

## **Identifying ovarian cancer with machine learning RNA methylation pattern analysis**

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High grade serous ovarian cancer remains one of the deadliest forms of cancer among women, largely in part due to the difficulty in early diagnosis and detection. Current methods for detecting ovarian cancer rely on imperfect biomarkers with poor sensitivity and specificity. New technologies are emerging which may have potential utility in improving ovarian cancer detection in the future. We hypothesize that we can modify and use an existing Machine Learning framework to identify ovarian cancer based on patterns found in the methylation of RNA extracted from benign and malignant tissue samples. With access to a large biobank of

samples we obtained RNA sequences of 109 patients which were then used to perform unsupervised training of a machine learning framework with an AUC of 94.6 and interrogate the framework for top CpG sites influencing the prediction using Shapley analysis. Prospective validation of this framework and investigation of top CpGs could result in a tool which could be applied to analyze clinical samples for the presence of ovarian cancer.

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