

Bayesian multiple logistic regression for metaanalysis in GWAS (B-LORE)

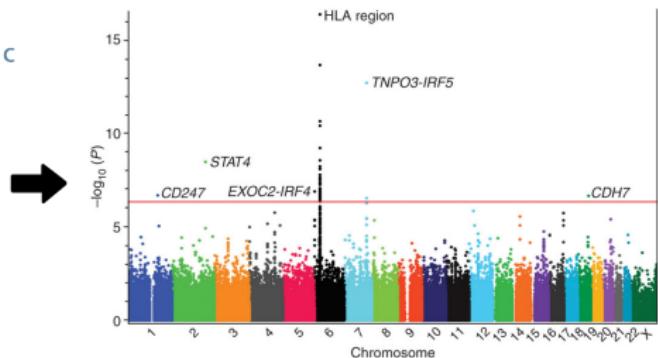
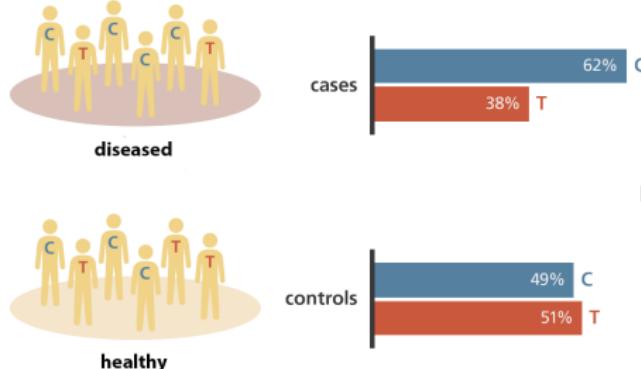
Saikat Banerjee

Max Planck Institute for Biophysical Chemistry

JULY 21, 2017



Genome-wide association studies (GWAS)



- ▶ Discovered thousands of variants associated with complex diseases

Association tests in GWAS

# of samples	Genotype (x)						Phenotype
	..	GA	TT	AT	GC	AC	..
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..	AA	TT	AA	GC	AA	..	y_3
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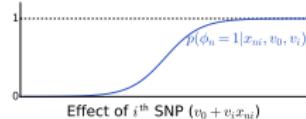
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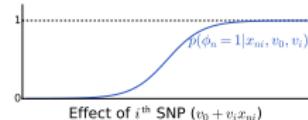
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- ▶ Is the coefficient v_i significantly different from 0? \Rightarrow P-values



Strengths

- Straightforward
- Computationally fast
- Conservative
- Easy to interpret

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Challenges

- Linkage disequilibrium
- Correlation vs coupling
- Genetic networks
- Low effect sizes

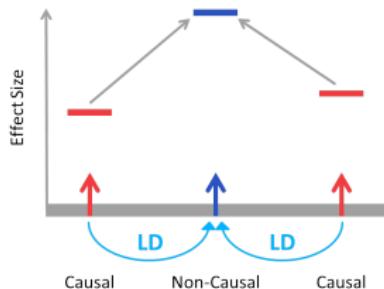
Univariate methods

Strengths

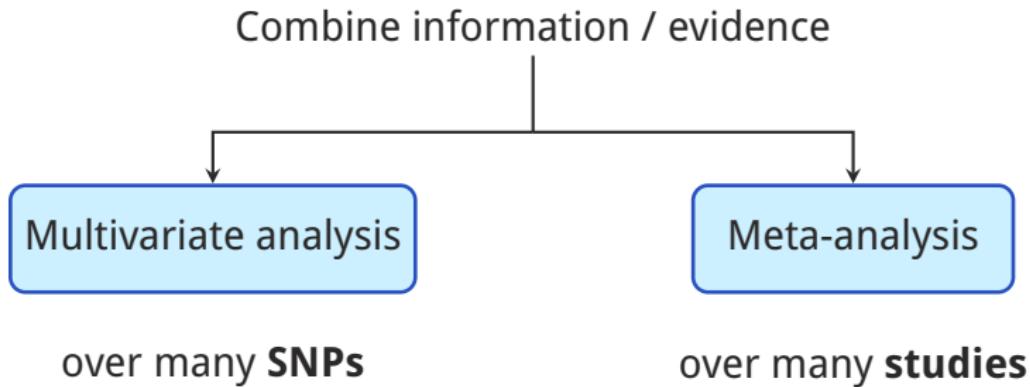
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How GWAS have improved?

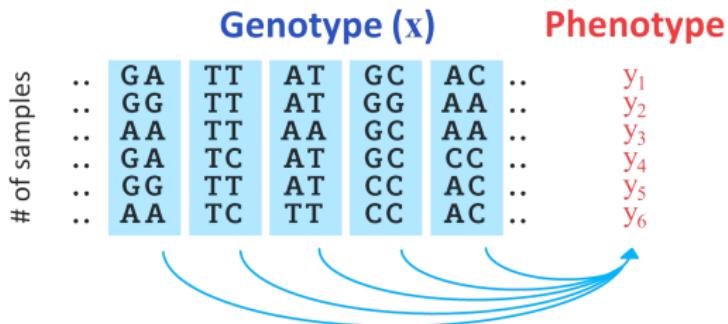


Multivariate methods

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Multivariate methods



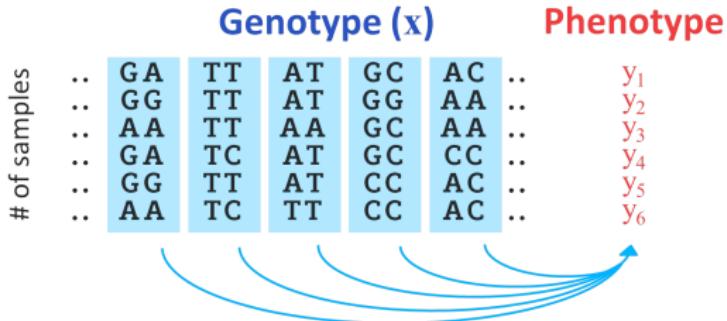
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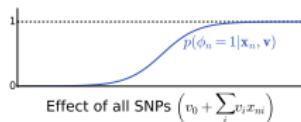
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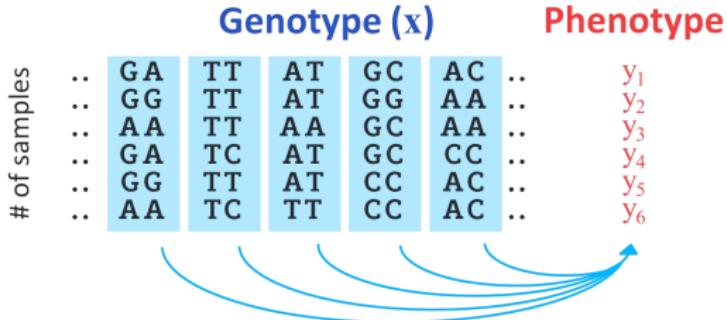


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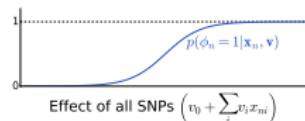
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- ▶ Multivariate methods perform better than univariate methods

