

Tests multiples et bornes post hoc pour des données hétérogènes

Soutenance de thèse

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Summary of contributions

- ▶ 2 published papers on previous works [Durand and Lessard (2016)], [Chatelain et al. (2018)]
- ▶ 1 paper in revision about optimal weighting arXiv:1710.01094
- ▶ 1 published paper about discrete tests [Döhler, Durand, and Roquain (2018)]
- ▶ 1 submitted paper about post hoc arXiv:1807.01470
- ▶ participation to 2 R packages: DiscreteFDR and sansSouci

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3. New post hoc bounds for localized signal

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1. Multiple testing basics

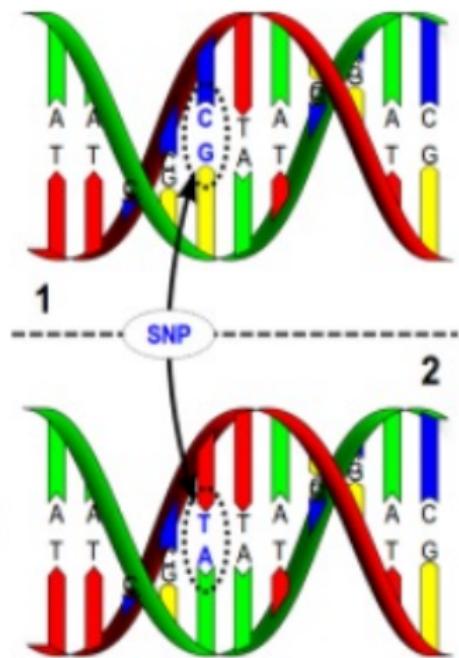
- From single to multiple tests
- Multiple testing procedures

2. Power optimality with groups and weighting

3. New post hoc bounds for localized signal

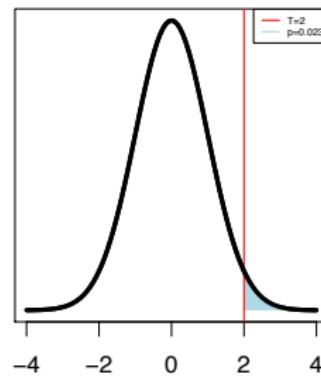
SNP association study

- ▶ A SNP = a location on the genome where there is variation
- ▶ Study the association of a SNP with a trait: case-control study
- ▶ Apply a **statistical test** to a measure $X \sim \mathcal{N}(\mu, 1)$
- ▶ Question: is $\mu = 0$ (no association) or > 0 ?



Single testing

- ▶ Null hypothesis H_0 : " $\mu = 0$ " versus alternative H_1 : " $\mu > 0$ "
- ▶ X in the tail of $\mathcal{N}(0, 1)$ \Rightarrow unrealistic \Rightarrow reject H_0
- ▶ \Leftrightarrow Reject H_0 if the p -value $p(X) = \bar{\Phi}(X)$ is small ($\leq \alpha$)



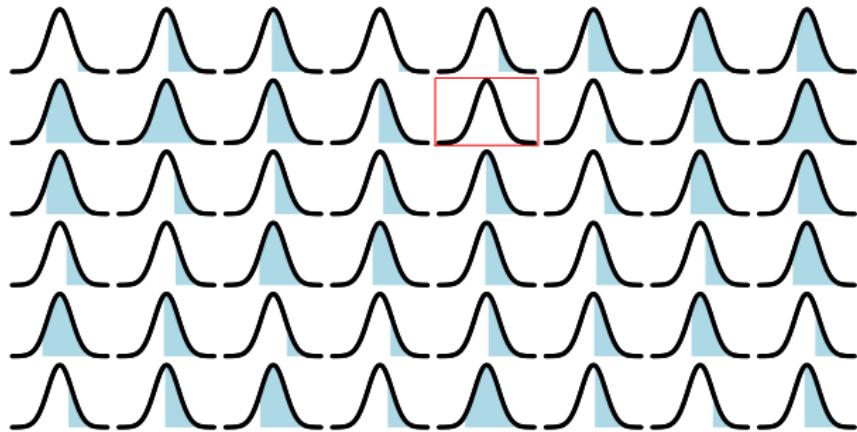
Probability to wrongly reject H_0

$$\mathbb{P}_{H_0}(p(X) \leq \alpha) \leq \alpha \text{ (uniformity under } H_0\text{)}$$

\implies false positive control

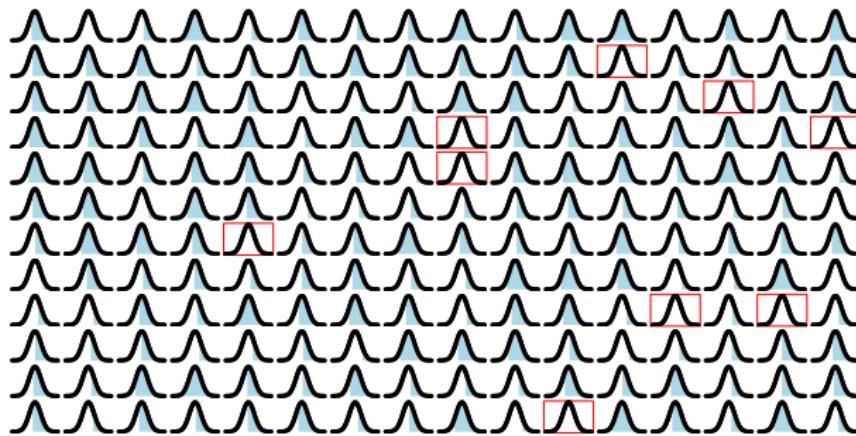
Multiple testing

- ▶ Now what if we test m SNPs at the same time?
- ▶ m null hypotheses $H_{0,i}$: " $\mu_i = 0$ " versus $H_{1,i}$: " $\mu_i > 0$ "
- ▶ Example if $m = 48$ and only noise (no signal):



Multiple testing

- $m = 192$, and only noise:



- $\mathbb{P}(\text{make at least one FP}) = 1 - (1 - \alpha)^m \xrightarrow[m \rightarrow \infty]{} 1$

Modern days applications

- $m = 10^4, 10^5, 10^6$
- Too many false positives if we keep using α as threshold

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Multiple testing procedures

- ▶ What we want: a rejection set R with a control on $V(R)$ the number of false positives in R

Bonferroni procedure

- ▶ Use α/m instead of α
- ▶ Then $\mathbb{P}(V(R) > 0) \leq \alpha$

This can be too stringent when:

- ▶ we want a lot of detections
- ▶ we allow some false positives

False Discovery Proportion (FDP) and False Discovery Rate (FDR)

$$\text{FDP}(R) = \frac{V(R)}{|R| \vee 1} \quad ; \quad \text{FDR}(R) = \mathbb{E} [\text{FDP}(R)]$$

Benjamini-Hochberg (BH) procedure

[Benjamini and Hochberg (1995)][Benjamini and Yekutieli (2001)]

- ▶ Sort p -values: $p_{(1)} \leq \dots \leq p_{(m)}$
- ▶ Let $\hat{k} = \max \left\{ k \in \llbracket 1, m \rrbracket : p_{(k)} \leq \alpha \frac{k}{m} \right\}$ or 0 if empty set
- ▶ Reject $H_{0,i}$ if $p_i \leq \frac{\alpha \hat{k}}{m}$
- ▶ Theorem: FDR of BH $\leq \alpha$ under independence or PRDS

Useful other formulation

$$\frac{\hat{k}}{m} = \max \left\{ u : \widehat{G}(u) \geq u \right\} = \mathcal{I}\left(\widehat{G}\right) \text{ where}$$

$$\widehat{G} : u \mapsto m^{-1} \sum_{i=1}^m \mathbb{1}_{\{p_i \leq \alpha u\}}, u \in [0, 1]$$

- ▶ \widehat{G} empirical c.d.f. of p -values (up to α)
- ▶ Useful for asymptotics ($m \rightarrow \infty$)

An illustration of $\mathcal{I}(\widehat{G})$

Last crossing point between \widehat{G} and the identity function

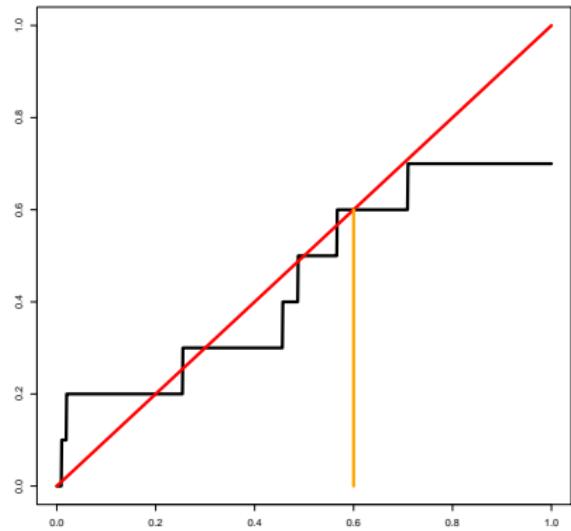
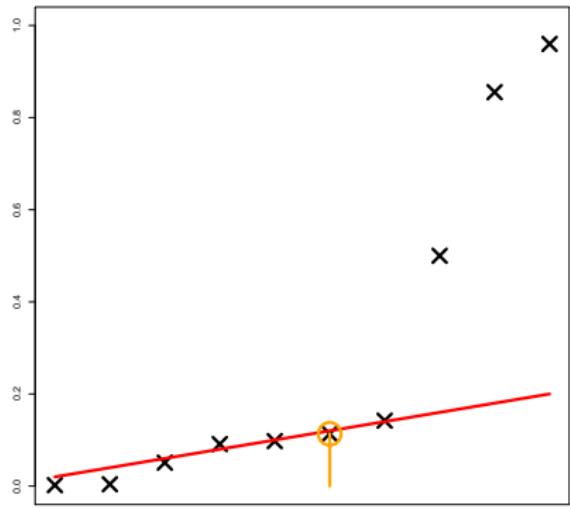


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Heterogeneity

Example: GWAS study

- ▶ Multiple SNPs tested, with heterogeneous Minor Allele Frequency (MAF)
- ▶ Distinguish SNPs with low and large MAF because this changes the power of tests
- ▶ ⇒ form two groups of SNPs

Multiple other examples [Cai and Sun (2009)]

- ▶ Sociologic studies, fMRI...

Setting

- ▶ G groups of sizes m_g with true null proportion $\pi_{g,0}$
- ▶ $p_{g,i} \sim \mathcal{U}([0, 1])$ under the null (noise); $p_{g,i} \sim F_g$ **strictly concave** under the alternative (signal)
- ▶ weak dependence [Storey, Taylor, and Siegmund (2004)] and technical assumptions

Quantities of interest

- ▶ we want FDR(R) control
- ▶ we study the optimality of the global **power**:

$$\text{Pow}(R) = m^{-1} \mathbb{E}[|R| - V(R)]$$

Main tool

Attribute **weights** to each group [Holm (1979)], [Genovese, Roeder, and Wasserman (2006)], [Blanchard and Roquain (2008)]...

