Resource Summary Report

Generated by dkNET on Apr 17, 2025

Happy

RRID:SCR_001395
Type: Tool

Proper Citation

Happy (RRID:SCR_001395)

Resource Information

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

Proper Citation: Happy (RRID:SCR_001395)

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 analysis software, software application, data processing software, software resource

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: Wellcome Trust

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Happy

Resource ID: SCR_001395

Alternate IDs: nlx_152594

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

Old URLs: https://sources.debian.org/src/r-other-mott-happy.hbrem/

Record Creation Time: 20220129T080207+0000

Record Last Update: 20250417T065042+0000

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 46 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

Perrier A, et al. (2024) Maternal inheritance of functional centrioles in two parthenogenetic nematodes. Nature communications, 15(1), 6042.

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

Watson A, et al. (2023) Longitudinal associations between weight status and academic achievement in primary school children. Pediatric obesity, 18(1), e12975.

Ho V, et al. (2022) The Acceptability of Digital Technology and Tele-Exercise in the Age of COVID-19: Cross-sectional Study. JMIR aging, 5(2), e33165.

Truong TH, et al. (2022) New approach to prepare cytocompatible 3D scaffolds via the combination of sodium hyaluronate and colloidal particles of conductive polymers. Scientific

reports, 12(1), 8065.

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.

Guiglielmoni N, et al. (2021) Overcoming uncollapsed haplotypes in long-read assemblies of non-model organisms. BMC bioinformatics, 22(1), 303.

Merchant RA, et al. (2021) Possible Sarcopenia and Impact of Dual-Task Exercise on Gait Speed, Handgrip Strength, Falls, and Perceived Health. Frontiers in medicine, 8, 660463.

Fernandes M, et al. (2020) Predicting Intensive Care Unit admission among patients presenting to the emergency department using machine learning and natural language processing. PloS one, 15(3), e0229331.

Hulsbosch LP, et al. (2020) Online mindfulness-based intervention for women with pregnancy distress: design of a randomized controlled trial. BMC pregnancy and childbirth, 20(1), 159.

Lorè NI, et al. (2020) Collaborative Cross Mice Yield Genetic Modifiers for Pseudomonas aeruginosa Infection in Human Lung Disease. mBio, 11(2).

Binenbaum I, et al. (2020) Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. BMC genomics, 21(1), 761.

Li X, et al. (2020) The genetic control of leaf and petal allometric variations in Arabidopsis thaliana. BMC plant biology, 20(1), 547.

Keele GR, et al. (2019) Determinants of QTL Mapping Power in the Realized Collaborative Cross. G3 (Bethesda, Md.), 9(5), 1707.

Kikas T, et al. (2019) The Effect of Genetic Variation on the Placental Transcriptome in Humans. Frontiers in genetics, 10, 550.

Vorobyev A, et al. (2019) Gene-diet interactions associated with complex trait variation in an advanced intercross outbred mouse line. Nature communications, 10(1), 4097.

Abdulkina LR, et al. (2019) Components of the ribosome biogenesis pathway underlie establishment of telomere length set point in Arabidopsis. Nature communications, 10(1), 5479.

Zhang J, et al. (2018) Identification of new loci involved in the host susceptibility to Salmonella Typhimurium in collaborative cross mice. BMC genomics, 19(1), 303.

Molenhuis RT, et al. (2018) Modeling the quantitative nature of neurodevelopmental disorders using Collaborative Cross mice. Molecular autism, 9, 63.