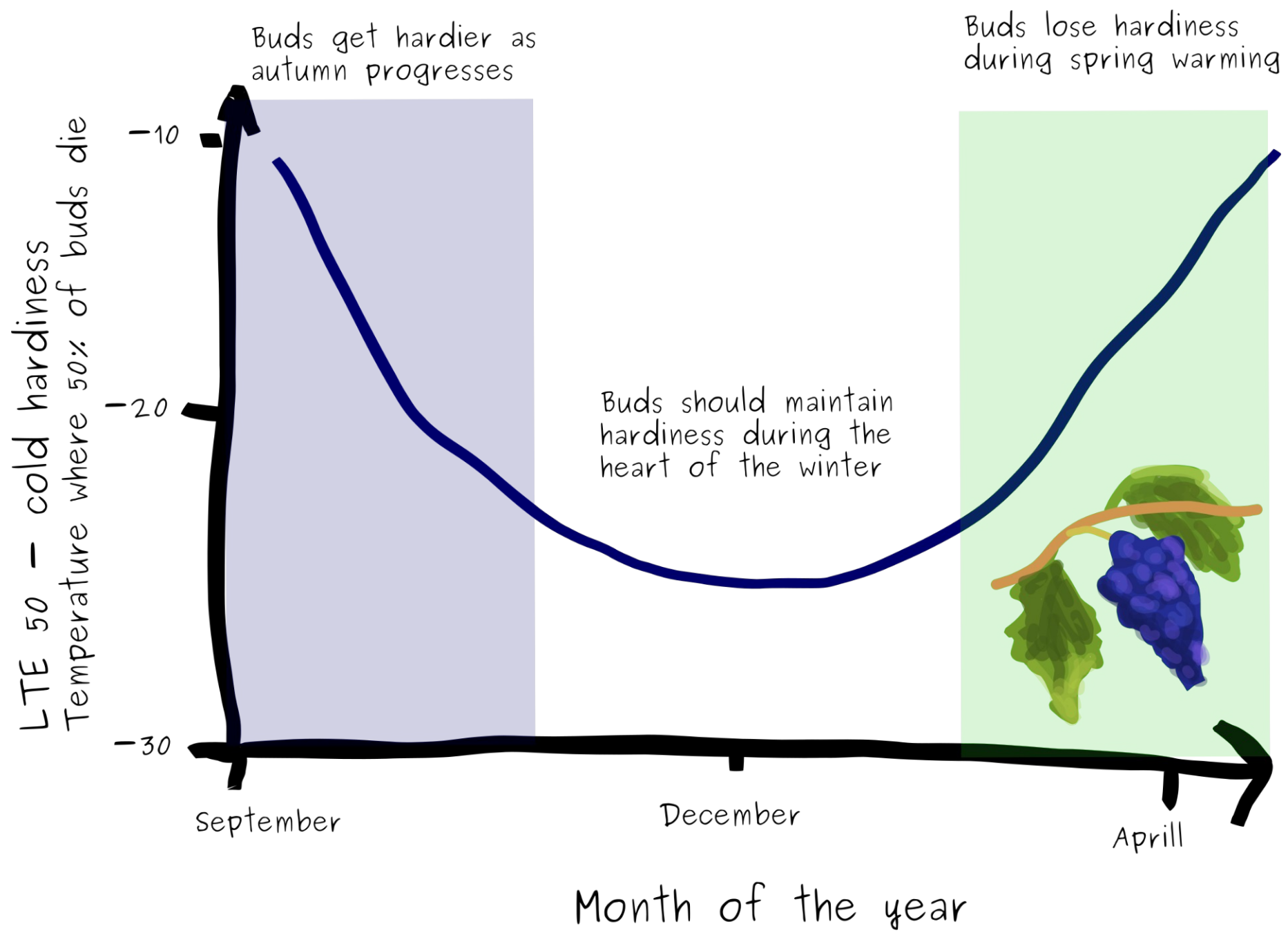


# Cold hardness model

Mixed model with three grouping factors on the intercept



# Background

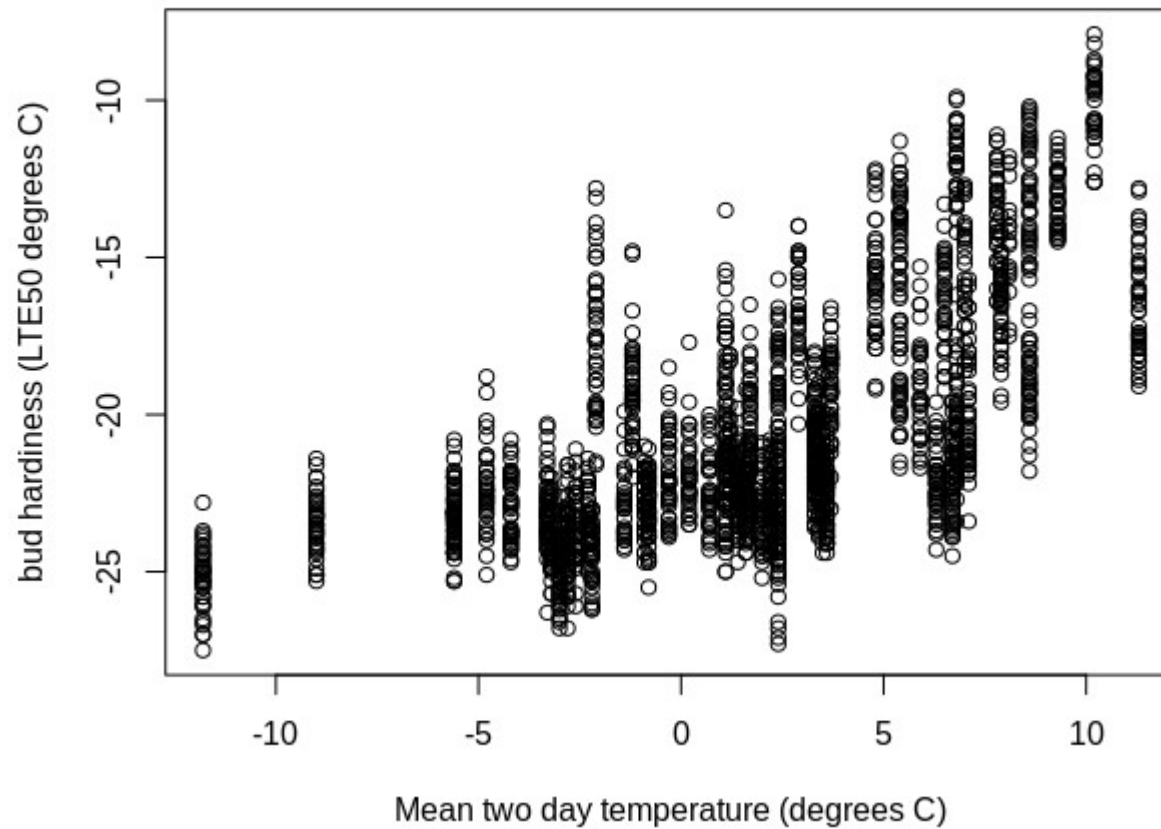
**Aim:** Partition the variation on winter hardiness (LTE50) into variation by variety, year and site location

# Background

**Question:** Is variety more influential than site in determining wine grape bud hardiness?

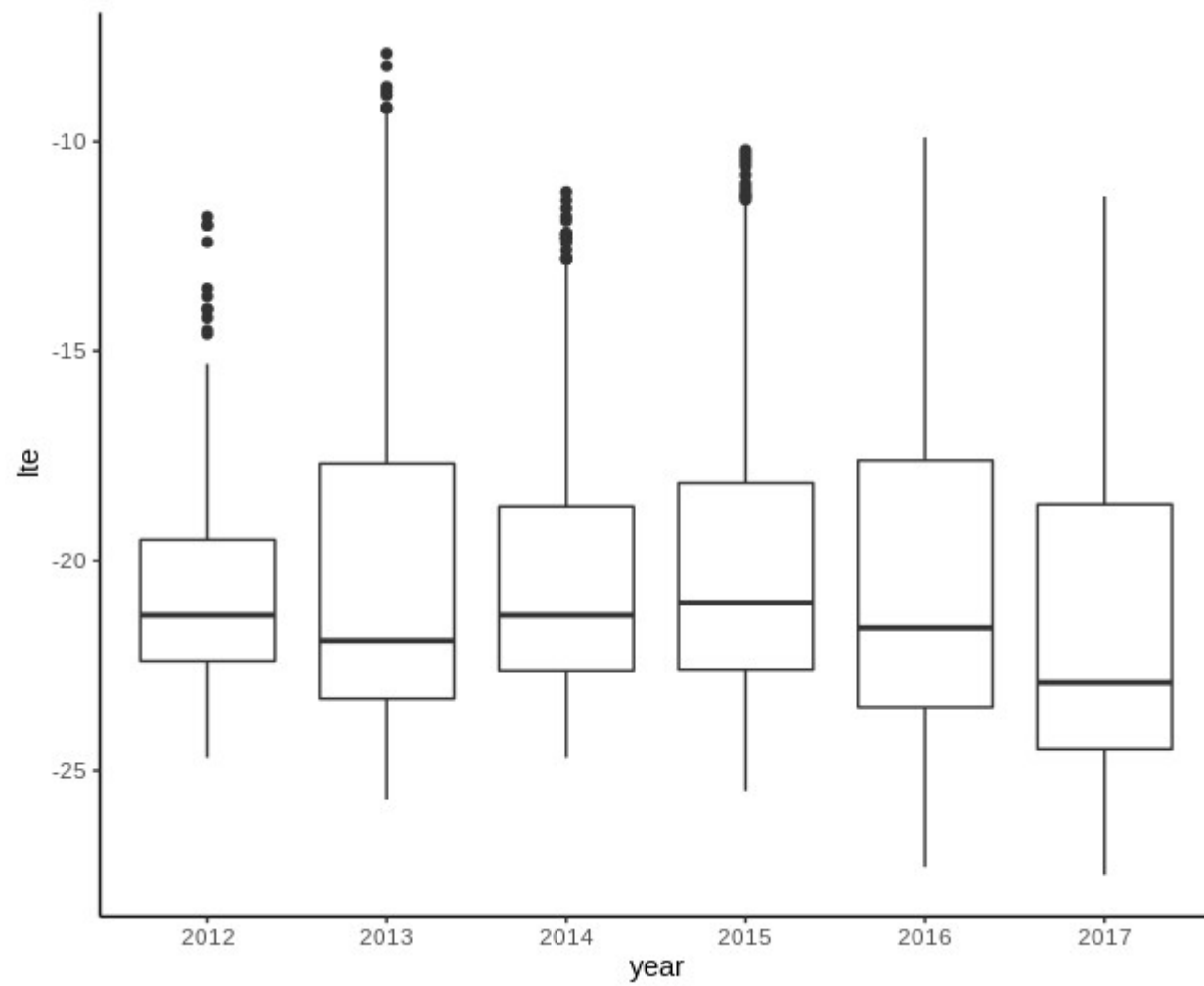
- Expect much less variation attributed to site if hardiness is controlled strongly by variety's physiology
- If lots of variation by site, this variation could be evidence of phenotypic plasticity, between clone variation or the effect of rootstock

