

COMPUTER SCIENCE  
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*Pattern Discovery Under Saturation Constraints*

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**Abstract:** The problem of characterizing and detecting surprisingly recurrent sequence patterns such as substrings or motifs and related associations or rules is pursued ubiquitously in order to compress data, unveil structure, infer succinct descriptions, extract and classify features, etc. In Molecular Biology, some such patterns are variously implicated in facets of biological structure and function. Because of that, Pattern Discovery constitutes one of the most battered, flourishing and arguably useful applications of Computational Molecular Biology. The very notion of a pattern still embodies subtleties and ambiguities, as do related concepts such as class and structure. And the discovery, particularly on a massive scale, of surprising patterns and correlations thereof poses interesting methodological and algorithmic problems, some of which appear to be hardly surmountable. This talk proposes a brief account of algorithmic pattern discovery under constraints of saturation, displays some of its applications, and highlights issues, products and challenges emerged in recent and current work.

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