

A Survey on Classification Analysis for Cancer Genomics: Limitations and Novel Opportunity in the Era of Cancer Classification and Target Therapies

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Abstract:

Advanced machine learning approaches are qualified for recognizing the too composite patterns in the massive datasets. We provide a perspective technical survey analysis in machine learning (ML), and deep learning (DL) approaches for genome analysis. It's quickly rising applications related to cancer diseases such as cancer diagnosis or subtypes of cancer through omics input data. It discusses effective approaches in the fields of genomics regulatory, pathogenicity, and variant calling. Moreover, the representation of ML's potential benefits due to the several technological platforms involved in its diagnosis, prognosis, and treatment. We concentrate on the most up-to-date knowledge of cancer classification models, targeted therapy, and define how genetic mutations inspire targeted therapy's responsiveness and highlight the different related issues in this era of precision medicine. Finally, we disuse limitations of the different approaches and hopeful ways of upcoming research in targeted therapy.

Keywords: Deep Learning, Genome Analysis, Precision Medicine, Cancer Classification Models, Classification Models, Omics

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Introduction

DNA molecule is translated to mRNA for the synthesis of proteins. Proteins are the primary factors in the utmost cellular processes. The process via which a fragment of DNA is reading besides transformed addicted to a protein has excessive awareness in several therapeutic analyses and biological. This process may affect diverse phases; however, the process's basis is the creature's DNA that converts according to the sequence of specific rules. Note to toward the full structure of DNA in a creature's cell the genome. The DNA consisted of four forms of roots – “Cytosine” (C), “Guanine” (G), “Thymine” (T), and “Adenine” (A), the genome of human is made up of completed 3 billion of these genomic letters. The genome can be measured to keep a series cleared on the character set {A, C, G, T}. A sequence of the genome can deliver over the DNA sequencing process. In the latest years, novel sequencing technologies, named Next Generation and Third Generation sequencing (NGS, TGS). The principal reason for cancer has situated a mutation in the genome, each inherited or established through an individual's life.