# Data

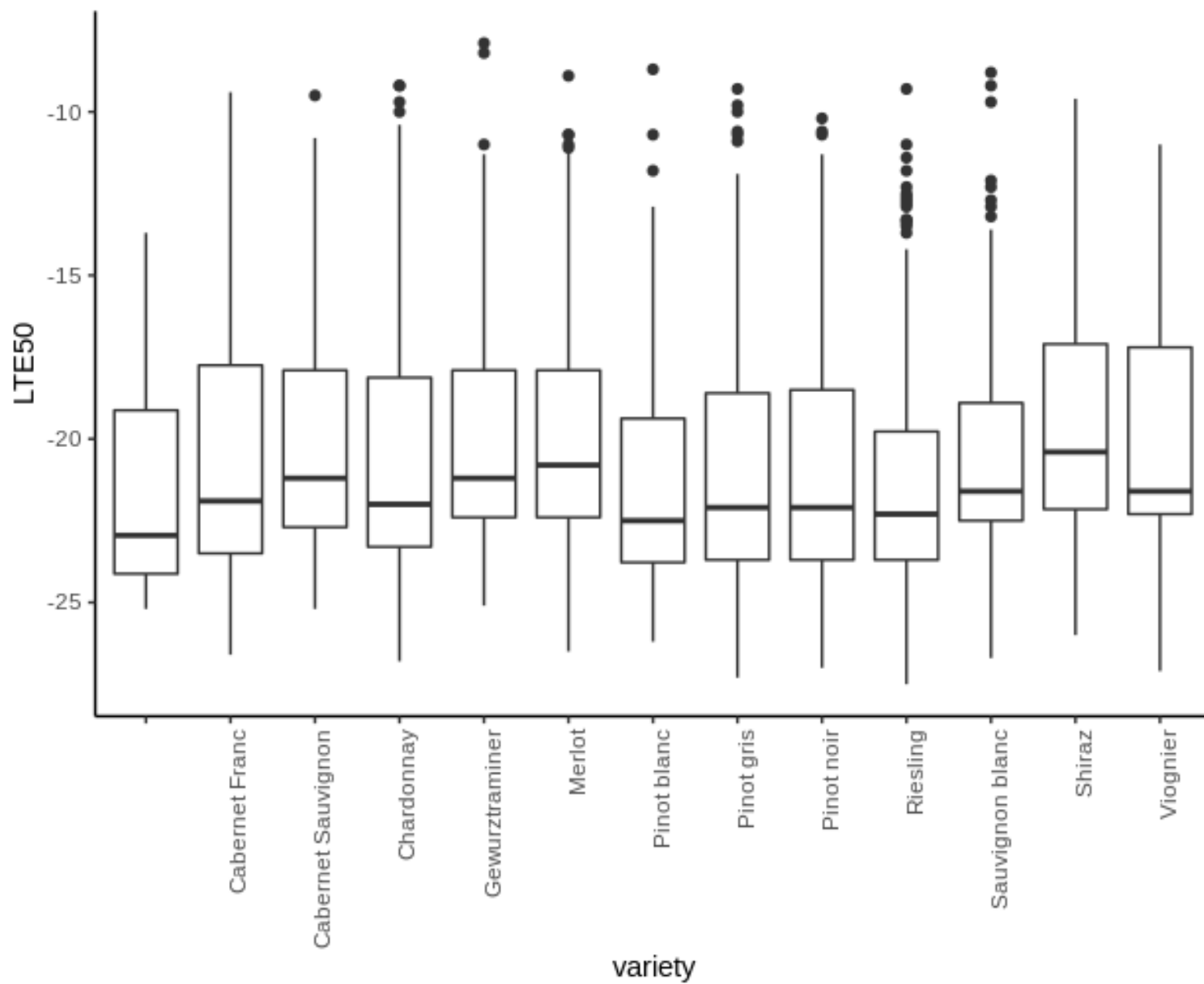


	Cabernet Franc	Cabernet Sauvignon	Chardonnay	Gewurztraminer	Merlot	Pinot blanc	Pinot gris	Pinot noir	Riesling	Sauvignon blanc	Shiraz	Viognier
Black Sage	59	59	59	0	59	59	59	59	94	24	59	0
Kelowna	0	0	0	35	0	0	0	59	59	0	0	0
Naramata Bench	0	0	59	0	0	0	59	35	35	0	0	0
OK Falls	0	0	59	59	0	0	59	0	0	0	0	0
Oliver	59	0	59	59	59	59	118	0	59	118	0	0
Osoyoos	35	177	59	0	94	0	0	59	0	0	247	35

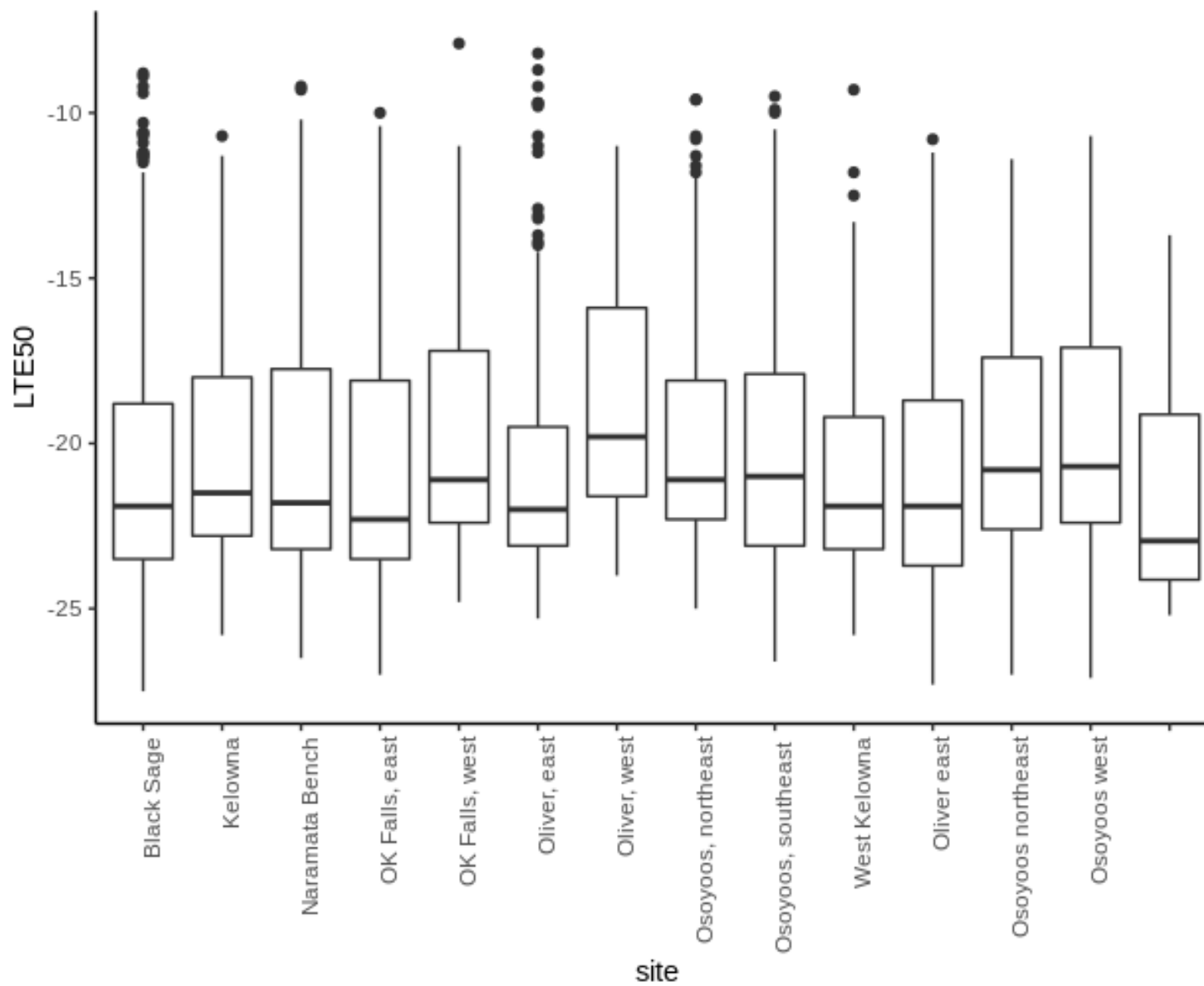
# Data



# Data



# Data





$$y_i \sim \text{normal}(\mu_i, \sigma)$$

$$\mu_i = \alpha_g + \alpha_{\text{var},i} + \alpha_{\text{site},i} + \alpha_{\text{year},i} + \beta^* x_i$$

$$\alpha_g \sim \text{normal}(-15, 12)$$

$$\beta \sim \text{lognormal}(0, 1)$$

$$\sigma \sim \text{truncated normal}(0, 5)$$

$$\alpha_{\text{var}} \sim \text{normal}(0, \sigma_{\text{var}})$$

$$\sigma_{\text{var}} \sim \text{truncated normal}(0, 5)$$

$$\alpha_{\text{site}} \sim \text{normal}(0, \sigma_{\text{site}})$$

$$\sigma_{\text{site}} \sim \text{truncated normal}(0, 5)$$

$$\alpha_{\text{year}} \sim \text{normal}(0, \sigma_{\text{year}})$$

$$\sigma_{\text{year}} \sim \text{truncated normal}(0, 5)$$

# Stan Model

Please see the R file  
LinearModelHardiness3Randoms.R

# Model fit

- (can open shiny stan from r code)

