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Authors

Kaiser, KA, Gadbury, GL

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Abstract

BACKGROUND/AIMS: The rising prevalence of human obesity worldwide has focused research on a variety of interventions that result in highly varied degrees of weight loss (WL). The advent of genomic testing has quantified estimates of both the contribution of genetic factors to the development of obesity as well as racial/ethnic variation of risk alleles across subpopulations. More recent studies have examined genetic associations with effectiveness of WL interventions, but to date are unable to explain a large proportion of the variance observed.

METHODS: We describe and provide two illustrations of statistical methods to estimate upper and lower bounds of WL treatment response heterogeneity (TRH) in the absence of genotypic data, using published summary statistics and a raw data set from WL studies.

RESULTS: Thirty-two studies had some evidence of a positive mean treatment effect with respect to the control intervention. Twelve of these 32 studies reported WL TRH. Of these 12, 3 demonstrated an estimated proportion of >5% of the sampled population having an outcome opposite the mean effect. In the raw data set, bounds estimations for change in waist circumference revealed tighter ranges in men than women.

CONCLUSION: Future studies may be able to take advantage of multiple approaches, including the method we describe, to identify and quantify the presence of TRH in studies of WL or related outcomes.