Approche statistique bayésienne pour l'estimation d'un risque de cancer radio-induit après exposition aux examens scanner durant l'enfance

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54èmes Journées de Statistique de la SFdS



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- Increasing number of computed tomography (CT) examinations in France:
  - Frequency between 2012 and 2017 : +17% [IRSN,2017]
- 13% of diagnostic procedures but 74% of the annual effective dose
- Higher radio-sensitivity of children [UNSCEAR,2013]
  - 1% of children received at least one CT scan during the year over the 2012-2018 period [IRSN,2017]

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#### Many epidemiological studies are underway

- Identify the existence of an association between the organ (radiation) doses following CT scans during childhood and a given cancer ⇒ If it exists, low risk!
- Estimate the magnitude of this association (and its uncertainty)

Study	Patients	CNS	Leukaemia
France [Foucault et al. (2022)]	100 560	Yes	Yes
United-Kingdom [Pearce et al. (2012)]	180 000	Yes	Yes
Australia [Mathews et al. (2013)]	680 000	Yes	Yes
Germany [Krille et al. (2015)]	45 000	Yes	No
Netherlands [Meulepas et al. (2019)]	168 000	Yes	No
<b>Taiwan</b> [Li et al. (2020)]	130 000	Yes	No
EPICT [Hauptmann et al. (2023)]	659 000	Yes	



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A recurrent criticism : Dosimetric uncertainty not accounted for in risk estimates



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## How are the organ doses estimated ?

#### Example : The NCICT software [Lee et al. 2015]



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## Different sources of dose uncertainty

- The input parameters of dosimetric models are uncertain
- The structure of the dosimetric models is uncertain



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If not or poorly accounted for, dose uncertainty may cause [Carroll et al, 2006; Keogh et al, 2020] :

- a bias in risk estimates (generally towards the null);
- an inadequate estimation of the associated confidence/credible intervals;
- a distortion of the dose-response relationship [Hoffmann et al, 2017];

 $\Rightarrow$  Misleading conclusions about the effect of organ (radiation) doses on the disease risk



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- Step 1: Simulate plausible organ doses values for each CT examination from a dosimetric model like NCICT using a 2-dimensional Monte-Carlo algorithm [Simon et al. (2015); Lee et al. (2019); Thierry-Chef et al. (2021)]
- Step 2:
  - Regression calibration : averaged dose vectors (derived from all organ doses realisations) are used as plug-in estimates for the true organ doses when estimating disease risks [Little et al. (2014); Hauptmann et al. (2023)]
  - Monte-Carlo Maximum Likelihood : Estimate the risk coefficient by maximizing an approximation of the likelihood integrated over all organ doses realisations over a grid of fixed values for this coefficient [Stayner et al. (2007)]
- Asymptotic confidence intervals



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- To propose an alternative approach :
  - Bayesian learning of a model made of modules (e.g., multilevels/hierarchical models) including the "black-box" dosimetric model provided by the NCICT software ⇒ Extension of the works by Richardson and Gilks, 1993; Hoffmann et al. 2017.
- To account for the difference between the patient's morphology and that of the NCICT phantom when modelling dose uncertainty



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Modelling the hazard rate of first diagnosis of a given cancer for patient i at age (in days) t ∈ [0, +∞[

$$h_i(t;\beta) = \lambda \times exp(\beta \times D_i^{cum}(t))$$

- $D_i^{cum}(t) = \sum_{u \le t-x} D_{i,k}^{real}(u)$ : : 2 or 5-years lagged cumulative radiation dose to the brain or the red bone marrow (RBM) (in Grays)
- D<sub>i,k</sub><sup>real</sup>(t): the true (unknown) organ dose received by patient i at age t for a CT examination of type k
- $\lambda > 0$  : Baseline hazard rate supposed to be constant over time
- β: Unknown risk coefficient
- Assumption : Non-informative censoring

Let  $D_{i,k}^{NCICT}$  be the organ dose estimated by the NCICT model for a CT examination of type k and a typical morphology (i.e., phantom selected from the age of patient *i*).



