

Application Note

skater: An R package for SNP-based Kinship Analysis and Benchmarking

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Abstract

Motivation: This section should specifically state the scientific question within the context of the field of study.

Results: This section should summarize the scientific advance or novel results of the study, and its impact on computational biology.

Availability: This section should state software availability if the paper focuses mainly on software development or on the implementation of an algorithm. Examples are: 'Freely available on the web at XXX.' Website implemented in Perl, MySQL and Apache, with all major browsers supported'; or 'Source code and binaries freely available for download at URL, implemented in C++ and supported on linux and MS Windows'. The complete address (URL) should be given. If the manuscript describes new software tools or the implementation of novel algorithms the software must be freely available to non-commercial users. Authors must also ensure that the software is available for a full TWO YEARS following publication. The editors of Bioinformatics encourage authors to make their source code available and, if possible, to provide access through an open source license.

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Supplementary information: Supplementary data are available at Bioinformatics Online.

1 Introduction

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2 The skater package

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3 Functions and usage

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3.1 Pedigree processing

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3.2 IBD segment analysis

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3.3 Additional features and built-in data

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4 Conclusion

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Acknowledgements

These should be included at the end of the text and not in footnotes. Please ensure you acknowledge all sources of funding, see funding section below.

Details of all funding sources for the work in question should be given in a separate section entitled ‘Funding’. This should appear before the ‘Acknowledgements’ section.

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- Grant numbers should be given in brackets as follows: ‘[grant number xxxx]’
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References