Assessment of Susceptibility Risk Factors for ADHD in Imaging Genetic Studies


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Abstract

Objective:
ADHD consists of a count of symptoms that often presents heterogeneity due to overdispersion and excess of zeros. Statistical inference is usually based on a dichotomous outcome that is underpowered. The main goal of this study was to determine a suited probability distribution to analyze ADHD symptoms in Imaging Genetic studies.

Method:
We used two independent population samples of children to evaluate the consistency of the standard probability distributions based on count data for describing ADHD symptoms.

Results:
We showed that the zero-inflated negative binomial (ZINB) distribution provided the best power for modeling ADHD symptoms. ZINB reveals a genetic variant, rs273342 (Microtubule-Associated Protein [MAPRE2]), associated with ADHD (p value = 2.73E-05). This variant was also associated with perivascular volumes (Virchow–Robin spaces; p values < 1E-03). No associations were found when using dichotomous definition.

Conclusion:
We suggest that an appropriate modeling of ADHD symptoms increases statistical power to establish significant risk factors.