2009 Working Se TMDL Documents

Linkage Analysis

Regional Water Quality Control Board – Santa Ana Region

Workshop 2
January 30, 2014

Purpose

- What is “linkage analysis”?
- Review linkage analysis in 2009 draft TMDLs/SSOs
  - Newport Bay watershed biodynamic model
  - Alternatives to biodynamic model considered
- Not in-depth review of selected biodynamic model input parameters or options
  - Relevant slides in reserve

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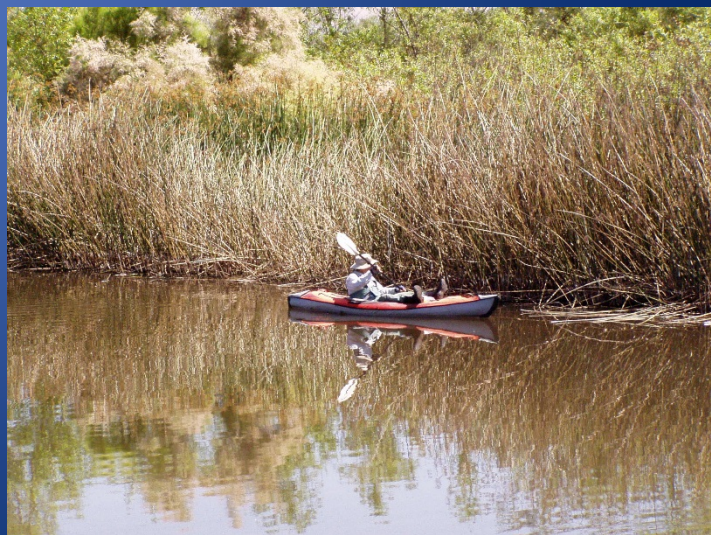
Linkage Analysis

- Investigates the relationship between Se in the environment, numeric Se targets and effects on beneficial uses

  - Used to determine allowable amount of Se inputs to surface waters



2009 Linkage Analysis

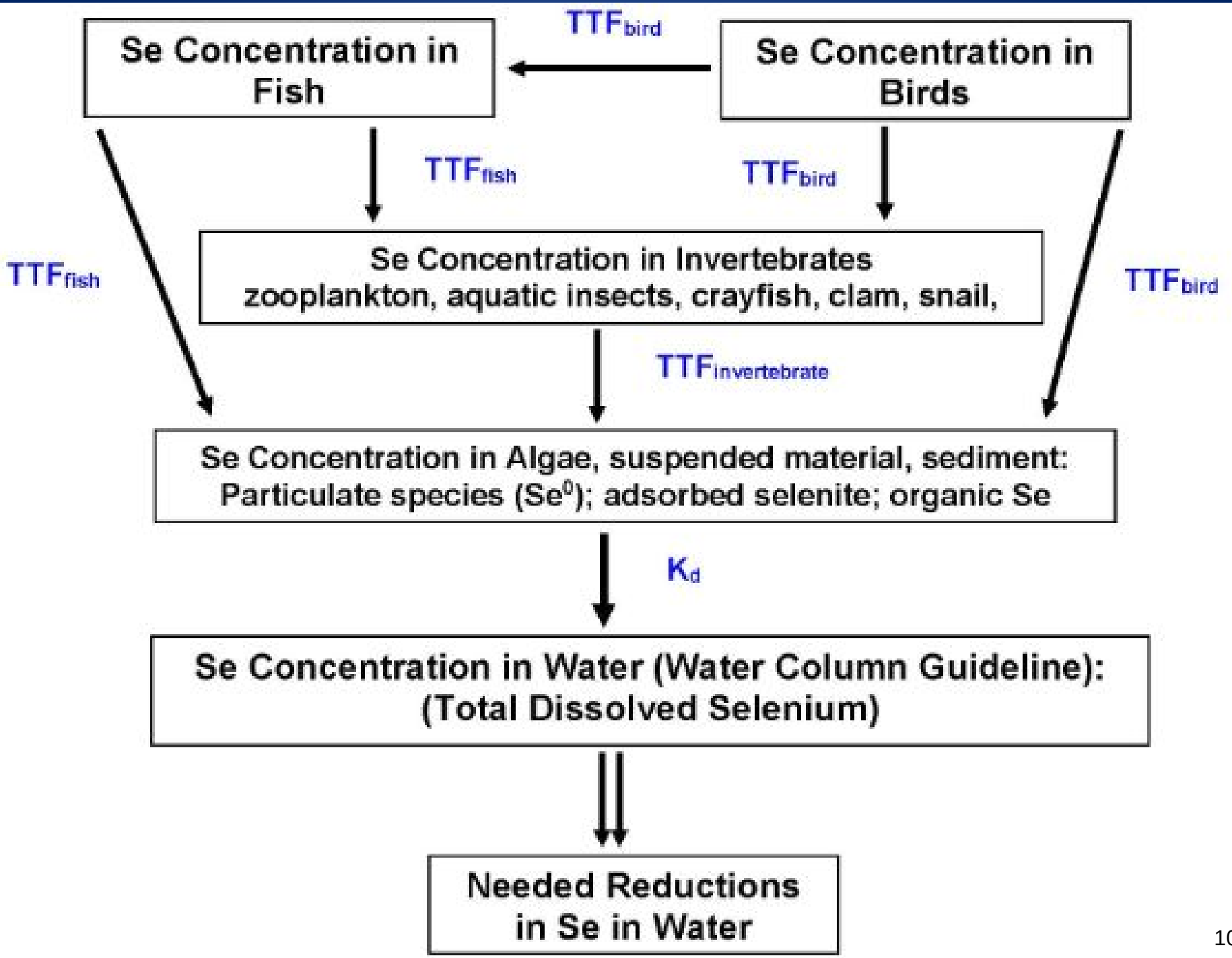
- Used the Presser-Luoma biodynamic model to translate tissue targets/SSOs to water column concentrations (guidelines):
- Consistent with 2006 Independent Advisory Panel (IAP) recommendations:
  - Account for spatial/temporal heterogeneity in Se transport and bioaccumulation processes
  - Approach must be capable of back-calculating Se water column concentrations
  - Modeling should be compatible with Presser–Luoma model for SF Bay: Newport Bay effort compatible with technical/regulatory framework for California

