New Model

$$y_{ij} = \mu + u_i + e_{ij}^*$$

- Properties of components:
  - μ: contains influences of known environment where observation y_{ij} was recorded (Herd, season, age, ...)
  - e_{ij}^*: random residuals corresponding to the unknown non-genetic effects that influence y_{ij}. Parameter of interest but the residual variance σ_e^2.
  - u_i: Effect that captures the sum of all single-loci breeding values:

$$u_i = BV_{i,A} + BV_{i,B} + BV_{i,C} + \dots$$

Sum of a large number of small effects

- $E(u_i) = 0$ because $E(BV_{i,A}) = E(BV_{i,B}) = \dots = 0$
- $\text{var}(u_i) = \sigma_{u_i}^2 = \sigma_{BV_{i,A}}^2 + \sigma_{BV_{i,B}}^2 + \dots$

Because, we want to include the total genetic-additive variance in our model, u_i must be a random effect.