Type d'offre : Corporate offer

Post date : 28.03.25

ASNR

PhD Offer l Generative AI & transfer learning between imaging modalities in cytogenetic biol. dosimetry

Informations générales

Contract type : Fixed-term contract

Contact :

Offer

Starting date : Mon 06/10/2025 - 12:00

ASNR :

L'**Autorité de sûreté nucléaire et de radioprotection** (ASNR) is an independent administrative authority created by the law of May 21, 2024, relating to the organization of the governance of nuclear safety and radiation protection to meet the challenge of reviving the nuclear industry. On behalf of the State, it oversees civil nuclear activities in France and carries out missions of expertise, research, training, and public information. The ASNR is composed of civil servants, public-law agents, and private-law employees.

Détail de l'offre (poste, mission, profil) :

Environment / Organization / Context

In situations involving nuclear, medical, or malicious radiological accidents, knowledge of the level of human exposure to ionizing radiation is crucial for determining the appropriate medical response. Complementing physical dosimetry, cytogenetic biological dosimetry is based on imaging techniques that detect radiation-induced chromosomal damage in circulating lymphocytes. This damage, known as chromosomal aberrations, is considered one of the most reliable biomarkers for estimating radiation exposure.

In previous work, computer vision and artificial intelligence models were developed to automatically detect chromosomal aberrations for two cytogenetic imaging modalities: Giemsa imaging and Fish3 imaging. In particular, this work revealed the possibility of using a "trans-modal" approach to switch from one imaging modality to another, enabling the development of a computer vision model for a third cytogenetic imaging modality: multi-Fish (M-Fish).

Mission

This thesis is a collaborative project between the Radiobiology of Accidental Exposure Laboratory at ASNR and the SAIRPICO project team at INRIA. It proposes to deploy generative AI and transfer learning tools around three themes: 1) the development of an AI model for image preselection in Glemsa/Fish3 modalities; 2) the conversion of automated aberration counting in Fish3 imaging into a radiation dose, taking into account confounding factors and associated uncertainties; and

finally, 3) the development of a new AI model for automated chromosomal aberration counting in M-Fish imaging.

TASK 1 - Development of artificial intelligence models for pre-selection of metaphase images in Giemsa and Fish-3 modalities (from Q4 2025 to Q2 2026)
Convolutional neural networks for classification will be trained on two databases (for each Giemsa and Fish modality) containing images classified into two labels by experts: non-exploitable images (approximately 1,000 for each modality) or exploitable images (approximately 5,000). The similarity between Giemsa images and the blue channel (DAPi) of Fish-3 images will be exploited using transfer learning methods to double the size of each training database.

TASK 2 - Dosimetric Validation of an AI Model for Counting Chromosomal Aberrations in Fish3 Imaging (Q3 2026 to Q1 2027)
The objective is to combine two deep learning models, one for aberration detection and the other for calibration curve regression, to provide a personalized estimate of dose and associated uncertainties.
Specifically, the first model will be trained on a database augmented by image-by-image generative artificial intelligence to classify chromosomes and identify chromosomal aberrations in Fish3. The second model will model the background rate (in the absence of ionizing radiation exposure) of chromosomal aberrations by incorporating individual demographic variables such as age, sex, and smoking status.

TASK 3 - Development of an AI model for counting chromosomal aberrations using M-Fish imaging (from Q2 2027 to Q2 2028)
Using five fluorescent probes (instead of three for the Fish3 technique), it is possible to stain each chromosome of a cell with a single color using the M-Fish technique. This would allow for a comprehensive count of all aberrations. However, the analysis time is very long and impossible to deploy in an operational accident context. Furthermore, the number of training images available is quite small (a few hundred). This thesis project proposes a two-step approach to address this problem: using transfer learning techniques to develop generative models of chromosomal aberrations in M-Fish from models trained to generate aberrations in the fish3 modality, and then using these synthetic images as data augmentation to develop an aberration classifier in M-Fish.

Required Qualifications

Candidates must hold a master's degree in applied mathematics, data science, or biostatistics. The successful candidate will work in close interdisciplinary collaboration with scientists with expertise in applied mathematics and radiobiology. The position includes data analysis and manuscript writing in collaboration with the research team. The successful candidate will be encouraged to present the project results at scientific conferences and to administrative authorities.

Job Location
Europe, France, Île-de-France, Hauts-de-Seine (92)

Lien vers l'offre sur le site dataia.eu :https://da-cor-dev.peppercube.org/node/1270