Improved data science methods for cytogenetic radiation biodosimetry

Retrospective biological dosimetry has been demonstrated to be essential for prompt determination of the dose received by individuals or groups of individuals potentially exposed to ionizing radiation (IR), after nuclear accidents (e.g., Chernobyl/Fukushima) or incidental overexposure in radiotherapy services or occupational settings. The whole-body absorbed dose is usually estimated by analyzing the biological damages produced by IR, at the cellular level. More precisely, data are collected by scoring chromosome aberrations such as radiation specific dicentrics, rings or micronuclei in peripheral human blood lymphocytes, from blood samples. This topic has been of great recent interest as it is the opinion of the international radiation protection community that it is now a case of 'when' rather than 'if' the next large scale (multi region, many thousands of exposed individuals) radiological accident or terrorist incident will take place. Moreover, this estimation may be crucial to clarify unclear radiation exposure scenarios and appease the "worried well" persons showing prodromal symptoms of a radiation exposure but without having received a dose high enough to cause acute health effects.

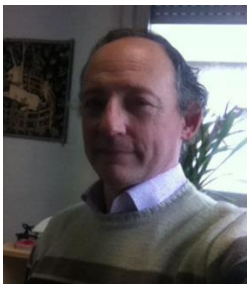
Several probabilistic models have been developed to describe the random occurrence of chromosome aberrations given the absorbed dose and estimate the received dose and its uncertainty, from frequentist or Bayesian statistical methods. However, the proposed models only account for the occurrence of a single type of chromosome aberration (i.e., dicentrics or rings or other abnormalities) to estimate the dose and its uncertainty. Thus, chromosome aberrations are analyzed separately from univariate models. However, different types of chromosome aberration may bring complementary information about the unknown dose of interest. Then, a promising way to improve the estimation of the dose and its uncertainty may be to allow several types of chromosome aberration to contribute simultaneously to the estimation of the dose. In this context, we propose:

- To build new probabilistic models to describe the random occurrence of multivariate chromosome aberrations given the absorbed dose;
- To develop and compare frequentist and Bayesian statistical methods to infer the proposed models;
- To validate the global methodology and highlight its potential benefits compared to univariate analyses, from real and simulated cytogenetic data

This is a cross disciplinary collaborative PhD project between the Universitat Autònoma de Barcelona (UAB) and the Institut de Radioprotection et de Sûreté Nucléaire (IRSN), with approximately 50% of time spent at UAB and 50% of time spent at IRSN. The successful candidate will be enrolled in the PhD program in Mathematics of the UAB having the opportunity to obtain an International Doctoral Research Component.

Supervisors

Pedro (Pere) Puig
Departament de Matemàtiques, Universitat Autònoma de Barcelona
http://www.uab.cat/web/maths-department-1210142393255.html
http://grupsderecerca.uab.cat/advancedstochasticmodelling/
Edifici C, 08913 Cerdanyola del Vallés (Barcelona), Spain.
ppuig@mat.uab.cat



Dr. Sophie Ancelet
PhD in biostatistics
Institut de Radioprotection et de Sûreté Nucléaire (IRSN),
https://www.irsn.fr/EN/Research/Research-organisation/Research-units/human-radiation-protection-unit/LEPID/Pages/laboratory-epidemiology.aspx
BP 17 92262 Fontenay-aux-Roses Cedex,France.
sophie.ancelet@irsn.fr

Some relevant publications

http://rspa.royalsocietypublishing.org/content/471/2174/20140588
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