

Accepted Manuscript

A simulations approach for meta-analysis of genetic association studies based on additive genetic model

Majnu John, Todd Lencz, Anil K Malhotra, Christoph U Correll, Jian-Ping Zhang

PII: S2214-5400(18)30018-5
DOI: doi:[10.1016/j.mgene.2018.02.004](https://doi.org/10.1016/j.mgene.2018.02.004)
Reference: MGENE 403

To appear in: *Meta Gene*

Received date: 17 November 2017
Revised date: 29 January 2018
Accepted date: 12 February 2018



Please cite this article as: John, Majnu, Lencz, Todd, Malhotra, Anil K, Correll, Christoph U, Zhang, Jian-Ping, A simulations approach for meta-analysis of genetic association studies based on additive genetic model, *Meta Gene* (2018), doi:[10.1016/j.mgene.2018.02.004](https://doi.org/10.1016/j.mgene.2018.02.004)

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

A simulations approach for meta-analysis of genetic association studies based on additive genetic model

Majnu John^{a,b,c,1}, Todd Lencz^{a,b,d}, Anil K Malhotra^{a,b,d}, Christoph U Correll^{a,b,d}, Jian-Ping Zhang^{a,b,d}

^aCenter for Psychiatric Neuroscience,
The Feinstein Institute of Medical Research,
Manhasset, NY.

^bPsychiatry Research, Zucker Hillside Hospital,
Northwell Health System,
Glen Oaks, NY.

^cDepartment of Mathematics,
Hofstra University,
Hempstead, NY.

^dDepartments of Psychiatry and of Molecular Medicine,
Hofstra Northwell School of Medicine,
Hempstead, NY.

Abstract

Meta-analysis of genetic association studies is being increasingly used to assess phenotypic differences between genotype groups. When the underlying genetic model is assumed to be dominant or recessive, assessing the phenotype differences based on summary statistics, reported for individual studies in a meta-analysis, is a valid strategy. However, when the genetic model is additive, a similar strategy based on summary statistics will lead to biased results. This fact about the additive model is one of the things that we establish in this paper, using simulations. The main goal of this paper is to present an alternate strategy for the additive model based on simulating data for the individual studies. We show that the alternate strategy is far superior to the strategy based on summary statistics.

Keywords:

genetic association studies; meta analysis; additive model; summary statistics; simulations; GWAS; 2×2 table; odds ratio

¹Corresponding author: 350 Community Drive, Manhasset, NY 11030. e-mail: mjohn5@northwell.edu, Phone: +01 718 470 8221, Fax: +01 718 343 1659

Download English Version:

<https://daneshyari.com/en/article/8389103>

Download Persian Version:

<https://daneshyari.com/article/8389103>

[Daneshyari.com](https://daneshyari.com)