

p-filter: Multilayer False Discovery Rate for grouped hypotheses

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Joint work with (the excellent) Rina Foygel Barber, Martin Wainwright and Mike Jordan



Multiple comparisons & FDR control

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Example

True signals



Data: $Z_i \sim \mathcal{N}(\mu, 1)$, $P_i = 1 - \Phi(Z_i)$ for 1000 hypotheses.

10×100 grid : $\mu > 0$ for 100 pixels, $\mu = 0$ for 900 pixels.

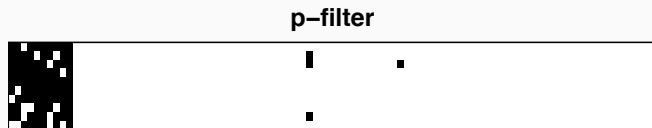
True signals have “small” p-values. Nulls have uniform p-values.

Example



Benjamini Hochberg with entry-level target $FDR = 0.2$.

Example



p-Filter with entry-level and column-level target $FDR = 0.2$

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- You may want to **group** together hypotheses that are likely to be null together or be non-null together.
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- In spatio-temporal applications, it might be natural to group hypotheses by space or time or space-time blocks. “Discovery at time/location x makes discoveries around x more likely”.
- In genetics, certain genes/proteins might be known to act together, or have similar molecular structure.
- We might have some prior guess about which hypotheses are more likely to be null or non-null.

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Partition 1 could be the set of all singletons,
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Partition 3 could be the set of all columns.
- Goal: select set $\hat{S} \subseteq [n]$ such that FDR is bounded simultaneously for partition $1, 2, \dots, M$.
Few falsely discovered singletons,
Few falsely discovered rows,
Few falsely discovered columns.

p-Filter: will discover $\hat{S} \subseteq [n]$ such that FDR is simultaneously controlled for all partitions.

Multilayer FDR

$$\alpha_{\text{indiv}} = 0.1$$

$$\alpha_{\text{group}} = 0.2$$

						Simes p-value
Group 1	0.03	0.01	0.18	0.04	0.08	0.05
Group 2	0.05	0.11	0.06	0.01	0.89	0.05
Group 3	0.14	0.12	0.58	0.11	0.11	0.18
Group 4	0.88	0.24	0.09	0.66	0.45	0.45

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FDR control with “internal consistency”:

Every rejected hypothesis is in some rejected group, and every rejected group contains at least one rejected hypothesis.

The p-Filter algorithm

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- Estimate FDP's for each partition: **correction**

$$\widehat{\text{FDP}}_m = \frac{t_m \cdot G_m}{|\hat{S}_m|} \leftarrow \begin{array}{l} \text{approx. \# false discoveries} \\ \text{\# discoveries} \end{array}$$

If $\widehat{\text{FDP}}_m > \alpha_m$, reduce t_m until $\widehat{\text{FDP}}_m$ is $\leq \alpha_m$ (discrete search)

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Note: Simes and BH are special cases when $M = 1$.

p-Filter controls FDR, finds max legal threshold

Theorem 2

p-Filter finds “maximum legal threshold”, and it controls FDR simultaneously $\forall m$:

$$\text{FDR for partition } m = \mathbb{E} \left[\frac{|\mathcal{H}_m^0 \cap \hat{S}_m|}{|\hat{S}_m|} \right] \leq \alpha_m \cdot \frac{|\mathcal{H}_m^0|}{G_m} \quad \forall m.$$

Furthermore, it halts in $G_1 + G_2 + \dots + G_M + 1$ outer loops.

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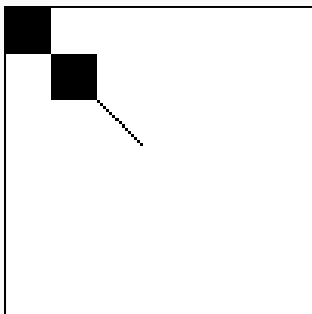
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Does not depend on order of specifying partitions.

