Bayesian multiple logistic regression improves loci prioritization and finemapping in case-control GWAS

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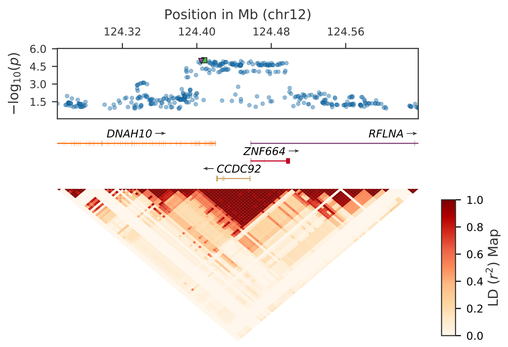
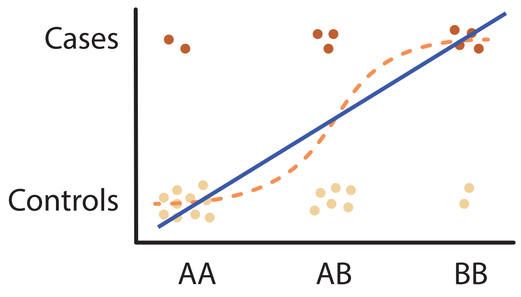
https://github.com/soedinglab/b-lore

1. Post-GWAS analyses using multiple regression could not utilize the benefits of logistic model



Linkage disequilibrium ☹



Linear model ☹

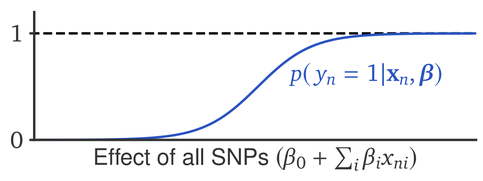
Challenges for using multiple logistic regression:

- The integration for the maximum likelihood cannot be solved analytically.
- MCMC sampling is computationally intractable.
- Solutions using Laplace and linear approximations essentially makes it a linear model.
- Metaanalysis requires knowledge of LD structure of the population.
- Limited to application on single genome-wide significant locus (cannot prioritize loci).

2. B-LORE uses logistic model and sparsity-inducing priors

Probability of n^{th} individual with genotype $\mathbf{x}_n$ to be diseased:

$$p\left(y_n = 1 \mid \mathbf{x}_n, \boldsymbol{\beta}\right) = \frac{\exp\left(\boldsymbol{\beta}^{\mathsf{T}}\mathbf{x}_n\right)}{1 + \exp\left(\boldsymbol{\beta}^{\mathsf{T}}\mathbf{x}_n\right)}$$



Prior on effect sizes given hyperparameters π and σ,

$$p\left(\beta_i \mid \pi, \sigma\right)$$

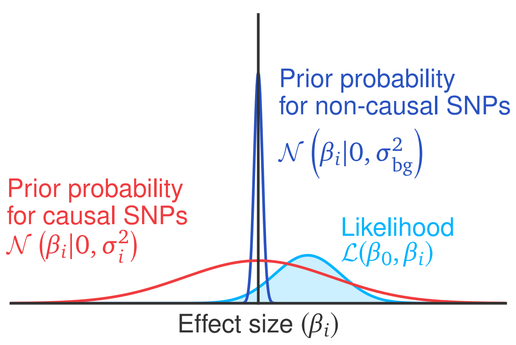
$$= \overbrace{\pi\,\mathcal{N}\left(\beta_i \mid 0, \sigma^2\right)}^{\text{Causal}} + \overbrace{(1-\pi)\,\delta_0}^{\text{Non-causal}}$$

$$= \sum_{z_i=0,1} \pi^{z_i}(1-\pi)^{(1-z_i)}\mathcal{N}\left(\beta_i \mid \mathbf{0}, \mathrm{diag}(\boldsymbol{\sigma}^{\mathbf{2}}_{\mathbf{z},\mathbf{i}})\right)$$