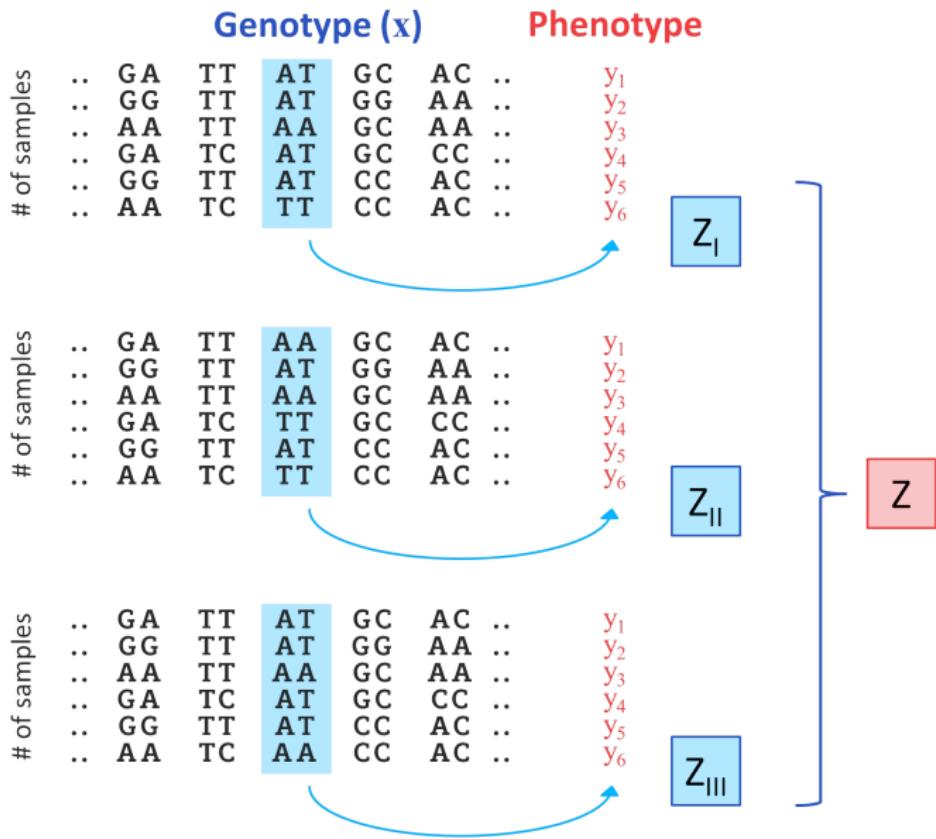


Meta-analysis

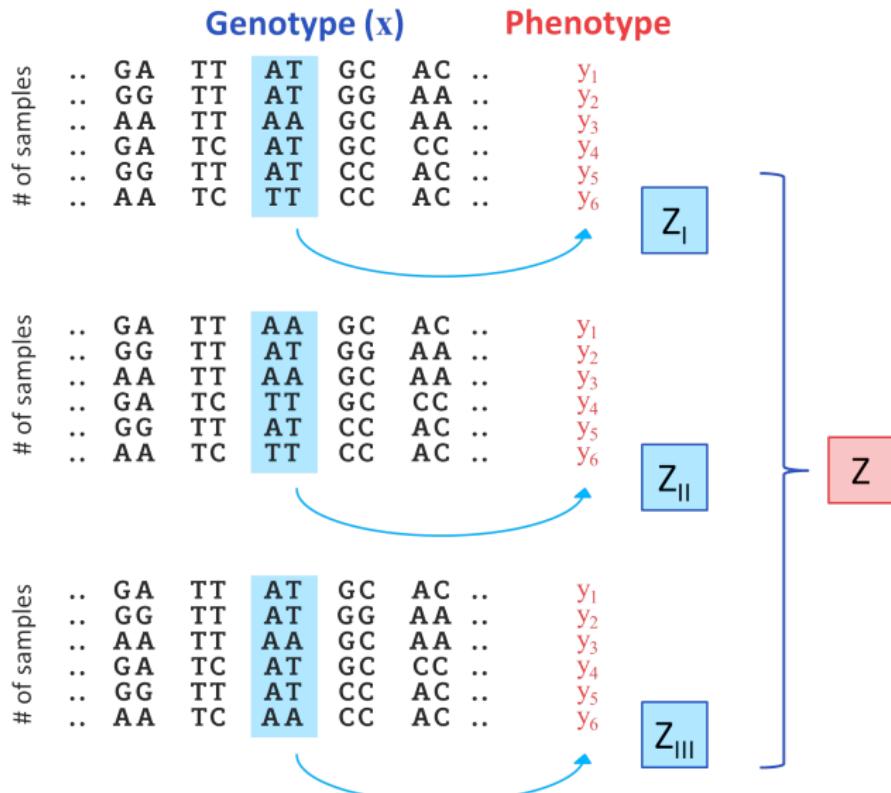
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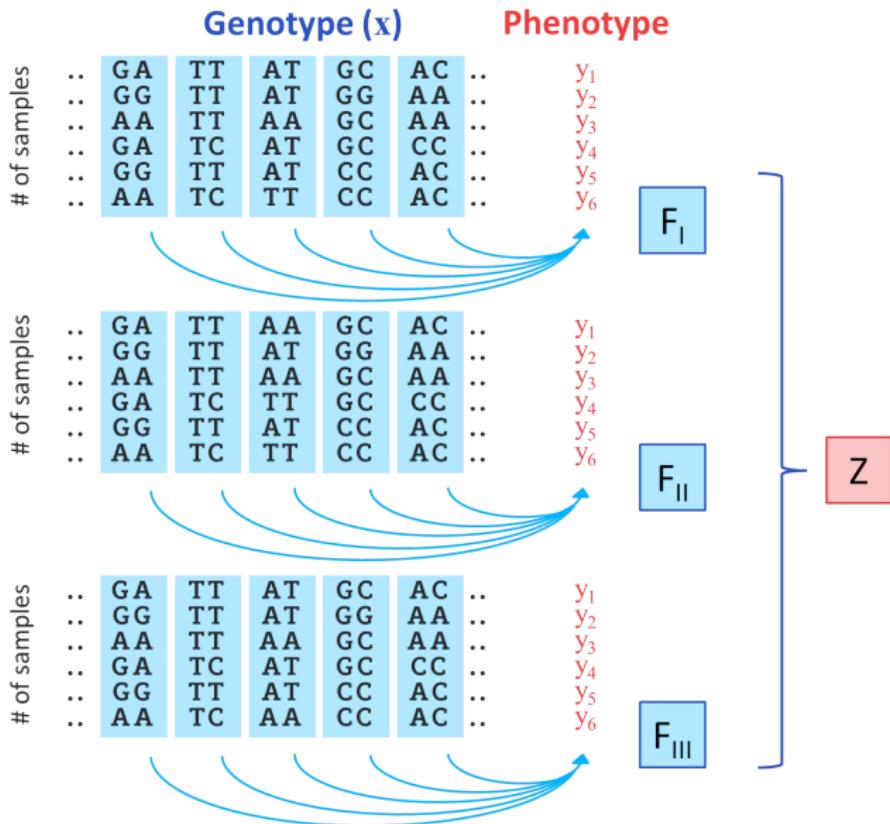
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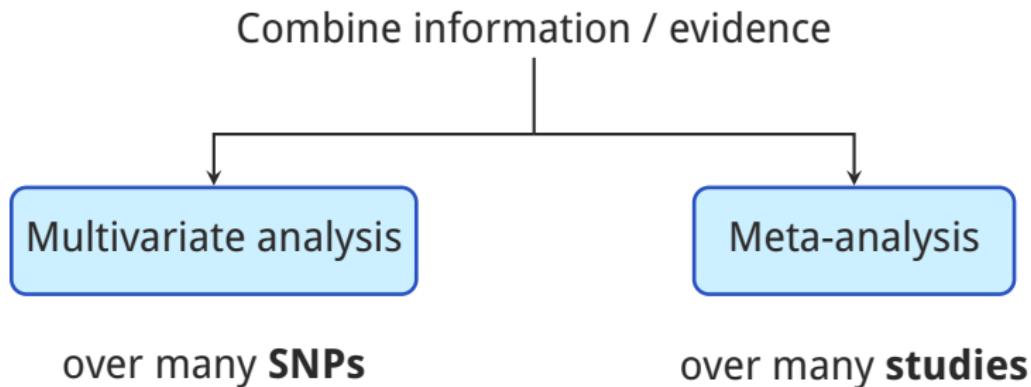
Goal of our method