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Weighted BH (WBH)

Take some weights $(w_g)_{1 \leq g \leq G}$, $w_g \geq 0$, apply BH to modified p -values
 $\tilde{p}_{g,i} = p_{g,i}/w_g$

Interpretation with the \mathcal{I} functional

Define

$$\hat{G}_w : u \mapsto m^{-1} \sum_{g=1}^G \sum_{i=1}^{m_g} \mathbb{1}_{\{\tilde{p}_{g,i} \leq \alpha u w_g\}}$$

and reject all $p_{g,i} \leq \alpha \hat{u} w_g$ with $\hat{u} = \mathcal{I}(\hat{G}_w) = \max \{u : \hat{G}_w(u) \geq u\}$.

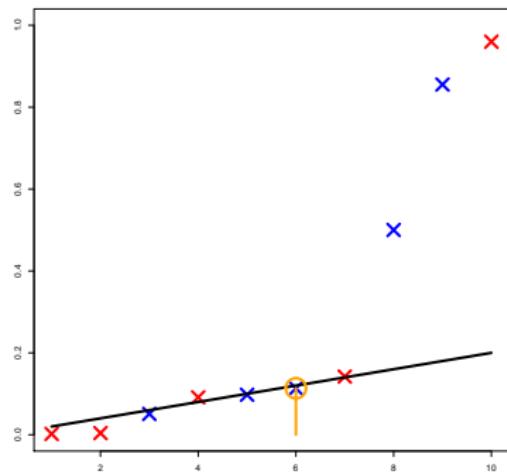
- A constraint is necessary for FDR control, for example:

$$w \in \mathcal{W} = \left\{ w \geq 0, \sum_{g=1}^G m_g w_g \leq m \right\}$$

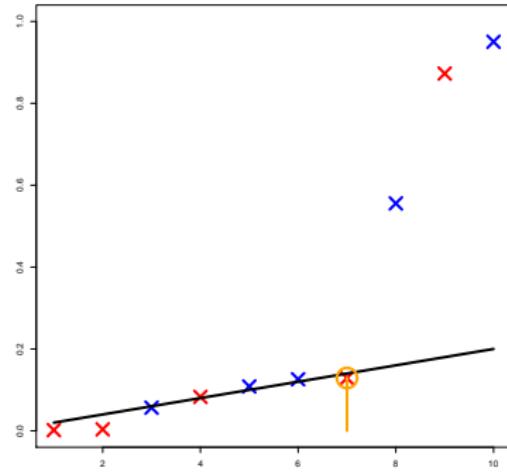
Unweighted vs Weighted BH procedure

Two groups with $w_1 + w_2 = 2$

- ▶ $w_1 = w_2 = 1$ (BH):



- ▶ $w_1 = 1.1, w_2 = 0.9$:



- ▶ Weights can increase detections \Rightarrow increase power ?

Multi-Weighting

[Roquain and van de Wiel (2009)]

- ▶ A generalization needed for the search for optimal power

Now weights are a function $u \mapsto W(u)$ for $u \in [0, 1]$. If

$\hat{G}_W : u \mapsto m^{-1} \sum_{g=1}^G \sum_{i=1}^{m_g} \mathbb{1}_{\{p_{g,i} \leq \alpha u W_g(u)\}}$ is nondecreasing,

then $\text{MWBH}(W) = \{(g, i) : p_{g,i} \leq \alpha \hat{u} W_g(\hat{u})\}$ with $\hat{u} = \mathcal{I}(\hat{G}_W)$.

Optimal weighting

- ▶ Fix u and w and define $R_{u,w}$ which rejects all $p_{g,i} \leq \alpha uw_g$
- ▶ Maximize its power for all u on the weight space \mathcal{W} :

Optimal oracle weights [Roquain and van de Wiel (2009)]

$$W_{or}^*(u) = \arg \max_{w \in \mathcal{W}} \text{Pow}(R_{u,w})$$

Theorem [Roquain and van de Wiel (2009)]

Existence and uniqueness of W_{or}^* if regularity assumptions on F_g and $\pi_{g,0} = \pi_0$.

Moreover, MWBH(W_{or}^*) has asymptotical:

- ▶ FDR control at level $\pi_0\alpha$
- ▶ Power optimality among all WBH procedures

Issues and consequences

- ① F_g 's are unknown in practice ! So is W_{or}^*
- ② The assumption $\pi_{g,0} = \pi_0$ removes some heterogeneity
- ③ $\sum_g m_g w_g \leq m \implies \pi_0 \alpha\text{-FDR control} \implies \text{conservativeness}$

Goal

- ▶ Estimate the oracle optimal weights
- ▶ enlarge \mathcal{W} in a way that incorporates $\pi_{g,0}$ estimators
- ▶ keep asymptotical results on FDR control and power optimality

⇒ Adaptive Data-Driven Optimal Weighting (ADDOW)

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π_0 estimation

- ▶ Each $\pi_{g,0}$ is estimated with $\hat{\pi}_{g,0}$
- ▶ $\widehat{\mathcal{W}} = \left\{ w : \sum_g m_g \hat{\pi}_{g,0} w_g \leq m \right\}$ allows larger weights than \mathcal{W} !
- ▶ Asymptotics: $\hat{\pi}_{g,0} \xrightarrow[m \rightarrow \infty]{\mathbb{P}} \tilde{\pi}_{g,0} \geq \pi_{g,0} \implies$ over-estimation (e.g. Storey)

Multiplicative Estimation (ME) case

There exists $C \geq 1$ such that $\tilde{\pi}_{g,0} = C\pi_{g,0} \forall g$

- ▶ Includes the consistent case $\tilde{\pi}_{g,0} = \pi_{g,0} \forall g$ ($C = 1$)
- ▶ Includes the case where $\hat{\pi}_{g,0} = 1$ and $\pi_{g,0} = \pi_0 \forall g$ ($C = 1/\pi_0$)

Definition of ADDOW

$$\text{ADDOW} = \text{MWBH}(\widehat{W}^*)$$

where

$$\forall u, \widehat{W}^*(u) = \arg \max_{w \in \widehat{\mathcal{W}}} \widehat{G}_w(u)$$

$\implies \widehat{W}^*$ maximizes the *number of rejections*

Key idea

Under (ME), maximizing the rejections is the same as maximizing the power

Remark : if $\hat{\pi}_{g,0} = 1 \ \forall g$, ADDOW=IHW [Ignatiadis et al. (2016)]

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Asymptotic FDR control

Theorem

$$\lim_{m \rightarrow \infty} \text{FDR}(\text{ADDOW}) \leq \alpha$$

Moreover if $\alpha \leq \tilde{\pi}_0$ and (ME):

$$\lim_{m \rightarrow \infty} \text{FDR}(\text{ADDOW}) = \frac{\alpha}{C}$$

By-product

If $\pi_{g,0} = \pi_0 \ \forall g$,

$$\lim_{m \rightarrow \infty} \text{FDR}(\text{IHW}) = \pi_0 \alpha.$$

Proofs inspired by [Roquain and van de Wiel (2009)], [Hu, Zhao, and Zhou (2010)] and [Zhao and Zhang (2014)].

Power optimality

Theorem

If (ME),

$$\lim_{m \rightarrow \infty} \text{Pow}(\text{ADDOW}) \geq \limsup_{m \rightarrow \infty} \text{Pow}(\text{MWBH}(\widehat{W}))$$

for any weight function sequence such that $\widehat{W}(u) \in \widehat{\mathcal{W}}$.

By-product

If $\pi_{g,0} = \pi_0 \forall g$,

$$\lim_{m \rightarrow \infty} \text{Pow}(\text{IHW}) \geq \limsup_{m \rightarrow \infty} \text{Pow}(\text{MWBH}(\widehat{W}))$$

for any weight function sequence such that $\sum_g m_g \widehat{W}_g(u) \leq m$.

Comparison with other methods

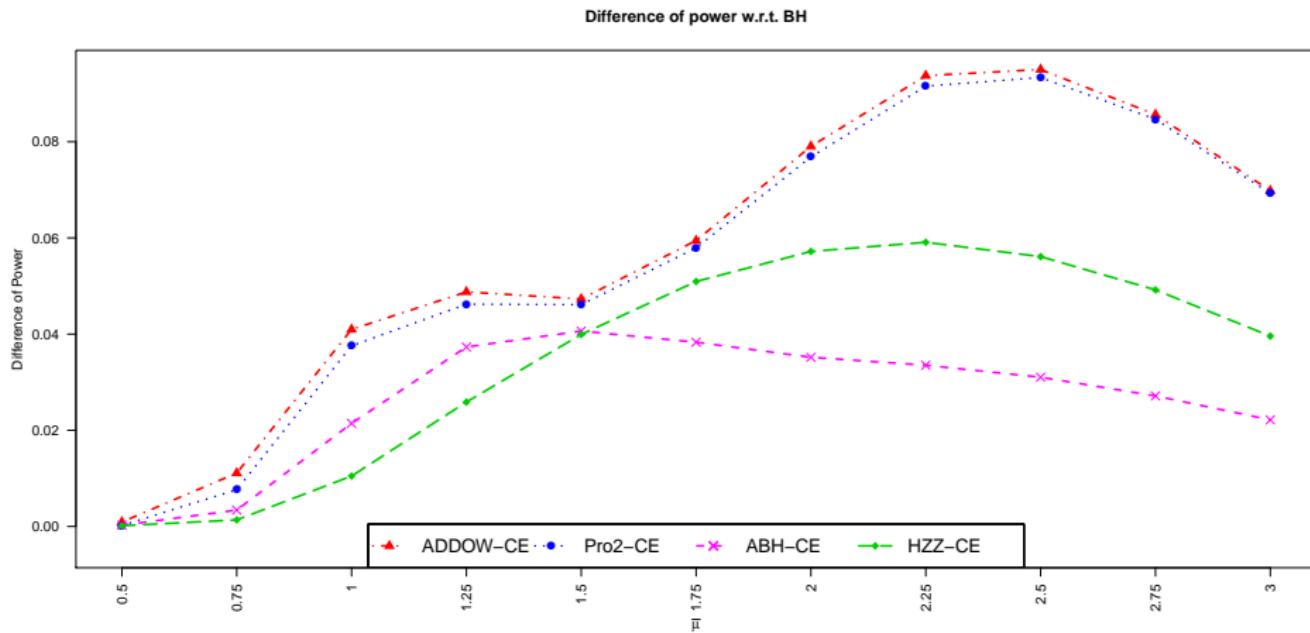
$\alpha = 0.05$, $\pi_{1,0} = 0.7$, $\pi_{2,0} = 0.8$, $m_1 = m_2 = 2000$, $\mu_1 = \bar{\mu}$ and $\mu_2 = 2\bar{\mu}$

