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Dear Editors,

We would like to submit our manuscript entitled "Eagle makes multi-locus association mapping on a genome-wide scale routine" for consideration in Bioinformatics.

We are looking to bring significant change to the area of genome-wide association studies by bringing a step-change to association mapping. Currently, data are analyzed, almost exclusively, on a locus-by-locus basis. More sophisticated multi-locus methods are available but are not being used in practice. We believe this poor uptake of multi-locus methods is due to them not scaling well with sample size, the results they produce being difficult to interpret, and many of the computer packages implementing these methods still sitting at the prototype stage. With *Eagle* we have solved these problems.

Eagle has the following advantages over its rivals
  • It is statistically superior by finding more true results while avoiding false results.
  • Its results are immediately interpretable.
  • Huge data sets can be analyzed in the same time as single-locus analysis.
  • The package has been developed with future development in mind.
  • Easy to install and easy to use (via our GUI).
  • It has extensive supporting resources (http://eagle.r-forge.r-project.org)

For the first time, geneticists will have access to a multi-locus association mapping tool that makes the analysis of GWAS data routine.

On behalf of the authors,

Dr Andrew George
CSIRO