Genomic BLUP

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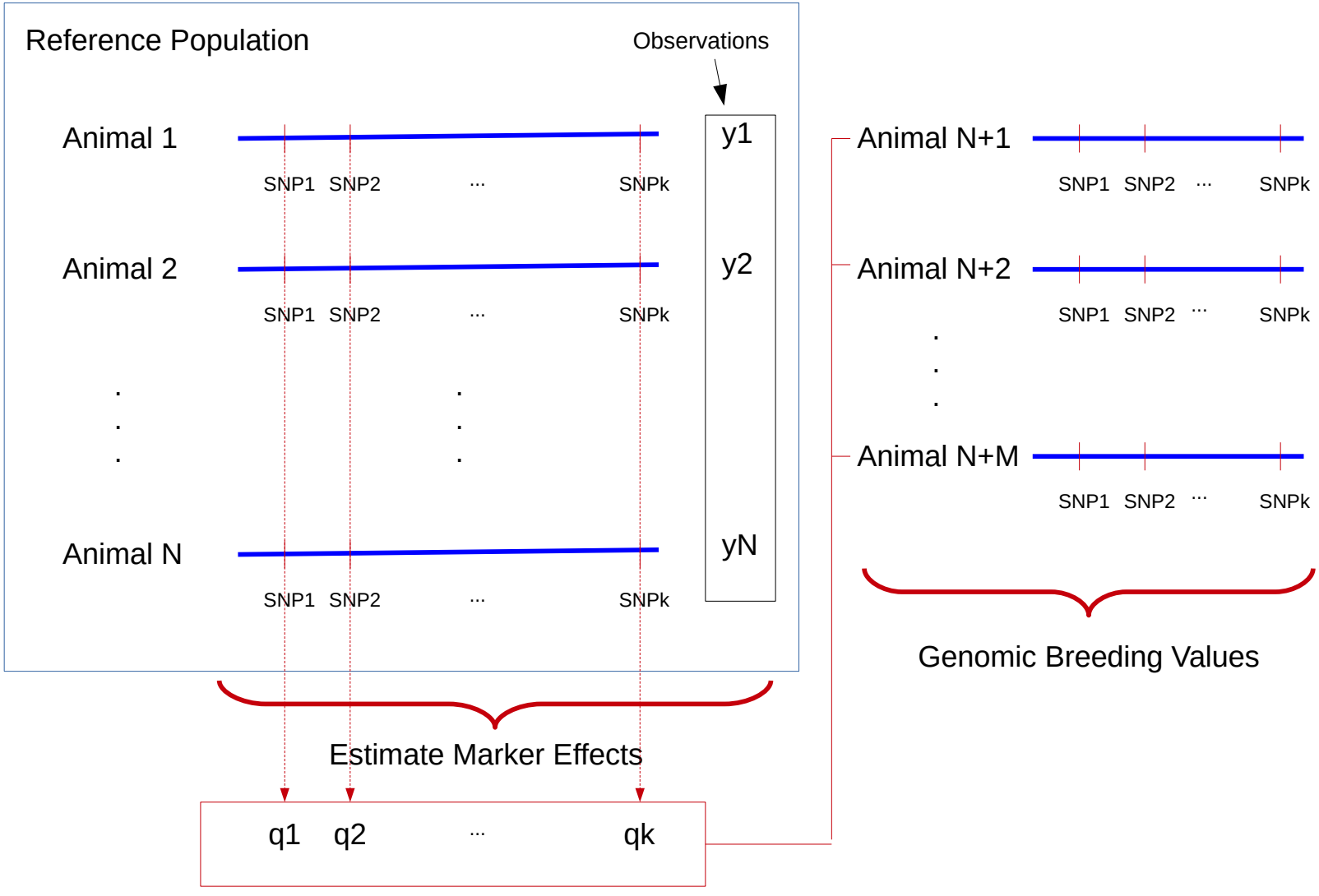
Genomic BIUP

1. Marker effect models (MEM): Linear mixed effects models with marker effects as random effects
2. Breeding-value based models (BVM): Genomic breeding values as random effects

Marker Effect Models



Marker Effect Models II

- Model

$$y = 1_n\mu + Mq + e$$

- Solution

$$\begin{bmatrix} 1_n^T 1_n & 1_n^T M \\ M^T 1_n & M^T M + \lambda_q * I \end{bmatrix} \begin{bmatrix} \hat{\mu} \\ \hat{q} \end{bmatrix} = \begin{bmatrix} 1_n^T y \\ M^T y \end{bmatrix}$$

