

ORAL PRESENTATIONS

Session A – AI in Biology

Olivier ARMANT

IRSN, France

Long term evolutionary impact of the Chernobyl nuclear accident on tree frog populations: perspectives for machine learning methods

Individual functional modifications shape the ability of wildlife populations to cope with anthropogenic environmental changes. But instead of adaptive response, a human-altered environment can generate a succession of deleterious functional changes leading to the extinction of the population. To study how persistent anthropogenic changes impacted local species, population status, we characterized population structure, genetic diversity and individual response on gene expression of the tree frog *Hyla Orientalis* along a gradient of radioactive contamination around the Chernobyl nuclear power plant. Using both supervised and unsupervised methods, we detected lower effective population size in populations most exposed to ionizing radiation that is not compensated by migrations from surrounding areas. We also highlighted a decreased body condition of frogs living in the most contaminated area, a peculiar transcriptomics signature and stop-gained mutations in genes involved in energy metabolism. Data integration with current (WGCNA) and novel machine learning methods is discussed.

Mohamedamine BENADJAOUD

IRSN, France

Statistical association between variables not jointly observed: a Bayesian latent modeling approach with applications in radiation biology.

Modern data-analysis fields, such as machine learning and statistics, for the most part study the isolated analysis of a “single dataset” where all the covariates (eventually with some missing values) are observed on the same unit subjects.

However, it is usually difficult to obtain a “single-source dataset” in which all the relevant variables are observed for the same individuals or units. In radiation biology for example, animal longitudinal studies generate a variety of data including molecular data, survival data, as well as histological and functionality end points. A simultaneous observation within the same animal of all these parameters is often impossible in practice since most of them require the animal sacrifice which precludes a direct observation of the future measures or events. Thus, connection between these covariates is often treated only qualitatively arguing analogy trends across the experiment groups.

To address this issue, we present an overview of several approaches based on Bayesian statistics and latent variable modeling which constrain the causal mechanism underlying the observations collected in multiple datasets. The proposed approach is illustrated on two studies: a study demonstrating the beneficial effect of exosomes derived human Mesenchymal Stem Cells on the survival of mice with radiation-induced gastrointestinal syndrome and a second study investigating

biomarkers of subclinical cardiac dysfunction in cohort of rats irradiated at several doses to the heart.

Judith REINDL

Universität der Bundeswehr, Germany

CeCILE – intelligent detection, tracking and cell cycle evaluation of eukaryotic cells on phase-contrast live-cell videos

To understand how tissue reacts to radiation, it is necessary to understand radiation effects on a single cell basis. The most notable reactions of cells to irradiation are cell cycle arrest, proliferation and cell death. Here, we present a completely new approach to investigate these biological endpoints in one experiment: A deep-learning based algorithm called CeCILE (Cell Classification and In-vitro Lifecycle Evaluation), which is used to detect and analyze cells on live-cell phase-contrast videos. With this method, we can observe and analyze the behavior and the health conditions of single cells over several days after treatment.

After irradiation up to six sample dishes containing the cells can be mounted on a microscope in parallel inside a stage-top incubator and are imaged for up to 5 days. The created videos can be analyzed by CeCILE, which is based on a faster RCNN algorithm for object detection and is trained on a hand-labeled dataset of microscopic videos. In these videos all cells were assigned to one of four classes, which defines the cells' state in the cell cycle. Then, a tracking algorithm assigns an individual ID to every cell in the video. The tracking is conducted employing hidden Markov models to simulate the cell movements and states and an embedded recursive Bayesian filter to infer their behavior. Furthermore, it provides an improved tracking with stable cell identification in complex scenes as well as the possibility to predict future states and fill previous gaps in trajectory caused by detection failures. In conclusion, we are able to investigate the behavior of irradiated cells in one simple experiment. Already the first published version of CeCILE showed that similar results compared to state-of-the-art assays could be achieved. With the inclusion of the tracking method, we are now able to go further by really inspecting the behavior of every single cell by evaluating the cell-cycle, the lineages and the circumstances of cell death.

