



General Electric
Housatonic River
Site, Rest of River

Public Meeting
January 5, 2005

Pittsfield, MA

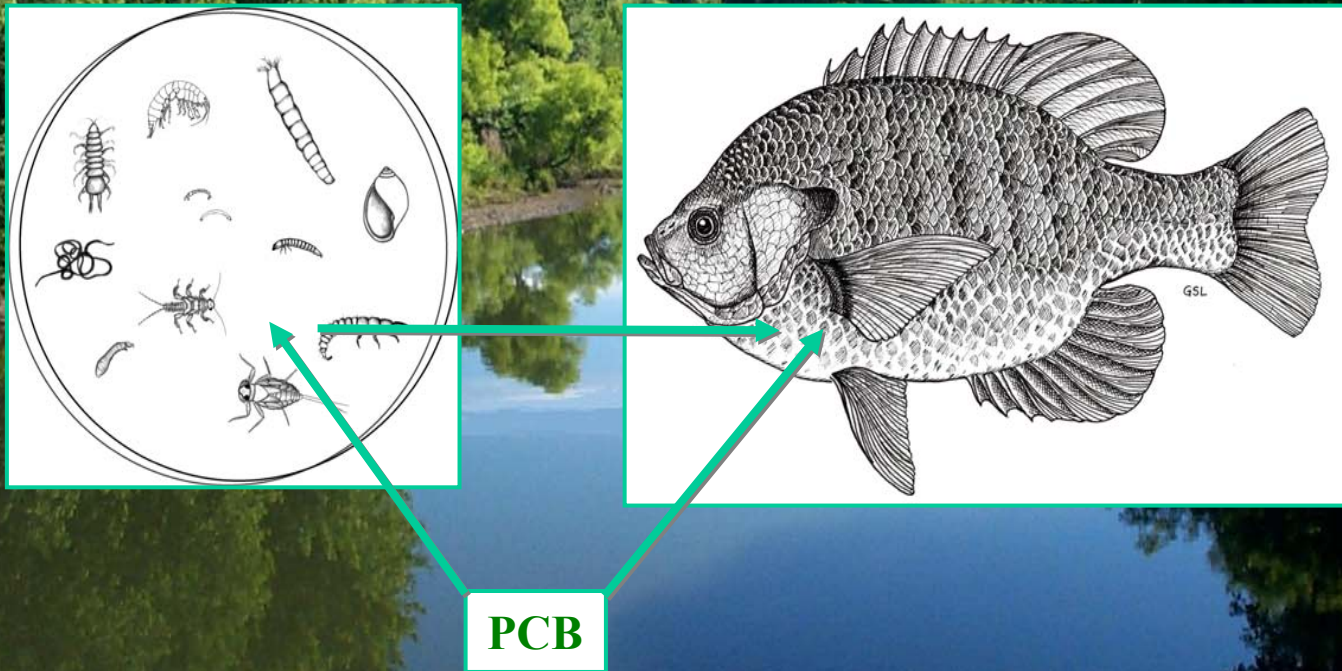
PCB Bioaccumulation Model Calibration: Food Chain Model (FCM)

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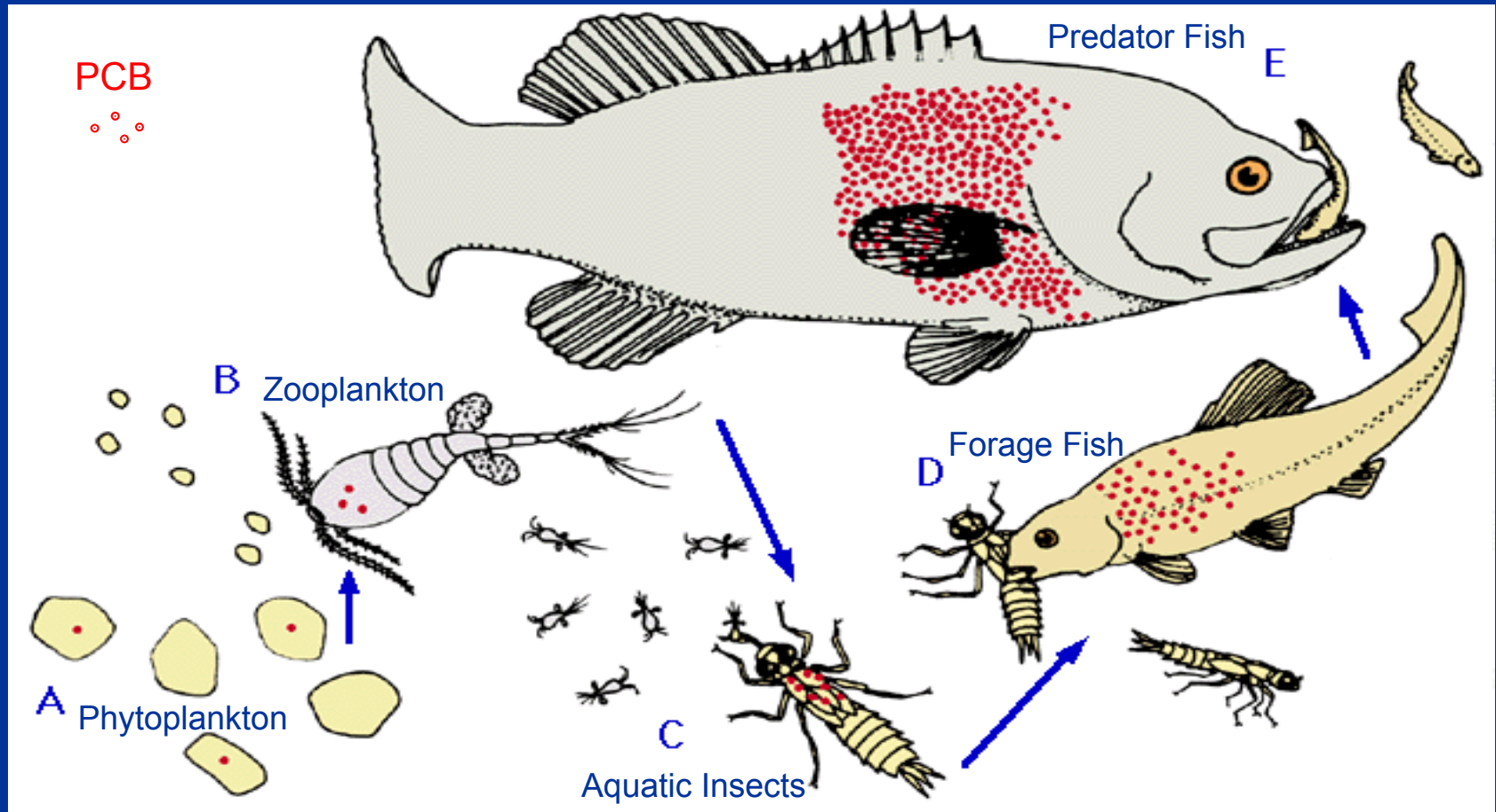