Parameter

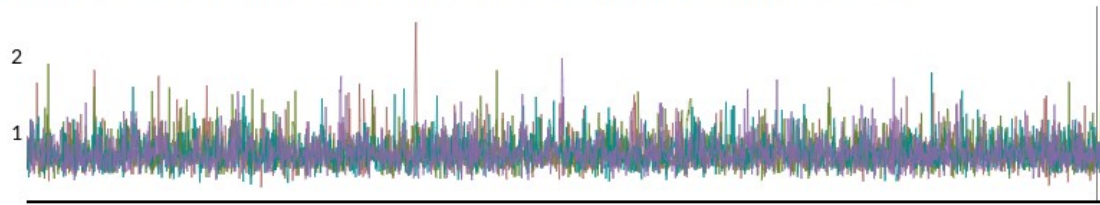
sigma\_v

Transformation

identity

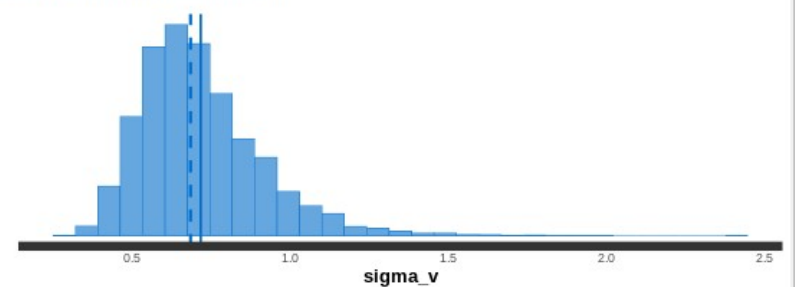
Transform

Use your mouse to select a range in the traceplot to zoom into. The other plots on the screen will update accordingly. Double-click to reset.

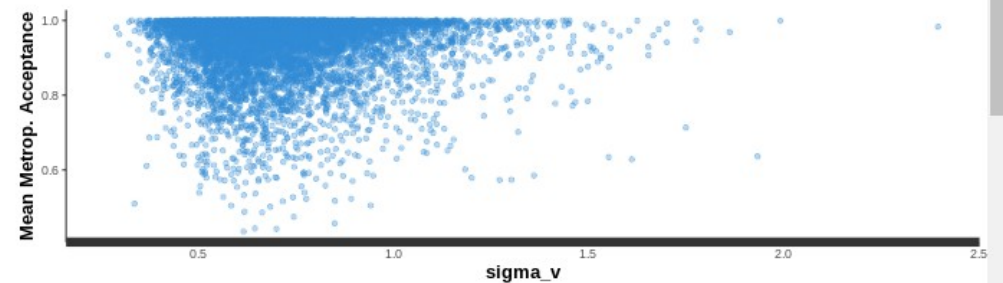
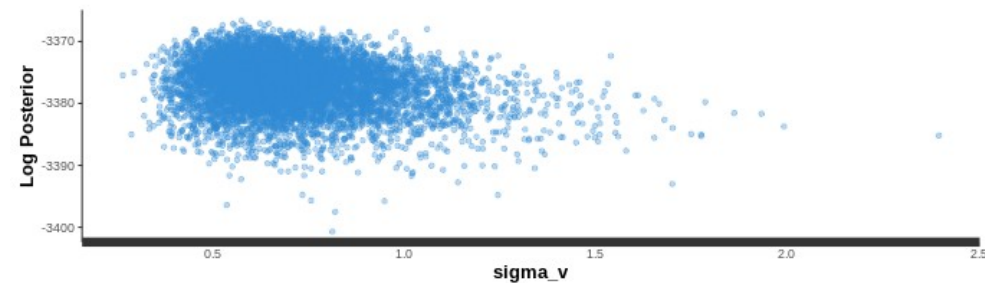


Parameter: sigma\_v

Lines are mean (solid) and median (dashed)

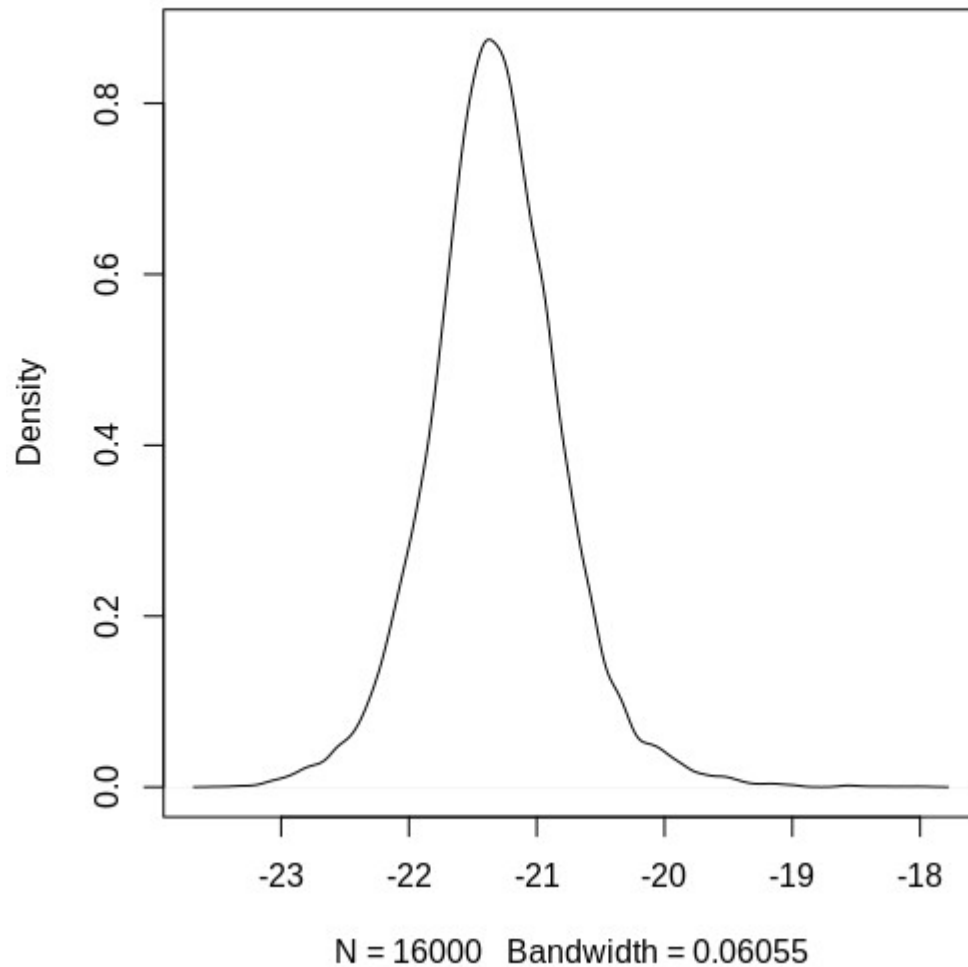


Large red points indicate which (if any) iterations encountered a divergent transition. Yellow indicates a transition hitting the maximum treedepth.



