

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

IcMLkin

RRID:SCR_025418

Type: Tool

Proper Citation

IcMLkin (RRID:SCR_025418)

Resource Information

URL: <https://github.com/COMBINE-lab/maximum-likelihood-relatedness-estimation>

Proper Citation: IcMLkin (RRID:SCR_025418)

Description: C++ program to infer biological relatedness from low coverage 2nd generation sequencing data. It uses information from genotype likelihoods rather than observed genotypes in maximum likelihood framework in order to estimate the overall coefficient of relatedness as well as individual kinship components between two samples. Maximum Likelihood Estimation of Biological Relatedness from Low Coverage Sequencing Data.

Synonyms: Maximum Likelihood Estimation of Relatedness

Resource Type: source code, software resource

Defining Citation: [DOI:10.1101/023374](https://doi.org/10.1101/023374)

Keywords: C++, Maximum Likelihood Estimation, Biological Relatedness, Low Coverage Sequencing Data,

Funding: NSF

Availability: Free, Available for download, Freely available

Resource Name: IcMLkin

Resource ID: SCR_025418

Record Creation Time: 20240621T053253+0000

Record Last Update: 20260801T042932+0000

Ratings and Alerts

No rating or validation information has been found for IcMLkin.

No alerts have been found for IcMLkin.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Gretzinger J, et al. (2025) Ancient DNA connects large-scale migration with the spread of Slavs. Nature, 646(8084), 384.

Xiong J, et al. (2025) The genomic history of East Asian Middle Neolithic millet- and rice-agricultural populations. Cell genomics, 100976.

Gretzinger J, et al. (2024) Evidence for dynastic succession among early Celtic elites in Central Europe. Nature human behaviour, 8(8), 1467.

DeCasien AR, et al. (2024) Evolutionary and biomedical implications of sex differences in the primate brain transcriptome. Cell genomics, 4(7), 100589.