A multiplicative Berkson error model:  $D_{i,k}^{real}(t) = D_{i,k}^{NCICT} \times B_k^D \times U_{i,k}^D(t)$ 

• 
$$U_{i,k}^{D}(t) \stackrel{\text{iid}}{\sim} logNormal\left(-rac{\sigma_{D,k}^{2}}{2}, \sigma_{D,k}^{2}
ight) \Rightarrow E\left(U_{i,k}^{D}(t)
ight) = 1$$

• Homoscedastic :  $\sigma_{D,k}^2 = \sigma_D^2$ ,  $B_k^D = B^D$ ,  $\forall k$ 

• Heteroscedastic :  $\sigma_{D,k}^2 = \sigma_{D,C(k)}^2$ ,  $B_k^D = B_{C(k)}^D$ ,  $\forall k \in C(k)$  (age, scanned body region)

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## A restricted version of the NCICT model

$$D^{NCICT}(organ, age, gender, model, kVp, filter, start, end, mAs, pitch) = \sum_{z=start}^{end} DC(organ, age, gender, kVp, filter, z) \times \frac{nCTDI_w(model, kVp, filter)}{pitch} \times \frac{mAs}{100}$$

- *DC*(*organ*, *age*, *gender*, *kVp*, *filter*, *z*) : dose coefficients estimated by Monte Carlo simulations. A table of previously estimated values is available.
- *nCTDI*<sub>w</sub>(*model*, *kVp*, *filter*) is the CT Dose Index per volumetric unit, normalised to 100 mAs and selected from the CTDI library [Lee and others, 2014].

A preliminary step: Identify the NCICT software input parameters that are most influential when estimating organ doses

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Let  $\mathbf{X} = (X_1, \dots, X_p)$  be the NCICT input parameters and Y the univariate outcome (a specific organ dose) of the (deterministic) dosimetric model f where Y = f(X).

• Sobol' indice associated to input *i* [Sobol (1993)]:



 $\Rightarrow$  When the input parameters are independent, Sobol' indices assign to each input parameter  $X_i$  a share of the variance of the organ dose estimate (Y).

• BUT some NCICT input parameters are dependent  $\Rightarrow$  We no longer have

$$1 = S_1 + S_2 + S_3 + S_{12} + S_{23} + S_{13} + S_{123}$$

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 $S_i = \frac{\mathbb{V}[\mathbb{E}(Y|X_i)]}{\mathbb{V}(Y)}$ 

Shapley effects [Owen (2014); looss et Prieur (2019)]

For any i in  $D = \{1, \ldots, p\}$ :

$$Sh_i = \frac{1}{p} \sum_{A \subseteq D_{-i}} {\binom{p-1}{|A|}}^{-1} \left( S_{A \cup \{i\}}^T - S_A^T \right) \qquad S_A^T = \frac{\mathbb{E}[\mathbb{V}(Y|X_{\bar{A}})]}{\mathbb{V}(Y)}$$

Two main properties:

- $Sh_i \geq 0$
- $\sum_i Sh_i = 1$

 $\Rightarrow$  An interaction effect is equitably shared between each parameter involved in this interaction.



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- Estimation of the Shapley effects from a single i.i.d input-output sample of PACS (Picture archive and communication system) data
- Consistent "given-data" estimates of the total Sobol' indices using a nearest-neighbor procedure [Broto et al. (2020); Il Idrissi et al. (2021)]
- *sensitivity* R package, and in particular the *shapleysobol\_knn* function, were used to estimate the Shapley effects
- Estimated Shapley effects for brain dose estimates associated with head examinations



#### • Identification of most influential parameters for each examination category :

Anatomical area	Brain dose	Bone marrow dose
Head	mAs, kVp, end	mAs, kVp, start, end, age
Chest	mAs, kVp, pitch	mAs, pitch
Abdomen-pelvis	kVp	kVp
Multiple	start	start

- Proportional Marginal Effects [Herin et al. (2022)] were also estimated :
  - known to be less sensitive to correlations and to provide more pronounced hierarchy than Shapley effects in highly correlated cases;
  - tends to favor the inputs proportionally to their marginal contributions to every possible "coalitions" ⇒ Proportional redistribution of interaction effects

#### ⇒ Similar conclusions



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# Continuous parameters uncertainty model (mAs, pitch, CTDI<sub>vol</sub>)



