# Identifying Multi-Omics Biomarkers that Predict Ovarian Cancer Survival

*Christopher Sullivan*
*University of Massachusetts, Dartmouth*

**Kosar Fateh,** Srinivasulu Yerukala Sathipati, PhD
*Center for Precision Medicine Research*

**Background**: Ovarian cancer remains one of the deadliest gynecologic malignancies worldwide. Its marked molecular heterogeneity limits accurate prognostic stratification and the identification of clinically meaningful biomarkers. Although multi-omics approaches have improved predictive modeling of patient survival, many prioritize predictive performance over biological interpretability, thereby limiting their potential for practical use in clinical settings. The purpose of this study was to develop a multi-omics biomarker prediction model of survival time in patients with ovarian cancer.

**Methods**: A retrospective cohort of ovarian cases was assembled using clinical data from The Cancer Genome Atlas (TCGA). A multi-stage machine learning framework was then developed using mRNA, microRNA, DNA methylation, copy number variation, protein expression, as well as clinical and survival data. Hierarchical feature selection was followed by a weighted ensemble of ElasticNet, Ridge Regression, Support Vector Regression, XGBoost, and Random Forest models to predict overall survival time. Model performance was evaluated by comparing predicted and observed survival times. Candidate biomarkers were subsequently validated through differential expression analysis across survival groups, Cox proportional hazards regression, and enrichment analyses.

**Results**: Compared with individual omics models, multi-omics integration substantially improved survival prediction, achieving a Pearson correlation of 0.75, a concordance index of 0.78, and a mean absolute error of 8.57 months between predicted and actual overall survival times. Among the individual molecular modalities, mRNA and microRNA were the strongest predictors of ovarian cancer survival. The framework identified a biologically coherent 20-biomarker signature, with the majority having prior established associations with ovarian cancer. These biomarkers converged on interconnected biological pathways underlying ovarian cancer progression, including immune regulation, tumor-associated macrophage signaling, tumor microenvironment interactions, post-transcriptional regulation by tumor-suppressive miRNAs, and the PI3K-Akt, MAPK, focal adhesion, hypoxia, apoptosis, and p53 signaling pathways.

**Conclusions**: This study produced an interpretable computational framework for predicting ovarian cancer survival. The close concordance between the identified biomarkers and established ovarian cancer biology also supports the plausibility and robustness of the proposed framework. Improved prognostic prediction of survival time with biological insight outlines a promising approach for multi-omics biomarker discovery and supporting future precision oncology research in ovarian and other forms of cancer.