README

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Methods based on On Online Control of False Discovery Rate, Javanmard & Montanari 2015

Definition 0.1 (Cluster-Adaptive LBORD). Let τ_i be the last rejection before hypothesis i. Let c_{i-1} be the number of consecutive rejections up to i-1. We apply a constant function as adaptive rejection boundary.

(0.2)
$$\alpha_i = \begin{cases} \beta_{i-\tau_i} & \text{for } c_{i-1} < r \\ m\alpha & \text{for } c_{i-1} \ge r \end{cases}$$

where $\{\beta\}$ is a converging decreasing infinite sequence summing to α , and r is a positive integer and $m\alpha < 1$.

Then update

(0.3)
$$c_i = \begin{cases} c_{i-1} + 1 & \text{if } p_i \text{ is rejected} \\ 0 & \text{if fails to reject.} \end{cases}$$

Remark 0.4. Intuitively, the parameter r represents the amount of evidence needed to admit a sequence as a cluster, and parameter m represents how much more liberal would clustered hypothesis receive.

1. Adaptive Forgiving LBORD

Definition 1.1 (Adaptive Forgiving LBORD). Let τ_i and c_{i-1} be as defined above. For each hypothesis i, use the rejection boundary

$$(1.2) \alpha_i = \beta_{i-\tau_i}$$

If the p-value is rejected, go to the next hypothesis, and update

$$(1.3) c_i = c_{i-1} + 1.$$

If p-value is not rejected. Test it again using

$$\zeta_i = \frac{1}{2}\alpha c_{i-1}$$

And update

$$(1.5) c_i = c_{i-1} - \frac{1}{\alpha}.$$

otherwise, set $c_i = 0$

Remark 1.6. The sequence of rejection produced by this algorithm divides into a set that is rejected by the first boundary (by β sequence) and a set rejected by the second boundary (by ζ sequence).

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