# Using AI Foundation models to Predict Cellular Expression in Cancer Tissue

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Every tumor contains a complex environment that influences disease development and treatment. Modern technologies can measure this activity, but are still expensive. This study investigates if AI can do this in a faster and more accessible way.

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This study builds on previous research at Lund University that developed Image2Count, a method that can estimate gene activity directly from microscope images of tissue. By analyzing the appearance of cells, the method can predict which genes are active and provide insight into biological processes inside the tissue.

The goal of this project was to investigate whether newer artificial intelligence models could improve Image2Count. These models have been trained on very large image datasets and may be better at recognizing patterns than the smaller model previously used. Because few studies have compared such models in this type of application, it is still unclear which approaches work best.

Three AI models were evaluated: Kronos, Deepcell, and Eva. Deepcell and Eva combine information from biological texts with image information, while Kronos relies only on what it sees in the images.

The models were tested on three datasets containing measurements of gene activity from tissue samples. The AI models first analyzed the images, and their outputs were then used to predict gene activity.

The results showed clear differences between the models. Kronos was particularly good at recognizing tissue structure and was the most reliable when applied to data it had not previously seen. Deepcell performed well for genes involved in immune responses and provided useful biological insights. Eva achieved strong results when tested on the same type of data it had been trained on. However, when the models were tested on a dataset that had previously been used to evaluate Image2Count, none of them outperformed the simpler model used in earlier work.

Overall, the results suggest that models trained only on images may be better at handling new datasets, while models that combine image and biological information can provide a deeper understanding of biological processes. At the same time, the study indicates that current large AI models still have limitations and are not yet able to consistently outperform smaller models designed for specific biological tasks.