

## Poster B-10

### PhenoLink - Linking phenotype to genotype



#### Authors:

Pieter Neerincx (*Laboratory of Bioinformatics, WUR*)

Blaise Alako (*Laboratory of Bioinformatics, WUR*)

Jack Leunissen (*Laboratory of Bioinformatics, WUR*)

**Short Abstract:** PhenoLink Project Linkage analysis studies provide genomic regions to narrow the search for genes involved in a certain trait. But there might still be dozens of candidate genes left after linkage analysis and screening all of them is a laborious task. The PhenoLink project provides a data-mining framework using mapping, co-expression and interaction data to rank candidate genes.

#### Long Abstract:

Abstract PhenoLink Project

Finding genes responsible for a certain genetic trait is a laborious task. Using linkage analysis studies the inheritance of known markers can be compared to the inheritance of a trait of interest. This enables researchers to pinpoint one or several marker-defined regions on the genome where one or more genes involved in the trait must be located. Even though linkage analysis narrows the search, there might still be dozens of genes left that could be involved. Screening all those candidate genes for involvement is a time and money consuming effort.

The PhenoLink project provides a data-mining framework to reduce the amount of wet-lab work by ranking candidate genes so the most promising candidates can be investigated first. The ranking is based on the idea that if a particular trait is expressed at a certain location (tissue) or during a certain time frame (developmental stage), at least some of the gene(s) involved must be expressed at the same location or during the same time frame. PhenoLink uses information from model species to complement information for the target organism.

The candidate gene prediction software is implemented as a workflow of web services each performing an atomic task. These web services were developed using the BioMOBY framework creating a highly modular setup that allows easy incorporation of web services developed by others and/or recycling of our web services for various other purposes.