# Results

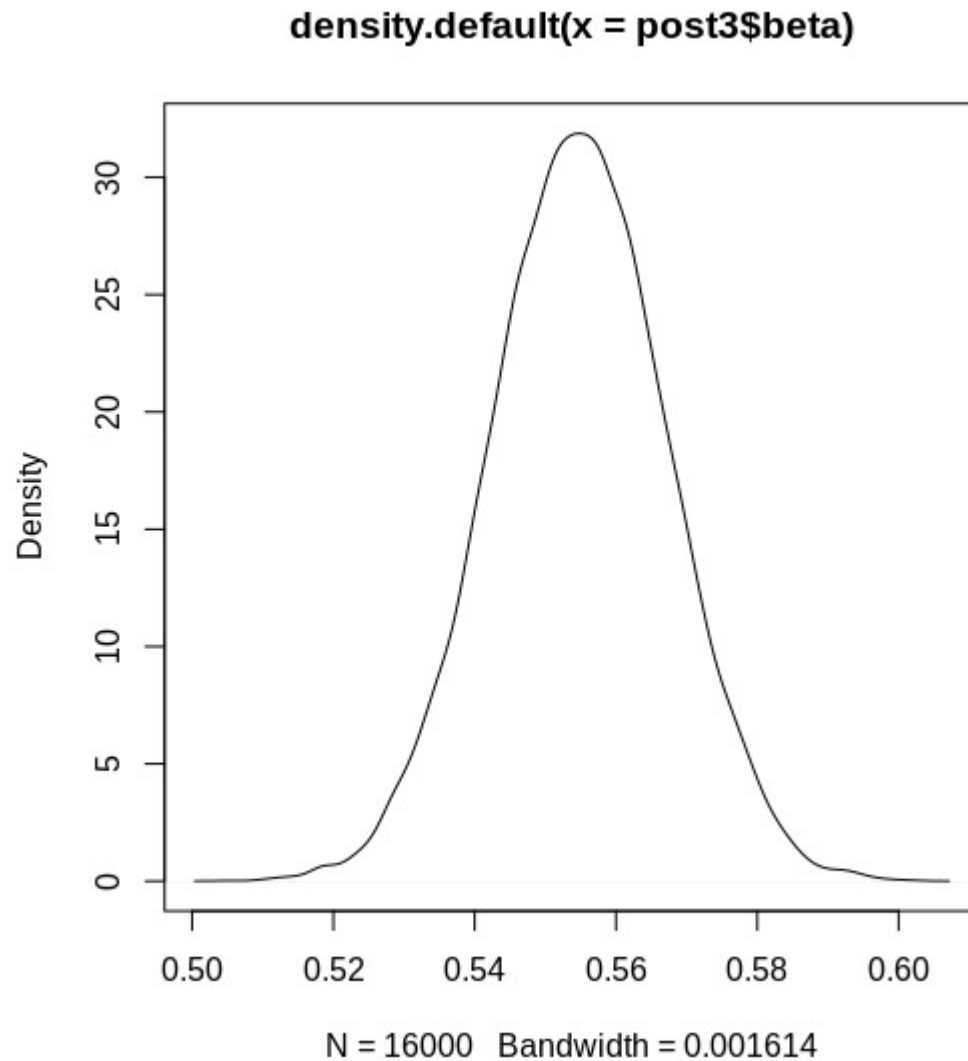
`density.default(x = post3$alpha)`



Mean = -21.3 degrees C

HPDI (0.89) = -22.1 : -20.52

# Results

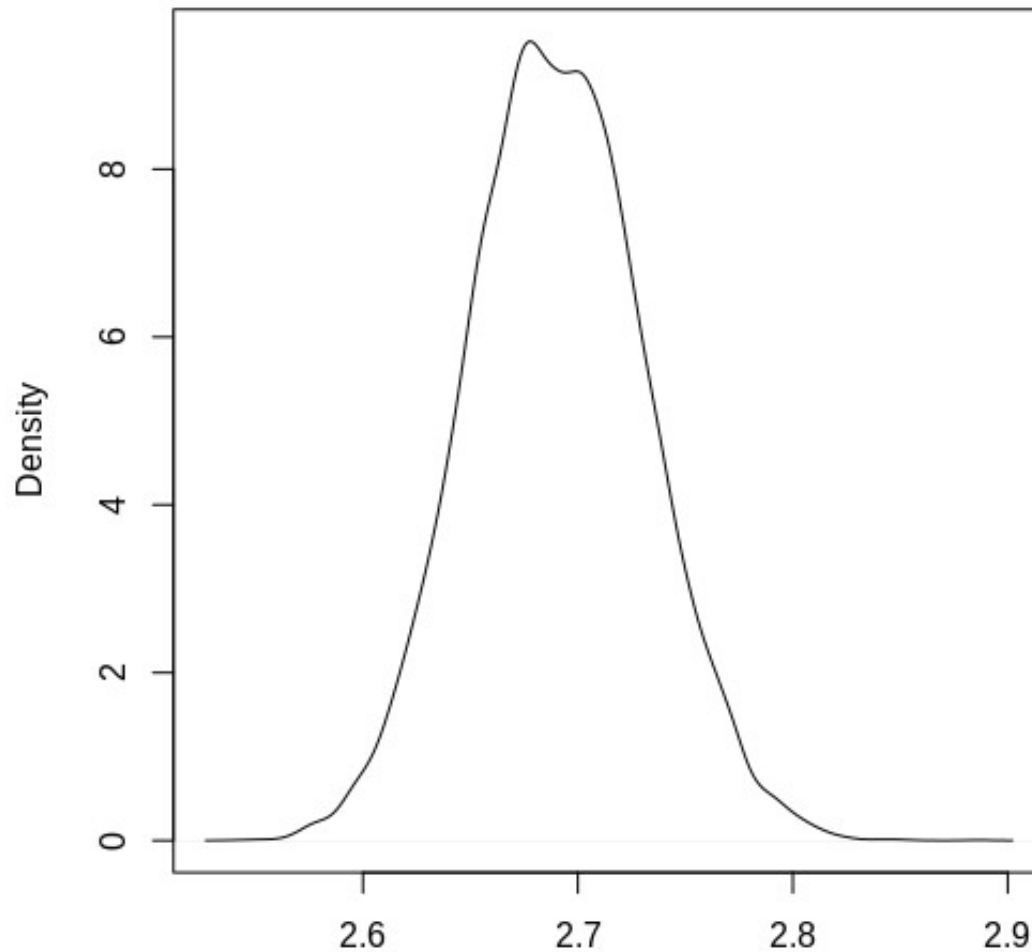


Mean = 0.55

HPDI (0.89) = 0.53 : 0.57

# Results

`density.default(x = post3$sigma_y)`



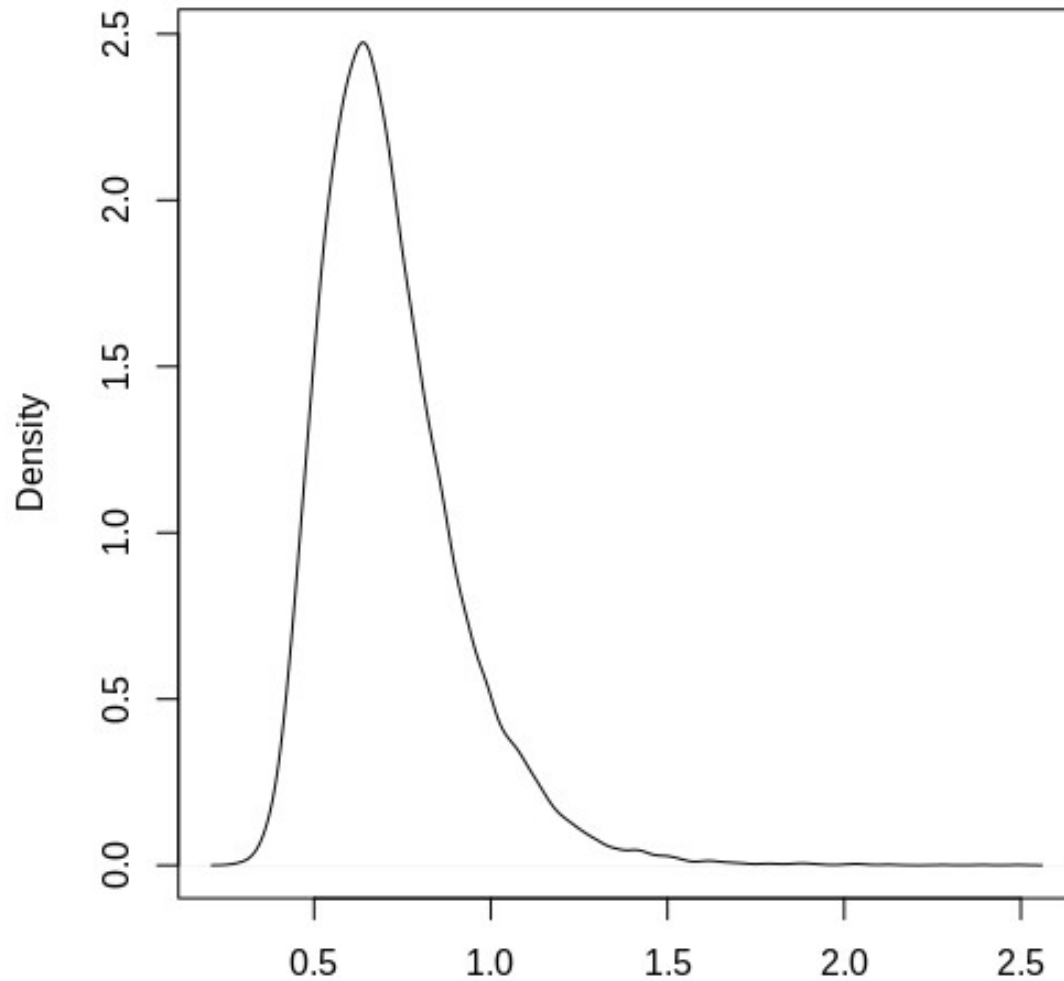
N = 16000 Bandwidth = 0.005278

Mean = 2.69

HPDI (0.89) = 2.62 : 2.75

# Results

`density.default(x = post3$sigma_v)`

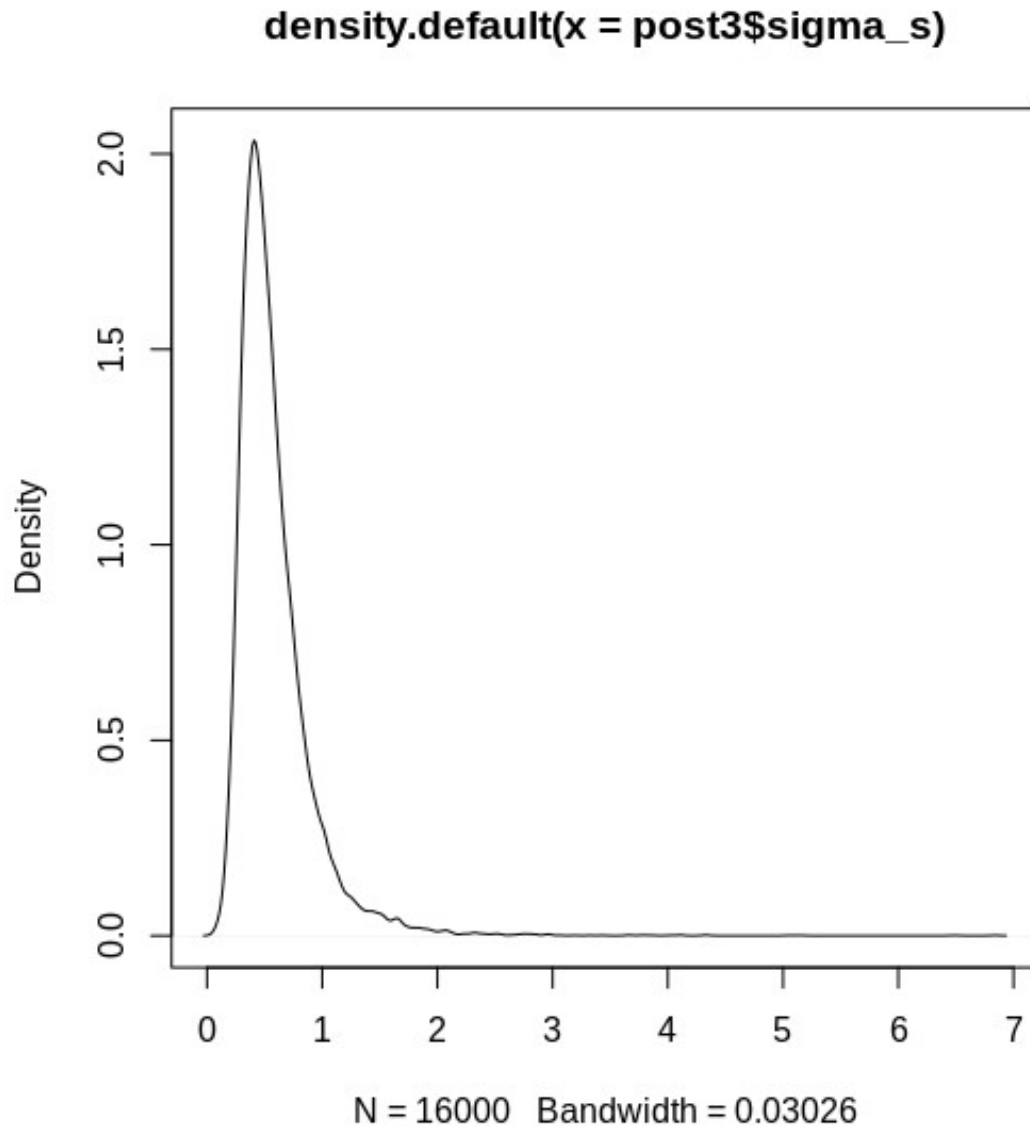


N = 16000 Bandwidth = 0.02281

Mean = 0.71

HPDI (0.89) = 0.43 : 0.98

