

POSTER PRESENTATION

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MamPhEA: a web tool for mammalian phenotype enrichment analysis

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Background

Most mouse (*Mus musculus*) mutants generated in laboratories have been designed to aid the study of human genetics, physiology or diseases progression. To date, nearly 9000 genes in the mouse genome have been mutated; these have been phenotyped in such a way that resembles human clinical examinations. The mutant phenotypes characterize the consequence of disturbing or disrupting the information output of a gene and thus are ideal to aid understanding of how genes function at the systems level. Therefore, enrichment analyses incorporating mouse mutant phenotypes are particularly useful in studying mammalian functional genomics in the post-genome era.

Results

We have developed MamPhEA (Mammalian Phenotype Enrichment Analysis), a web application dedicated to understanding functional properties of mammalian gene sets based on mouse mutant phenotypes [1]. It allows users to conduct enrichment analysis on predefined or user-defined phenotypes, gives users the option to specify phenotypes derived from null mutations, produces easily comprehensible results, and supports analyses on genes of all mammalian species with a fully sequenced genome. MamPhEA is freely available at <http://evol.nhri.org.tw/MamPhEA/>. Figure 1

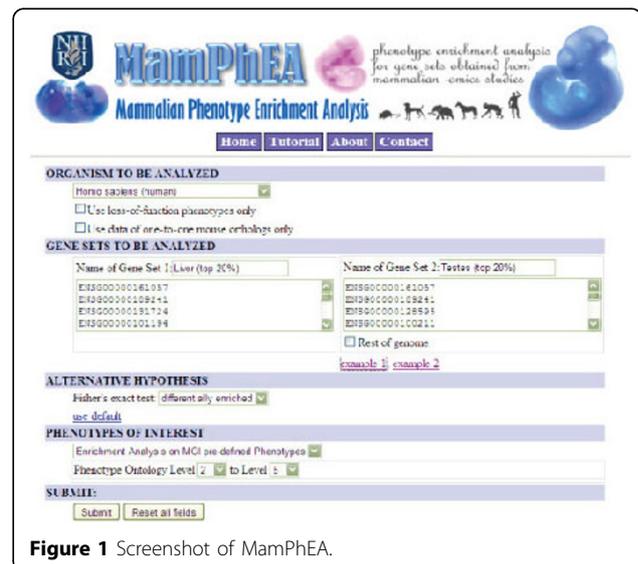


Figure 1 Screenshot of MamPhEA.

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Reference

1. Weng Meng-Pin, Liao Ben-Yang: MamPhEA: a Web tool for Mammalian Phenotype Enrichment Analysis. *Bioinformatics* 2010.

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