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Making the most of what we have: application of extrapolation approaches in wildlife transfer models

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INTRODUCTION

The assessment of the exposure wildlife to ionising radiation for planned, existing and accidental scenarios requires predictions to be made of the transfer of a wide range of radionuclides to a diversity of species. Most models assessing the exposure of wildlife use a simple concentration ratio ($CR_{\text{wo-media}}$) relating the whole organism activity concentration to that in the environmental medium (i.e. soil, air or water). For many of the radionuclide-species combinations that require assessment we have no empirical data. When empirical data are lacking, predictions are often made using transfer parameter values derived using extrapolation approaches, though the clarity on the use of such approaches varies between publications/models. For instance, the $CR_{\text{wo-media}}$ value for an organism of similar taxonomy may be assumed (e.g. a mammal value may be used to model birds if data for the latter are lacking). Many of the extrapolation approaches used do not appear to have been validated or scientifically assessed.

Recently, we published a report evaluating extrapolation techniques (<http://bit.ly/1zisRBf>) starting from a consideration of how the most commonly used performed against additional data as it has become available (Brown *et al.* 2013). Here we focus on two aspects of the report: (i) development of simplified allometric models, and (ii) the demonstration of an alternative approach to the $CR_{\text{wo-media}}$ model. The report also provides an assessment of the application of Bayesian statistics (Hosseini *et al.* 2013) and stoichiometry to provide radioecological transfer parameters.

A SIMPLIFIED ALLOMETRIC APPROACH

Size (expressed as mass) affects rates of many biological processes from cellular metabolism to population dynamics. The dependence of a biological variable (Y) on body mass (M) is typically characterised by an allometric scaling law of the form: $Y = aM^b$ where a and b (the allometric exponent) are constants.

Kleiber (1932) found that basal metabolic rate across groups of mature animals ranging from a ring dove (< 200 g body mass) to a steer (about 680 kg body mass) was proportional to mass to the power of 0.74. Following further analyses, which demonstrated similar exponents, Kleiber suggested that 'metabolic body size' (now generally referred to as 'metabolic live weight') could be determined as $M^{0.75}$ where M is the mass of the animal (Kleiber 1947); this has since become known as *Kleiber's law*. There have been many compilations of allometric relationships for biological parameters across large mass ranges and a multitude of animal and plant species (see Beresford and Vives i Batlle (2013) for examples).

There are specific radioecological parameters which have been shown to scale allometrically, with relationships for biological half-life across species having been reported in the 1970's. In more recent years, the application of allometry to radioecology has received revived attention during the development of models to predict the exposure of wildlife to radionuclides. One reason for this attention is the potential of allometry to help address the lack of $CR_{wo-media}$ data for the large number of organism-radionuclide combinations which may need to be assessed.

Allometric relationships for the biological half-lives in mammals/birds often scale as mass to the power of $c. 0.25$ which can be explained on the basis of the relationship between the biological half-life and the metabolic rate. Sheppard (2001) proposed that, if it is accepted that there is an approximation of the exponent applicable for all elements (i.e. in the case of biological half-life, 0.25), then only an estimation of the multiplicand is needed for any given element. In Beresford and Vives i Batlle (2013) we derive an approach to estimate the multiplicand for radionuclide biological half-life ($T_{B1/2}$), such that:

$$T_{B1/2} = \frac{\ln 2}{a_I f_I} CR_{wo-diet} M^{0.25}$$

where M is mass (kg), $CR_{wo-diet}$ is the ratio between the activity concentration in an organism (fresh mass) to that in its diet (dry mass), f_I is the gastrointestinal absorption coefficient and a_I is the multiplicand in the allometric model describing the daily dry matter intake rate of food. For mammals and birds a_I values are readily available as are $CR_{wo-diet}$ and f_I estimates for many radionuclides.

In Beresford and Vives i Batlle (2013) we tested this model against available $T_{B1/2}$ values for Cs, I, Sr and Co in mammals with body masses ranging from $c. 10$ g to 80 kg. All predictions were within a factor of five of the observed values when the model was parameterised appropriate to the feeding strategy of each species. Subsequently, we have further tested the model considering additional elements (Ag, Po and Zn) and some data for birds in addition to mammals. With the exception of a prediction of the $T_{B1/2}$ of Po in rat, all estimates were within a factor of seven of the measured values.

Application to reptiles?

Whilst proposed for homeothermic vertebrates we are aware that allometric models for $T_{B1/2}$ have been used to make predictions for reptiles and amphibians. In Beresford and Wood (submitted) we demonstrate that this does not give good predictions against available data for

reptiles. However, by adapting the above equation to take into account the lower metabolic rate of reptiles and, where possible, finding reptile specific values for $CR_{wo-diet}$, f_1 and a_I , predictions can be obtained within a factor of 5 of the available data (data were available for Cs, Sr and Ra for species of reptiles covering a *c.* 50-fold mass range). This is considered acceptable, given that allometry is not an exact mathematical law but a method to produce generalised relationships.