$$= \sum_{z_i=0,1} p\left(\mathbf{z} \mid \pi\right)\mathcal{N}\left(\beta_i \mid \mathbf{0}, \mathrm{diag}(\boldsymbol{\sigma}^{\mathbf{2}}_{\mathbf{z},\mathbf{i}})\right)$$

where, $\sigma^2_{\mathbf{z},i} = z_i\sigma^2$

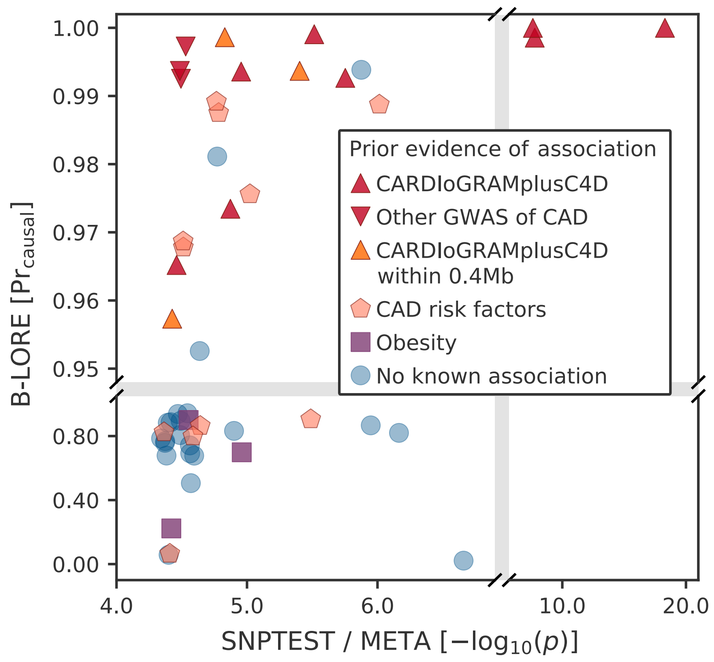
$z_i \in \{0,1\} \Rightarrow$ Indicator variable of causality

