



Making the most of what we have: application of extrapolation approaches in radioecological transfer modelling

Nicholas A. Beresford, Michael D. Wood, Jordi Vives i Batlle, Justin E. Brown, Ali Hosseini, Tamara L. Yankovich, Clare Bradshaw & Neil Willey

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www.star-radioecology.org www.radioecology-exchange.org

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

..... because we will never have everything we want









•How well do ERICA extrapolation approaches work?

- Bayesian statistics
- Stoichiometry
- Transfer coefficient v's concentration ratio
- •<u>Allometry</u>

An alternative approach to CR for wildlife



Contents lists available at SciVerse ScienceDirect Journal of Environmental Radioactivity iournal homepage: www.elsevier.com/locate/ienvrad

ournal of Environmental Radioactivity 126 (2013) 399-41

Approaches to providing missing transfer parameter values in the ERICA Tool - How well do they work?

I.E. Brown a.*, N.A. Beresford b, A. Hosseini a

Journal of Environmental Radioactivity 126 (2013) 376-387 Contents lists available at SciVerse ScienceDirect



Journal of Environmental Radioactivity ournal homepage: www.elsevier.com/locate/jenvra



A. Hosseini a.*, K. Stenberg^b, R. Avila^b, N.A. Beresford^c, J.E. Brown^a



A new approach to predicting environmental transfer of radionuclides to wildlife: A demonstration for freshwater fish and caesium

N.A. Beresford ^{a,*}, T.L. Yankovich ^b, M.D. Wood ^c, S. Fesenko ^d, P. Andersson ^e, M. Muikku ^f, N.J. Willey ^g

Journal of Environmental Radioactivity

Volume 138. December 2014. Pages 116-121

A new simplified allometric approach for predicting the biological half-

Science of the Total Environment 463-464 (2013) 284-293

Contents lists available at SciVerse ScienceDirect

Science of the Total Environment

iournal homepage: www.elsevier.com/locate/scitotenv

life of radionuclides in reptiles

N.A. Beresford^{a, b,} Å · M.D. Wood^b



DELIVERABLE (D-N°3.2)

Evaluation of extrapolation approaches to provide radioecological parameters

Editors: N.A. Beresford (NERC-CEH, UK), J.E. Brown (NRPA, Norway), J. Vives i Batlle (SCK-CEN, Belgium), A. Hosseini (NRPA, Norway), C. Bradshaw (SU, Sweden)

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DOI 10.1007/s00411-013-0481-x

ORIGINAL PAPER

Estimating the biological half-life for radionuclides in homoeothermic vertebrates: a simplified allometric approach

N. A. Beresford · J. Vives i Batlle



Journal of Environmental Radioactivity Available online 4 April 2015 In Press, Corrected Proof - Note to users



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

Nicholas A. Beresford* . 🛓 🖾 , Michael D. Wood*, Jordi Vives i Batlle*, Tamara L. Yankovich*, Clare Bradshaw[®], Neil Willev

Open Access funded by Natural Environment Research Council

STAR Concentration ratios are generic (e.g. Cs)



0.23±0.17

 0.64 ± 1.0



0.10±0.10

0.70

$CR = \frac{Activity \ concentration \ in \ organism \ (or \ meat)(Bq \ kg^{-1} \ FM)}{Activity \ concentration \ in \ diet(Bq \ kg^{-1} \ DM)}$



Concentration ratios are generic (e.g. Cs)



0.23±0.17



 0.64 ± 1.0



0.10±0.10



0.70



0.40-0.85



0.40±0.20



0.46



0.48±0.06



0.27±0.11



0.53



0.73±0.40

STAR Allometry in Radioecology

•Size affects rates of all biological processes from cellular metabolism to population dynamics

•The dependence of a biological variable Y on a body mass M is typically characterised by an allometric scaling law of the form:

$Y = aM^b$

where *a* and *b* are constants



b most often = 'quartile values':

- mammals & birds metabolic rates scale as M^{0.75} (*Kleiber's Law* 1932)
 - ≻M^{0.75} is often referred to as *metabolic live-weight*
- life-span scales as M^{0.25}
- food, water and inhalation rates scale as $M^{0.75}$

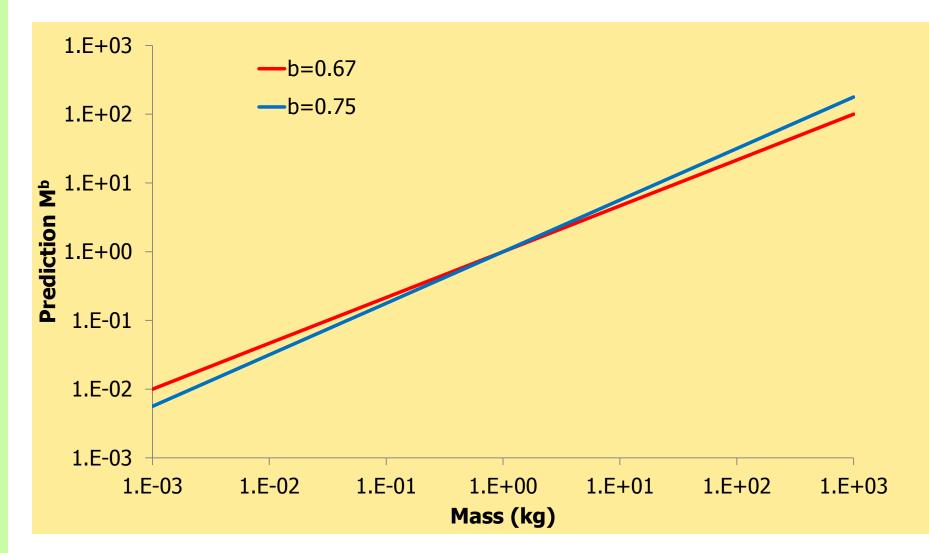


b most often = 'quartile values':

