The dynamics of metal accumulation and toxicity relationships (BIMBAM)

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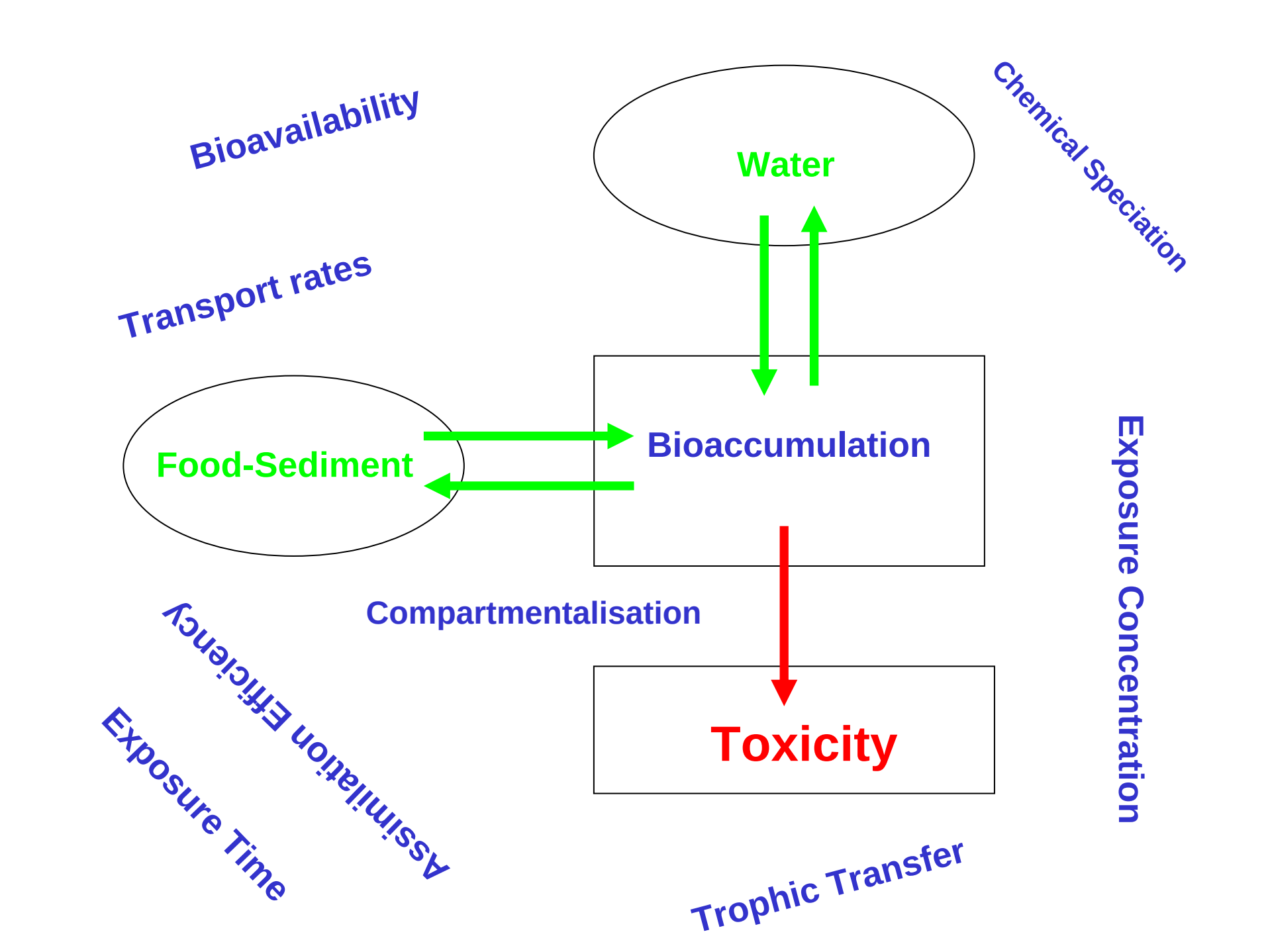
