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Proceedings

SY05.01 | **Computer Aided Diagnosis**

Structure, Function, And Predictive Diagnosis Algorithms

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Introduction/ Background

Background: Predictive diagnosis (PD) is a component of tissue based diagnosis. It is based upon immunohistochemical (IHC) and molecular genetic (MG) measurements of structures and functions. It predicts the outcome of individual cancer treatment.

Aims

To develop computerized analysis of microscopic images in relation to prognosis evaluation of cancer patients.

Methods

Theory: Structures are related to object – associated visual information that remains constant within the period of observation. Functions display with changes either in relation to contemporary structures or to the background or to both. Structures are usually visible in hierarchical spatial order, functions in both spatial and time oriented order. Functions usually alter or destroy one or several structures at a certain order which might cause the breakdown of the whole system, especially if higher order structures are involved. In microscopy the idea can be mapped on the diagnostic sequence that starts with conventional diagnosis (adenocarcinoma) followed by IH (receptor expression, EGFR), and ends with MG (k-ras). PD can be automatically derived from analysis of digitized images; and of potential (therapeutic) interactions between the different images (steps). The sequence results in:

1. Analysis of image quality, and evaluation of regions of interest (ROI).
2. Assessment of an automated conventional diagnosis.
3. Analysis of IH expression and quantification.
4. Analysis of intra-cellular pathways either by IH or fluorescent techniques.
5. Analysis of therapeutic interactions and evaluation of prognosis.

Results

Interpretation and Experiences: Image quality evaluation and standardization are mandatory to assure constant quality and reproducibility of the analysis results, such as ROI finding, colour intensity, diagnosis assessment, and IH quantification. The automated investigation of MG pathways and the final PD classification are not problematic. Each component contributes to potential interaction (drug regime), which all together add to evaluate the patient's prognosis. Perspectives: Graph theory defining nodes by structure and edges by function seems to be an adequate tool to construct an algorithm, which can be embedded in an open access data banks of individually tuned predictive diagnosis systems.

References:

[1] Kayser K., Borkenfeld S., Carvalho R., Kayser G., The concept of entropy in histopathological diagnosis and targeted therapy, diagnostic pathology 2015, 1:97.

[2] Sharma H., Zerbe N., Lohmann S., Kayser K., Hellwich O., Hufnagl P., A review of graph- based methods for image analysis in digital histopathology, diagnostic pathology 2015, 1:6.