Resource Summary Report

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SDMINP

RRID:SCR_009377
Type: Tool

Proper Citation

SDMINP (RRID:SCR_009377)

Resource Information

URL: https://www.dkfz.de/en/epidemiologie-krebserkrankungen/software/software.html

Proper Citation: SDMINP (RRID:SCR_009377)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 24,2023. Software program for fast calculation of empirical and adjusted p-values for correlated and uncorrelated hypotheses in multiple testing experiments. It is based on the Free Step-Down Resampling Method for controlling the Family Wise Error Rate, originally proposed by Westfall and Young (1993), and implements a variation of the efficient algorithm of Ge et al. (2003), in which the originally necessary re-sampling effort was reduced considerably and the method made computationally more feasible. The program is independent of the underlying test statistic and works with provided observed and permutation test statistics. (entry from Genetic Analysis Software)

Abbreviations: SDMINP

Synonyms: Step-Down MIN P-value

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, python 2.3.5, unix, linux, ms-windows

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SDMINP

Resource ID: SCR_009377

Alternate IDs: nlx_154612

Old URLs: http://www.dkfz.de/SDMinP/

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260905T133251+0000

Ratings and Alerts

No rating or validation information has been found for SDMINP.

No alerts have been found for SDMINP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.