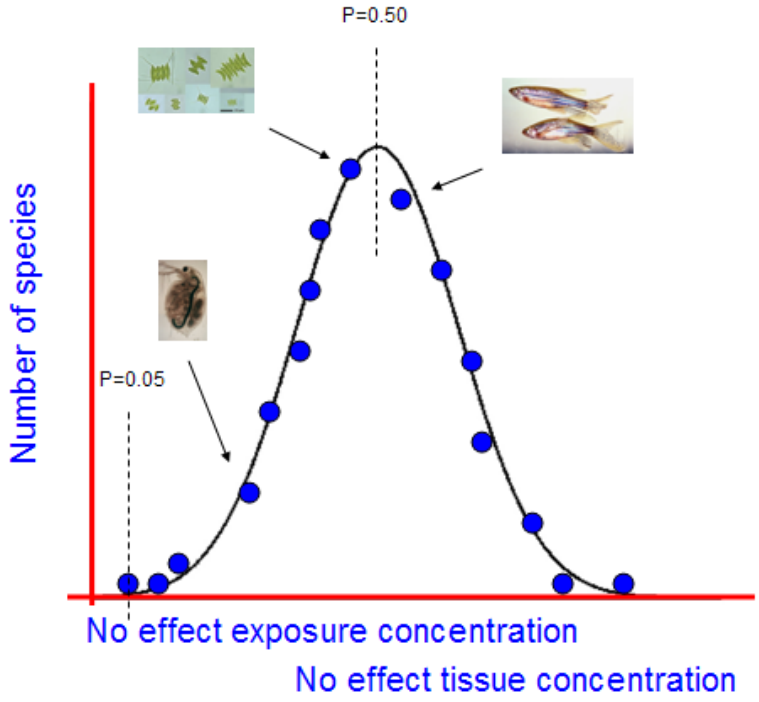
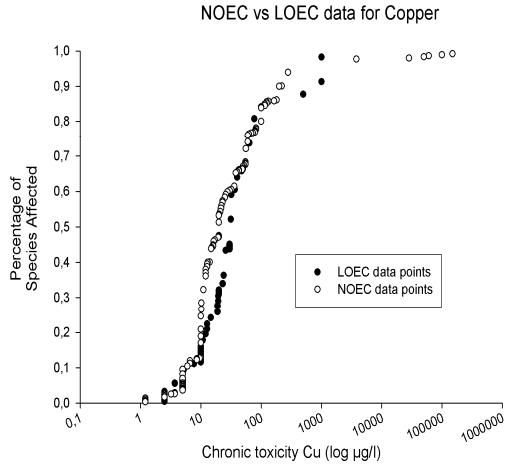
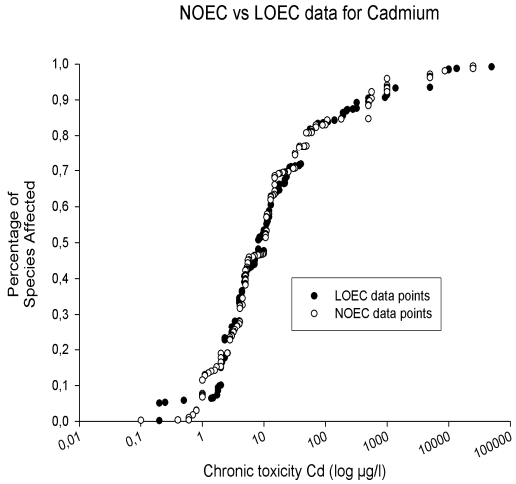
Metals in the Environment,1-2 April 2009, Hamburg, Germany


