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Mining the coding and non-coding genome for cancer drivers

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Highlights

- 20 • A review of current computational programs for prioritizing or scoring
mutations in the coding and non-coding genome;
- A summary of non-coding elements and their mutations involved in cancer;
- A precise categorization of software for calling cancer mutations, scoring
mutations, and identifying potential cancer driving mutations;
- 25 • Perspectives for the development of computational tools for non-coding
mutation assessment.

Abstract

Progress in next-generation sequencing provides unprecedented opportunities to fully
characterize the spectrum of somatic mutations of cancer genomes. Given the large number of
30 somatic mutations identified by such technologies, the prioritization of cancer-driving events

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