

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

FLOSS

RRID:SCR_000836

Type: Tool

Proper Citation

FLOSS (RRID:SCR_000836)

Resource Information

URL: <http://faculty.washington.edu/browning/floss/floss.htm>

Proper Citation: FLOSS (RRID:SCR_000836)

Description: Software application that performs ordered subset analysis using MERLIN's output .lod file created with the --perFamily option. Ordered subset analysis uses covariate information to identify a more homogenous subset of families for linkage analysis. The homogeneous subset of families does not need to be specified a priori, and the covariates can include environmental exposures, quantitative traits, or linkage scores at another locus in the genome. The evidence for linkage is evaluated with a permutation test. (entry from Genetic Analysis Software)

Abbreviations: FLOSS

Synonyms: FLexible Ordered SubSet analysis

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, bio.tools

Resource Name: FLOSS

Resource ID: SCR_000836

Alternate IDs: biotools:floss, nlx_154319

Alternate URLs: <https://bio.tools/floss>

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260805T044014+0000

Ratings and Alerts

No rating or validation information has been found for FLOSS.

No alerts have been found for FLOSS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.