Bioavailability
Water
Chemical Speciation
Transport rates
Food-Sediment
Bioaccumulation
Exposure Concentration
Compartmentalisation
Toxicity
Assimilation Efficiency
Exposure Time
Trophic Transfer

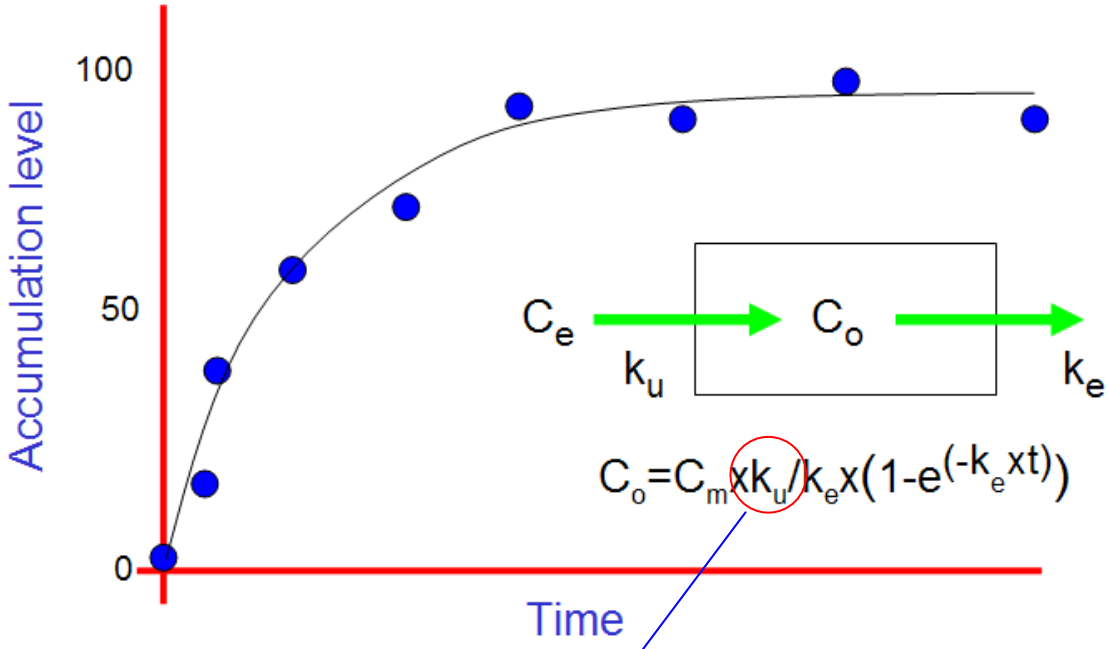
Metal toxicity species sensitivity distributions

