The small-animal dedicated SPECT scanner (Molecubes), equipped with three collimators (rat, general-purpose (GP) and high-sensitivity (HS) mouse), has recently been installed in our institute. The aim of this study was to optimize acquisition protocols and reconstruction parameters for theranostic preclinical studies.
Uniformity and spatial resolution were investigated using dedicated phantoms (uniform cylinder and Derenzo) with both Tc-99m and Lu-177 according to standardized methods. Images were acquired with the three collimators and reconstructed with attenuation correction varying the number of iterations. In addition, a biomimetic mouse phantom was used to optimize acquisition parameters. Organs and tumours were filled with different concentrations of Tc-99m, mimicking a typical tracer biodistribution. Gold standard images obtained with an administered activity of 10 MBq acquired for 30 min were compared to images obtained with lower activities and longer acquisition times.
Uniformity coefficient-of-variations with Tc-99m were 20 %, 18 % and 7 % for rat, GP and HS collimators respectively after 50 iterations, worsening to 76 %, 60 % and 22 % after 500 iterations. Under equal conditions, Lu-177 exhibited poorer uniformity values, due to the tracer lower radiation yield. Spatial resolutions with both radionuclides were 2 mm, 1 mm and 2 mm for rat, GP and HS collimators respectively after 50 iterations and 1.6 mm, 0.7 mm and 1.4 mm after 500 iterations. Acceptable image quality with Tc-99m compared to gold standard was obtained lowering injected activity to 1 MBq and rising the acquisition time from 30 to 120 min.
Based on our findings, 50 iterations provide a good compromise between uniformity and spatial resolution with shorter reconstruction time. For Lu-177, HS collimator and longer acquisition times are required compared to Tc-99m to achieve adequate image quality. Satisfactory image quality can be obtained with 120 min and low dose of Tc-99m. Similar measurements with Lu-177 are ongoing.

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Nuovi ambiti - multidisciplinare

Abstract PO.01.290

Machine learning integration of multi-modal data in DM1 patients allows to reveal subgroups underlying genomic classes

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Myotonic Dystrophy type 1 (DM1) is an expansion repeat disorder which mainly involves neuromuscular and central nervous systems. DM1 diagnosis is based on the detection of a CTG triplet in the DMPK gene, whose length affects clinical manifestations (DOI: https://doi.org/10.1007/s10072-024-07826-9). The genotype-phenotype correlation is not fully clear and needs a deeper understanding. Moreover, the possible presence of interruption patterns within the main expansion motif should have a stabilizing effect on the phenotype and deserves to be investigated.
The dataset was composed of 36 adult DM1 patients enrolled at Ospedale Bellaria, Bologna. Multi-modal data was collected from disease-specific clinical scales, a comprehensive neuropsychological test battery to evaluate multiple cognitive domains, morphological and advanced brain MR images. Genomic data was acquired through Southern blot technique. Each of these groups of features was separately pre-processed and standardized. Data integration followed a machine learning unsupervised approach, exploiting PacMap embedding and K-means clustering, with silhouette score evaluation. Finally, Mann-Whitney U test was used to assess significant statistical differences between clusters.
Three well-separated clusters emerged from the silhouette score evaluation, consisting of 16, 12 and 8 samples. Genomic classes are distributed among them. U test revealed significant differences among several features. Memory, visuo-spatial and global cognition functions are the neuropsychological features that mainly differ from cluster to cluster. For what concerns imaging, frontal, parietal and temporal cortical regions resulted to be discriminative.
The two larger clusters show deficits in some cognitive areas, together with the narrowing of related brain regions, especially in the left hemisphere. These findings must be further investigated and correlated with genomic information. Results will be integrated with interruption patterns analysis, which are currently being characterized by nanopore long reads sequencing, that allows to accurately sequence repeated regions detecting changes and insertions in the main repeat motif.

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Nuovi ambiti - multidisciplinare

Abstract PO.01.294

Optimizing AI models for haematological malignancies with federated learning: simulations and experiments

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Federated Learning (FL) is a machine learning framework that enables privacy-preserving collaboration between institutions. Instead of transferring sensitive data to a central server, FL allows individual entities to learn locally and shares only AI model parameters. FL has enormous potential in haematology, where scarce and sensitive data and diverse datasets are analysed. A platform to perform FL experiments has been developed by the EU project GenoMed4All, whose reliability and robustness must be tested.
FL was implemented for Myelodysplastic Syndrome (MDS) and Sickle Cell Disease (SCD) datasets, of 4427 and 65 patients, respectively. For MDS, a DeepSurv model predicted overall survival, while for SCD, a Logistic Regression predicted the emergence of silent cerebral infarction. Models' performances were assessed through C-index and F1-score, respectively. FL tests were conducted exploiting both simulations using Flower library and experiments utilizing the GenoMed4All platform. The MDS and SCD datasets were distributed across 3 clients, each one with a different number of samples. Simulations were performed on a single