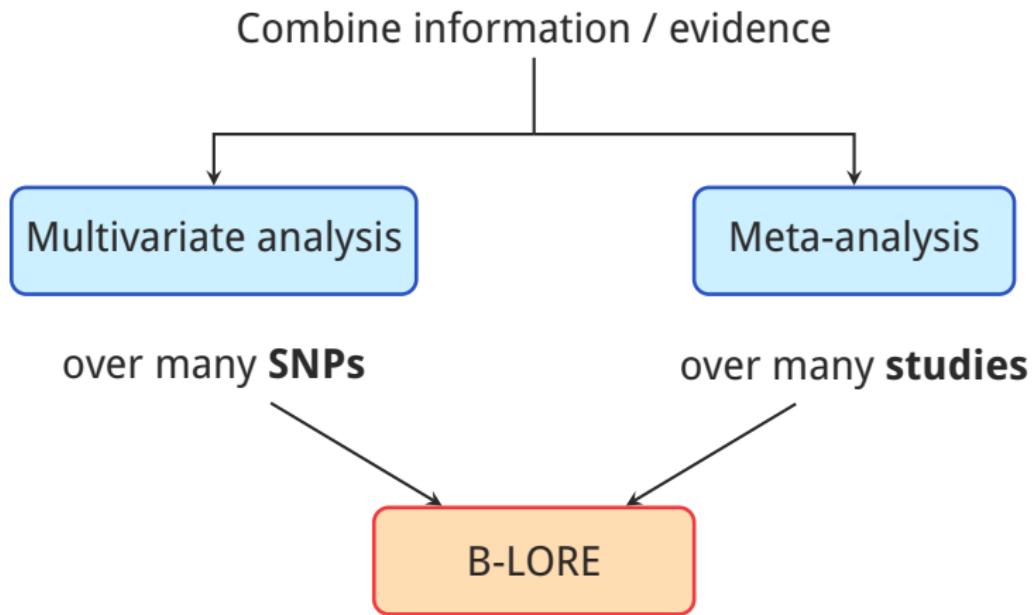
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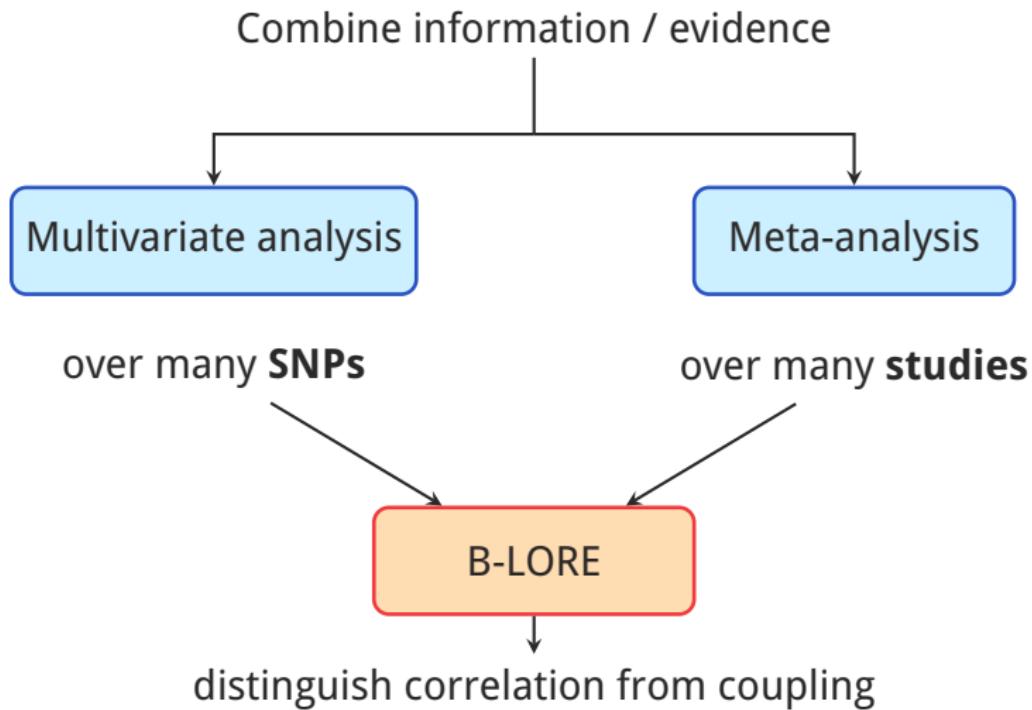
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Bayesian variable selection regression (BVSR)

BIMBAM

Servin and Stephens, *PLoS Genetics* 2007
Guan and Stephens, *Ann. Appl. Stats.* 2011

$$y_n = v_0 + \sum_i v_i x_{ni} + \epsilon, \quad \text{with} \quad \epsilon \sim \mathcal{N}(0, \tau^{-1}) \quad \text{Quantitative phenotype}$$

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- ▶ Likelihood for N patients:

$$p(\mathbf{y} | \mathbf{x}, \mathbf{v}, \tau) = \mathcal{N}(\mathbf{y} | \mathbf{x}^\top \mathbf{v}, \tau^{-1} \mathbb{I})$$

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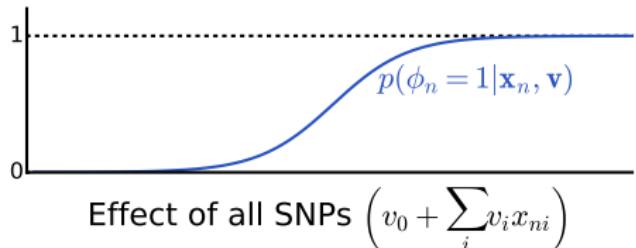
- ▶ Number of SNPs \gg samples → Overfitting
- ▶ Effective priors on \mathbf{v} for sparsity

Bayesian variable selection logistic regression (BVSLR)

B-LORE

Banerjee and Söding, *manuscript prepared 2017*

$$p(\phi_n = 1 | \mathbf{x}_n, \mathbf{v}) = \text{lf}\left(v_0 + \sum_i v_i x_{ni}\right)$$

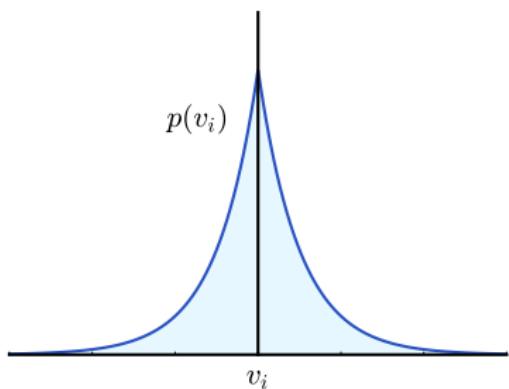


- Likelihood for N patients:

$$p(\boldsymbol{\phi} | \mathbf{x}, \mathbf{v}) = \prod_{n=1}^N p(\phi_n | \mathbf{x}_n, \mathbf{v}) = \prod_{n=1}^N \frac{\exp(\phi_n \mathbf{v}^\top \mathbf{x}_n)}{1 + \exp(\mathbf{v}^\top \mathbf{x}_n)}$$

LASSO penalisation

- ▶ Constraint: $\sum_i |v_i| \leq t$, where $t(> 0)$ is a *tuning parameter*.
- ▶ Applied as a Lagrangian penalty to the joint log-likelihood.