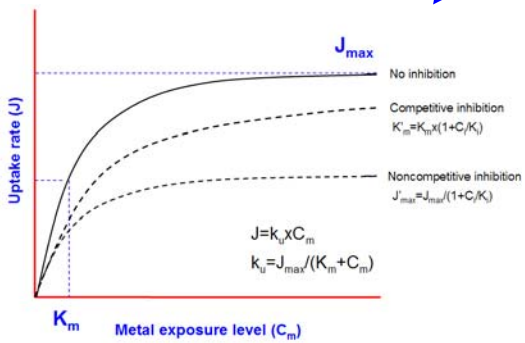


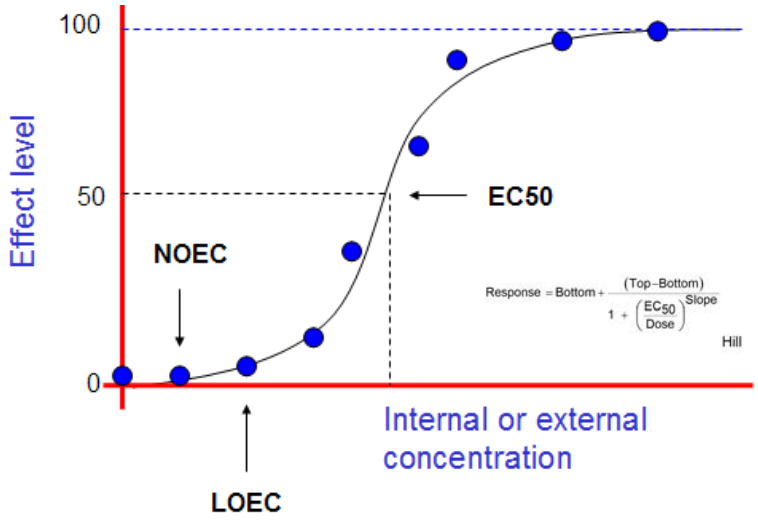


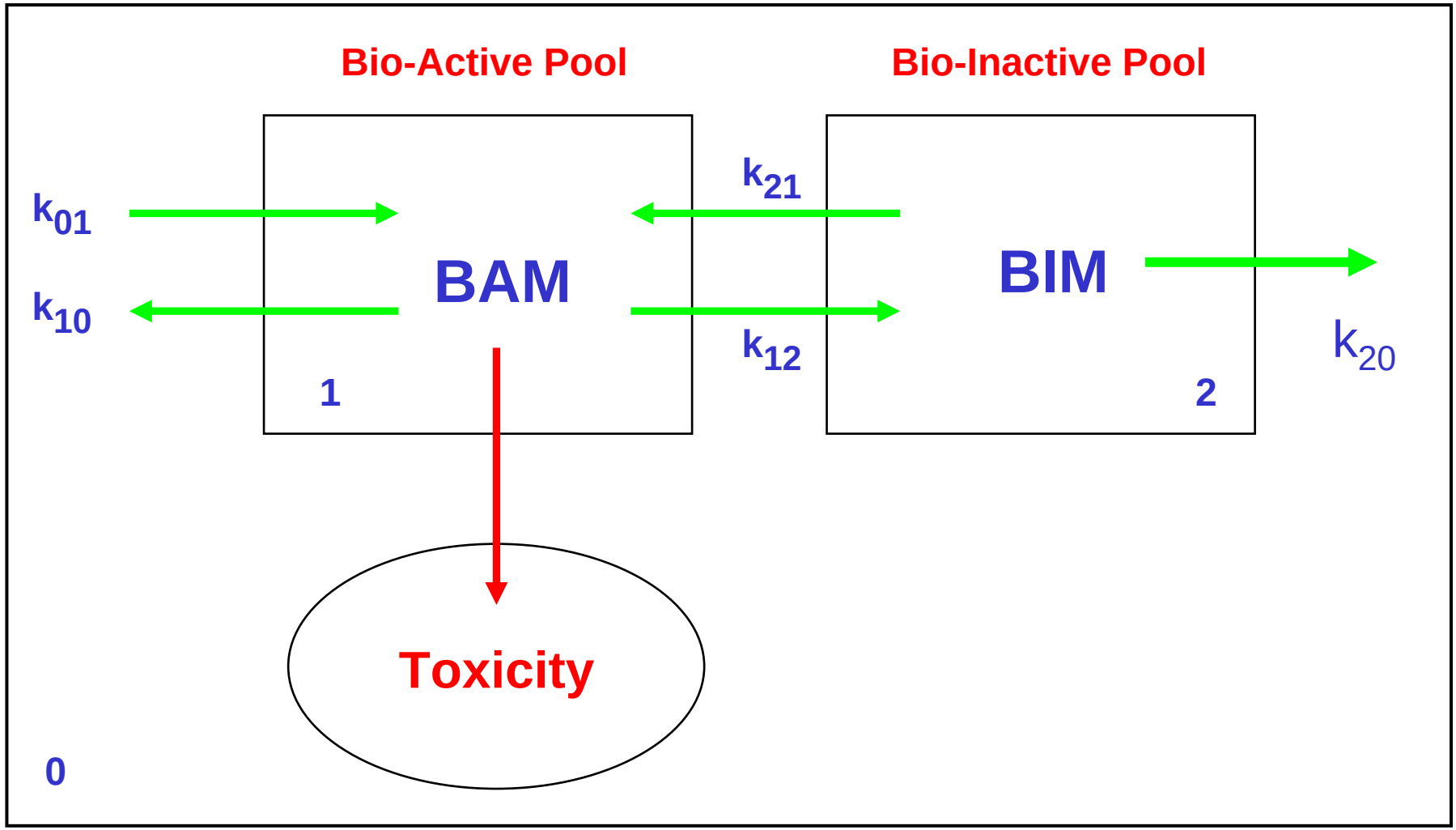


Exposure accumulation toxicity relationship



