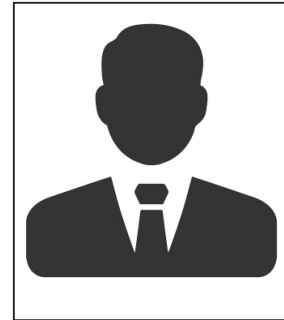


Title: Digital histopathology analysis tools based on supervised machine learning: pros and cons

Caterina Facchin

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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 inter-operator variability. However, we and other have experienced some limitations. Supervised ML is strongly encouraged for homogeneous staining quantifications, in which the pathologist can control the learning phase and choose appropriate input and output data (quality control). Subsequent, ML algorithms need to be well trained on a large amount of high-quality labeled images, to accurately segment and classify each image. The chosen images should include enough diversity to be representative of the entire dataset.

In addition, the choice of ML-algorithm is fundamental, and it reflects the complexity of the desired histological analysis. If 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 classifier 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).

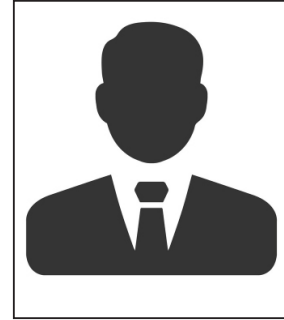
Biography

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

Danielle Chew

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Post mortem Computed Tomography (PMCT) in the 21st century has become an integral feature in forensic medicine. Hanging is the most common method of suicide in the United Kingdom, peaking amongst those aged 45-54 years. This study examined the two methodologies at post mortem to determine if they were complimentary in identifying the cause of death in suspected hanging cases. This study examined 19 cases (mean age, 44) between January and August 2020 at the iGene CT facility in the Coroners mortuary in Stoke-on-Trent. Retrospective images produced using a 'Siemens SOMATOM go. All CT' scanner in a range of different parameters (e.g. KV, pitch, rotation time, slice thickness (mm), increment (mm), Kernel and window) were evaluated. Post mortem reports from the external examinations at the Coroners mortuary were anonymised and made available for analyses in comparison to the PMCT data. Tabulated parameters of the written statements as qualitative data were generated and evaluated using descriptive statistical analyses. There are case examples where PMCT is the superior methodology in identifying and interpreting fracture of the hyoid bone where post mortem external presentation showed inconsistencies. From the data available from the 19 cases in 2020, this suggests that PMCT is complimentary to the current conventional method of the external post mortem examination to more confidently identify neck trauma in suspected hanging cases. The documentation and clinical terminology used in reporting post mortem neck trauma findings requires the development of best practice guidelines to make reporting more consistent.

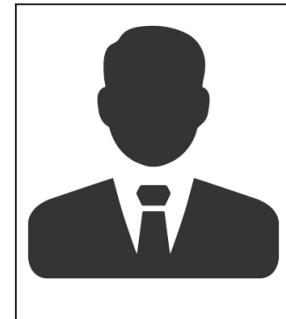
Biography

My name is Danielle Chew and I am a PhD researcher at Staffordshire University. My research focuses on the use of Post-Mortem Computed Tomography as a diagnostic tool within the UK Coronial System to accurately and efficiently diagnose the Cause of Death. My PhD research will build on the foundation of results formulated in my undergraduate research. My current working title is; To what extent can PMCT be used as a singular analytical method of autopsy to conclusively identify the cause of death in cases within Stoke on Trent and North Staffordshire.

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

Dmitri Atiakshin

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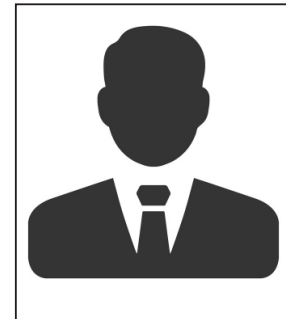
Received: May 17, 2022; Editor assigned: May 18, 2022, Reviewed: May 25, 2022, QC No. Q-00001;
Published: August 08, 2022, Invoice No. PPB-0000F3

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



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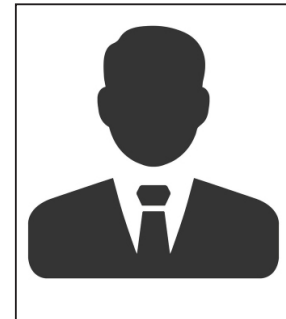
Salmonella (S.) enterica serovar typhi is the common cause of bloodstream infections leading to systemic febrile illness and typhoid. S. typhi is a host restricted bacterium that becomes the leading cause of death in developing countries, spread through the fecal-oral route. The current research aimed to investigate the prevalence of multidrug-resistance and extensively drug-resistant 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-sulfame-

thoxazole 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.