Bioaccumulation



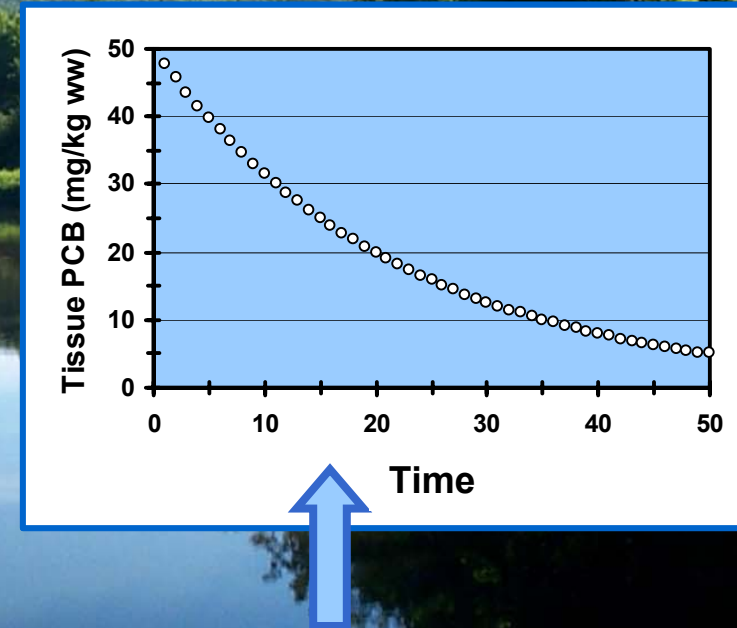
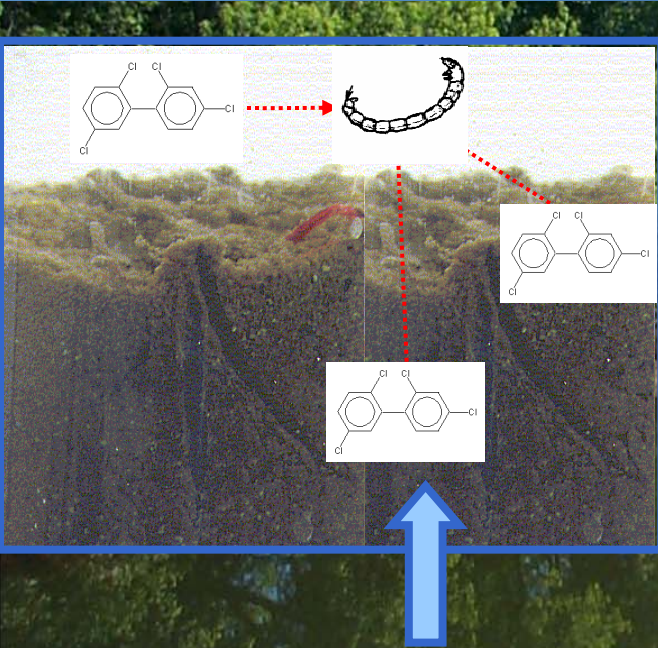
- Bioaccumulation = the process by which living things accumulate contaminants from their environment
- Occurs by **feeding** and by **contact** with water and solids

Biomagnification



- Biomagnification: concentration in the food chain
 - PCBs both bioaccumulate and biomagnify

Purpose of Bioaccumulation Model



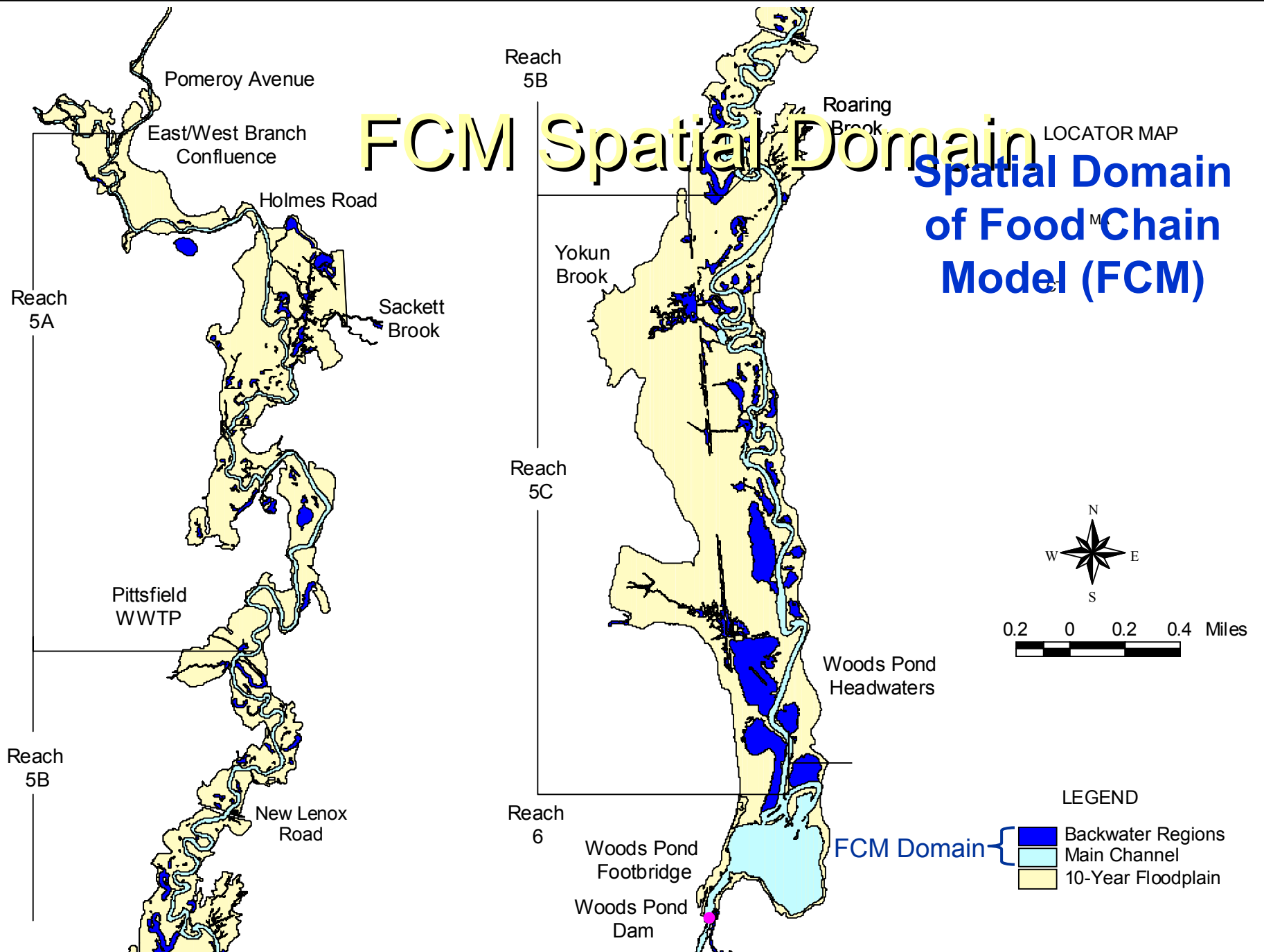
1. Identify how aquatic organisms obtain PCB burdens (e.g., from water or sediment)

2. Estimate the time needed for PCBs in biota tissue to be reduced to "safe" levels.

FCM Spatial Domain

Spatial Domain of Food Chain Model (FCM)