4 methods compared with $\hat{\pi}_{g,0} = \pi_{g,0}$ (oracle) and varying signal parameter $\bar{\mu}$:

- ▶ ADDOW
- ▶ Pro2 [Zhao and Zhang (2014)]
- ▶ HZZ [Hu, Zhao, and Zhou (2010)]
- ▶ Adaptive BH

Comparison with other methods

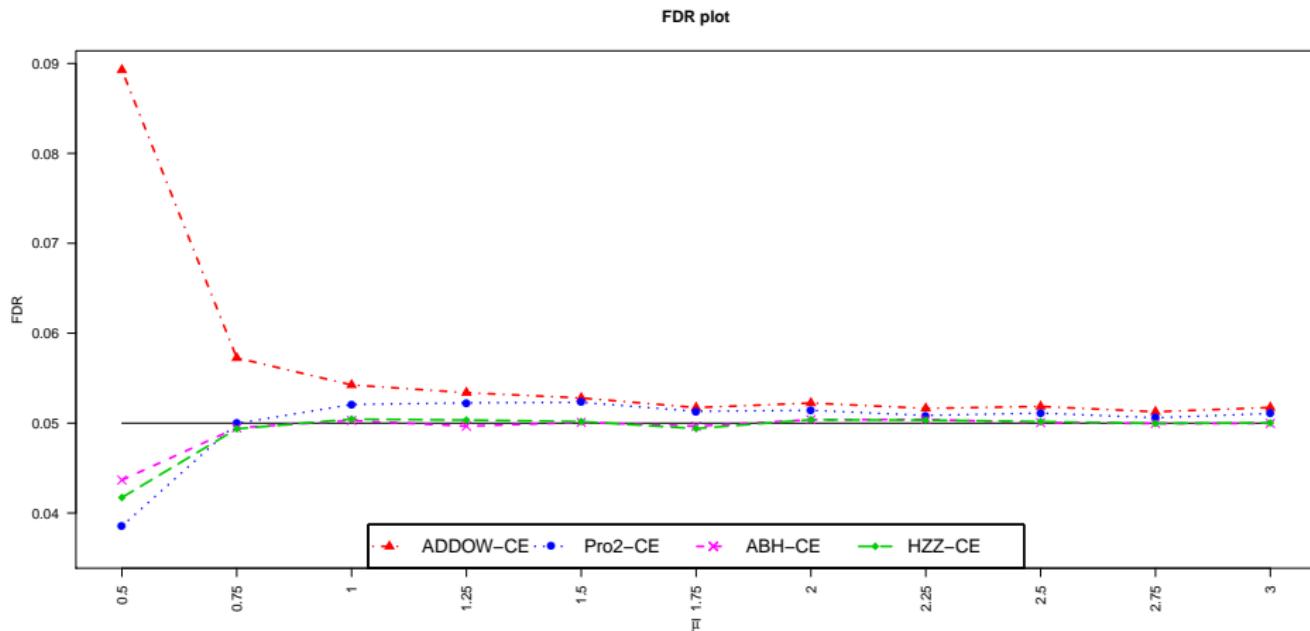
$\alpha = 0.05$, $\pi_{1,0} = 0.7$, $\pi_{2,0} = 0.8$, $m_1 = m_2 = 2000$, $\mu_1 = \bar{\mu}$ and $\mu_2 = 2\bar{\mu}$



- ADDOW > Pro2 > HZZ & ABH

Comparison with other methods

$\alpha = 0.05$, $\pi_{1,0} = 0.7$, $\pi_{2,0} = 0.8$, $m_1 = m_2 = 2000$, $\mu_1 = \bar{\mu}$ and $\mu_2 = 2\bar{\mu}$

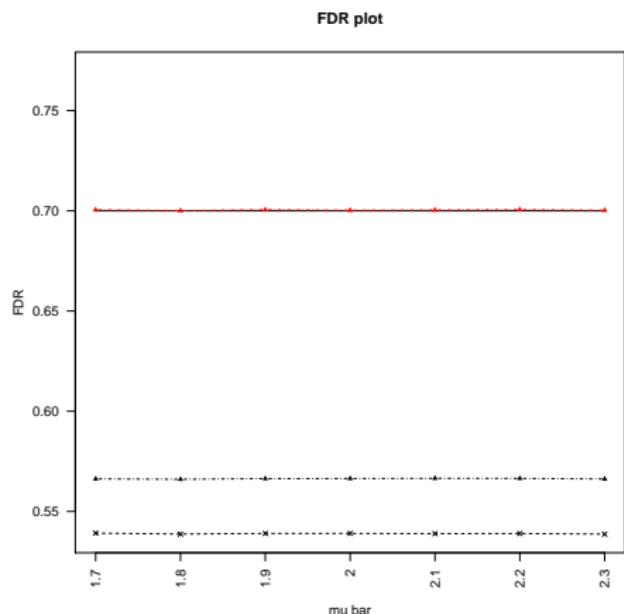
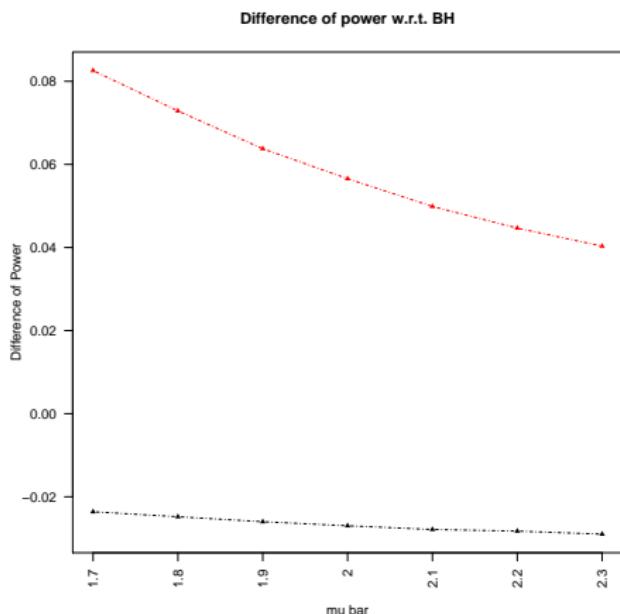


- Overfitting for ADDOW and Pro2

BH better than IHW?

$\alpha = 0.7$, $\pi_{1,0} = 0.05$, $\pi_{2,0} = 0.85$, $m_1 = 1000$, $m_2 = 9000$, $\mu_1 = 2$ and $\mu_2 = \bar{\mu}$

- ADDOW with oracle $\hat{\pi}_{g,0}$ vs IHW vs BH with heterogeneous $\pi_{g,0}$



- Remark: $m = 10^4$ here and no overfitting

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Outlook

- ▶ Optimal asymptotical properties but with restrictive dependence assumptions and finite sample overfitting
- ▶ Incorporate the dependence ?
- ▶ Use a better estimator of the rejections than \hat{G}_w ? LCM ?
- ▶ FDR bound in finite sample ? (done in [\[Ignatiadis and Huber \(2017\)\]](#) with folds and censoring)
- ▶ Convergence rates ? With more regularity assumptions on F_g ?

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Replication crisis

- ▶ Published results/experiments impossible to reproduce
- ▶ 70% fail rate (*Nature* poll)

A possible explanation: *p*-hacking [Wasserstein and Lazar (2016)]

- ▶ Pre-selecting variables that seem significant, exclude others from experiment
- ▶ Theoretical results no longer hold
- ▶ Results poorly interpretable and non reproducible

Toy example

- ▶ GWAS study with 10^6 genetic variants
- ▶ MTP over only the 10 smallest *p*-values
- ▶ Distribution of 10 smallest \neq distribution of 10 *p*-values taken at random

Our general problem

Confidence bounds on any set of selected variables [Goeman and Solari (2011)]

A confidence (post hoc) bound is a (random) function \hat{V} such that

$$\mathbb{P} \left(\forall S \subset \mathbb{N}_m, V(S) \leq \hat{V}(S) \right) \geq 1 - \alpha$$

- ▶ Hence for any selected \hat{S} , $\mathbb{P} \left(V(\hat{S}) \leq \hat{V}(\hat{S}) \right) \geq 1 - \alpha$ holds
- ▶ Not a classic MTP: a guarantee over any selected set instead of a rejected set
- ▶ Originates from [Genovese and Wasserman (2006)], [Meinshausen (2006)]

BNR methodology

[Blanchard, Neuvial, and Roquain (2018)]

Key concept: reference family

- $\mathfrak{R} = (R_k, \zeta_k)$ (random) with Joint Error Rate (JER) control:

$$\mathbb{P}(\forall k, V(R_k) \leq \zeta_k) \geq 1 - \alpha$$

- Confidence bound only on the members of \mathfrak{R}
- \implies Derivation of a global confidence bound
- Flexible approach: we choose \mathfrak{R}

Two different interpolation bounds

- $V_{\mathfrak{R}}^*(S) = \max \{|S \cap A|, \forall k, |R_k \cap A| \leq \zeta_k\}$ difficult to compute
- $\overline{V}_{\mathfrak{R}}(S) = \min_k (\zeta_k + |S \setminus R_k|) \wedge |S|$ less sharp but easy to compute

Simes bound

[Goeman and Solari (2011)], [Blanchard, Neuville, and Roquain (2018)]

Choice of \mathfrak{R} :

- ▶ Fix $\zeta_k = k - 1, \forall 1 \leq k \leq m$
- ▶ $R_k = \{i : p_i < \alpha k / m\}$

Simes bound formula

$$V_{\mathfrak{R}}^*(S) = \overline{V}_{\mathfrak{R}}(S) = \min_k \left(k - 1 + \sum_{i \in S} \mathbb{1}_{\{p_i \geq \alpha k / m\}} \right) \wedge |S|$$

Based on:

- ▶ Simes inequality and PRDS for JER control
- ▶ Nestedness of R_k 's for $V_{\mathfrak{R}}^*(S) = \overline{V}_{\mathfrak{R}}(S)$

New approach

Opposite to Simes approach of BNR

- ① Deterministic R_k 's with a localized structure (e.g. chromosomes).
Requires to compute $V_{\mathfrak{R}}^*$
- ② Over-estimate $V(R_k)$ in each R_k with a simple method
 - ▶ Example with the DKWM inequality [Dvoretzky, Kiefer, and Wolfowitz (1956)], [Massart (1990)] (independence needed):
 - ▶ $\zeta_k =$

$$|R_k| \wedge \min_{0 \leq \ell \leq |R_k|} \left[\frac{C}{2(1-p_{(\ell)})} + \left(\frac{C^2}{4(1-p_{(\ell)})^2} + \frac{\sum_{i \in R_k} \mathbf{1}\{p_i > p_{(\ell)}\}}{1-p_{(\ell)}} \right)^{1/2} \right]^2,$$

where $C = \sqrt{\frac{1}{2} \log \left(\frac{K}{\alpha} \right)}$ (union bound)