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 - ≻M^{0.75} is often referred to as *metabolic live-weight*
- life-span scales as M^{0.25}
- food, water and inhalation rates scale as $M^{0.75}$

Much debate re if *b* is quartiles or tertiles (thirds) BUT:

STAR Allometry in Radioecology





b most often = 'quartile values':

metabolic rates scale as M^{0.75} (*Kleiber's Law* 1932)
M^{0.75} is often referred to as *metabolic live-weight*life-span scales as M^{0.25}
food, water and inhalation rates scale as M^{0.75}

All potential useful for radioecological models, but:



Allometry in Radioecology

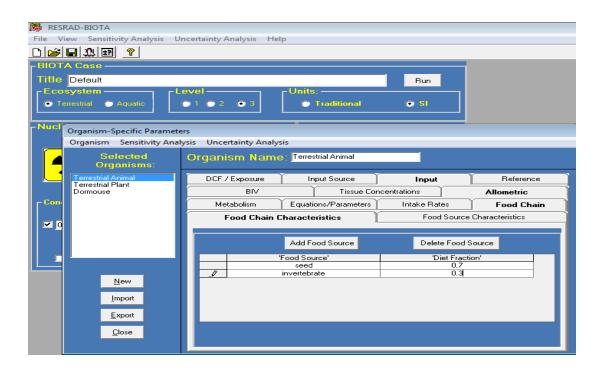
• For (some) radionuclides the biological half-life (often *c*. M^{0.25}) scales allometrically

STAR Allometry in Radioecology

• For (some) radionuclides the biological half-life (often *c*. M^{0.25}) scales allometrically

Option to model terrestrial/riparian birds/mammals in RESRAD-BIOTA

Model performed comparable to CR model in intercomparisons





T_{B1/2} scaling to M^{0.25} (for mammals & birds) makes
 <u>sense</u>:

$$T_{B1/2} = \frac{M \ln 2}{\varepsilon_a B_r}$$

•Kleiber's law $(B_r = aM^{0.75})$, so:

$$T_{B1/2} = \frac{\ln 2}{a\varepsilon_a} M^{0.25}$$

 B_r = metabolic rate (kg d⁻¹); ε_a is a proportionality constant between the rate of biological loss of a radionuclide from the organism and the metabolic rate of the organism







If $T_{B1/2}$ scales to $M^{0.25}$ then just need an estimate of $a_B (T_{B1/2} = a_B M^{0.25})$ (after Sheppard 2001)







If $T_{B1/2}$ scales to $M^{0.25}$ then just need an estimate of $a_B (T_{B1/2}=a_B M^{0.25})$ (after Sheppard 2001)

GREAT!

But how do you estimate a_B ?





easy after four pages of algebra





 $a_{B} = \frac{\ln 2}{a_{I} f_{I}} CR_{org-diet}$

- f_1 = gastrointestinal absorption coefficient
- a_I = constant on allometric relationship describing dry matter intake

 $CR_{org-diet}$ and f_1 generally available & a_1 values are documented for different animal types (e.g. Nagy 2001)





$$a_{B} = \frac{\ln 2}{a_{I}f_{1}}CR_{org-diet}$$

 $T_{B1/2} = a_R M^{0.25}$ and

f_1 = gastrointestinal absorption coefficient

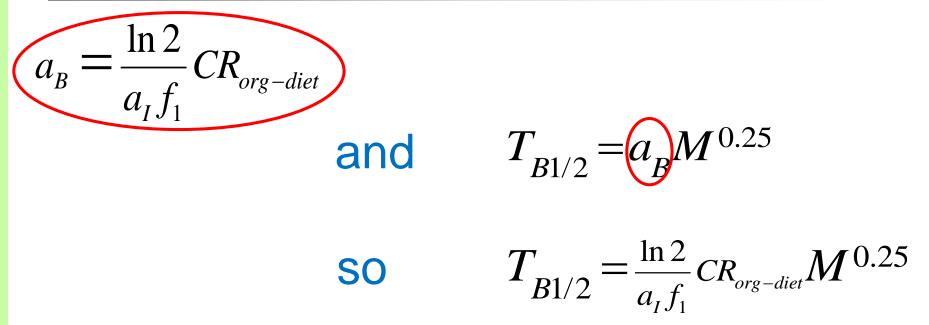
 a_I = constant on allometric relationship describing dry matter intake

 $CR_{org-diet}$ and f_1 generally available & a_1 values are documented for different animal types (e.g. Nagy 2001)



The answer is:





- f_1 = gastrointestinal absorption coefficient a = constant on allometric relationship describing dry m
- a_l = constant on allometric relationship describing dry matter intake

 $CR_{org-diet}$ and f_1 generally available & a_1 values are documented for different animal types (e.g. Nagy 2001)





IAEA MODARIA WG produced a database of *c*.
 1900 T_{B1/2} values

STAR partners led development for each ecosystem

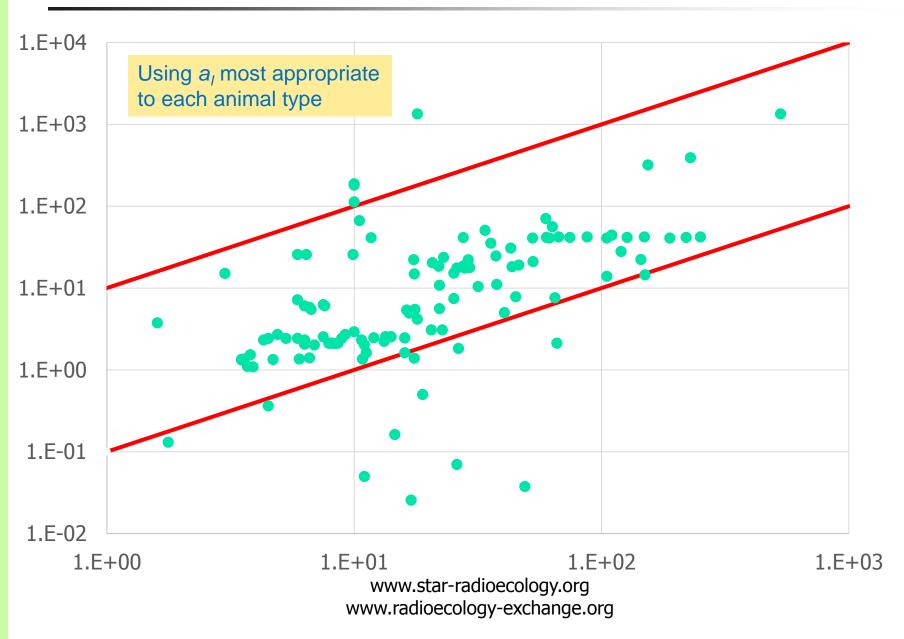
- 123 values for mammals and birds used as blind test
 - Body mass 8 g to 70 kg
 Ag, Co, Cs, I, Na, Nb, Ru, Se, Sr & Zn