LOCATOR MAP



Model Linkages

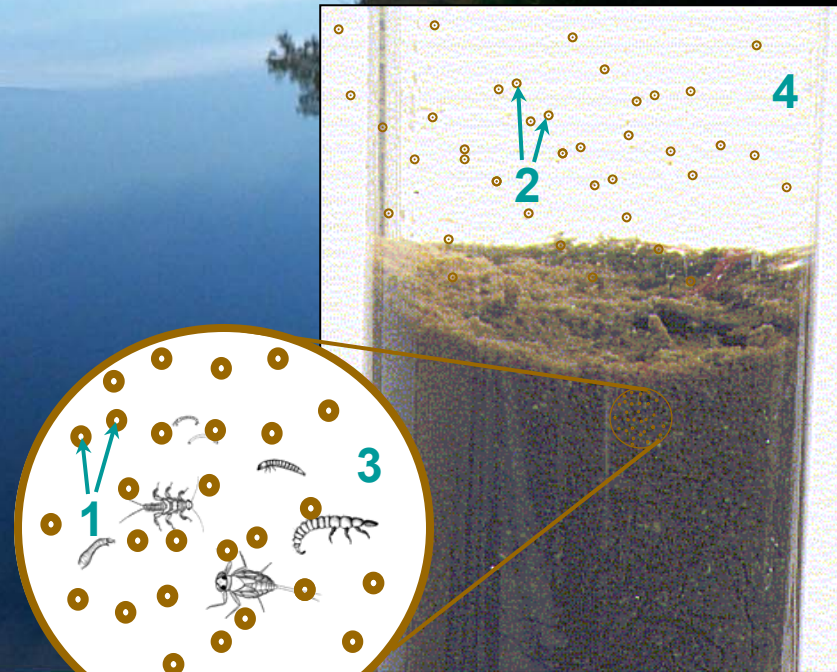
PCB Exposure Inputs
(EFDC)

Temperature
(HSPF)

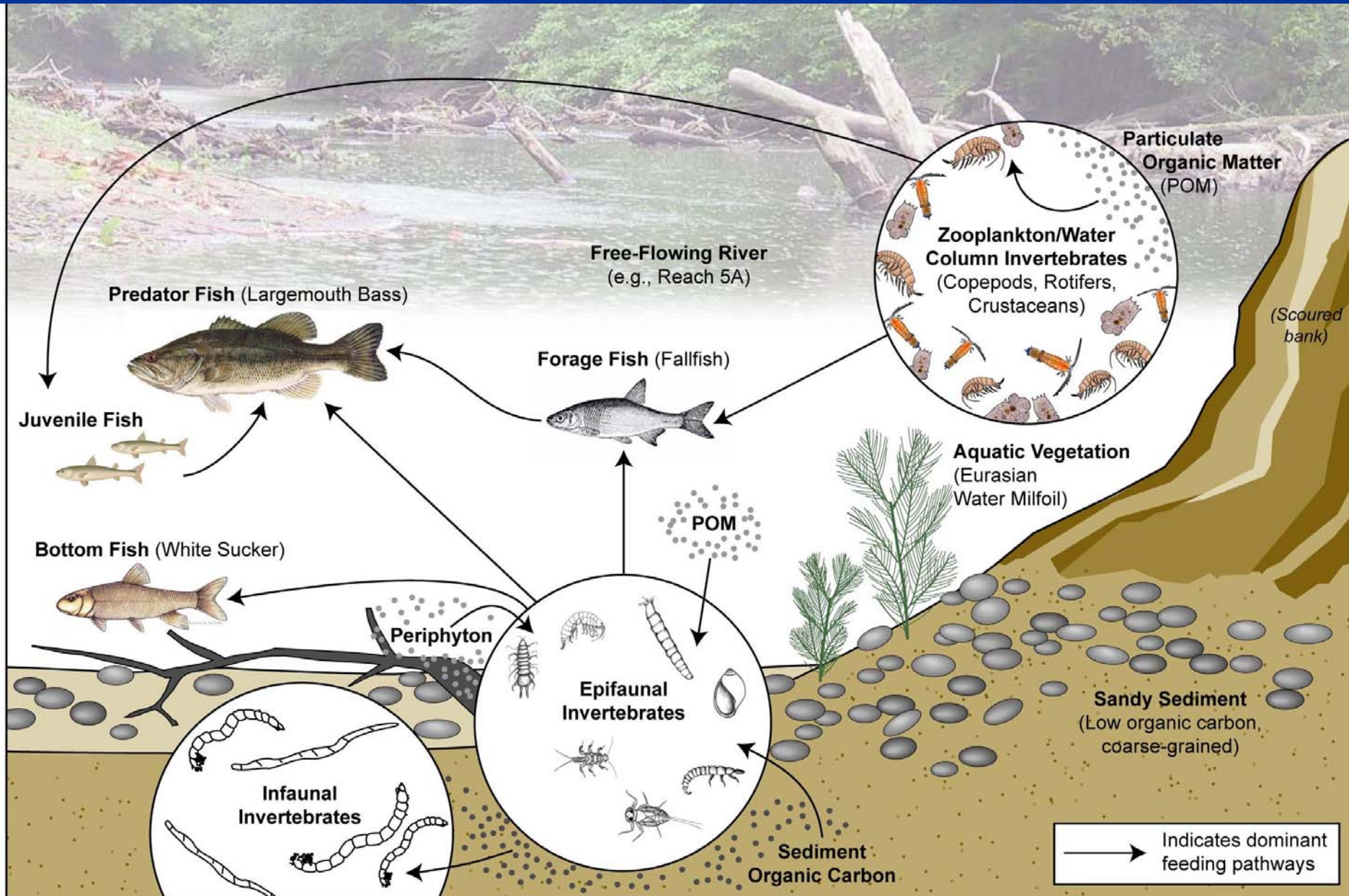
Bioaccumulation Model
(FCM)

Exposure Inputs from EFDC:

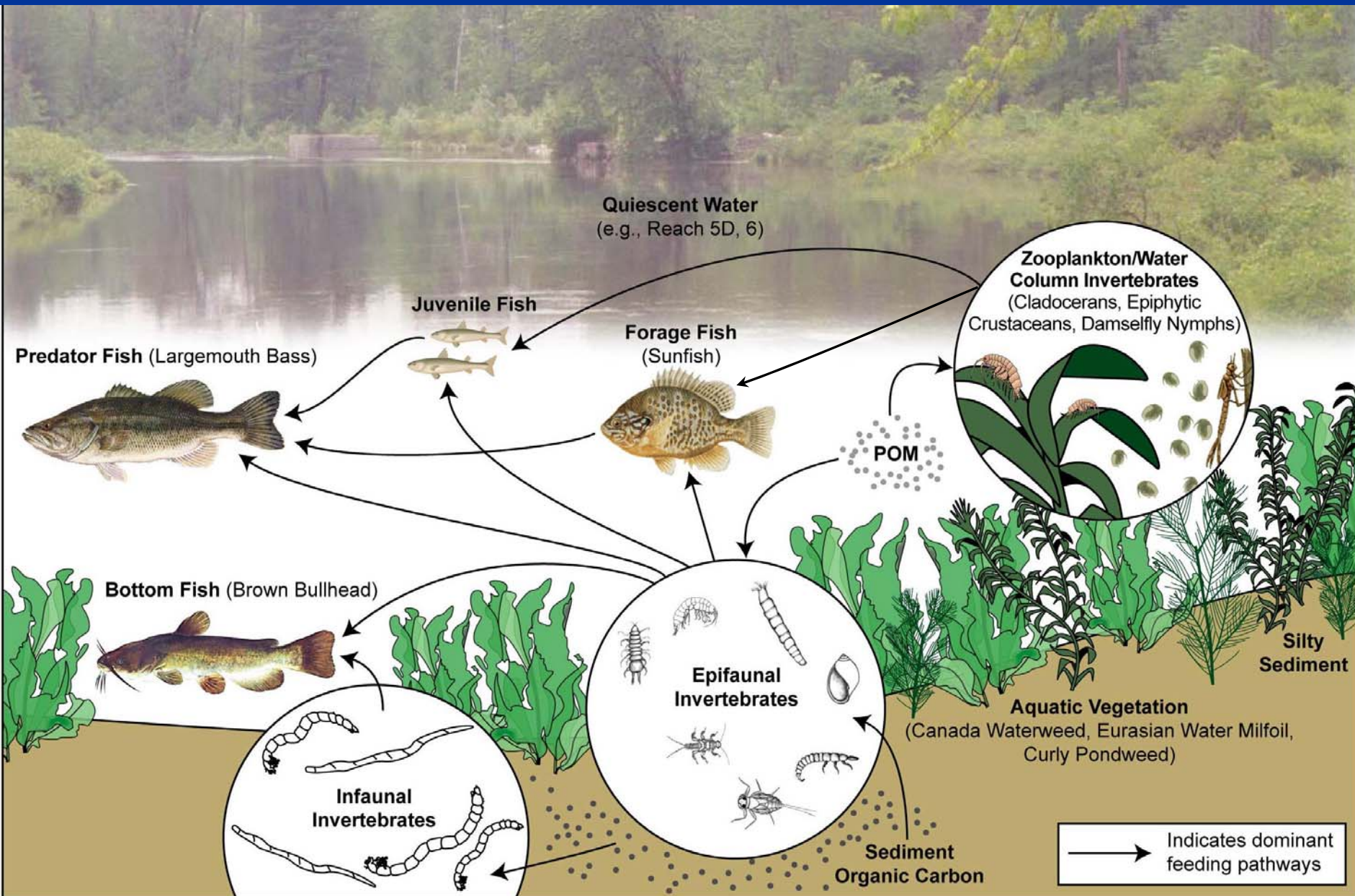
1. PCB in bed sediment organic carbon
2. PCB in water column organic matter (POM)
3. Dissolved PCB in sediment pore water
4. Dissolved PCB in water column