Session B – AI in Medicine

Igor PECHERSKY

ANAGOG Ltd., Israel

Foundation models in biomedical research

The report presents an overview of recent developments in the field of foundation models, which are large-scale pre-trained models that use self-supervision. These models have been shown to be capable of rivaling the performance of human experts on challenging tasks, such as answering complicated questions, generating coherent contexts, summarizing ideas, reasoning, and planning. Through their ability to engage in in-context learning, these systems are capable of adapting to the prompt given by a user and generating content that is pertinent to both the query and the context. Recently, it was shown that these systems might be successfully used to generate new molecular structures with prescribed properties, predict protein-ligand interactions, and identify potential drug targets.

The report highlights the potential applications of these models in biomedical research, such as drug discovery, personalized medicine, and causal interpretation of high-throughput omics experiments. Special attention is given to the practical recommendations for available architectures, repositories, tools, and platforms.

Nadav RAPPOPORT

Ben-Gurion University, Israel

What can we tell from routine laboratory test results?

An essential part of the clinical decision-making process depends on interpreting different laboratory test values. This process is usually performed by scanning the results and looking for abnormal values. One of the core limitations is that the scan for abnormalities is done marginally, where every test is considered independently of the results of the other laboratory tests. Such practice can miss information in higher dimensions where a result of a laboratory test is assessed given the results of other laboratory tests.

Using multidimensional laboratory test results, we defined a new measure of 'abnormality'. We showed that this measure might be useful for alerting physicians for patients at risk for illnesses otherwise overlooked.

Moreover, we showed that routine laboratory test results can be used to estimate biological age. Biological age may be of higher importance than chronological age, yet biological age is not trivial to estimate. We trained a machine-learning-based model to predict age using routine laboratory tests.

We trained an XGBoost model using data from about 472,000 individuals aged 37–82 years old. The model achieved an RMSE of about 6 years. Subjects, predicted by the model to be younger than their actual age, were found to be healthier as they had fewer diagnoses, fewer operations, and a lower prevalence of specific diseases than age-matched controls. On the other hand, subjects predicted to be older than their chronological age had no significant differences in the number of diagnoses, number of operations, and specific diseases than age-matched controls.

Chen NADLER

Hadassah Medical Center, Israel

Artificial Intelligence used in Oral and Maxillofacial Imaging

Artificial Intelligence is tremendously being used in medicine, especially in medical imaging. Oral Maxillofacial imaging includes pathologies of both the hard and the soft tissue in the jaws and their surrounding structures (such as the salivary glands). Research of AI in the OMF field focuses on diagnosis, image quality and treatment planning. My talk will introduce the development of AI in OMF by showing examples of studies we conducted on both 2D (panoramic imaging) and 3D (cone-beam CT) imaging in detecting dental restorations and jaw lesions, respectively. AI is an important research and clinical tool which is developing exponentially. It is my belief that this tool will help the clinical community by providing better treatment planning and promoting patients' health.

Dental cone beam CT (CBCT) is used for various indications including treatment planning of dental implants, extraction, root canal treatment and bone pathologies may include incidental findings which may be clinically important and if left untreated, may cause teeth displacement, bone expansion, bone fracture or development of malignancy. Therefore, scanning and interpretation of the entire imaged volume is needed. Currently, reporting of dental CBCT is not routinely done, due to a combination of lack of trained clinicians and enforcement of the need for a report. Furthermore, an increasing number of CBCT scans are being performed. Our study aimed to develop an algorithm to detect, segment and display benign jaw lesions in CBCT.

MATERIALS & METHODS: Our study included 41 CBCT scans with and 41 without histologically confirmed, benign jaw lesions from 3 different CBCT machines. They were assigned into training (50 cases - 20,214 slices), validation (10 cases - 4,530 slices), and testing (22 cases – 6,795 slices) datasets. MASK-RCNN was used to detect the bone lesion in each axial slice. The algorithm further identified the spatial location of the lesion, in sequential axial slices.

RESULTS: The developed algorithm was able to detect all 11 CBCT scans with bone lesions, with an accuracy of 100%. The sensitivity ranged between 82.0%-100% with a total sensitivity of 95.9% and the final precision ranged between 92.4%-100% with a total precision of 98.8%. Following the segmentation of the BIOLs in each case, the dice coefficient ranged between 66.8%-93.0% with an average of $83.5\% \pm 7.8\%$.