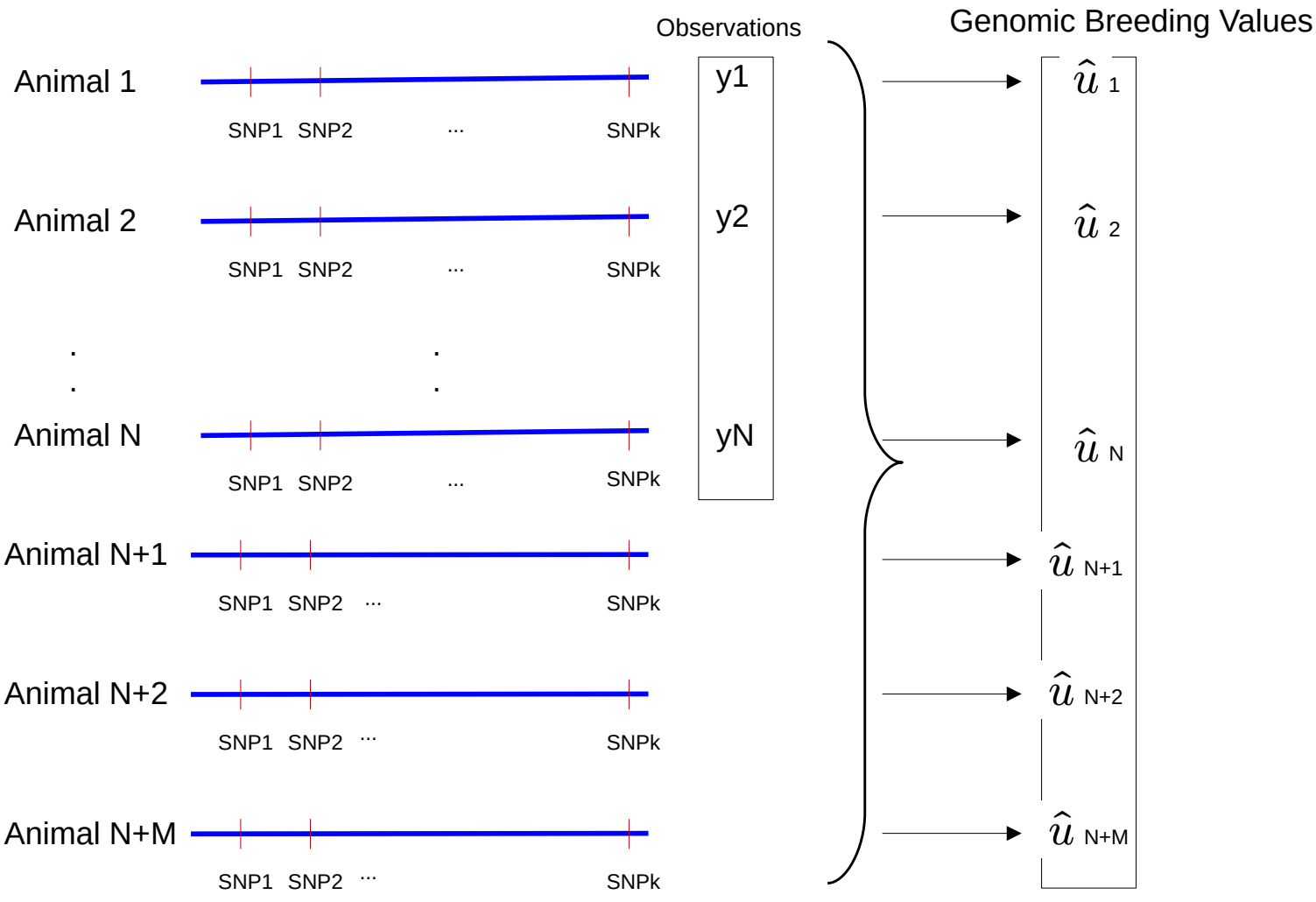
with $\lambda_q = \sigma_e^2/\sigma_q^2$.

Genomic Breeding Values from MEM

For animal i with genotype information stored in row i of Matrix M, predicted genomic breeding value $\hat{u}_i$ is

$$\hat{u}_i = M_i \cdot \hat{q}$$

Breeding Value Models



Breeding Value Models II

- Model

$$y = Xb + Zu + e$$

- Solution

$$\begin{bmatrix} X^T X & X^T Z \\ Z^T X & Z^T Z + \lambda_u * G^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^T y \\ Z^T y \end{bmatrix}$$

with $\lambda_u = \sigma_e^2 / \sigma_u^2$.

Genomic Relationship Matrix

$$u = U \cdot q$$

with $U = M - P$ and P has columns $2p_j - 1$ with p_j being the frequency of the positive allele at locus j.

$$var(u) = G * \sigma_u^2$$

$$var(u) = UU^T * \sigma_q^2$$

$$\sigma_u^2 = 2 \sum_{j=1}^{m} p_j(1 - p_j)\sigma_q^2$$

Genomic Relationship Matrix II

$$var(u) = G * \sigma_u^2 = UU^T \sigma_q^2$$

$$G = \frac{UU^T}{2 \sum_{j=1}^{m} p_j(1 - p_j)}$$

How Does GBLUP Work

How do we get predicted genomic breeding values for young animals

$$\begin{bmatrix} X^T X & X^T Z & 0 \\ Z^T X & Z^T Z + G^{(11)} & G^{(12)} \\ 0 & G^{(21)} & G^{(22)} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_1 \\ \hat{u}_2 \end{bmatrix} = \begin{bmatrix} X^T y \\ Z^T y \\ 0 \end{bmatrix}$$

$$\hat{u}_2 = -\left(G^{22}\right)^{-1} G^{21} \hat{u}_1$$