A multiplicative Berkson error model :  $P_{i,k}^{real}(t) = P_k^{prot} \times B_k^P \times U_{i,k}^P(t)$ 

• 
$$U_{i,k}^{P}(t) \stackrel{\text{iid}}{\sim} \log Normal\left(-\frac{\sigma_{P,k}^{2}}{2}, \sigma_{P,k}^{2}\right) \Rightarrow E\left(U_{i,k}^{P}(t)\right) = 1$$

• Homoscedastic :  $\sigma_{P,k}^2 = \sigma_P^2$ ,  $B_k^P = B^P$ ,  $\forall k$ 

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Image: A math a math

## Discrete parameters uncertainty model

(kVp,landmarks of the scanned body region)



	Parameter	Prior distribution		
-	Disease submodel			
	$\lambda = \lambda'  imes 10^{-7}$	$\lambda' \sim \mathcal{G}(1,1)$		
	$\beta$	$\mathcal{N}(0, 10^6)$		
-	Morphol	ogy uncertainty submodel		
	$\sigma_D$	$\mathcal{HC}(0,5)$ [Gelman (2006)]		
	$\sigma_{D,C(k)}$	$\mathcal{HC}(0,Z),  Z \sim U(0,100)$		
	B	$\mathcal{LN}(-50,100)$		
	$B_{C(k)}^{D}$	$\mathcal{LN}(-s^2/2,s^2),  s \sim U(0,100)$		
-	NCICT input p	arameters uncertainty submodel		
	$\sigma_P$	$\mathcal{HC}(0,5)$		
	$\sigma_{P,C(k)}$	$\mathcal{HC}(0,Z),  Z \sim U(0,100)$		
	B	$\mathcal{LN}(-50,100)$		
	$B^P_{C(k)}$	$\mathcal{LN}(-s^2/2,s^2),  s \sim U(0,100)$		
_	$p_{x,.}^{L}$	$Dirichlet(0, 5, \ldots, 0, 5)$		



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## • High-dimensional posterior distribution

- Over 500,000 latent variables to be estimated (but informed by external PACS data)
- Around 170,000 pseudo-observations
- Hamiltonian Monte-Carlo algorithm implemented in the R package rstan
  - Targeted Effective Sample Size : 4000
  - Importance of model parameterization ! (Ex : using standard normal distributions, 20
    - $\rightarrow$  2 days of calculations for the most complex model)
- Comparison of the predictive performance of proposed models using the Leave-one-out information criterion (LOOIC) [Vehtari et al. (2017)]



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## Application to the French CT cohort

- Set up in France in 2009 by IRSN
- 100 560 patients who:
  - Received at least one CT scan for a non-cancer pathology
  - Before the age of 10 years
  - Between 2000 and 2011
  - In one of the 21 participating university hospitals.
- Follow-up until a diagnostic of cancer, the death, the 18th birthday or the 31st December 2016



### Some statistics

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- 50 cases of central nervous system (CNS) tumours
- 35 cases of leukaemia
- Mean age at inclusion : 3 years / Mean follow-up : 9 years
- Patients without cancer predisposing factors : 97%



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## A transfer learning approach

- No pair of values  $(P_{i,k}^{real}(t), P_k^{prot})$  is available in the French CT cohort database  $\Rightarrow$  Information required to learn about  $\sigma_P$ ,  $\sigma_{P,C(k)}$ ,  $B^P$ ,  $B_{C(k)}^P$  !
- Idem for  $\sigma_D$  ,  $\sigma_{D,C(k)}$ ,  $B^D$ ,  $B^D_{C(k)}$ ,  $p^L_{x,y}$
- 8848 CT examinations collected in the PACS database ⇒ True technical parameters values associated with CT examinations + associated radiological protocols ⇒ Pair of values (P<sup>real</sup><sub>i,k</sub>(t), P<sup>prot</sup><sub>k</sub>) were defined.
- Different morphologies were simulated from growth curves: dose estimation based on age (typical phantom morphology) versus dose estimation based on weight and height  $\Rightarrow$  **Pair of values**  $(D_{i,k}^{real}(t), D_i, k^{NCICT})$  were defined
- Assumption: These pairs of values follow the same multiplicative Berkson error models than in the French CT cohort
- Joint Bayesian inference of our multilevel models from both the French CT cohort data and the PACS data

