

JOINT EVENT ON

20th Euro-Global Summit on

Cancer Therapy & Radiation Oncology

and

2nd International Oncologist & Diagnostics Conference

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miniABS (mini Absolute Breast Cancer Subtyper)

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Human breast cancer has been classified into several distinct molecular intrinsic subtypes based on gene expression profile for molecular-based treatment. Although there are many well-known gene-expression-based classification such as PAM50, subtyping using these methods are affected by the composition of patients and data preprocessing method, which is less reproducible mainly due to the relativity of gene expression within the cohort and different normalization method. While recent studies try to build an absolute classifier that utilizes internal gene expression comparisons for single sample classification, there has been no trial to build an RNA-seq based absolute classifier to meet the recent demand for NGS-based diagnosis. Here, we present a new classification method based on pairs of absolute gene expression within a single sample. In the performance test using four machine learning techniques, we showed that our RNA-seq specific classifier with minimal gene set achieved up to 88% accuracy increasing from 74% of conventional methods. We have also demonstrated that this classifier can be applied to a variety of data derived from other gene expression quantification techniques due to the methodology we applied.

Biography

Mikyoung Seo majored in Bioinformatics at Ajou University College of Medicine, Korea, and is currently a PhD candidate at Yonsei University College of Medicine, Korea. She is developing a classifier for breast cancer using machine learning algorithms, and is conducting fusion gene research and translational research in disease.

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