Conceptual Model – Upstream PSA



Conceptual Model – Downstream PSA



Bioaccumulation Processes

$$\frac{dv_i}{dt} = \underbrace{K_{ui}c}_b + \underbrace{\alpha_c \sum_{j=1}^n C_{ij}v_j}_a - \underbrace{(K_i + G_i)v_i}_{c \& d}$$

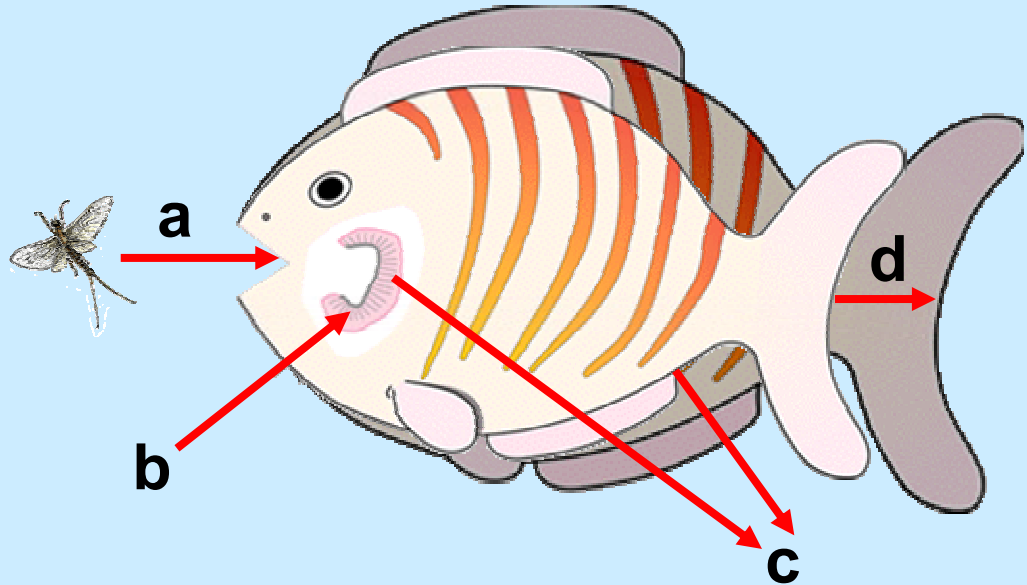
- PCB Uptake:**

- a. Dietary uptake
- b. Respiration

- PCB Elimination**

- c. Depuration (elimination via gill and feces)
- d. Growth dilution

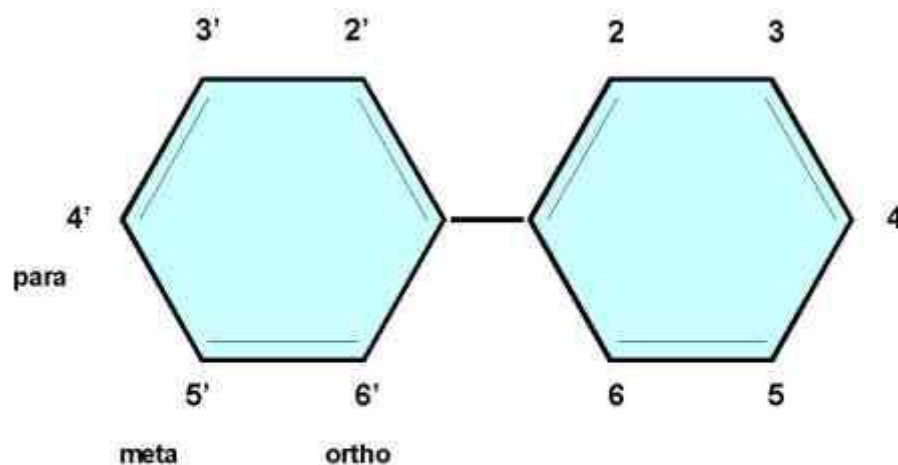
- Fish modeled as “time-dependent”; invertebrates modeled as “steady-state”:



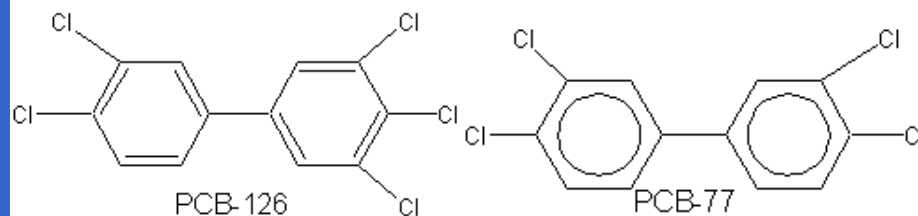
$$v_i = \frac{\text{uptake}}{\text{loss}} = \frac{a + b}{c + d}$$

Contaminants Simulated

- **Total PCBs** (similar to Aroclor 1260)
- 9 Individual congeners
 - “Dioxin-like” PCBs: (PCB-77, PCB-123, PCB-126)
 - High-concentration PCB congeners: (PCB-101, PCB-118, PCB-138, PCB-156, PCB-177, PCB-183)



