

# Resource Summary Report

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## SNPHARVESTER

RRID:SCR\_008536

Type: Tool

### Proper Citation

SNPHARVESTER (RRID:SCR\_008536)

### Resource Information

**URL:** <http://bioinformatics.ust.hk/SNPHarvester.html>

**Proper Citation:** SNPHARVESTER (RRID:SCR\_008536)

**Description:** Software tool for detecting epistatic interactions in genome-wide association studies (entry from Genetic Analysis Software)

**Abbreviations:** SNPHARVESTER

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic, java

**Resource Name:** SNPHARVESTER

**Resource ID:** SCR\_008536

**Alternate IDs:** nlx\_154643

**Record Creation Time:** 20220129T080248+0000

**Record Last Update:** 20260919T195755+0000

### Ratings and Alerts

No rating or validation information has been found for SNPHARVESTER.

No alerts have been found for SNPHARVESTER.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 6 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

Tang DY, et al. (2024) SEEI: spherical evolution with feedback mechanism for identifying epistatic interactions. BMC genomics, 25(1), 462.

Tuo S, et al. (2018) FDHE-IW: A Fast Approach for Detecting High-Order Epistasis in Genome-Wide Case-Control Studies. Genes, 9(9).

Tuo S, et al. (2017) Niche harmony search algorithm for detecting complex disease associated high-order SNP combinations. Scientific reports, 7(1), 11529.

Jiang X, et al. (2015) Learning Predictive Interactions Using Information Gain and Bayesian Network Scoring. PloS one, 10(12), e0143247.

Lee JY, et al. (2013) A SNP Harvester Analysis to Better Detect SNPs of CCDC158 Gene That Are Associated with Carcass Quality Traits in Hanwoo. Asian-Australasian journal of animal sciences, 26(6), 766.

Anuniação O, et al. (2013) Using information interaction to discover epistatic effects in complex diseases. PloS one, 8(10), e76300.