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Discovering patterns in biological sequences is a fundamental problem. For example, the identification of patterns in DNA sequences led to the identification of open reading frames, the identification of gene promoter elements, intron/exon sites and SH RNA, the location of RNA degradation signals, the identification of alternative bonding sites, etc. in protein sequences, patterns led to domain identification, location of protease cleavage sites, identification of signalling peptides, protein interactions, identification of protein degradation elements, identification of protein trading elements, discovery of short functional motifs, etc. We are studying (l, d) the theme to search for a problem or to plant a Search theme (PMS). PMS accepts both input n strings and two integers l and d. Returns all M sequences of l length that occur in each input string, where each occurrence differs from M in most positions d. Another phrasing is the PMS quorum (qPMS), where the theme appears in at least q% of strings. Introducing qPMS9, a parallel precision qPMS algorithm that offers significant improvements to the runtime on DNA and protein data sets. qPMS9 addresses challenging CASES of DNA (l, d)(28, 12) and (30, 13). Source code is available on the 2Discovering patterns in biological sequences is a fundamental problem. 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