Conference or Workshop Item

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Is the use of wildlife group-specific concentration ratios justified?

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INTRODUCTION

Many of the currently available wildlife dose assessment models use concentration ratios ($CR_{wo\text{-}media}$) to predict the transfer of radionuclides to wildlife (Wood *et al*., 2013). The concentration ratio ($CR_{wo\text{-}media}$) is a constant that describes the ratio between the activity concentration of a radionuclide in the whole- organism and the activity concentration of that radionuclide in a reference environmental medium (e.g. soil or filtered water). It has been demonstrated that the transfer component of dose assessment models is a major source of variability in model predictions (e.g. Johansen *et al*., 2012; Wood *et al*., 2009; Yankovich *et al*., 2010). Therefore, there is a need to ensure that the $CR_{wo\text{-}media}$ values used for model parameterisation are fit-for-purpose.

The Wildlife Transfer Database (WTD; www.wildlifetransferdatabase.org/) provides the most comprehensive international compilation of $CR_{wo\text{-}media}$ values for wildlife (Copplestone *et al*., 2013; Howard *et al*., 2013). Developed to support activities of the International Atomic Energy Agency (IAEA) and the International Commission on Radiological Protection (ICRP), the WTD now contains over 100,000 $CR_{wo\text{-}media}$ values. To provide $CR_{wo\text{-}media}$ values for use in wildlife dose assessment models, the WTD has been used to generate summary statistics for broad wildlife groups (the terrestrial wildlife groups included within the WTD are presented in Table 1). The group-specific summary statistics include weighted mean and standard deviation (both arithmetic and geometric) and range.

Large variability is a characteristic of many of the organism-radionuclide datasets within the WTD, even within individual input data sets. In this paper we use a statistical technique that we developed recently for the analysis of summarised datasets (Wood *et al*., 2013) to evaluate the current approach of summarising wildlife group-specific $CR_{wo\text{-}media}$ values.

RECONSTRUCTING SUMMARISED $CR_{wo\text{-}media}$ DATASETS

The datasets that underpin the WTD include summarised data (i.e. a single data entry line within the database is often given as number of observations in the study (n_i), arithmetic mean (μ_i) and standard deviation (σ_i) rather than an individual $CR_{wo\text{-}media}$ value). However, in some cases, the n_i and μ_i are presented in source publications, but not σ_i. This leads to some problems when summarising the data (most especially for geometric mean and standard deviation) (Wood *et al*., 2013). To enable statistical evaluation of the data within the WTD, we developed a methodology for generating a reconstructed database, i.e. a database in which all entry lines are single $CR_{wo\text{-}media}$ values (Wood *et al*., 2013). Given that $CR_{wo\text{-}media}$ values tend to be lognormally distributed, the summarised data from each individual study are used to generate a lognormal distribution. This distribution is then sampled n_i times to approximate the underlying dataset from which the summarised values were derived. The methodology is described in full in Wood *et al.* (2013) and briefly outlined here.

Table 1. Terrestrial organism groupings and sub-categories defined within the Wildlife Transfer Database (Copplestone *et al.*, 2013)

Broad group	Available sub-categories
Amphibian	-
Annelid	
Arachnid	-
Arthropod	
	Arthropod - Carnivorous
	Arthropod - Detritivorous
	Arthropod - Herbivorous
Bird	
	Bird – Carnivorous
	Bird – Herbivorous
	Bird – Omnivorous
Mollusc - gastropod	-
Grasses and herbs	-
	Grasses
	Herbs[a]
Lichens and Bryophytes	-
Mammal	
	Mammal – Carnivorous
	Mammal - Herbivorous[b]
	Mammal - Omnivorous
	Mammal - Marsupial[c]
	Mammal - *Rangifer* spp.
Reptile	-
	Reptile – Carnivorous
	Reptile – Herbivorous
Shrub	-
Tree	-
	Tree - Coniferous
	Tree - Broadleaf

