates vary across different hypothetical samples.

$$\beta = (\beta_0, \beta_1, \beta_2)$$



$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$

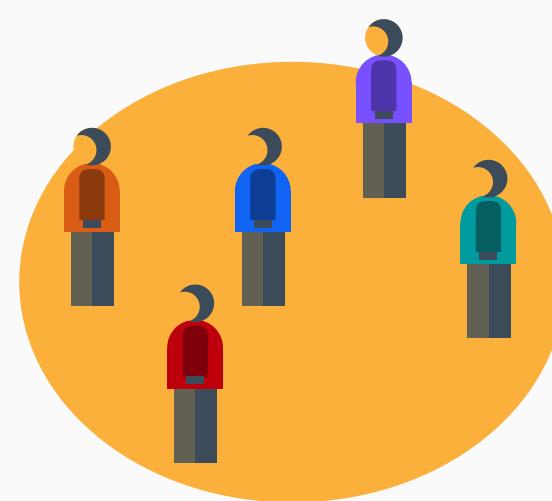


$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$

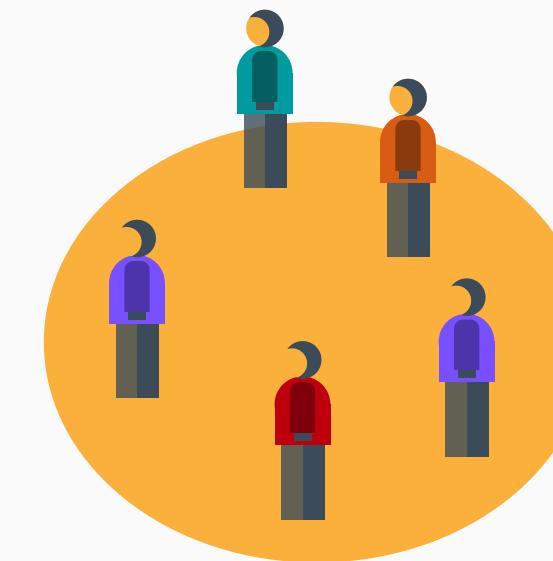
FREQUENTIST FRAMEWORK

One population with unknown parameters. Estimates vary across different hypothetical samples.

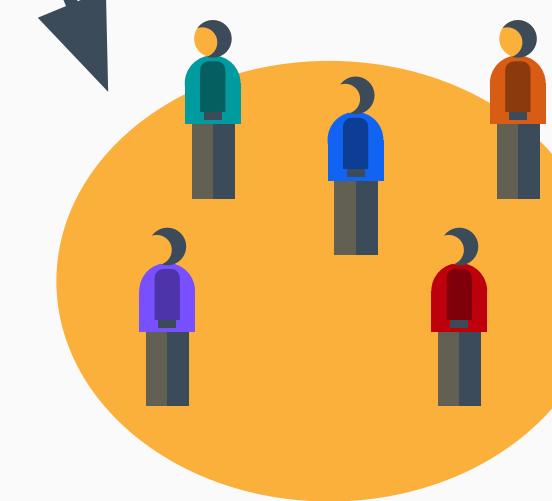
$$\beta = (\beta_0, \beta_1, \beta_2)$$



$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$



$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$

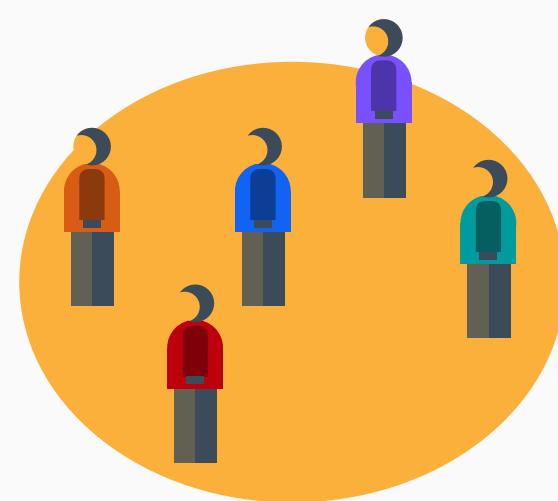
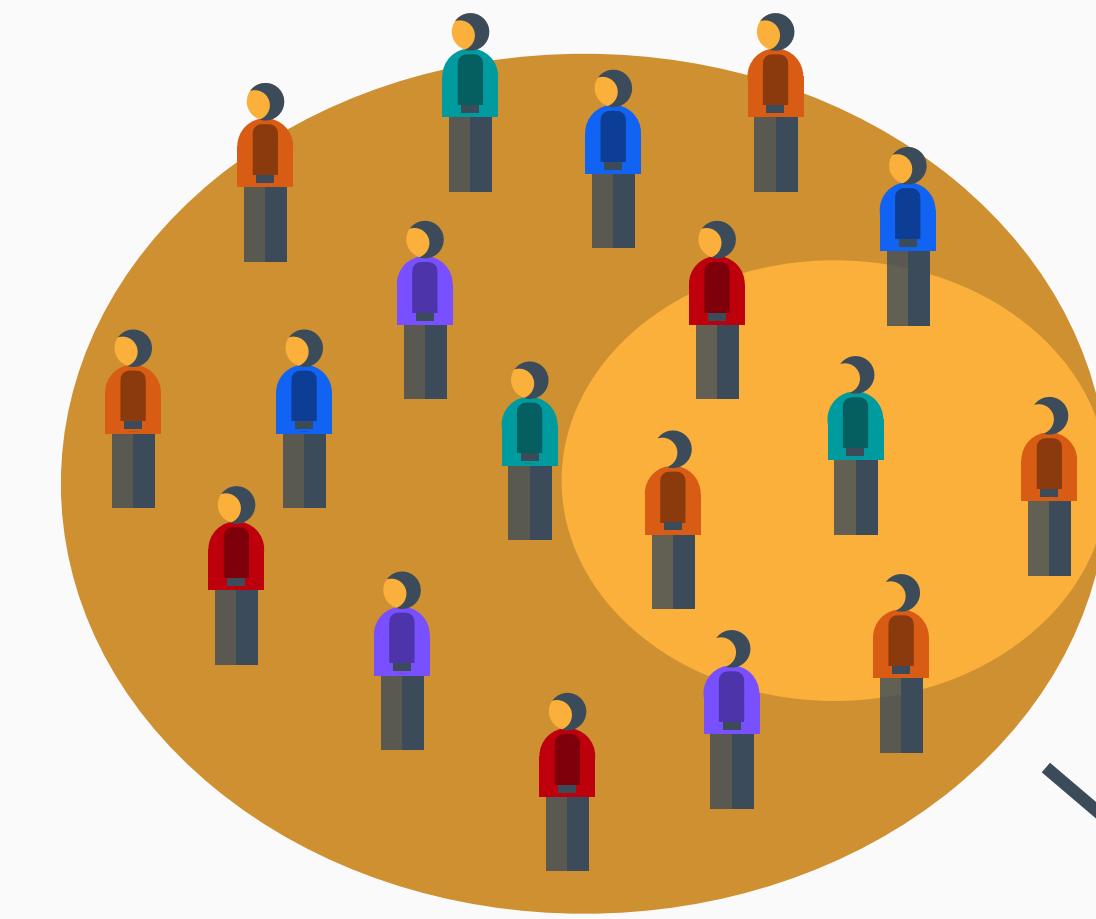


$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$

FREQUENTIST FRAMEWORK

One population with unknown parameters. Estimates vary across different hypothetical samples.

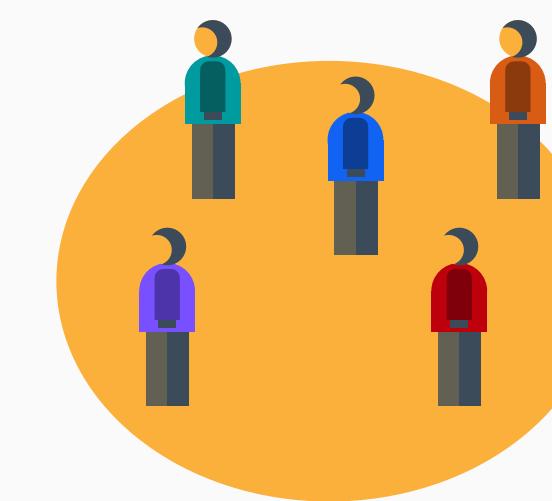
$$\beta = (\beta_0, \beta_1, \beta_2)$$



$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$



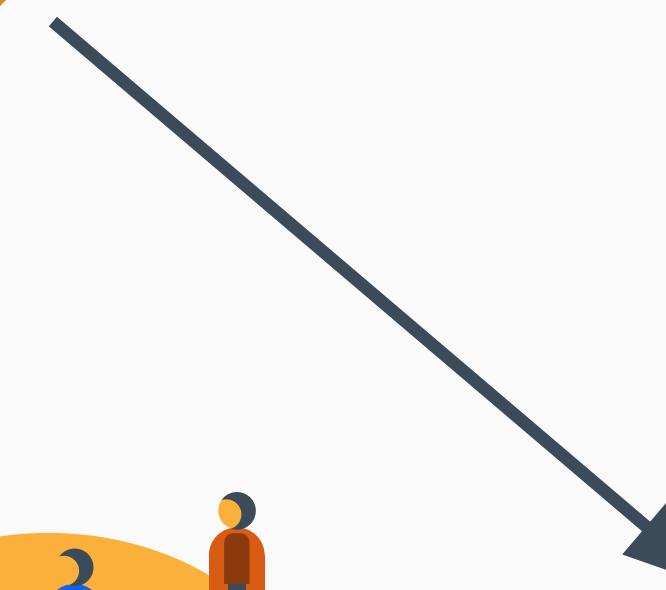
$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$



$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$



$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2)$$



BAYESIAN STATISTICAL PARADIGM

- The Bayesian paradigm is defined by the idea that there is one sample of size N that we observe (no hypothetical samples)
- We imagine numerous hypothetical populations that could have produced our particular sample of data, each with unique parameter values (e.g., many values of β_0 , β_1 , and β_2)
- The sample data are locked into place, and parameter values vary across different hypothetical populations

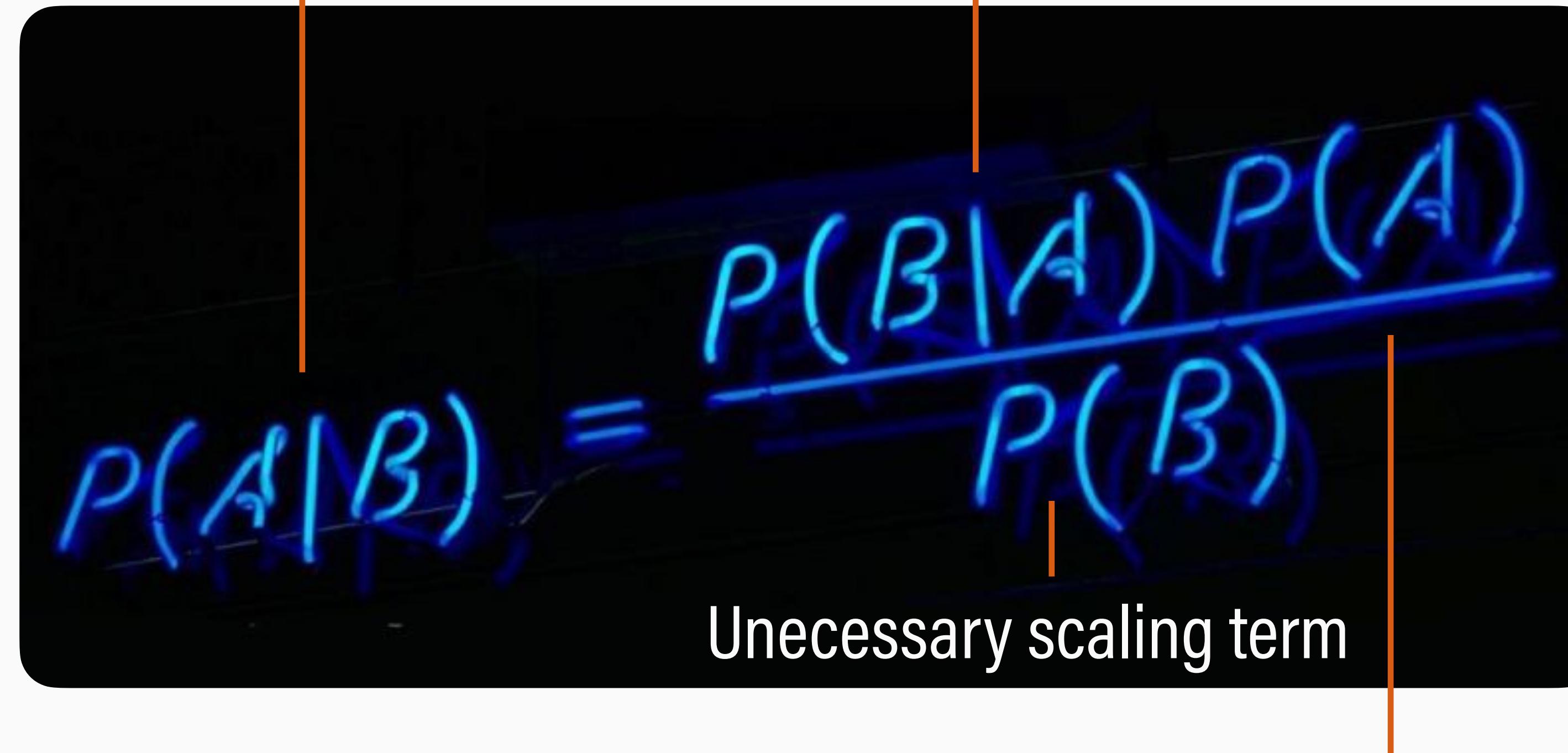
BAYES' THEOREM

Posterior = parameters (A) given the data (B)

Frequentist likelihood = data (B) given the parameters (A)

$$P(A|B) = \frac{P(B|A) P(A)}{P(B)}$$

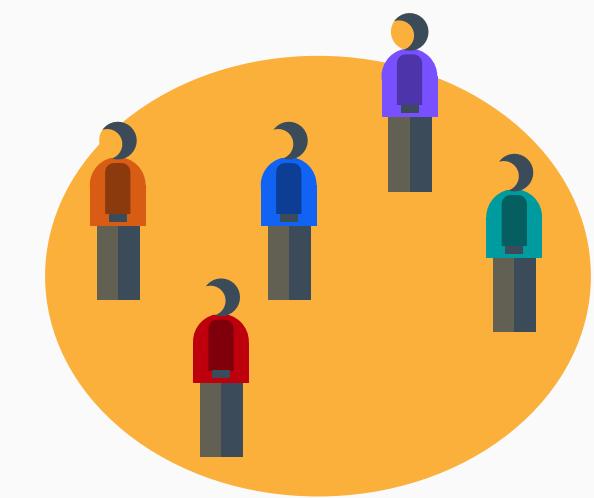
Unecessary scaling term



Prior = a priori belief about parameters (A)

BAYESIAN FRAMEWORK

One sample of size N

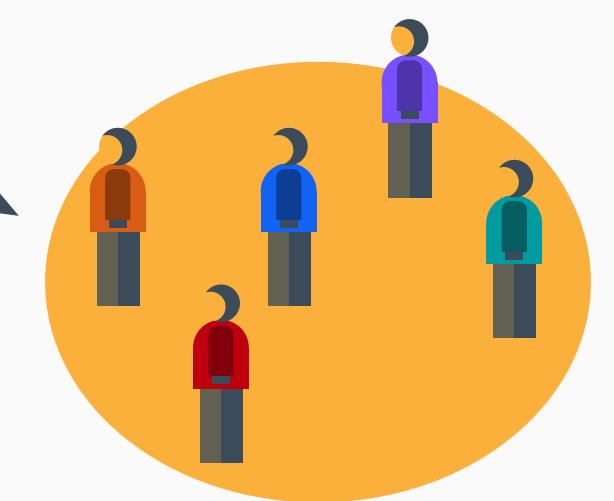


BAYESIAN FRAMEWORK

$$\beta = (\beta_0, \beta_1, \beta_2)$$

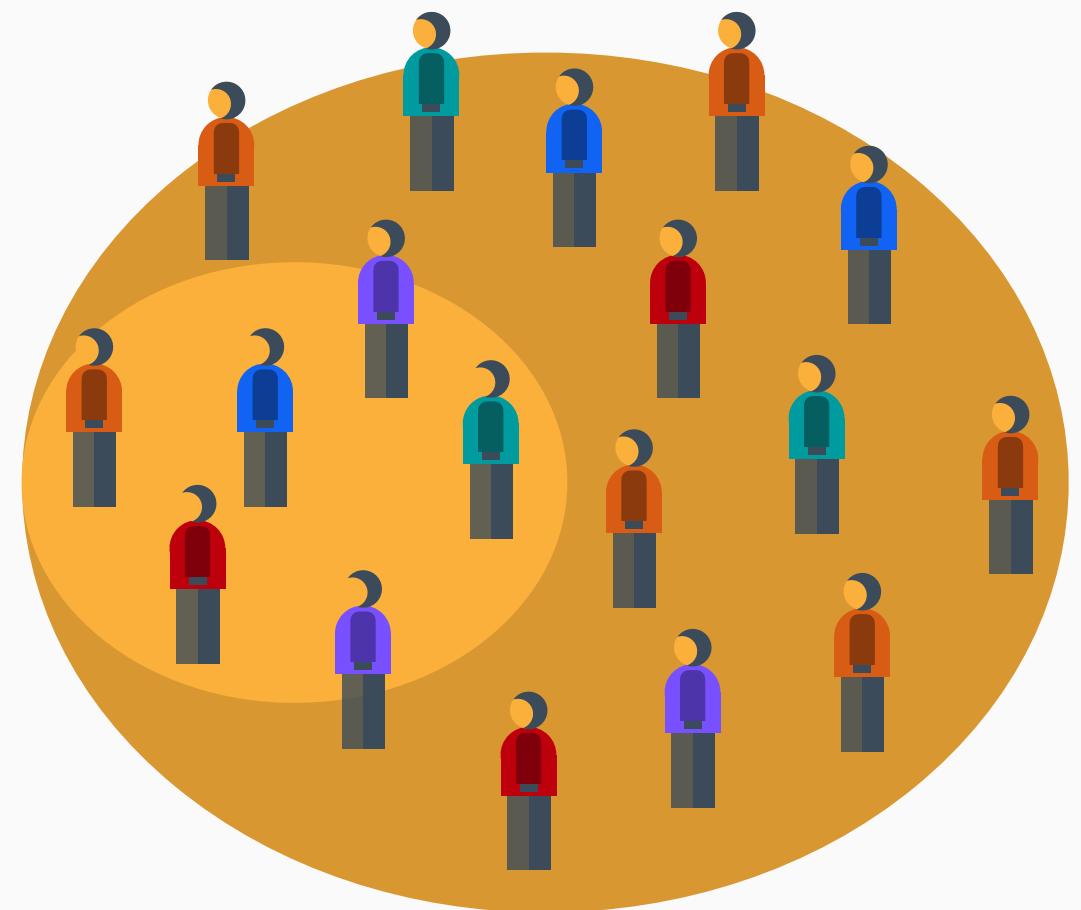


One sample of size N. Parameter
values vary across different
hypothetical populations.

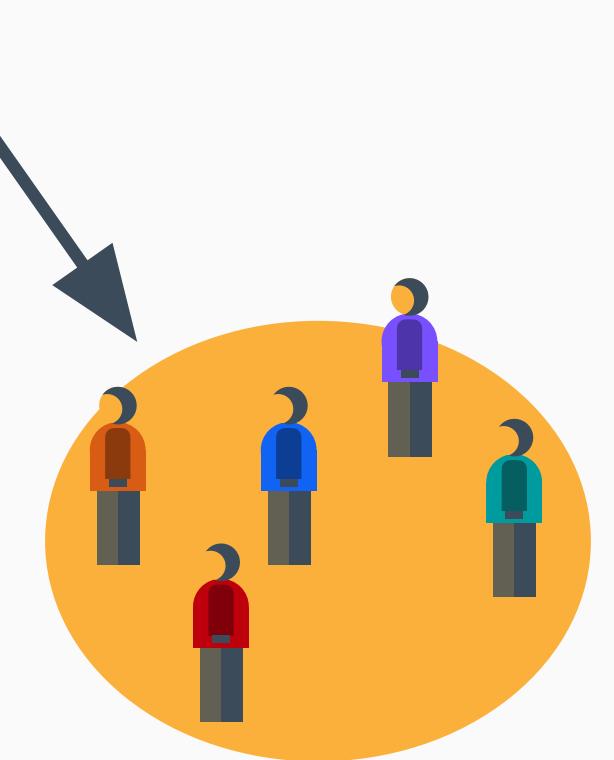


BAYESIAN FRAMEWORK

$$\beta = (\beta_0, \beta_1, \beta_2)$$



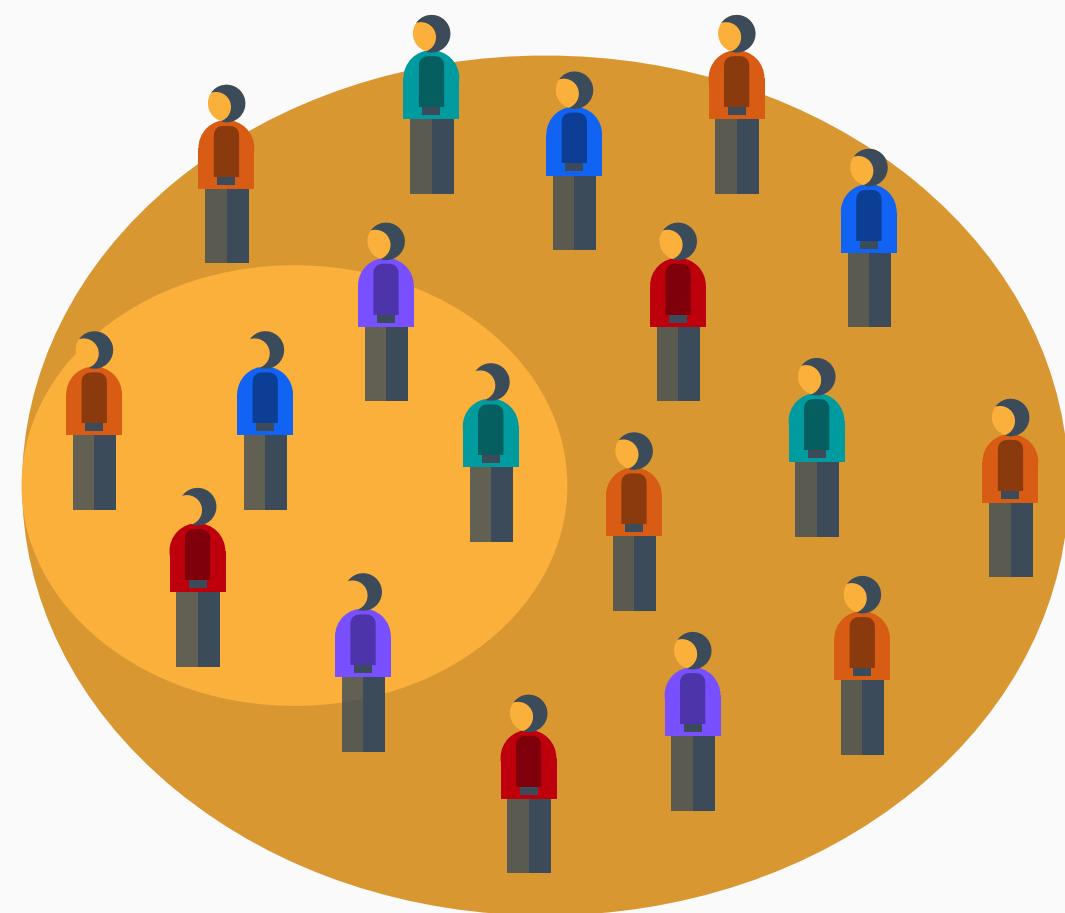
$$\beta = (\beta_0, \beta_1, \beta_2)$$



One sample of size N. Parameter
values vary across different
hypothetical populations.

