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Could the CRISP3 gene be a potential prognostic biomarker for cervical cancer?

CBBL COMPUTATIONAL BIOLOGY AND BIOINFORMATICS LABORATORY

(Bio-IA Project)
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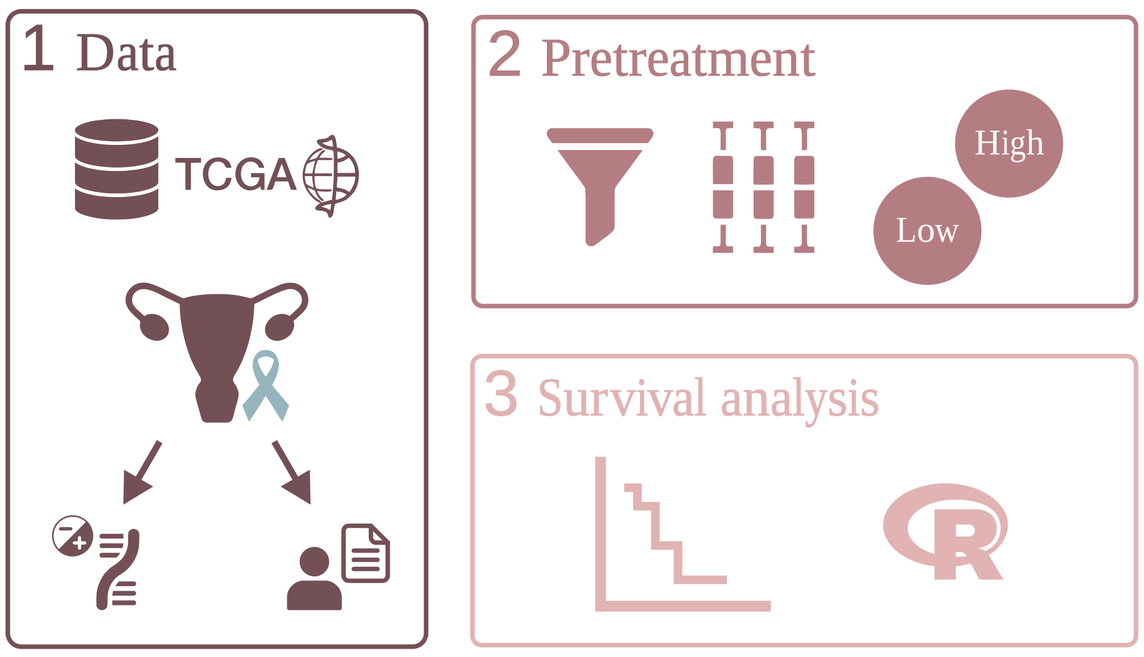
Introduction and Objective

Cervical cancer is a disease of the female reproductive system, being the third most frequent and deadly neoplasia in women [1]. Cervix modifications that promote cancer progression are associated with human papillomavirus infection accompanied by gene expression alterations [2,3]. Therefore, transcriptomic analyses may unveil underlying molecular mechanisms behind the disease, as well as identify novel biomarkers [4]. These describe a normal/abnormal organism state, and can be either diagnostic, prognostic or predictive [5]. In this context, the present study aims to relate gene expression to data available in public repositories in order to analyze potential prognostic biomarkers for cervical cancer.