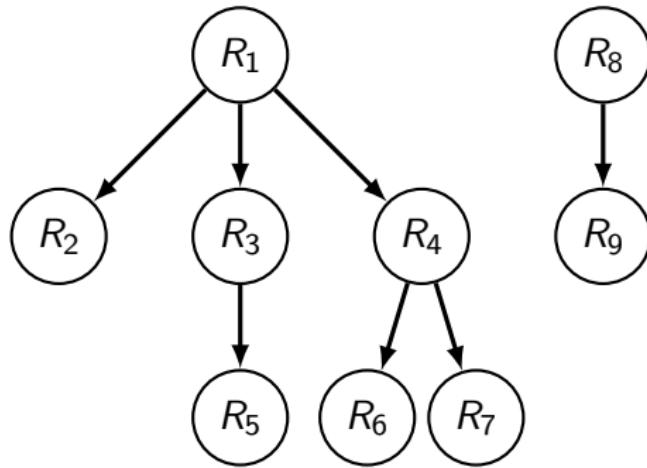
- ▶ Other estimators possible

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Choice of R_k : Forest structure

- ▶ $\forall k, k' \in \mathcal{K}, R_k \cap R_{k'} \in \{R_k, R_{k'}, \emptyset\}$
- ▶ Includes nested families or totally disjoint families



Main points

- ① Accommodates to realistic localization structures
- ② There is a simple algorithm to compute $V_{\Re}^*(S)$ with this structure

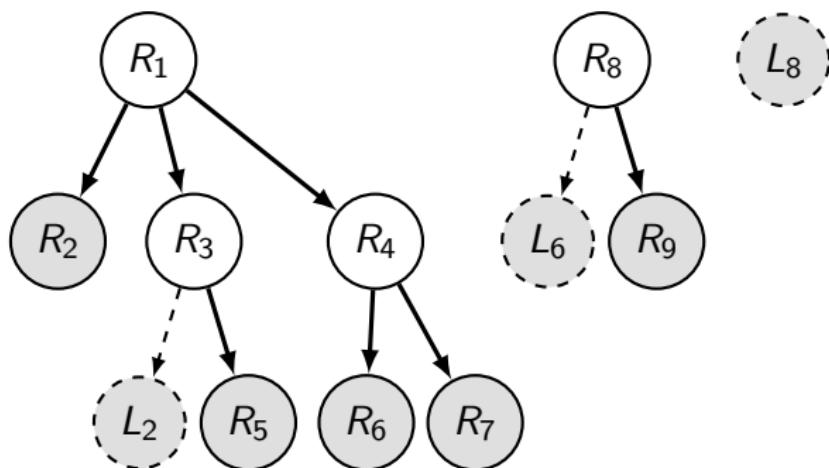
Properties of forest structures

Proposition

There is a partition $(L_n)_{1 \leq n \leq N}$ of \mathbb{N}_m (the leaves) such that each R_k can be written as a union $\bigcup_{i \leq n \leq j} L_n$.

Proposition

Each forest structure can be completed to include all leaves.



New interpolation bounds

Recall: $\bar{V}_{\mathfrak{R}}(S) = \min_k (\zeta_k + |S \setminus R_k|) \wedge |S|$

Definition

For any $q \leq K$,

$$\tilde{V}_{\mathfrak{R}}^q(S) = \min_{Q \subset \mathcal{K}, |Q| \leq q} \left(\sum_{k \in Q} \zeta_k \wedge |S \cap R_k| + \left| S \setminus \bigcup_{k \in Q} R_k \right| \right),$$

and

$$\tilde{V}_{\mathfrak{R}}(S) = \tilde{V}_{\mathfrak{R}}^K(S).$$

Property

$$V_{\mathfrak{R}}^*(S) \leq \tilde{V}_{\mathfrak{R}}(S) \leq \tilde{V}_{\mathfrak{R}}^{K-1}(S) \leq \cdots \leq \tilde{V}_{\mathfrak{R}}^2(S) \leq \tilde{V}_{\mathfrak{R}}^1(S) = \bar{V}_{\mathfrak{R}}(S)$$

Main results

Theorem

For a reference family with a forest structure and $\ell = \text{number of leaves}$,

$$V_{\mathfrak{R}}^*(S) = \tilde{V}_{\mathfrak{R}}(S) = \tilde{V}_{\mathfrak{R}}^\ell(S).$$

Lemma

There is a simple algorithm to compute $\tilde{V}_{\mathfrak{R}}$ if \mathfrak{R} is complete.

Lemma

Completing the family does not change $V_{\mathfrak{R}}^*$ and $\tilde{V}_{\mathfrak{R}}$.

Corollary

There is a simple algorithm to compute $V_{\mathfrak{R}}^*(S)$ by:

- ① Completing the family
- ② Travel across the forest from the leaves

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Outlook

- ▶ Incorporation of local structure \implies better power
- ▶ DKWM inequality involves independence
- ▶ Other over-estimators of true nulls ? [Blanchard, Neuvial, and Roquain (2018)], [Hemerik and Goeman (2018)]
- ▶ Other families combining BNR approach and deterministic regions ?
 - ▶ $\mathfrak{R} = (R_{k,i_k}, \zeta_{k,i_k})_{\substack{k \in \mathcal{K} \\ 1 \leq i_k \leq |R_k|}}$

Conclusion

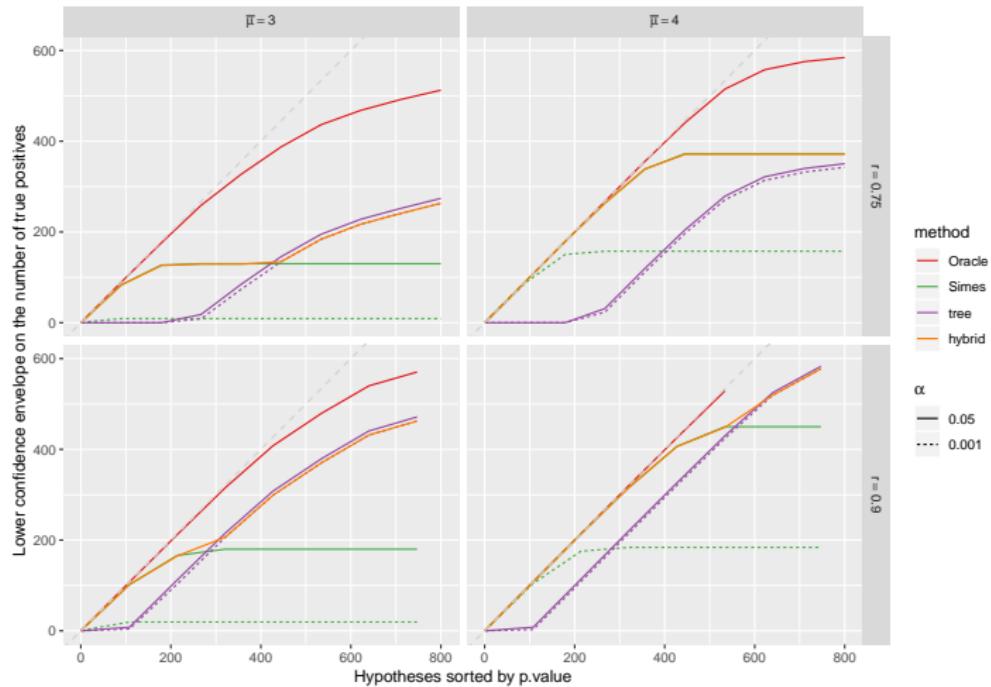
3 different ways to tackle heterogeneity in multiple testing:

- ▶ heterogeneity under the alternative with groups and weights
- ▶ heterogeneity under the discrete null
- ▶ localization heterogeneity with post hoc bounds

Next step: combine them all?

Hybrid bound

- $V_{\text{hybrid}}^{\gamma}(\alpha, S) = \min(V_{\text{Simes}}((1 - \gamma)\alpha, S), V_{\text{tree}}(\gamma\alpha, S))$
- $\gamma = 0.02$: favors Simes, convenient thanks to V_{tree} relation to α



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Multi-Weighting

A practical way to compute $\mathcal{I}(\widehat{G}_W)$

No need to compute $W(u)$ for each u !

$\forall k \in \llbracket 1, m \rrbracket$, compute all $\frac{\rho_i}{W_i(\frac{k}{m})}$ and take q_k the k -th smallest.

Let $q_0 = 0$.

Then $\mathcal{I}(\widehat{G}_W) = m^{-1} \max\{k \in \llbracket 0, m \rrbracket : q_k \leq \alpha \frac{k}{m}\}$.

About the computation of \widehat{W}^*

Key ideas

- ▶ Compute only $\widehat{W}^*(u)$ for $u = \frac{1}{m}, \frac{2}{m}, \dots, \frac{m-1}{m}, 1$
- ▶ Fixing u , $w \mapsto \widehat{G}_w(u)$ only jumps at the $\frac{p_{g,i}}{\alpha u}$ \implies let $\widehat{W}_g^*(u) = \frac{p_{g,i_g}}{\alpha u}$ such that $\sum m_g \widehat{\pi}_{g,0} \frac{p_{g,i_g}}{\alpha u} \leq m$ and $\sum_g i_g$ is maximal
- ▶ $\widehat{G}_w(u)$ nondecreasing in u AND w : try to reject 1 hyp, then 2, then 3... for $u = \frac{1}{m}$, when fail at k hyp, try to reject k hyp for $u = \frac{2}{m}, \dots$

Proof ideas

- ▶ $\widehat{G}_{\widehat{W}^*}(\hat{u}) \xrightarrow{\mathbb{P}} G_{W^*}^\infty(u^*)$ by LLN and careful use of maximality
- ▶ Then $\hat{u} \xrightarrow{\mathbb{P}} u^*$ by continuity of $\mathcal{I}(\cdot)$
- ▶ Then $\widehat{W}^*(\hat{u}) \xrightarrow{\mathbb{P}} W^*(u^*)$ by reductio ad absurdum
- ▶ $\Rightarrow \text{FDP} = \frac{m^{-1} \sum_g \sum_i \mathbb{1}_{\{p_{g,i} \leq \alpha \hat{u} \widehat{W}_g^*(\hat{u}) \text{ and } H_{g,i} \text{ true}\}}}{\widehat{G}_{\widehat{W}^*}(\hat{u})} \xrightarrow{\mathbb{P}}$
 $\frac{\alpha \sum_g \pi_g \pi_{g,0} u^* W_g^*(u^*)}{u^*} = \alpha \sum_g \pi_g \pi_{g,0} W_g^*(u^*) \leq \alpha$ (weight space choice)
- ▶ under (ME), maximize rejections \Leftrightarrow maximize power because we can write $\sum_g \pi_g \pi_{g,0} U(\alpha u w_g) \leq \frac{\alpha u}{C} \sum_g \pi_g \tilde{\pi}_{g,0} w_g \leq \frac{\alpha u}{C} \Rightarrow$ no dependence in w in $G_w^\infty - P_w^\infty$!

