

Statistics >

Download:

- [PDF](#)
- [PostScript](#)
- [Other formats](#)

Current browse context:

stat.ME

[< prev](#) | [next >](#)

[new](#) | [recent](#) | [1010](#)

Change to browse by:

[q-bio](#)

[q-bio.GN](#)

[stat](#)

References & Citations

- [NASA ADS](#)

Bookmark([what is this?](#))



Methodology

A Bayesian Method for Detecting and Characterizing Allelic

Heterogeneity and Boosting Signals in Genome- Wide Association Studies

Zhan Su, Niall
Cardin, the
Wellcome Trust
Case Control
Consortium,
Peter Donnelly,
Jonathan
Marchini

*(Submitted on 22
Oct 2010)*

The
standard
paradigm
for the
analysis
of
genome-
wide
association
studies