Structure of Polychlorinated Biphenyl (PCB) Molecule

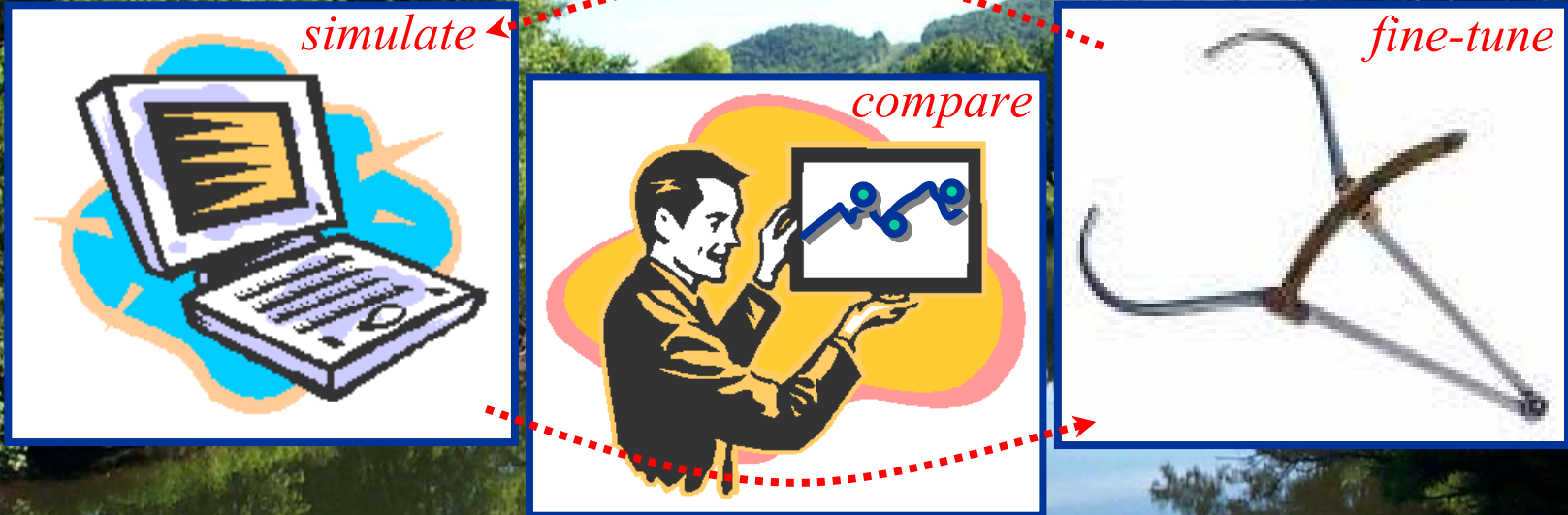




Model Parameterization

- Energy balance parameters (e.g., sediment energy density, lipids, protein, food energy content);
- Invertebrate “rate parameters” (growth rates, respiration rates, and PCB elimination rates);
- Fish growth rates;
- Fish respiration rates;
- Chemical-specific parameters (e.g., PCB assimilation efficiency, partitioning constants);
- **Invertebrate and fish feeding preferences.**

General Calibration Strategy



- Kept most parameters uncalibrated (e.g., used initial estimate from literature review)
- Some small-scale refinements to initial parameter estimates made to improve model
- Parameters always constrained to ranges of scientifically plausible values



Example Calibration Procedures



Fallfish [cyprinid
benthivore]

(Average respiration
rate between sucker
and dace)

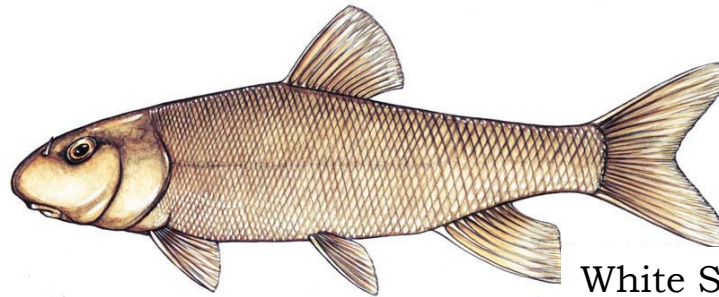


Shiner

[Small
cyprinids]



Dace



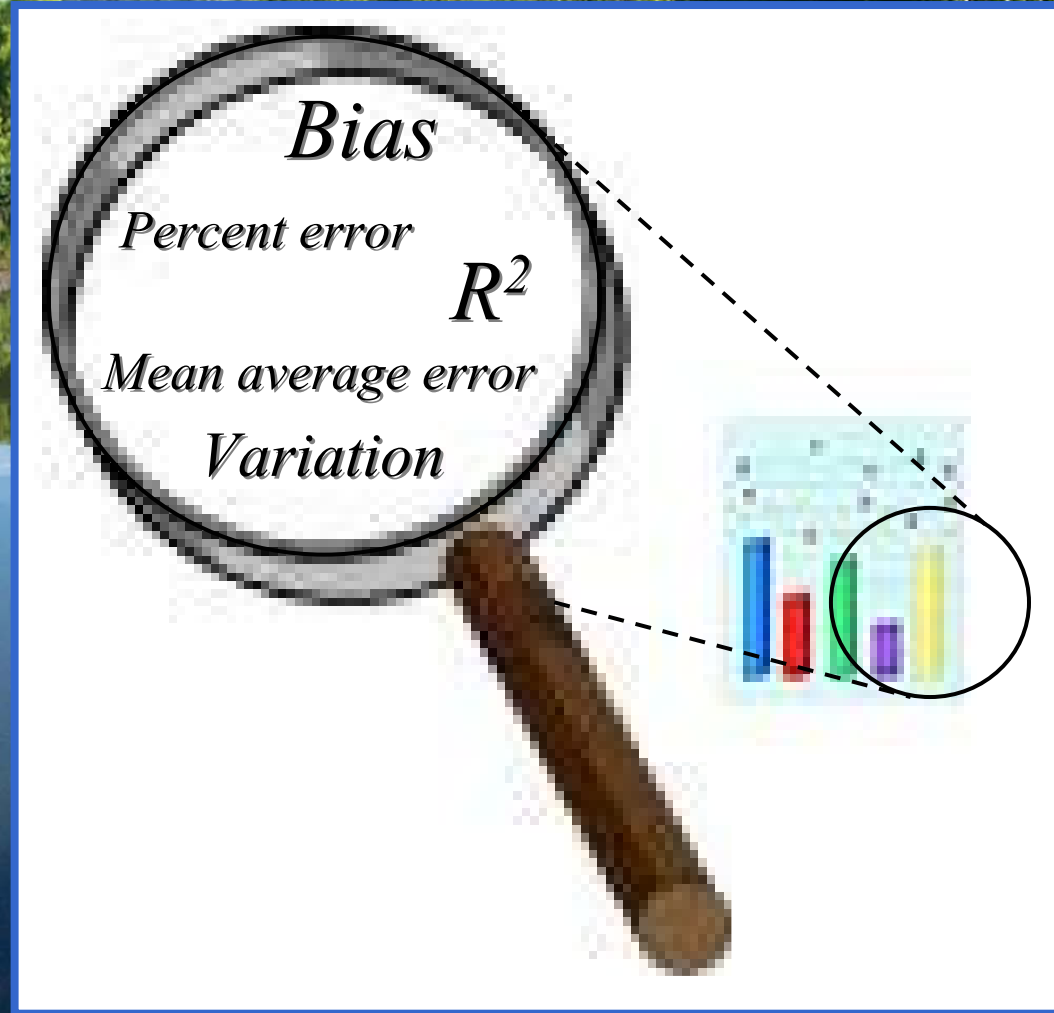
White Sucker [large benthivore]

