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	Sommario/riassunto	New sequencing technologies have broken many experimental barriers to genome scale sequencing, leading to the extraction of huge quantities of sequence data. This expansion of biological databases

established the need for new ways to harness and apply the astounding amount of available genomic information and convert it into substantive biological understanding. A complilation of recent approaches from prominent researchers, Bioinformatics: High Performance Parallel Computer Architectures discusses how to take advantage of bioinformatics applications and algorithms o