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: 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). HAPPY's analysis is essentially two stage; ancestral haplotype reconstruction using dynamic programming, followed by QTL testing by linear regression: * Assume that at a QTL, a chromosome originating from the progenitor strain, labelled s, contributes an unknown additive amount Ts to the phenotype, so that the expected genetic effect for a diploid individual with ancestral alleles labelled s,t at the trait locus is Ts+Tt; a test for a QTL is equivalent to testing for differences between the Ts's. * A dynamic-programming algorithm is used to compute the probability Fn(s,t) that a given individual has the ancestral alleles s, t at locus labelled n, conditional upon all the genotype data for that individual. Then the expected phenotype is 2 Sums Ts Sumt Fn(s,t), and the Ts are estimated by a linear regression of the observed phenotypes on these expected values across all individuals, followed by an analysis of variance to test whether the progenitor estimates differ significantly. * The method's power depends on the ability to distinguish ancestral haplotypes across the interval; clearly the power will be lower if all markers in a region have the same type of non-informative allele distribution, but the markers can share information where there is a mixture. HAPPY is written in ANSI C. It has been compiled and tested on various UNIX platforms (Linux, IRIX, SunOS). It requires the NAG C library, so you will need a license for this product in order to compile the program locally. The source code for HAPPY is available for non-commercial users only by anonymous ftp.
**Resource Type:** Resource, software resource, software application, data analysis software, data processing software, source code

**References:** PMID:11050180

**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

**Parent Organization:** Wellcome Trust Centre for Human Genetics

**Funding Agency:** Wellcome Trust

**Availability:** Non-commercial, Commercial use with permission

**Website Status:** Last checked up

**Abbreviations:** HAPPY

**Resource Name:** Happy

**Resource ID:** SCR_001395

**Alternate IDs:** nlx_152594

**Alternate URLs:** http://www.well.ox.ac.uk/~rmott/happy.html

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**Ratings and Alerts**

No rating or validation information has been found for Happy.

No alerts have been found for Happy.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 37 mentions in open access literature.

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


Cao Y, et al. (2017) Low Mood Leads to Increased Empathic Distress at Seeing Others'
Pain. Frontiers in psychology, 8, 2024.