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Model	HR* per 10 mGy (95% CI)	LOOIC
CNS tumors (case	es=50)	
Frequentist estimation	1,05 (1,01 - 1,09)	
No effect of radiation exposure ( $\beta = 0$ )		1381
Uncorrected	1,04 (0,97 - 1,08)	1382
Berkson homoscedastic	1,04 (0,97 - 1,07)	1611
Berkson + Bias heteroscedastic <sup>a</sup>	1,03 (0,97 - 1,06)	1383
Leukaemia (cases	s=35)	
Frequentist estimation	1,17 (1,07 - 1,27)	
No effect of radiation exposure ( $\beta = 0$ )		803
Uncorrected	1,15 (0,99 - 1,23)	1172
Berkson homoscedastic	1,15 (1,02 - 1,22)	789
Berkson + Bias heteroscedastica	1,10 (1,01 - 1,16)	791

<sup>a</sup>Latent structure with the smallest LOOIC on PACS data.

\* Hazard Ratio:  $exp(\beta \times 10)$ 



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Construction of informative prior probability distributions from the English cohort



Posterior probability distribution of the Hazard Ratio per 10 mGy



#### Aim :

- Sevaluate the ability of LOOIC to make a relevant model selection
- (a) Evaluating the effect of misspecification of Berkson error models on risk estimation



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Organ doses were the ones from the French CT cohort :

- Without adding a multiplicative Berkson error on the NCICT input parameters
- After multiplying the NCICT input parameters :
  - by an homoscedastic Berkson error component
  - by an heteroscedastic Berkson error component and a systematic bias component

 $\Rightarrow$  True values of Berkson error model parameters = Posterior medians estimated from the French CT cohort

- Generate failure times for 10,000 individuals according to the Cox disease model to obtain cancer incidence rates similar to the ones observed in the French CT cohort.
- Generate 100 replicated datasets for each scenario

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Estimation	$\widehat{\beta}^{a}$	Mean	95%	Model
model		relative	coverage rate	selection <sup><math>b</math></sup>
		bias		
		$\beta = 0, 0$	)05	
$\beta = 0$				0
Cox	0,005	0,01	0,98	99
		$\beta = 0$	)	
$\beta = 0$				0
$Cox\;(\beta>0)$	$10^{-3}$			0

<sup>a</sup>Posterior median averaged over 100 replicated datasets

<sup>b</sup>Proportion of simulated data sets for which the LOOIC of the simulation model is lower than the LOOIC of the other competing model with a difference of at least 8 points [Sivula et al. (2020)]



Estimation model	$\widehat{\beta}^{a}$	Mean	95%	
		relative	coverage rate	
		bias		
Berkson error (homoscedastic)				
$Cox,\ \beta = 0$	Cox, $\beta = 0,02$			
Uncorrected	0,02	-0,01	98	
Berkson error (homoscedastic)	0,02	0,03	100	
Berkson error + bias (heteroscedastic)				
Cox, $\beta = 0,04$				
Berkson error (homoscedastic)	0,01	-0,65	0	
Berkson error + bias (heteroscedastic)	0,04	-0,02	94	

<sup>a</sup>Posterior median averaged over 100 replicated datasets



## Discussion

Bayesian inference of the proposed multilevel models on the French CT cohort showed:

- A weak but statistically significant positive association between CT scans exposure during childhood and the risk of leukaemia
- No statistically significant association between the risk of CNS tumours and CT scans exposure
- A weak impact of dosimetric uncertainties on cancer risk estimates

Strenghts:

- Use of two recent variance-based global sensitivity indices
- Use of a Bayesian multilevels approach :
  - Flexible modelling approach to describe different sources of uncertainty
  - Allows to integrate external information
  - Allows for the joint inference of all unknown quantities (e.g., true organ doses and risk)

Weaknesses :

- Using the LOOIC for model selection in case of multilevel models ? What else?
- Transfer learning : Possible underestimation of the variance of dose uncertainty. What about adding similarity parameter(s) ?

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## Thank you for your attention !

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