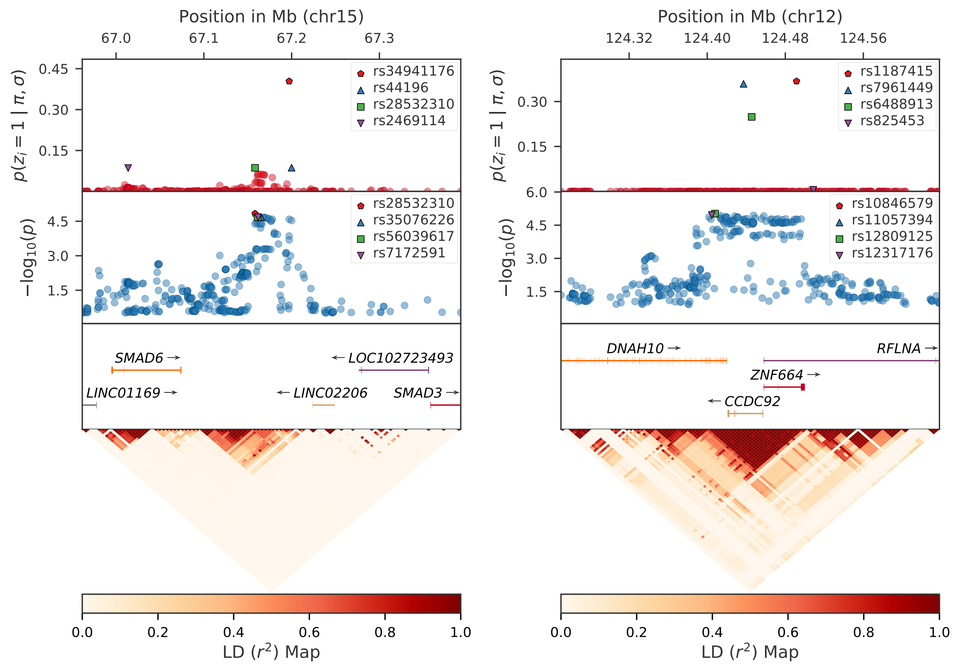


- $z_i = 1$ SNP i is causal
- $z_i = 0$ SNP i is non-causal

3. Latex equation plate

5. Meta-analysis example: B-LORE discovers novel loci associated with coronary artery disease





Meta-analysis of 5 cohorts, Germal Myocardial Infarction Family Studies (GerMIFS I-V) – 6234 cases and 6848 controls.

4. Inference

Prediction of causality of each locus.

The probability for a locus to be causally associated with the disease is

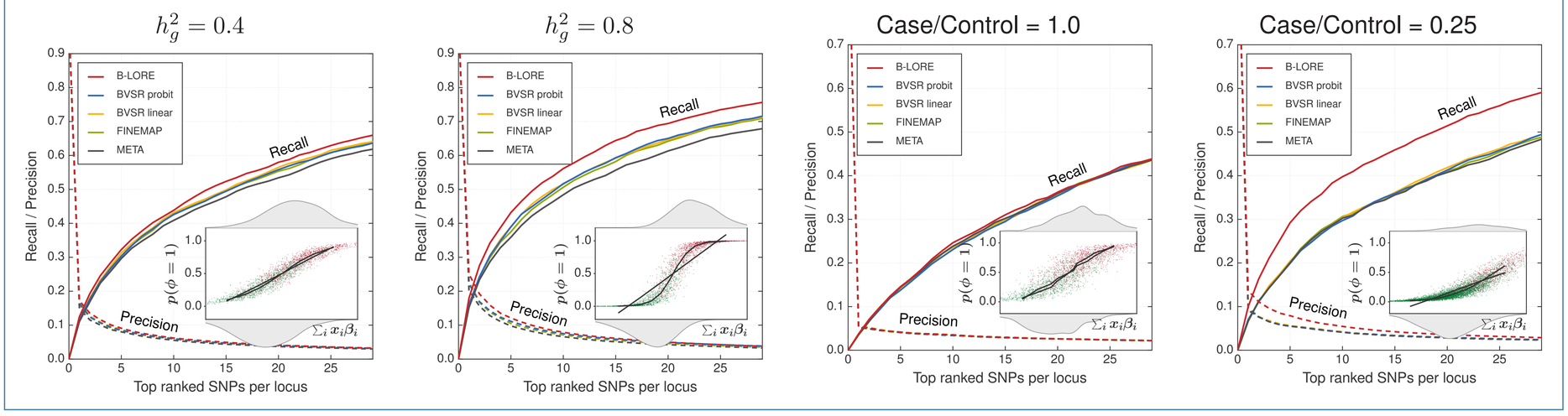
$$\begin{aligned}\text{Pr}_{\text{causal}} &= p\left(\text{locus is causal} \mid \mathbf{y}, \mathbf{X}, \hat{\pi}, \hat{\sigma}\right)\\ &= 1 - p\left(\mathbf{z} = 0 \mid \mathbf{y}, \mathbf{X}, \hat{\pi}, \hat{\sigma}\right)\end{aligned}$$

Statistical finemapping of causal variants.

The posterior probability for SNP i to be causal is

$$p\left(z_i = 1 \mid \mathbf{y}, \mathbf{X}, \hat{\pi}, \hat{\sigma}\right)$$

6. Examples of non-linear regimes in case-control GWAS



7. References

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2. Servin *et al.* PLOS Genet 2007, doi:10.1371/journal.pgen.0030114
3. Guan *et al.* Ann Appl Stat 2011, doi:10.1214/11-AOAS455
4. CARDIoGRAMplusC4D Nat Genet 2015, doi:10.1038/ng.3396

8. Acknowledgement

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