

# Resource Summary Report

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## FLOSS

RRID:SCR\_000836

Type: Tool

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### Proper Citation

FLOSS (RRID:SCR\_000836)

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### 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:** 20260829T183038+0000

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### Ratings and Alerts

No rating or validation information has been found for FLOSS.

No alerts have been found for FLOSS.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.