sADDOW $_{\beta}$

Stabilization for weak signal

- ▶ ADDOW overfits so FDR control lost with weak signal in finite sample
- ▶ We should prefer BH then
- ▶ \implies test if there is signal before choosing the procedure, like KS tests

Definition

$$\text{sADDOW}_{\beta} = \begin{cases} \text{ADDOW} & \text{if } \phi_{\beta} = \mathbf{1}_{\{Z_m > q_{\beta,m}\}} = 1 \\ \text{BH} & \text{if } \phi_{\beta} = \mathbf{1}_{\{Z_m > q_{\beta,m}\}} = 0 \end{cases}$$

with $Z_m = \sqrt{m} \sup_{u \in [0,1]} (\widehat{G}_{\widehat{W}^*}(u) - \alpha u)$ and $q_{\beta,m}$ the $(1 - \beta)$ quantile of Z_{0m} (independent copy of Z_m under full null, and independence).

sADDOW $_{\beta}$

Stabilization for weak signal

Main idea (under independence)

Weak signal $\implies Z_m$ close to Z_{0m} in distribution, and

$$\begin{aligned}\text{FDR}(\text{sADDOW}_{\beta}) &= \mathbb{E} [\phi_{\beta} \text{FDP}(\text{ADDOW}) + (1 - \phi_{\beta}) \text{FDP}(\text{BH})] \\ &\leq \mathbb{E} [\phi_{\beta} + \text{FDP}(\text{BH})] \\ &\leq \mathbb{P}(Z_m > q_{\beta,m}) + \frac{m_0}{m} \alpha \\ &\lesssim \mathbb{P}(Z_{0m} > q_{\beta,m}) + \frac{m_0}{m} \alpha \\ &\leq \beta + \frac{m_0}{m} \alpha\end{aligned}$$

- $\beta \rightarrow 0$?

sADDOW $_{\beta}$ equivalent to ADDOW

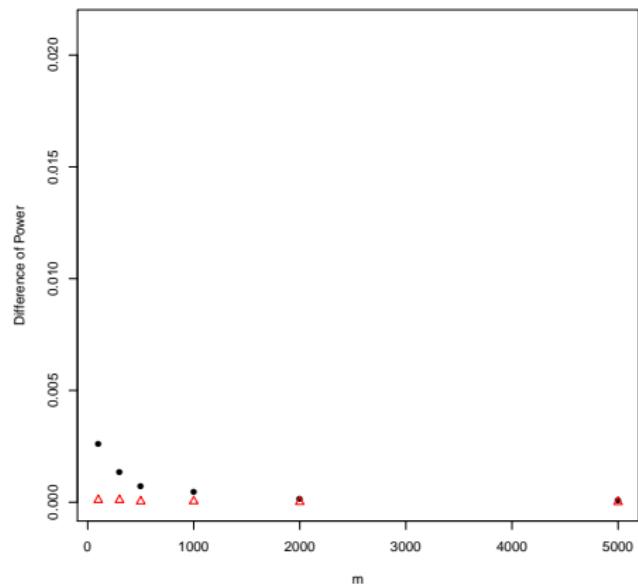
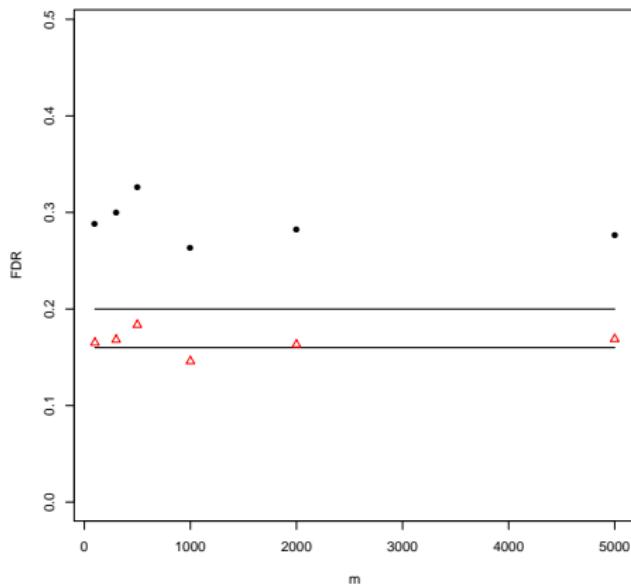
Theorem

sADDOW $_{\beta}$ is asymptotically equivalent to ADDOW because $\phi_{\beta} \xrightarrow{a.s.} 1$ when $m \rightarrow \infty$, even if $\beta = \beta_m \rightarrow 0$ not too slowly ($\beta_m \geq \exp(-m^{1-\nu}), \nu > 0$).

Proof relies on the DKWM inequality [Massart (1990)]

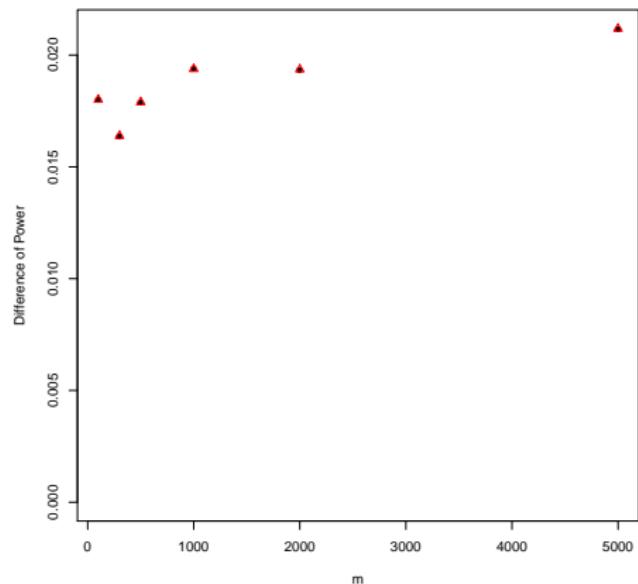
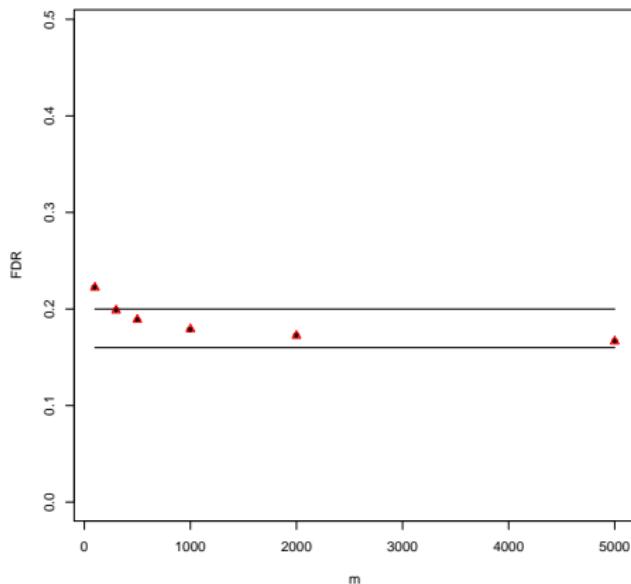
Stabilization for weak signal : $\bar{\mu} = 0.01$

$\pi_1 = \pi_2 = 0.5$, $\pi_0 = 0.8$, $\mu_1 = \bar{\mu}$, $\mu_2 = 2\bar{\mu}$, 1000 replications



Stabilization for strong signal : $\bar{\mu} = 3$

$\pi_1 = \pi_2 = 0.5$, $\mu_1 = \bar{\mu}$, $\mu_2 = 2\bar{\mu}$, 1000 replications



Closed testing for post hoc inference

Designed for FWER control [Marcus, Eric, and Gabriel (1976)]

- ▶ Form $H_{0,I} = \bigcap_{i \in I} H_{0,i}$ all intersection hypotheses
- ▶ Have a collection of α level local test ϕ_I
- ▶ Examples:
 - ▶ Bonferroni test $\phi_I = 1$ if $\exists i \in I : p_i \leq \alpha/|I|$
 - ▶ Simes test $\phi_I = 1$ if $\exists i \in I : p_{(i:I)} \leq \alpha i / |I|$ (under PRDS)
- ▶ Test $H_{0,I}$ only if all $H_{0,J}$, $J \supseteq I$, are rejected
- ▶ Reject the individual hypotheses $H_{0,i}$ such that $H_{0,\{i\}}$ has been rejected that way
- ▶ Then $\text{FWER}(\text{Closed testing}) \leq \alpha$

Closed testing for post hoc inference

[Goeman and Solari (2011)]

Main idea

The closed testing provides more information than just the individual rejects:

- ▶ Let \mathcal{X} the set of all I such that we rejected $H_{0,I}$
- ▶ Simultaneous guarantee over all $H_{0,I}$, $I \in \mathcal{X}$:

$$\mathbb{P}(\forall I \in \mathcal{X}, H_{0,I} \text{ is false}) \geq 1 - \alpha$$

Confidence bound derivation:

- ▶ $V_{GS}(S) = \max_{\substack{I \subseteq S \\ I \notin \mathcal{X}}} |I|$ is a confidence bound because

$$\begin{aligned}\exists S, |S \cap \mathcal{H}_0| > V_{GS}(S) &\implies \exists S, S \cap \mathcal{H}_0 \in \mathcal{X} \\ &\implies \exists I \in \mathcal{X}, H_{0,I} \text{ is true}\end{aligned}$$

- ▶ $V_{GS}(S) = V_{\mathfrak{R}}^*(S)$ with $\mathfrak{R} = (I, |I| - 1)_{I \in \mathcal{X}}$

DKWM use

- ▶ Let $S \subset \mathbb{N}_m$
- ▶ $N_t(S) = \sum_{i \in S} \mathbf{1}\{p_i(X) > t\}$
- ▶ $v = |S \cap \mathcal{H}_0|$

$$v \leq \min_{t \in [0,1)} \left(\frac{\sqrt{\log(1/\lambda)/2}}{2(1-t)} + \left\{ \frac{\log(1/\lambda)/2}{4(1-t)^2} + \frac{N_t(S)}{1-t} \right\}^{1/2} \right)^2$$