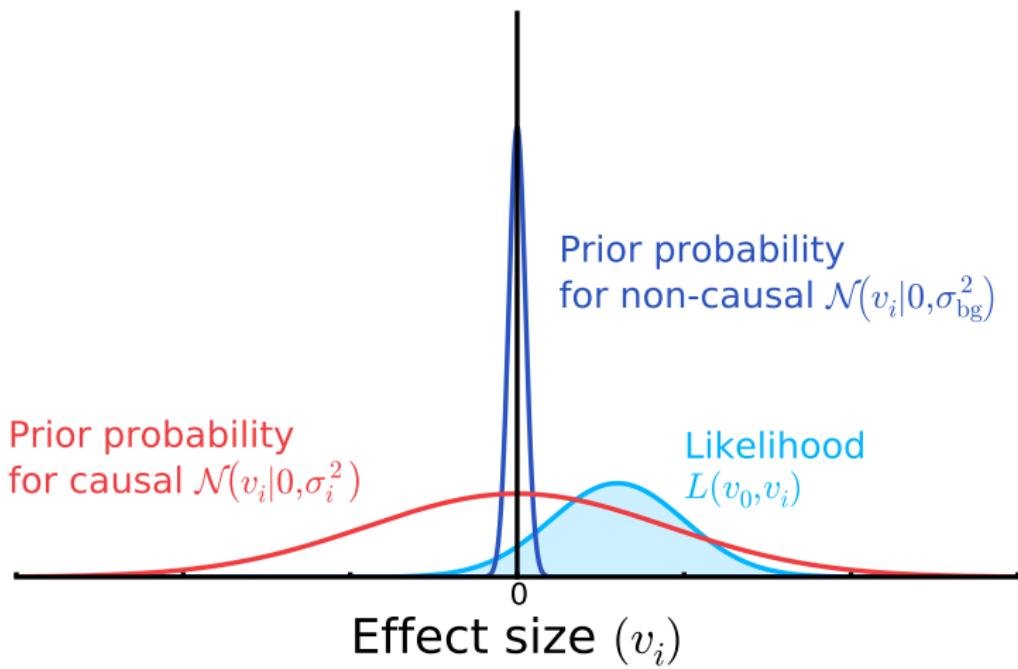
LASSO penalty assumes implicit Laplace prior \rightarrow more zero-valued coefficients.

Problems:

- ▶ Multicollinearity
- ▶ Variability in penalty parameter

Sparsity in BVSR (BIMBAM) / BVSLR (B-LORE)

Looks at both **null hypothesis** and **alternate hypothesis**



Priors in BVSR (BIMBAM)

$$p(\mathbf{y} | \mathbf{x}, \mathbf{v}, \tau) = \mathcal{N}(\mathbf{y} | \mathbf{x}^\top \mathbf{v}, \tau^{-1} \mathbb{I})$$

$$p(\tau) = \text{Gamma}\left(\frac{\lambda}{2}, \frac{\kappa}{2}\right)$$

$$p(v_0 | \tau) = \mathcal{N}(v_0 | 0, \sigma_\mu^2 / \tau)$$

$$p(v_i | \tau) = \underbrace{(1 - \pi) \delta_0}_{\text{Non-causal}} + \underbrace{\pi \mathcal{N}(v_i | 0, \sigma_a^2 / \tau)}_{\text{Causal}}$$

Hyperparameters $\Rightarrow \lambda, \kappa, \pi, \sigma_\mu, \sigma_a$

Priors in BVSLR (B-LORE)

$$p(\phi | \mathbf{x}, \mathbf{v}) = \prod_{n=1}^N \frac{\exp(\phi_n \mathbf{v}^\top \mathbf{x}_n)}{1 + \exp(\mathbf{v}^\top \mathbf{x}_n)}$$

$$p(v_i | \theta) = \underbrace{(1 - \pi) \mathcal{N}(v_i | 0, \sigma_{bg}^2)}_{\text{Non-causal}} + \underbrace{\pi \mathcal{N}(v_i | \mu, \sigma^2)}_{\text{Causal}}$$

Hyperparameters $\theta \Rightarrow \pi, \mu, \sigma_{bg}, \sigma$

Causality configurations

$$\begin{aligned} p(v_i | \boldsymbol{\theta}) &= \underbrace{(1 - \pi) \mathcal{N}(v_i | 0, \sigma_{\text{bg}}^2)}_{\text{Non-causal}} + \underbrace{\pi \mathcal{N}(v_i | \mu, \sigma^2)}_{\text{Causal}} \\ &= \sum_{z_i=0,1} \pi^{z_i} (1 - \pi)^{(1-z_i)} \mathcal{N}(v_i | \mu_{\mathbf{z},i}, \sigma_{\mathbf{z},i}^2) \\ \mu_{\mathbf{z},i} &= z_i \mu \quad \text{and} \quad \sigma_{\mathbf{z},i}^2 = \sigma_{\text{bg}}^2 + z_i [\sigma^2 - \sigma_{\text{bg}}^2] \end{aligned}$$

$\mathbf{z} \in \{0,1\}^I \Rightarrow \text{Causality configurations}$

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

Optimising the hyperparameters

$$p(v_i | \theta) = \sum_{z_i=0,1} \pi^{z_i} (1-\pi)^{(1-z_i)} \mathcal{N}(v_i | \mu_{\mathbf{z},i}, \sigma_{\mathbf{z},i}^2)$$

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Evidence approximation: Maximising the marginal likelihood

$$\begin{aligned} mL(\boldsymbol{\theta}) &= p(\boldsymbol{\phi} | \mathbf{x}, \boldsymbol{\theta}) \\ &= \int p(\boldsymbol{\phi} | \mathbf{x}, \mathbf{v}) p(\mathbf{v} | \boldsymbol{\theta}) d\mathbf{v} \rightarrow \max \end{aligned}$$

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Laplace approximation (?)

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Quasi-Laplace approximation

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$$p(\boldsymbol{\phi} | \mathbf{x}, \mathbf{v}) \mathcal{N}(\mathbf{v} | \boldsymbol{\mu}_{\mathbf{z}}, \text{diag}(\boldsymbol{\sigma}_{\mathbf{z}}^2))$$
$$= p(\boldsymbol{\phi} | \mathbf{x}, \mathbf{v}) \mathcal{N}(\mathbf{v} | \tilde{\boldsymbol{\mu}}, \text{diag}(\tilde{\boldsymbol{\sigma}}^2)) \times \frac{\mathcal{N}(\mathbf{v} | \boldsymbol{\mu}_{\mathbf{z}}, \text{diag}(\boldsymbol{\sigma}_{\mathbf{z}}^2))}{\mathcal{N}(\mathbf{v} | \tilde{\boldsymbol{\mu}}, \text{diag}(\tilde{\boldsymbol{\sigma}}^2))}$$
$$\propto \mathcal{N}(\mathbf{v} | \tilde{\boldsymbol{\mu}}, \tilde{\boldsymbol{\sigma}}^2)$$

