

Computer Aided Scoring and Analysis (CASA) for Rapid and Robust Detection of Biological Molecules in Tissue Microarrays

Published date: Feb. 1, 2012

Technology description

Summary

Tissue Microarray (TMA) technology is a technique that allows tissue samples to be miniaturized and biologically characterized. The results can be stored digitally and analyzed manually for the expression of biological molecules which can permit the diagnosis or prognosis of disease. Despite its practical use, the current method of manually analyzing TMA samples is subjective and lacks the standardization and concordance needed to support consistent interpretation of the results. This leads to a low correlation in the results obtained amongst different laboratories and detection agents. The current invention, Computer Aided Scoring and Analysis (CASA), provides a means of rapidly and consistently analyzing the expression patterns of biological molecules in large quantities of tissue samples. This software uses novel algorithms which normalize the pixel data obtained from digital images of the samples, statistically determines which biological molecules are diagnostic markers for the disease, and compares these data to normal, as well as diseased or abnormal tissue samples, to diagnose or predict susceptibility to the disease. In some applications, two or more biological molecules can be simultaneously screened or identified using two or more detection agents making the CASA system amenable to methods such as cluster analysis. This type of analysis can not only identify groups of antigens that are associated with a disease, but can also combine this information with characteristics of the patient population, such as age, gender or ethnicity to achieve a predictive output. The CASA system can analyze data from a broad range of detection agents such as antibodies, radionuclides, dyes and quantum dots making it a very attractive tool for high throughput TMA analysis.

The system has already been used successfully for the diagnosis and prognosis of non-small cell lung cancer in tissue samples and can be adapted for use in many diseases where changes in the expression of one or more biological molecule will to be detected.

Application area

Large scale diagnosis of tissue expression patterns of biological molecules

Rapid, robust tissue diagnosis or prognosis of disease Compatible with wide range of detection agents

Institution

NIH - National Institutes of Health





叶先生

电话: 021-65679356 手机: 13414935137 邮箱: yeyingsheng@zf-ym.com