# **Resource Summary Report**

Generated by dkNET on Apr 18, 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: 20250416T063537+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 dkNET.

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.