

- Result of Step 1: Estimates  $\hat{g}$  for marker effects
- Step 2: From estimates of marker effects, genomic breeding values are computed by summing up appropriate marker effects for each genotyped animal.

Animal 1: Genotype:

$$G_1 G_2 \quad H_1 H_2 \quad \dots \quad I_1 I_1$$

$$0 \cdot \hat{g}_1 + 0 \cdot \hat{g}_2 + \dots + 1 \cdot \hat{g}_k = \hat{g}_1$$

Direct genomic  
breeding value  
for animal 1.

Animal 2:  $G_2 G_2 \quad H_1 H_1 \quad \dots \quad I_2 I_2$

$$(-1) \cdot \hat{g}_1 + 1 \cdot \hat{g}_2 + \dots + (-1) \cdot \hat{g}_k = \hat{g}_2$$

Animal N: --

$\hat{g}_v$