

A background image of a foggy forest with many trees and a blue horizontal band across the middle.

Innovar Meeting

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We simulate the data considering two types of variables:

- ▶ Genotype (categorical variable)
- ▶ Temperature (numeric variable)

In the *temperature* variable, we apply a clustering process, such that

$$\mathbf{t} = \prod_{j=1}^J \pi_j \mathcal{N}(\mu_j, \sigma_j)$$

where π_j represents the weight of the j^{th} component, with $\sum_{j=1}^J \pi_j = 1$.



$$y_i = g_{gen_i} + e_{env_i} + \epsilon_i$$

where $i = 1, \dots, n$, $gen_i = 1, \dots, l$, $env_i = 1, \dots, J$

$$g_i \sim N(\mu_g, \sigma_g^2)$$

$$e_j \sim N(\mu_e, \sigma_e^2)$$

$$\epsilon_i \sim N(0, \sigma^2)$$

$$t_i \sim N(\mu_{env_i}, \omega^2)$$

$$env_i \sim Cat(\pi_{1:J})$$

$$\mu_j \sim N(0, 100^2), \omega^2 \sim IG(\alpha, \beta), \pi \sim Dirichlet(1)$$



The configuration of our simulation was

- ▶ 6 genotypes
- ▶ 3 groups
- ▶ 60 observations
- ▶ Mean of the groups: -5,10,30.



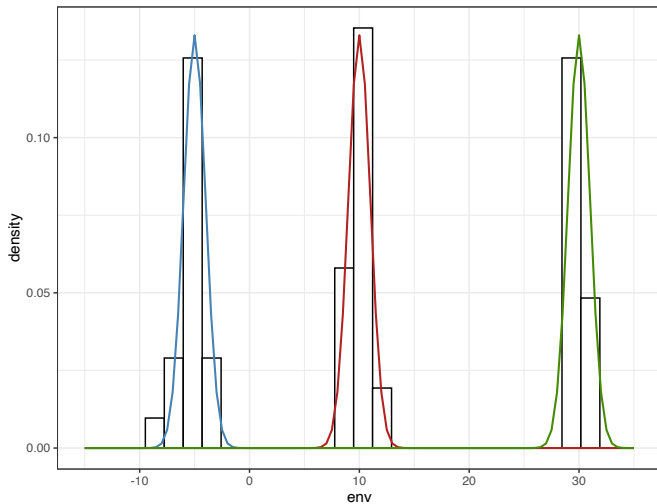
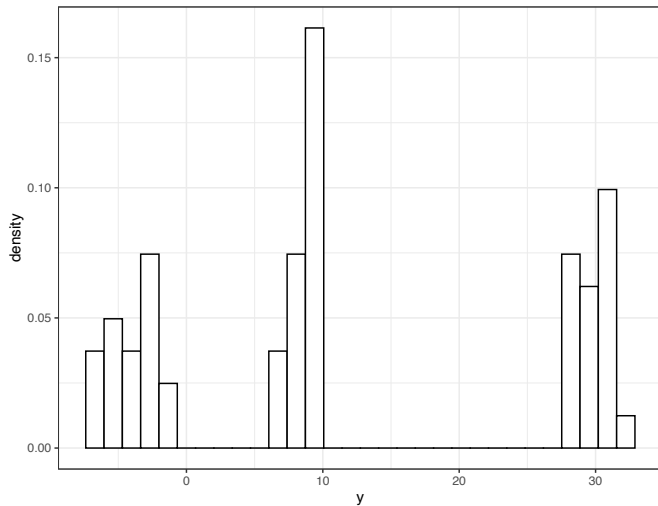


Figure: Temperature.



Figure: y .

The configuration of the second simulation was

- ▶ 3 groups of genotypes
- ▶ 3 groups of environments
- ▶ 100 observations
- ▶ Mean of the groups (env): -5,10,30.
- ▶ Mean of the groups (gen): -1,0,1.



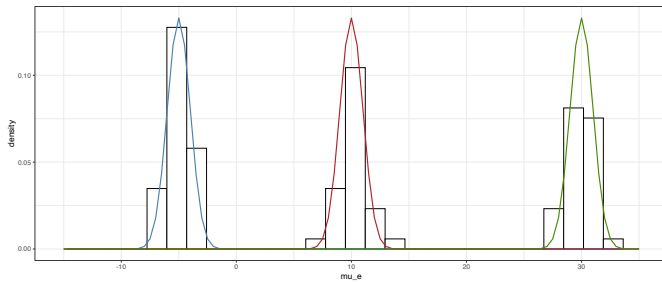


Figure: Temperature.

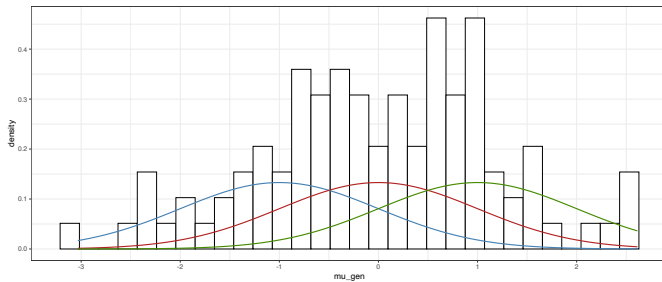


Figure: Temperature.



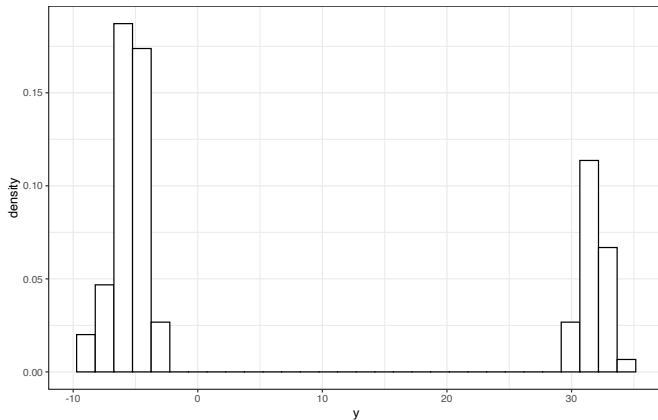


Figure: y .

