Improving Techniques and Technology for CELLULAR AND MOLECULAR PATHOLOGY

ABSTRACTS

29th November 2016 - 1st December 2016
Location: Online

EuroSciCon
This event will share best practice, and discuss new and improved methodologies for the cellular and molecular analysis of disease.

This event has [CPD accreditation](www.lifescienceevents.com/path16)

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#PathESC

This abstract book will be finalised two weeks before the event
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Invited Speakers Abstracts

Can Deep Learning Revolutionise Digital Pathology?
Dr Francesco Ciompi, Radboud University Medical Center, Nijmegen, Netherlands
Deep Learning has the potential to revolutionise the field of digital pathology. In this talk, I will present the results of recent research in my lab, in which deep learning has been successfully applied to obtain state of the art performance in classification at whole slide image level.

Radioligands for quantifying the glia response after brain injury and neuropsychiatric diseases
Dr. Cornelius K. Donat, Imperial College London, London, United Kingdom
Neuroinflammation is a commonly observed following brain injuries and neuropsychiatric diseases, mediated via glia activation. Activated glia cells upregulate certain proteins, such as the 18 kDa translocator protein or imidazoline-2 binding sites. These proteins can be quantified with selective radioligands and therefore provide biomarkers of brain injury and inflammation. We have investigated the glia response with new radioligands in different animal models of traumatic brain injury and post-mortem tissue of patients with depression, schizophrenia and bipolar disorder. Our results show that glia targets provide interesting biomarkers for assessing brain injury and could potentially be used to quantify therapeutic effects.

Computational Imaging of Digital Pathology and Precision Medicine
Dr Anant Madabhushi, Department of Biomedical Engineering, Case Western Reserve University, Cleveland, Ohio, USA
For a number of cancers, tumor grade (morphologic appearance on tissue as assessed qualitatively or semiquantitatively by a pathologist) has been found to be highly correlated with disease outcome. However pathologic grade tends to suffer from significant interobserver variability. Digitization of histological samples, or whole slide imaging, facilitates a quantitative approach towards evaluating disease progression and predicting outcome, while also facilitating the adoption of telepathology. Recently, research groups (including our own) have begun to show that computer extracted measurements of tumor morphology (e.g. capturing nuclear orientation, texture, shape, architecture) from routine H&E stained cancer tissue images can predict disease aggressiveness and treatment outcome. By computationally interrogating the entire tumor landscape and its most invasive elements from a standard H&E slide, these approaches can allow for more accurate capture of tumor heterogeneity, disease risk and hence the most appropriate treatment strategy.

How to use protein biomarkers to assess and monitor brain injury
Dr Eric Thelin, Department of Clinical Neuroscience, Karolinska Institutet, Stockholm, Sweden
There is an increasing amount of brain specific proteins that have been shown to function as markers of tissue fate. Subsequent sampling of S100B, Neuron-specific enolase (NSE), Glial Fibrillary Acidic Protein (GFAP) and Neurofilament-Light (NF-L) in serum and cerebrospinal fluid could aid the physician in assessing the severity of the brain injury and guide different diagnostic modalities and treatment strategies. By implementen brain specific proteins into the multi-modal monitoring of unconscious patients suffering from different cerebral pathologies, it is possible to provide a global biomarker of tissue fate and functional outcome.

Oral Presentation Abstracts
Oral presentations will be added after the submission deadline
Day 1:

Day 2:

Day 3:

**Poster Presentation Abstracts**

Poster abstracts will be finalised weeks before the event