Resource Summary Report

Generated by NIF on Apr 21, 2025

BOOSTRAPPER

RRID:SCR_009135
Type: Tool

Proper Citation

BOOSTRAPPER (RRID:SCR_009135)

Resource Information

URL: http://bioinfo.ebc.ee/download/

Proper Citation: BOOSTRAPPER (RRID:SCR_009135)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 16,2023. Robust haploblock border reliability estimation tool implemented for LD based haploblock detection method. The most important new features are bootstrapping and overlapping block borders. (entry from Genetic Analysis Software)

Abbreviations: BOOSTRAPPER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, ms-window, linux

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BOOSTRAPPER

Resource ID: SCR_009135

Alternate IDs: nlx_154250

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250421T053719+0000

Ratings and Alerts

No rating or validation information has been found for BOOSTRAPPER.

No alerts have been found for BOOSTRAPPER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Andreson R, et al. (2008) Predicting failure rate of PCR in large genomes. Nucleic acids research, 36(11), e66.

Andreson R, et al. (2006) SNPmasker: automatic masking of SNPs and repeats across eukaryotic genomes. Nucleic acids research, 34(Web Server issue), W651.