CONCLUSIONS: Our deep-learning-based algorithm successfully detected jaw lesion in CBCT axial slides. Our study is unique since it focused on lesions in various jaw locations, with different CBCT machines and different scanning protocols. We currently expand our study to include other jaw lesions. We believe that our algorithm may be used to demonstrate incidental bone lesions, thus promote a more conservative treatment and improve patients' health.

Talia YESHUA

Jerusalem College of Technology, Israel

Using diverse image processing and machine learning tools for automatic diagnosis of medical and biological images

In our medical image diagnosis lab, we collaborate with researchers and physicians from various departments including radiology, orthopedic surgery, urology, otorhinolaryngology, microbiology, and oral medicine. Our partners create the image databases and raise the clinical needs for a variety of image diagnoses, such as detecting autoimmune diseases, detecting and segmenting benign and cancerous tumors, assessing kidney function, and measuring DNA growth rate. The role of our laboratory is to choose what are the most suitable AI tools to reach the optimal automatic diagnosis. We use image processing, machine learning, and deep learning tools for classifying the images, measuring new quantitative parameters, and detecting pathologies. During this lecture, some of the tools used for automatic diagnosis will be briefly reviewed and the advantages of combining several AI tools for the finest diagnosis will be demonstrated.

Laila C. ROISMAN

Shaare Zedek Medical Center & I3LUNG group, Israel

I₃LUNG: Integrative science, Intelligent data platform for Individualized LUNG cancer care with Immunotherapy

Lung cancer is a major cause of cancer-related death worldwide, with 470,000 new cases and more than 390,000 deaths in Europe alone¹. Non-Small Cell Lung Cancer (NSCLC) is the most common histology, accounting for around 85% of all cases. Immunotherapy (IO) has revolutionized the care paradigm for advanced NSCLC, with 30-50% of patients potentially benefiting from IO in the long term. However, this also means a substantial share of patients are exposed to the risk of IO-associated toxicities, denied other treatment alternatives, and incur substantial costs to the medical system without a reasonable chance of response. To reduce this economic burden and improve patient outcomes, personalized patient selection is essential, which requires a better understanding of tumour features, its microenvironment, and its interactions with the host. Currently, Programmed Death-Ligand 1 (PD-L1) is the only biomarker used to predict IO efficacy, despite its limited predictive performance. Other markers, such as baseline clinical features, Tumour Mutational Burden (TMB), tumour microenvironment (TME), microRNA (miRNA), immune gene signatures, and the gut microbiome have been tested in retrospective studies of randomized clinical trials, but with uncertain results. To address this complexity, Artificial Intelligence (AI) frameworks and Machine Learning (ML) processes, which can synthesize and correlate data from multiple sources and develop learning methods, are a powerful tool to construct decision-making (DM) tools that provide personalized predictions of response to treatment. In I₃LUNG study, we aim to achieve the highest performance in personalized medicine through AI/ML models based on multimodal patient data and images, and to implement an AI/ML model in a real-life setting.

Gavriel FIALKOFF

Hebrew University of Jerusalem, Israel

Deconvolution of cell-free nucleosomes and inferring tissue-of-origin and transcription programs in autoimmune hepatitis plasma

Liquid biopsy methods have emerged in the past two decades as a powerful tool for non-invasive diagnosis and disease monitoring in several pathological contexts. While most methods rely on sequence changes, a few recent methods attempt to identify tissue-of-origin also in the absence of such changes, based on DNA methylation, fragmentation patterns and more. cfChIP-seq, a recently published method for chromatin immunoprecipitation and sequencing of cell-free nucleosomes, holds the promise of further inferring the transcription programs taking place in the dying cells. However, a significant barrier hindering this possibility is the preceding unsolved challenge of quantifying the unknown types and proportions of tissues composing the cell-free DNA.

Many deconvolution methods were proposed for genomic data, the majority of them aimed at decomposing bulk RNA-seq data to its cell-type components based on cell-type specific markers. Despite the availability and good performance of these methods, cfChIP-seq data requires tailored adjustments for various reasons related to the nature of the assay (e.g., background reads derived from non-specific antibody binding) and the chromatin dynamic which practically excludes the possibility of achieving a complete reference atlas of all cell states.

