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MEDIPS: genome-wide differential coverage analysis of sequencing data derived from DNA enrichment experiments

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Abstract

MOTIVATION:

DNA enrichment followed by sequencing is a versatile tool in molecular biology, with a wide variety of applications including genome-wide analysis of epigenetic marks and mechanisms. A common requirement of these diverse applications is a comparison of read coverage between experimental conditions. The amount of samples generated for such comparisons ranges from few replicates to hundreds of samples per condition for epigenome-wide association studies. Consequently, there is an urgent need for software that allows for fast and simple processing and comparison of sequencing data derived from enriched DNA.

RESULTS:

Here, we present a major update of the R/Bioconductor package MEDIPS, which allows for an arbitrary number of replicates per group and integrates sophisticated statistical methods for the detection of differential coverage between experimental conditions. Our approach can be applied to a diversity of quantitative sequencing data. In addition, our update adds novel functionality to MEDIPS, including correlation analysis between samples, and takes advantage of Bioconductor's annotation databases to facilitate annotation of specific genomic regions.

AVAILABILITY AND IMPLEMENTATION:

The latest version of MEDIPS is available as version 1.12.0 and part of Bioconductor 2.13. The package comes with a manual containing detailed description of its functionality and is available at <http://www.bioconductor.org>.

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