# Results

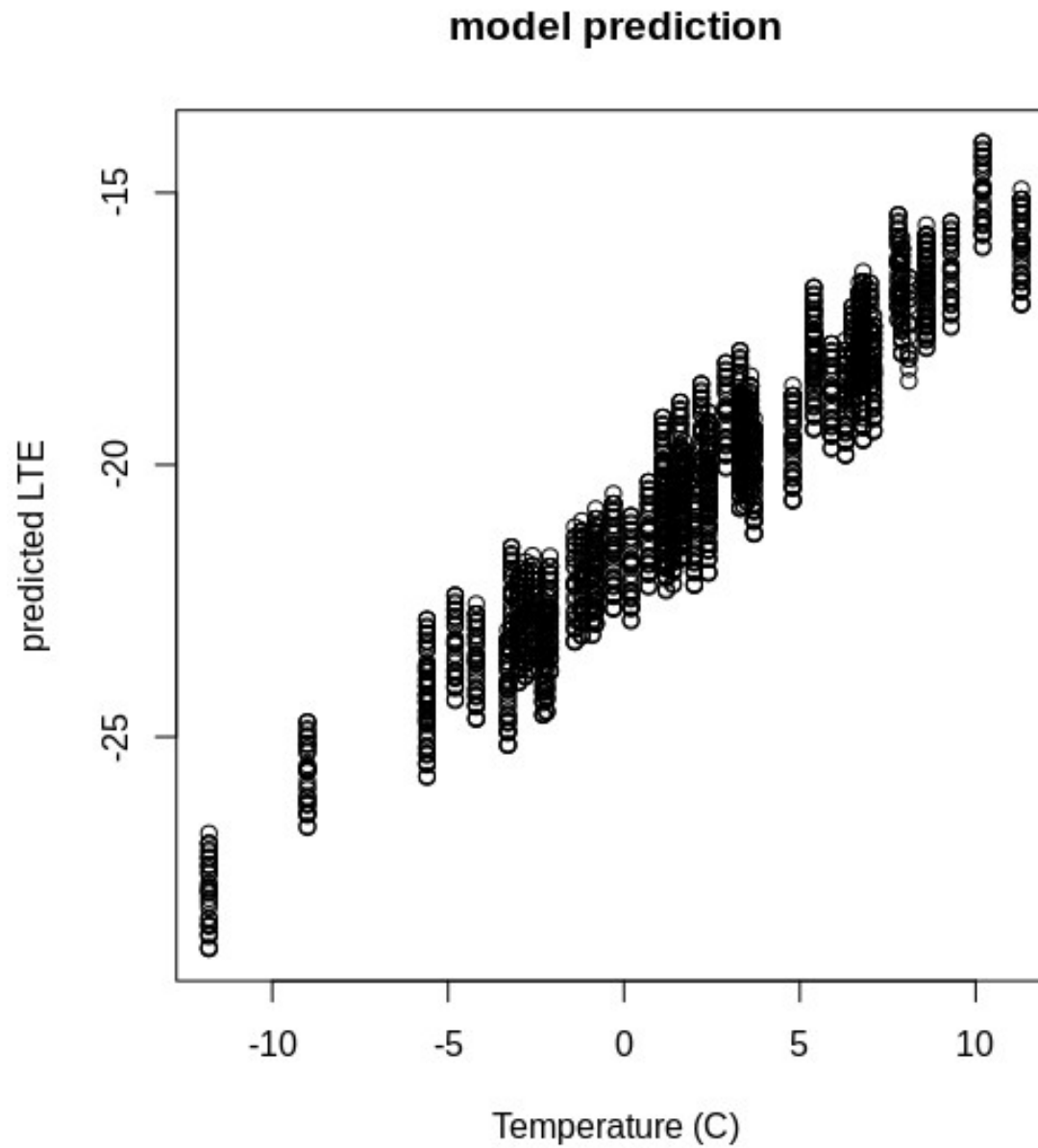


Mean = 0.58

HPDI (0.89) = 0.19 : 0.94

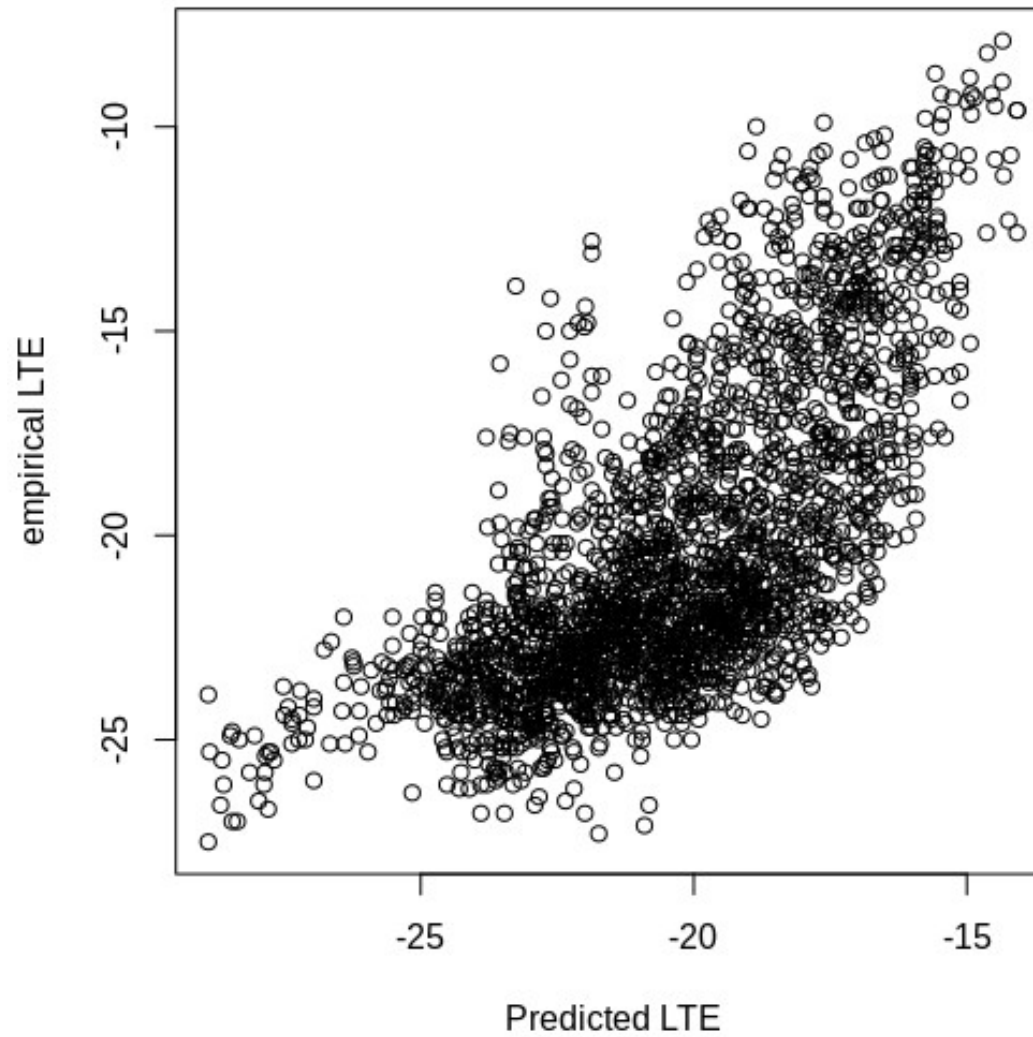


# Results

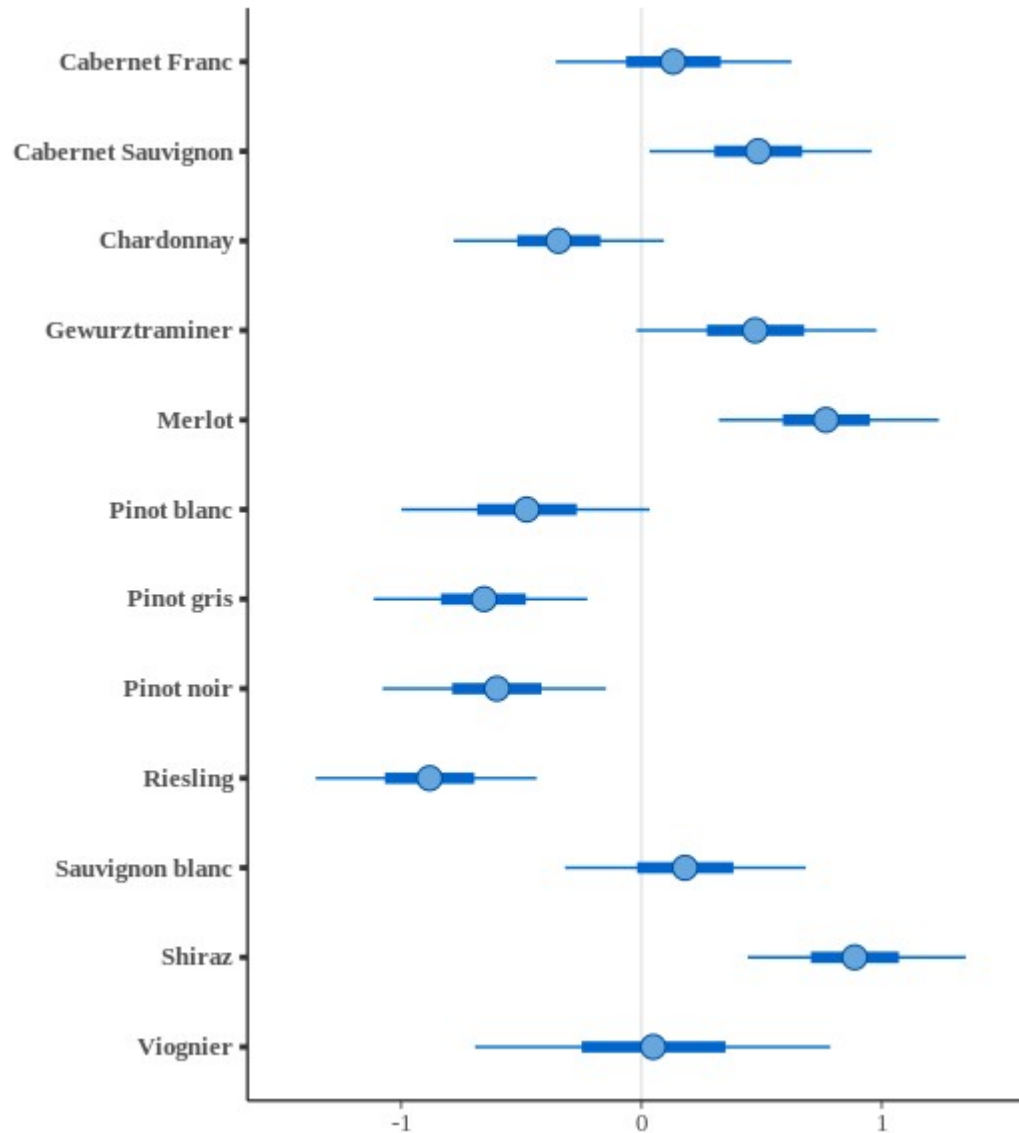


# Results

estimated lte against predicted lte

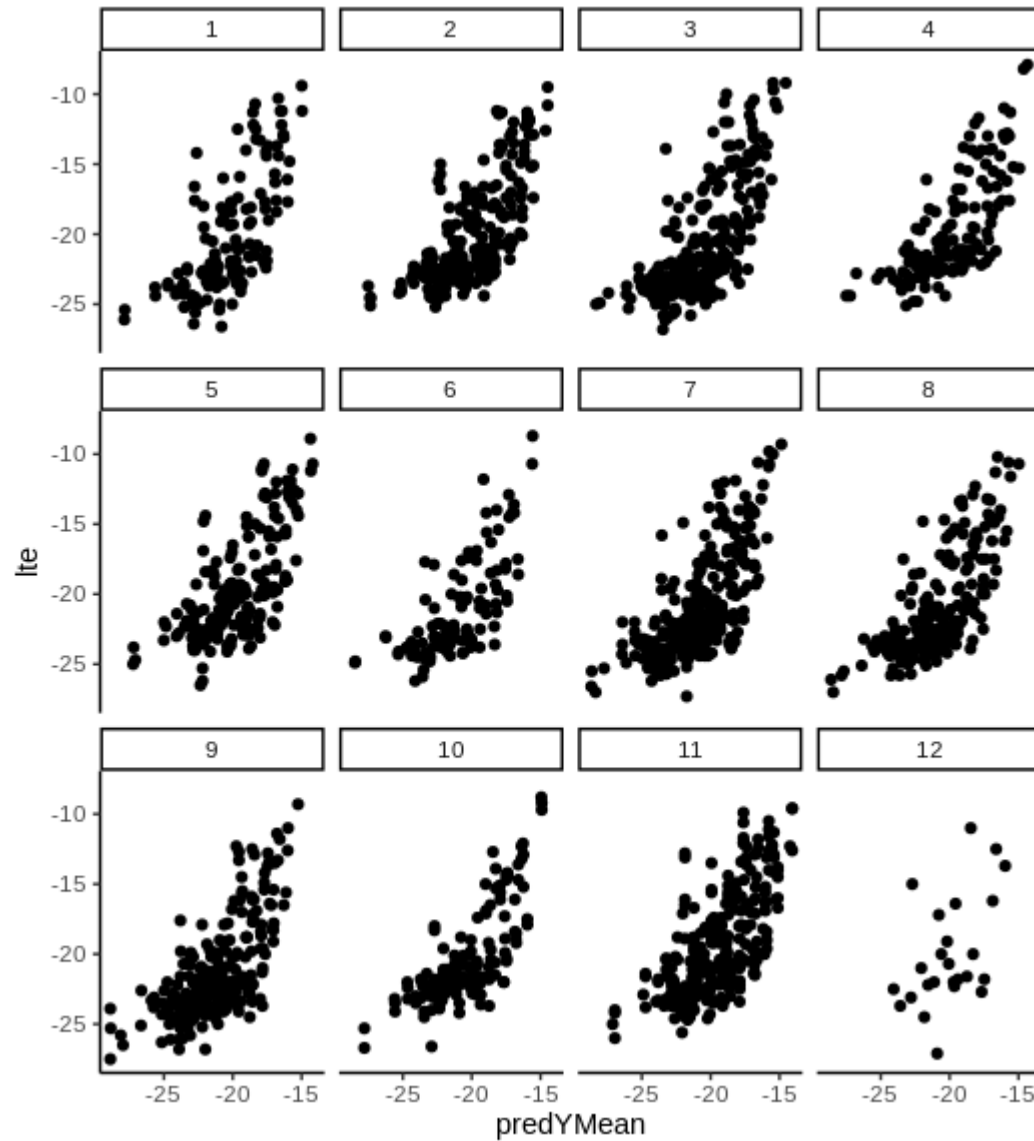


# Results



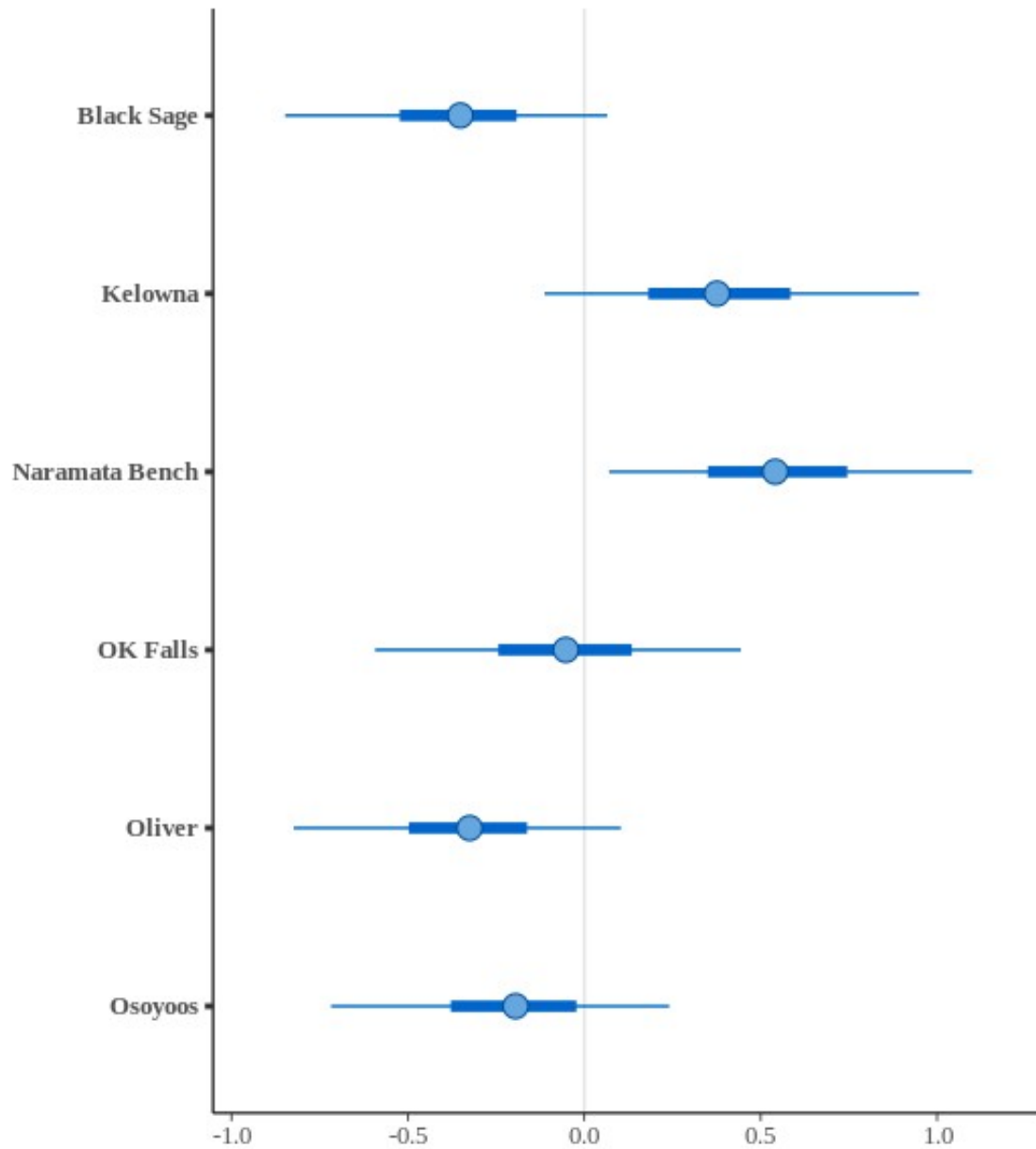
Variation by variety

# Results



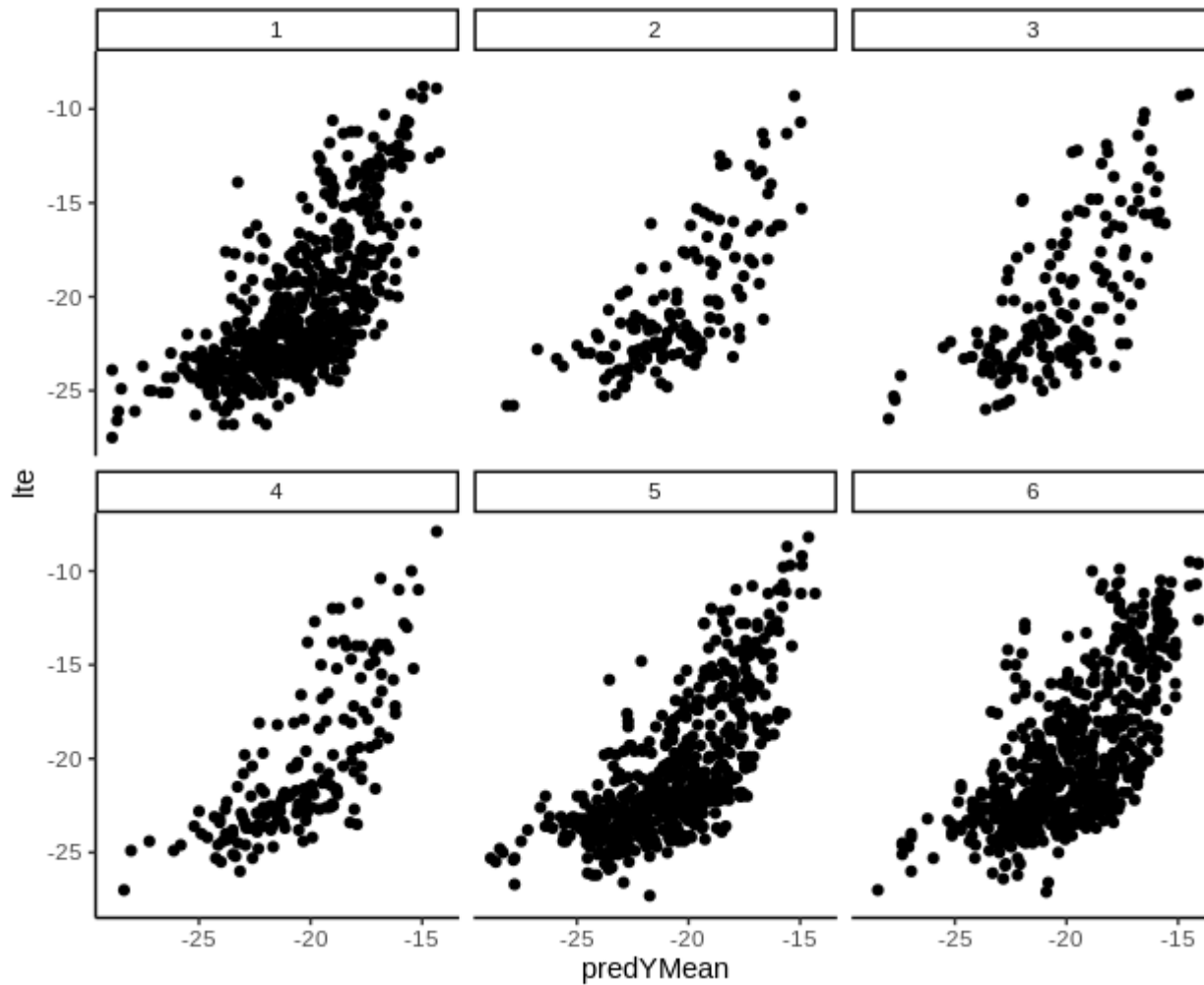
Variation by variety

# Results



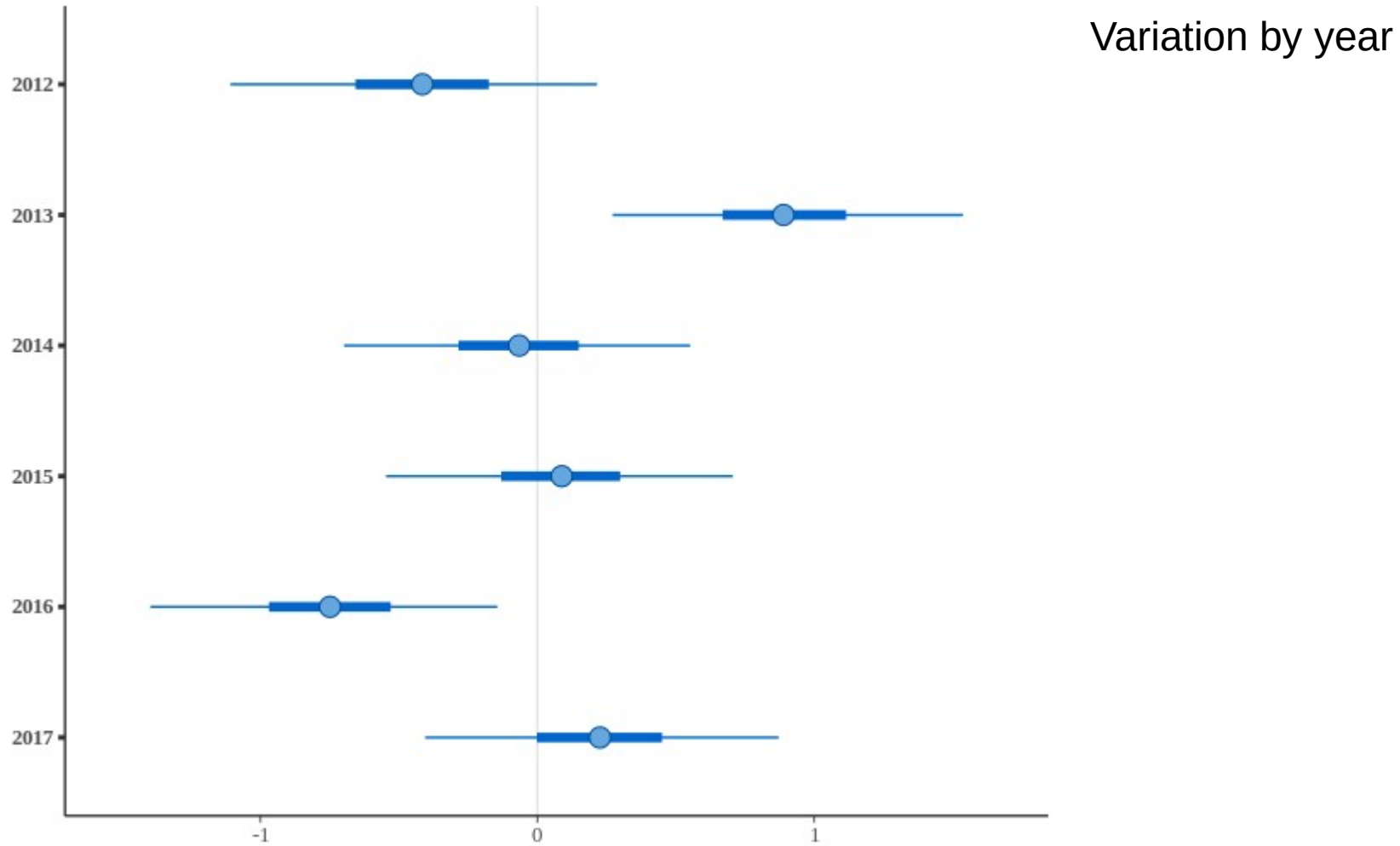
Variation by site location

# Results

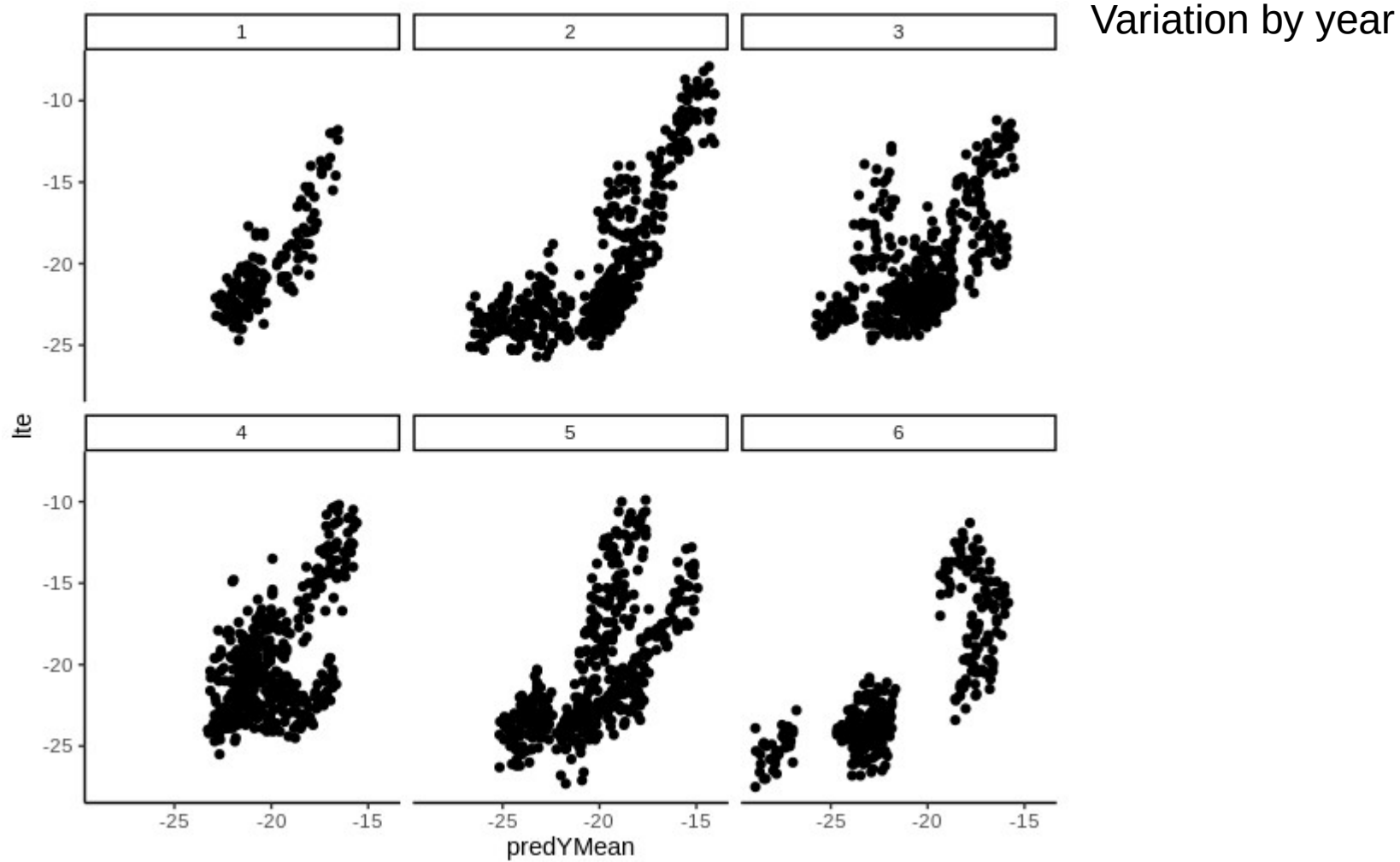


Variation by site location

# Results



# Results





# Plan for next model

- Include random slopes for variety
- Assume that varieties that are more cold tolerant should also have steeper slopes so they can get in and out of cold tolerance quicker
- Not including site at the moment

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

$$\mu_i = \alpha_{y_i} + \alpha_{v_i} + \beta_{y_i} \cdot \text{temp}_i$$

$$\begin{bmatrix} \alpha_v \\ \beta_v \end{bmatrix} \sim \text{MVNormal} \left( \begin{bmatrix} \alpha \\ \beta \end{bmatrix}, S \right)$$

$$S = \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} R \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix}$$

$$\alpha \sim \text{Normal}(-15, 12)$$

$$\beta \sim \text{Normal}(0, 1)$$

$$\sigma \sim \text{Normal}(0, 5)$$

$$\sigma_y \sim \text{Normal}(0, 5)$$

$$\sigma_\alpha \sim \text{Normal}(0, 5)$$

$$\sigma_\beta \sim \text{Normal}(0, 1)$$

$$R \sim \text{LKJcorr}(2)$$

# STAN code

- See `stan_model_slope.stan`

# Not working - warning

Left-hand side of sampling statement ( $\sim$ ) may contain a non-linear transform of a parameter or local variable.

