## **Resource Summary Report**

Generated by dkNET on May 9, 2025

# forqs

RRID:SCR\_000643

Type: Tool

### **Proper Citation**

forqs (RRID:SCR\_000643)

#### **Resource Information**

URL: https://bitbucket.org/dkessner/forqs

**Proper Citation:** forgs (RRID:SCR\_000643)

**Description:** Software for forward-in-time population genetics simulation that tracks individual haplotype chunks as they recombine each generation. It also also models quantitative traits and selection on those traits.

Abbreviations: forgs

Synonyms: Forward-in-time simulation of Recombination, and Selection, Quantitative traits

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

**Defining Citation: PMID:24336146** 

**Keywords:** c++, linux, osx, windows, command line, simulation, recombination, quantitative trait, selection, haplotype pattern

**Funding:** NHGRI HG002536; NHGRI R01 HG007089; NSF EF-0928690

Availability: BSD License

Resource Name: forqs

Resource ID: SCR\_000643

Alternate IDs: OMICS\_02196

**Record Creation Time:** 20220129T080202+0000

Record Last Update: 20250508T064647+0000

## **Ratings and Alerts**

No rating or validation information has been found for forqs.

No alerts have been found for forqs.

### **Data and Source Information**

Source: SciCrunch Registry

# Usage and Citation Metrics

We have not found any literature mentions for this resource.