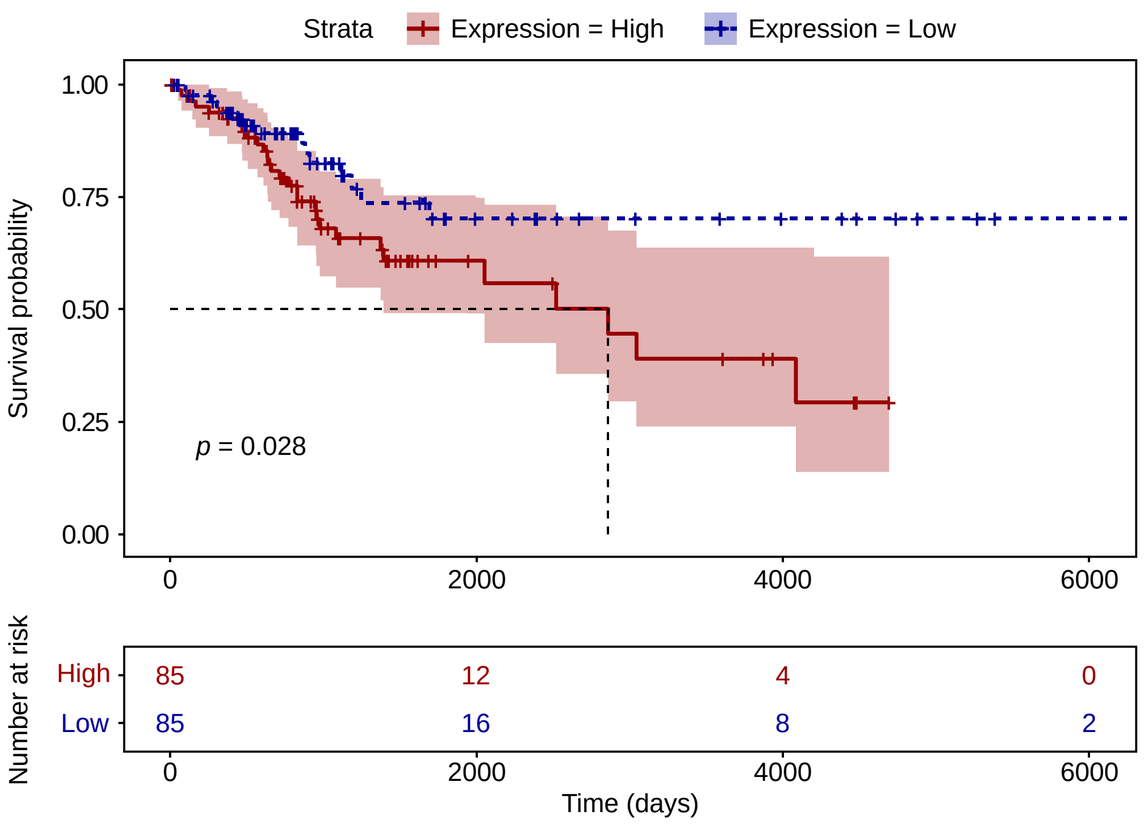
Materials and Methods

RNA-seq gene expression and clinical data of patients diagnosed with cervical cancer were retrieved from The Cancer Genome Atlas [6,7]. A pretreatment step took place to filter, normalize and categorize the gene expression data. 19 differentially expressed genes during the course of cervical carcinogenesis identified in a previous study (not yet published) were analyzed. The Kaplan-Meier method was used to estimate the survival probability for patients. The Mantel-Haenszel test was employed to compare survival curves between groups of high-expression and low-expression for each gene (cutoff by median expression), taking $p<0.05$ as significant. All procedures described made use of R programming language.



Results and Discussion

As a result, only the CRISP3 gene showed potential as a prognostic biomarker in cervical cancer. The analysis revealed a higher survival in patients with low gene expression ($p=0.028$). However, the literature reports a negative regulation for CRISP3 throughout cervical carcinogenesis [8]. In this case, the lower survival in high gene expression patients may be associated with a more aggressive variant of the disease. The same gene has been found upregulated in prostate cancer, where it plays a role in neoplasia onset and progression due to shifts in cellular adhesion [9]. Despite the function of the glycoprotein encoded by CRISP3 not being completely understood, it appears to operate in processes such as cellular adhesion, innate and adaptive immunity, and fertility, depending on the tissue where it is expressed [10].



Final Considerations

This study contributes evidence for a prognostic biomarker in cervical cancer and insights into the related molecular mechanisms. Nevertheless, additional analyses beyond the scope of a computational methodology are still needed to verify and confirm the potential of CRISP3.

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