If it does, you need to include a target += statement with the log absolute determinant of the Jacobian of the transform.

Left-hand-side of sampling statement:

`a_b_variety ~ multi_normal_lpdf(...)`

Parameter

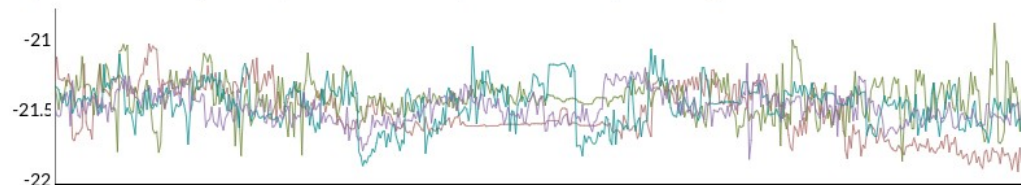
alpha\_g

Transformation

identity

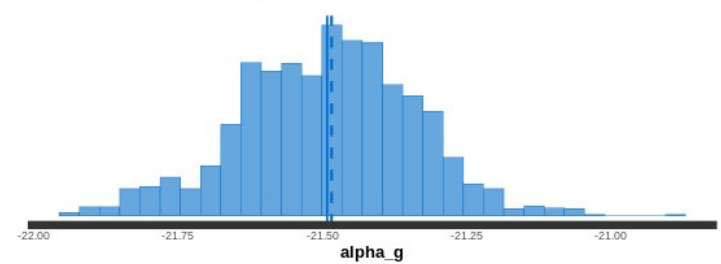
Transform

Use your mouse to select a range in the traceplot to zoom into. The other plots on the screen will update accordingly. Double-click to reset.

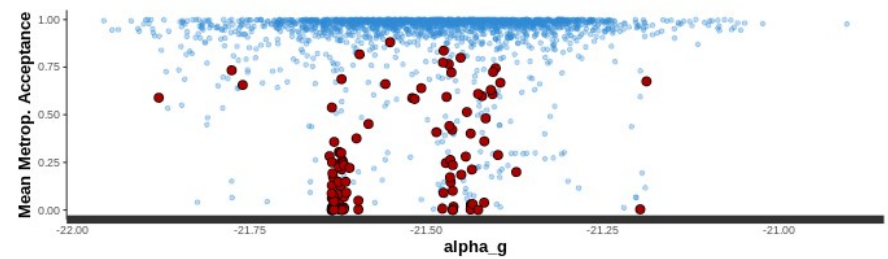
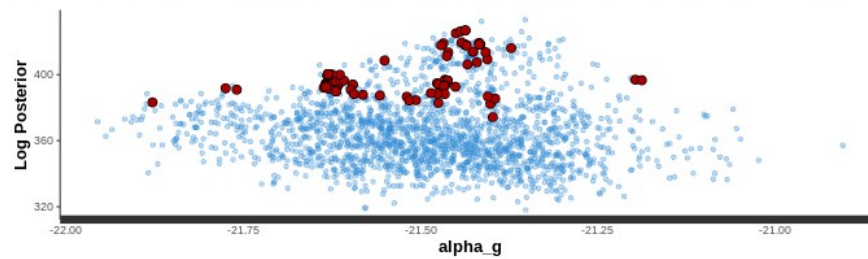


Parameter: alpha\_g

Lines are mean (solid) and median (dashed)



Large red points indicate which (if any) iterations encountered a divergent transition. Yellow indicates a transition hitting the maximum treedepth.

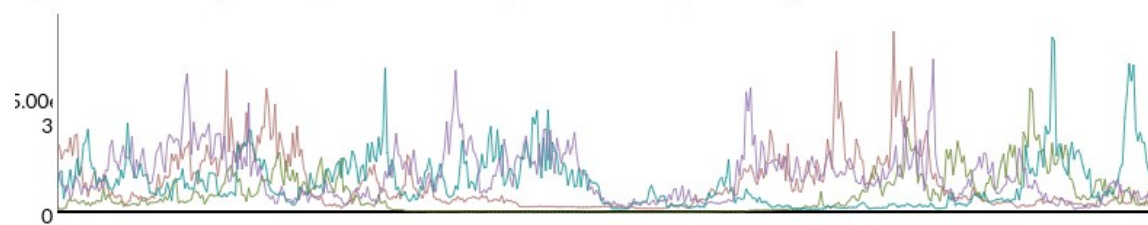


var\_sigma[2]

identity

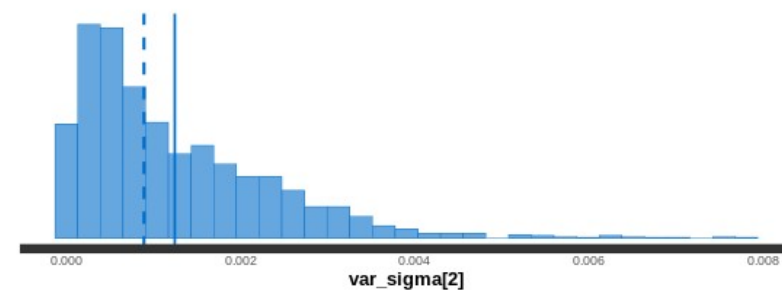
Transform

Use your mouse to select a range in the traceplot to zoom into. The other plots on the screen will update accordingly. Double-click to reset.

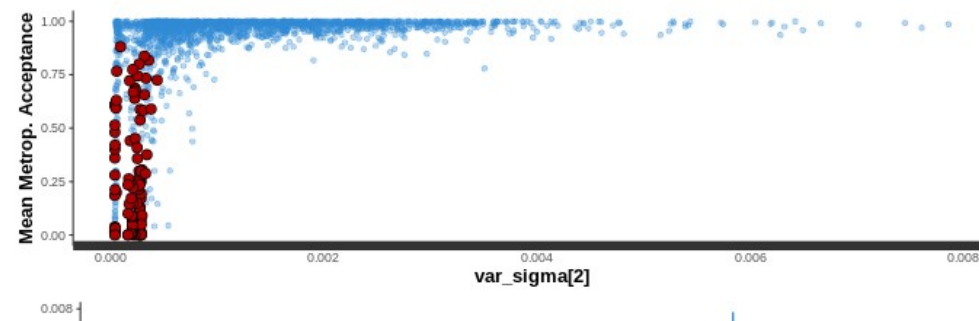
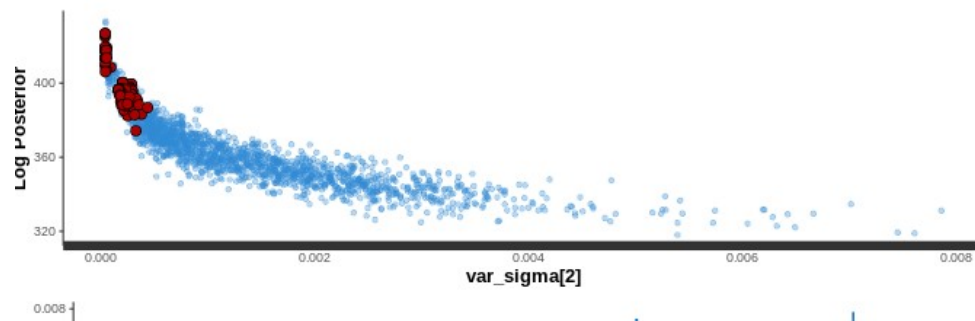


Parameter: var\_sigma[2]

Lines are mean (solid) and median (dashed)



Large red points indicate which (if any) iterations encountered a divergent transition. Yellow indicates a transition hitting the maximum treedepth.



Parameter

Rho[1,1]

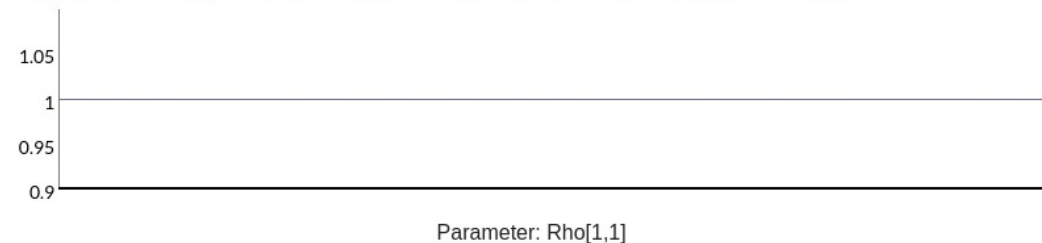
Transformation

identity

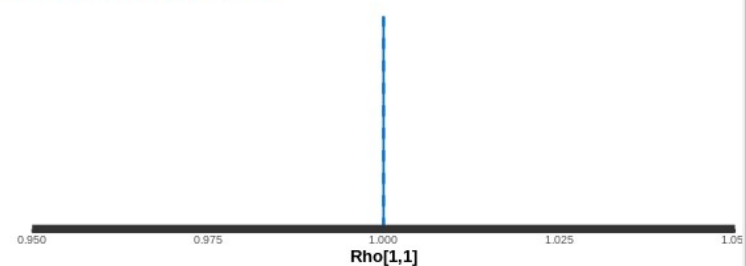
Transform

itions.

Use your mouse to select a range in the traceplot to zoom into. The other plots on the screen will update accordingly. Double-click to reset.



Lines are mean (solid) and median (dashed)



Large red points indicate which (if any) iterations encountered a divergent transition. Yellow indicates a transition hitting the maximum treedepth.

