MULTIPLE TESTING IN CONTINGENCY TABLES

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We propose a simple method for testing the independence in rxc contingency tables using multiple testing procedures and confidence intervals for the multinomial proportions. We compare this novel method with some recent approaches based on multiple testing procedures and residual analysis for contingency tables [Kim, S.B., Tsui, K-L. and Borodovsky, M. (2006) 'Multiple testing in large-scale contingency tables: inferring patterns of pair-wise amino acid association in β-sheets', Int. J. Bioinformatics Research and Applications, Vol. 2, No. 2, pp.193–217]. Finally, we apply the proposed methodology to identify patterns of codons associations for two species: Homo sapiens and Pan troglodytes.

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