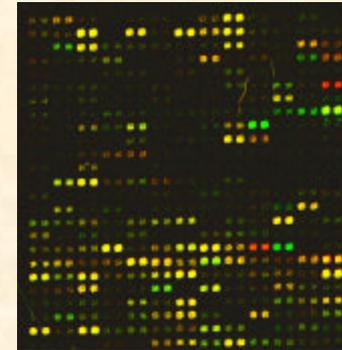


Gene regulatory networks in hair and skin biology

Mouse Genetics and Functional Genomics Program – December 2002

Contact: Brynn Jones (865) 574-3966

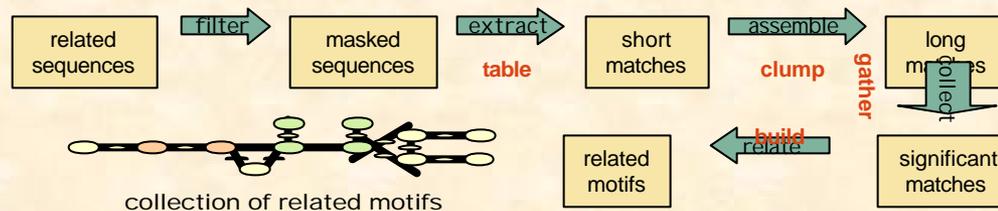
Objective: Combine experimental and bioinformatic approaches to understand the molecular basis of gene regulatory networks



Experimental — Empirically identify co-regulated genes using large scale (~ 22,000 mouse genes) microarrays

Current applications:

- Genes differentially expressed in skin of near naked hairless (Hr^n) mice
- Time course analysis of genes that mediate the response of primary mouse keratinocytes to an elevation of media calcium content



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Computational — Develop new algorithms for discovery of gene regulatory elements

Current algorithm features:

- applicable to any collection of related genomic sequence (co-regulated genes, orthologs of a specific gene, etc.)
- independent of global sequence alignment
- insensitive to sequence(s) that do not contain a motif of interest
- can incorporate general genomic information, such as mutation rates or expected nucleotide frequencies