

New Model:

- no longer compute breeding values as with the single locus model, because we do not know the locations in the genome that are relevant for a given trait of interest.
- all that can be done is to predict breeding values based on phenotypic information, but using the developed genetic model.

- Principle of prediction:
predicted breeding value (\hat{u})

$$\hat{u} = b * (y - \mu)$$

Diagram illustrating the components of the prediction equation:

- \hat{u} : predicted breeding value
- b : Step 2 (indicated by a green arrow)
- y : Observation (circled in red, with a red arrow pointing to the word "Observation")
- μ : appropriate mean performance (circled in green, with a green arrow pointing to the text)
- Step 1: A bracket under the term $(y - \mu)$ is labeled "Step 1" in green.