Radionuclide biological half-life values for terrestrial and aquatic wildlife

Submitted J. Environ. Radioact.

N.A. Beresford^{1,2}, K. Beaugelin-Seiller³, J. Burgos⁴, M. Cujic⁵, S. Fesenko⁶, A. Kryshev⁷, N. Pachal⁸, A. Real⁹, B.S. Su⁸, K. Tagami¹⁰, J. Vives i Batlle¹¹, S. Vives-Lynch¹², C. Wells¹, M.D. Wood²

Measured v's predicted T_{B1/2}







- In USDoE five elements have T_{B1/2} relationships which <u>do not</u> scale to c. 0.25 but to c. 0.8
 - ➢ Am, Ce, Eu, Pu & Th
 - ≻ Why?
 - None have biological role??
- Reptiles ($B_r = aM^{0.80-0.92}$)













Alternative to CR approach for wildlife



- Simple
- Widely adopted

 $CR = \frac{Activity concentration in biota whole body (Bq kg^{-1} fresh weight)}{Activity concentration media ((filtered water (Bq l^{-1}) or soil (Bq kg^{-1} dry weight))}$

CR_{wo-media} approach MMM









Sr CRs IAEA TRS479 Max:Min

Highly variable

 No data for many wildlife-radionuclide combinations

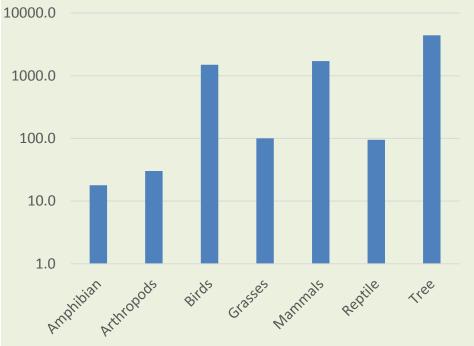


Table A.4. Bee (*Apidea*): concentration ratio values (units of Bq/kg fresh weight per Bq/kg dry weight).

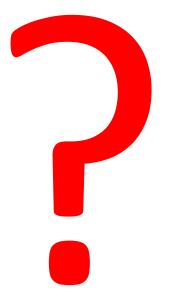
No empirical data.

Table A.5. Frog (Ranidae): concentration ratio values (units of Bq/kg fresh weight per Bq/kg dry weight).

Element	Arithmetic mean	Arithmetic standard deviation	Geometric mean	Geometric standard deviation	п	Ref ID
Am	1.0E-01	2.6E-02	1.0E-01	1.3E+00	7	486
Cd	1.5E-02	7.9E-03	1.3E-02	1.7E+00	5	213
Cs	5.5E-01	9.0E-01	2.8E-01	3.2E+00	105	188, 205, 256, 486
Pb	3.1E-03	2.2E-03	2.6E-03	1.9E+00	6	213
Sr	1.5E+00	1.4E+00	1.1E+00	2.2E+00	14	188, 486

ICRP Pub-114





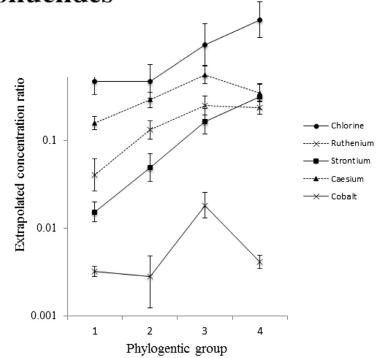


Radiat Environ Biophys (2010) 49:613–623 DOI 10.1007/s00411-010-0320-2

ORIGINAL PAPER

Phylogeny can be used to make useful predictions of soil-to-plant transfer factors for radionuclides

Neil J. Willey



STAR An alternative to the CR_{wo-media}

Radiat Environ Biophys (2010) 49:613–623 DOI 10.1007/s00411-010-0320-2

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Phylogeny can be used to make useful predictions of soil-to-plant transfer factors for radionuclides

Neil J. Willey

Can we use this approach for other organisms

• STAR - example freshwater fish and Cs

Journal of Environmental Radioactivity 126 (2013) 299-31

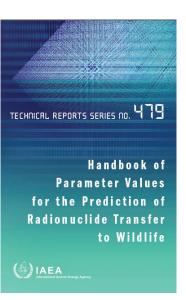


Establishing a database of radionuclide transfer parameters for freshwater wildlife

T. Yankovich^{a,*}, N.A. Beresford^b, S. Fesenko^c, J. Fesenko^d, M. Phaneuf^e, E. Dagher^f, I. Outola^g, P. Andersson^h, K. Thiessenⁱ, J. Ryan^j, M.D. Wood^k, A. Bollhöfer¹, C.L. Barnett^b, D. Copplestone^m

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CrossMark



STAR An alternative to the CR_{wo-media}

Adapted approach used by Willey for plants
 Residual Maximum Likelihood (REML)

Generates an adjusted mean (or relative value) taking into account inter-site variability

