11.S: Genomics and Systems Biology (Summary)

- Genomics and related technologies differ from other techniques of molecular biology largely because of their scale; they allow many different genes (or gene products) to be studied in parallel.
- DNA sequencing can be applied to either a single gene, or in the case of genomics, to a large number of genes.
- Most DNA sequencing relies on the incorporation of dye-labeled terminator molecules, which create products that differ in length and end in a known nucleotide. The products can then be separated based on length, and the identity of the last based in each fragment can be determined based on fluorescence.
- Next-generation sequencing technologies have further reduced costs of sequencing, through miniaturization and parallelization.
- Physical maps are ordered sets of clones containing overlapping pieces of DNA, which together represent large pieces of chromosomes.
- Whole genomes may be sequenced using either a clone-by-clone approach, which required a physical map, or by a shotgun approach, in which small fragments are randomly sequenced.
- Genome analysis does not end after sequence acquisition; various features of the genome including genes (and their introns, exons, etc.) must be identified through a process called annotation.
- Functional genomics techniques including microarray analysis correlate transcript abundance with particular tissue samples. Genes whose transcripts are highly abundant under certain biological conditions may cause or respond to that condition.

Key Terms

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<tr>
<th>genome</th>
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<td>genomics</td>
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proteomics
transcriptomics
ddNTP
terminator nucleotide
capillary electrophoresis
chromatogram
next-generation sequencing

BAC
clone-by-clone sequencing
whole genome shotgun
genome annotation
functional genomics
microarray

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