In this work I will discuss the considerations involved in deconvolution of cell free nucleosomes, suggest a Poisson regression model for estimating cell-type composition and inferring transcription programs and present results from applying this model on cfChIP of autoimmune hepatitis patients.

Session C – AI in Medicine

Moshe YANOVSKIY

Yair Y. SHAKI

Jerusalem College of Technology, Israel

Ethical challenges of using AI in medical decision making: in search for solutions

Many ethical problems have been addressed in the literature. Most issues are not new and were broadly discussed for decades, like the “moral hazard” of asymmetric information (AI developer – AI developer’s expert – medical practitioner-patient). Various conflicts of interest could jeopardize proper AI systems deployment. For example, fear of competition could encourage practitioners to deliver biased feedback on AI application efficiency, while AI developers could overestimate the advantages of their products. A relatively new ethical problem is the capacity of experts and developers to promote their choices, imposing it on practitioners and eventually on patients, under the veil of anonymity.

As usual, these challenges mobilized many believers in the magic of governmental regulation as the universal solution to any grave problems. It is true that governments (lawmakers) could properly establish responsibility for AI in medicine applications that caused harm and define some standards of transparency for these systems. However, governmental intervention routinely comes with numerous costs and specific moral challenges. Government is neither a perfect unbiased, impartial and enlightened machine, nor an assembly of angels. So governmental regulations imposed upon AI developers could aggravate the challenge of an anonymous decision maker choosing the fate of patients without their consent. Government officials interested in more spending (Niskanen model) and in more discretionary power (Jasay model) could inflict harm by promoting their (officials’) special interests rather than the interests of the patients.

Excessive responsibility of AI developers could harm patients not less than lack of responsibility, discouraging development of AI medical tools. Damage potentially caused by AI tools should be considered in comparison to other medical tools; present software tools are probably the best, though still rather poor, analogy.

So even the governmental capacity to define responsibility for wrongdoings or to establish transparency standards in medical AI applications should be prudently examined and restricted to avoid above mentioned side effects, probably overweighting the benefits of governmental intervention.

Chen SAGIV

DeePathology Ltd., Israel

Why AI should ultimately be the playground for medical doctors and how it works for Computational Pathology

AI has revolutionized the world in the last decade, and the revolution still goes on. The impact of AI on medical diagnosis, selection of the right treatment and drugs' development is enormous. Hundreds of AI solutions for various problems in healthcare have been developed and it is expected that many more will be developed in future. While the problems are usually presented by the medical experts, the solutions are being developed by AI experts. A recent trend in AI brings

the power of solutions' creation to the hands of the medical experts, with platforms that provide AI solutions' creation for specific domains. This is how medical experts are able to explore AI solutions to day-to-day problems and develop these solutions by themselves. We will give an example of this paradigm in the domain of computational pathology.

Yaakov HACHOEN-KERNER

Jerusalem College of Technology, Israel

Detection of anorexic girls in blog posts written in Hebrew using a combined heuristic AI and NLP methods

In this study, we aim to detect in social media texts written in Hebrew girls who are suspected of being anorexic. We constructed a dataset containing 100 blog posts written by females who are probably anorexic, and 100 blog posts written by females who are likely to be non-anorexic. The construction of this dataset was supervised and approved by an international expert on anorexia. We tested several text classification (TC) methods, using various feature sets (content-based and style-based), five classical machine learning (ML) methods, three RNN models, four BERT models, three basic preprocessing methods, three feature filtering methods, and parameter tuning. Several insights were found as follows. A set of 50-word n-grams (mostly word unigrams) given by an expert was found as a good basic detector. A heuristic process based on the random forest ML method has overcome a combinatorial explosion and led to significant improvement over a baseline result at a significance level of $P=0.01$. Application of an iterative process that tests combinations of “k out of n_0 ” where $n_0 < n$ (n is the number of feature sets) lead to an accuracy score of 90.63%, using a combination of 300 features from ten feature sets.