1. Cyprinid respiration in Reach 5A (above)
2. Seasonal fish growth (restricted to growing season)



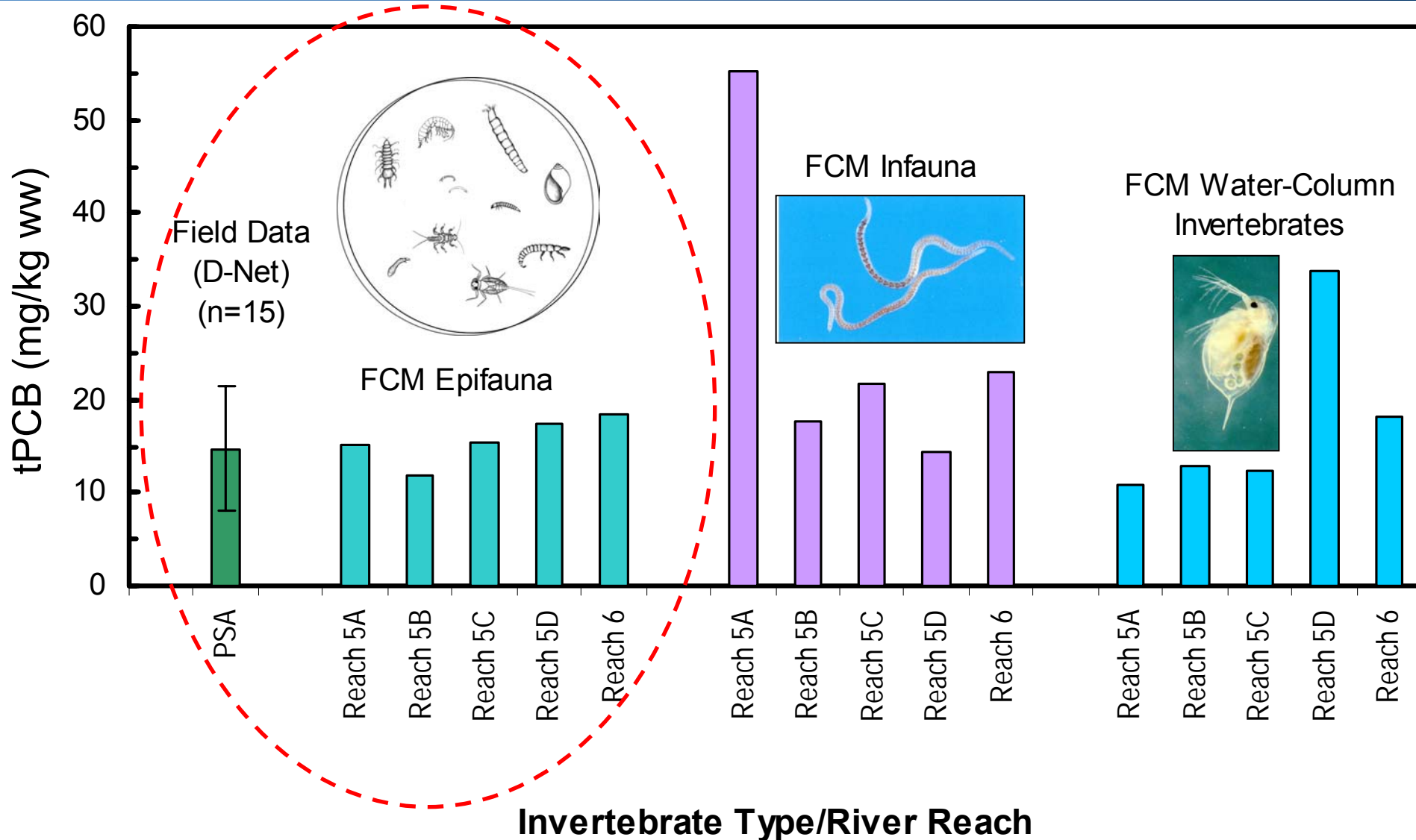
Model Performance Measures

1. “Goodness-of-fit” statistics
2. Visual inspection of simulated versus measured PCBs:
 - by fish age
 - by species
3. Model bias check



