Resource Summary Report

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Differential Methylation Analysis Package

RRID:SCR_019148
Type: Tool

Proper Citation

Differential Methylation Analysis Package (RRID:SCR_019148)

Resource Information

URL: https://www.otago.ac.nz/chatterjee-lab/tools/index.html

Proper Citation: Differential Methylation Analysis Package (RRID:SCR_019148)

Description: Software package for large scale genomic DNA methylation analysis. Filters and processes aligned bisulphite sequenced data to generate comprehensive reference methylomes in different units for any genome. Processes aligned SAM files of multiple samples to provide reliable and statistically significant differentially methylated regions, then relate them to proximal genes and CpG features with reasonable rapidity.

Abbreviations: DMAP

Resource Type: software application, software toolkit, data analysis software, data processing software, software resource

Defining Citation: PMID:24608764

Keywords: Genomic DNA methylation, DNA methylation analysis, bisulphite sequenced data, reference methylomes generation, genome, aligned SAM files processing, differentially methylated regions

Funding: National Centre for Growth and Development and Health Research Council ; New Zealand

Availability: Free, Freely available

Resource Name: Differential Methylation Analysis Package

Resource ID: SCR_019148

Record Creation Time: 20220129T080343+0000

Record Last Update: 20250525T031612+0000

Ratings and Alerts

No rating or validation information has been found for Differential Methylation Analysis Package.

No alerts have been found for Differential Methylation Analysis Package.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.