Summary

This method is built upon the Benjamini and Hochberg method in the previous paper. They argue that the old method, when applied to genomics, which often has many hypotheses to test, is too conservative. The method they propose is similar to Benjamini and Hochberg method, but with an extra parameter to scale the p-values, which can be estimated.

Reaction

Another interesting paper on multiple comparisons, which is still used today. They briefly talk about the bias variance tradeoff when choosing lambda, but it seems like choosing lambda is somewhat arbitrary which could lead to multiple interpretations of this method.

Questions

The paper is related to genomics, but I wonder if there is another field that this would be relevant too. We talked about the fmri paper which may be one such example.

I’m still unsure of how lambda is chosen. Do you just look at the p-values and choose what you think looks good? Are there any tricks to choosing it or is it that straight forward?