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ABSTRACT

Motivation: Many tools for GWAS and NGS in Bioconductor. Very few tools for pooled seq gwas in R. large datasets in R because of new hig performance packages. Works well on desktop and cluster configurations. Open source on github, sample dataset available. Fast and intuitive methods for biology scientist to perform gwas analysis. Time consuming

[illegible]

Availability: genewiseR is open source and easily downloadable at [github](#) here. The

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1 INTRODUCTION

Text Text. Figure 1 shows that the above method Text Text Text Text Text Text Text Text Text Text Text Text Text Text. (Bag *et al.*, 2001) wants to know about text follows.

(1)

2 APPROACH

Equation (1) Text Text Text Text Text Text Text Text Text Text Text
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that the above method Text Text Text Text Text Text Text Text Text
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3 METHODS

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- for bulleted list, use itemize
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