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Analytical solution

$$mL(\boldsymbol{\theta}) = p(\boldsymbol{\phi} | \mathbf{x}, \boldsymbol{\theta})$$

$$\approx D' \sum_{\mathbf{z}} p(\mathbf{z} | \boldsymbol{\theta}) \frac{|\text{diag}(\boldsymbol{\lambda}_{\mathbf{z}})|^{\frac{1}{2}}}{|\boldsymbol{\Lambda}_{\mathbf{z}}|^{\frac{1}{2}}} \exp \left(-\frac{1}{2} \boldsymbol{\mu}_{\mathbf{z}}^\top \text{diag}(\boldsymbol{\lambda}_{\mathbf{z}}) \boldsymbol{\mu}_{\mathbf{z}} + \frac{1}{2} \mathbf{v}_{\mathbf{z}}^\top \boldsymbol{\Lambda}_{\mathbf{z}} \mathbf{v}_{\mathbf{z}} \right)$$

where

$$\boldsymbol{\Lambda}_{\mathbf{z}} := \tilde{\boldsymbol{\Lambda}} - \text{diag}(\tilde{\boldsymbol{\lambda}}) + \text{diag}(\boldsymbol{\lambda}_{\mathbf{z}})$$

$$\mathbf{v}_{\mathbf{z}} := \boldsymbol{\Lambda}_{\mathbf{z}}^{-1} [\tilde{\boldsymbol{\Lambda}} \tilde{\mathbf{v}} + \text{diag}(\boldsymbol{\lambda}_{\mathbf{z}}) \boldsymbol{\mu}_{\mathbf{z}} - \text{diag}(\tilde{\boldsymbol{\lambda}}) \tilde{\boldsymbol{\mu}}]$$

- ▶ Optimization can be done by gradient descent methods (e.g. L-BFGS).

Inference of causality in BVSLR (B-LORE)

Using the definition of conditional probability,

$$p(\mathbf{z} | \boldsymbol{\phi}, \mathbf{x}, \boldsymbol{\theta}) = \frac{p(\boldsymbol{\phi}, \mathbf{z} | \mathbf{x}, \boldsymbol{\theta})}{p(\boldsymbol{\phi} | \mathbf{x}, \boldsymbol{\theta})}$$

The posterior probability for SNP i to be causal is

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$$p(z_i = 1 | \boldsymbol{\phi}, \mathbf{x}, \boldsymbol{\theta}) = \sum_{\mathbf{z}: z_i = 1} p(\mathbf{z} | \boldsymbol{\phi}, \mathbf{x}, \boldsymbol{\theta})$$

The probability for a locus to be causal = 1 – probability of *not* having a single causal SNP

$$p(\text{locus is causal} | \boldsymbol{\phi}, \mathbf{x}, \boldsymbol{\theta}) = 1 - p(\mathbf{z} = \mathbf{0} | \boldsymbol{\phi}, \mathbf{x}, \boldsymbol{\theta})$$

BVSLR can be extended to multiple studies

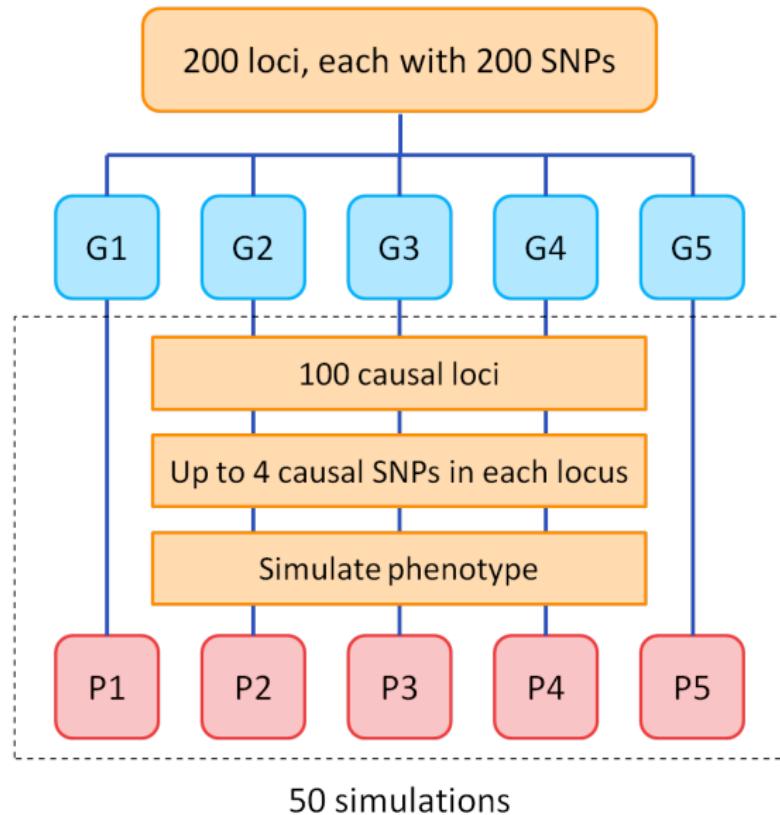
$$\begin{aligned} mL(\boldsymbol{\theta}) &= p(\boldsymbol{\phi} | \mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_S, \boldsymbol{\theta}) \\ &= \int p(\boldsymbol{\phi} | \mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_S, \mathbf{v}) p(\mathbf{v} | \boldsymbol{\theta}) d\mathbf{v} \rightarrow \max \end{aligned}$$

Assuming the quasi-Laplace approximation holds for each study,

$$\begin{aligned} \prod_{s=1}^S [p(\boldsymbol{\phi} | \mathbf{x}_s, \mathbf{v}) \mathcal{N}(\mathbf{v} | \tilde{\boldsymbol{\mu}}_{\mathbf{z},s}, \text{diag}(\tilde{\sigma}_{\mathbf{z},s}^2))] &\propto \prod_{s=1}^S \mathcal{N}(\mathbf{v} | \tilde{\mathbf{v}}_s, \tilde{\boldsymbol{\Lambda}}_s^{-1}) \\ &= \mathcal{N}(\mathbf{v} | \tilde{\mathbf{v}}, \tilde{\boldsymbol{\Lambda}}^{-1}) \end{aligned}$$

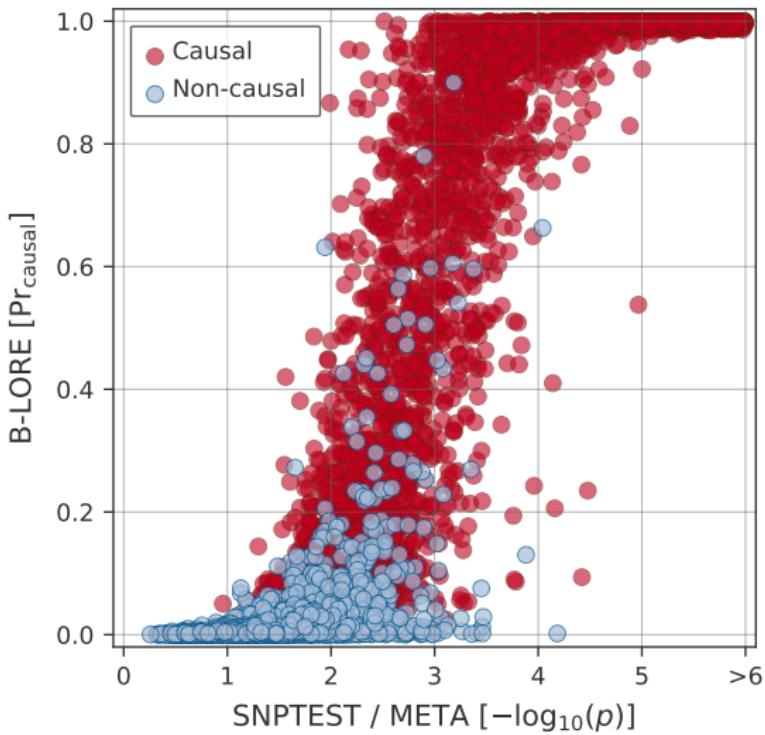
where $\tilde{\boldsymbol{\Lambda}} = \sum_{s=1}^S \tilde{\boldsymbol{\Lambda}}_s$ and $\tilde{\mathbf{v}} = \tilde{\boldsymbol{\Lambda}}^{-1} \sum_{s=1}^S \tilde{\boldsymbol{\Lambda}}_s \tilde{\mathbf{v}}_s$

Simulation details



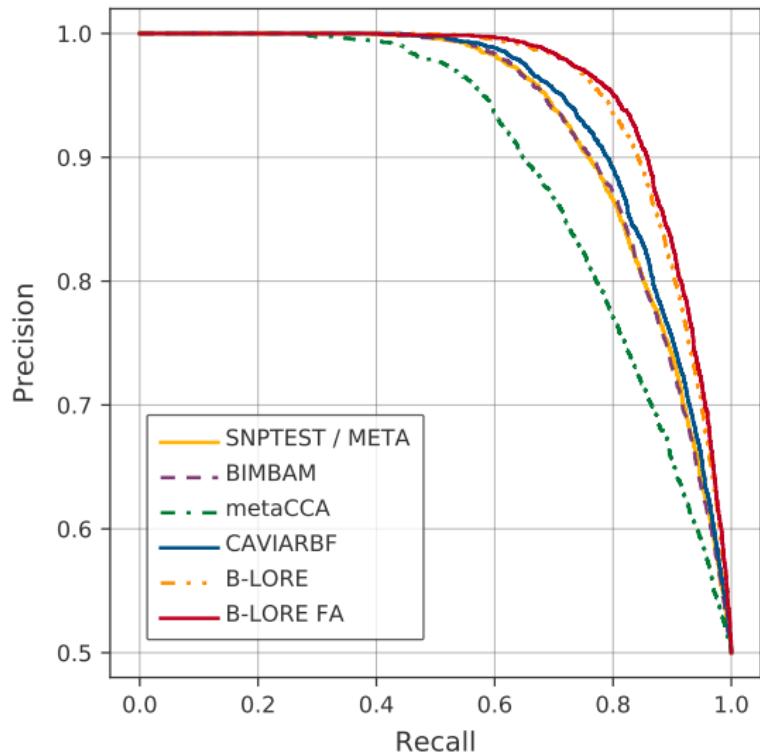
- ▶ B-LORE
- ▶ BIMBAM
- ▶ SNPTEST / META
- ▶ metaCCA
- ▶ PAINTOR
- ▶ CAVIARBF
- ▶ FINEMAP

Prediction of causal loci



- ▶ 5000 causal loci (100 from each of the 50 simulations)
- ▶ 5000 non-causal loci (100 from each of the 50 simulations)

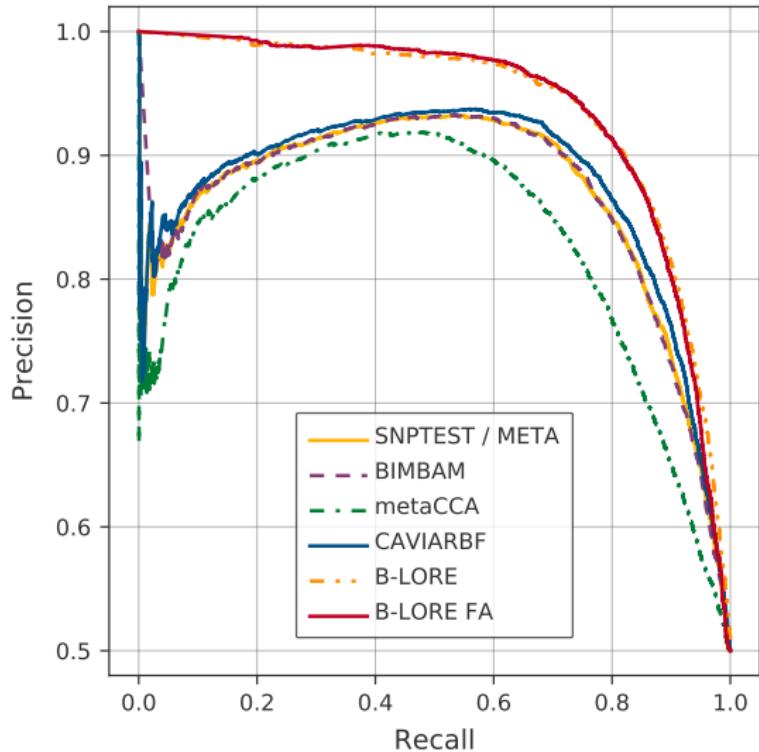
Prediction of causal loci



$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}}$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

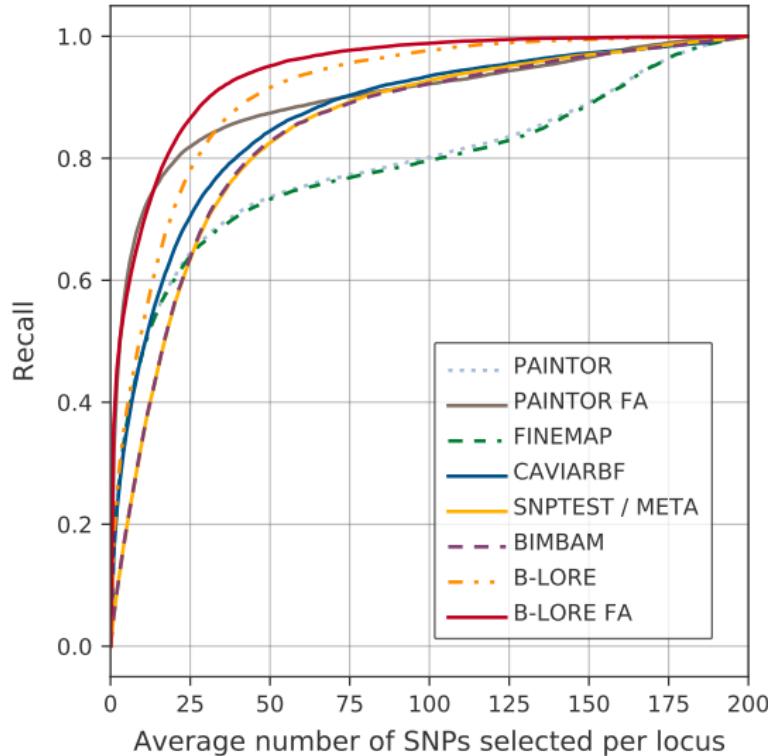
If there are non-causal loci in LD with causal regions



$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}}$$
$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

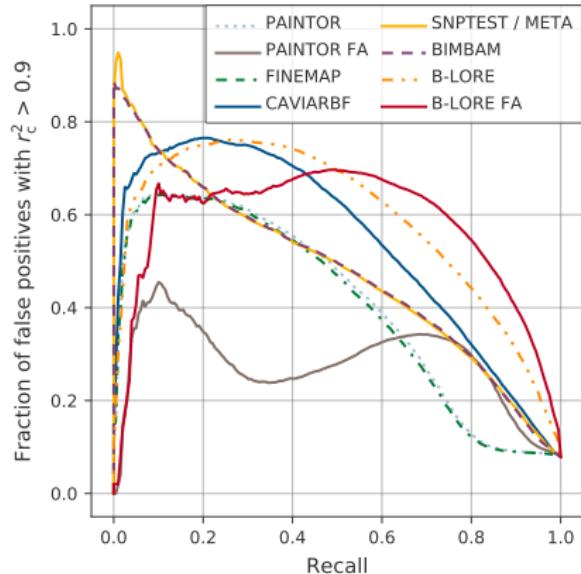
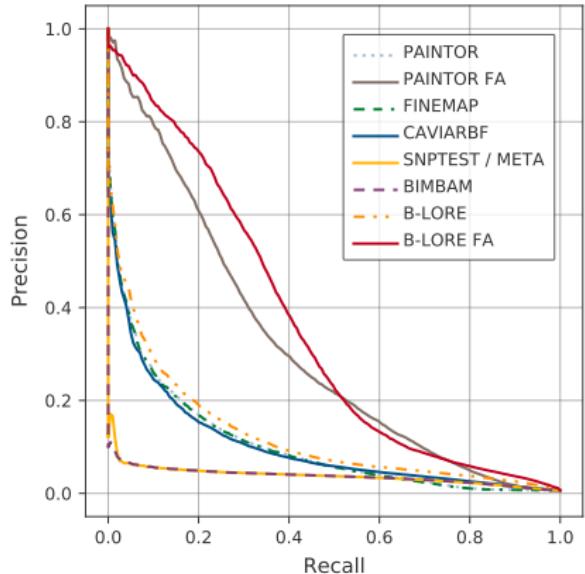
- ▶ 8 loci (out of 200) in LD with each other were introduced in the simulation

Finemapping causal variants



- ▶ Comparable to CAVIARBF up to 20% recall

Functional annotation improves finemapping

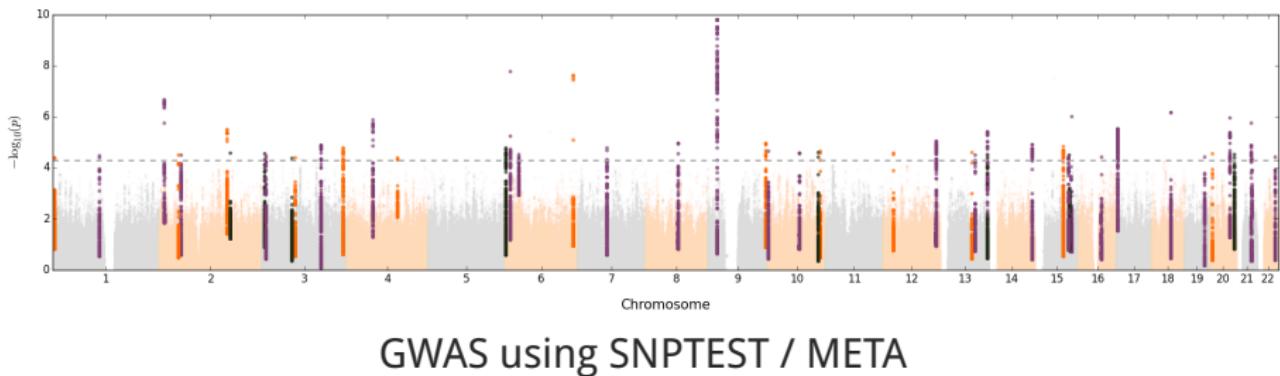


Association with coronary artery diseases (CAD)

- ▶ 5 GERMIFS cohorts
- ▶ 6228 cases, 6854 controls
- ▶ Imputed with 1000G Phase 1

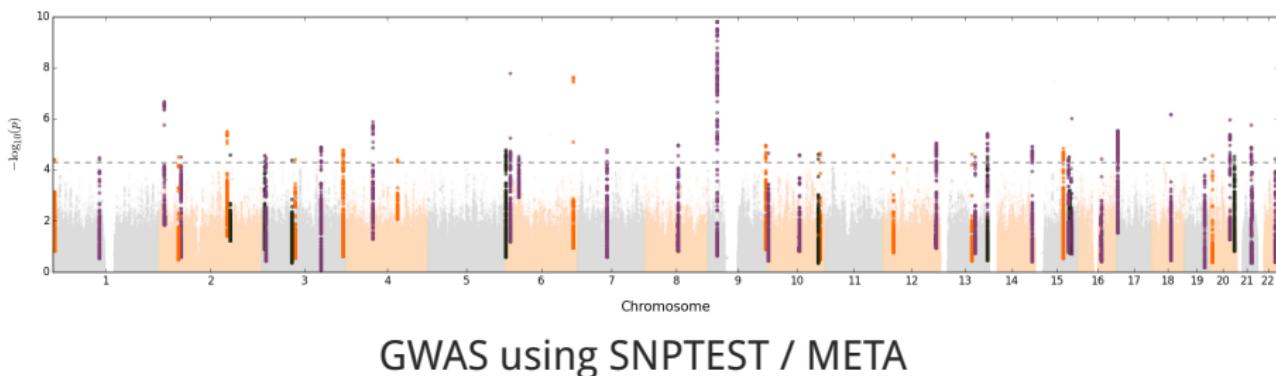
Association with coronary artery diseases (CAD)

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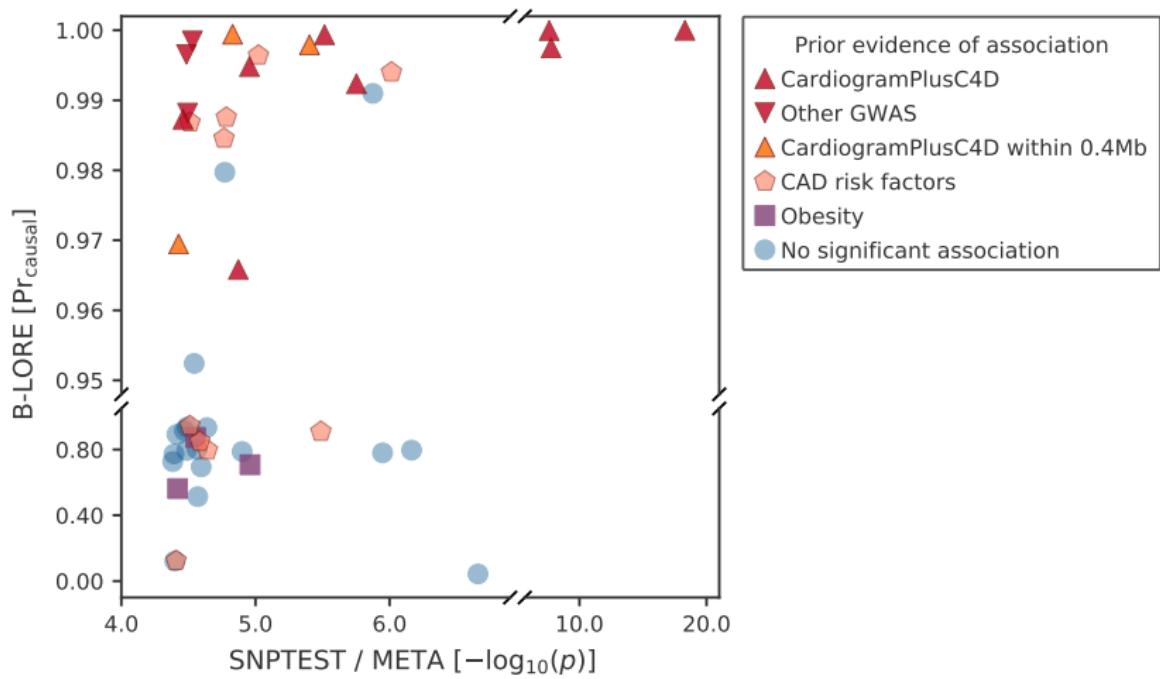
Association with coronary artery diseases (CAD)

- ▶ 5 GERMIFS cohorts
- ▶ 6228 cases, 6854 controls
- ▶ Imputed with 1000G Phase 1



- ▶ Applied B-LORE on these 45 loci, selecting 400 SNPs at each locus.