computer, that acts as central server and generates virtual clients and then compared to the FL platform results.
FL aggregation allowed to improve models' performance for both MDS and SCD use case. In particular, clients with less samples benefits from FL training. In general, federated training performed better than isolated training and allowed to achieve performances close to centralized training, where all datasets are merged. Numerical results from simulations and runs on FL platform were comparable and validated the platform robustness.
Experiments confirmed the benefits of FL for MDS and SCD use cases and assessed the reliability of the GenoMed4All platform. Results' improvements could be also achieved by different strategies of model parameters' aggregation during the FL training. These findings open the possibility of implementing FL for other haematological tasks.

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Nuovi ambiti - multidisciplinare

Abstract PO.01.300

Horizon scanning of virtual clinical trial platforms and digital twins in Italy

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The AIFM4VCT working group (WG) of the Italian Association of Medical Physics (AIFM) was established to foster networking and advance the development and application of in-silico frameworks and digital twins in Virtual Imaging Trials (VITs) in medicine. We conducted a horizon scanning of the state-of-the-art to assess the implementation of VITs in Italy.
The review focuses explicitly on the development of virtual platforms and digital twins and their role in VITs, highlighting their application fields: diagnostic radiology, nuclear medicine, and radiotherapy. Independent researchers from the AIFM4VCT group carried out a literature search covering the last five years. Specific keywords (Italy as affiliation/digital phantom/computer-generated model/simulated phantom/in-silico medicine/virtual imaging/computational twin) were employed in freely available literature databases.
The selected research topics covered analysis of diagnostic and screening modalities; therapies and personalized medicine; development and implementation of 3D digital phantoms (e.g., for single organs, anatomical districts, and pathologies); and related applications of artificial intelligence tools. About 80 original papers, including research and conference papers, reviews, and technical notes, were collected. The papers were stratified based on the anatomical district (breast, abdomen, chest, etc.) and application. The studies were analyzed and discussed in terms of strengths and weaknesses across all application fields. The review underlined a growing interest of the medical physics community in developing VIT platforms and their potential impact in clinical settings. However, especially in nuclear medicine, VITs are still in their early stages but hold significant potential in revolutionizing personalized medicine, improving patient outcomes, and transforming healthcare delivery. The need for stakeholders, validation, and standardization approaches is evident, as is the need to engage legislative bodies in adopting in-silico tests supporting medical device development and clinical decisions.
AIFM4VCT WG recognized the potential in the Italian community to develop and adopt VITs to advance personalized medicine through networking opportunities.

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Nuovi ambiti - multidisciplinare

Abstract PO.01.303

Photo-thermal therapy for selective killing of human cardiac fibroblasts

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Cardiovascular diseases are the leading cause of death in Western countries, and cardiac fibrosis is a condition found in several cardiovascular pathologies. Fibrosis may be an organism's response to myocardial infarction; moreover, pathologies like diabetes, can stimulate the fibrotic process. The fibrotic process is a response to maintaining the structural integrity of the organ, but it compromises its contractile capacity, leading to cardiac dysfunction. Cardiac fibroblasts (CF) play a central role in the fibrotic process.
Photothermal therapy (PTT) is a non-invasive medical treatment that exploits the ability of plasmonic nanoparticles to convert light radiation into thermal energy, generating localized heat. In this work, gold nanorods (AuNRs) are exploited as light-heat converters to study for the first time the feasibility of a PTT approach for the selective ablation of CFs that does not damage surrounding cells.
Absorption spectroscopy and cell viability analysis were performed as preliminary measurements to characterize the photothermal properties of the system composed of AuNRs and CFs. The selectivity of the treatment was verified by irradiating with a continuous wave laser emitting at 808 nm a mixed cell culture consisting of AuNRs-treated CFs and untreated CFs, expressing Green Fluorescent Protein (GFP). A fluorescent live/dead assay assessed cell death.
A concentration-dependent red shift of the longitudinal plasmon bands of AuNRs is observed by absorption spectroscopy. AuNRs-loaded CFs undergo a temperature increase proportional to the AuNRs concentration upon laser irradiation, which causes cell death. Fluorescence images of the mixed culture after the irradiation show that the AuNRs-loaded CFs were dead, while the viability of non-loaded CFs was preserved.
These results demonstrate the potential of AuNRs for selective ablation of human cardiac fibroblasts and show how PTT could become an important tool in the hands of the next generation of medical physicists, enabling them to develop next-generation cancer treatments that combine various techniques.