[a] Any non-woody plant which does not fall into one of the other categories; [b] Excludes *Rangifer* spp. (reindeer and caribou) in recognition of the high transfer of some elements to this group compared to other mammals; [c] No distinction made between marsupials based on feeding strategy

For each individual study for which summarised data are provided, the arithmetic mean ($\mu_{\ln x}$) of the natural logarithms (ln) of the underlying data values (x) and the corresponding standard deviation ($\sigma_{\ln x}$) are derived:

$$\mu_{\ln x} = \ln \mu_x - \frac{1}{2}\sigma_{\ln x}^2 \tag{1}$$

$$\sigma_{\ln x} = \sqrt{\ln\left(1 + \frac{\sigma_x^2}{\mu_x^2}\right)} \tag{2}$$

Assuming that the underlying data are lognormal, $\mu_{\ln x}$ and $\sigma_{\ln x}$ should describe a normal distribution. To sample n_i times within this distribution a random number generator is used to derive n_i random percentile values and the value of $\ln x$ at each percentile is determined. These values can then be reverse transformed to the corresponding value of x in the original scale ($\exp^{\ln x} = x$).

$\ln x$ can be standardised to derive the standard normal distribution random variable z, which defines the distance in standard deviation units between $\ln x$ and the arithmetic mean of the natural logarithms of variable x:

$$z = \frac{\ln x - \mu_{\ln x}}{\sigma_{\ln x}} \tag{3}$$

For the purposes of the analysis presented here, we needed to derive values of $\ln x$ for specific percentiles, so equation 3 was modified to:

$$z_p = \frac{\ln x_p - \mu_{\ln x}}{\sigma_{\ln x}} \tag{4}$$

where z_p is the value of z at probability p, x_p is the value of x at probability p and all other terms have been defined. Equation 4 was rearranged to calculate x_p:

$$x_p = \exp\left(\sigma_{\ln x} z_p + \mu_{\ln x}\right) \tag{5}$$

The calculated values of x_p for each study from which summarised data had been reported were used to replace the summarised data line for that study within the subsequent data analysis.

For studies reporting $n_i > 1$ and an arithmetic mean (μ_i) but not an arithmetic standard deviation (σ_i), σ_i was estimated from the arithmetic mean of the coefficient of variation (CV) for each of the studies that reported both arithmetic mean and standard deviation:

$$CV = \frac{\sigma_i}{\mu_i} \tag{6}$$

For each radionuclide, the arithmetic mean of the CVs (CV_μ) for the wildlife group was used to estimate the missing arithmetic standard deviation values (σ_i):

$$\sigma_i = CV_\mu \cdot \mu_i \tag{7}$$

To facilitate the application of this approach to other summarised datasets, we have developed a macro-enabled spreadsheet that will automatically perform the calculation approach described above. This spreadsheet is freely available for download at https://wiki.ceh.ac.uk/x/PgC6Cw.

EVALUATING WILDLIFE GROUP-SPECIFIC $CR_{wo\text{-}media}$ VALUES

Using the reconstructed database, it is possible to use standard statistical techniques to compare different groups of $CR_{wo\text{-}media}$ values. In Wood *et al.* (2013) we used a General Linear Model with Tukey's pairwise comparisons to analyse log-transformed $CR_{wo\text{-}media}$ values for different wildlife group sub-categories. The analysis revealed some statistically-significant differences in terrestrial wildlife group sub-category $CR_{wo\text{-}media}$ values (e.g. mammals categorised by feeding strategy). However, further investigation suggested that biases and limitations within the underlying datasets of the WTD could explain many of the differences observed. We reached similar conclusions in a limited evaluation of the freshwater data in Beresford *et al.* (2013).

We are now repeating this analysis at the level of wildlife group, using terrestrial data as an example, and will present our initial findings at the International Conference on Radioecology and Environmental Radioactivity in Barcelona in September 2014.

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