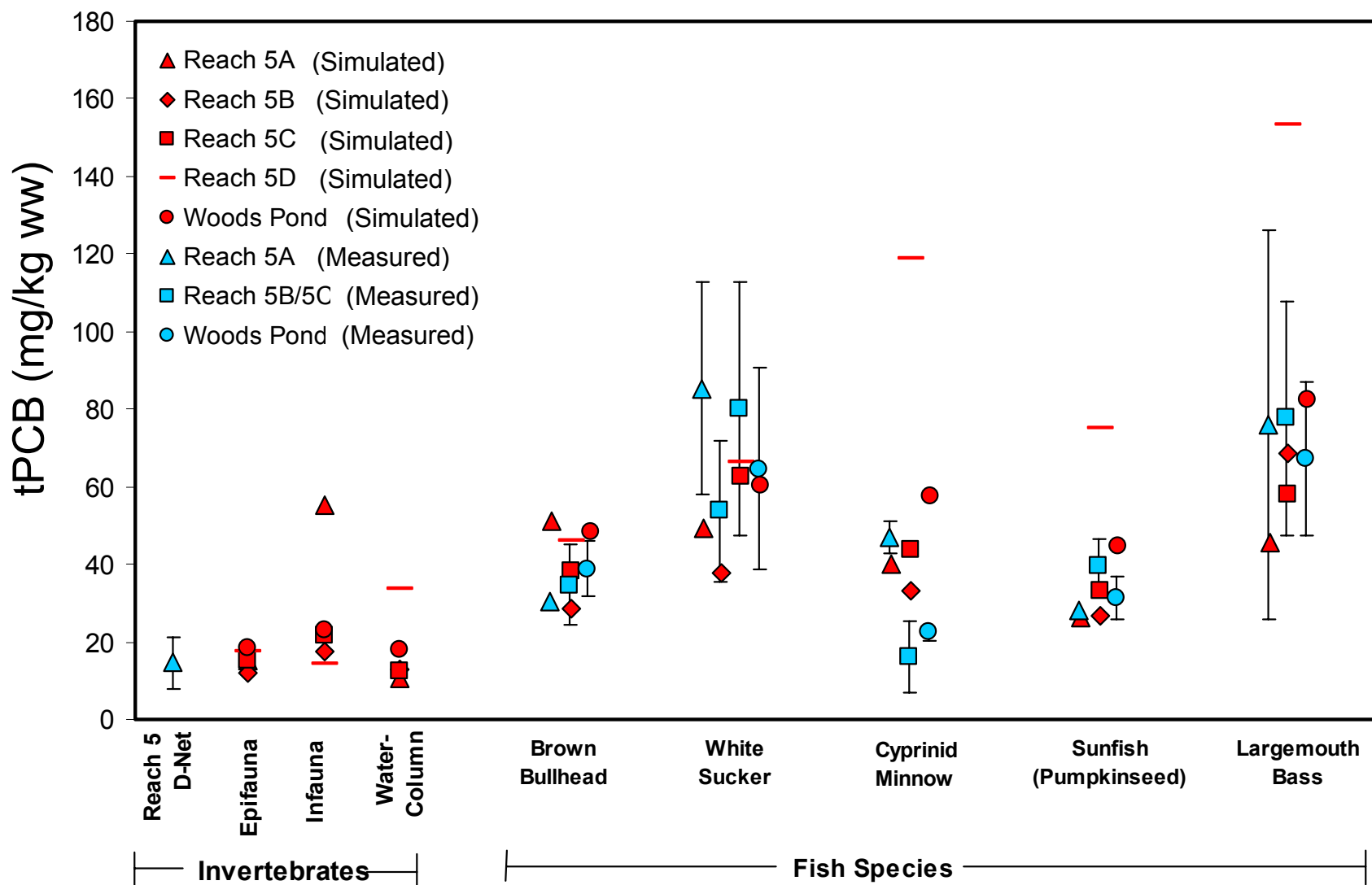


PCBs in Invertebrates (Simulated Versus Measured) – Linked FCM Model



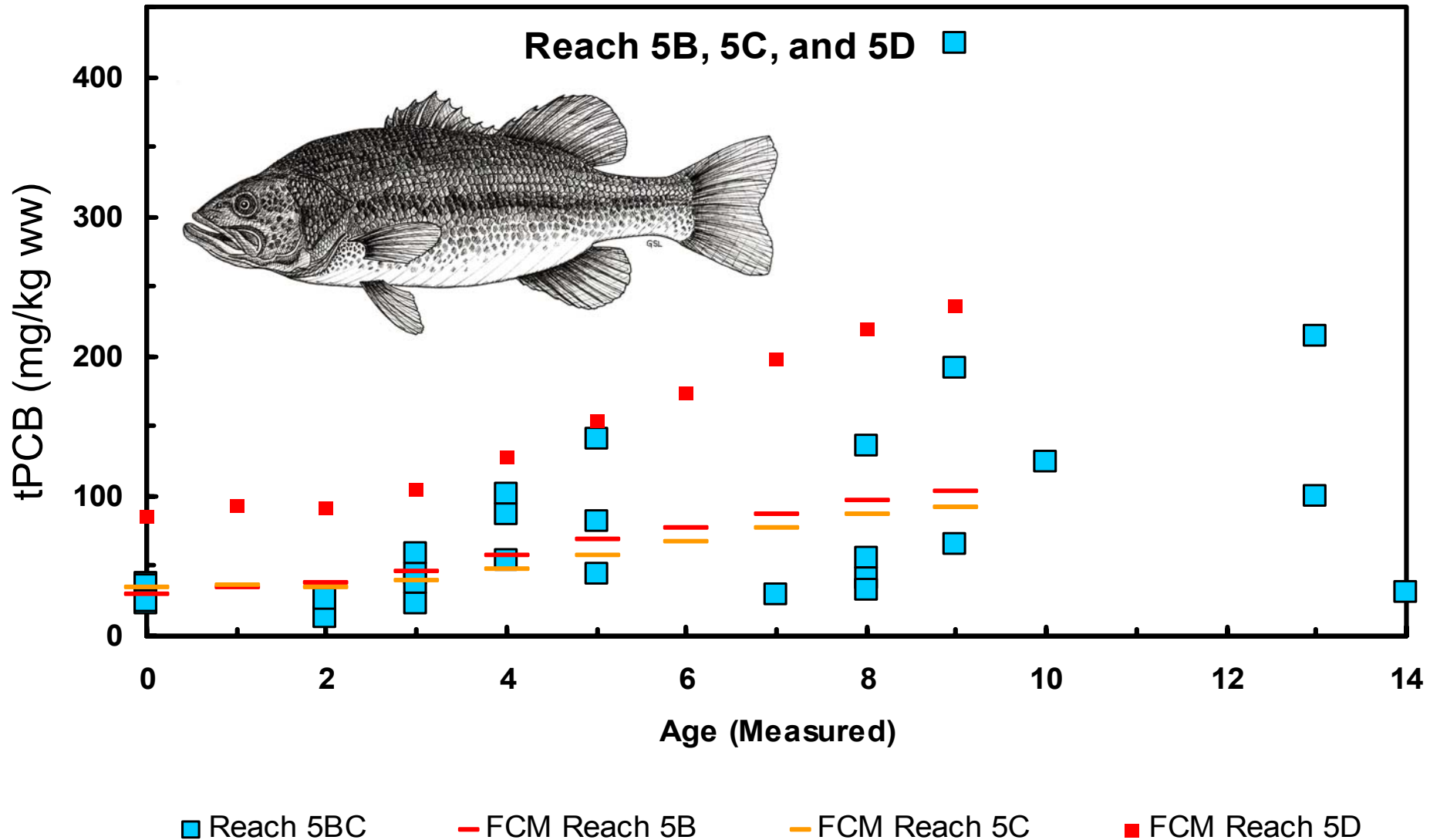


Comparison of Measured Biota Tissue tPCB Concentrations to Linked Model Simulations

