

Bruce J. Aronow, PhD

Professor, Director of Bioinformatics Core

Department of Pediatrics; Division of Biomedical Informatics

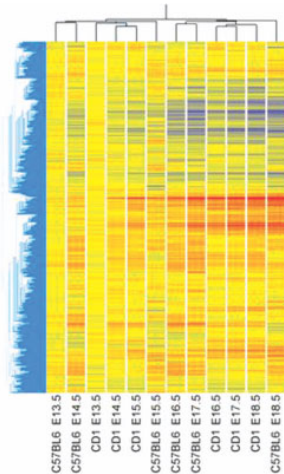
Description of Research:

Dr. Aronow and his group in Biomedical Informatics have pursued the application of functional genomics approaches to the characterization of biological systems using whole-genome analyses of the structure, function, and expression of genes, transcripts and proteins. He has developed web-accessible resources and performed a series of detailed comparative functional genomics analyses between different organisms to identify highly conserved biological structures, processes, and disease states. To apply these approaches to improve the study and understanding of human disease, particularly that of the gastrointestinal tract, he has sought to develop bioinformatics applications and databases that facilitate the detection of (1) conserved structural features that contribute to gene regulation and gene function (2) harmful polymorphisms or mutations that confer disease risk, and (3) improved recognition of gene-anatomy and gene-disease associations for large-scale application to functional genomics analyses using both gene expression database mining and biomedical literature and knowledge abstraction and mining.

Collaborations:

Drs. Aronow and Bezerra collaborate on studies addressing pathogenic mechanisms of bile duct injury in biliary atresia. He also works with Dr. Denson on identifying genomic signatures in inflammatory bowel disease from responders and non-responders. Dr. Aronow works with Dr. Grabowski on the microarray analysis for signature transcriptome pathways in liver, spleen, and intestine of acid β -glucosidase or lysosomal acid lipase knockout mice. He also works with Dr. Potter in defining the transcriptome of the developing kidney, and with Dr. Rothenberg to define the expression profile of genes involved in children with eosinophilic esophagitis.

Representative Figure:



Hierarchical and gene clustering of gene expression in embryonic mouse colon. Hierarchical clustering of 13,484 filtered genes normalized to E13.5 in outbred CD-1 and inbred C57BL/6 mice identified two major groups (E13.5–E15.5 and E16.5–E18.5). Horizontal bars on the right indicate genes that are down-regulated (Group 1-blue) or upregulated (Group 2-red) 2-fold or greater relative to E13.5. Red, increased expression; yellow, equal; blue, decreased expression. Fig. 3 from *Genesis*, 2005; 41: 1-12.