

# A Multi-Omics Classifier For Prediction Of Androgen Deprivation Treatment Response In Prostate Cancer Patients

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## Abstract

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**Abstract:**

Despite the advancement in the management of prostate cancer in recent years, treatment strategies are only efficient against localized disease while managing metastatic cancer remains a challenge. As a result, the global burden of the disease has remained significant. Efficient and personalized management of the disease before metastasis is therefore of prime importance. In this study, we developed a classifier to predict the response of prostate cancer patients to treatment leveraging on multi-omics datasets provided by The Cancer Genome Atlas (TCGA). Our investigation using ten machine learning algorithms reveals that tree-based algorithms had better predictive performance than probabilistic models such as Naive Bayes and kernel-based methods such as Support Vector Machines. We also investigated the performance of all possible omics combinations. Our results show that there is an overall increase in performance when multiple omics datasets are used in contrast to single omics strategies. We have predicted for the first time, possible androgen deprivation treatment response outcomes for 68 prostate cancer patients with missing phenotype values in the TCGA dataset.

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**I. Introduction**

Prostate cancer (PCa) constitutes a significant global burden, ranking fifth among the prevalent causes of death in men in 2020 [1]. The heterogeneity of PCa is influenced by several factors such as gene expression, pattern of tumor growth and androgen receptor status [2]. Therefore, strategies for combating PCa differs depending on the stage of the disease.

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