BAYESIAN FRAMEWORK

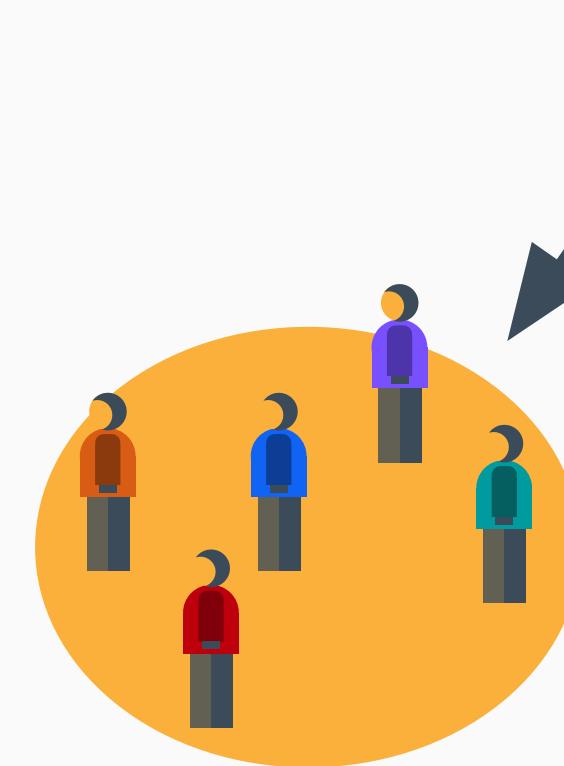
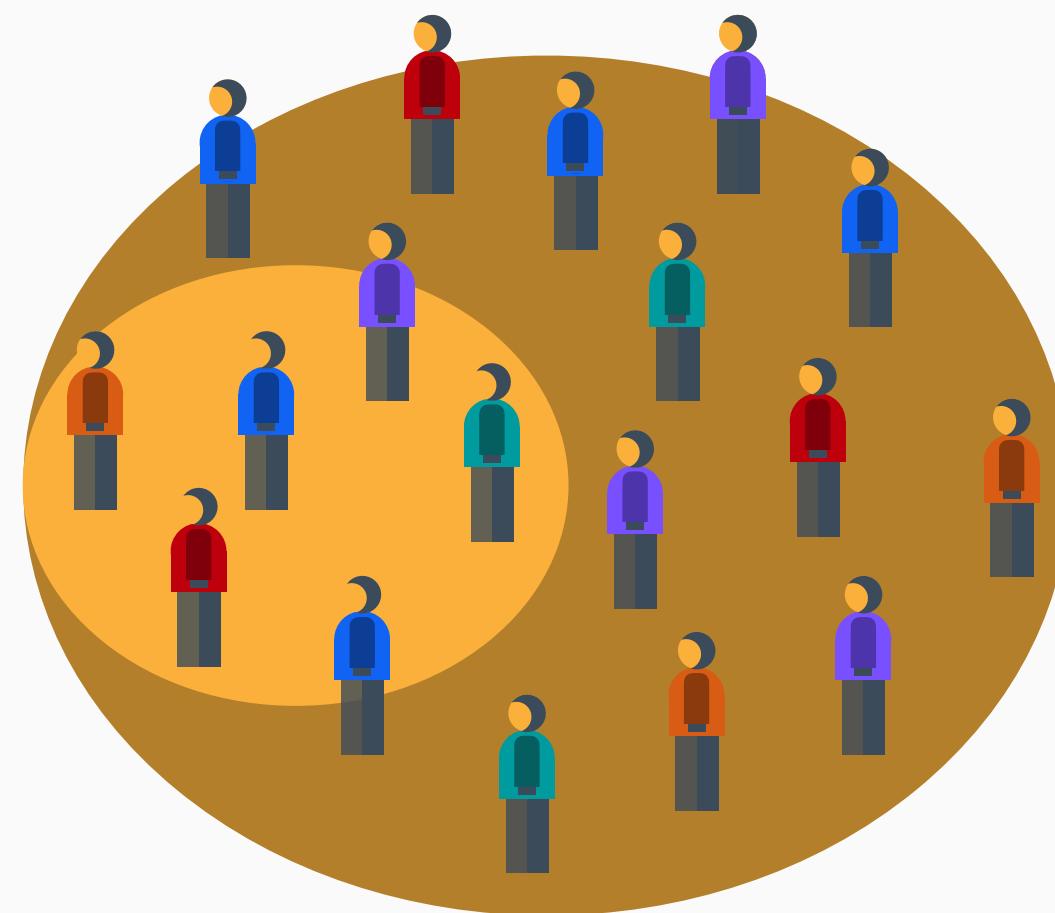
$$\beta = (\beta_0, \beta_1, \beta_2)$$



$$\beta = (\beta_0, \beta_1, \beta_2)$$



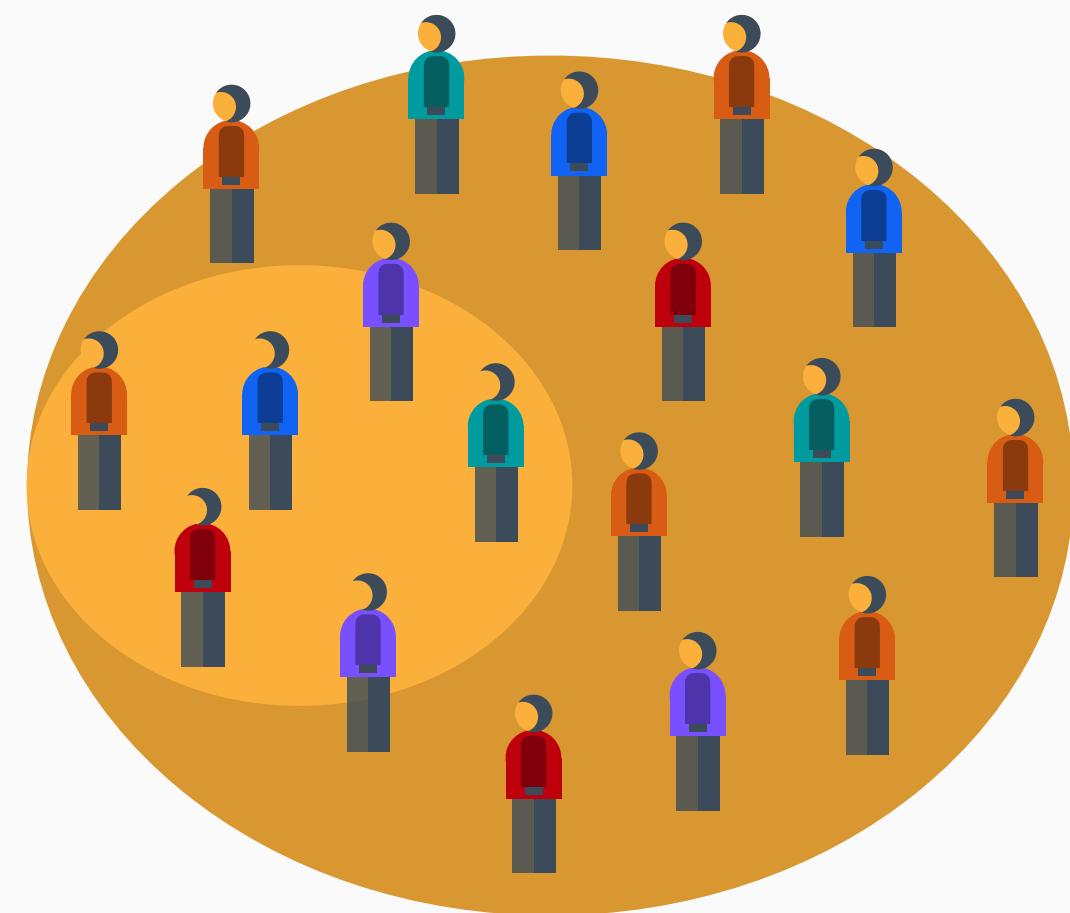
$$\beta = (\beta_0, \beta_1, \beta_2)$$



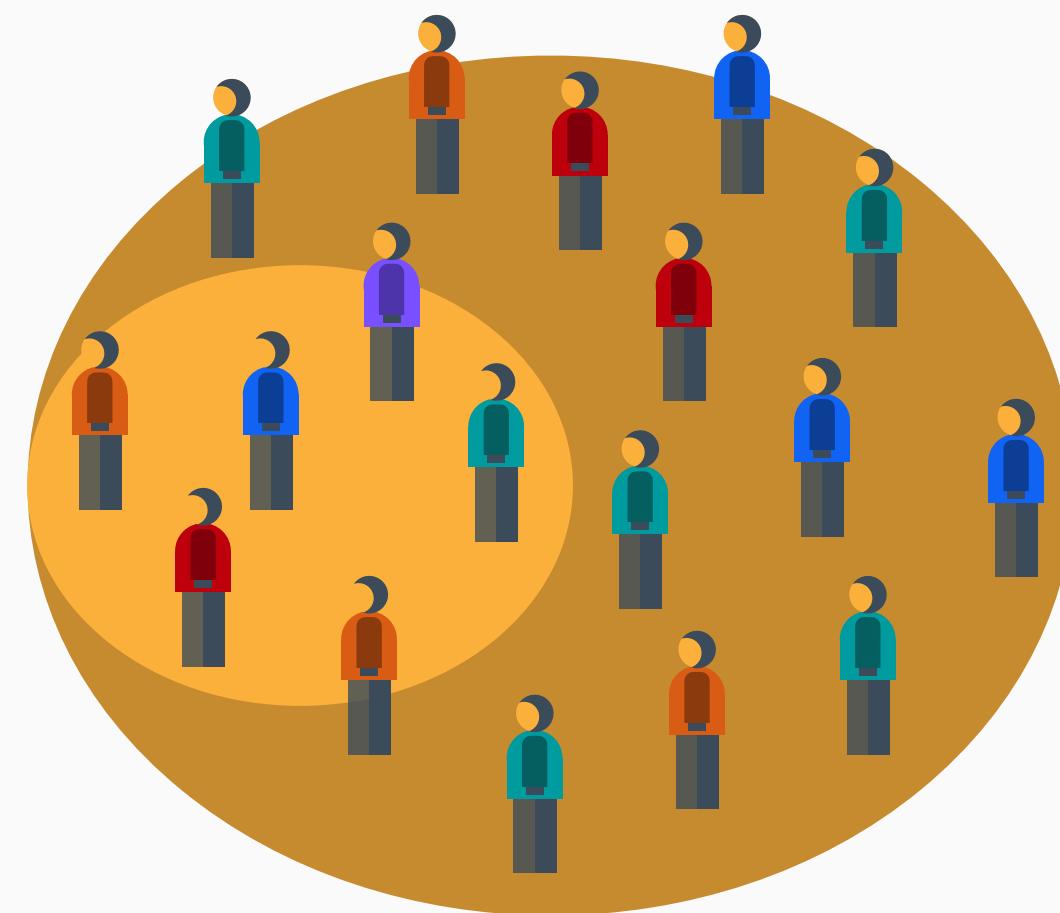
One sample of size N. Parameter values vary across different hypothetical populations.

BAYESIAN FRAMEWORK

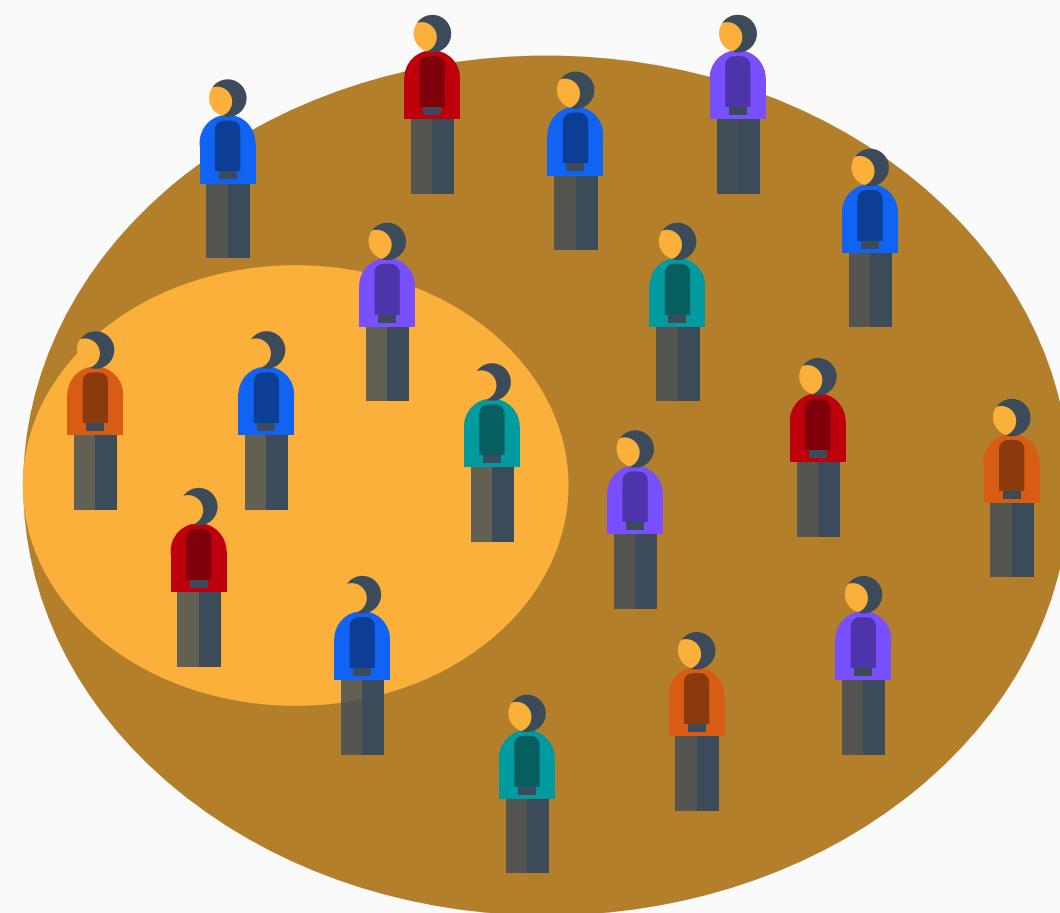
$$\beta = (\beta_0, \beta_1, \beta_2)$$



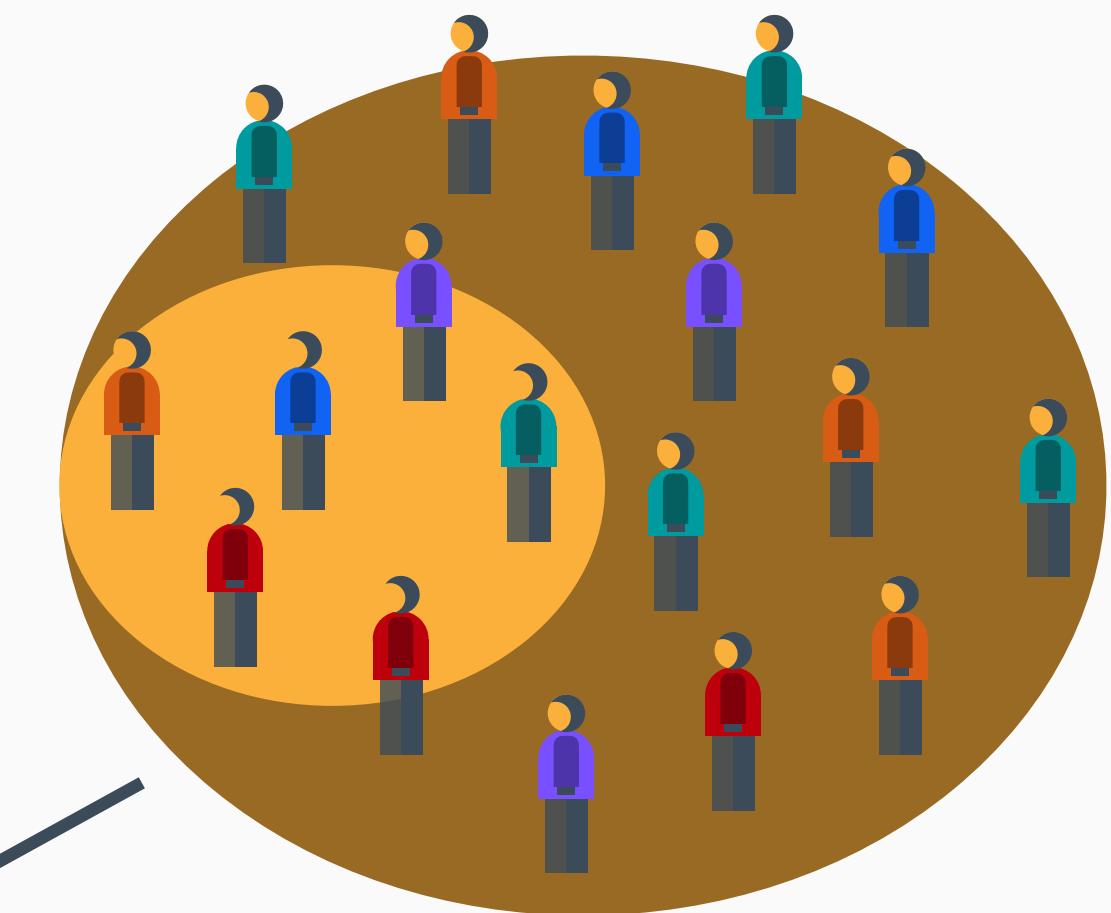
$$\beta = (\beta_0, \beta_1, \beta_2)$$



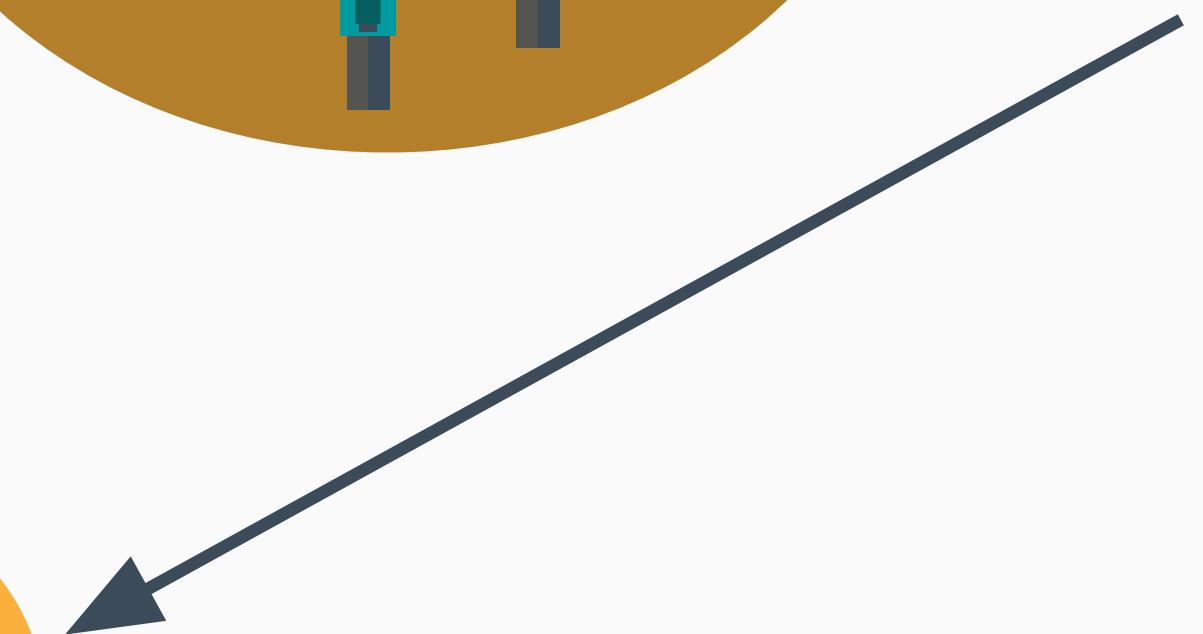
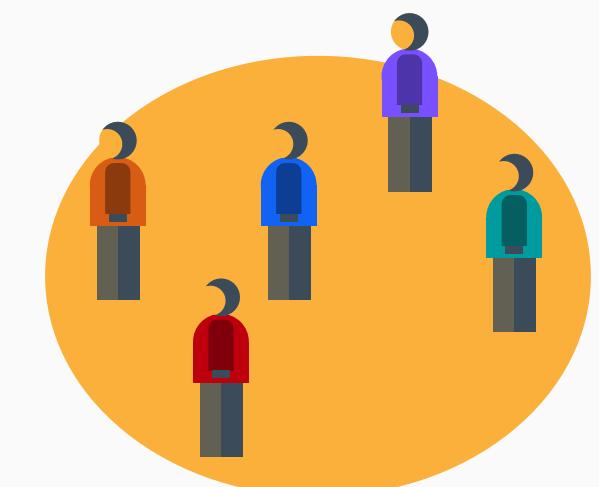
$$\beta = (\beta_0, \beta_1, \beta_2)$$



$$\beta = (\beta_0, \beta_1, \beta_2)$$



One sample of size N. Parameter values vary across different hypothetical populations.



FREQUENTIST VS. BAYESIAN SUMMARY

Frequentist

- The parameter is a fixed quantity, estimates vary across different samples
- Statements about probability, precision, and confidence refer to estimates
- Probability = the long run frequency of an event across many different samples

Bayesian

- There is a single sample, and parameters vary across different populations
- Statements about probability, precision, and intervals refer to the parameter
- Probability = our degree of certainty about a parameter after analyzing data

OUTLINE

- 1 Analysis Example
- 2 Frequentist vs. Bayesian Statistical Paradigms
- 3 Maximum Likelihood Estimation
- 4 MCMC Estimation
- 5 MCMC Diagnostics
- 6 Checking MLM Assumptions

MAXIMUM LIKELIHOOD ESTIMATION

- Maximum likelihood (ML) estimation identifies the population parameters that are most likely to have produced the data
- Like ordinary least squares regression, maximum likelihood estimates (MLEs) minimize the sum of squared residuals
- Normal curve functions define two layers of MLM residuals

ITERATIVE OPTIMIZATION ALGORITHMS

- Unlike OLS, multilevel models do not have closed-form equations where you plug in data and solve for the estimates
- ML requires iterative optimizers (Newton's or EM algorithm) that cyclically update the parameters
- Each successive step adjust estimates to improve fit (decrease residuals) until the data-model fit is maximized

REVIEW: ESTIMATING VARIANCES

- OLS can be viewed as two-steps: (1) Use all N data points to estimate coefficients, (2) subtract the “spent” degrees of freedom (df) from the N and estimate the residual variance
- Computing the variance with $N - 1$ as a divisor gives unbiased estimates, whereas using N attenuates variability estimates
- The degrees of freedom adjustment for residual variances in regression similarly uses $N - \# \text{ predictors} - 1$

FIML VERSUS REML ESTIMATORS

- Full information maximum likelihood (FIML) does use bias-reducing degrees of freedom adjustments
- Level-2 variance estimates are attenuated when the number of clusters is small because no degrees-of-freedom adjustment is applied (e.g., they use J rather than $J - 1$)
- Restricted maximum likelihood (REML) addresses this bias, estimating variances with df-like adjustments

FIML VS. REML COMPARISON

- FIML estimates of the level-2 residual variance are slightly lower because they do not adjust for degrees of freedom spent estimating the coefficients

| Parameter | REML | | FIML | | Bayesian MCMC | |
|---------------------------------|-------------|-----------|-------------|-----------|---------------|-----------|
| | Est. | Std. Err. | Est. | Std. Err. | Est. | Std. Err. |
| Fixed intercept | 5.05 | 0.12 | 5.05 | 0.12 | 5.00 | 0.13 |
| Sleep (within-person) | 0.17 | 0.01 | 0.17 | 0.01 | 0.17 | 0.01 |
| Sleep (between-person) | 0.58 | 0.09 | 0.58 | 0.08 | 0.60 | 0.09 |
| Random intercept variance | 1.83 | -- | 1.80 | -- | 1.84 | 0.25 |
| Residual within-person variance | 1.31 | -- | 1.30 | -- | 1.31 | 0.04 |

OUTLINE

- 1 Analysis Example
- 2 Frequentist vs. Bayesian Statistical Paradigms
- 3 Maximum Likelihood Estimation
- 4 MCMC Estimation
- 5 MCMC Diagnostics
- 6 Checking MLM Assumptions

WHY CHOOSE MCMC?

