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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

Availability: genewiseR is open source and easily downloadable at github here. The

Contact: jain.nehil@gmail.com

1 INTRODUCTION

$$\sum x + y = Z \tag{1}$$

2 APPROACH

3 METHODS

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| row3 | row3 | row3 | row3 |
| row4 | row4 | row4 | row4 |

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4 DISCUSSION

5 CONCLUSION

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- 3. this is item, use enumerate

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