Presser- Luoma Biodynamic Model

Uses an ecosystem-scale methodology

- Conceptualizes ecosystem
  - Incorporates site-specific foodweb structure

- Quantifies processes for each step
  - Mass balance — partitioning (K_d)
  - Biodynamics — diet and tissue Se transfers (Trophic transfer factors: TTFs)
- Key input parameters: Tissue targets, $K_{d,}$ TTFs

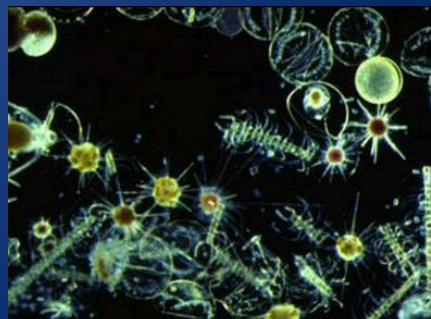

Se Concentration in Fish
TTFbird
Se Concentration in Birds
TTFfish
TTFbird
TTFfish
Se Concentration in Invertebrates
zooplankton, aquatic insects, crayfish, clam, snail,
TTFbird
TTFinvertebrate
Se Concentration in Algae, suspended material, sediment:
Particulate species (Se0); adsorbed selenite; organic Se
Kd
Se Concentration in Water (Water Column Guideline):
(Total Dissolved Selenium)
Needed Reductions
in Se in Water

Elements of the Biodynamic Model

Partitioning Coefficient (K_d)

K_d = particulate Se concentration/water column Se concentration

- Represents dynamics of Se transformations within water and particulate matter
  - Reflects the largest bioconcentration step of Se from the aqueous phase to organisms (10^6-fold increase) via microorganisms (e.g., algae, bacteria)



Elements of the Biodynamic Model

Partitioning Coefficient (K_d)

K_d = particulate Se concentration/water column Se concentration

- Suspended particulate material is representative of the organic-rich, fine-grained (bioavailable) biomass present in water bodies
  - Se measured in suspended particulate material integrates Se uptake by microorganisms in multiple compartments (e.g., algae, detritus, sediment, biofilms)

Elements of the Biodynamic Model

Trophic Transfer Factors[1]

$$C_{organism} = (AE)(IR)(C_{diet})/k_e$$

$$TTF = (AE * IR)/k_e$$

$$TTF = C_{organism}/C_{diet} \quad \text{and} \quad C_{organism} = TTF^* C_{diet}$$

Where:

AE = assimilation efficiency

IR = ingestion rate

k_e = efflux rate

[1] simplified

Data Needed to Adapt the Presser-Luoma Model to the Newport Bay Watershed

- Temporally and spatially matched data sets across all media: water, particulates, tissue
- Conceptual model of Se transfer pathways
- Seasonal patterns of waterborne Se concentrations, species and loading (dissolved and total)
- Surficial sediment Se concentrations
- Estimated assimilation efficiencies and transfer factors: inorganic Se sources to tissue accumulation
- Se concentrations in food chain biota (dietary items)
- Se concentrations in larger/higher level trophic level predators such as fish and birds (model end product)

Newport Bay Biodynamic Model

USGS staff successfully adapted the Presser-Luoma model to the Newport Bay watershed

- Generated multiple model runs for a variety of foodwebs and waterbodies in the watershed
  - Used proposed tissue-based site-specific objectives
  - Back-calculated water column Se concentrations from the tissue numbers
- Validated model using observed site-specific Se concentrations in invertebrates, fish, and bird species
  - Predicted Se concentrations in the range of observed Se concentrations in most cases

Newport Bay Biodynamic Model Runs

- The waterbody-specific K_ds and the TTF for birds selected by Regional Board staff differed slightly from those selected by USGS staff
  - Selected K_ds using the Basin Plan waterbody designations
  - Used TTF for birds of 1.4 as recommended by CH2M Hill (vs. 1.8 used by USGS)
- ❖ Based on the conceptual model and data collected in the watershed, insect-based foodweb is of most concern

Newport Bay Biodynamic Model

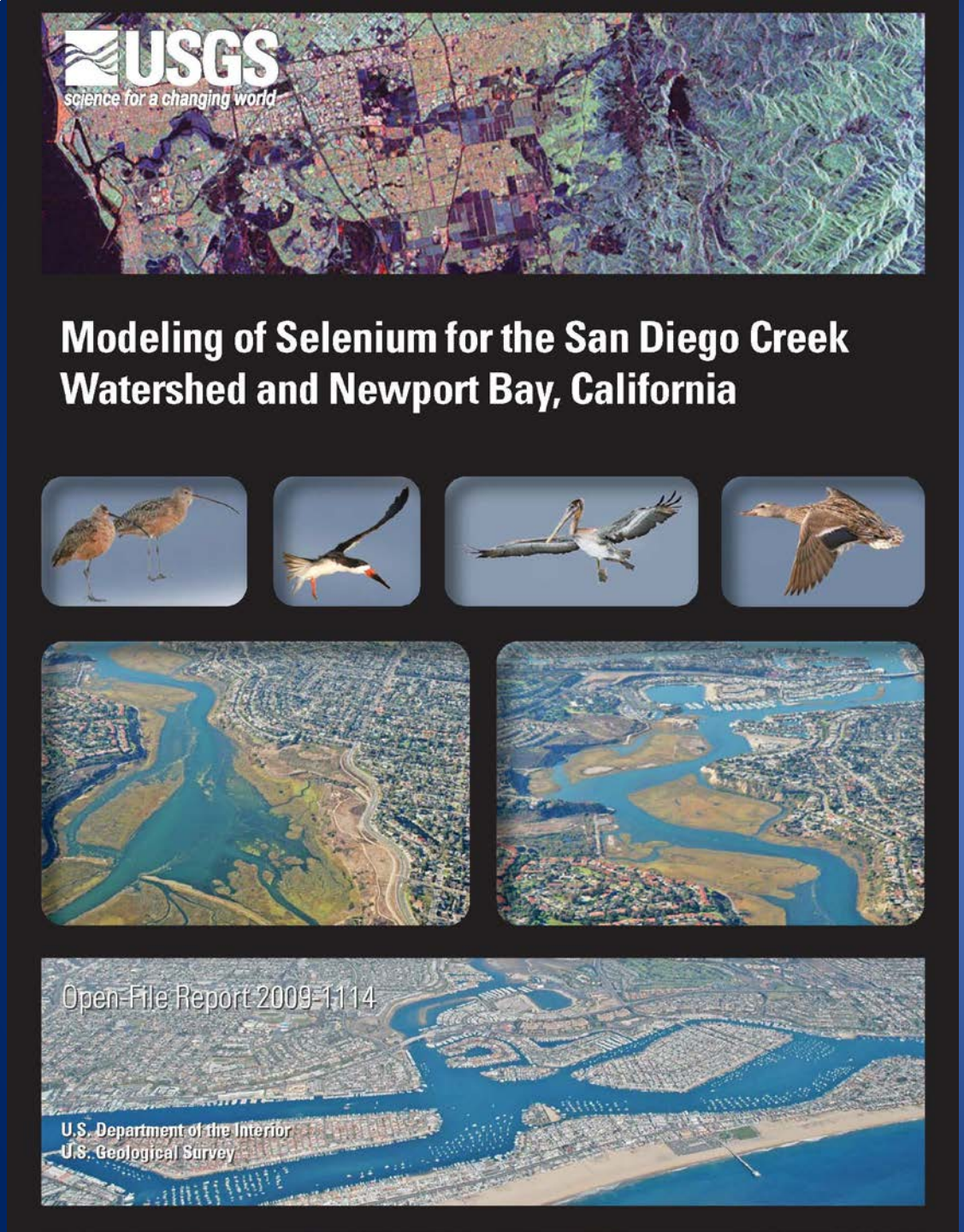
Watershed scenarios modeled included:

