

Optimal Multiple Testing with Prior Information

Edgar Dobriban¹ Kristen Fortney² Stuart K. Kim² Art B.
Owen¹

¹Statistics, Stanford

²Developmental Biology & Genetics, Stanford

August 30, 2015

Overview

Motivating example: Genomics of human longevity

New Method

Motivating example: Human longevity

- ▶ 25-30 % heritable
- ▶ Genome-Wide Association Studies (GWAS)
 - ▶ centenarians vs controls
 - ▶ test 500K SNPs (single-nucleotide polymorphisms)
 - ▶ usually t-test/z-test
- ▶ Only one DNA polymorphism (APOE/TOMM40) associated
- ▶ Challenges:
 - ▶ Few centenarians
 - ▶ Small effects

Our approach

- ▶ Leverage information from age-related diseases
 - ▶ Focus on smaller set of variants that protect from disease
- ▶ Many large prior GWAS:
 - ▶ coronary artery disease (CAD) $n > 20K$.
 - ▶ type II diabetes (T2D)
 - ▶ ...
- ▶ How?

P-value weighting

- ▶ null hypothesis H_i : i -th SNP is not associated to longevity
- ▶ Use weighted Bonferroni method:
 - ▶ reject H_i if $P_i \leq qw_i$
 - ▶ weights $w_i \geq 0$, $\sum_{i=1}^J w_i = J$
 - ▶ controls FWER at $\alpha := Jq$
- ▶ How to choose weights?
- ▶ Optimize expected number of discoveries: Spjøtvoll (1972); Benjamini and Hochberg (1997); Rubin et al. (2006); Roeder and Wasserman (2009); Eskin (2008); Peña et al. (2011) ...

Gaussian p-value weighting

- ▶ for each SNP have a **test statistic** $T_i \sim \mathcal{N}(\mu_i, 1)$ in current study
- ▶ test $H_i : \mu_i = 0$ against $\mu_i < 0$
- ▶ information about μ_i from **prior studies**: $\mu_i \sim \mathcal{N}(\eta_i, \sigma_i^2)$.
- ▶ *Bayes weights* maximize expected number of discoveries $R(w)$:

$$\begin{aligned} \max_{w \in \mathbb{R}^J} \quad & \mathbb{E}_\mu \mathbb{E}_T R(w) \\ \text{s.t. } \quad & w_i \geq 0, \quad \sum_{i=1}^J w_i = J. \end{aligned}$$

- ▶ non-convex optimization
- ▶ formulated by Westfall et al. (1998), algorithm for small J

Main results

- ▶ We give efficient methods to find the weights.
- ▶ Let $\gamma = (\sigma^2 + 1)^{1/2}$, and

$$c(\eta, \gamma; \lambda) = -\frac{\eta + \gamma\{\eta^2 + 2(\gamma^2 - 1)\log(\gamma\lambda)\}^{1/2}}{\gamma^2 - 1}.$$

- ▶ **Theorem 1:** If the significance level $q \in [0, 1]$ is small enough, then the optimal Bayes weights are

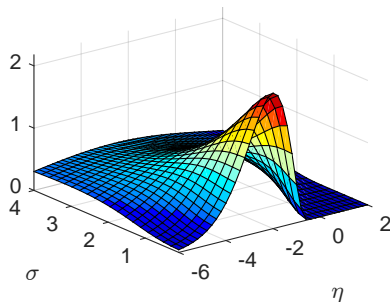
$$w_i = w(\eta_i, \gamma_i; \lambda) = \Phi\{c(\eta_i, \gamma_i; \lambda)\}/q$$

- ▶ $\lambda \geq 1$ is the unique constant s.t. $\sum_{i=1}^J w(\eta_i, \gamma_i; \lambda) = J$.
 - ▶ weights can be found by 1D line search

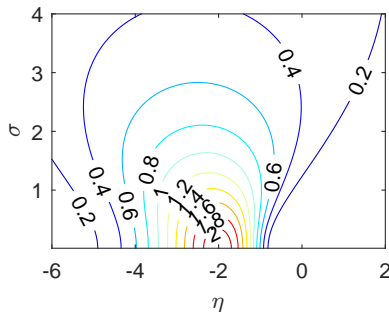
Main results

- ▶ **Theorem 2:** For any significance level q , the weights can be found nearly exactly in $O(J \log J)$ steps.
 - ▶ we find it remarkable, non-convex optimization hard in general
 - ▶ use duality, reduce to 1D line search

Bayes weights



(a) Surface



(b) Contour

Figure : An instance of Bayes weights $w(\eta, \sigma)$, a function of prior mean η and standard error σ . The weight of the i -th p-value is $w(\eta_i, \sigma_i)$.