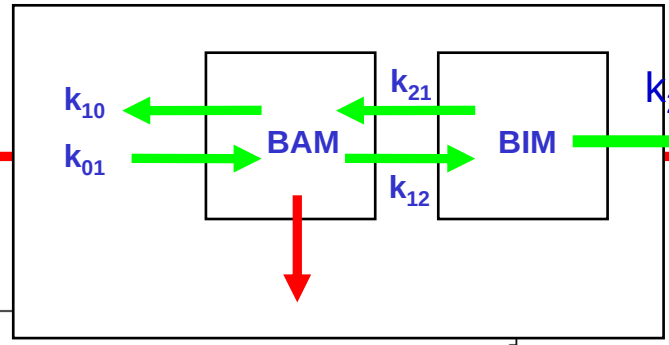


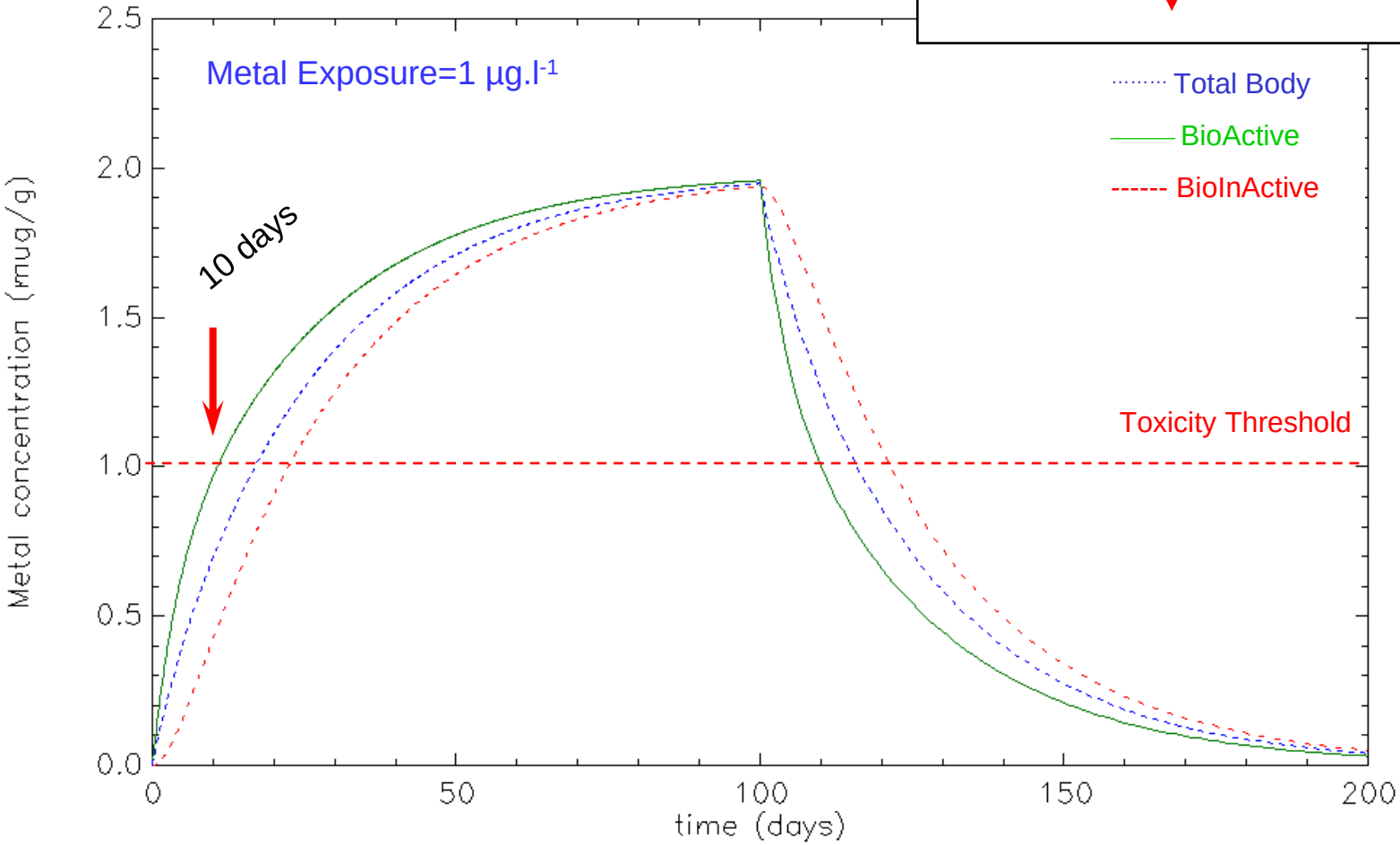




BIM-BAM Metal Accumulation Toxicity Model

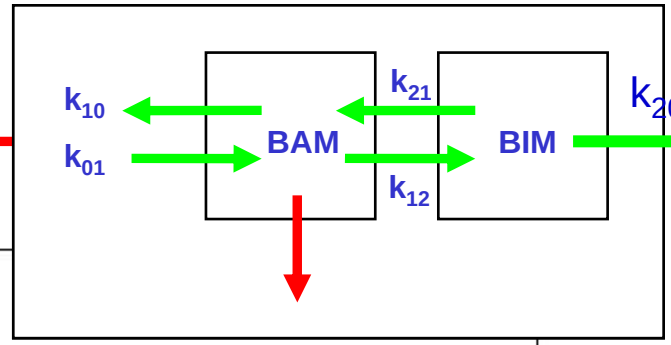
Metal Accumulation – Toxicity 2 Pool Model