STAR An alternative to the CR_{wo-media}

Adapted approach used by Willey for plants
 Residual Maximum Likelihood (REML)

Generates an adjusted mean (or relative value) taking into account inter-site variability

Initial data source Yankovich et al (2013)
 REML requires site/study contains more than one species (one of which must occur at another site)

Supplemented with additional data (can mix CR and activity concentration data)

≻597 data entries including 10 orders, 14 families, 33 genera & 53 species



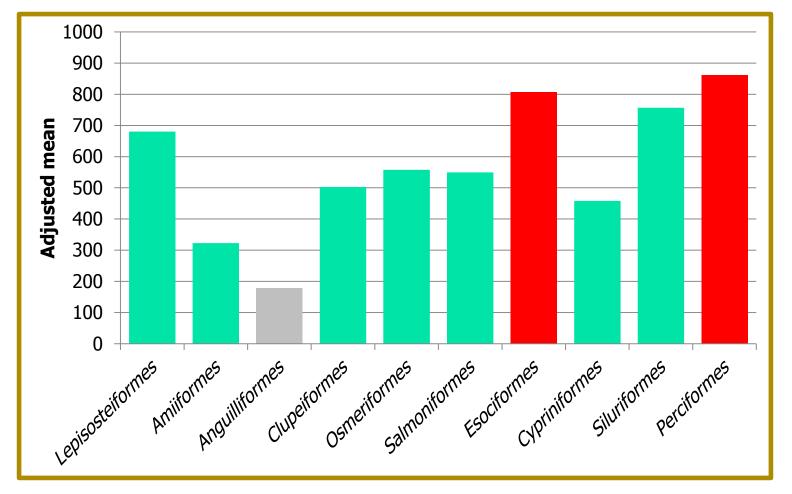


Generates *adjusted mean* (or relative value) – taking into account inter-site variability



Output (by order)





Ignore the number it's all relative





The REML model outputs can be used to predict the radionuclide (Cs) activity concentrations in unknown species from the results of a species which has been sampled at a specific site



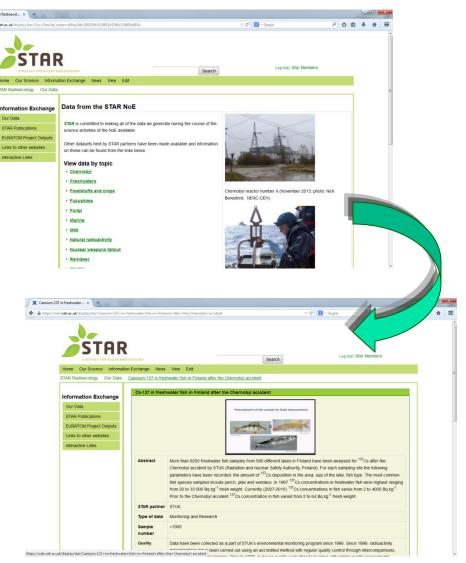


STUK had made data available from lakes monitoring programme through STAR

Not used within REML analyses

Used data from 1988 to test:

27 lakes11 species





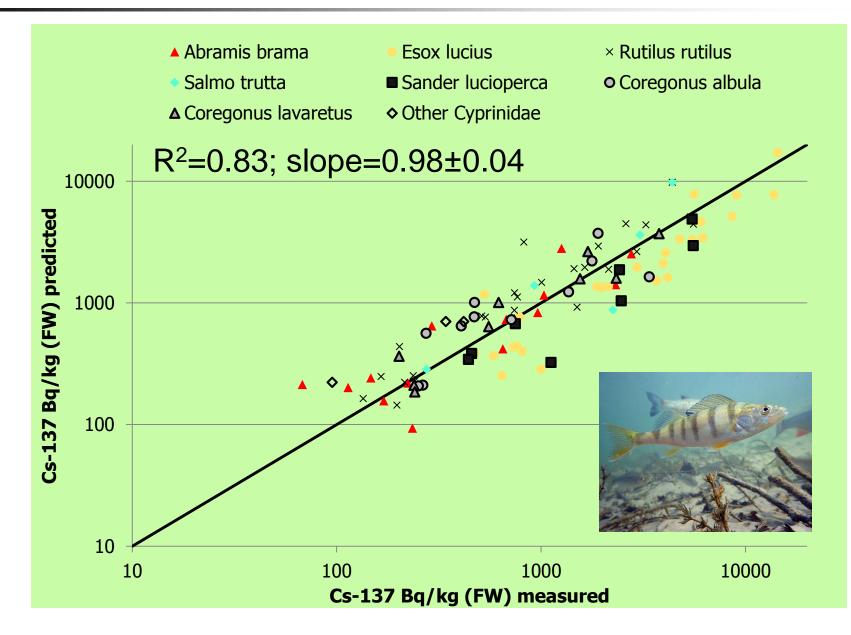


- Perca fluviatilis present at all 27 sites
- Assumed to be the 'known' species
- Concentrations in all other species estimated as:

Cs137 activity conc. in perch $\times \frac{REML \ value \ species \ X}{REML \ value \ perch}$