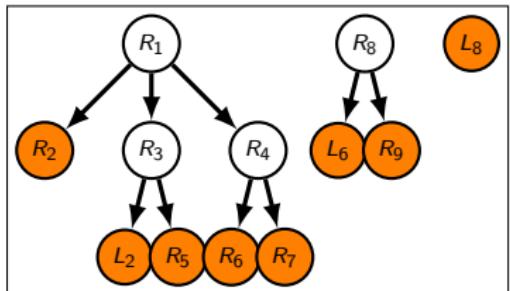
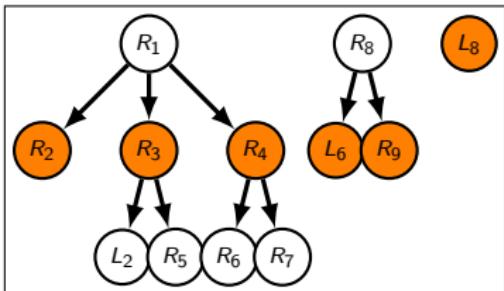
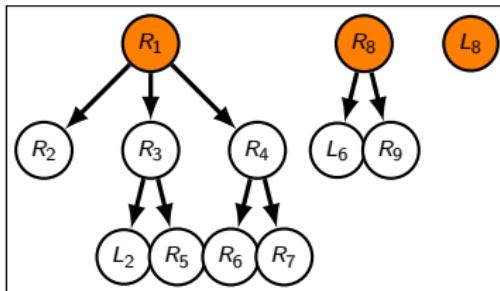
comes from

$$v^{-1} \sum_{i=1}^v \mathbf{1}\{U_i > t\} - (1-t) \geq -\sqrt{\log(1/\lambda)/(2v)}, \quad \forall t \in [0,1],$$

with probability at least $1 - \lambda$ (U_1, \dots, U_v i.i.d. uniform, $N_t(S)$ dominates $\sum_{i=1}^v \mathbf{1}\{U_i > t\}$ by independence)

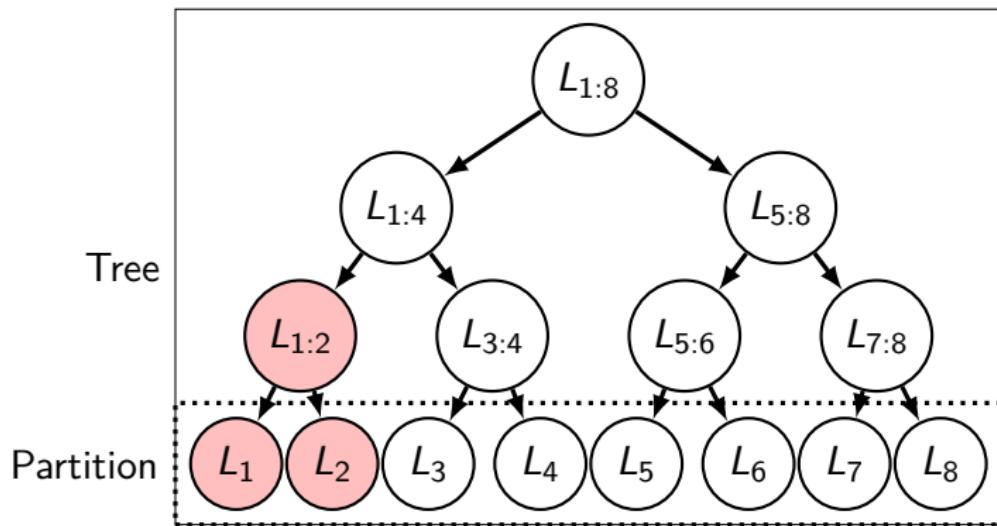
- ▶ $S = R_k$ and $\lambda = \alpha/K$ (union bound)

Forest algorithm

 \mathcal{K}_3  \mathcal{K}_2  \mathcal{K}_1 

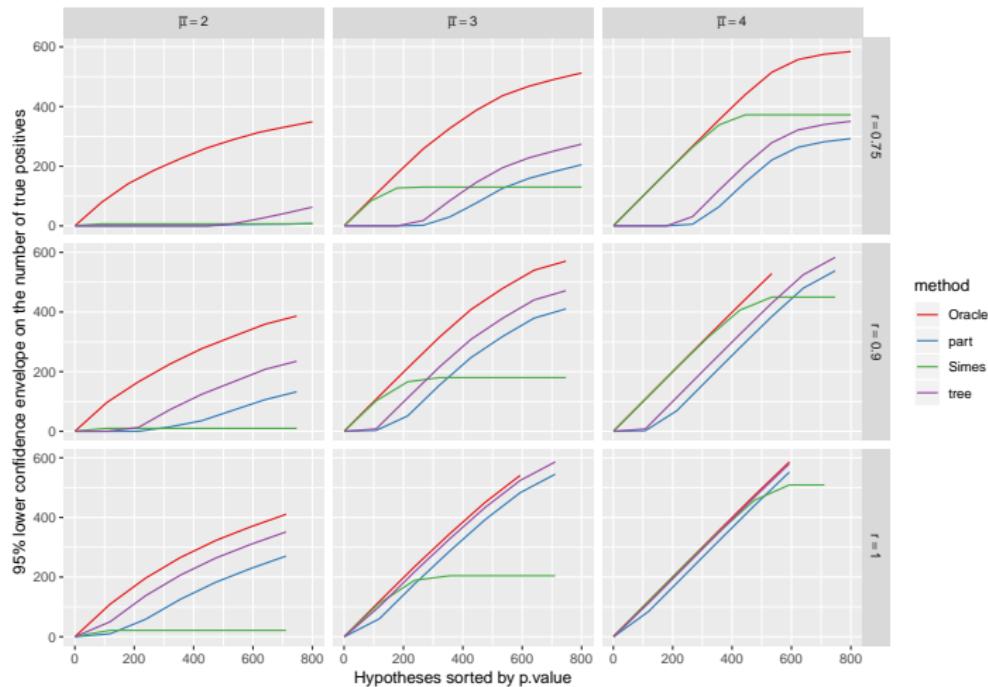
Comparison of Simes vs 2 new bounds

- ▶ V_{tree} and V_{part} : complete binary tree or only the leaves partition
- ▶ Signal in adjacent leaves, to test V_{tree} w.r.t V_{part}
- ▶ Parameters: signal $\bar{\mu}$ and signal proportion in active leaves r



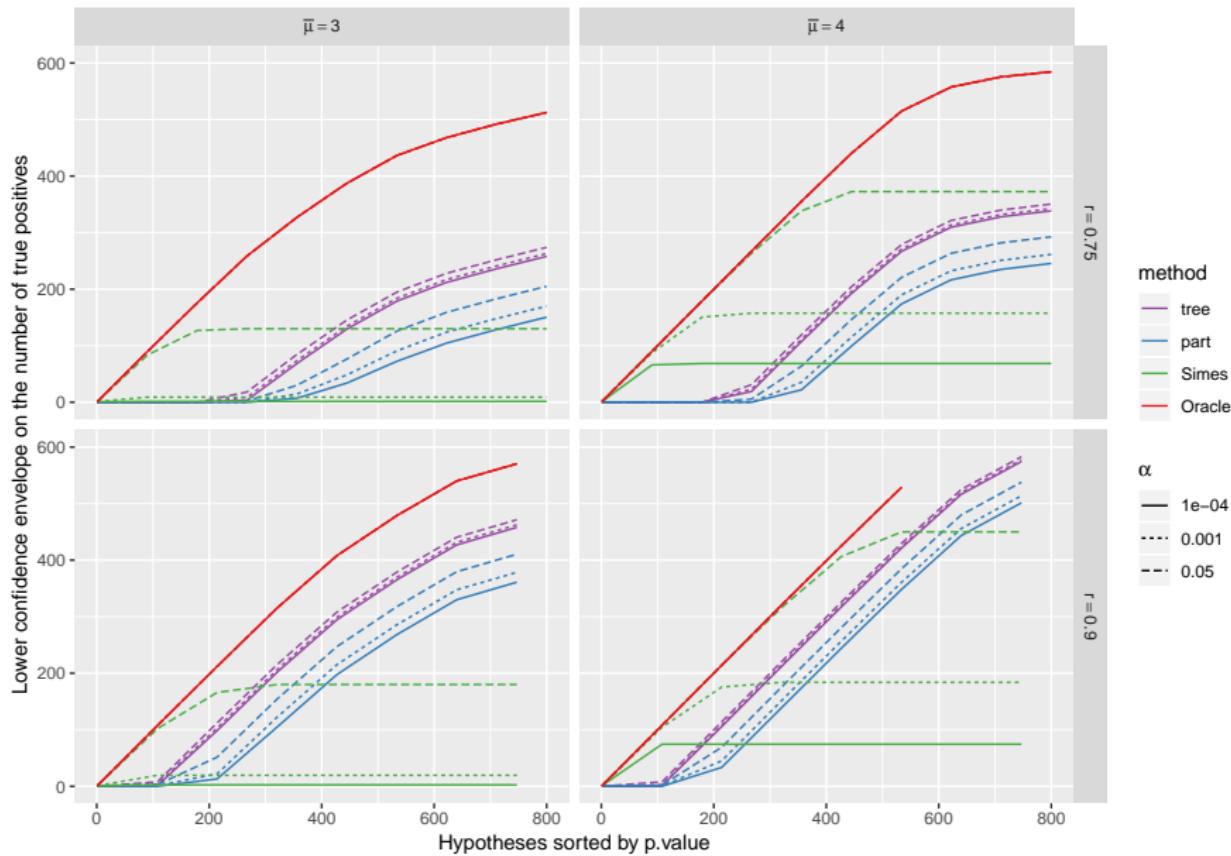
Comparison of Simes vs 2 new bounds

- The choice of S favors the Simes bound of BNR
- Simes better with $\bar{\mu}$, new bounds better with r
- V_{tree} better than V_{part} , despite union bound penalty



Comparison of 3 bounds

Influence of α



An example of discrete test

Fisher's exact test

- ▶ GWAS study
- ▶ Testing association between allele A and a phenotype (1) of interest

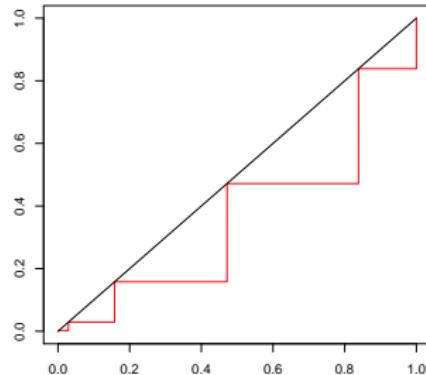
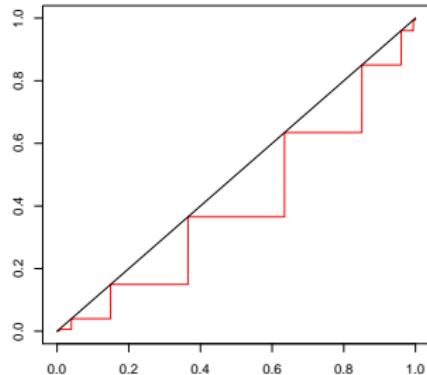
	Phenotype 1	Phenotype 2	Total
Allele A	$n_{1,A}$	$n_{2,A}$	n_A
Allele a	$n_{1,a}$	$n_{2,a}$	n_a
Total	n_1	n_2	N

- ▶ For large samples, χ^2 approximation: $E_{1,A} = \frac{n_1 n_A}{N}$, $\frac{(n_{1,A} - E_{1,A})^2}{E_{1,A}} + \dots$ follows χ^2 distribution under H_0
- ▶ What if we want an exact test ?
- ▶ Under H_0 , conditionally to n_1 and n_A , $n_{1,A} \sim \mathcal{H}(n_1, n_2, n_A)$, hypergeometric hence discrete

Issue of discrete p -values

Super-uniformity rather than uniformity under H_0

Let's see the c.d.f. of $\mathcal{H}(30, 30, 10)$ and $\mathcal{H}(14, 42, 6)$.