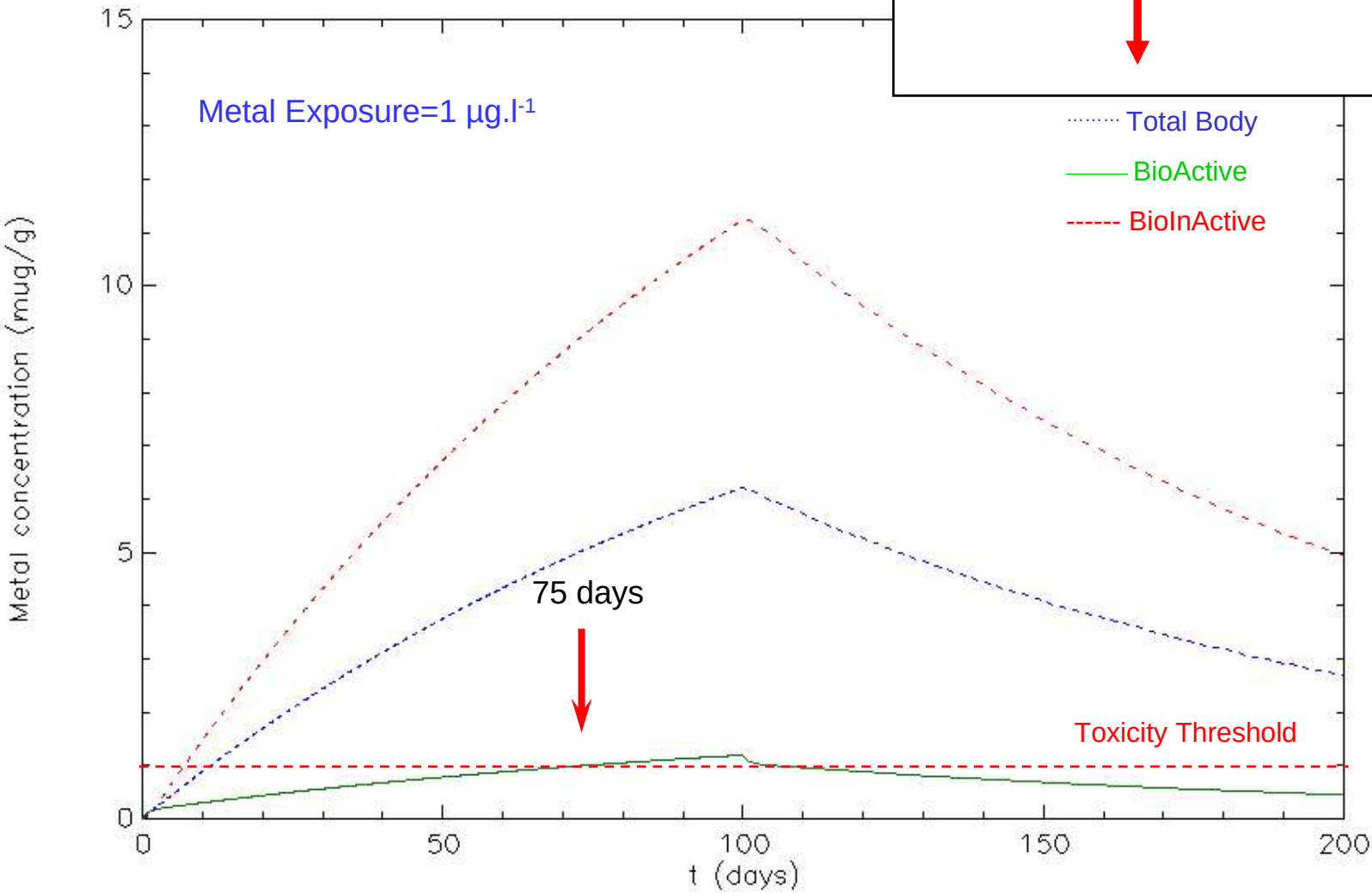




k(0,1)=0.1 - k(1,0)=0.1 - k(2,1)=0.1 - k(1,2)=0.1

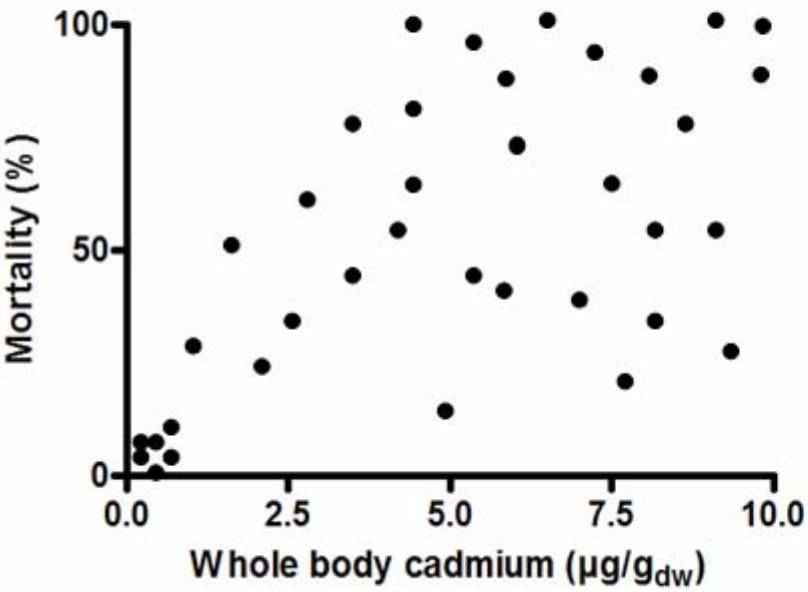
Metal Accumulation – Toxicity 2 Pool Model

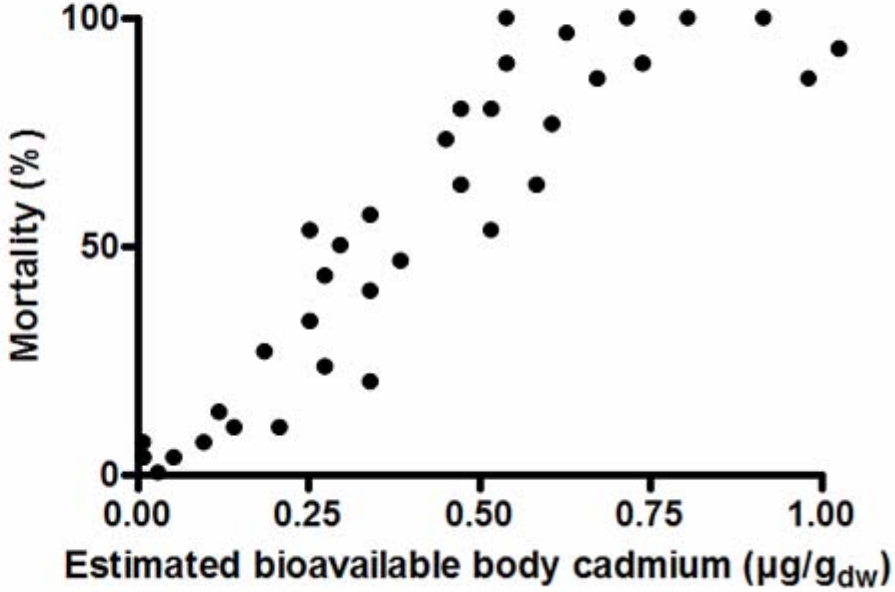




k(0,1)=0.1 - k(1,0)=0.1 - k(2,1)=0.1 - k(1,2)=1

Cadmium accumulation and toxicity in carp and estimated internal availability





Lessons learned

Metal uptake from water is function of the free metal ion activity in the exposure solution but...

Competitive and non-competitive effectors modifying the binding and transport characteristics of membrane channels and carriers have to be taken into account.

Some metal complexes appear to be labile and others directly available for uptake.

Water is not the only exposure route and food and sediments may contribute to toxicity.

Metal toxicity is not a direct function of metal uptake and accumulation. Hence a single critical body residue does not exist.

The kinetics of internal compartmentalization into biologically active and less active pools is key to understanding exposure toxicity relationships.

The development of dynamic models linking exposure to accumulation and toxicity provide a powerful means to explain the variation observed in toxicity within and among species.

The future of the BLM

The BLM is a simple model describing exposure toxicity relationships in a pragmatic manner.

Today it only considers water borne metal toxicity but it can be easily expanded to include other routes (i.e. from a single layer to a muti-layer BLM).

BLMs are developed for a limited number of species and the basis for across species extrapolation needs a fundamental underpinning.