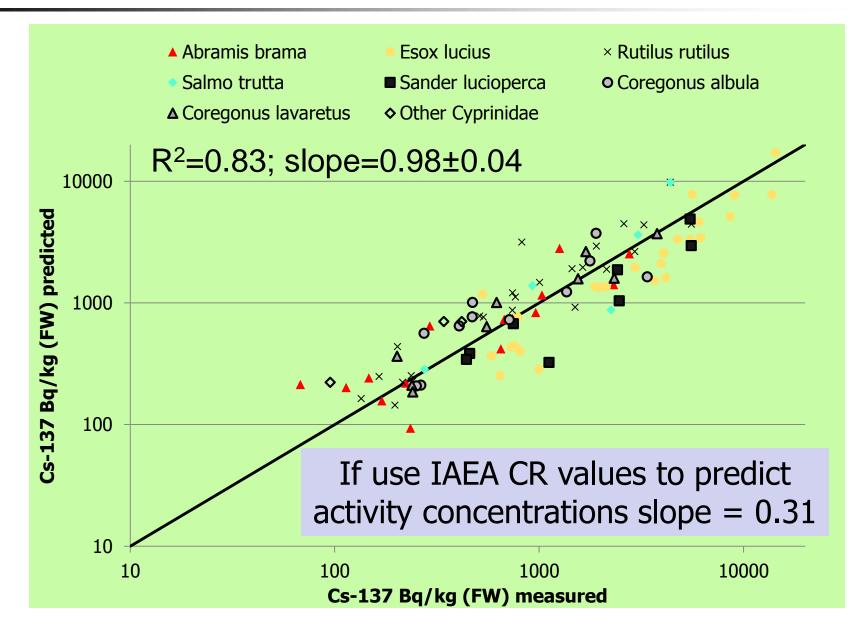




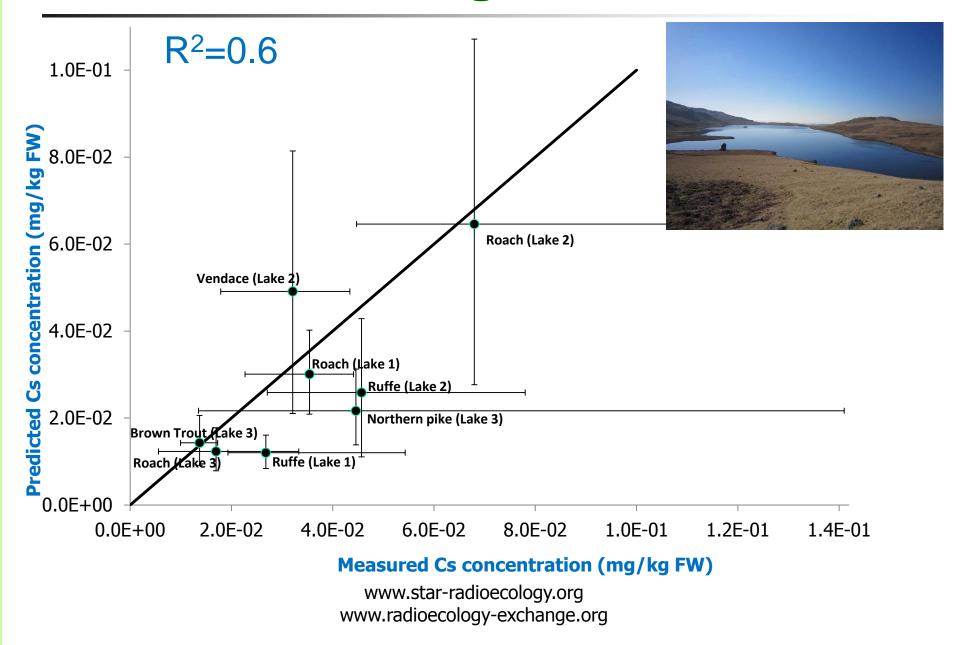








STAR Stable Cs English lakes



Simon Burnard







We've tried it, but all that follows is provisional!

- Reference assumed = site
- Maybe some data to remove



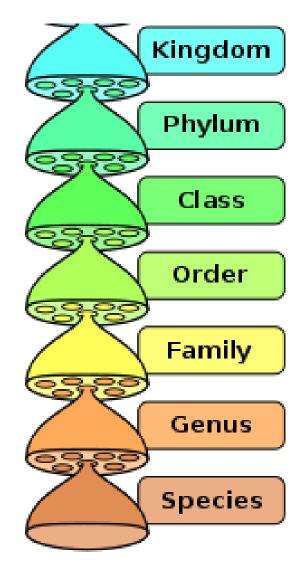
Transfer - Exposure - Effects:

integrating the science needed to underpin radioactivity assessments for humans and wildlife