B-LORE predictions

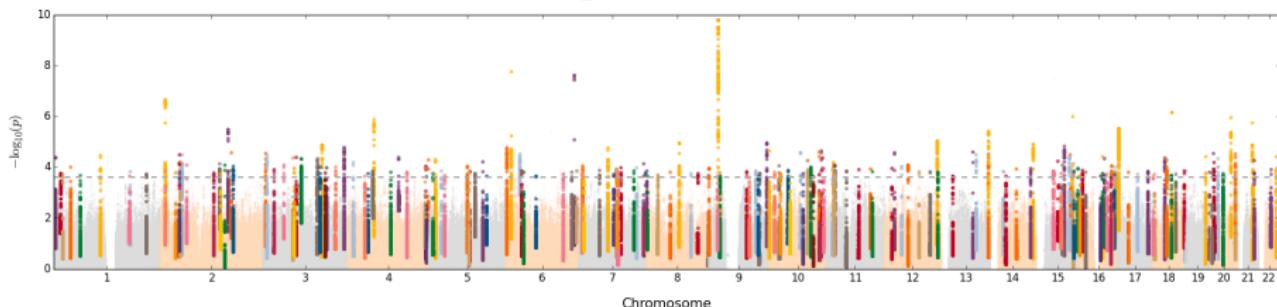


Top B-LORE predicted loci (not discovered in CardiogramPlusC4D)

Region	<i>P</i> r	Gene	Comments
6p21.3	0.998	C6orf10-BTNL2	GWAS for CAD in Han Chinese, 2012
15q25	0.997	IL-16	GWAS for CAD in Han Chinese, 2012
12q24	0.996	ZNF664	GWAS hit for HDL-C, TG, 2015
15q25	0.994	AKAP13	GWAS for BP in Koreans, 2011
4q13.1	0.991	desert	-
2p16	0.988	NRXN1	GWAS for CAD in OHGS1 + WTCCC2, 2015
3q28	0.988	IL1RAP	Mediation via IL-33, 2010
13q21.1	0.987	ARHGEF1	Regulates Blood Pressure, 2010
6p25	0.985	MYLK4	Downregulated in heart failure, 2014
7q11.22	0.980	AUTS2	-
3p26	0.952	desert	-

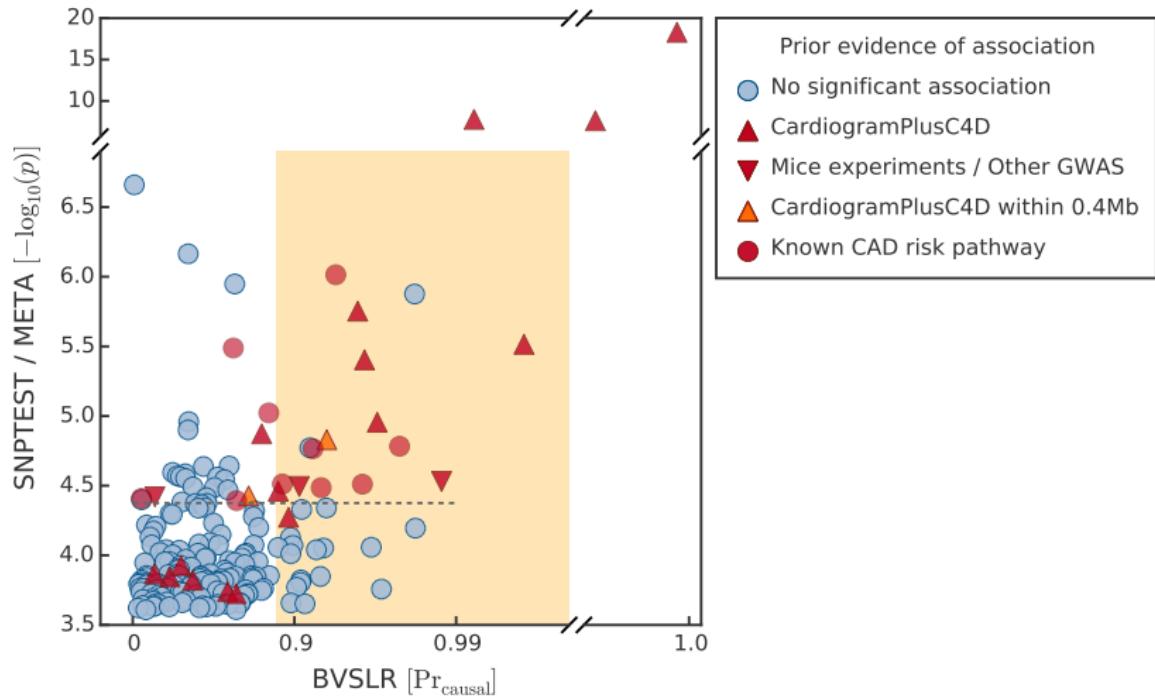
Extension to 200 loci

GWAS using SNPTEST / META



- ▶ Applied B-LORE on these 200 loci, selecting 400 SNPs at each locus.

Extension to 200 loci



Summary

- ▶ Multivariate analysis in meta studies
- ▶ High (German) precision
- ▶ Predicts new associations in CAD

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Outlook

- ▶ Submission
- ▶ GWAS-GTEx combined analysis
- ▶ Age-at-onset: Quantitative phenotype for CAD?
- ▶ New statistic for trans-eQTL analysis?

Many thanks to ...



Johannes Söding



Heribert Schunkert



Jeanette Erdmann

Many thanks to ...



Johannes Söding



Heribert Schunkert



Jeanette Erdmann



AG Söding

Many thanks to ...



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Heribert Schunkert



Jeanette Erdmann

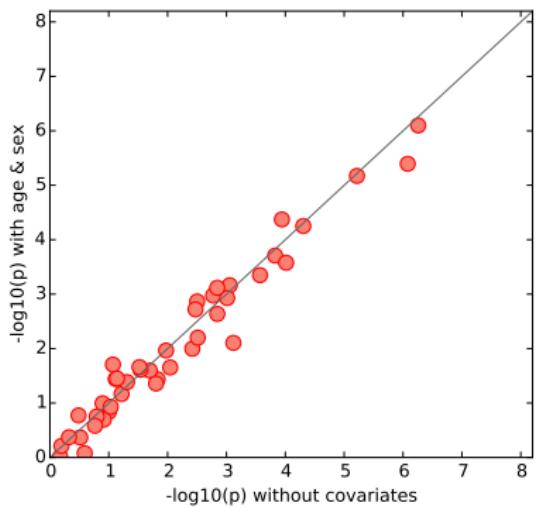


AG Söding

Thank you!

Risk correction can be improved

Pirinen *et al.*, Nat. Gen. 2012



Liability correction