Benjamin MILGROM

Jerusalem College of Technology, Israel

Autoencoders in depth sensing for vision enhancement

We present image enhancement by increasing the depth of field of the imaging system using a coded phase mask. The improvement is performed by combining image processing algorithms, based on machine learning using autoencoders. An added value of the improvement is passive range estimation, which defines areas of interest in the image according to the distance from the lens. The presented algorithm is specially adapted for machine vision applications, as well as for improving the orientation of the visually impaired by means of a relatively cheap and simple-to-operate component.

Avi ROSENFELD

Jerusalem College of Technology, Israel

Quantifying artificial intelligence for better prediction of cancer

We outline several ground-breaking directions for how explainable artificial intelligence (XAI) can be quantified and applied for improved AI safety in medicine. We present a brief overview of XAI within the context of medical safety. We develop

four metrics for quantifying XAI: The D metric based on performance differences between the explanation's logic and the system's actual performance, the R metric to quantify the number of rules outputted by the explanation, the F metric to quantify the number of features used to generate that explanation, and the S metric to quantify the stability of the explanation. We provide a specific example for how all four of these metrics can be applied to better quantify AI safety to detect several types of cancer.

Moshe AMITAY

Jerusalem College of Technology, Israel

Deep convolutional neural network for screening carotid calcification in dental panoramic radiographs

Ischemic stroke, a leading global cause of death and disability, is commonly caused by carotid arteries atherosclerosis. Carotid artery calcification is a well-known marker of atherosclerosis. Such calcifications are classically detected by ultrasound screening. In recent years it was shown that these calcifications can also be inferred from routine panoramic dental radiographs. In this work, we focused on the panoramic dental radiographs taken from 500 patients. We manually labeled the patient's carotids and applied a convolutional neural network (CNN) classifier to automatically detect carotid calcification. Applying the algorithm in healthcare units and dental clinics has the potential of reducing stroke events and their mortality and morbidity consequences.

Ori ASHUSH

Jerusalem College of Technology, Israel

Feature harmony classification for the detection of handwriting disorders

Handwriting is used to diagnose a variety of disorders and is known as a biomarker for early detection of a variety of diseases characterized by motor symptoms. Many clinical tests have been developed to identify various disorders and diseases using the patient's handwriting. Machine learning and deep learning methods have been tailored to build intelligent models and tools to support clinician's decisions using the patients' handwriting. Each of the models is trained on a specific disorder and used to detect one specific disorder. Motivated by experience in the field of occupational therapy, we define the concept of "harmonic handwriting". Our hypothesis is that various handwriting disorders are characterized by non-harmonic handwriting. Rather than using a subset of features to characterize specific problems, we explore multiple parameters of handwriting as a whole and attempt to determine the level of its harmony and how fluid the handwriting is in multiple parameters. We then use this to classify and detect handwriting deficiencies. We use methods such as random forests and neural nets on different datasets of handwriting captured on a Wacom tablet (DCD, Dysgraphia, Parkinson's, Alzheimer's) from subjects of various ages (children and adults) and discuss our findings.

Willian A. DA SILVEIRA
Staffordshire University, UK

Space Omics: Challenges and Opportunities for Artificial Intelligence

Dr da Silveira will present the field of Space Omics, their current opportunities and challenges and how Artificial Intelligence can contribute to the development of the field.

POSTERS

Ruth COHEN-ARBIV, Avi ROSENFELD
Bar-Ilan University, Israel, and Jerusalem College of Technology, Israel

Creating the best decision tree for assisting practitioners to diagnose cancer

The goal of our research is to develop algorithms to determine the best decision tree to use in order to teach a medical practitioner to perform a classification task. Specifically, we taught people (practitioners or lay experiment participants?) how to diagnose suspected cancer using a decision tree. After the learning process, we tested the diagnostic ability of the people via new cases presented to them. Based on the results of the experiment, we built an agent that used Machine Learning to determine which decision tree was best to present so that the people's cancer understanding was maximized as quantified by their predictive accuracy. We found that too complicated tree was hard to understand, thus impairing the ability to correctly diagnose cancer. Conversely, too simple tree was easy to understand, but also impaired performance as it oversimplified the medical information. Thus, the agent needed to find the best balance between these extremes so it could maximize his performance while not overloading practitioners with too much information. We present initial results of this agent's success in helping people predict esophageal cancer.