

Resource Summary Report

Generated by [NIF](#) on Sep 2, 2026

TreeMix

RRID:SCR_021636

Type: Tool

Proper Citation

TreeMix (RRID:SCR_021636)

Resource Information

URL: <https://bitbucket.org/nygcresearch/treemix>

Proper Citation: TreeMix (RRID:SCR_021636)

Description: Software tool for inferring patterns of population splits and mixtures in history of set of populations.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:23166502](#)

Keywords: Inferring patterns, population splits, common ancestor, population mixtures, ancestral populations, ancestral populations graph, allele frequencies

Availability: Free, Freely available

Resource Name: TreeMix

Resource ID: SCR_021636

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260829T182722+0000

Ratings and Alerts

No rating or validation information has been found for TreeMix.

No alerts have been found for TreeMix.

Data and Source Information

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Kou Y, et al. (2026) Haplotype-resolved T2T genome and population resequencing provide insights into the domestication and mogroside biosynthesis of *Siraitia grosvenorii* (Cucurbitaceae). *Horticulture research*, 13(7), uhag103.

Jain R, et al. (2026) Layers in the sand: The genetic imprint of migration, culture, and Indus craft in the Thar Desert. *HGG advances*, 7(3), 100623.

Zhu XL, et al. (2025) Potential risk of dipterocarps in the marginal Asian rainforests: low population size and high genomic erosion. *BMC biology*, 23(1), 161.

Zhao Y, et al. (2025) The origin and evolution of cultivated rice and genomic signatures of heterosis for yield traits in super-hybrid rice. *BMC biology*, 23(1), 153.

Floridia V, et al. (2025) Uncovering the architecture of production-driven introgression in Cinisara cattle breed. *BMC genomic data*, 26(1), 47.

Xia X, et al. (2025) Orogeny and High Pollen Flow as Driving Forces for High Genetic Diversity of Endangered *Acer griseum* (Franch.) Pax Endemic to China. *International journal of molecular sciences*, 26(2).

Floridia V, et al. (2025) Genomic insights on the history and selection trajectories of the Comune di Sicilia goat. *BMC genomic data*, 26(1), 78.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Reeves IM, et al. (2025) Admixture Increases Genetic Diversity and Adaptive Potential in Australasian Killer Whales. *Molecular ecology*, 34(23), e17689.

Pongsanarm T, et al. (2025) Genetic and geographical insights call for early conservation of Mae Hong Son's blue mahseer to prevent population crisis. *PloS one*, 20(2), e0313505.

Schmidtman C, et al. (2021) Assessing the genetic background and genomic relatedness of red cattle populations originating from Northern Europe. *Genetics, selection, evolution : GSE*, 53(1), 23.

Fitak RR, et al. (2021) OptM: estimating the optimal number of migration edges on population trees using Treemix. *Biology methods & protocols*, 6(1), bpab017.

Sudrajat P, et al. (2020) An insight into the evolutionary history of Indonesian cattle assessed by whole genome data analysis. *PloS one*, 15(11), e0241038.

Gómez-Bahamón V, et al. (2020) Speciation Associated with Shifts in Migratory Behavior in an Avian Radiation. *Current biology* : CB, 30(7), 1312.

Kim JY, et al. (2019) Dissection of soybean populations according to selection signatures based on whole-genome sequences. *GigaScience*, 8(12).