- MCMC readily handles complex missing data problems, including:
 - Mixed metrics (normal, ordinal, nominal, skewed, count, latent)
 - Nonlinear effects (interactions, curvilinear effects)
 - Multilevel data (random coefficients, interactions)
 - Latent variable modeling (interactions)
- FIML estimators for these scenarios are far more limited

MARKOV CHAIN MONTE CARLO (MCMC)

- MCMC estimation samples model parameters and the missing values from distributions of plausible values
- MCMC breaks a complex problem involving multiple unknowns (parameters and missing values) into separate steps
- Each step estimates one unknown at a time, treating the current values of all other quantities as known constants

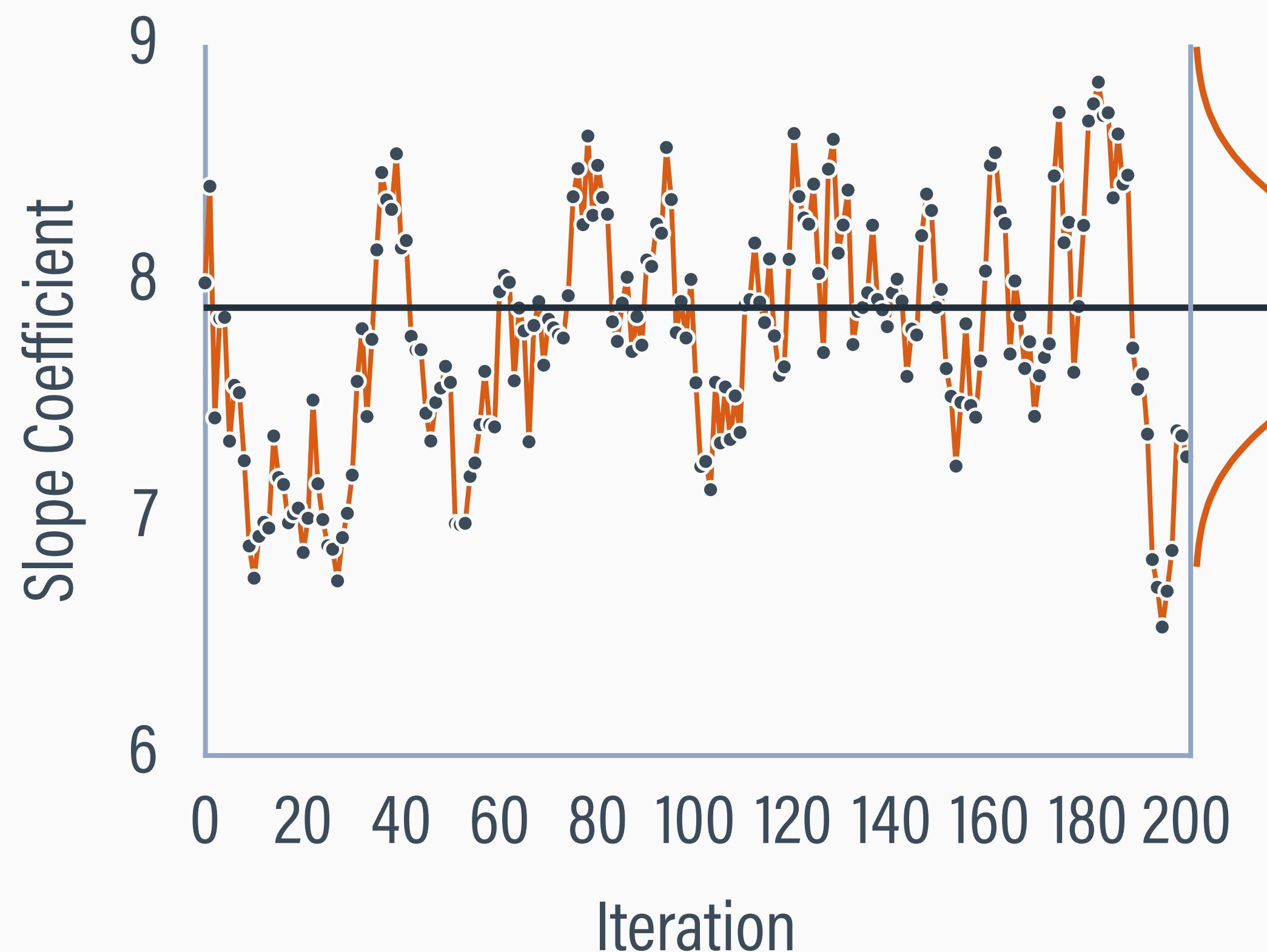
MCMC ALGORITHM



- » Do for $t = 1$ to T iterations
 - » Estimate regression coefficients
 - » Estimate random intercept residuals
 - » Estimate level-2 intercept variance
 - » Estimate level-1 residual variance
 - » Impute missing data
- » Repeat

MEANING OF ESTIMATION

- MCMC uses computer simulation to “sample” parameters from a distribution
- Estimates continually vary across iterations in a random pattern
- Each iteration gives plausible parameter values that could have produced our data



DISAGGREGATED ANALYSIS

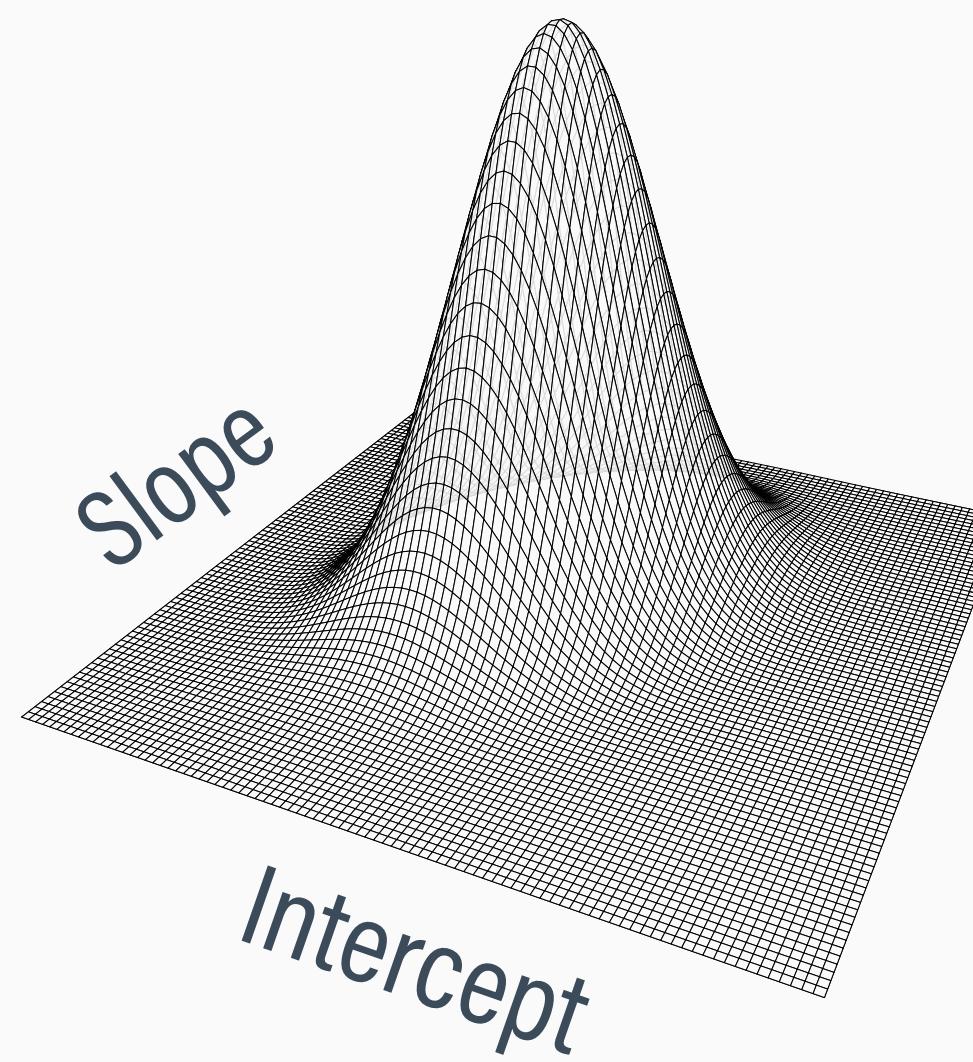
- Affect regressed on within- and between-person sleep

$$p\text{affect}_{ij} = \beta_0 + \beta_1(\text{sleep}_{ij}^W) + \beta_2(\text{sleep}_j^B) + u_{0j} + \varepsilon_{ij}$$

- Each iteration yields population parameter values that could have plausibly produced this same of data
- The goal is to summarize the parameter distributions

PARAMETER-GENERATING DISTRIBUTIONS

- MCMC draws coefficients from a multivariate normal distribution, with least-squares estimates defining shape
- MCMC draws variances from an inverse gamma distribution with its shape determined by the df and residual SS

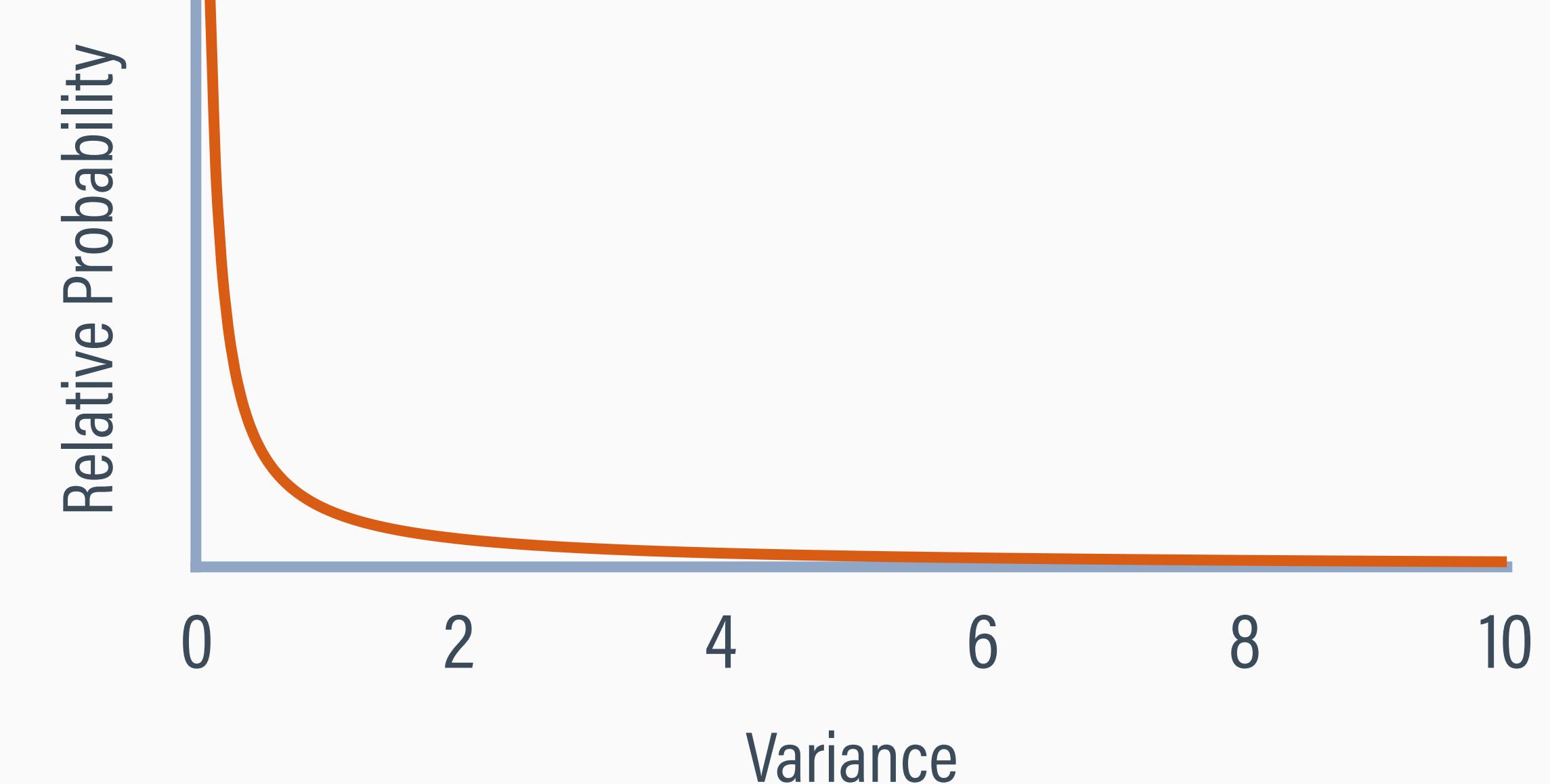
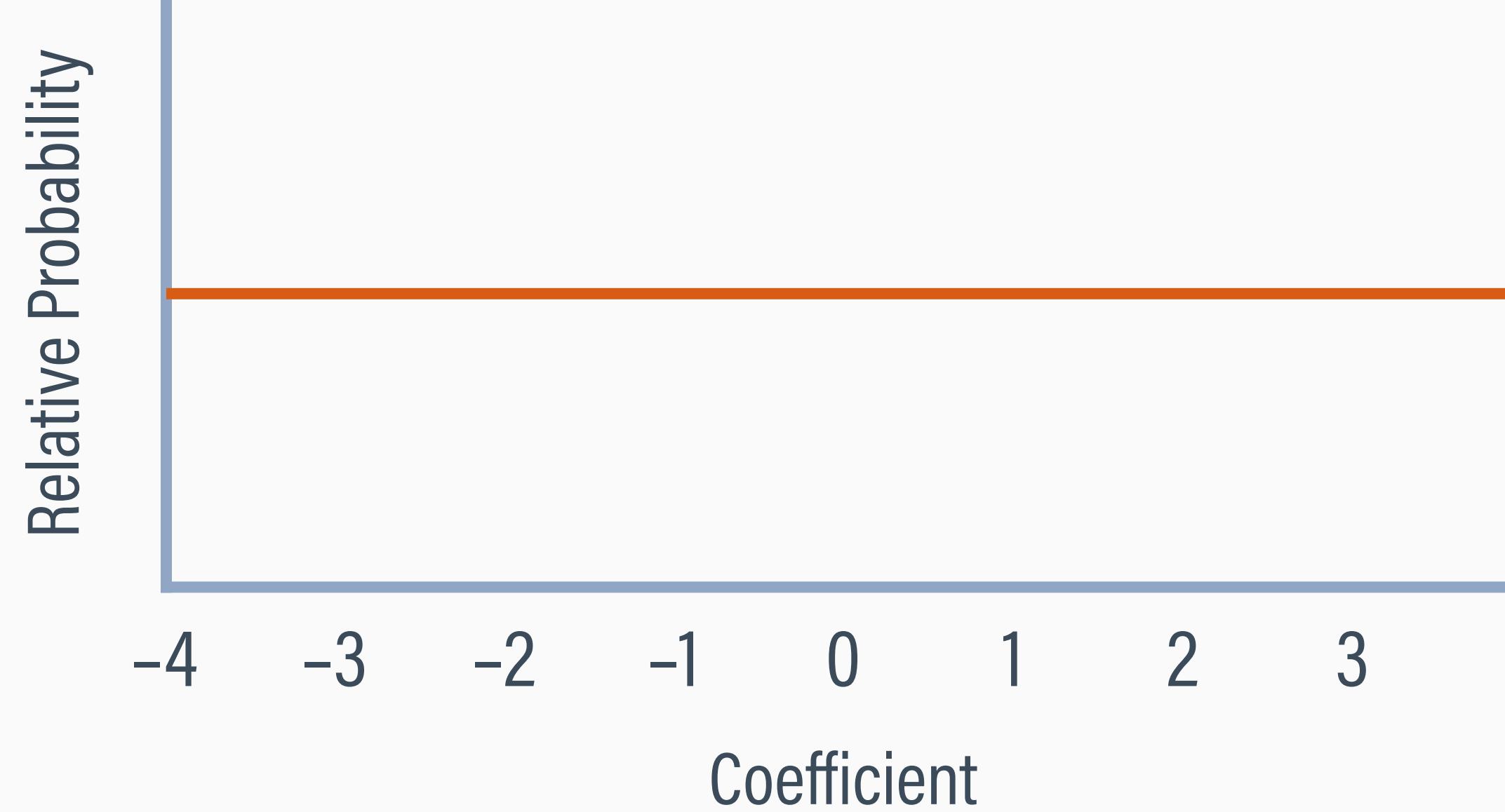


PRIOR DISTRIBUTIONS

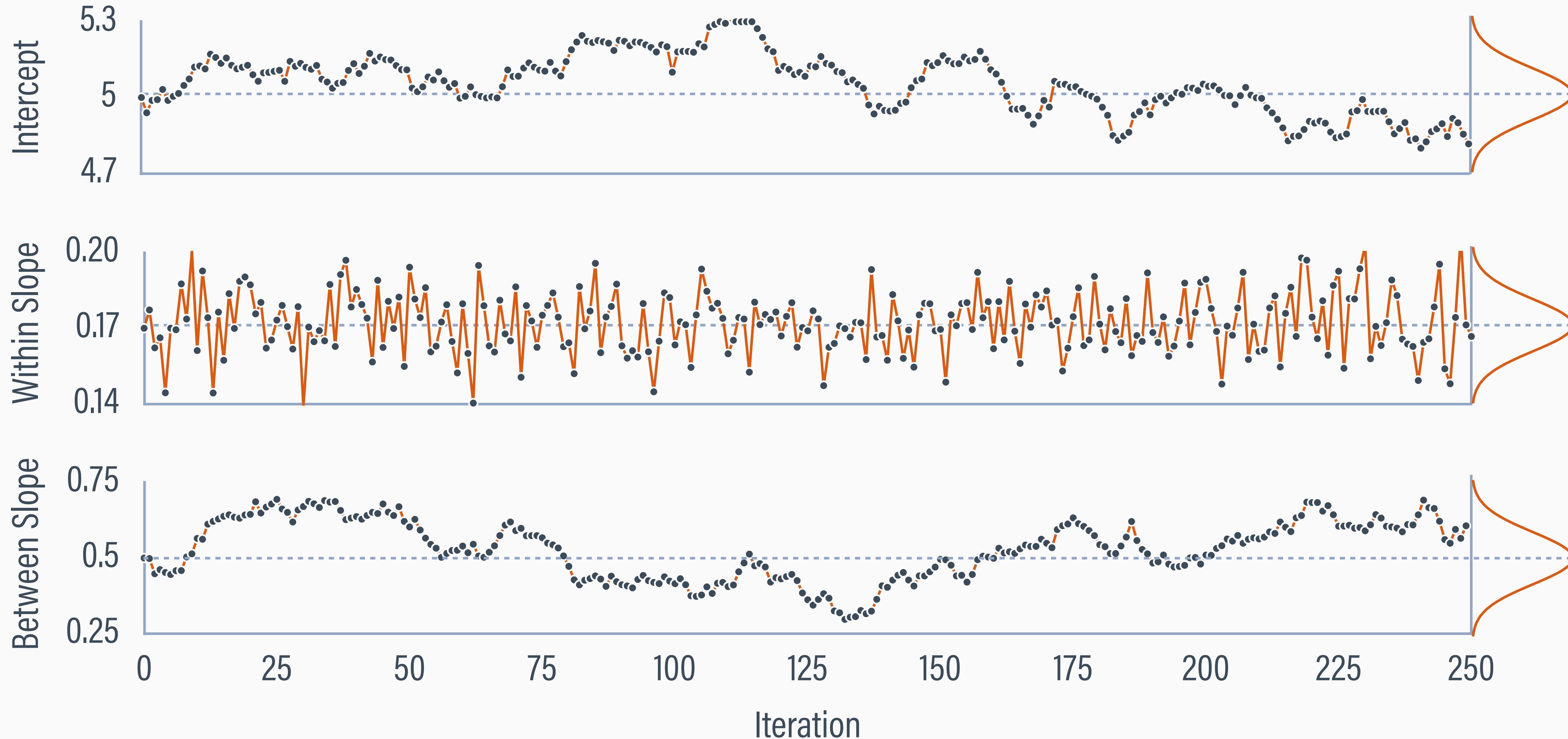
- Bayesian analyses require prior distributions that encode our beliefs about the parameter values prior to analyzing the data
- Conceptually, prior distributions function like secondary inputs that augment the data during estimation
- It is common to use non-informative (diffuse) priors that impart as little information as possible (let the data do the talking)

PRIOR DISTRIBUTIONS

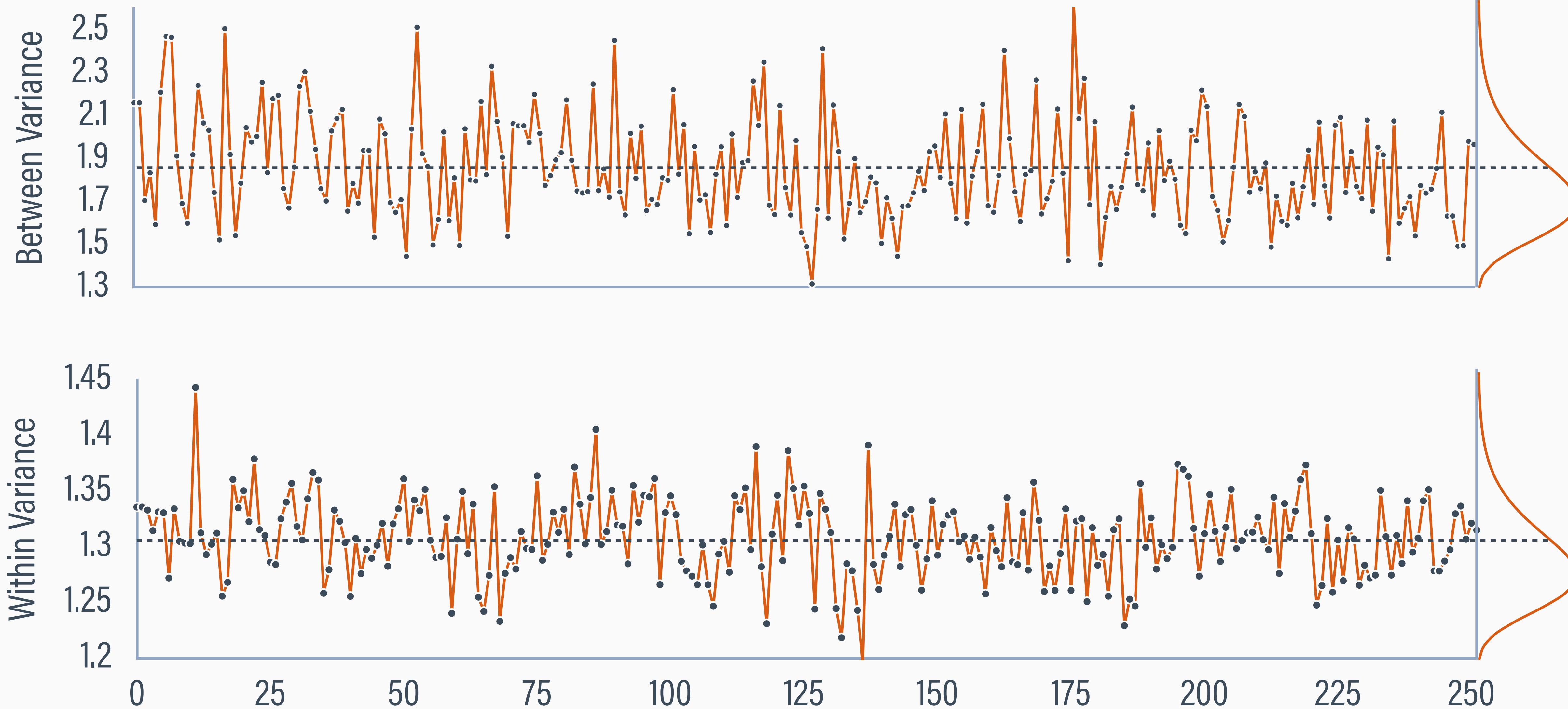
- A diffuse prior for means and coefficients conveys that all possible parameter values are equally likely a priori
- Diffuse priors for variances are slightly informative, and different options function like df adjustments in regression



COEFFICIENTS FROM 250 MCMC CYCLES



VARIANCES FROM 250 MCMC CYCLES



SUMMARIZING MCMC ESTIMATES

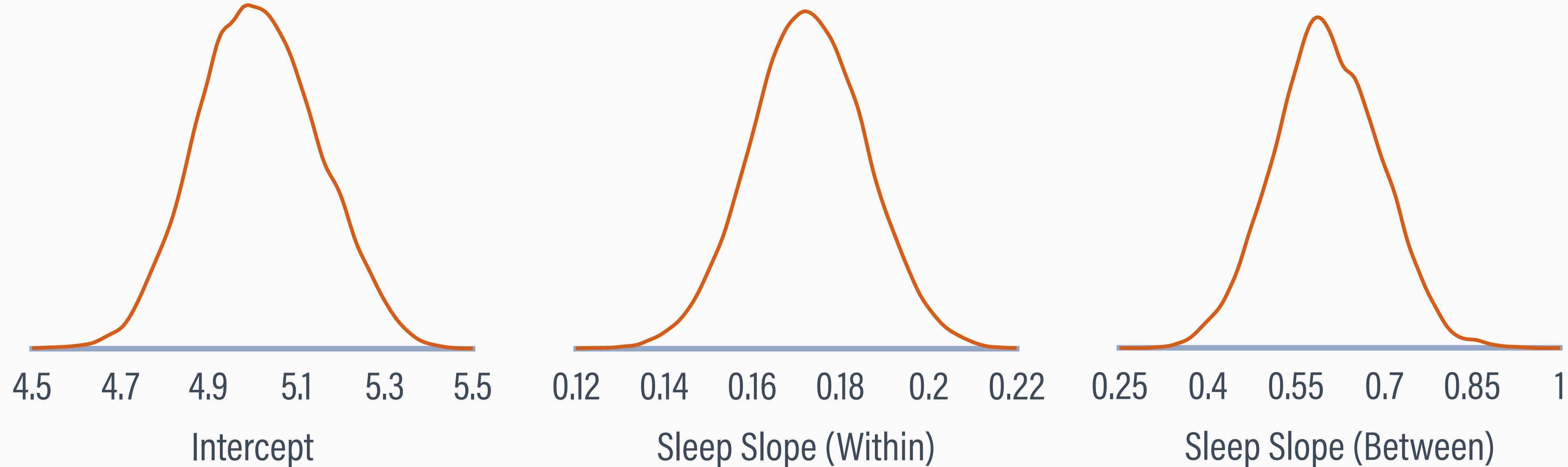
- MCMC iterates for thousands of cycles, and each cycle produces estimates based on one fixed-in data set
- MCMC estimation yields a distribution of parameters—called a posterior—that averages over thousands of imputations
- The posterior is a distribution of plausible parameter values that could have produced our particular data