STAR Terrestrial

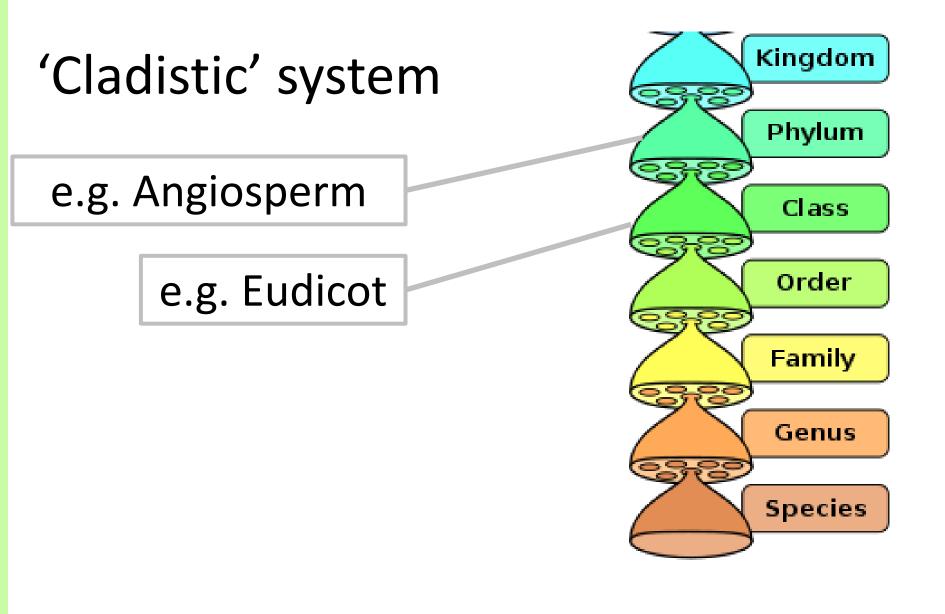




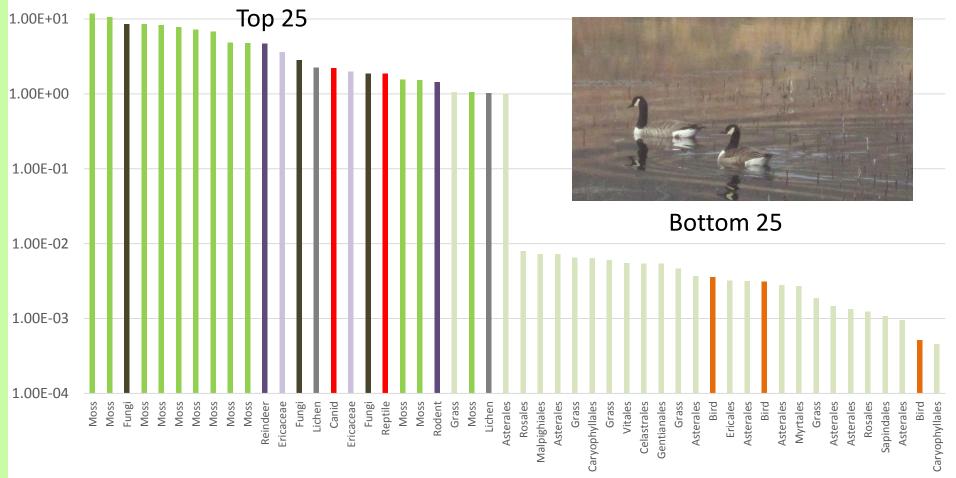


Terrestrial - plants





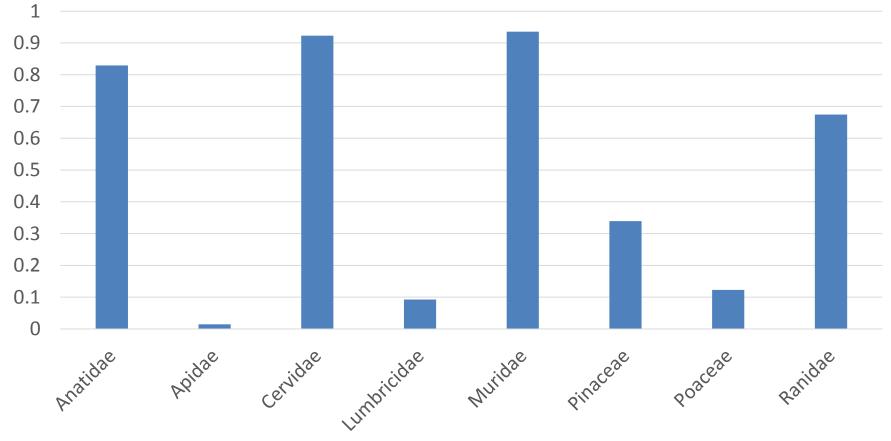
STAR Example output: Cs by genus



REML adjusted mean

202 Genus





REML adjusted mean

Predictions v measurements

Radiat Environ Biophys (2014) 53:125–149 DOI 10.1007/s00411-013-0493-6

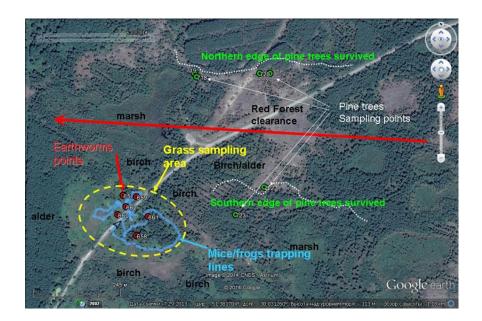
ORIGINAL PAPER

COMET

COordination and iMplementation of a pan European instrumenT for Radioecology

Transfer parameters for ICRP reference animals and plants collected from a forest ecosystem

C. L. Barnett · N. A. Beresford · L. A. Walker · M. Baxter · C. Wells · D. Copplestone



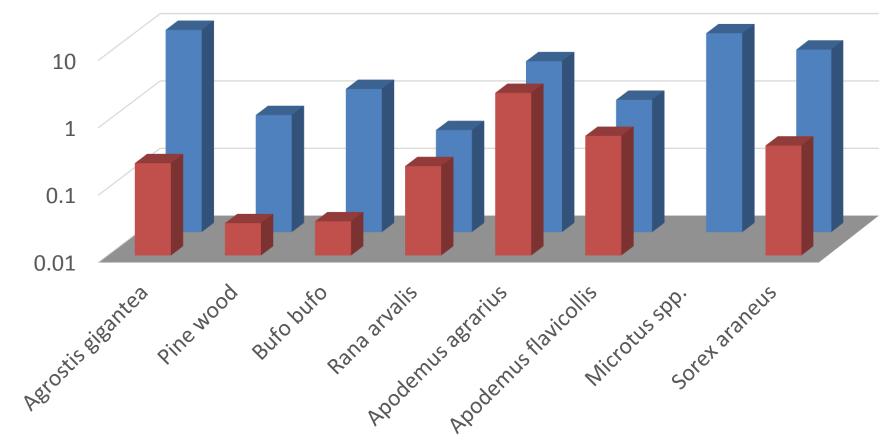








Sr-90 Cs-137



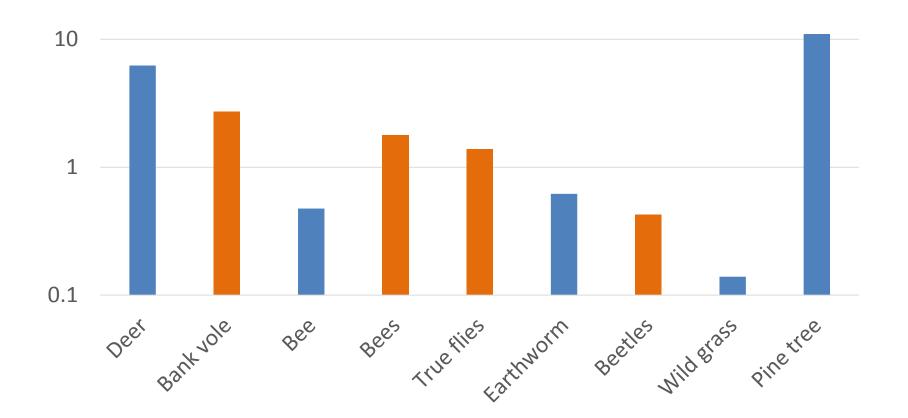
Cs known = Myodes (genus level) Sr known = Cricetidae (family level)



