



C)

Step 1: Estimate posterior genetic liability for each individual using Gibbs sampling

$$\hat{l}_g = E \left(l_g \mid \begin{array}{c} \text{Case-control status} \\ \text{for genotyped} \\ \text{individual} \end{array} ; \begin{array}{c} \text{Family history} \\ \text{(case-control} \\ \text{status)} \end{array} ; \underbrace{\begin{array}{c} \text{Gender} \quad \text{Age} \quad \text{Birth year} \end{array}}_{\text{For all family members}} ; \begin{array}{c} \text{Population} \\ \text{prevalence by age,} \\ \text{sex, and birth year} \end{array} \right)$$

Step 2: Perform GWAS (BOLT-LMM) with estimated genetic liability as outcome

$$\hat{l}_g = x_j \beta_j + \dots$$

Predicted genetic liability

Effect of the j^{th} genetic variant

Additional covariates, PCs, sex, age, random effects, etc.