Happy
RRID:SCR_001395
Type: Tool

Proper Citation

Happy (RRID:SCR_001395)

Resource Information

URL: http://www.well.ox.ac.uk/happy/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28, 2023. Software package for Multipoint QTL Mapping in Genetically Heterogeneous Animals (entry from Genetic Analysis Software) The method is implemented in a C-program and there is now an R version of HAPPY. You can run HAPPY remotely from their web server using your own data (or try it out on the data provided for download).

Abbreviations: HAPPY

Synonyms: reconstructing HAPlotYpes

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

Defining Citation: PMID:11050180, DOI:10.1073/pnas.230304397

Keywords: qtl, quantitative trait locus, r, c, gene, genetic, genomic, ansi c, unix, irix, sunos, linux, animal model, trait, map, genotype, phenotype, haplotype, linear regression, data set, qtl mapping

Funding Agency: Wellcome Trust

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Happy
**Ratings and Alerts**

No rating or validation information has been found for Happy.

No alerts have been found for Happy.

**Data and Source Information**

**Source:** SciCrunch Registry

**Usage and Citation Metrics**

We found 45 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.

Fleck SJ, et al. (2024) High quality genomes produced from single MinION flow cells clarify polyploid and demographic histories of critically endangered Fraxinus (ash) species. Communications biology, 7(1), 54.

Chang HS, et al. (2023) Emotional tones of voice affect the acoustics and perception of Mandarin tones. PloS one, 18(4), e0283635.


Dorman A, et al. (2021) Genetic mapping of novel modifiers for ApcMin induced intestinal
polyps’ development using the genetic architecture power of the collaborative cross mice. BMC genomics, 22(1), 566.