COEFFICIENT DISTRIBUTIONS

Median = 5.01
Std. Dev. = 0.14
95% CI = (4.76, 5.28)

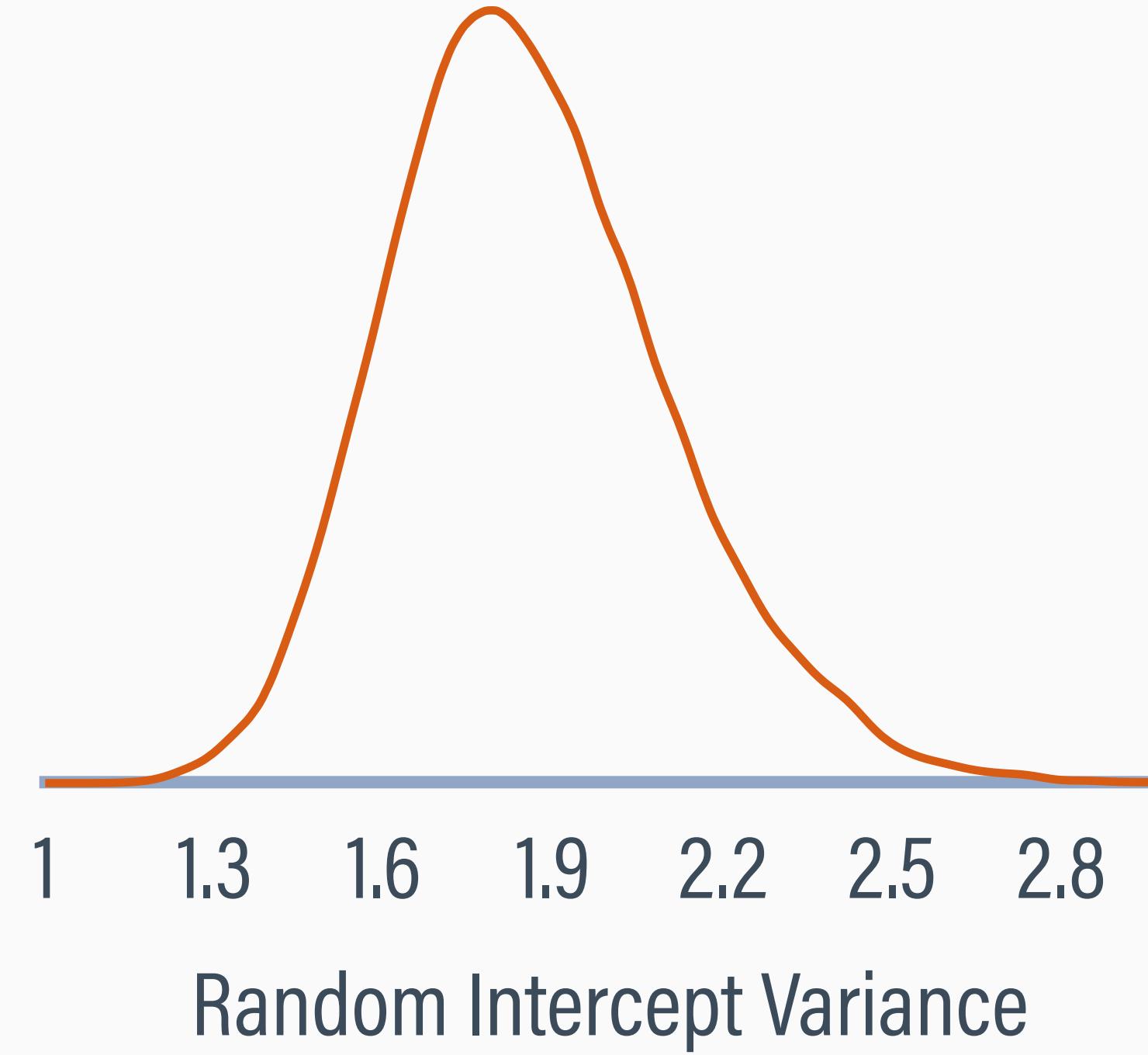
Median = 0.17
Std. Dev. = 0.01
95% CI = (0.15, 0.20)

Median = 0.60
Std. Dev. = 0.09
95% CI = (0.43, 0.78)

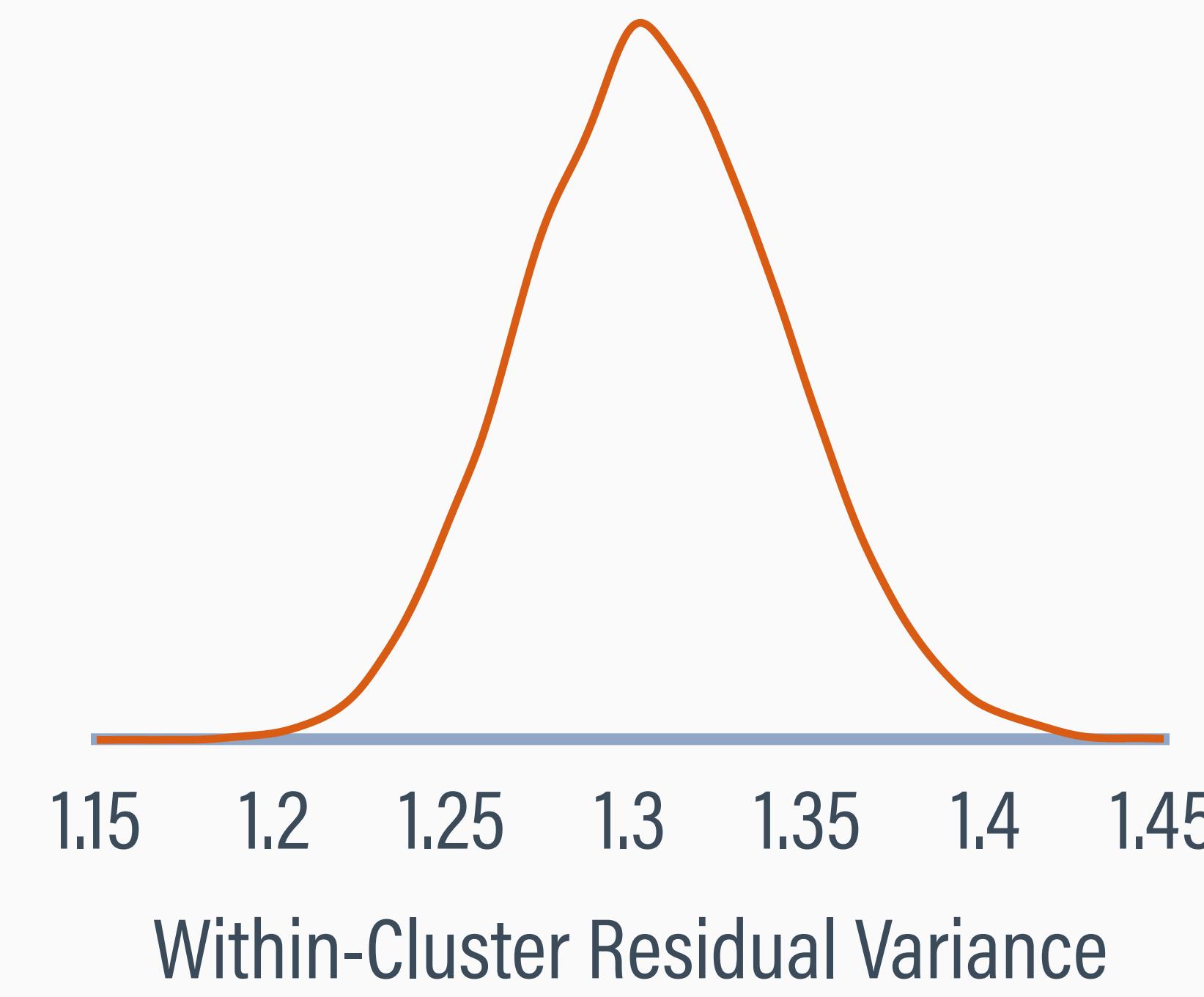


VARIANCE DISTRIBUTIONS

Median = 1.84
Std. Dev. = 0.25
95% CI = (1.43, 2.40)



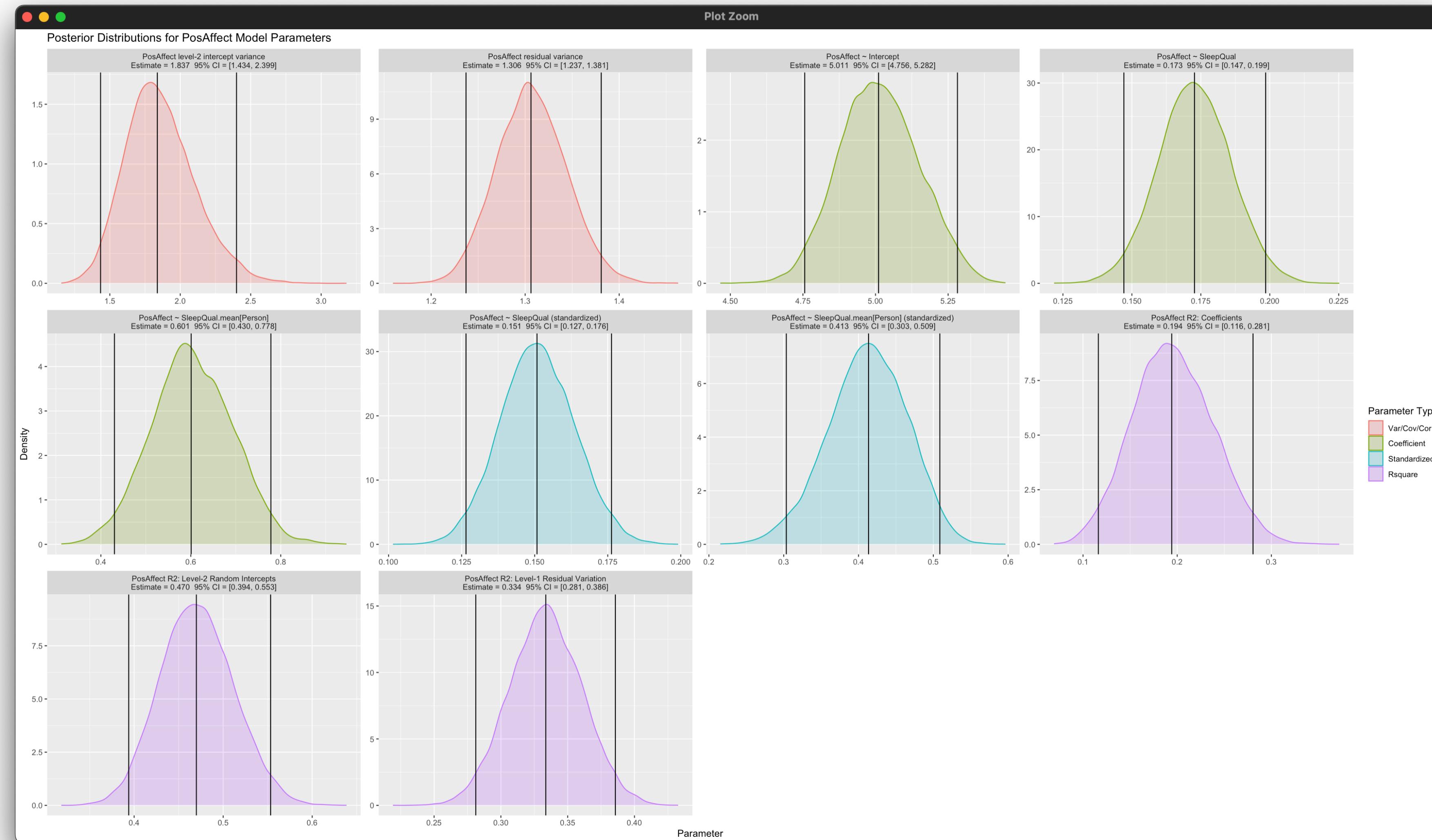
Median = 1.31
Std. Dev. = 0.04
95% CI = (1.24, 1.38)



RBLIMP SCRIPT

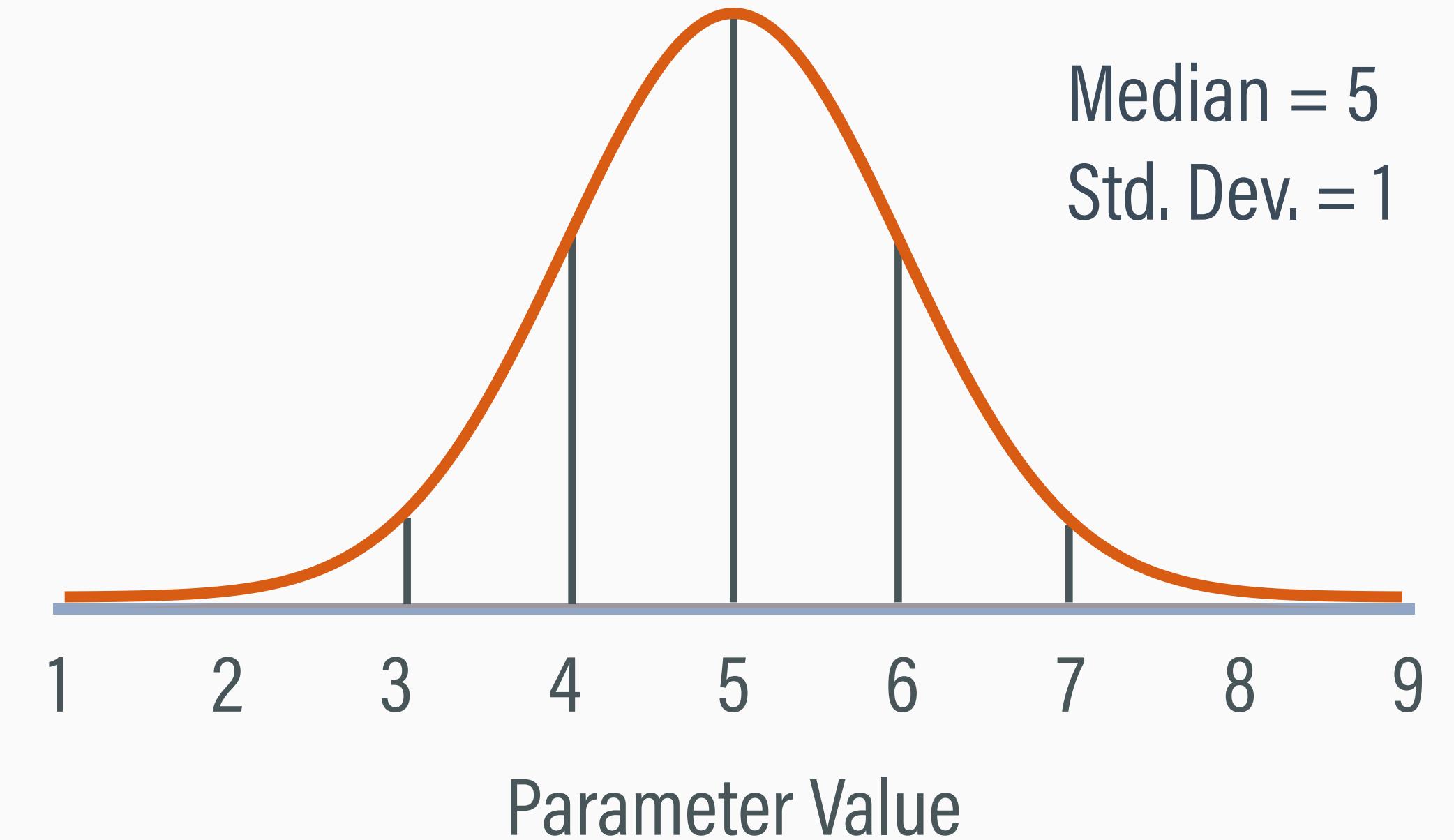
```
model <- rblimp(  
  data = PainDiary,  
  clusterid = 'Person',  
  center = 'grandmean = SleepQual.mean; groupmean = SleepQual',  
  model = 'PosAffect ~ intercept SleepQual SleepQual.mean | intercept',  
  seed = 90291,  
  burn = 10000,  
  iter = 10000)  
  
output(model)  
posterior_plot(model)
```

PARAMETER PLOTS (RBLIMP ONLY)



POSTERIOR MEDIAN AND STD. DEV.

- The posterior median and standard deviation quantify the most likely parameter value and uncertainty
- Analogous to a point estimate and standard error but no reference to other hypothetical samples



BLIMP OUTPUT

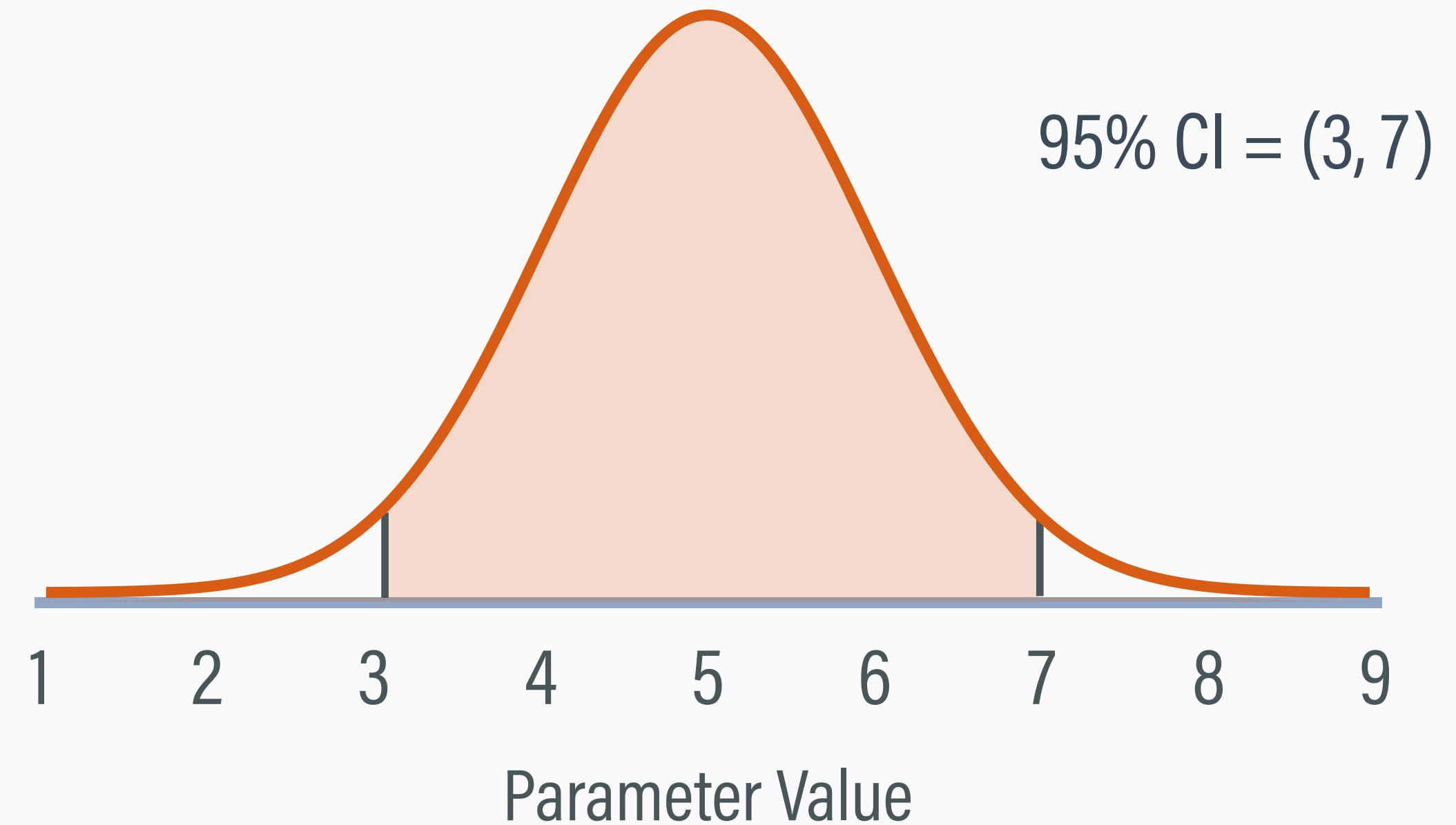
Outcome Variable: PosAffect

Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|-------------------------------|----------|--------|-------|-------|----------|--------|----------|
| <hr/> | | | | | | | |
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.839 | 0.246 | 1.436 | 2.399 | --- | --- | 5051.168 |
| Residual Var. | 1.307 | 0.037 | 1.238 | 1.380 | --- | --- | 8227.580 |
| <hr/> | | | | | | | |
| Coefficients: | | | | | | | |
| Intercept | 4.997 | 0.133 | 4.761 | 5.277 | 1423.604 | 0.000 | 154.295 |
| SleepQual | 0.173 | 0.013 | 0.147 | 0.199 | 174.595 | 0.000 | 9302.345 |
| SleepQual.mean[Person] | 0.598 | 0.094 | 0.416 | 0.788 | 40.936 | 0.000 | 161.345 |
| <hr/> | | | | | | | |
| Standard Deviations: | | | | | | | |
| L2 : SD(Intercept) | 1.356 | 0.090 | 1.198 | 1.549 | --- | --- | 5041.908 |
| Residual SD | 1.143 | 0.016 | 1.113 | 1.175 | --- | --- | 8223.888 |
| <hr/> | | | | | | | |
| Standardized Coefficients: | | | | | | | |
| SleepQual | 0.151 | 0.013 | 0.127 | 0.176 | 142.389 | 0.000 | 1996.211 |
| SleepQual.mean[Person] | 0.412 | 0.055 | 0.297 | 0.513 | 55.809 | 0.000 | 169.087 |
| <hr/> | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.193 | 0.044 | 0.112 | 0.286 | --- | --- | 175.664 |
| by Level-2 Random Intercepts | 0.471 | 0.042 | 0.392 | 0.555 | --- | --- | 414.230 |
| by Level-1 Residual Variation | 0.334 | 0.027 | 0.280 | 0.387 | --- | --- | 511.829 |

95% CREDIBLE INTERVALS

- The 95% credible interval gives limits spanning 95% of the parameter's range
- Akin to a confidence interval, but references a range of highly plausible parameter values for one data set



BLIMP OUTPUT

Outcome Variable: PosAffect

Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|-------------------------------|----------|--------|-------|-------|----------|--------|----------|
| <hr/> | | | | | | | |
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.839 | 0.246 | 1.436 | 2.399 | --- | --- | 5051.168 |
| Residual Var. | 1.307 | 0.037 | 1.238 | 1.380 | --- | --- | 8227.580 |
| <hr/> | | | | | | | |
| Coefficients: | | | | | | | |
| Intercept | 4.997 | 0.133 | 4.761 | 5.277 | 1423.604 | 0.000 | 154.295 |
| SleepQual | 0.173 | 0.013 | 0.147 | 0.199 | 174.595 | 0.000 | 9302.345 |
| SleepQual.mean[Person] | 0.598 | 0.094 | 0.416 | 0.788 | 40.936 | 0.000 | 161.345 |
| <hr/> | | | | | | | |
| Standard Deviations: | | | | | | | |
| L2 : SD(Intercept) | 1.356 | 0.090 | 1.198 | 1.549 | --- | --- | 5041.908 |
| Residual SD | 1.143 | 0.016 | 1.113 | 1.175 | --- | --- | 8223.888 |
| <hr/> | | | | | | | |
| Standardized Coefficients: | | | | | | | |
| SleepQual | 0.151 | 0.013 | 0.127 | 0.176 | 142.389 | 0.000 | 1996.211 |
| SleepQual.mean[Person] | 0.412 | 0.055 | 0.297 | 0.513 | 55.809 | 0.000 | 169.087 |
| <hr/> | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.193 | 0.044 | 0.112 | 0.286 | --- | --- | 175.664 |
| by Level-2 Random Intercepts | 0.471 | 0.042 | 0.392 | 0.555 | --- | --- | 414.230 |
| by Level-1 Residual Variation | 0.334 | 0.027 | 0.280 | 0.387 | --- | --- | 511.829 |

MCMC AS COMPUTATIONAL FREQUENTISM

- Several recent innovations in the multilevel modeling literature (e.g., “dynamic” models with lagged effects) are available only via MCMC estimation
- This has led to a perspective in which MCMC is used for computational purposes rather than philosophical appeal (computational frequentism; Levy & McNeish, 2021)
- Essentially, MCMC results are surrogates for frequentist point estimates, standard errors, and test statistics

