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An Importance on how RNA Sequencing and Radiomics Work Together to Treat Breast Cancer

Marika Milan*

Department of Medical Surgical Sciences, Sapienza University of Rome, 04100 Latina, Italy

Introduction

Breast cancer is one of the most common cancers among women worldwide. The disease is characterized by the uncontrolled growth of breast cells, and if not detected early, it can spread to other parts of the body, resulting in a poor prognosis for patients. Over the years, there have been significant advances in the diagnosis and treatment of breast cancer, but the disease remains a major health challenge. In recent years, there has been growing interest in the use of radiomics and RNA sequencing as complementary tools in the diagnosis and treatment of breast cancer. This essay will focus on the synergy of radiomics and RNA sequencing in breast cancer. Radiomics is a rapidly evolving field that uses advanced imaging techniques to extract quantitative features from medical images. These features can be used to identify patterns in the images that are associated with specific diseases or conditions.

In the case of breast cancer, radiomics can be used to analyze mammography, ultrasound, MRI, and PET/CT images to identify features that are associated with the disease. Radiomics has the potential to provide a non-invasive, objective, and quantitative method for the diagnosis, prognosis, and treatment of breast cancer. RNA sequencing is a technique used to determine the sequence of RNA molecules in a biological sample. The technique allows researchers to identify the genes that are expressed in a particular tissue or cell type. In the case of breast cancer, RNA sequencing can be used to identify the genes that are overexpressed or under expressed in cancerous breast tissue compared to normal breast tissue. This information can be used to develop new targeted therapies for breast cancer [1].

Description

The synergy of radiomics and RNA sequencing in breast cancer has the potential to revolutionize the diagnosis, prognosis, and treatment of the disease. By combining the two techniques, researchers can identify imaging features that are associated with specific gene expression patterns. This information can be used to develop personalized treatment plans for breast cancer patients. One of the key advantages of radiomics and RNA sequencing is their ability to identify subtypes of breast cancer. Breast cancer is a heterogeneous disease that can be divided into several subtypes based on the expression of different genes. Each subtype has a different prognosis and response to treatment. Radiomics and RNA sequencing can be used to identify the subtypes of breast cancer and develop personalized treatment plans for each patient [2].

For example, radiomics can be used to identify imaging features that are associated with the expression of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2). These receptors are commonly used to classify breast cancer into subtypes. RNA sequencing can be used to confirm the expression of these receptors and identify additional genes that are overexpressed or under expressed in the tumor. This information can be used to develop personalized treatment plans that target the specific genes that are driving the growth of the tumor. Another advantage of radiomics and RNA sequencing is their ability to predict the response to treatment. Traditional methods for predicting the response to treatment, such as measuring tumor size, have limitations. Tumor size can be affected by factors such as inflammation, edema, and necrosis, which may not accurately reflect the response to treatment. Radiomics and RNA sequencing can provide a more accurate prediction of the response to treatment by identifying imaging features and gene expression patterns that are associated with treatment response. For example, radiomics can be used to identify imaging features that are associated with the response to chemotherapy. RNA sequencing can be used to identify genes that are overexpressed or under expressed in tumors that are resistant to chemotherapy. This information can be used to develop personalized treatment plans for breast cancer patients that are more likely to respond to chemotherapy [3-5].

Conclusion

RNA sequencing is a high-throughput sequencing technique that can be used to measure gene expression levels and identify changes in gene expression that are associated with cancer. RNA sequencing can provide a more comprehensive understanding of the molecular mechanisms underlying breast cancer and may lead to the identification of new therapeutic targets. RNA sequencing has been used to identify gene expression signatures that are associated with breast cancer subtypes. For example, RNA sequencing to identify a gene expression signature that can classify breast cancer into four molecular subtypes. The authors found that this classification was associated with differences in prognosis and response to therapy. RNA sequencing has also been used to identify new therapeutic targets in breast cancer. RNA sequencing to identify a novel therapeutic target for HER2-positive breast cancer.

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Conflict of Interest

There are no conflicts of interest by author.

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***Address for Correspondence:** Marika Milan, Department of Medical Surgical Sciences, Sapienza University of Rome, 04100 Latina, Italy; E-mail: marikamilan@iu.edu*

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