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## ABSTRACT

### Motivation:

R is the language of choice for statistical analysis in genomic research. This is because of its open source nature and the advance collection of R packages for statistical tests and visualisation of data. In GWAS studies, pooled sequencing is gaining popularity. Many tools exist to work with next-gen sequencing data in a gwas study; Bioconductor and Python are the go to places. Very few packages and tools exist for pooled seq gwas in R. This is mainly because of slow speed and memory constraints for R when working with large datasets. New high performance computing techniques in R have enabled the fulfillment of this gap. Works well on desktop and cluster configurations. Open source. Fast and intuitive methods for biology scientist to perform gwas analysis.

**Results:** The availability of genewiseR on github makes it easy for scientists to install the package in their development environment is perform gwas analysis with ease. Because of addition on bootstrapping feature for p-values of snps, this package allow scientist to identify noise in their data and reduce the dataset early on in their gwas analysis.

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

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## 1 INTRODUCTION

- what is gwas?
- why pool seq and why new skills and large datasets?
- why snps to genes?
- study design to make use of genewiseR

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## 2 DESCRIPTION

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- Hypothesis testing, QC with bootstrapping
- Multiple testing correction
- Snps to Genes
- Calc gene level statistics
- LD assesment
- Utilities required by biologist

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\*to whom correspondence should be addressed

**Table 1.** This is table caption

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row3	row3	row3	row3
row4	row4	row4	row4

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**Fig. 1.** Caption, caption.

**Fig. 2.** Caption, caption.

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### 3 EXAMPLE

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## 4 VALIDATION OR CONCLUSION

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## ACKNOWLEDGEMENT

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*Funding:* Text Text Text Text Text Text Text Text.

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