

Resource Summary Report

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READ

RRID:SCR_026958

Type: Tool

Proper Citation

READ (RRID:SCR_026958)

Resource Information

URL: <https://bitbucket.org/tguenther/read/src/master/>

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Description: Software tool to infer family relationships for degraded samples. Used to infer degree of relationship (up to second degree, i.e. nephew/niece-uncle/aunt, grandparent-grandchild or half-siblings) for pair of low-coverage individuals.

Synonyms: Relationship Estimation from Ancient DNA

Resource Type: software application, software resource

Defining Citation: [PMID:29684051](#)

Keywords: infer family relationships, degraded samples, infer degree of relationship,

Funding: European Research Council ;
Swedish Research Council ;
Uppsala Multidisciplinary Center for Advanced Computational Science

Availability: Free, Freely available

Resource Name: READ

Resource ID: SCR_026958

Record Creation Time: 20250517T055756+0000

Record Last Update: 20260810T040921+0000

Ratings and Alerts

No rating or validation information has been found for READ.

No alerts have been found for READ.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Zenczak M, et al. (2026) Genetic genealogy of the Piast dynasty and related European royal families. *Nature communications*, 17(1).

Nedoluzhko A, et al. (2025) Ancient DNA analysis of elite nomadic warrior from Chinge-Tey I funerary commemorative complex in the "Valley of the Kings", Tuva. *BMC genomics*, 26(1), 220.

Saag L, et al. (2025) North Pontic crossroads: Mobility in Ukraine from the Bronze Age to the early modern period. *Science advances*, 11(2), eadr0695.

Wang R, et al. (2025) East and West admixture in eastern China of Tang Dynasty inferred from ancient human genomes. *Communications biology*, 8(1), 219.

Sun L, et al. (2025) The demic expansion of Yangshao culture inferred from ancient human genomes. *BMC biology*, 23(1), 186.

Wang J, et al. (2025) Ancient DNA reveals a two-clanned matrilineal community in Neolithic China. *Nature*, 643(8074), 1304.

Zou Y, et al. (2025) Ancient genomes from the Yellow River Bend reveal long-distance population interactions between the Central Plains, Steppe, and southern China. *Cell reports*, 44(8), 116034.

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

Heraclides A, et al. (2024) Palaeogenomic insights into the origins of early settlers on the island of Cyprus. *Scientific reports*, 14(1), 9632.

Seki RP, et al. (2024) National Politics' Role in Developing Primary Health Care Policy for Maternal Health in Papua New Guinea: A Qualitative Document Analysis. *Global health, science and practice*, 12(5).

Varga GIB, et al. (2024) Archaeogenetic analysis revealed East Eurasian paternal origin to the Aba royal family of Hungary. *iScience*, 27(10), 110892.

Valentim O, et al. (2024) "This Is Me" an Awareness-Raising and Anti-Stigma Program for Undergraduate Nursing Students: A Pre-Post Intervention Study. *Nursing reports (Pavia, Italy)*, 14(4), 2956.

Shapaer T, et al. (2024) Elevated BEAN1 expression correlates with poor prognosis, immune evasion, and chemotherapy resistance in rectal adenocarcinoma. *Discover oncology*, 15(1), 446.

Ye J, et al. (2024) Secular trend of gout incidence in the UK: an age-period-cohort analysis. *BMJ open*, 14(1), e079665.

Palladino R, et al. (2024) Trajectories and management of vascular risk following the diagnosis of multiple sclerosis: A population-based matched cohort study between 1987 and 2018 in England. *Multiple sclerosis (Houndmills, Basingstoke, England)*, 30(13), 1653.

Langley K, et al. (2023) Can a nation-wide e-cohort of ADHD and ASD in childhood be established using Welsh routinely available datasets? *BMJ open*, 13(8), e071851.

Bandyopadhyay A, et al. (2023) Factors associated with low school readiness, a linked health and education data study in Wales, UK. *PloS one*, 18(12), e0273596.

Marsh WA, et al. (2023) Inferring biological kinship in ancient datasets: comparing the response of ancient DNA-specific software packages to low coverage data. *BMC genomics*, 24(1), 111.

Wang CC, et al. (2021) Genomic insights into the formation of human populations in East Asia. *Nature*, 591(7850), 413.

Capodiferro MR, et al. (2021) Archaeogenomic distinctiveness of the Isthmo-Colombian area. *Cell*, 184(7), 1706.