Biography

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

Title: Personalized and Precision Medicine (PPM) as a Unique Healthcare Model to Be Set Up via Translational Applications and Upgraded Business Modeling to Secure the Human Healthcare, Wellness and Biosafety



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A new systems approach to diseased states and wellness result in a new branch in the healthcare services, namely, personalized and precision medicine (PPM). To achieve the implementation of PPM concept, it is necessary to create a fundamentally new strategy based upon the recognition of biomarkers and thus the targets to secure the grand future of drug design and drug discovery.

Each decision-maker values the impact of their decision to use PPM on their own budget and well-being, which may not necessarily be optimal for society as a whole. It would be extremely useful to integrate data harvesting from different databanks for applications such as prediction and personalization of further treatment to thus provide more tailored measures for the patients resulting in improved patient outcomes, reduced adverse events, and more cost effective use of the latest health care resources including diagnostic (companion ones), preventive and therapeutic (targeted molecular and cellular) etc.

PPM, genomics and AI are those of the most rapidly emerging areas of biomedical research and the most promising technologies for improving health care and health outcomes. Examples include the use of AI for improved DNA sequencing and SNP analysis to target specific cell and tissue types, biosensors for

specific molecules in vivo, and point-of-care molecular diagnostic devices enabled by genomics- and AI tools.

The enormous development of genomics research has raised great expectations concerning its impact on PPM aiming to customize medical practice with a focus on the individual, based on the use of genetic tests, identification of genomic biomarkers, and development of targeted drugs. Personal genomics is an area of genomics focusing specifically on the sequencing and analysis of one person's genome, and then giving them their genomic information.

PPM is a developing trend for the future of intensive care medicine. In this sense, the impact of physiology and pathology allows a modular approach, as its various aspects are under development in sometimes unrelated areas of PPM. Integration of the concepts will provide a true challenge for the future, requiring collaboration between clinicians, physiologists, pathologists, bio-designers and bioengineers and remaining a real challenge to bioindustry.

Pathology and Physiology are the central specialties of PPM. It is pathology that provides the skills, infrastructure, and scientific vision we need to lead the way in science-driven biobanking, and it is pathology that can help to ensure optimal research use of

human biosamples, In this sense, molecular diagnostics has a long tradition in pathology, especially in clinical one, where various OMICS-analyses of cancers are being incorporated into diagnostic and decision-making algorithms to secure a way where the pathologists continue to play an essential role in developing and implementing molecular profiling tests in practice and communicate the results and their relevance with clinician

Although “the next-generation pathologists” have already been launched, further and continuous educational efforts must fully implement the paradigm shift into diagnostic molecular pathology practice and reinvent it as a leading diagnostic discipline in the PPM era. Most of the approved and validated predictive biomarkers in PPM still require further optimization and standardization.

The combination of comprehensive biobanking and the next wave of theranostic pathology technologies provides a natural, externally visible infrastructure that now allows pathology as a discipline – to engage directly with the biotechnology and pharma sector. We’re at an exciting junction in pathology’s growth as a medical specialty, and pathology-driven biobanking is becoming both central to our core expertise and, even more importantly, a powerful enabler for many of the most promising growth areas of our discipline: PPM healthcare, clinical trials and drug development, theranostics, and functional assessment and monitoring of disease. In the context of these changes and challenges, the pathology can play a fundamental role in both clinical practice and research.

We stress that implementation of PPM thus requires a lot be-

fore the current model “physician-patient” could be gradually displaced by a new model “medical advisor-healthy person-at-risk”. This is the reason for developing global scientific, clinical, social, and educational projects in the area of PPM to elicit the content of the new branch. In short, PPM will transform the way doctors practice and will shake up the entire pharmaceutical value chain.

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 I.M. 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 Lab of Clinical Immunology, Helmholtz Eye Research Institute in Moscow. From 1995 through 2004 - a Chair of the Dept for Clinical Immunology, Moscow Clinical Research Institute (MONIKI). In 1993-1996, Dr Suchkov was a Secretary-in-Chief of the Editorial Board, Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK.