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Robust joint statistical tests for DNA methylation data

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T he detection of differential methylation between the control and case group of a disease of interest remains a challenging task. Reliable result depends on a correct employment of robust statistical tests. In the past, the hypothesis testing for methylation data is mainly focused on the equality of means while the intrinsic variability in the methylation data has often been ignored. Many statistical tests that could incorporate the variability into the testing procedure rely on the assumption of either normality or absence of outliers. Consequently, these tests are not very robust when applied to real data. In this talk, we will present three robust statistical tests that can test the equality of both means and variances simultaneously. Results from simulation studies and real data analyses suggest that our proposed methods are more powerful and robust in comparison with other three bench mark testing procedures.

Recent Publications

- 1. Gold N, Frasch M, Herry C, Richardson B and Wang X (2018) A doubly stochastic change point detection algorithm for noisy biological signals. Frontiers in Computational Physiology and Medicine 8:1112.
- 2. Li X, Qiu W, Morrow J, Weiss J, Fu Y and Wang X (2015) A comparative study of tests for homogeneity of variances with application of DNA methylation data. PLOS One 10(12):e0145295.
- 3. Wang Q, Gold N, Frasch M, Huang H Â and Wang X (2015) Mathematical model of cardiovascular and metabolic responses to umbilical cord occlusions in fetal sheep. Bulletin of Mathematical Biology 77(12):2264-2293.

Biography

Xiaogang Steven Wang is currently a Professor in Statistics at the Department of Mathematics and Statistics, York University, Toronto, Canada. He was an expertise in bioinformatics, data mining, machine learning and biostatistics. He developed several effective clustering algorithms including one for categorical data and one for protein data. He also worked on developing algorithms for handling nonstationary biological times series data. Besides of machine learning, he has been working on analyzing DNA methylation data.