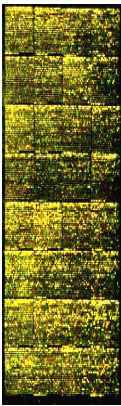


Molecular Mechanisms of Aging and Longevity

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We use the model organism *C. elegans* (a tiny worm) to study aging. We use DNA microarrays to measure changes in gene expression in aging and long-lived mutant worms. We collect a huge amount of data on the entire “transcriptome” in every experiment, and there is a wealth of information buried in this data, waiting for students to dig it out! We hope to use this information to find the biological basis for aging and the regulation of longevity.



C. elegans microarray

C. elegans

Projects:

1. Global analysis of gene transcription profiles from large data sets of aging, longevity mutants, environmental stresses, xenobiotic treatments, etc., to discover regulatory mechanisms and pathways.

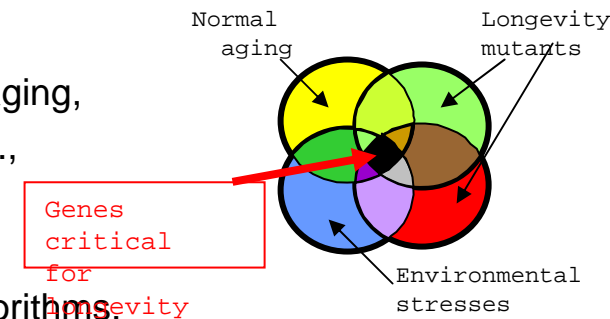
2. Algorithm development to integrate time into traditional clustering algorithms.



3. Motif analysis to discover regulatory sequences in co-regulated genes.

4. Integration of genetic and biochemical data to build biological networks that relate to longevity regulation.

5. Any interesting aging-related bioinformatic project.



QuickTime™ and a TIFF (Uncompressed) decompressor are needed to see this picture.

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