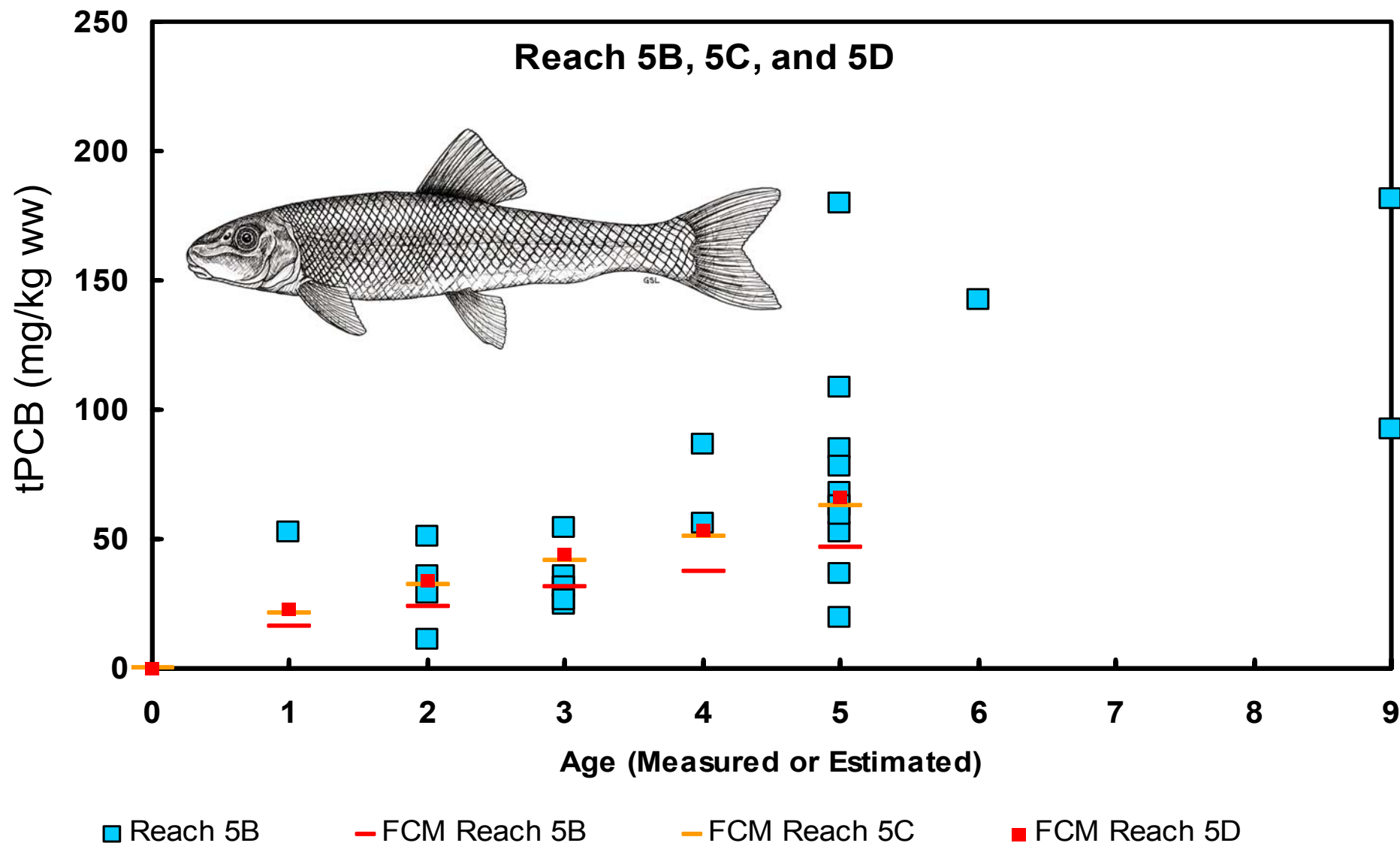




Largemouth Bass – tPCB Versus Age

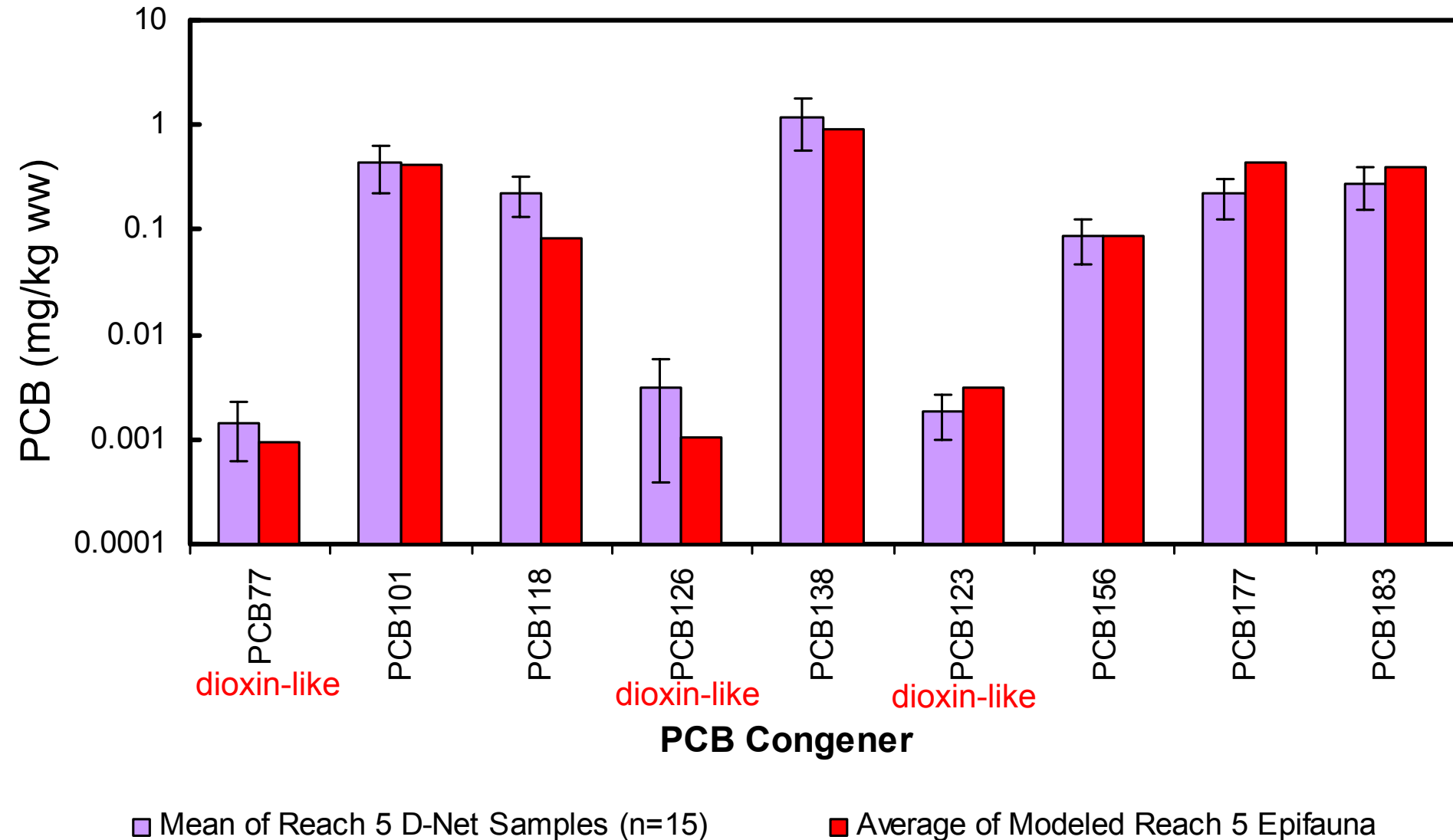


White Sucker – tPCB Versus Age



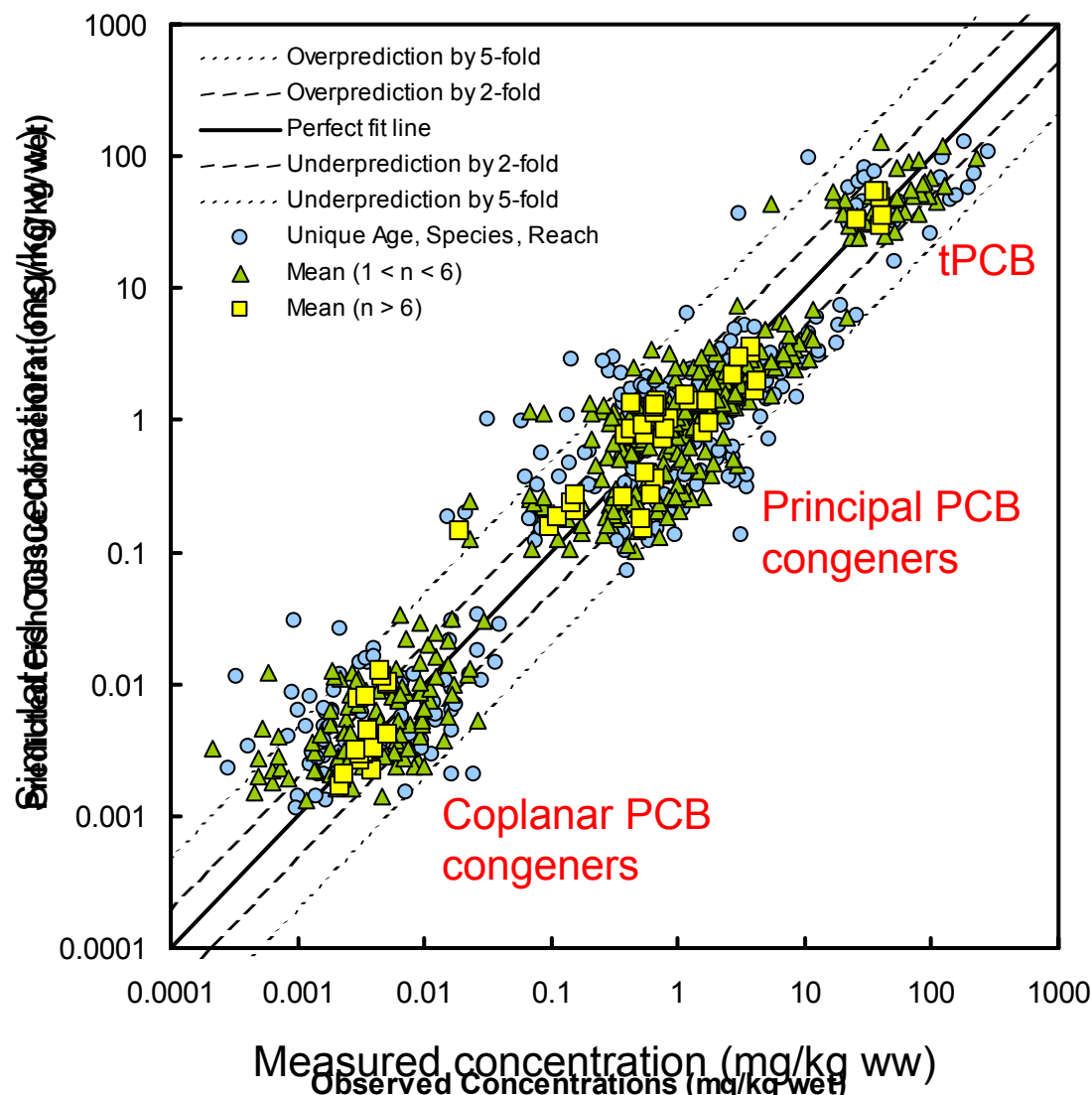


PCB Congeners in Invertebrates: FCM Simulations Versus Field Measurements



Check for Model Bias

- Looked for systematic over- or under-predictions
- No bias observed as function of:
 - PCB type
 - Trophic level
 - Age or lipid





Conclusions

- Successfully predicted PCB burdens at multiple levels of the aquatic food chain (tPCBs, congeners)
- Calibration performance criteria specified in the MFD/QAPP were achieved



Questions?

