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Importance of Dose Reference Level in Pediatric Computed Tomography

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Abstract

Radiation dosimetry is vital in minimizing health risks associated with ionizing radiation, especially for pediatric patients who are more sensitive and at higher risk. Chest radiography and computed tomography (CT) are common procedures for diagnosing pediatric patients, but the distribution of radiation dose in CT is different and often results in higher effective doses. To ensure patient safety, the As Low As Reasonably Achievable (ALARA) principle should be followed, and diagnostic Reference Levels (DRLs) should be established. DRLs serve as crucial tools to optimize dose and achieve high-quality diagnostic imaging while minimizing radiation risks. This article focuses on studying the variables for the verification, validation, and creation of a dose reference level in CT for pediatric patients in Rio de Janeiro, Brazil. International standards such as ICRP 135 and Radiation Protection N° 185 are used as references. The study considers factors such as weight, height, age, scan time, number of images, CTDIvol, collimation, and beam energy. The procedures analyzed are divided into head, chest, and abdomen. Probability models, specifically the T-Student Distribution method, will be used to analyze the data and determine diagnostic reference levels. Excel and Python will be used for data analysis and statistical tests. The expected results include the determination of specific diagnostic reference levels for pediatric CT in Rio de Janeiro, reducing the risk of cancer induction, and minimizing excessive doses. In conclusion, establishing dose reference levels for pediatric CT is crucial for radiological protection. Specialized DRLs that consider the unique characteristics of pediatric patients are necessary to ensure optimized dose and radioprotection for all pediatric groups undergoing CT. (author)



Brain Volumetric Analysis of Muscular Dystrophy Pediatric Patients Using MRI Images

Abstract

Muscular Dystrophy is a term used to describe a series of genetic illnesses that affect the development of skeletal muscles, which also causes a series of brain anomalies such as atrophy, white matter abnormalities, and ventricular enlargement [Angelini C. (2019)]. Specifically, around 30% of patients with Duchenne Dystrophy present cognitive deficit and intellectual disability, co morbid with lecture and attention deficits, hyperactivity, autism spectrum disorder, epilepsy, and obsessive-compulsive disorder [Septien L. (1991)], and in some cases a cerebral atrophy that progresses over time [Doorenweerd N. (2014)]. In our research, we analyzed MRI images of brains of Mexican pediatric patients of muscular dystrophy, along with a control group, using the software FreeSurfer compare volumetric differences on cortical and subcortical structures, and differences on total gray and white matter. The normality of the structure's volume distributions was analyzed using the Shapiro-Wilk test. Several structures, both cortical and subcortical, presented a substantial augmented volume compared to control. A handful of cortical structures showed a substantially diminished volume. A better understanding of how brain volumetric differences affects the development of Muscular Dystrophy will allow to develop accurate models to improve the quality of life of its patients. (author)





Development and Initial Validation of an Innovative Analytical Tool for Preclinical Evaluations of PET Radiopharmaceuticals for in Vivo Investigations of Neurological Disease

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Abstract

Preclinical research represents the first important milestone in the clarification and investigation of clinically relevant diseases. In addition, preclinical research significantly supports the development of therapies. Small animal positron emission tomography (µ-PET) plays an important role in this context, as it is able to image and quantify functional, physiological and biochemical processes in vivo. Despite various established µ-PET data analysis programs, the analysis of in vivo acquired image data remains a major challenge in medicine due to the multitude of medical questions, the complexity of disease patterns, and the establishment of new radiotracers. Therefore, the aim of this PhD thesis is to develop and establish a suitable, usable evaluation tool for a simple and efficient analysis of acquired µ-PET data, which extends the spectrum of already existing programs. The developed nuclear medicine data processing analysis tool (NU_DPA) was implemented in Matlab and tested and established on the basis of three preclinical experimental or test series. The data series are µ-PET datasets of different stroke rat brain models using the following radiotracers: 2-[18F]fluoro-2-deoxy-glucose ([18F]FDG), which accumulates homogeneously in the brain and [68Ga]fucoidan, which specifically accumulates at p-selectin. The NU_DPA involves automatic segmentation of a volume-of-interest (VOI) from the full PET image and the subsequent alignment of the VOI using a PET template (averaged PET dataset). This PET template is created from the own acquired PET data. By embedding a suitable anatomical MR atlas (customizable), the aligned PET data can be assigned to individual atlas-specific sub-regions. Such a sub-classification of the VOI allows a more detailed analysis and evaluation of the radiotracer accumulation. Furthermore, NU_DPA offers the possibility of a semi-quantitative evaluation of the PET image data based on three different parameters, the normalized activity, the standardized uptake value and the uptake ratio. The Matlab-integrated statistical algorithms provide an additional option for statistical evaluation of the previously calculated semi-quantitative parameters. The NU_DPA program thus represents a semi-automatic data evaluation program that enables both the registration and the semi-quantitative evaluation of PET image data within a series of experiments and it has already been successfully tested for the radiotracers [18F]FDG and [68Ga]fucoidan in animal models. To the best of our current knowledge, there is no known data analysis program that can semiautomatically analyze PET image data using the added atlas and is potentially suitable for homogeneous and target-specific accumulating radiotracers.





