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ISPR'2023 　　　　　　　　3/23/23
To: Suzan Anwar >

ISPR'2023 Pre-notification for paper 72

Dear Suzan Anwar,

On behalf of the Program Committee, we are pleased to inform you that your paper entitled " Breast Cancer Radiogenomics Data Generation Using Combined Generative Adversarial Networks GANs" has been accepted for presentation at ISPR'2023. Congratulations on this achievement!

However, please note that the acceptance rate for the conference is limited by Springer CCIS, and we kindly request that you confirm your participation by responding to this email within the next 48 hours.

AnyScanner

Breast Cancer Radiogenomics Data Generation Using Combined Generative Adversarial Networks GANs

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Abstract. Radiogenomics is a newly emerging field that integrates genomics with medical imaging data. The aim of this field is to elucidate the associations between gene expression data and imaging phenotypes, especially in cancer. However, radiogenomics is hindered by the expensive cost of genetic screening tests which leads to the unavailability of numerous big datasets for paired imaging and genetic data. Big data is crucial for training machine learning-based techniques for analysis relating to radiogenic studies. Currently, fake data is generated on only one of the two radiogenomic types; genomic or medical imaging data are generated separately. In this paper, we propose a deepfake approach implemented by combining two Generative Adversarial Networks (GANs) to create fake image data that are hardly differentiable from the original to improve Breast cancer diagnosis. To evaluate the model, a survey is developed and distributed among the participants to measure their ability to differentiate the original from the Deepfakes images. The results showed that the model-generated fake images cannot be distinguished from the authentic images and are relatively satisfying using the PyTorch framework.

1   Introduction

Radiogenomics is a promising field with many valuable potentials, such as shedding light on underlying disease mechanisms, survival estimation, and treatment response prediction. Existing approaches for generating fake data can create either genomic data or medical imaging separately. These approaches ignore the associations between the disease's genetic mutations and their effect on the structure and function of human tissues and organs. Generating big fake genomic data with existing realistic imaging data will have a broad scientific impact as it will improve cancer diagnosis prediction access to life's domains.