BLIMP OUTPUT

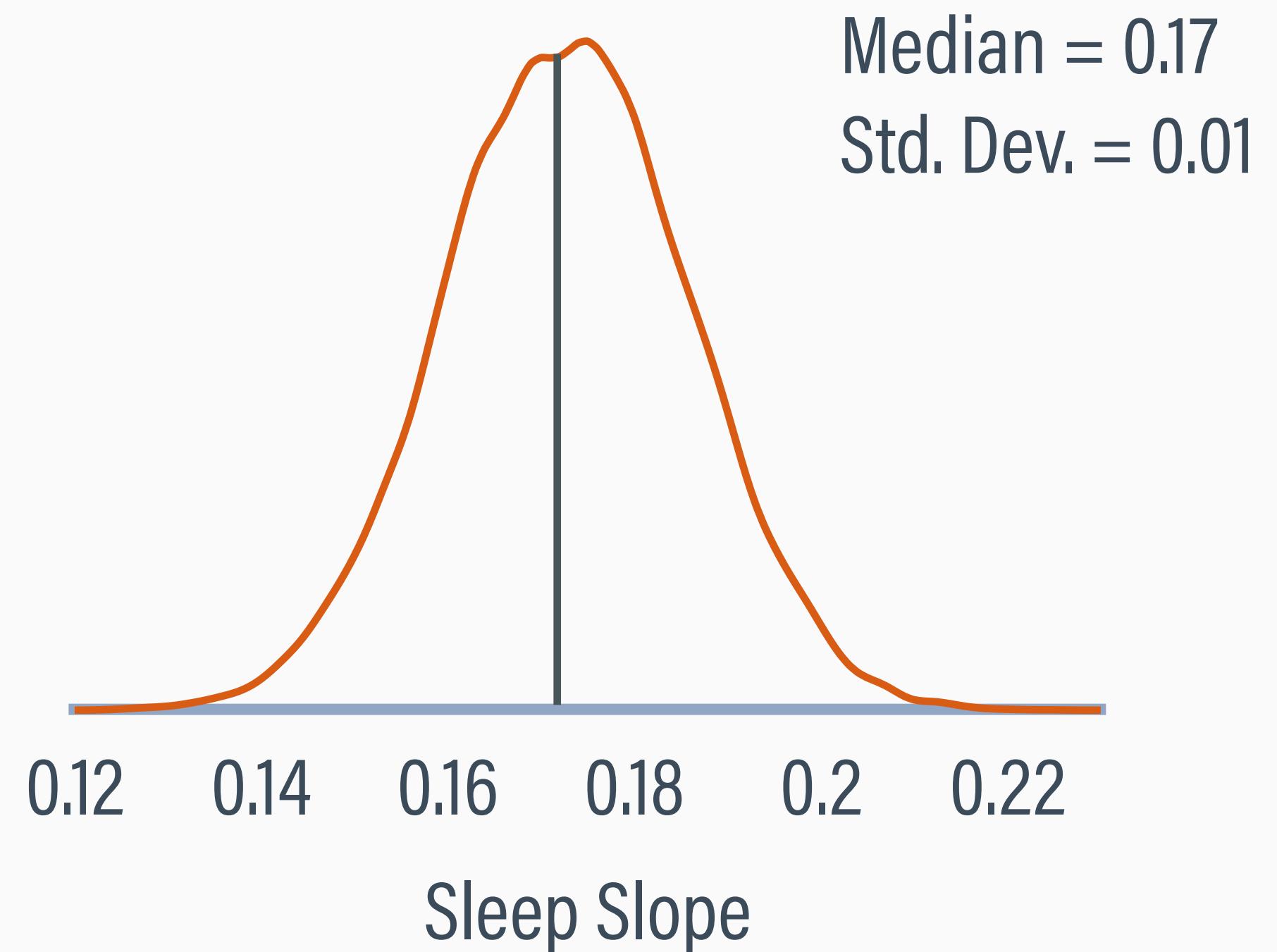
Outcome Variable: PosAffect

Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|-------------------------------|----------|--------|-------|-------|----------|--------|----------|
| <hr/> | | | | | | | |
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.839 | 0.246 | 1.436 | 2.399 | --- | --- | 5051.168 |
| Residual Var. | 1.307 | 0.037 | 1.238 | 1.380 | --- | --- | 8227.580 |
| <hr/> | | | | | | | |
| Coefficients: | | | | | | | |
| Intercept | 4.997 | 0.133 | 4.761 | 5.277 | 1423.604 | 0.000 | 154.295 |
| SleepQual | 0.173 | 0.013 | 0.147 | 0.199 | 174.595 | 0.000 | 9302.345 |
| SleepQual.mean[Person] | 0.598 | 0.094 | 0.416 | 0.788 | 40.936 | 0.000 | 161.345 |
| <hr/> | | | | | | | |
| Standard Deviations: | | | | | | | |
| L2 : SD(Intercept) | 1.356 | 0.090 | 1.198 | 1.549 | --- | --- | 5041.908 |
| Residual SD | 1.143 | 0.016 | 1.113 | 1.175 | --- | --- | 8223.888 |
| <hr/> | | | | | | | |
| Standardized Coefficients: | | | | | | | |
| SleepQual | 0.151 | 0.013 | 0.127 | 0.176 | 142.389 | 0.000 | 1996.211 |
| SleepQual.mean[Person] | 0.412 | 0.055 | 0.297 | 0.513 | 55.809 | 0.000 | 169.087 |
| <hr/> | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.193 | 0.044 | 0.112 | 0.286 | --- | --- | 175.664 |
| by Level-2 Random Intercepts | 0.471 | 0.042 | 0.392 | 0.555 | --- | --- | 414.230 |
| by Level-1 Residual Variation | 0.334 | 0.027 | 0.280 | 0.387 | --- | --- | 511.829 |

ILLUSTRATION: WITHIN-CLUSTER SLOPE

- The most likely population slope for these data (the posterior median) is $\beta_1 = 0.17$, and the parameter's standard deviation is 0.01
- From a computational frequentism lens, these can serve as MCMC-generated point estimates and standard errors



BLIMP OUTPUT

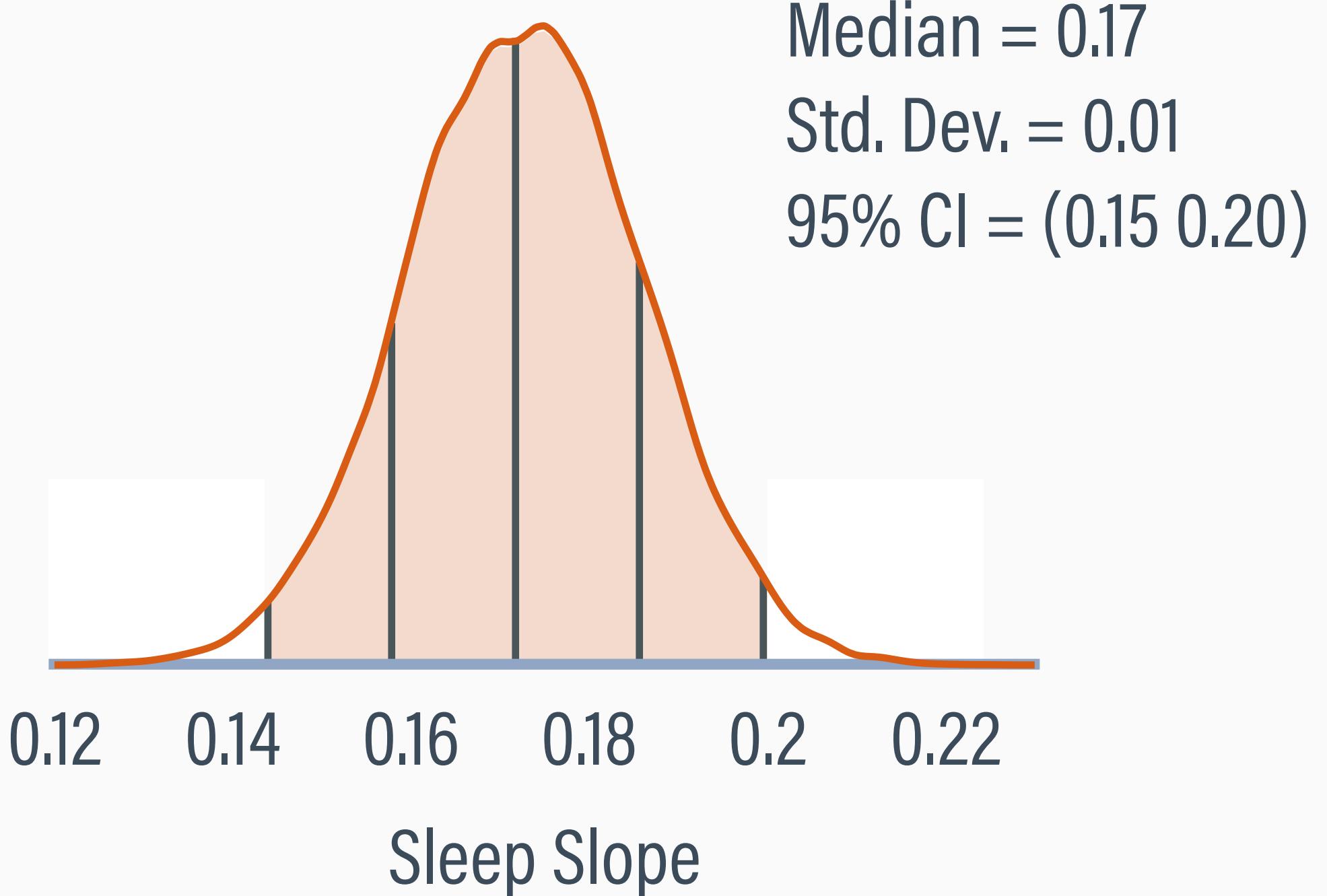
Outcome Variable: PosAffect

Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|-------------------------------|--------------|--------------|-------|-------|----------|--------|----------|
| <hr/> | | | | | | | |
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.839 | 0.246 | 1.436 | 2.399 | --- | --- | 5051.168 |
| Residual Var. | 1.307 | 0.037 | 1.238 | 1.380 | --- | --- | 8227.580 |
| <hr/> | | | | | | | |
| Coefficients: | | | | | | | |
| Intercept | 4.997 | 0.133 | 4.761 | 5.277 | 1423.604 | 0.000 | 154.295 |
| SleepQual | 0.173 | 0.013 | 0.147 | 0.199 | 174.595 | 0.000 | 9302.345 |
| SleepQual.mean[Person] | 0.598 | 0.094 | 0.416 | 0.788 | 40.936 | 0.000 | 161.345 |
| <hr/> | | | | | | | |
| Standard Deviations: | | | | | | | |
| L2 : SD(Intercept) | 1.356 | 0.090 | 1.198 | 1.549 | --- | --- | 5041.908 |
| Residual SD | 1.143 | 0.016 | 1.113 | 1.175 | --- | --- | 8223.888 |
| <hr/> | | | | | | | |
| Standardized Coefficients: | | | | | | | |
| SleepQual | 0.151 | 0.013 | 0.127 | 0.176 | 142.389 | 0.000 | 1996.211 |
| SleepQual.mean[Person] | 0.412 | 0.055 | 0.297 | 0.513 | 55.809 | 0.000 | 169.087 |
| <hr/> | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.193 | 0.044 | 0.112 | 0.286 | --- | --- | 175.664 |
| by Level-2 Random Intercepts | 0.471 | 0.042 | 0.392 | 0.555 | --- | --- | 414.230 |
| by Level-1 Residual Variation | 0.334 | 0.027 | 0.280 | 0.387 | --- | --- | 511.829 |

ILLUSTRATION, CONTINUED

- 95% of the plausible parameter values that could have produced these data range between 0.15 and 0.20
- From a computational frequentism lens, these can serve as MCMC-generated confidence interval limits



BLIMP OUTPUT

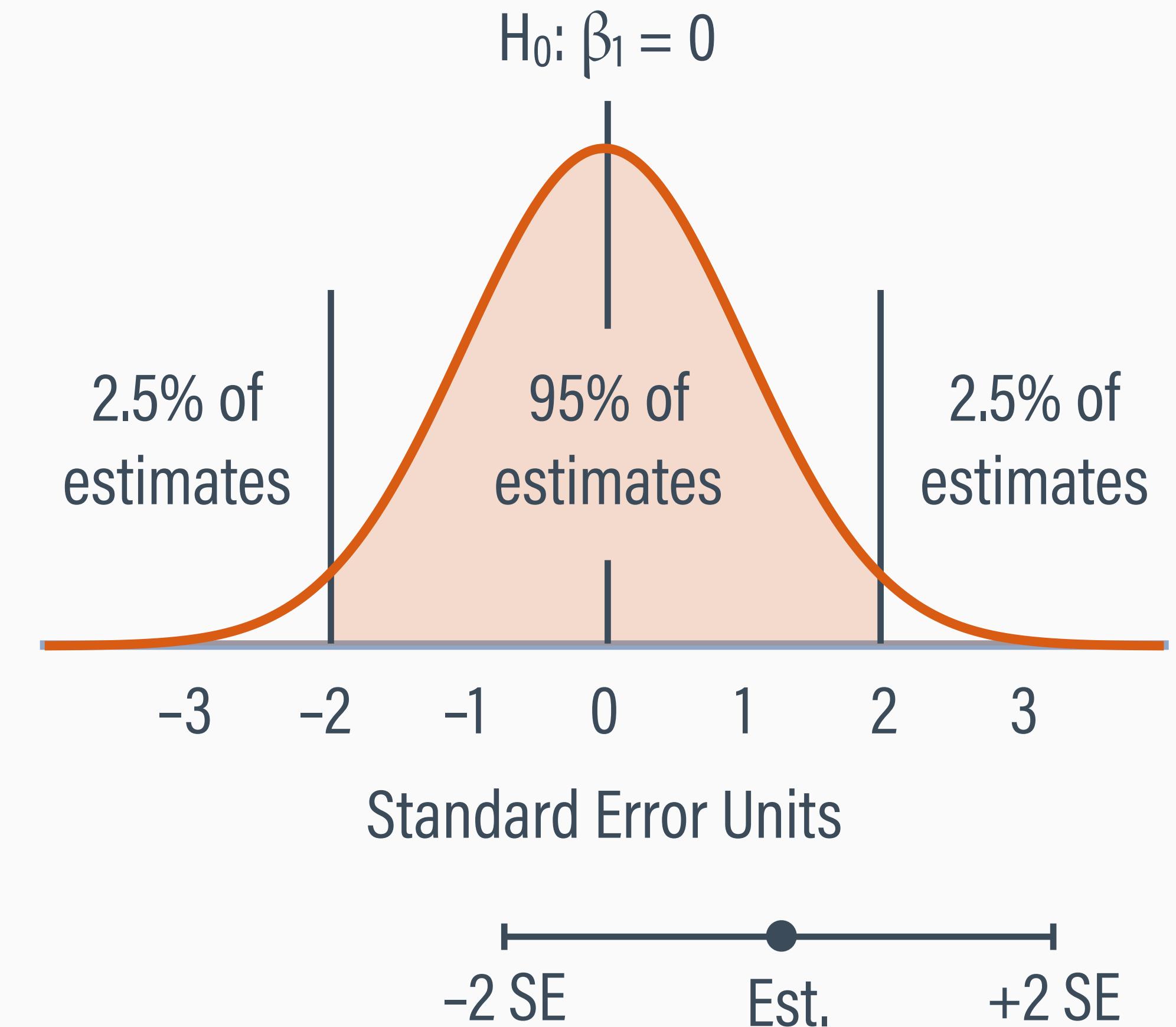
Outcome Variable: PosAffect

Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|-------------------------------|----------|--------|-------|-------|----------|--------|----------|
| <hr/> | | | | | | | |
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.839 | 0.246 | 1.436 | 2.399 | --- | --- | 5051.168 |
| Residual Var. | 1.307 | 0.037 | 1.238 | 1.380 | --- | --- | 8227.580 |
| <hr/> | | | | | | | |
| Coefficients: | | | | | | | |
| Intercept | 4.997 | 0.133 | 4.761 | 5.277 | 1423.604 | 0.000 | 154.295 |
| SleepQual | 0.173 | 0.013 | 0.147 | 0.199 | 174.595 | 0.000 | 9302.345 |
| SleepQual.mean[Person] | 0.598 | 0.094 | 0.416 | 0.788 | 40.936 | 0.000 | 161.345 |
| <hr/> | | | | | | | |
| Standard Deviations: | | | | | | | |
| L2 : SD(Intercept) | 1.356 | 0.090 | 1.198 | 1.549 | --- | --- | 5041.908 |
| Residual SD | 1.143 | 0.016 | 1.113 | 1.175 | --- | --- | 8223.888 |
| <hr/> | | | | | | | |
| Standardized Coefficients: | | | | | | | |
| SleepQual | 0.151 | 0.013 | 0.127 | 0.176 | 142.389 | 0.000 | 1996.211 |
| SleepQual.mean[Person] | 0.412 | 0.055 | 0.297 | 0.513 | 55.809 | 0.000 | 169.087 |
| <hr/> | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.193 | 0.044 | 0.112 | 0.286 | --- | --- | 175.664 |
| by Level-2 Random Intercepts | 0.471 | 0.042 | 0.392 | 0.555 | --- | --- | 414.230 |
| by Level-1 Residual Variation | 0.334 | 0.027 | 0.280 | 0.387 | --- | --- | 511.829 |

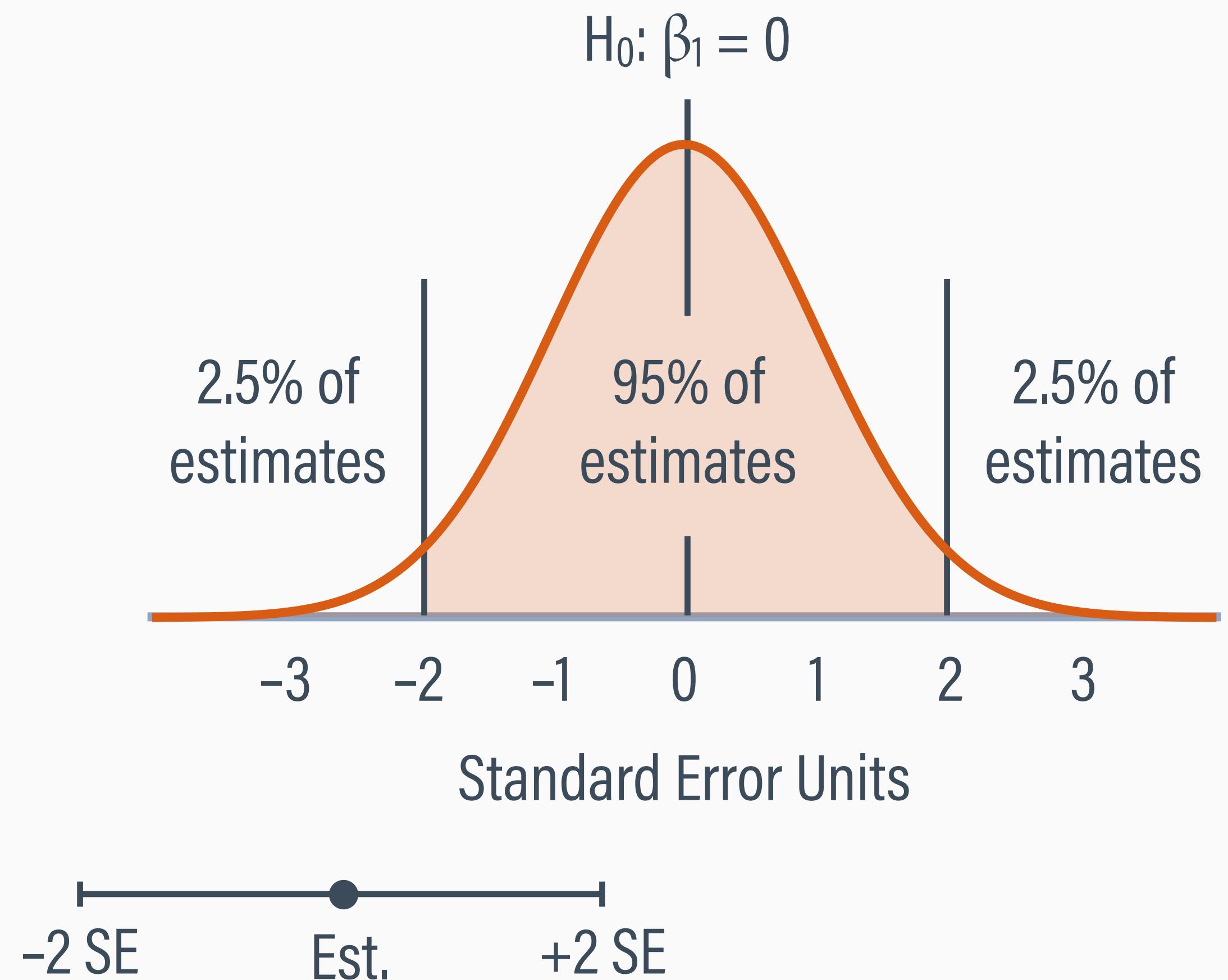
SIGNIFICANCE TESTING VIA INTERVALS

- A confidence interval applies the ± 2 standard error band to an estimate
- If the 95% confidence interval includes zero, the estimate cannot be in the critical region, and $p > .05$



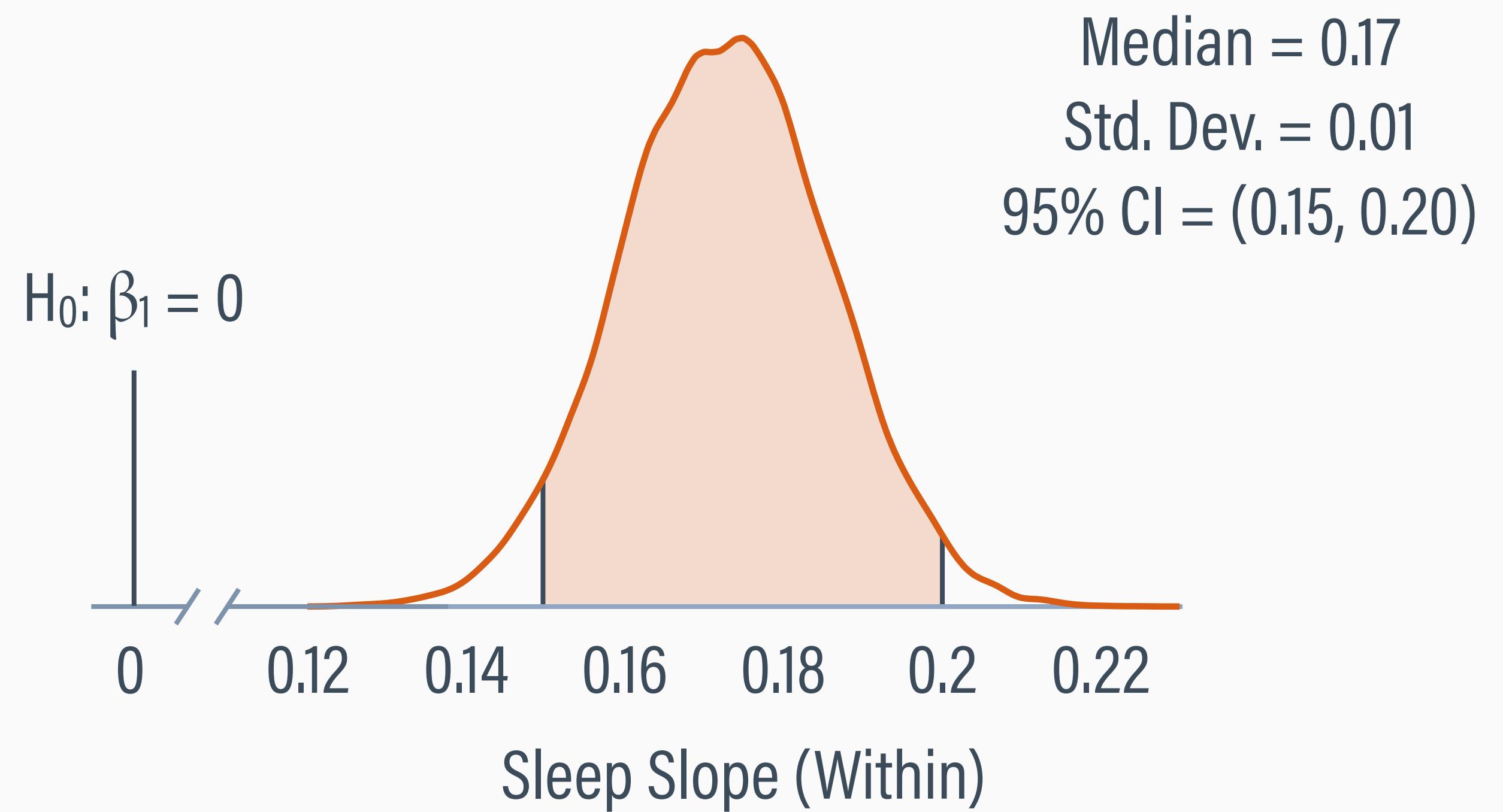
SIGNIFICANCE TESTING VIA INTERVALS

- A confidence interval applies the ± 2 standard error band to an estimate
- If the 95% confidence interval does not include zero, the estimate must be in the critical region, and $p < .05$



SIGNIFICANCE TEST ILLUSTRATION

- The 95% credible interval (0.15, 0.20) does not include zero, so we refute the null hypothesis ($p < .05$)
- A population slope equal to zero is unlikely to have produced these data



FREQUENTIST WALD TEST

- The Wald chi-square is an alternate test statistic that equals the square of the z-statistic (or t-test)

$$\chi^2_{\text{ML}} = \frac{(\hat{\theta} - \theta_0)^2}{\text{SE}^2} = \frac{(\text{estimate} - \text{null})^2}{(\text{standard error})^2} = z^2$$

- Multivariate versions of the Wald test can evaluate multiple parameters simultaneously

MCMC WALD TEST

- The MCMC-based Wald test (Asparouhov & Muthén, 2021) replaces the point estimate and standard error with the parameter's mean and standard deviation

$$\chi^2_{\text{MCMC}} = \frac{(\theta - \theta_0)^2}{\text{SD}^2} = \frac{(\text{posterior mean} - \text{null})^2}{(\text{posterior standard deviation})^2} = z^2$$

- MCMC quantities replace FIML estimates in the test statistic

BLIMP OUTPUT

Outcome Variable: PosAffect

Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|-------------------------------|----------|--------|-------|-------|----------|--------|----------|
| <hr/> | | | | | | | |
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.839 | 0.246 | 1.436 | 2.399 | --- | --- | 5051.168 |
| Residual Var. | 1.307 | 0.037 | 1.238 | 1.380 | --- | --- | 8227.580 |
| <hr/> | | | | | | | |
| Coefficients: | | | | | | | |
| Intercept | 4.997 | 0.133 | 4.761 | 5.277 | 1423.604 | 0.000 | 154.295 |
| SleepQual | 0.173 | 0.013 | 0.147 | 0.199 | 174.595 | 0.000 | 9302.345 |
| SleepQual.mean[Person] | 0.598 | 0.094 | 0.416 | 0.788 | 40.936 | 0.000 | 161.345 |
| <hr/> | | | | | | | |
| Standard Deviations: | | | | | | | |
| L2 : SD(Intercept) | 1.356 | 0.090 | 1.198 | 1.549 | --- | --- | 5041.908 |
| Residual SD | 1.143 | 0.016 | 1.113 | 1.175 | --- | --- | 8223.888 |
| <hr/> | | | | | | | |
| Standardized Coefficients: | | | | | | | |
| SleepQual | 0.151 | 0.013 | 0.127 | 0.176 | 142.389 | 0.000 | 1996.211 |
| SleepQual.mean[Person] | 0.412 | 0.055 | 0.297 | 0.513 | 55.809 | 0.000 | 169.087 |
| <hr/> | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.193 | 0.044 | 0.112 | 0.286 | --- | --- | 175.664 |
| by Level-2 Random Intercepts | 0.471 | 0.042 | 0.392 | 0.555 | --- | --- | 414.230 |
| by Level-1 Residual Variation | 0.334 | 0.027 | 0.280 | 0.387 | --- | --- | 511.829 |

WALD TEST INTERPRETATION

- The test refutes the null hypothesis that the population within-person regression slopes equals zero
- $\chi^2(1) = 174.60, p < .001$
- If the null is true in the population, a slope as large as the one from the data would result in fewer than 1 out of 1000 random samples (this is a 100% frequentist interpretation!)