Information Technologies and Computational Methods for Management, Optimization and Precision Medicine in Medical Imaging Departments

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<u>Abstract</u>

The healthcare industry demands information technologies and computational methods to improve productivity and offer personalized assistance to patients. This work aimed to develop and explore information systems and computational methods to improve the management, optimize the exams, and provide new biomarkers and artificial intelligence signatures for decision making in medical imaging facilities. We developed software based on Workflow Based Approach (WBA) concept and computational methods using Python language to improve the management and optimize the exam protocols. A framework to access new biomarkers and artificial intelligence (AI) signatures was developed and validated in COVID-19 CT patients, 18F-FDG-PET/CT cervical cancer and 18F-FDG-PET/CT Hodgkin lymphoma patients. This framework was feasible for robustness analysis: repetitivity (error < 5%), reproducibility (intraclass correlation coefficient, ICC > 90%) and clinical correlation (p < 0.05). The overall performance of predictive models was AUC=0.74 and AUC=0.96 for 18F-FDG-PET/CT cervical cancer and 18F-FDG-PET/CT Hodgkin lymphoma, respectively. A new Al software to support thorax CT COVID-19 diagnoses was implemented and validated within PACS/Viewer. Without the support of software, physicians performed with mean sensitivity and specificity of 83.4% and 64.3%, respectively. When they were assisted with Al software, mean sensitivity and specificity were 87.1% and 91.1%, respectively. In addition, Al software improved the inter-rater reliability from moderate to substantial agreement in a Cohen's Kappa scale. (author)



Central Nervous System Radiotracer Development: Bench to Bedside

International Atomic Energy Agency (2024), Radiochemistry and Radiation Technology Section, Vienna, Austria

<u>Abstract</u>

This publication provides an overview of central nervous system (CNS) radiotracer development, discussing different aspects and stages of development. Non-invasive neuroimaging with radiotracers can provide functional information at the cellular level and contributes substantially to understanding the complex mechanisms of the functioning and pathophysiological processes in the human brain and is useful in certain diseases for patient stratification, treatment response monitoring and as an aided technique for drug development. The success of the development of clinically significant radiotracers depends on many factors such as the selected biological target, specificity and affinity of the radio ligand, pharmacokinetics of radiotracer and others. The information provided in the document will be useful to researchers, students and professionals engaged in the development and deployment of CNS radiotracers for clinical, research or drug development applications.





Brain Tissues Have Single-Voxel Signatures in Multi-Spectral MRI

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Abstract

Since the seminal work of Brodmann and Vogt and Vogt, it has been known that different brain regions have unique cyto- and myeloarchitectural features. Classifying brain tissue and other tissues on the basis of their intrinsic characteristics has been a long-standing endeavour in the field of magnetic resonance (MR). The idea of classifying tissues based on their T1 and T2 relaxation times can be traced back to before the advent of magnetic resonance imaging (MRI). In fact, Lauterbur used it to motivate MRI, and rightly so; the high soft tissue contrast resulting from T1 and T2 times in the human body is a cornerstone of today's radiology, which frequently uses relaxation time weighted MR images. The first automated approaches to classifying tissues based on intrinsic MR features were introduced in the 1980s. For example, although successful classifications have been reported for up to ten tissue classes, the limited set of input features restricted the ability to achieve classifications for a higher number of tissue classes. For this reason, atlas-based approaches have been introduced with great success, using spatial information to reduce the number of potential tissue classes at a given position. In the present study, I investigated the feasibility of a global brain classification based on intrinsic MR features in cooperation with an interdisciplinary team. To this end, I exploited several technological advances. First, I used a 7 Tesla scanner of the latest generation, which provides an increased contrast-to-noise ratio for many MR contrasts. Second, I used a novel diffusion MR technique, q-space trajectory imaging. This can be used to measure not only the voxel-averaged diffusion metrics, but also the variance of diffusion tensors within a voxel, which is relevant in many regions of cortical grey matter with more than one dominant fibre orientation. Third, I used a chemical exchange saturation transfer (CEST) sequence. The resulting magnetisation transfer (MT) contrast appears to be a suitable marker of myelination that can be used to distinguish and segment different cortical regions.