Forward genomics matches a given pattern of phenotypic differences between species to genomic differences using a genome-wide screen. In our implementation, we measure the divergence of the coding region of genes in mammals. Given an ancestral phenotypic trait that is lost in independent mammalian lineages, we have shown that searching for genes that are more diverged in all trait-loss species can discover genes that are involved in the given phenotype.

News

- Sept 27, 2012: The forward genomics approach used in Phenotree has been published in Cell Reports.
- Sep, 2012 - Phenotree V1.0 is released!