Simulation results

True signals



p-Filter: entries + rows + columns (3 partitions)

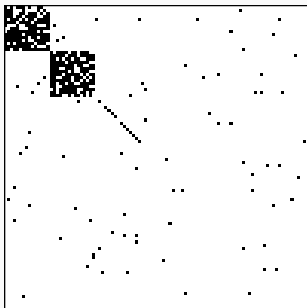
BB: entries + rows (2 partitions, constrained to be hierarchical)

BH: entries only

Target FDR: $\alpha_{\text{entries}} = \alpha_{\text{rows}} = \alpha_{\text{columns}} = 0.2$

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BH



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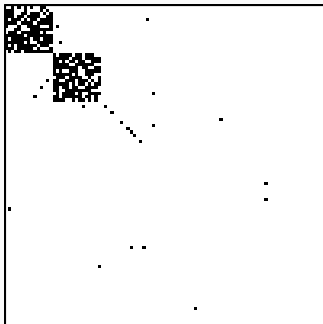
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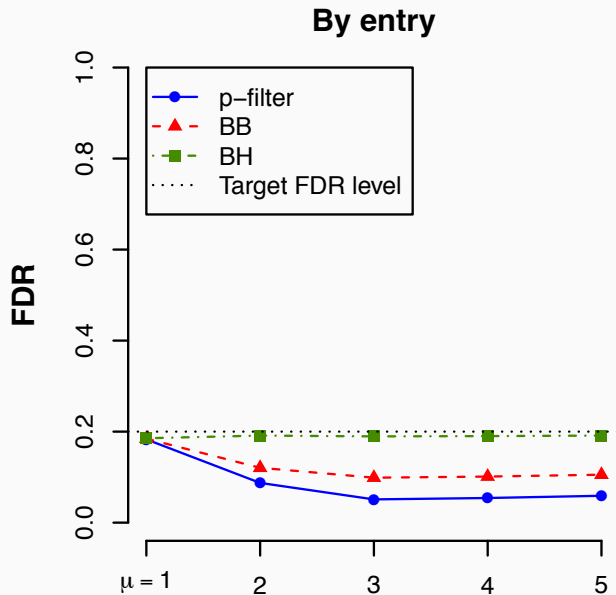
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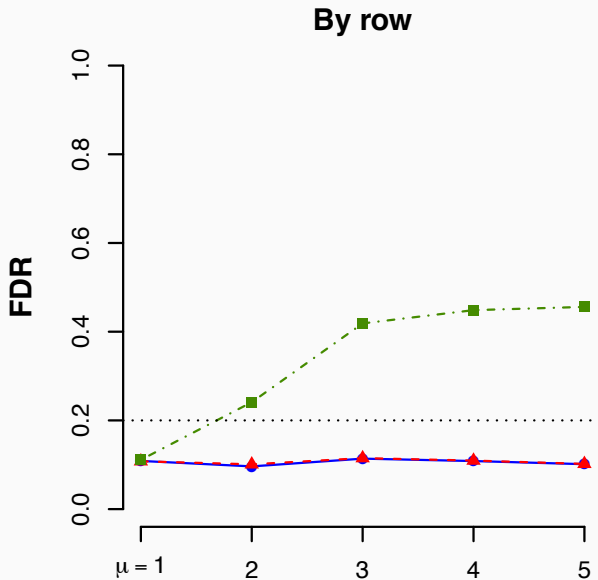
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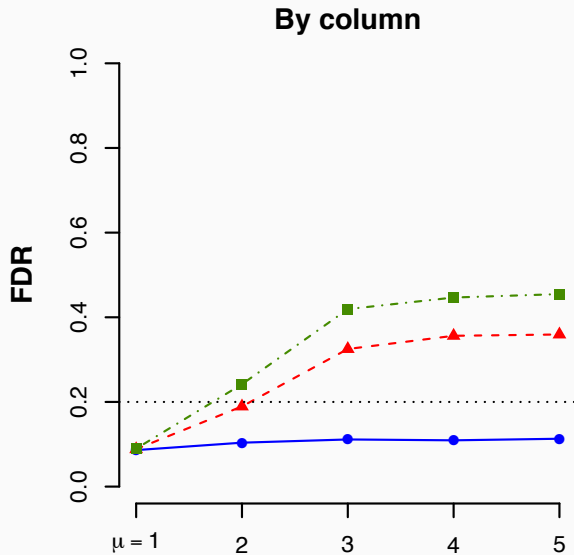
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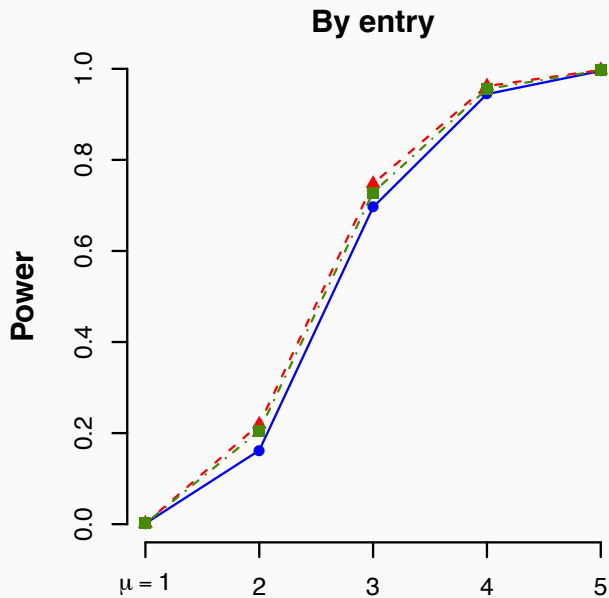
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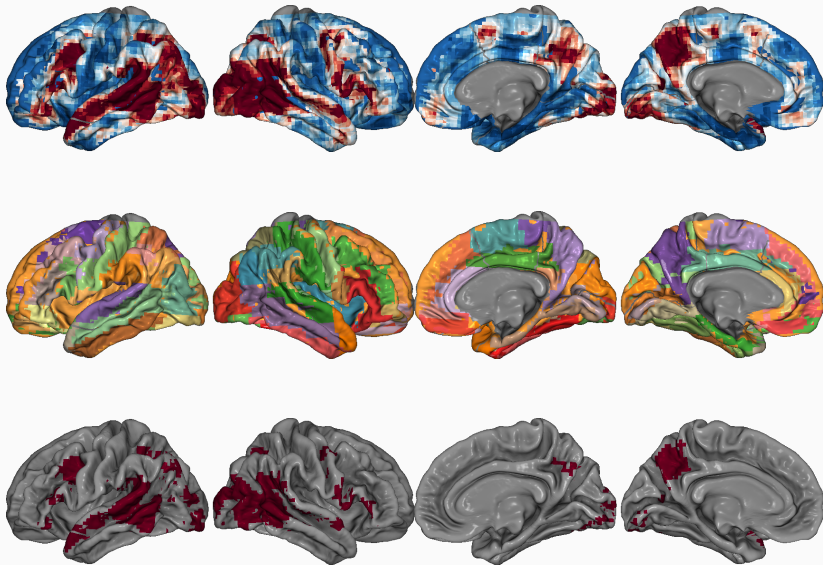
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A neuroscience example

- 8 subjects read Chapter 9 of Harry Potter, 1 word = 0.5 sec.
- fMRI recording: 40,000 voxels, 1 scan = 2 sec.
- Consider semantic features of the text (NLP techniques).
- Try to find dependence between text presented at time t with voxel activity at time $t + \delta$, for delay $\delta = 0, 2, 4, 6, 8$ sec.
- One p-value per voxel, per delay δ .
- Can group by space, time or space-time blocks.

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Big Picture¹

Summary:

- $m = 1$: p-Filter is a strict generalization of BH and Simes.

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- Can incorporate weights, at hypothesis and group level.
- Can incorporate “null-proportion” estimation.
- Can have overlapping groups, incomplete partitions, etc.

Orthogonal Works (in progress):

- Improved algorithms for online FDR.

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