

Interactive comment on “Multi-compartment kinetic-allometric model of radionuclide bioaccumulation in marine fish” by Roman Bezhenar et al.

Anonymous Referee #2

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The authors present a multi-compartment model for radionuclide bioaccumulation in fish. The compartments for this model are muscle, bones, and organs. Uptake can be by direct absorption through gills, or from food. Transfer is also allowed between compartments. The model was tested on a set of radionuclides, with good agreement with lab experiments. The model was implemented into the POSEIDON-R, and applied to several real-world scenarios. This seems to work better than the previous single-compartment model that was previously used.

Overall, the paper is detailed and well-written. The authors present a novel method, integrated into a current software with applications to real-world problems.

C1

My major concern about the work here is in the comparison between the MCKA model and one-compartment or equilibrium models. The Forsmark results seem to show improvements in estimates from the MCKA model as opposed to the one-compartment model and Equilibrium models. However, I'm not convinced that it's not just because of poor-quality estimates of parameters for the one-compartment model and equilibrium. The equilibrium model consistently underpredicts by a factor of ~ 10 for ^{54}Mn over a period of decades. If you want a fair comparison for the underlying model, then you need to make sure they all the parameters are consistent. Are the parameters consistent between models? That is, you could use the MCKA model to estimate equivalent one-compartment parameters and BAF parameters such that the equilibrium concentrations are all identical. In that case, are the results significantly different? If the results are still different, then you have shown that your additional model complexity is needed for higher accuracy in these dynamic problems. If they aren't, then it just shows that your method can be used to estimate these factors for a given ecosystem model. This would still be an excellent finding, as it will help with model building, but it wouldn't be necessary to explicitly track all the concentrations inside the model. Judging from the results in figure 2, it looks like the inter-compartment equilibrium is reached quite quickly (< 2 days?) in this case, the system should behave identically to a single-compartment system, should it not?

If this issue is resolved then I would highly recommend publication.

Specific comments:

I. 127 Not sure what is meant by “The equations under (17) is used”

Should define BAF in equation somewhere. You may also note that IAEA uses concentration ratio CR or concentration factor CF to describe what you are using as bioaccumulation factor BAF, while you use CR for something different.

I believe the IAEA document only has BAF_{wb}, not BAF_{food}, does it not?

C2

l. 229 “shown the importance of including in the model of the digestive tract compartment describing highly non-equilibrium transfer dynamics” this seems to show the importance of kinetics in the modeling, but not the digestive compartment per se, as opposed to just using a single compartment.

The half-life of ^{54}Mn is only 312 days, so could be relevant compared to the biological half-lives. Was this accounted for in the modeling?

l. 321 using compartments here as spatial regions may be confusing.

Technical corrections:

Figure 1 should be regenerated in higher-quality.

Regarding eq. 1-3, you describe all variables except C_i

l. 125 should be λ_g

Figures 2-4 are low quality JPG. Avoid using lossy compression (jpg) on graphs – use lossless (e.g., png) or vector graphics (pdf/svg/wmf).

l. 240 space before ^{60}Co

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