Predicted:Measured

100

Known = Muridae (family level)







Photos: http://www.ceh.ac.uk/tree





Allometry of transfer parameters in marine biota Jordi Vives i Batlle, Belgian Nuclear Research Centre, SCK+CEN, Mol, Belgium, E-mail: ivibatli@sckcen.be

N.A. Beresford, NERC Centre for Ecology & Hydrology, CEH Lancaster, UK. E-mail: nab

Introduction

Exchange rate and bioaccumulation of radionuclides in biota are commonly represented by two simple parameters: the biological half-life of elimination (T_{BLG}) and the concentration ratio (CR). This study presents an interpolation method to calculate these parameters for radionuclides in marine biota based on allometric scaling.

Objective

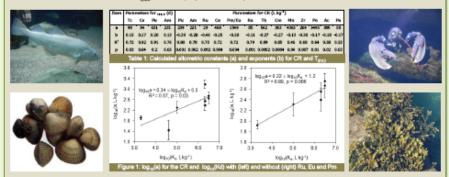
investigate the hypothesis that, for marine blota, b would be close to the slope of -1/4 frequently found in alignmetric relationships in blology, and that a would depend on the individual properties of compounds formed by radionucides in the marine environment.

Materials and methods

Power relationships of the type Y = a × M^p were fitted to a CR and T_{BL2} database for Tc, I, Cs, Pu and Am in fish, crustaceans, molluscs, plants and plankton reported in Vives i Battle et al. (2007). To this was added data for 29 additional elements. To discriminate potentially significant relationships, we used the criteria r² > 0.7, p-value of 2-tailed Student T-test < 0.05 and N > 2.

Results

For CR, the mean value of b for statistically valid relationships was -0.26 ± 0.09. For those radionuclides we also found a significant linear relationship between log₁₀(a) and log₁₀(K₄) (Figure 1), showing particle-reactive (or sediment seeking) radionuclides to have the highest log. (a) values. These relationships present an opportunity to estimate CR when data are lacking, from M and Kg. The mean value of b for the 4 elements with valid $T_{1/28}$ relationships (R² value > 0.7) was 0.16 ± 0.03.



An anomaly for the allometric relationships for marine organisms with respect to those for terrestrial organisms is that the actinides and lanthanides scale with an exponent similar to other elements for marine organisms, unlike the case for terrestrial blota.

Conclusions

The observed scaling of the CR to $M^{0.26 \pm 0.09}$ is compatible with metabolic theory scaling to to M^{46} , given that the CR is an activity concentration relative to mass and to activity in the medium. The observed scaling of T_{BLR} to $M^{40.16 \pm 0.03}$ is slightly outside theory predictions that turnover rates scale with M-4, but compatible with the range +0.15 to +0.30 quoted in USDoE (2002). The elements for which the CR scales allometrically are mostly lanthanides and actinides. Association of a with the K is strongest for particleseeking elements, most likely binding to biological / organic matter (e.g. food). As food ingestion relates to metabolism, and hence, to body mass via Kleiber's law, the resultant CR will scale allometrically (Beresford et al., 2015).

Beresford, N.A., Wood, M.D., Vives i Batlie, J. et al. (2015). Making the most of what we have: application of extrapolation approaches in radioecclogical wildlife transfer models. Journal of Environmental Radioactivity Special Isaue: ICRER, Barcelona, Barcelona, Online-published, http://dc.doi.org/10.1016/j.jenvrad.2015.03.022. USDoE (2002). DOE Standard: A Graded Approach for Evaluating Radiation Doses to Aquatic and Terrestrial Biota. DOE STD-1153-2002, Washington DC, 58 pp. Vives i Batlie, J., Wilson, R.C., McDonald, P. (2007). Allometric methodology for the calculation of biokinetic parameters for marine biota. Sci. Total. Environ. 388: 256 - 269.

Marine Allometry



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Application of Bayesian statistics in radioecology

Hosseini A.1, Brown, J.E.1, Beresford, N.A2, Stenberg K.3, Avlia, R.3

¹ Nerwegian Rediation Protection Authority, P.O. Box 55, N-1332 Øxtenia, Nerwey, ² Centre for Ecology and Hydrology, CEH-Lancester Environment Centre, Library Avenue, Beihigg, Lancester LA 1 4AP, UK, ³ Feolia AB, S-167 51 Bromme, Sweden.

INTRODUCTION

Quantification of fisk to wildlife as a consequence of releases of radioactivity to the environment requires the determination of activity concentrations in various environmental media and selected plants and animals. A simple and widely used method to model radionuclide transfer from soil and water to biota is through the application of concentration ratios (CR)

A common step in data collations required to populate CR (and other) databases is the pooling or combining of data to produce more robust estimates for the parameters of interest However, the contribut data are usually estructed from different studies with variable sample does and different measures of averages and variation. Another common issue is the application of different extrapolation approaches to derive missing banafer parameter values.

BAYESIAN APPROACH

The procedure for assigning a probability distribution to a model parameter, such as CR. can be divided into two main steps:

selection of a probability model or distribution type and

etimation of the distribution parameters.

It is usually assume that the CRs are log-normally distributed. Now what remains is to discuss how to estimate the distribution parameters, i.e. the geometric mean (GM) and geometric standard deviation (GSD). For this purpose, below we introduce three methods regarding utilization of the various related datasets information in our other to generate motion of robust estimates of GM and GSD, all based on the application of Bayes' theorem (Bayes, 1700).

