AdaPT: Interactive Multiple Testing with Side Information

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Side Information

Setting: hypotheses $H_1, \ldots, H_n$ with p-values $p_1, \ldots, p_n$

Observe side information $x_i \in \mathcal{X}$ for each H_i

Examples:

- Identifying differentially expressed genes with "prioritization scores" (priors, auxiliary information, etc.)
- Spatiotemporal testing;
- Clinical meta-analysis;

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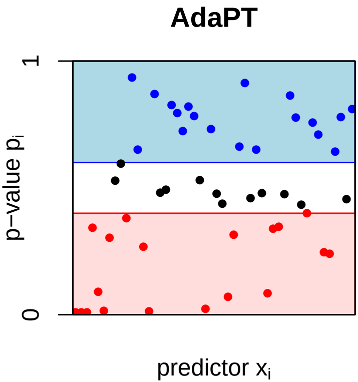
Goal: produce hypothesis-specific p-value thresholds s_i's and control False Discovery Rate (FDR).

AdaPT, Visualized



Step t:

Covariate-dependent threshold $s_t(x)$

Mirror image $1 - s_t(x)$

$$\widehat{\mathrm{FDP}}_t = \frac{\#\text{ blue points} + 1}{\#\text{ red points} \vee 1}$$

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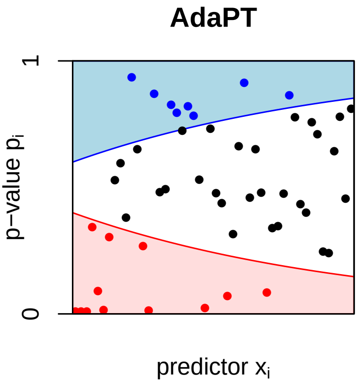

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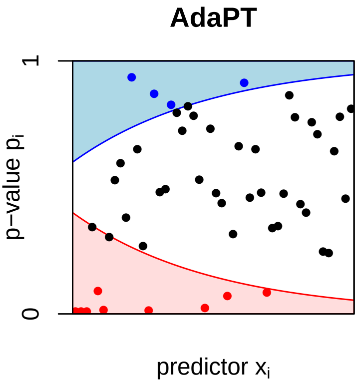

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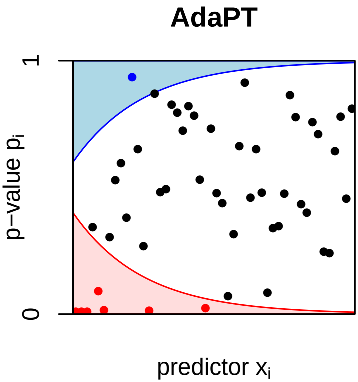

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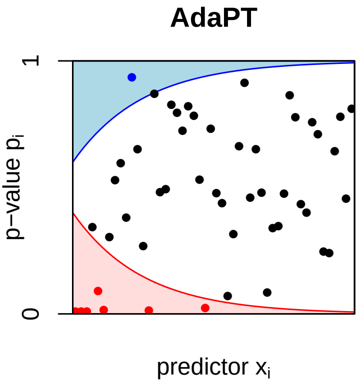

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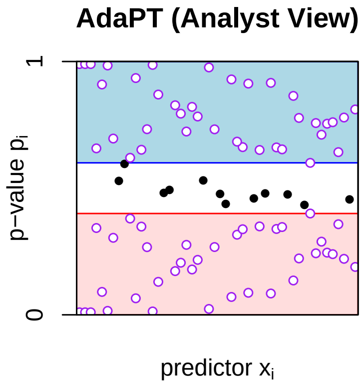
Stop when $\widehat{\mathrm{FDP}}_t \leq \alpha$, and reject all red points

AdaPT, "Analyst View"

Define partially masked p-values:

$$\tilde{p}_{t,i} = \begin{cases} p_i & s_t(x_i) < p_i < 1 - s_t(x_i) \\ \{p_i,\ 1 - p_i\} & \text{otherwise.} \end{cases}$$



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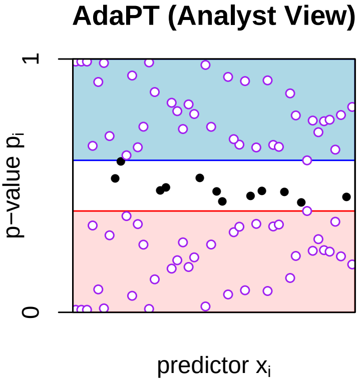

To select $s_{t+1}(x)$, we can use:

- $x_1, \ldots, x_n$
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Any such update rule is OK

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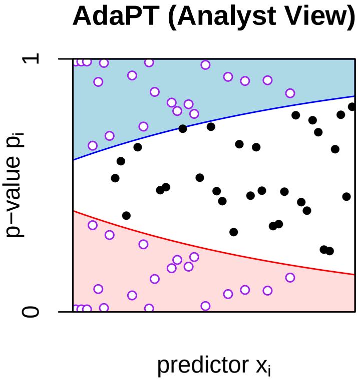

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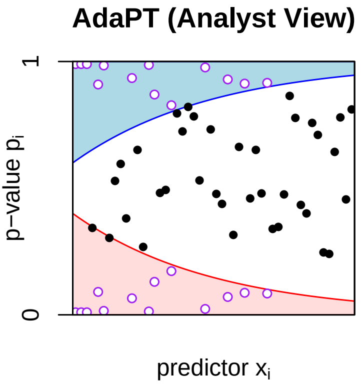

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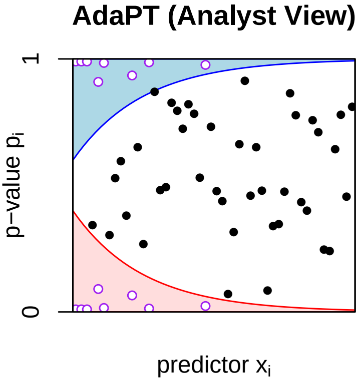

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Don't worry. Use your favorite model to guide the update!

THANKS!