Statement of the Problem: In both preclinical and clinical settings, histological images are now digitalized into high resolution images. Big data sets of images seek digital tools for fast and precise analysis and diagnosis. Machine learning (ML)-based software are commonly used for various images analysis: detection, segmentation and classification. Here, we describe advantages and disadvantages of ML-supervised based digital histopathology image tools based on the literature review.

Review-based observations: ML-based software can significantly reduced image analysis time and int

a complex analysis is needed, more complex ML-based tools should be applied. For example, for simple staining quantification ML-FIBER is considered as easy-to use, fast and reproducible but lack of complex analysis and it requires specific image formats as input. Other software must be considered to quantify the image features. For instance, Ilastik software uses a random

forest classifer in the learning step, which helps to characterize by a set of generic (nonlinear) features (color and texture) and it supports up to three spatial plus one spectral dimension, calculating all dimensions in the feature analysis. Additionally, higher image processing can require deep neural networks in order to extract higher-level features from the raw input (used for cell characterization).

Biography

Caterina Facchina is a postdoctoral researcher at McGill University working on anti-cancer drug discovery and biomarker identification. She obtained her PhD in medical imaging at the University of Paris, where she started her research on image analysis 2D and 3D. She is Vice-President Academic of the Postdoctoral Association of McGill University and she is an active member of the American Society for Investigative Pathology (ASIP).

Title: A Comparison of Post Mortem Computed Tomography and External Examination of the Neck in Suspected Hanging Cases
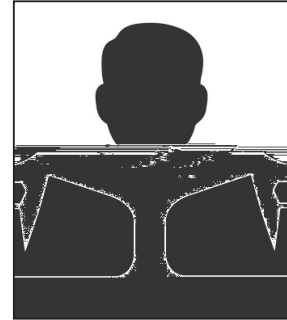
PhD researcher at Staffordshire University, United Kingdom

Title: Carboxypeptidase A3—A Key Component of the Protease Phenotype of Mast Cells

Dmitri Atiakshin

Peoples' Friendship University of Russia, Moscow, Russia

Carboxypeptidase A3 (CPA3) is a specific mast cell (MC) protease with variable expression. This protease is one of the preformed components of the secretome. During maturation of granules, CPA3 becomes an active enzyme with a characteristic localization determining the features of the cytological and ultrastructural phenotype of MC. CPA3 takes part in the regulation of a specific tissue microenvironment, affecting the implementation of innate immunity, the mechanisms of angiogenesis, the processes of remodeling of the extracellular matrix, etc. Characterization of CPA3 expression in MC can be used to refine the MC classification, help in a prognosis, and increase the effectiveness of targeted therapy

Biography

Dr.Dmitri Atiakshin Research and Educational Resource Center for Immunophenotyping, Digital Spatial Profiling and Ultrastructural Analysis Innovative Technologies, Peoples' Friendship University of Russia, Moscow, Russia.

Title: An Update on the Prevalence And Drug-Resistant Profiling of Salmonella Typhi Isolated From Tertiary Care Centres in Faisalabad, Pakistan
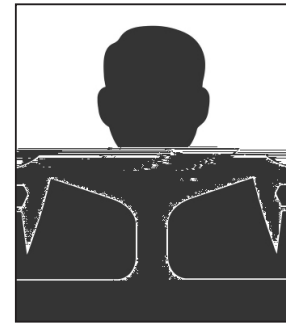
Farhat Jabeen

Student of M.Phil (Microbiology) at University of Agriculture, Faisalabad, Pakistan

Salmonella (S.) enterica serovar typhi is the common cause of bloodstream infections leading to systemic febrile illness and typhoid. S. typhi is a host restricted bacterium that becomes the leading cause of death in developing countries, spread through the fecal-oral route. The current research aimed to investigate the prevalence of multidrug-resistance and extensively drug-resistance S. typhi isolated from the blood samples of typhoid patients. A total of 120 samples were collected from three tertiary care centers in Faisalabad, Punjab, Pakistan. Blood culture positive samples were inoculated and purified on SS-Agar and XLD agar. For the serovar characterization, Gram's staining and biochemical tests were executed, which exhibited positive results for catalase and methyl red and confirmed biochemically the test organism is S. typhi. After the phenotypic confirmation through biochemical tests, Antibiotic Susceptibility Testing (AST) was accomplished using the first and second line of antibiotics. Data were analyzed statistically, and an overall 10% prevalence of S. typhi in the research area was calculated. The 25% isolated S. typhi strains were observed as multidrug-resistant bacteria, 58.9% of S. typhi isolates were reported as extensively drug-resistant while 16.7% displayed an unusual antibiogram pattern, showing susceptibility merely against trimethoprim-sulfamethoxazole and tetracycline and exhibited a resistance pattern against all the other used antibiotics. These sequels are concerning because they will force us to rely on second-line medications. Moreover, the impact of COVID-19, development of mutation in the drug-resistant genes (i.e. azithromycin), and misuse of antibiotics lead to the occurrence of resistance and unusual antibiogram patterns.

https://www.omicsonline.org/clinical-experimental-pathology.php

Biography

Biography: Sergey Suchkov was born in the City of Astrakhan, Russia, in a family of dynasty medical doctors. In 1980, graduated from Astrakhan State Medical University and was awarded with MD. In 1985, Suchkov maintained his PhD as a PhD student of the IM Sechenov Moscow Medical Academy and Institute of Medical Enzymology. In 2001, Suchkov maintained his Doctor Degree at the National Institute of Immunology, Russia.

From 1989 through 1995, Dr Suchkov was being a Head of the Ladi   te