OUTLINE

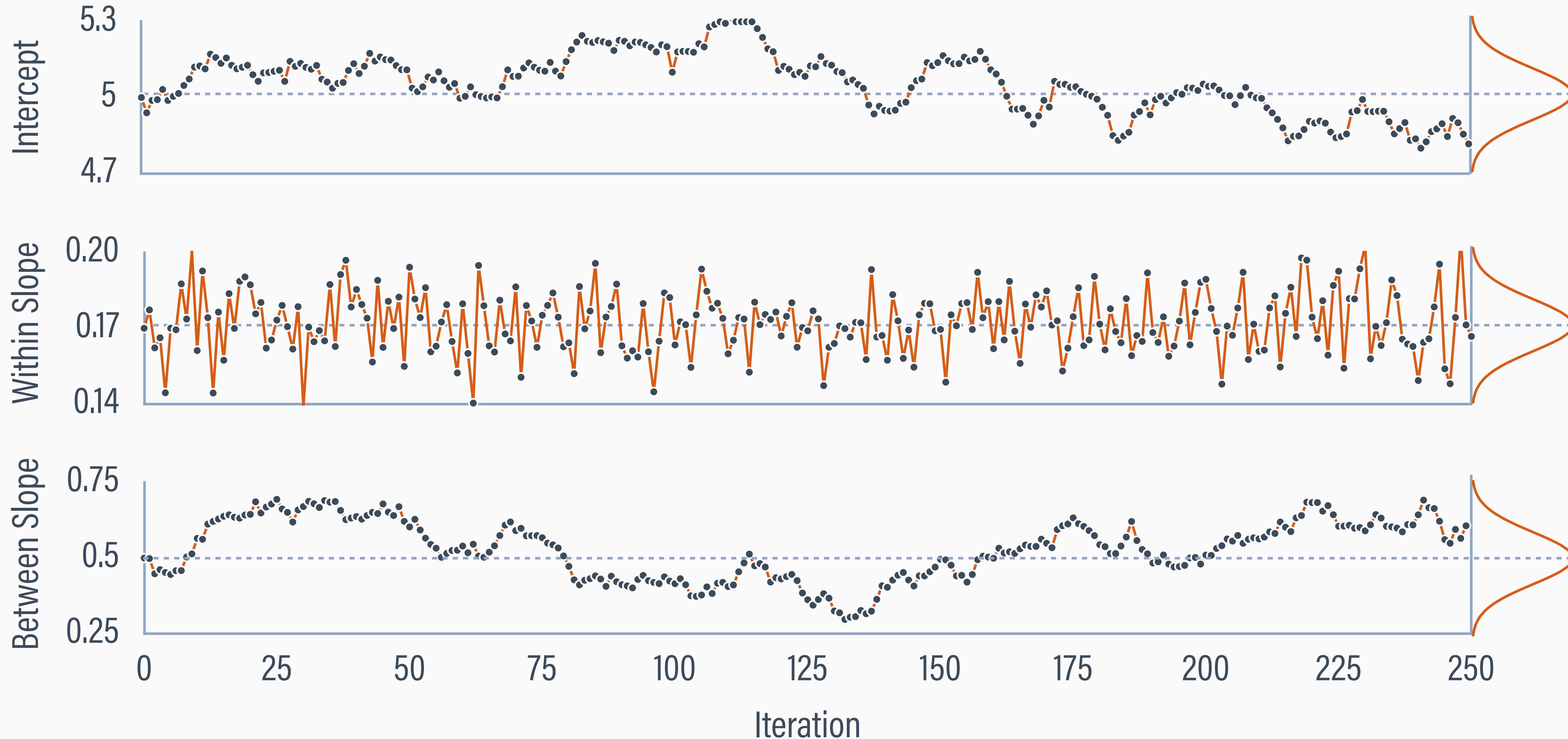
- 1 Analysis Example
- 2 Frequentist vs. Bayesian Statistical Paradigms
- 3 Maximum Likelihood Estimation
- 4 MCMC Estimation
- 5 MCMC Diagnostics
- 6 Checking MLM Assumptions

MCMC ALGORITHM

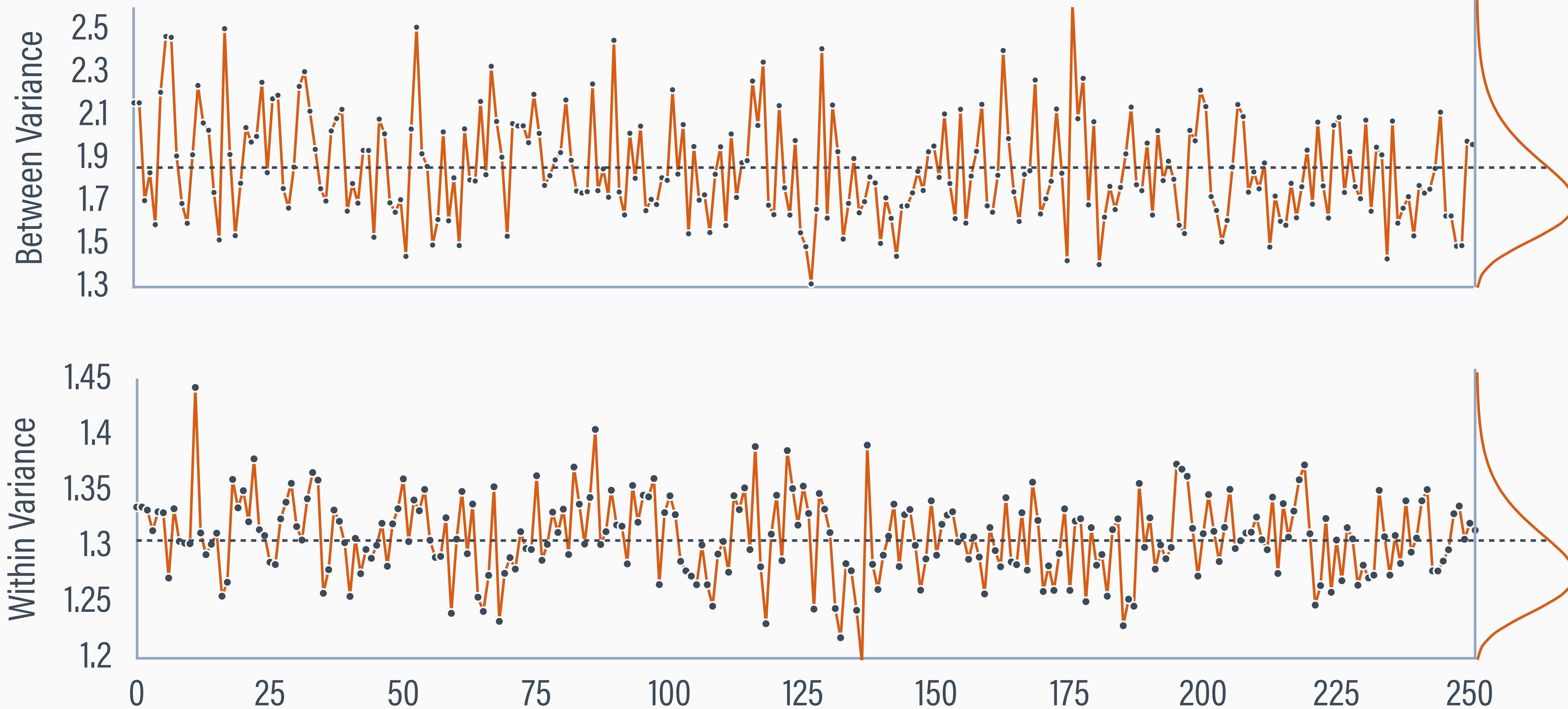


- » Do for $t = 1$ to T iterations
 - » Estimate regression coefficients
 - » Estimate random intercept residuals
 - » Estimate level-2 intercept variance
 - » Estimate level-1 residual variance
 - » Impute missing data
- » Repeat

COEFFICIENTS FROM 250 MCMC CYCLES



VARIANCES FROM 250 MCMC CYCLES



MCMC CONVERGENCE

- MCMC parameter values continually fluctuate across cycles
- MCMC converges when posterior distributions are stationary, meaning that parameter values oscillate around a stable mean, and their variation doesn't change with additional iterations
- MCMC should “warm up” until convergence, after which parameter values are saved for the distributional summaries

MCMC ALGORITHM SETTINGS

BURN: 10000;

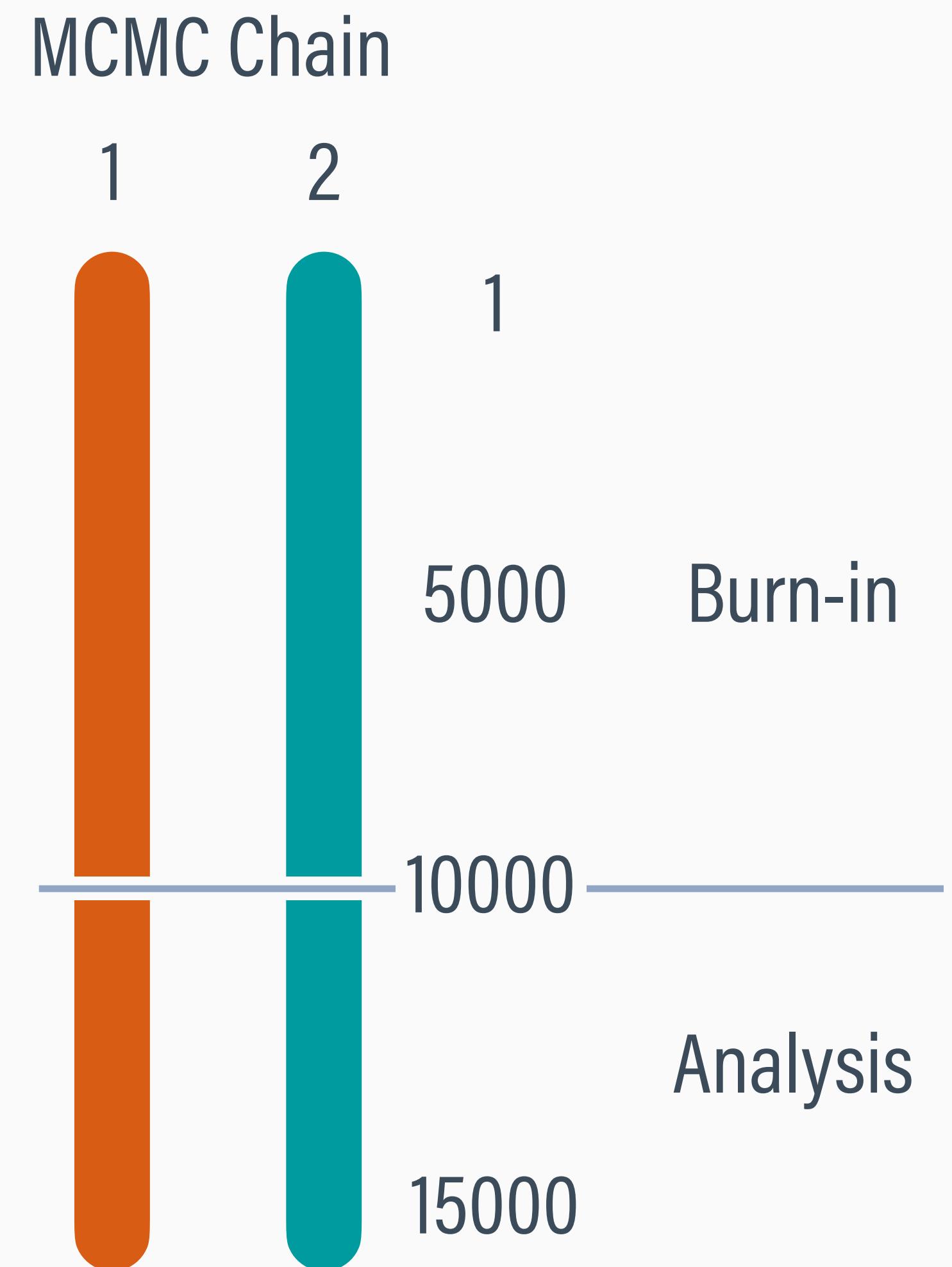
warm up iterations (per chain)

ITERATIONS: 10000;

analysis iterations (both chains)

SEED: 90291;

random number seed

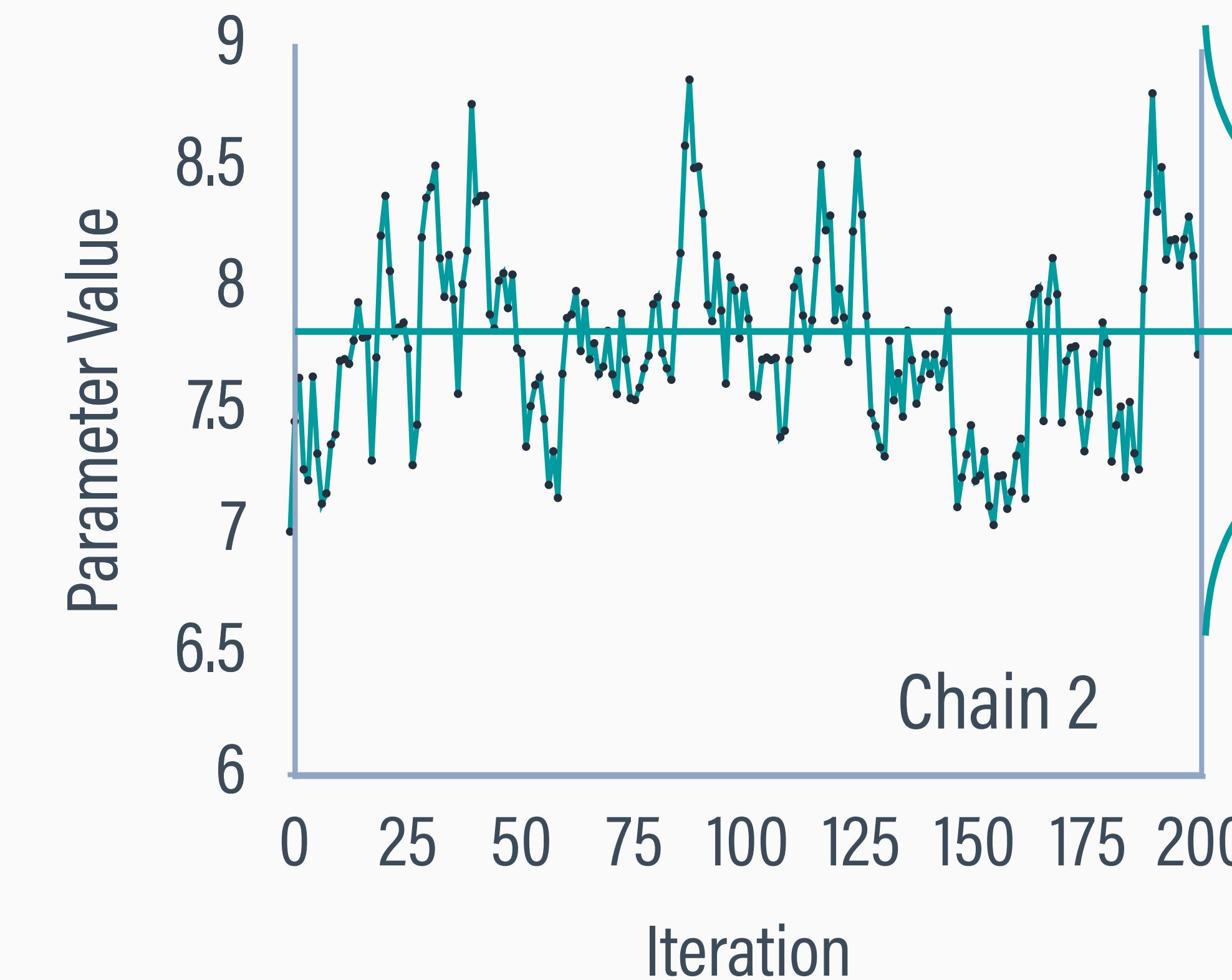
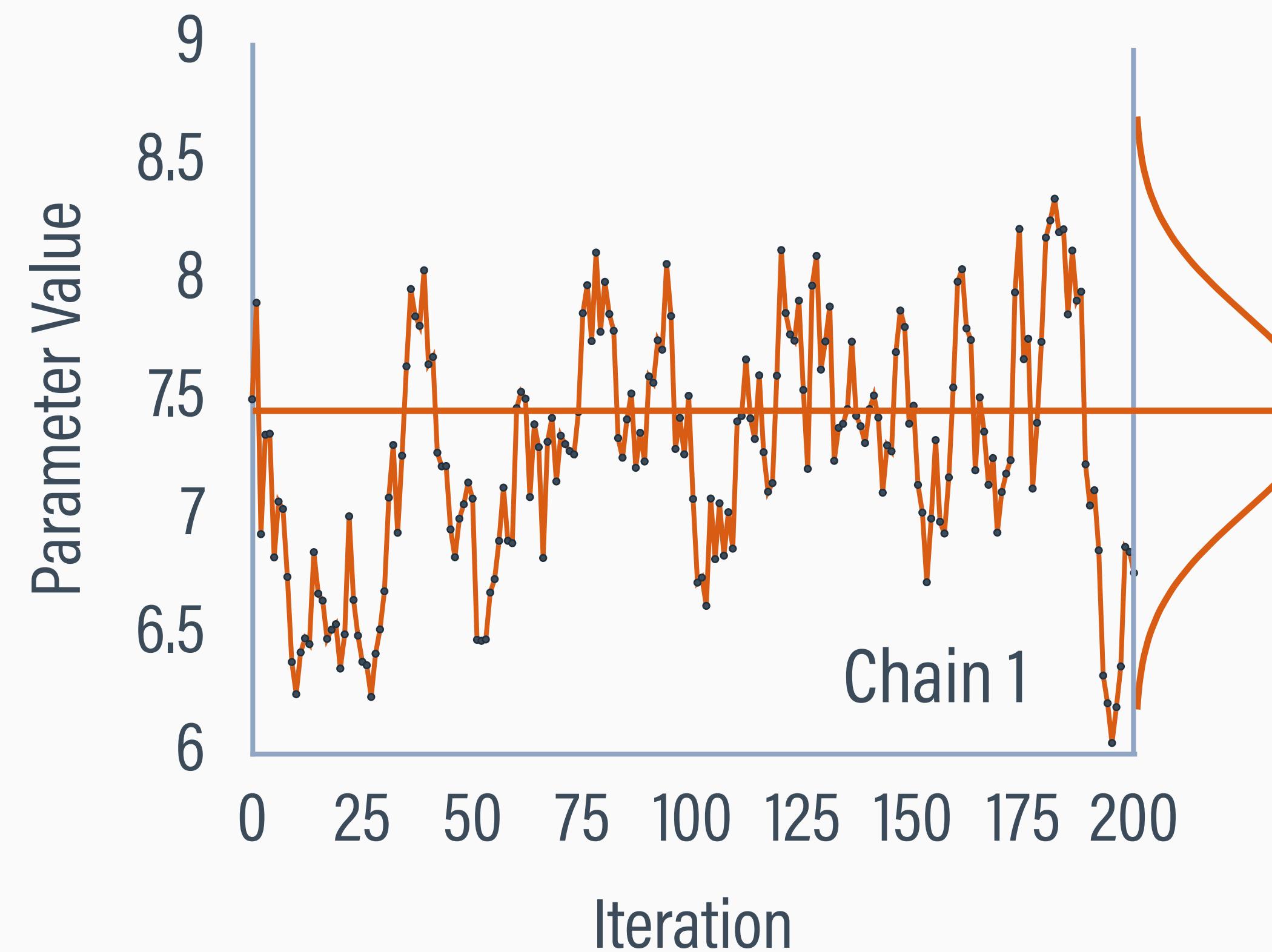


POTENTIAL SCALE REDUCTION FACTOR

- The potential scale reduction factor (PSRF) compares the similarity of parameters generated from two MCMC processes
- MCMC converges when the two unique processes (chains) give parameter values with same mean and spread
- PSRFs for all parameters should be < 1.05