AN ALTERNATIVE TO THE CR APPROACH TO PREDICT RADIONUCLIDE TRANSFER TO WILDLIFE

The application of the concentration ratio ($CR_{wo-media}$) to predict radionuclide activity concentrations in wildlife from those in soil or water has become the widely accepted approach for environmental assessments. Recently, both the ICRP and IAEA have produced compilations of $CR_{wo-media}$ values for application in environmental assessment. However, the $CR_{wo-media}$ approach has many limitations most notably that the transfer of most radionuclides is largely determined by site-specific factors (e.g. water or soil chemistry). Furthermore, there are few, if any, values for many radionuclide-organism combinations.

In Beresford *et al.* (2013) we propose an alternative approach and, as an example, demonstrated and tested this for caesium and freshwater fish. Using a Residual Maximum Likelihood (REML) mixed-model regression we analysed a dataset comprising 597 entries for 53 freshwater fish species from 67 sites. The REML analysis generated a mean value for each species on a common scale after REML adjustment taking account of the effect of the inter-site variation. Using an independent dataset, we subsequently tested the hypothesis that the REML model outputs can be used to predict radionuclide (in this case radiocaesium) activity concentrations in unknown species from the results of a species which has been sampled at a specific site. From the outputs of the REML analysis we accurately predicted ^{137}Cs activity concentrations in different species of fish from 26 Finnish lakes using ^{137}Cs activity concentrations in *Perca fluviatilis* as our model input (Figure 1); these data had not been used in our initial analyses to establish our model.

The approach is now being further investigated for a wide range of radionuclides, and organisms in freshwater, terrestrial and marine ecosystems through the NERC RATE programme's TREE project (<https://wiki.ceh.ac.uk/x/PwZgD>) in collaboration with the EU EURATOM project COMET (www.comet-radioecology.org).

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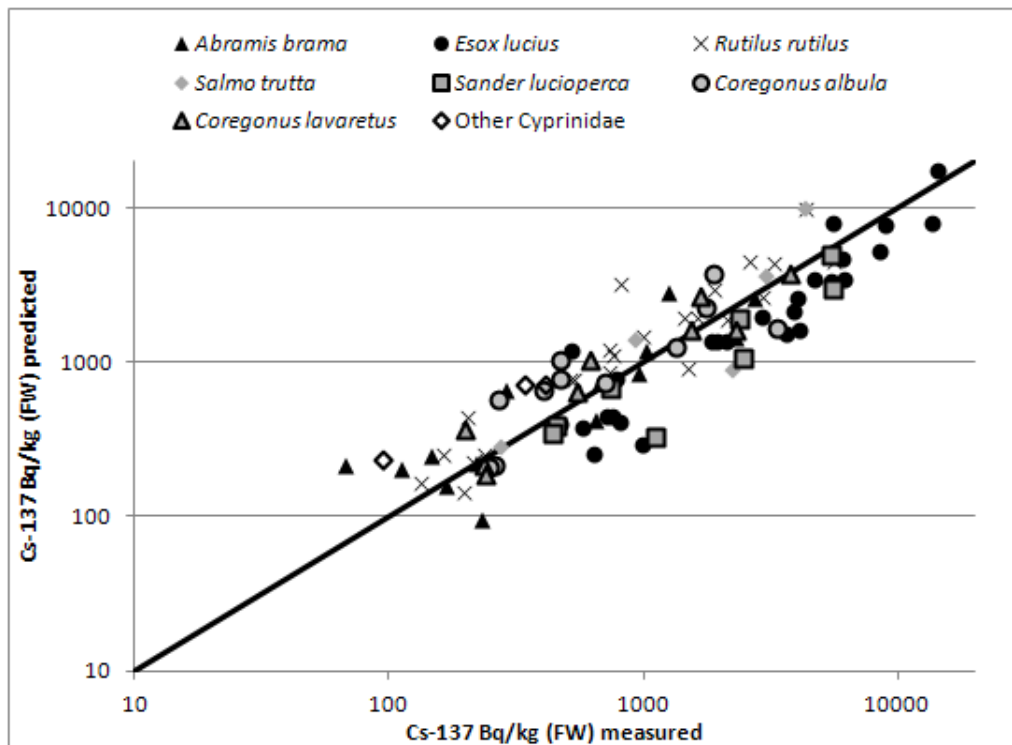


Figure1. Comparison of measured ^{137}Cs activity concentrations in fish collected from 26 Finnish lakes with predicted activity concentrations using the outputs of the REML model (the line is a 1:1 relationship).

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