Further theoretical results

- ▶ as $\sigma \rightarrow 0$, the Bayes weights tend to the Spjotvoll weights of Spjotvoll (1972); Rubin et al. (2006); Roeder and Wasserman (2009)
- ▶ as $\sigma \rightarrow \infty$, a symmetry-breaking occurs
 - ▶ the weighting scheme $(1/q, \dots, 1/q, \varepsilon, \dots, \varepsilon)$ dominates uniform weighting
 - ▶ due to the extreme non-convexity of objective
 - ▶ reinforces that previous results are remarkable

Empirical results

- ▶ apply to GWAS: *i*GWAS or informed GWAS
- ▶ longevity: leads to new loci that replicate. Fortney et al., submitted
- ▶ simulations: compares favorably to alternatives (more power)
- ▶ data analysis: slight advantage over existing methods
 - ▶ use GWAS both as prior and current traits
 - ▶ several pairs: e.g., eGFR creatinine → coronary artery disease (CAD)
 - ▶ only our method could improve power, when averaged over all pairs studied
- ▶ all computational results **reproducible**

Simulation

- ▶ In Gaussian model, generate $J = 1000$ random means and variances iid $\eta_i \sim \mathcal{N}(0, 1)$, $\sigma_i \sim |\mathcal{N}(0, 1)|$
- ▶ Set $q = 10^{-2}$
- ▶ Compare weighting methods
 - ▶ unweighted testing: $w_i = 1$
 - ▶ Bayes weighting: prior parameters $\eta_i, \phi\sigma_i^2$
 - ▶ exponential weighting: $w_i \propto \exp(-\beta\eta_i)$, (Roeder et al., 2006)
 - ▶ filtering: test top effects $|\eta_i| \geq |M|$, with equal weights
- ▶ Compute the power as the objective function divided by J

Simulation

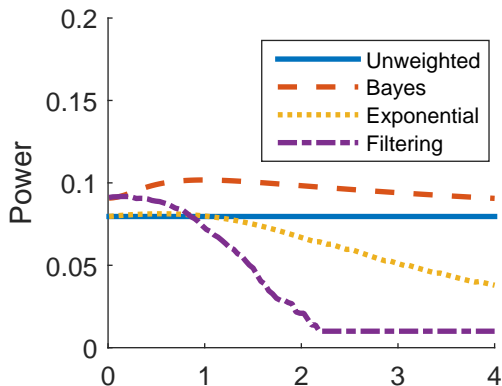


Figure : Power of four p-value weighting methods as a function of their parameter. Bayes as a function of the dispersion ϕ ; exponential as a function of β ; and filtering as a function of $|M|$.

Conclusion

- ▶ new p-value weighting method - Bayes weights/iGWAS
 - ▶ control type I error (optimal for FWER control)
 - ▶ use prior information
 - ▶ Box (1980)'s vision: be Bayesian when predicting and frequentist when testing
- ▶ **general**: Gaussian tests
- ▶ **easy to use**: only summary statistics from prior studies
- ▶ **computationally efficient**

Additional information

- ▶ Software
 - ▶ R package **pweight** for p-value weighting on CRAN.
 - ▶ MATLAB package from github.com/dobriban
- ▶ Reference: Dobriban et al. (2015): Optimal multiple testing under a gaussian prior on the effect sizes, *Biometrika*, to appear. *arXiv:1504.02935*.
- ▶ Acknowledgements
 - ▶ Supported by grants from the AFAR/EMF and the NIH/NIA (AG025941), and NSF grants DMS-1407397, DMS-1418362.
 - ▶ Helpful feedback: E. Eskin, J. Habiger, W. Su, J. Wang
- ▶ Contact
 - ▶ dobriban@stanford.edu
 - ▶ web.stanford.edu/~dobriban
- ▶ Thank you!

- Benjamini, Y. and Hochberg, Y. (1997). Multiple hypotheses testing with weights. *Scandinavian Journal of Statistics*, 24(3):407–418.
- Box, G. E. P. (1980). Sampling and Bayes' inference in scientific modelling and robustness (with Discussion). *Journal of the Royal Statistical Society. Series A (General)*, 143(4):383–430.
- Dobriban, E., Fortney, K., Kim, S. K., and Owen, A. B. (2015). Optimal multiple testing under a gaussian prior on the effect sizes. *arXiv preprint arXiv:1504.02935*. *Biometrika*, to appear.
- Eskin, E. (2008). Increasing power in association studies by using linkage disequilibrium structure and molecular function as prior information. *Genome research*, 18(4):653–660.
- Peña, E. A., Habiger, J. D., and Wu, W. (2011). Power-enhanced multiple decision functions controlling family-wise error and false discovery rates. *The Annals of Statistics*, 39(1):556–583.
- Roeder, K., Bacanu, S.-A., Wasserman, L., and Devlin, B. (2006). Using linkage genome scans to improve power of association in genome scans. *The American Journal of Human Genetics*, 78(2):243–252.
- Roeder, K. and Wasserman, L. (2009). Genome-wide significance levels and weighted hypothesis testing. *Statistical Science*, 24(4):398.
- Rubin, D., Dudoit, S., and Van der Laan, M. (2006). A method to increase the power of multiple testing procedures through sample splitting. *Statistical Applications in Genetics and Molecular Biology*, 5(1).

Spjotvoll, E. (1972). On the optimality of some multiple comparison procedures. *The Annals of Mathematical Statistics*, 43(2):398–411.

Westfall, P. H., Krishen, A., and Young, S. S. (1998). Using prior information to allocate significance levels for multiple endpoints. *Statistics in Medicine*, 17(18):2107–2119.