$p(\theta y) = \frac{p(y \theta)p(\theta)}{\theta}$	~	hitelihood × prior
$\int p(y \theta)p(\theta)d\theta$		∫(Elethood×prim)de

Here, the posterior distribution describes our state of knowledge about the desired parameter 0 (i.e. GM or GSD) after considering the data. The likelihood function describes how probable the current data are given the parameter 0. The prior represents the present state of our knowledge based on an initial consideration of the parameter 0.

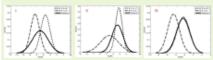
A JOINT PRICE DISTRIBUTION FOR THE MEAN AND VARIANCE

This Dayesian inference method is based on the assumption that the available empirical data for the case of interest and the existing historical (iterature) data are exchangeable and can be considered as being from the same population. In this case, the other data carries information on both the mean and variance of the distribution and can be used to deline a joint prior distribution (Geiman et al. 2004)

OR data for 8 species of bat are used here to illustrate a typical situation where we can apply this approx

	Ciello	104034		- 444	6115
		bowniong-cored	5	0.11	3.1
Table 1. Date for eight bat		Common Neofula	20	0.10	2.7
species sampled in the		Daubenten	2	001	3.9
Chevroltyl exclusion zone	-	Locard Hourkday	5	0.04	1.6
(Tom Gaudrak et al., 2010)		Homeser Reviseda	- 51	0.10	4.4
		Fort-selected	10	0.04	1.7
		Sandra .	12	0.24	421
		Impectio Plotstalle	2	0.29	41

Let us assume that our aim is to derive a PDF for the CR of the Dauberton species of bat (Code X in Table 1). Since only 2 data points are available for this species, maximum Itelihood estimates (e.g. sample mean and variance) will not work well. However, freme are data available for other 7 bat species that can be considered more or less representative (analogues) for the species of interest.



we show three different cases where Dauberton's data (X) is combined with data of three various analogues: It species G (N=2) as analogue leads to the largest posterior GGD among all tried analogues because of the total few observations, ii) species E (θ = 1 () as an analogue has a smaller GSD than data and leads to smaller posterior median GSD, III) species D with N=51 is used as analogue and almost completely dominates the data (N=2)

HIERARCHICAL MODEL: PRIOR IMPLICITLY DERIVED FROM DATA OF SEVERAL SIMILAR

The second approach is applicable when considering a number of related units (such as species or elements which share some common balks) or groups of measurements that are believed to be similar with regards to the parameter of interest. The approach is called hierarchical updating and can be used to obtain estimates for all unfolgroups simulane outs, letting the units borrow drength from the owned induster (Morris, 1993). The webbo differs an alternative to using alter separate estimates or a complete pooled estimate and the estimates from hierarchical models are therefore sometimes called partially pooled estimates (Geiman et al., 2004).



INDEPENDENT PRIOR DISTRIBUTIONS FOR THE NEAN AND VARIANCE

The third Bayesian updating technique considered is applicable to situations where, in addition to data for the case of interest, there is available either relevant historical data or information, but these do not tell us anything about the variance of the case of interest. In such a situation, the prior distributions of mean and variance are specified independently and here are often referred to as servicopiggate pfor distributions. If no pfor information is unstable for the variance, a so called non-informative pfor for the variance can be used.

no Bavesian statistics to revise the ERICA Tool.

The first major update of ERICA Tool (Brown et al. 2008) released November 2014 (http://www.erica.loci.eu/). Upon updating the ERICA Tool CR databases nome decisions had to be made in dealing with cases where available data were limited. To improve the situation in terms of deriving more robust parameter estimates the Bayesian semi-conjugate approach was applied. The approach was as follows: after identifications of cases where NuS. The updated gap-Siling options. available in the ERICA Tool, were consulted to discern which analogues would have been used if no data were available for these cases. In this way a surrogale organizer or radionacide has been assigned for each case where possible and further these have been used as priors in the process. of updating.

	Doubles.	Species.	H			40	Here editoriales	
			Relation	Date				
able 3. Sume	Ċe .	80		3	628+0	5.58+0	8249+0	APR-0
angles from the field (DRCA Text)	2	80	118		2.58+1	3,88+1		
des Chickinkase	Cal	Castoneon		5	7.48+0	5.28+0	1228+4	5,798+0
ete neur passader	Cal	MORAL - DVD+0	44		1/18+5	4.811+5		
mattes have been	Ce	Folyshaete worm		3	8,31+0	1008+4	8,0391+3	1,308+4
hed based on the	Ce	MORAL-DVDVD	- 42		5.38+0	1,38+4		
earlien of the scien panel-	- Pa	Machinagee		4	1.48+0	1/28+0	1.448+0	1,378+0
agaie mellod.	- Bu	Thyloparkton	- 11		121844	228+4		
	Pa	Folyshaete worm		3	1.518+0	2,218+3	1.538+3	2.028+3
	14	MORES-DIVISIO	146		1,15+0	1.4848		

Exystian approaches require specification of prior distributions for parameter values. In the context of the work discussed here, priors have been used to take into account the existing external information/data and also to describe our 'belief' about the relevancy of these data for our case of Interest. As priors represent additional knowledge which would not be considered if we were only using likelihood function, considering them is not only a necessary step in the process of learning and acquiring knowledge, but also a crucial element for coming to the right conclusion (itrustrike 2010). Given that the prior knowledge (external data/information) is valid, this approach provides more robust parameter estimates as compared to when only limited site or study specific empirical data are used. Bayesian approaches have a much witter applicability to radioscological proteines and are bailed considered within the COMIT (www.comit-radioscological) proteines.

A full description of the methodology presented here, and discussion of its application within radioecology, can be found in Hosseini et al. (2013).

REFERENCES

Bayesian

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www.star-radioecology.org www.radioecology-exchange.org