

# Resource Summary Report

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## HAPSIMU

RRID:SCR\_009235

Type: Tool

### Proper Citation

HAPSIMU (RRID:SCR\_009235)

### Resource Information

**URL:** <http://l.web.umkc.edu/liujian/>

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**Description:** Software platform that is based on real haplotype data from the HapMap ENCODE project that can simulate heterogeneous populations with various known and controllable structures under the continuous migration model or the discrete model. Moreover, both qualitative and quantitative traits can be simulated using additive genetic model with various genetic parameters designated by users. (entry from Genetic Analysis Software)

**Abbreviations:** HAPSIMU

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

**Keywords:** gene, genetic, genomic, c++

**Resource Name:** HAPSIMU

**Resource ID:** SCR\_009235

**Alternate IDs:** nlx\_154394

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20260829T183106+0000

### Ratings and Alerts

No rating or validation information has been found for HAPSIMU.

No alerts have been found for HAPSIMU.

### Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Mourad R, et al. (2011) A hierarchical Bayesian network approach for linkage disequilibrium modeling and data-dimensionality reduction prior to genome-wide association studies. BMC bioinformatics, 12, 16.

Zhang F, et al. (2008) HAPSIMU: a genetic simulation platform for population-based association studies. BMC bioinformatics, 9, 331.

Liu J, et al. (2007) Bayesian mapping of quantitative trait loci for multiple complex traits with the use of variance components. American journal of human genetics, 81(2), 304.