Super-uniformity under H_0

$$\mathbb{P}(p \leq u) \leq \mathbb{P}(U \leq u) = u$$

i.e under the null, our p -values are usually larger than uniforms

Issue of discrete p -values

Super-uniformity rather than uniformity under H_0

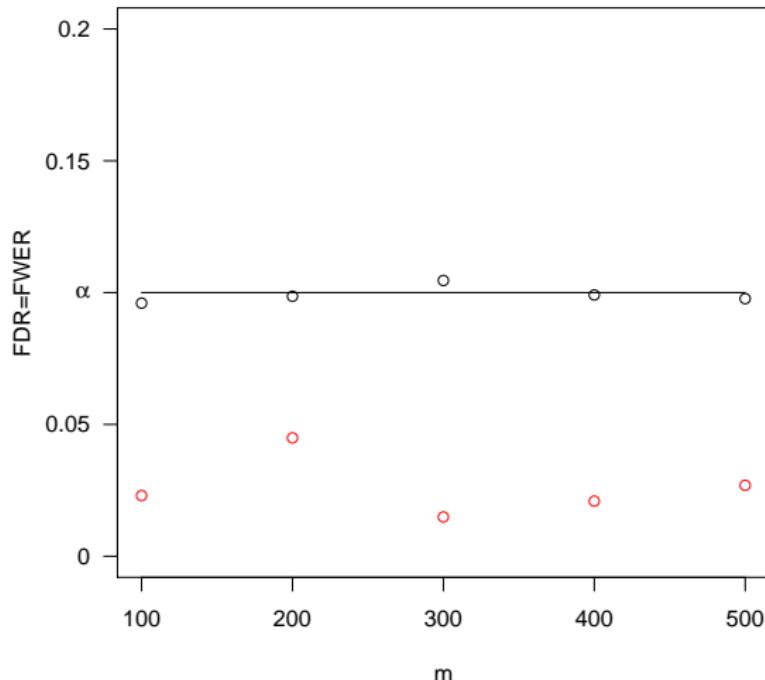
Problem

Usual MT procedures designed for uniformity

- ▶ As discrete p -values are larger than uniforms, classic thresholds are too conservative \implies loss of power

Issue of discrete p -values

Toy example: BH under full null, $m/2$ p -values $\sim \mathcal{H}(30, 30, 10)$, and $m/2$ p -values $\sim \mathcal{H}(14, 42, 6)$



In this section

- ▶ New procedures that use heterogeneous discrete distributions
- ▶ New FDR bounds and FDR control of our procedures
- ▶ Numerical illustrations

Back to BH (again)

- ▶ Reject all $p_i \leq \alpha \frac{\hat{k}}{m}$ where $\hat{k} = \max\{k : p_{(k)} \leq \alpha k/m\}$

Step-up procedure, critical constants

- ▶ Take a nondecreasing sequence (τ_k) , the critical constants
- ▶ Reject all $p_i \leq \tau_{\hat{k}}$ where $\hat{k} = \max\{k : p_{(k)} \leq \tau_k\}$

Examples:

- ▶ BH: $\tau_k = \alpha k/m$
- ▶ BY [Benjamini and Yekutieli (2001)]: $\tau_k = \alpha k / (m \times \sum_{i=1}^m i^{-1})$

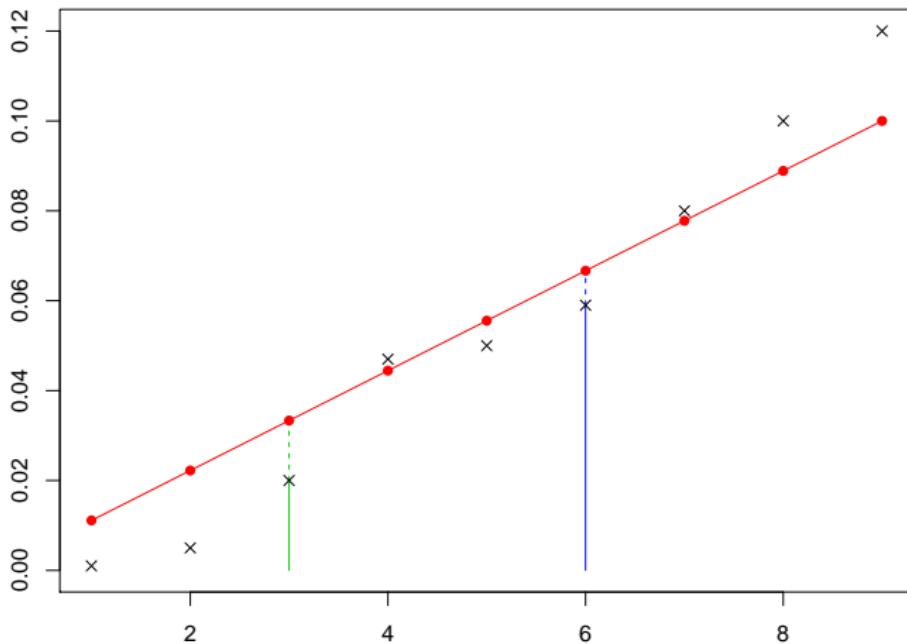
Step-down procedure

- ▶ Reject all $p_i \leq \tau_{\hat{k}}$ where $\hat{k} = \max\{k : \forall k' \leq k, p_{(k')} \leq \tau_{k'}\}$

Example:

- ▶ HB [Holm (1979)]: $\tau_k = \alpha / (m + k - 1)$

Step-up, step-down



Heyse procedure

[Heyse (2011)]

A step-up procedure

With $\tau_k = \max\{t \in \mathcal{A} : \bar{F}(t) \leq \alpha k/m\}$, where $\bar{F}(t) = \frac{1}{m} \sum_{i=1}^m F_i(t)$, F_i (known) c.d.f. under the null, \mathcal{A} discrete support of p -values

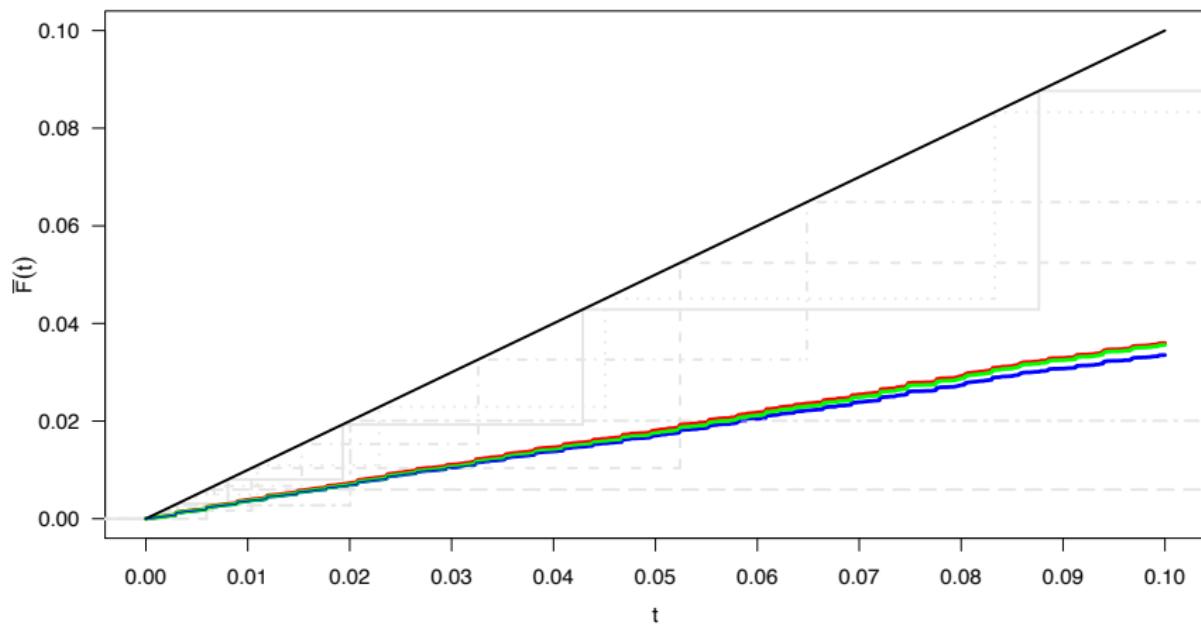
Main ideas:

- ▶ “Invert” \bar{F} at $\alpha k/m$
- ▶ As $\bar{F}(t) \leq t$, this yields larger critical values than BH
- ▶ The more $\bar{F}(t)$ is small compared to t , the larger are the τ_k
- ▶ But heterogeneity also needed, otherwise Heyse = BH (because $F_i(t) = t$ when $t \in \mathcal{A}_i$)

