

Poster presentation

## Gene Expression-Based Cross Species Tissue Mapping

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These days, genomes of many species are being rapidly completed. Some of them already available are: Human genome, Mouse genome, Fly genome, Zebra fish genome, Nematode genome.

Many similarities and homologies exist between the genes of one species and another, for example between mouse and human. So by studying genes from one species may help to find genes which might be responsible for certain diseases and defects occurring in other species. If experiments carried out on animals are conclusive then they can be applied to human beings.

That's why there are numerous research going to study genomics among different species. To do tissue mapping, there are several ways for e.g. Expert mapping, Cell type mapping and Gene expression. This project used Gene Expression approach to study tissue mapping between the mouse, *mus musculus* and the fly *Drosophila melanogaster*.

The main steps in the project are:

Step 1 – is to get the 28 stages representing the mouse embryo anatomy  
Step 2 – is to get the expressed genes in these 'tissues', excluding 'house Keeping' genes. This will be somehow based on a score to be decided later for a gene to be classified as 'Expressed gene'.  
Step 3 – is to look for homologous genes which are expressed in developmental fly.  
Step 4 – is to find the mapping of tissues in developmental fly.  
Step 5 – is to establish and save the mapping (if any) in a database.

Benefit(s) of the project: Establish a database of tissue mappings available to the scientific community working

on proteomics and genomics; evaluate this approach of using gene expression for tissue mapping. Extend the project to other species.

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