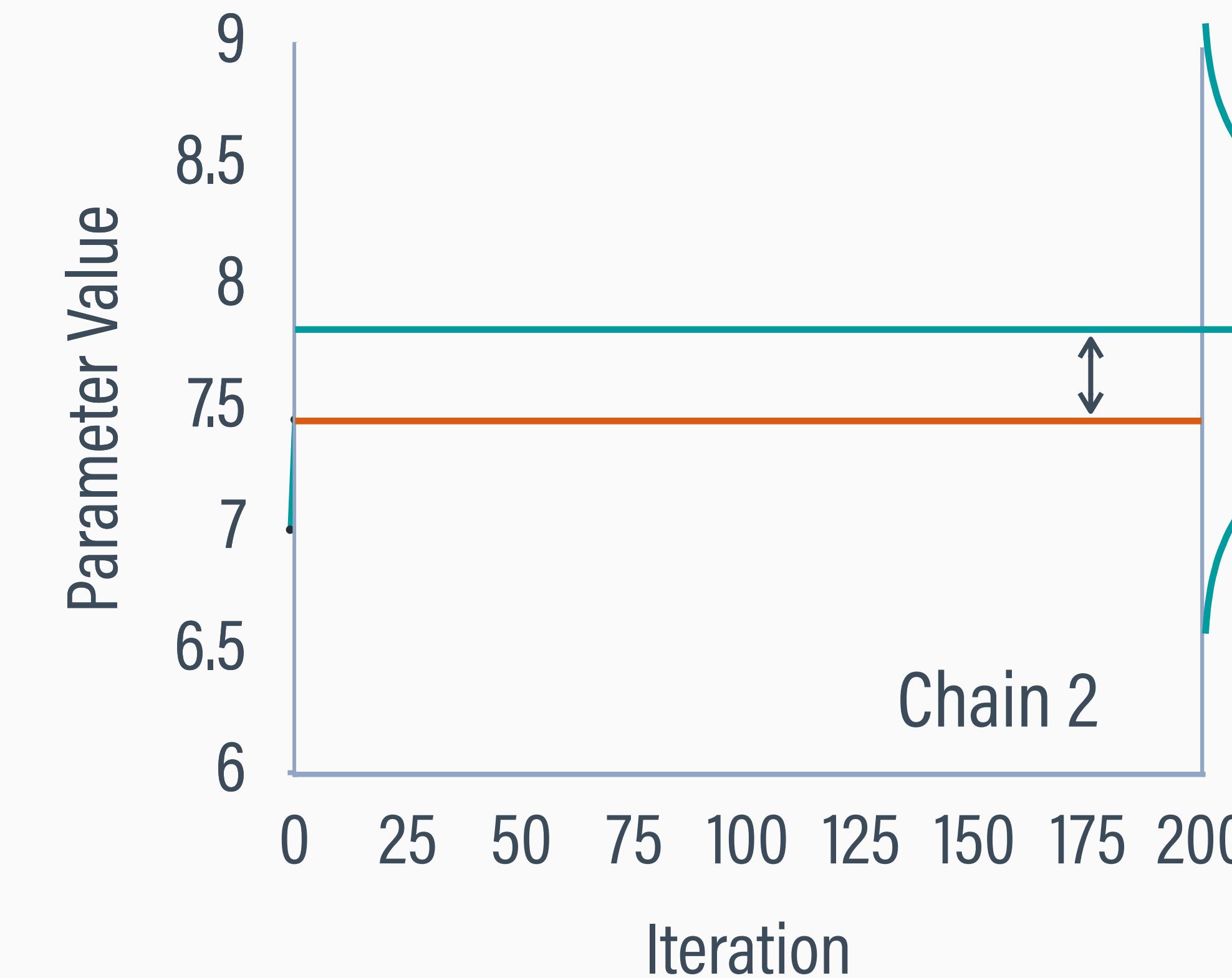
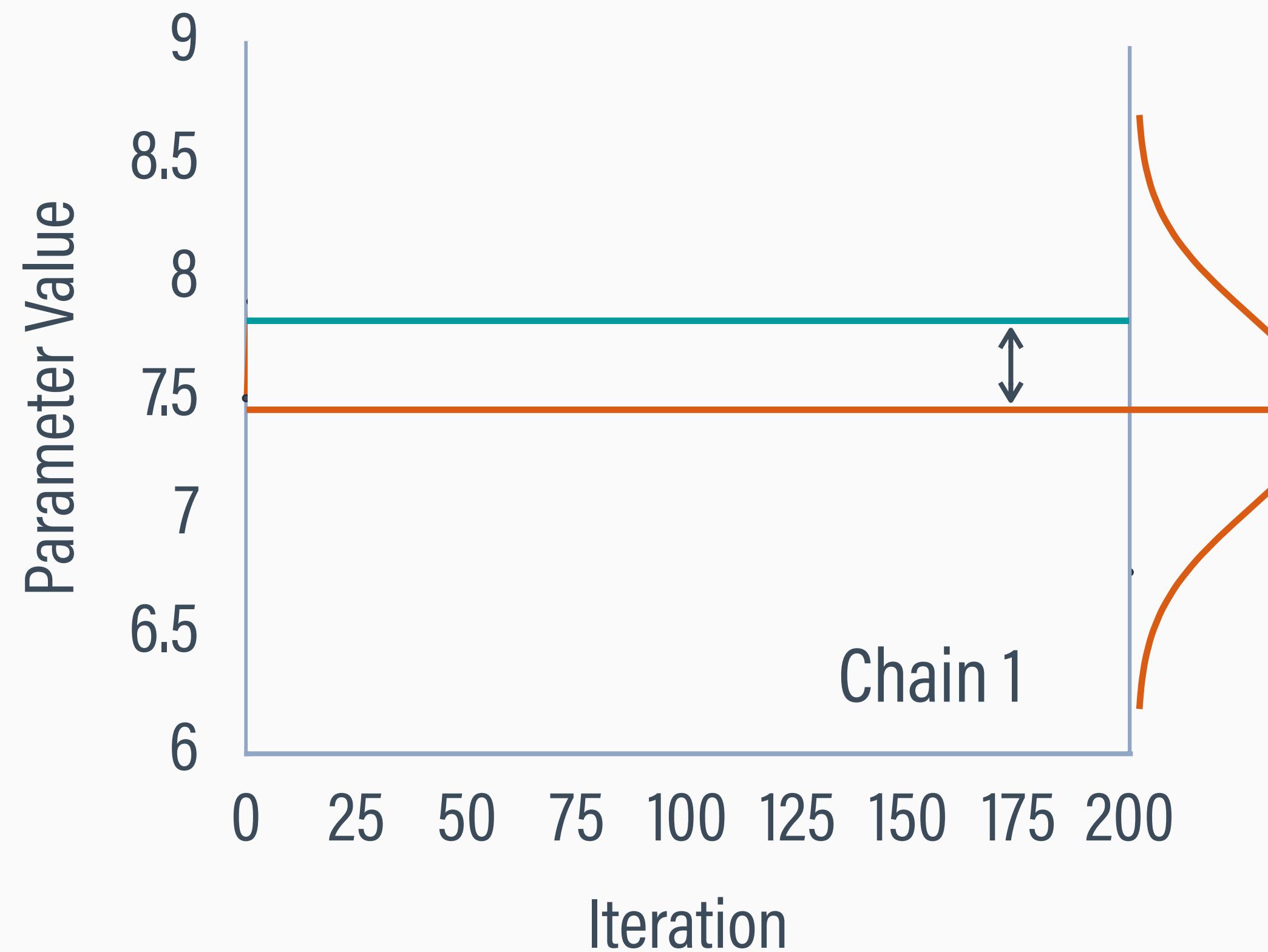
POTENTIAL SCALE REDUCTION FACTOR

$$\text{PSRF} = \sqrt{\frac{\text{mean difference between chains} + \text{within-chain variation}}{\text{within-chain variation}}}$$



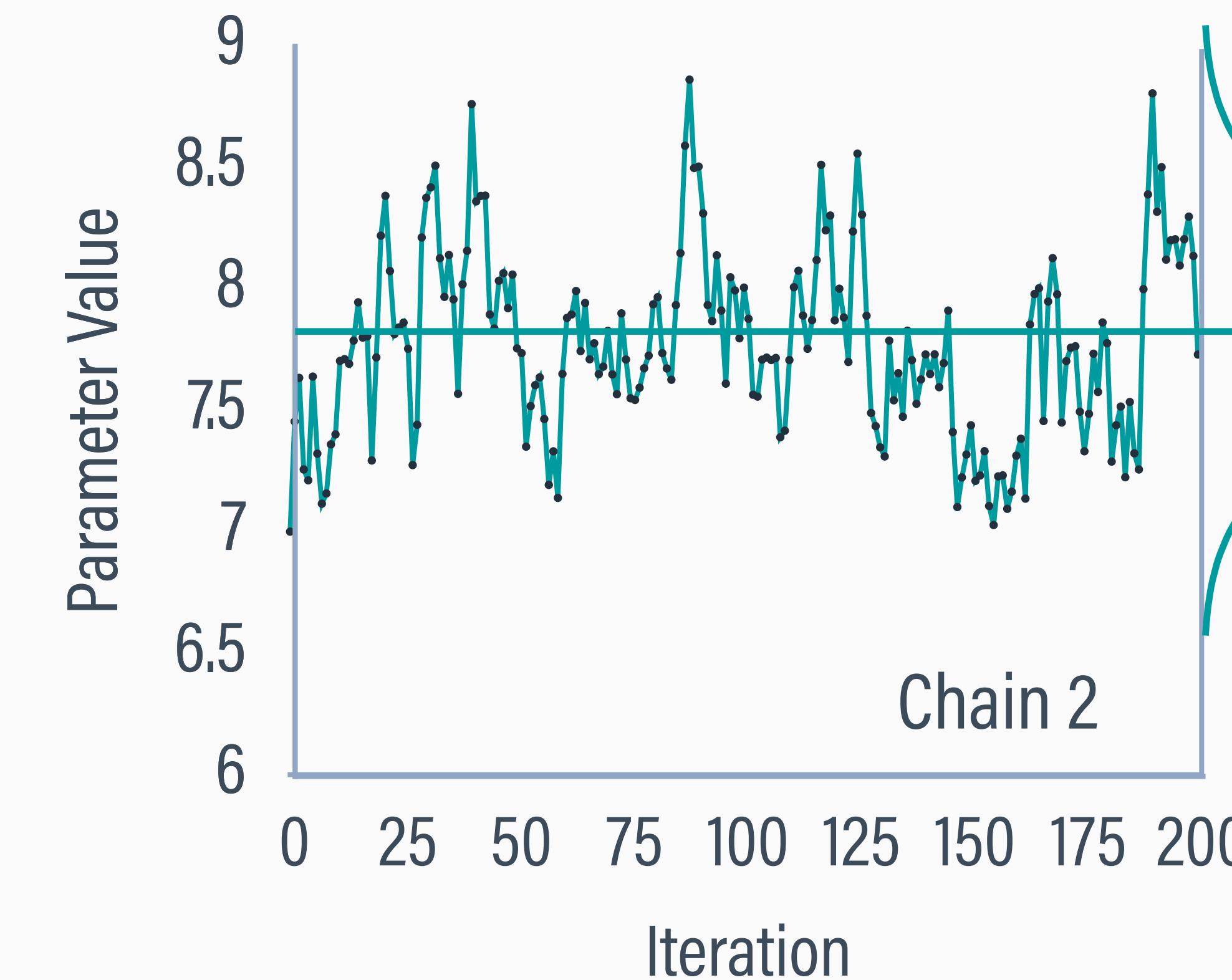
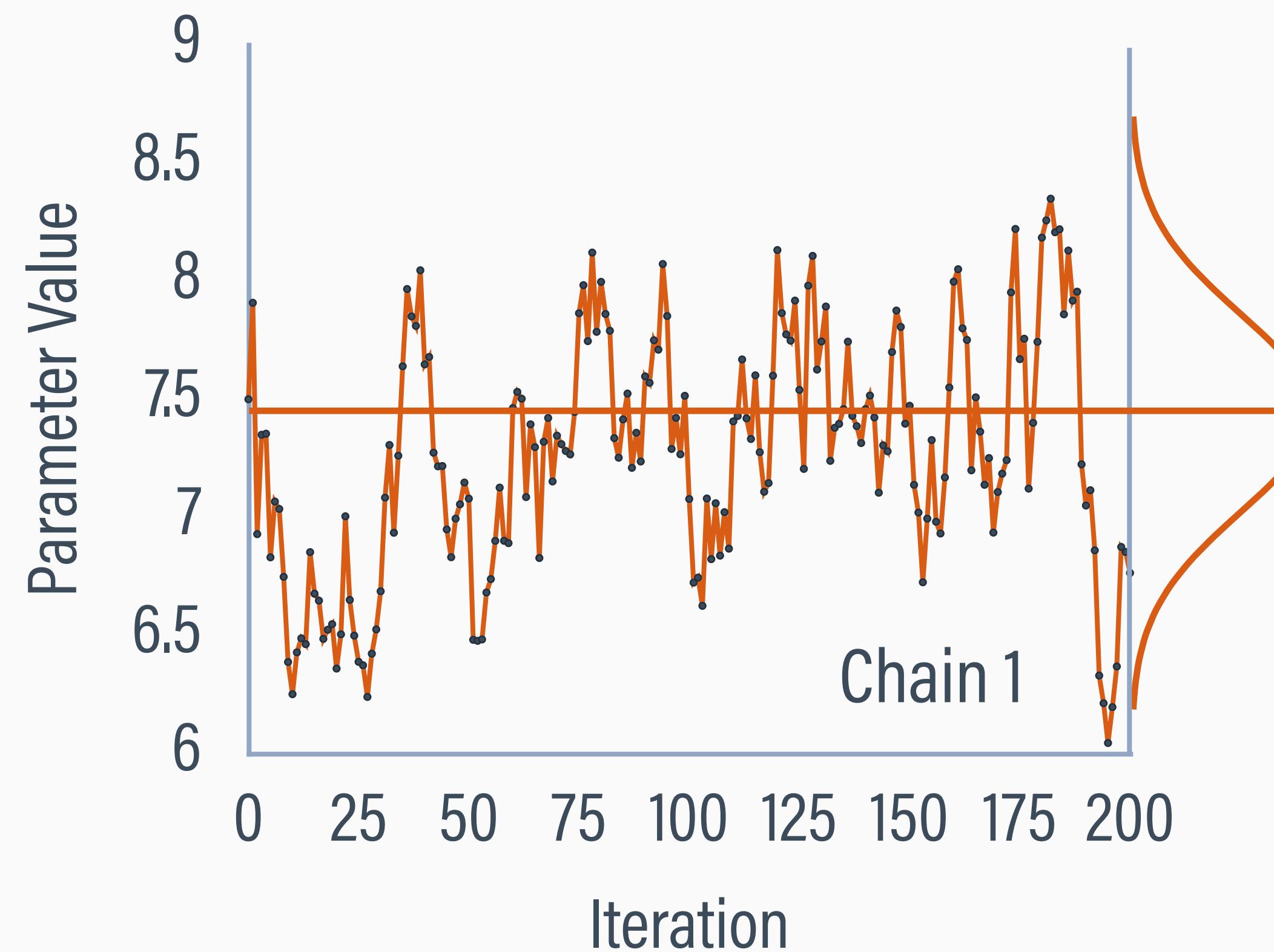
BETWEEN-CHAIN MEAN DIFFERENCE

$$\text{PSRF} = \sqrt{\frac{\text{mean difference between chains} + \text{within-chain variation}}{\text{within-chain variation}}}$$



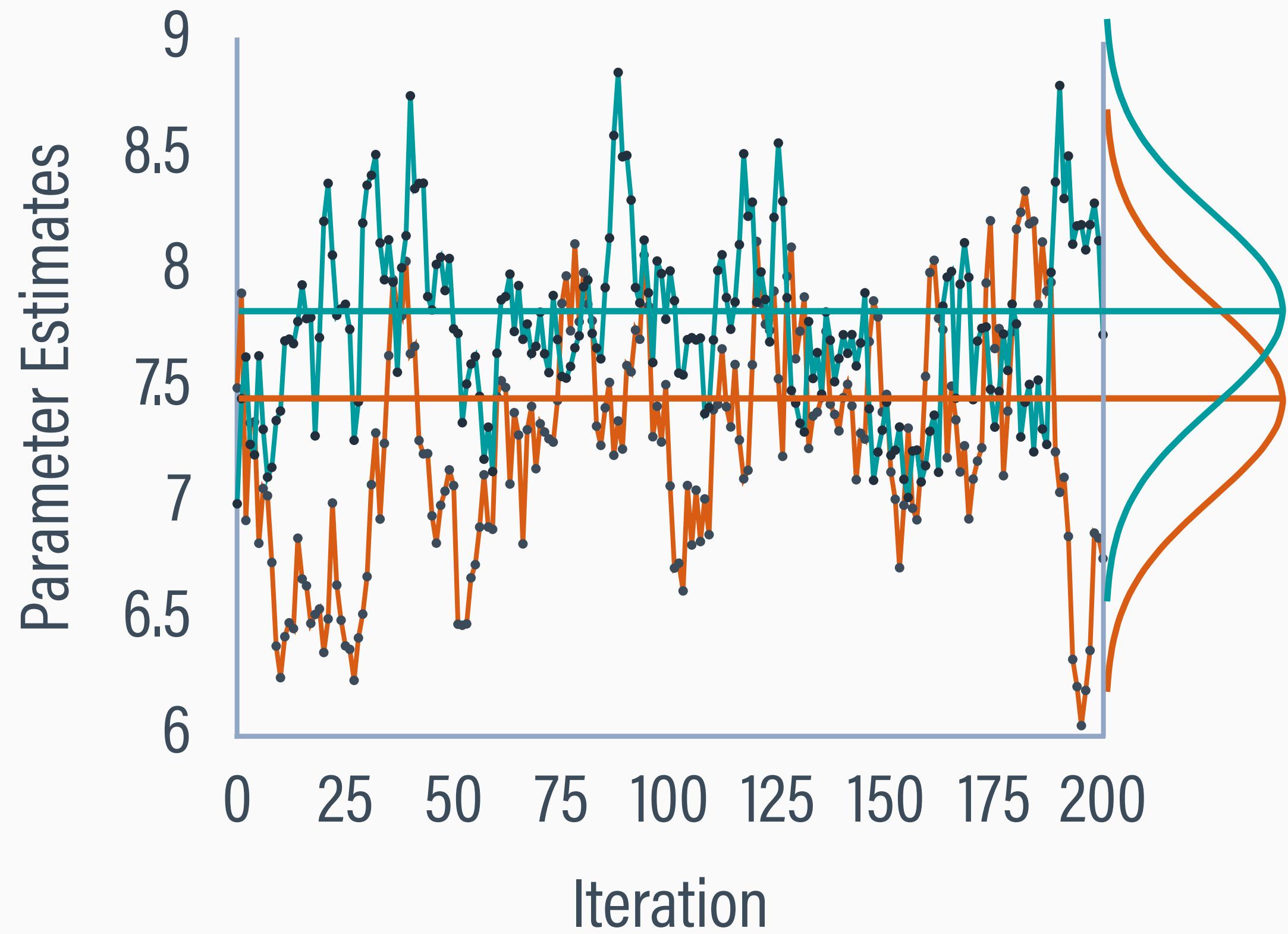
WITHIN-CHAIN VARIATION

$$\text{PSRF} = \sqrt{\frac{\text{mean difference between chains} + \text{within-chain variation}}{\text{within-chain variation}}}$$

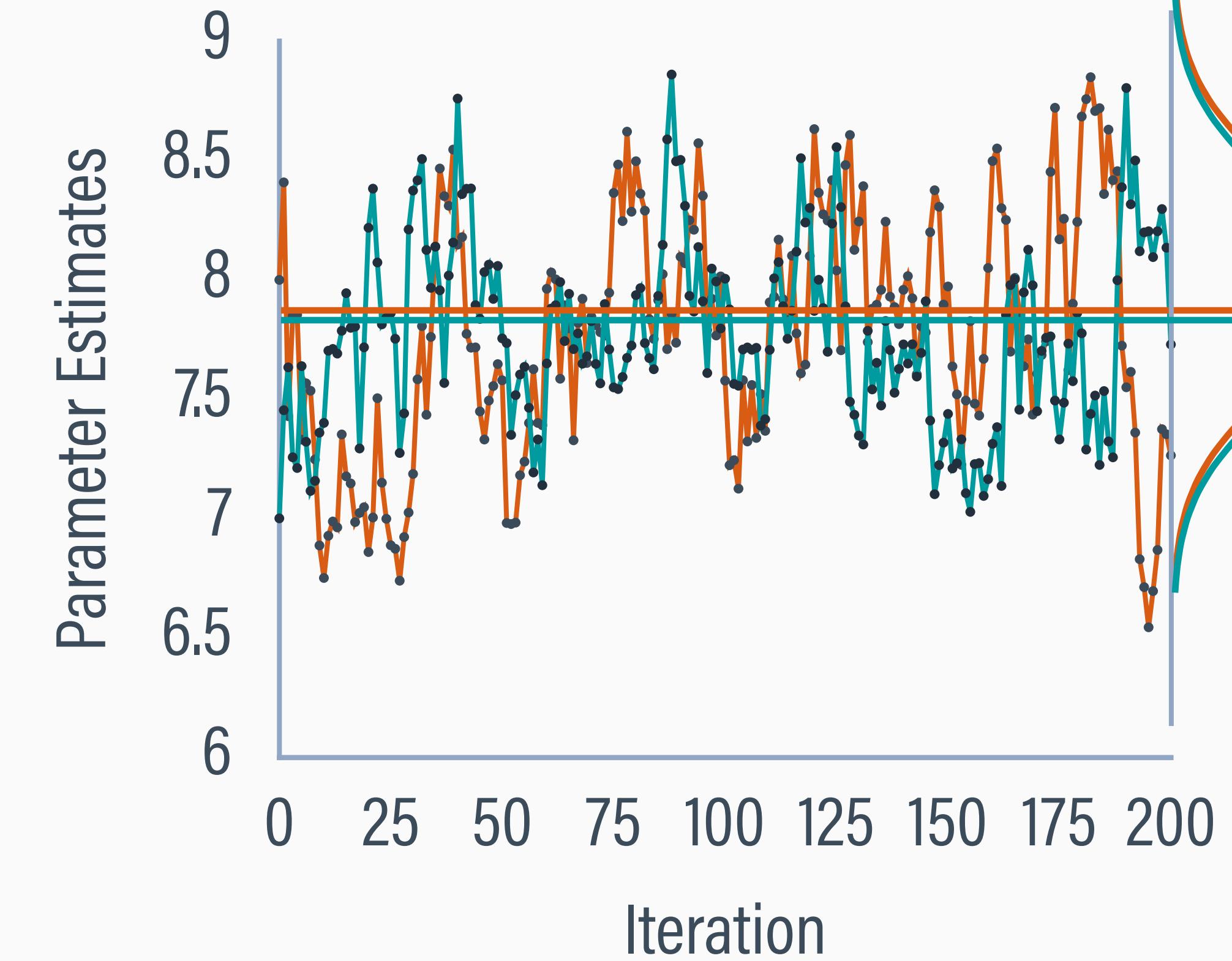


CONVERGENCE

MCMC has not converged because between-chain mean difference is large ($\text{PSR} > 1.05$)



MCMC has converged because between-chain mean difference is very small ($\text{PSR} < 1.05$)



PSRF DIAGNOSTIC OUTPUT

The number of burn-in iterations is sufficient because the highest PSRF across all parameters is < 1.05 at the end of the burn-in period

BURN-IN POTENTIAL SCALE REDUCTION (PSR) OUTPUT:

NOTE: Split chain PSR is being used. This splits each chain's iterations to create twice as many chains.

| Comparing iterations across 2 chains | Highest PSR | Parameter # |
|--------------------------------------|-------------|-------------|
| 251 to 500 | 1.428 | 3 |
| 501 to 1000 | 1.387 | 3 |
| 751 to 1500 | 1.076 | 5 |
| 1001 to 2000 | 1.161 | 11 |
| 1251 to 2500 | 1.064 | 11 |
| 1501 to 3000 | 1.046 | 3 |
| 1751 to 3500 | 1.100 | 11 |
| 2001 to 4000 | 1.029 | 3 |
| ... | ... | ... |
| 3501 to 7000 | 1.023 | 3 |
| 3751 to 7500 | 1.024 | 3 |
| 4001 to 8000 | 1.006 | 3 |
| 4251 to 8500 | 1.019 | 5 |
| 4501 to 9000 | 1.013 | 5 |
| 4751 to 9500 | 1.012 | 3 |
| 5001 to 10000 | » 1.031 | 3 |

CONCLUSIONS

- PRSFs indicated that a 10,000-iteration warm-up (burn-in) period was sufficient for achieving convergence
- The highest (worst) PSRF was < 1.05 after $\sim 4,000$ iterations
- Two independent MCMC chains were producing similar parameters (same mean and spread) after $\sim 4,000$ iterations
- Always inspect the PSRFs before interpreting results!

EFFECTIVE SAMPLE SIZE DIAGNOSTIC

- Effective sample size reflects the number of independent MCMC samples after accounting for autocorrelation
- Values above ~ 100 are viewed as sufficient, and lower values indicate the need for additional iterations
- Low values (high autocorrelation) indicate that a parameter has weak data support from the data

BLIMP OUTPUT

Outcome Variable: PosAffect

Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|--------------------------------------|----------|--------|-------|-------|----------|--------|----------|
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.839 | 0.246 | 1.436 | 2.399 | --- | --- | 5051.168 |
| Residual Var. | 1.307 | 0.037 | 1.238 | 1.380 | --- | --- | 8227.580 |
| Coefficients: | | | | | | | |
| Intercept | 4.997 | 0.133 | 4.761 | 5.277 | 1423.604 | 0.000 | 154.295 |
| SleepQual | 0.173 | 0.013 | 0.147 | 0.199 | 174.595 | 0.000 | 9302.345 |
| SleepQual.mean[Person] | 0.598 | 0.094 | 0.416 | 0.788 | 40.936 | 0.000 | 161.345 |
| Standard Deviations: | | | | | | | |
| L2 : SD(Intercept) | 1.356 | 0.090 | 1.198 | 1.549 | --- | --- | 5041.908 |
| Residual SD | 1.143 | 0.016 | 1.113 | 1.175 | --- | --- | 8223.888 |
| ... | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.193 | 0.044 | 0.112 | 0.286 | --- | --- | 175.664 |
| by Level-2 Random Intercepts | 0.471 | 0.042 | 0.392 | 0.555 | --- | --- | 414.230 |
| by Level-1 Residual Variation | 0.334 | 0.027 | 0.280 | 0.387 | --- | --- | 511.829 |

CONCLUSIONS

- Diagnostics show that 10,000 post-warm-up iterations provided adequate precision (all N_{eff} values > 100)
- The lowest N_{eff} values (~154 to 161) occurred for level-2 mean parameters—they rely on the number of clusters rather than the full N , so they naturally have less support from the data
- Additional iterations would improve these values
- Always inspect the N_{eff} values before interpreting results!