Heyse procedure

An illustration

- ▶ Compensation effect from heterogeneity



Heyse procedure

Problem

Heyse procedure does not control the FDR

Counter-examples exist

In the following

Build upon Heyse ideas but with FDR control

HSU and HSD

Slight modifications of \bar{F}

$$\bar{F}_{\text{SU}}(t) = \frac{1}{m} \sum_{i=1}^m \frac{F_i(t)}{1 - F_i(\tau_m)}; \quad \bar{F}_{\text{SD}}(t) = \frac{1}{m} \sum_{i=1}^m \frac{F_i(t)}{1 - F_i(t)}$$

where

$$\tau_m = \max\{t \in \mathcal{A} : \bar{F}_{\text{SD}}(t) \leq \alpha\}$$

HSU

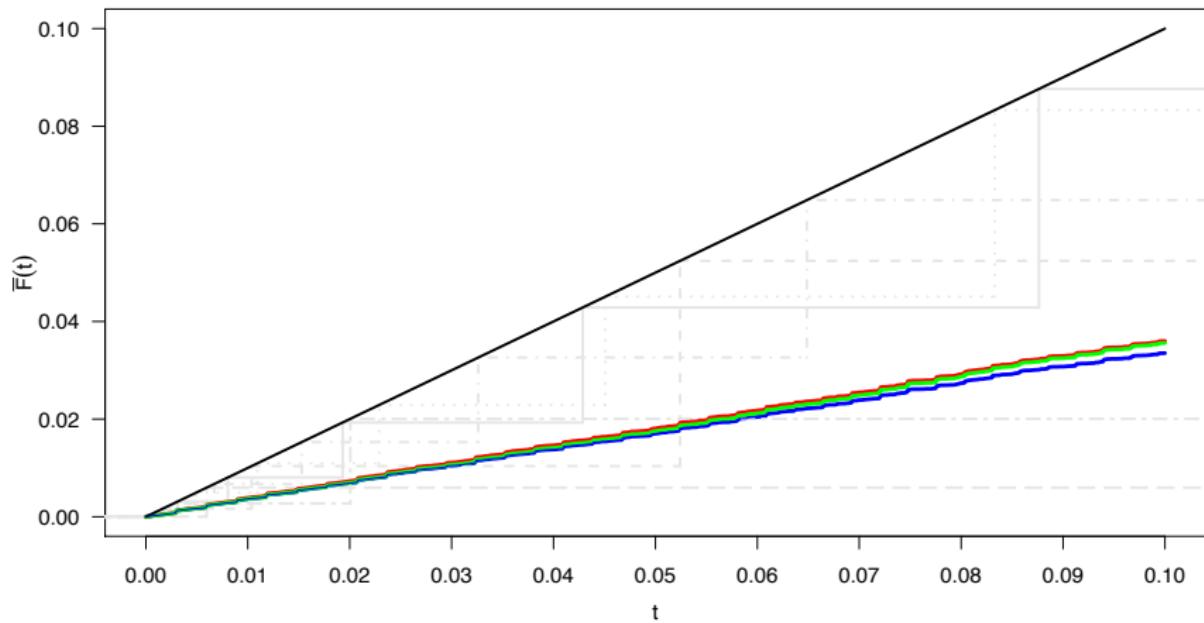
SU with $\tau_k = \max\{t \in \mathcal{A} : t \leq \tau_m, \bar{F}_{\text{SU}}(t) \leq \alpha k/m\}, k \leq m-1$

HSD

SD with $\tau_k = \max\{t \in \mathcal{A} : \bar{F}_{\text{SD}}(t) \leq \alpha k/m\}, k \leq m$

HSU and HSD

- ▶ $\bar{F}_{\text{SU}}, \bar{F}_{\text{SD}} \geq \bar{F}$
- ▶ But not that much!



AHSU ans AHSD

Adaptive procedures

AHSU

SU with $\tau_k =$

$$\max \left\{ t \in \mathcal{A} : t \leq \tau_m, \left(\frac{F(t)}{1-F(\tau_m)} \right)_{(1)} + \cdots + \left(\frac{F(t)}{1-F(\tau_m)} \right)_{(m-k+1)} \leq \alpha k \right\},$$
$$k \leq m-1$$

AHSD

SD with

$$\tau_k = \max \left\{ t \in \mathcal{A} : \left(\frac{F(t)}{1-F(t)} \right)_{(1)} + \cdots + \left(\frac{F(t)}{1-F(t)} \right)_{(m-k+1)} \leq \alpha k \right\}, \quad k \leq m$$

AHSU ans AHSD

Why “adaptive” ?

Back to HB

- ▶ SD with $\tau_k = \alpha/(m + k - 1)$
 - ▶ Sequential point of view: if $p_{(1)} \leq \alpha/m$, then at most $m - 1$ true nulls, let's see if $p_{(2)} \leq \alpha/(m - 1) \dots$
 - ▶ Adapts to the quantity of signal
 - ▶ Controls the FWER
-
- ▶ HSD is the discrete version of GBS [Gavrilov, Benjamini, and Sarkar (2009)]:
$$\tau_k = \frac{\alpha k}{m - (1 - \alpha)k + 1}$$
 - ▶ GBS itself is the FDR version of HB

New FDR bounds

Under independence

Theorem

$$\text{FDR}(\mathbf{SU}(\tau)) \leq \min \left(\sum_{i=1}^m \max_k \frac{F_i(\tau_k)}{k}, \right.$$
$$\left. \max_k \frac{1}{k} \left(\left(\frac{F(\tau_k)}{1 - F(\tau_m)} \right)_{(1)} + \cdots + \left(\frac{F(\tau_k)}{1 - F(\tau_m)} \right)_{(m-k+1)} \right) \right)$$

New FDR bounds

Under independence

Theorem

$$\text{FDR}(\mathbf{SD}(\tau)) \leq \min \left(\sum_{i=1}^m \max_k \frac{F_i(\tau_k)}{k}, \right.$$
$$\left. \max_k \frac{1}{k} \left(\left(\frac{F(\tau_k)}{1 - F(\tau_k)} \right)_{(1)} + \cdots + \left(\frac{F(\tau_k)}{1 - F(\tau_k)} \right)_{(m-k+1)} \right) \right)$$

Direct corollaries

Corollary

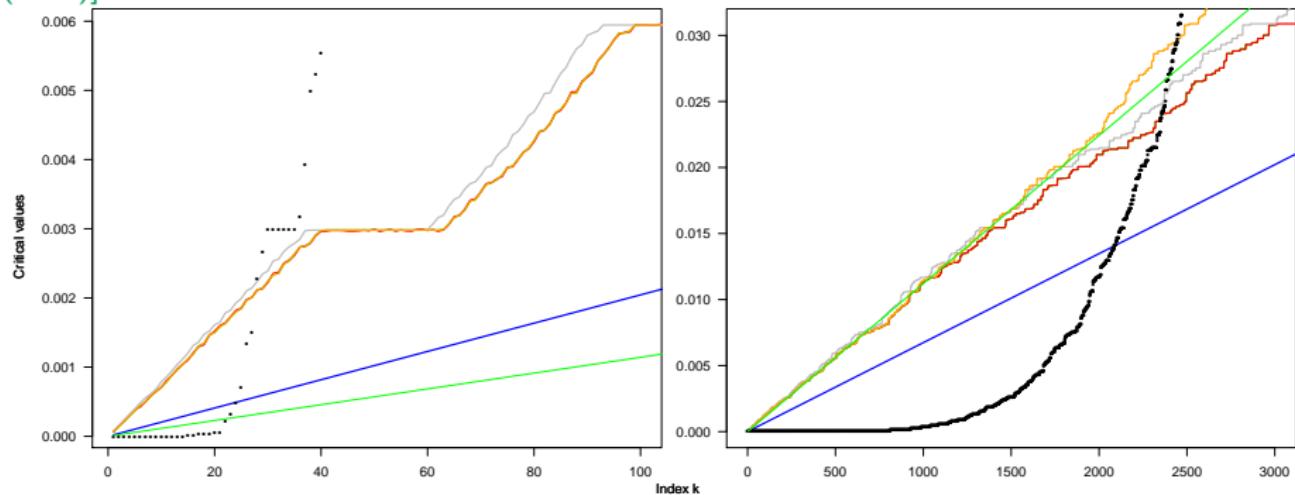
HSU, HSD, AHSU, AHSD all control the FDR under independence

Also recovery of other results

- ▶ FDR control under independence of BH and GBS
- ▶ [Blanchard and Roquain (2009)] recovered in a special case
- ▶ [Roquain and van de Wiel (2009)] recovered in finite sample \Rightarrow connection with weighting

Real data analysis

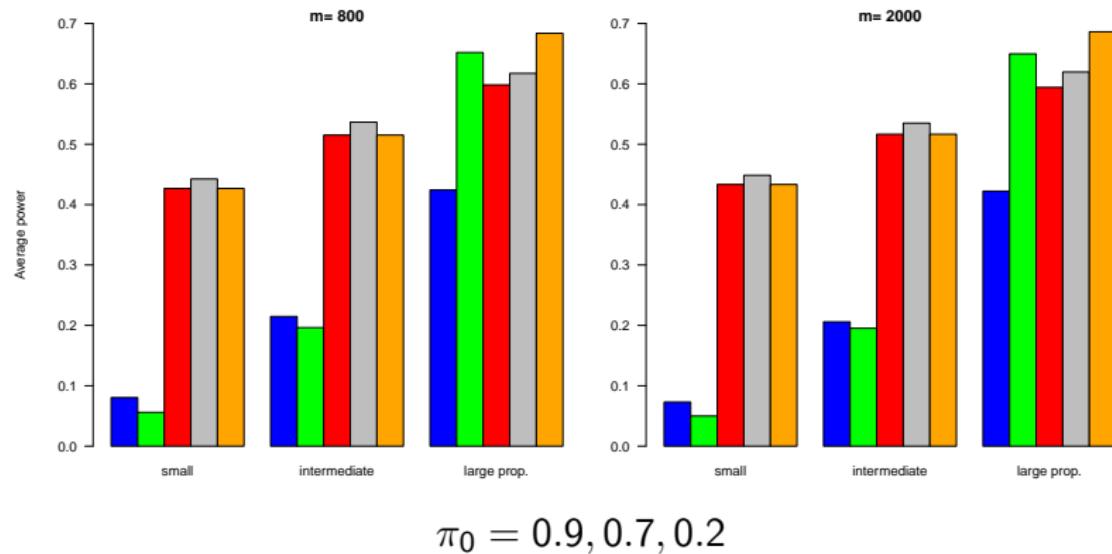
Pharmacovigilance data [Heller and Gur (2011)] and methylation data [Chen and Doerge (2015)]



- ▶ Blue: BH
- ▶ Red: HSU
- ▶ Green: Storey with $\lambda = 1/2$ but without censoring [Storey, Taylor, and Siegmund (2004)]
- ▶ Orange: AHSU
- ▶ Grey: Heyse

Simulations

Fisher's exact test on m contingency tables



Conclusion

- ▶ New powerful procedures well-suited for discrete tests under independence
- ▶ New bounds also relevant in other contexts (i.e. weighting)
- ▶ Positive dependence ? Any dependence ? [Döhler (2016)]
- ▶ π_0 estimation ?

A discrete procedure always better than BH: RBH

SU procedure

With $\tau_k = \lambda_\alpha k/m$, $\lambda_\alpha = \max\{\lambda \in [0, 1] : \Psi(\lambda_\alpha) \leq \alpha\}$, and

$$\Psi(\lambda) = \min \left(\lambda, \max_{1 \leq k \leq m} \left(\frac{1}{k} \sum_{i=1}^m \frac{F_i(\lambda k/m)}{1 - F_i(\lambda)} \right) \right)$$

- ▶ FDR control by the new FDR bounds
- ▶ If $\Psi(\lambda_\alpha) = \alpha$ then RBH always better than BH because $\alpha \leq \lambda_\alpha$