

Presentation title: Transcriptomics 101

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Abstract

The transcriptome is the full complement of RNA transcripts expressed in given biological sample. It is the active part of the genome, and understanding how the transcriptome changes can give us insight into which pathways are active in a particular biological system or pathological state. Microarrays have been the workhorse of transcriptomics for many years now, however the development of new sequencing technologies has sparked a revolution within the field.

High-throughput sequencing technologies can generate hundreds of millions of short tags (typically only 25-50nt) from a single experiment, and this capacity is enabling a new wave of genomic-based research. Not only is this technology being used for genomic sequencing, re-sequencing, and epigenomic applications, but several groups have recently applied this technology to sequence RNA for gene-expression studies (RNAseq). Some of the benefits of using RNAseq over microarrays to study gene-expression data include: (i) the potentially unlimited dynamic range of expression; (ii) the greater sensitivity of the sequencing data; (iii) the improved ability to discriminate regions of high sequence identity; and (iv) the ability to profile transcription without prior assumptions of which genomic regions are expressed. No prior knowledge of bioinformatics, microarrays, or next-generation sequencing will be required for this lecture.