OUTLINE

- 1 Analysis Example
- 2 Frequentist vs. Bayesian Statistical Paradigms
- 3 Maximum Likelihood Estimation
- 4 MCMC Estimation
- 5 MCMC Diagnostics
- 6 Checking MLM Assumptions

MLM ASSUMPTIONS

- Associations are linear
- Level-1 residuals are normal with constant variation across level-1 units (days) and level-2 units (persons)
- Level-2 random intercept residuals are normal with constant variation across level-2 units (persons)

$$u_{0j} \sim N(0, \sigma_u^2) \quad \varepsilon_{ij} \sim N(0, \sigma_\varepsilon^2)$$

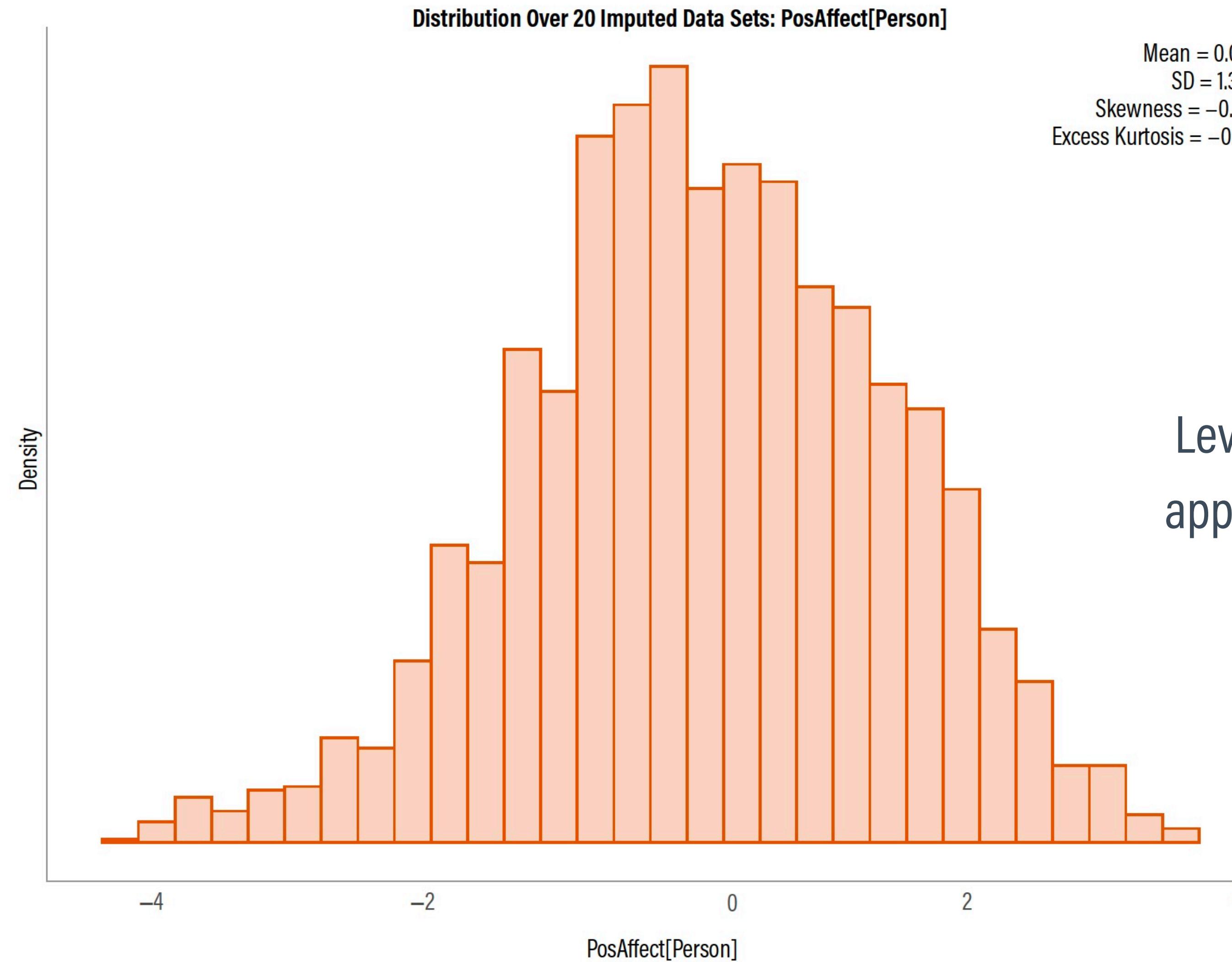
RESIDUAL DIAGNOSTICS

- Each MCMC iteration produces different parameter values—and thus different predicted values and residuals
- Residuals from different MCMC steps can be saved to create multiple datasets for plotting
- The `univariate_plot` function (imported at the top of the `rblimp` scripts) graphs residuals from multiple `rblimp` data sets

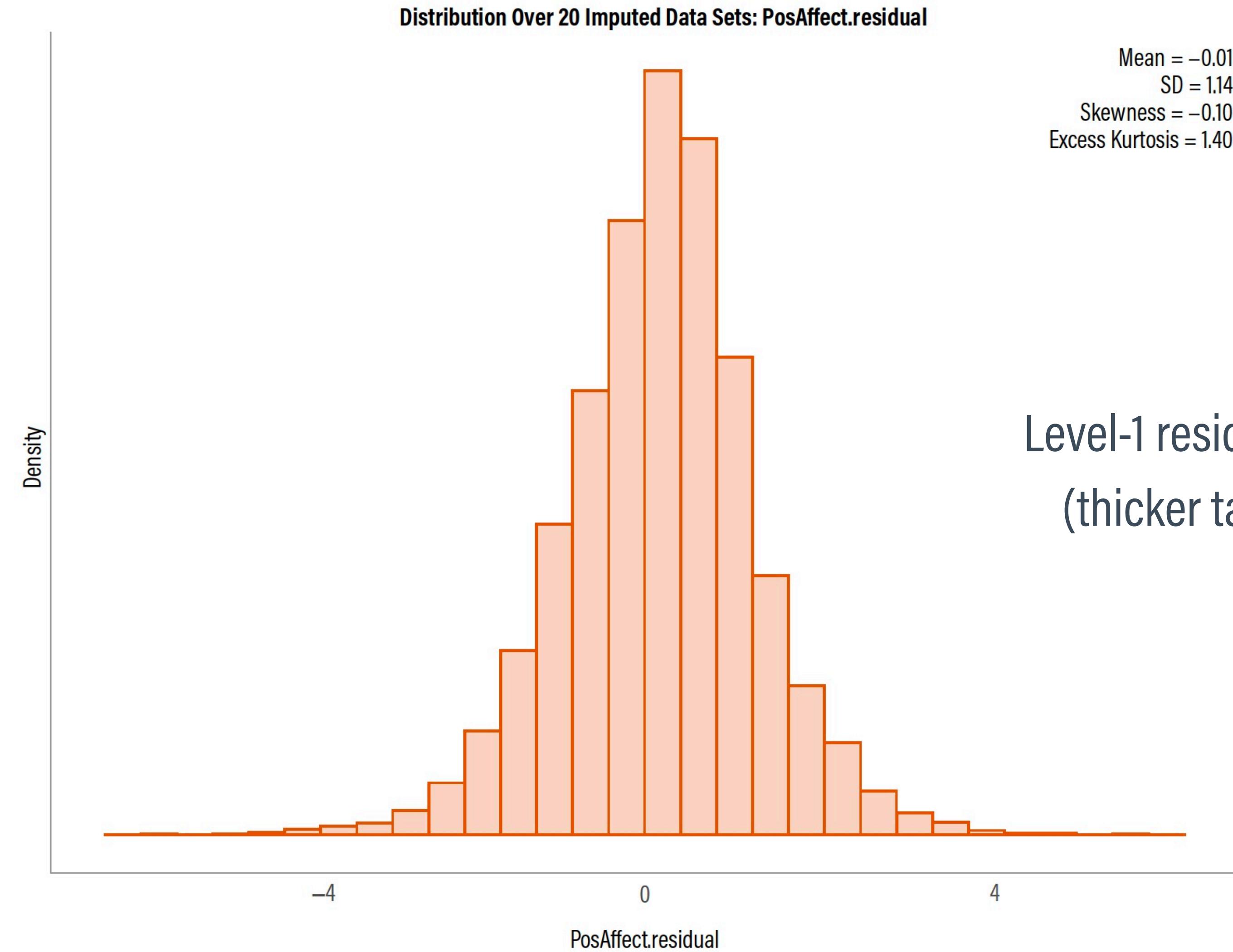
RBLIMP SCRIPT 3 (MODEL 2)

```
model2 <- rblimp(  
  data = PainDiary,  
  clusterid = 'Person',  
  center = 'grandmean = SleepQual.mean; groupmean = SleepQual',  
  model = 'PosAffect ~ intercept SleepQual SleepQual.mean | intercept',  
  seed = 90291,  
  burn = 10000,  
  iter = 10000,  
  nimps = 20)  
  
output(model2)  
univariate_plot(vars = c('PosAffect[Person]', 'PosAffect.residual'), model = model, stats = T)  
bivariate_plot(PosAffect.residual ~ SleepQual, standardize = 'y', model = model2)  
bivariate_plot(PosAffect[Person] ~ SleepQual.mean[Person], standardize = 'y', model = model2)
```

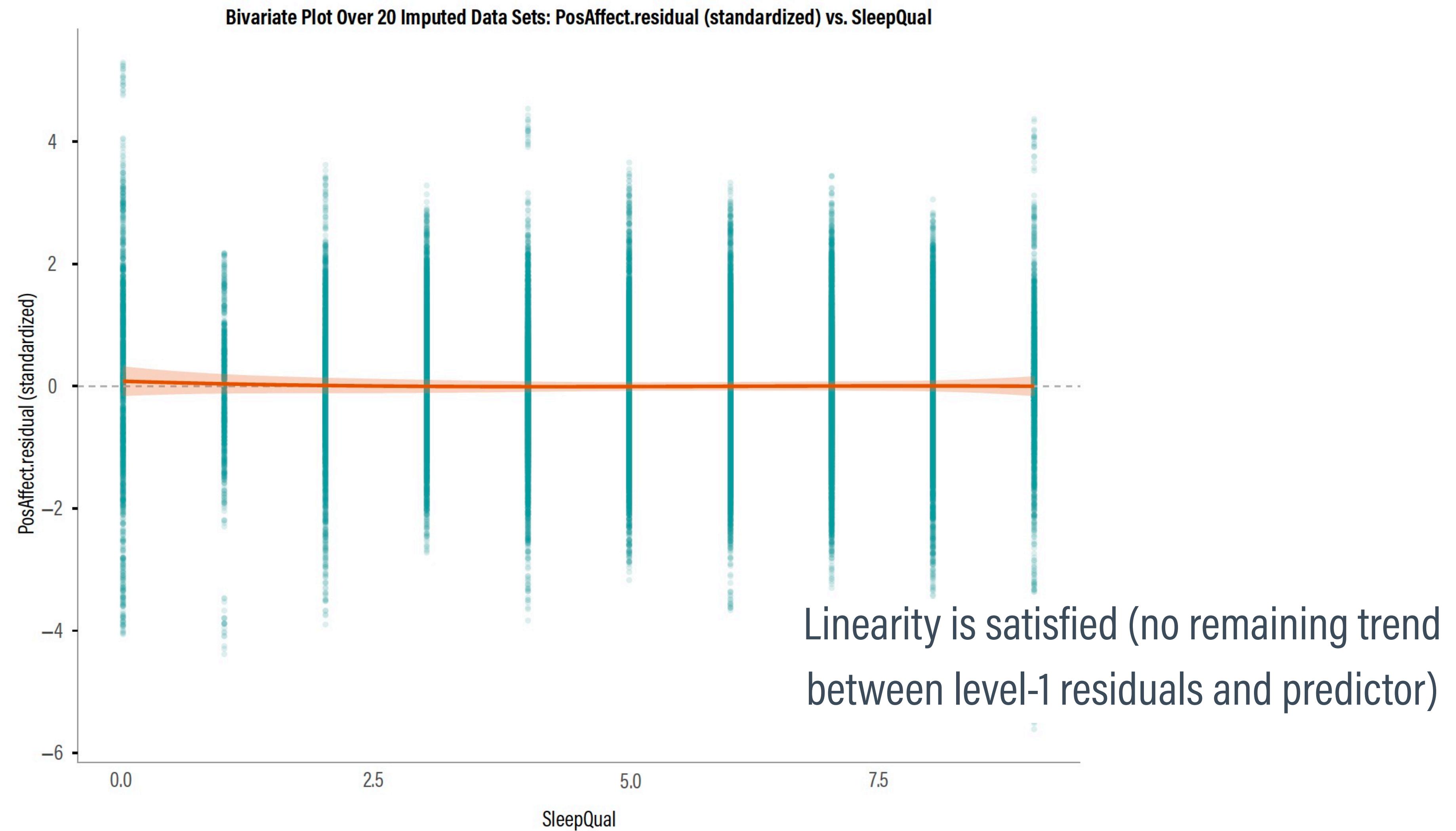
LEVEL-2 RESIDUALS



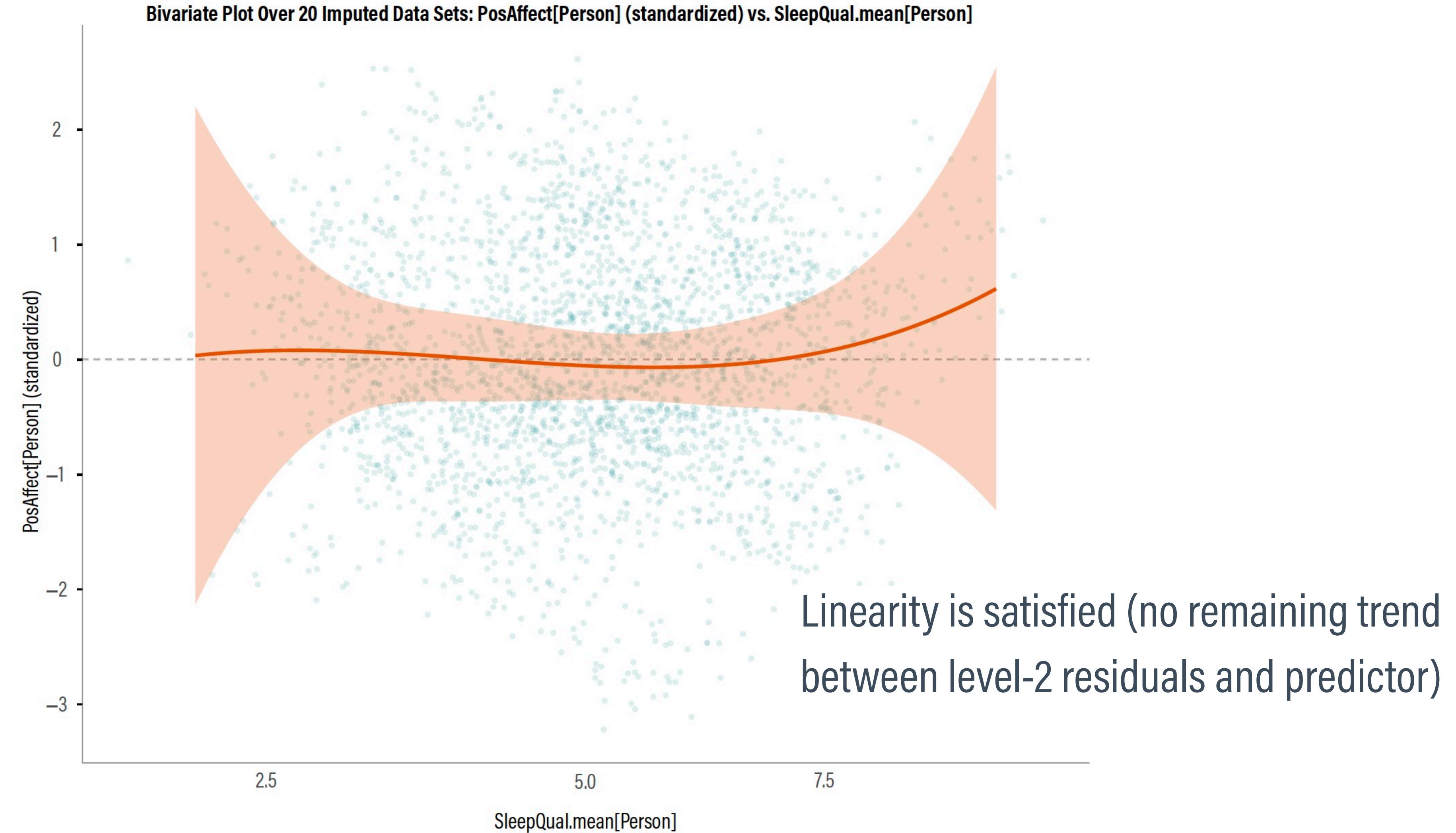
LEVEL-1 RESIDUALS



LEVEL-1 RESIDUALS BY LEVEL-1 PREDICTOR



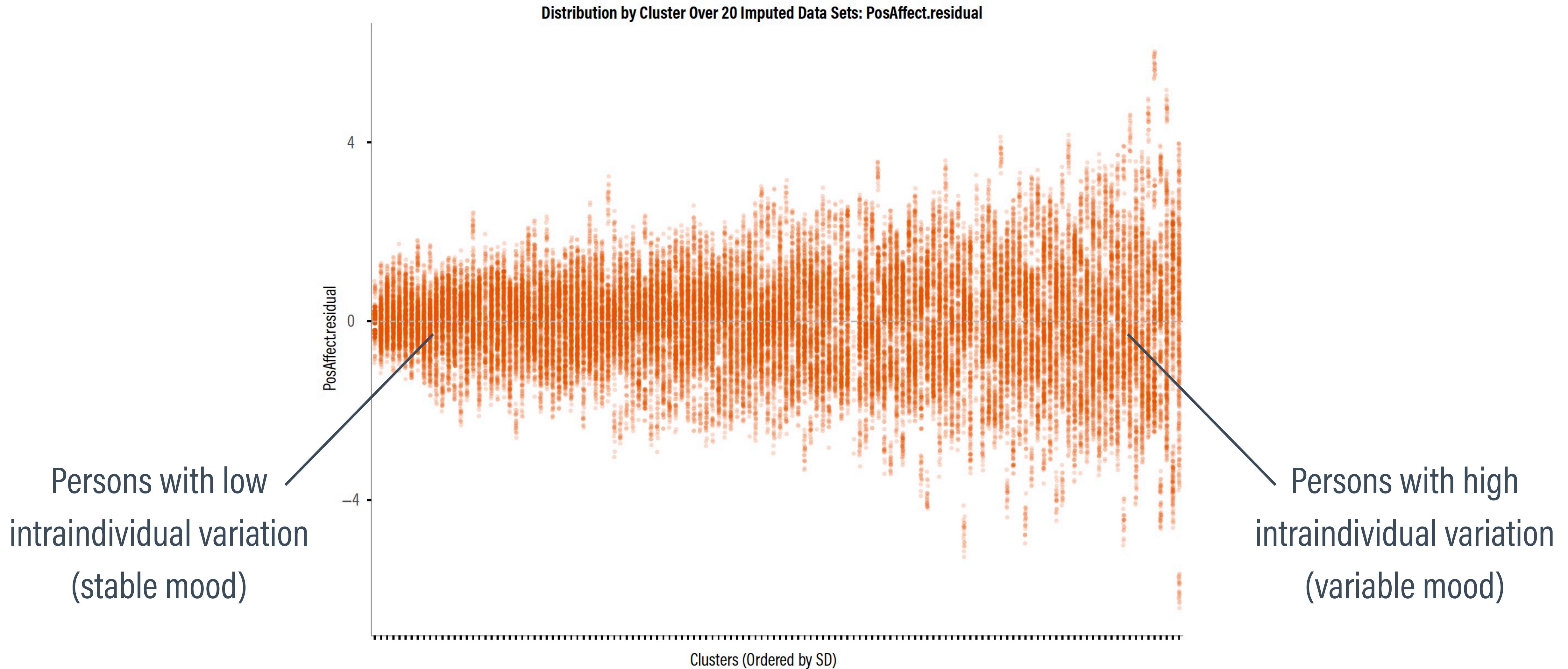
LEVEL-2 RESIDUALS BY LEVEL-2 PREDICTOR



VARIANCE HETEROGENEITY

- MLMs assume that the residual variance is constant (homogeneous) across clusters
- This assumption is often at odds with intensive data, where intraindividual variability differs across people (some have stable mood, others have large day-to-day fluctuations)
- Nonnormal (positively kurtotic) residuals are often a symptom of variance heterogeneity

LEVEL-1 RESIDUALS BY CLUSTER



SENSITIVITY ANALYSIS

- Blimp fits MLMs with cluster-specific variation
- Treat this as a sensitivity analysis: fit a model with cluster-specific residual variation (person-specific intraindividual variability) and evaluate whether the results change
- Are the main conclusions affected by assumptions about variance heterogeneity?

BLIMP STUDIO SCRIPT 3.2

DATA: PainDiary.dat;

VARIABLES: Person Day PosAffect NegAffect Pain WorkGoal LifeGoal SleepQual Female Education
Employment MarStatus NumDiagnose ActivityLevel PainAccept Catastrophize Stress Anxiety;

CLUSTERID: Person;

CENTER:

grandmean = SleepQual.mean; # defines the fixed (average) intercept as the grand mean

groupmean = SleepQual; # cwc with level-2 latent group means

MODEL: PosAffect ~ intercept SleepQual SleepQual.mean | intercept; # .mean invokes latent means

BURN: 10000;

ITERATIONS: 10000;

SEED: 90291;

OPTIONS: hev;

RBLIMP SCRIPT 3 (MODEL 3)

```
model3 <- rblimp(  
  data = PainDiary,  
  clusterid = 'Person',  
  center = 'grandmean = SleepQual.mean; groupmean = SleepQual',  
  model = 'PosAffect ~ intercept SleepQual SleepQual.mean | intercept',  
  seed = 90291,  
  burn = 10000,  
  iter = 10000,  
  options = 'hev')  
output(model3)
```

BLIMP OUTPUT

 = level-2 estimate

 = level-1 estimate

Outcome Variable: PosAffect

Group Mean Centered: SleepQual

| Parameters | Estimate | StdDev | 2.5% | 97.5% | ChiSq | PValue | N_Eff |
|-------------------------------|--------------|--------|-------|-------|----------|--------|----------|
| <hr/> | | | | | | | |
| Variances: | | | | | | | |
| L2 : Var(Intercept) | 1.845 | 0.251 | 1.438 | 2.418 | --- | --- | 4565.552 |
| Heterogeneity Index | 0.241 | 0.042 | 0.174 | 0.336 | --- | --- | 3676.792 |
| Q25% Residual Var. | 0.656 | 0.036 | 0.587 | 0.727 | --- | --- | 6552.527 |
| Q50% Residual Var. | 1.066 | 0.055 | 0.963 | 1.180 | --- | --- | 8295.850 |
| Mean Residual Var. | 1.337 | 0.050 | 1.249 | 1.443 | --- | --- | 6775.414 |
| Q75% Residual Var. | 1.747 | 0.096 | 1.573 | 1.955 | --- | --- | 7606.960 |
| <hr/> | | | | | | | |
| Coefficients: | | | | | | | |
| Intercept | 5.051 | 0.150 | 4.760 | 5.352 | 1140.408 | 0.000 | 69.000 |
| SleepQual | 0.167 | 0.013 | 0.143 | 0.191 | 178.266 | 0.000 | 6998.401 |
| SleepQual.mean[Person] | 0.622 | 0.094 | 0.435 | 0.799 | 43.951 | 0.000 | 94.442 |
| <hr/> | | | | | | | |
| ... | | | | | | | |
| <hr/> | | | | | | | |
| Proportion Variance Explained | | | | | | | |
| by Coefficients | 0.200 | 0.044 | 0.115 | 0.287 | --- | --- | 101.893 |
| by Level-2 Random Intercepts | 0.463 | 0.042 | 0.387 | 0.550 | --- | --- | 242.871 |
| by Level-1 Residual Variation | 0.211 | 0.023 | 0.170 | 0.258 | --- | --- | 430.938 |

MODEL COMPARISON

- The stability of estimates between models suggests that the results were not materially affected by variance heterogeneity

| Parameter | MCMC (Homogeneous) | | | MCMC (Heterogeneous) | | |
|---------------------------------|--------------------|-----------|--------|----------------------|-----------|--------|
| | Est. | Std. Dev. | p | Est. | Std. Dev. | p |
| Fixed intercept | 5.00 | 0.13 | < .001 | 5.05 | 0.13 | < .001 |
| Sleep (within-person) | 0.17 | 0.01 | < .001 | 0.17 | 0.01 | < .001 |
| Sleep (between-person) | 0.60 | 0.09 | < .001 | 0.62 | 0.09 | < .001 |
| Random intercept variance | 1.84 | 0.25 | — | 1.85 | 0.25 | — |
| Residual within-person variance | 1.31 | 0.04 | — | 1.07 | 0.06 | — |