- invertebrates→fish
  (for lower trophic level fish such as fathead minnow)
- invertebrates→fish→fish
  (for piscivorous fish such as large-mouth bass)
- invertebrates→birds
  (for shorebirds such as black-neck stilts)
- invertebrates→fish→birds
  (for piscivorous birds such as terns)

Newport Bay Model Results

Table 9-3. Range in Water Column Guidelines Predicted by the Newport Bay Watershed Biodynamic Model Using Fish (5 µg/g dw) and Bird Egg Tissue (8 µg/g dw) SSOs					
Freshwater (µg/L)					
Lower Peters Cyn Wash	San Diego Creek (All Sites)	IRWD Wetlands	UCI Wetlands	Santa Ana Delhi Channel	Big Canyon Creek
5.0 – 11.5	5.0 – 13	6.0 – 9.0	2.0 – 2.6	12 - 28	0.9 – 1.4
Saltwater (µg/L)					
Upper Newport Bay (water column)	Upper Newport Bay (benthos)	Lower Newport Bay (water column)	Lower Newport Bay (benthos)	All Newport Bay (water column)	All Newport Bay (benthos)
11 – 20	0.109 – 0.184	5.0 – 8.0	0.04 – 0.07	2.5 – 6.0	0.06 – 0.110

Range in water column guidelines (WCGs) based on lowest and highest Se concentrations in water predicted by the model for both fish and birds using both the median and 75th percentile K_ds for each waterbody/ waterbody combination modeled (results from all model scenarios are shown in Table 9-2 in the 2009 draft staff report)



Details of the Adaptation of the Presser-Luoma Biodynamic Model to the Newport Bay Watershed

Development of the Newport Bay Biodynamic Model

Requested information provided to USGS staff

- Calculated partitioning coefficients (K_ds)
  - Median and 75th percentile
- Recommended trophic transfer factors for both fresh and saltwater organisms
  - Invertebrates (insects, bivalves, worms)
  - Fish (prey and predator fish)
  - Aquatic-dependent birds (herbivorous, omnivorous, piscivorous)

Newport Bay Biodynamic Model

Watershed scenarios modeled using both the median and 75th percentile K_ds included:

- invertebrates→fish
  (for lower trophic level fish such as fathead minnow)
- invertebrates→fish→fish
  (for piscivorous fish such as large-mouth bass)
- invertebrates→birds
  (for shorebirds such as black-neck stilts)
- invertebrates→fish→birds
  (for piscivorous birds such as terns)

Regional Board Staff Revisions to the Newport Bay Biodynamic Model

- K_ds selected by Regional Board staff differed slightly from those selected by USGS staff
  - The Basin Plan defines the waterbodies in the Newport Bay watershed differently than how they were segregated in the USGS modeling runs
  - RB staff used the Basin Plan designated waterbodies for SDC (Reach 1 and Reach 2) and Newport Bay (Upper and Lower bay)
  - Added additional water column and bed sediment data for UNB

Regional Board Staff Revisions to the Newport Bay Biodynamic Model

Waterbodies and waterbody combinations modeled:

- Peters Canyon Wash
- Lower San Diego Creek (Reach 1)
- IRWD Wetlands
- UCI Wetlands
- San Diego Creek – all sites (includes PCW and IRWD and UCI wetlands)
- Santa Ana Delhi Channel
- Big Canyon Creek (stream areas)
- Upper Newport Bay (water column food web)
- Upper Newport Bay (benthic food web)
- Lower Newport Bay (water column food web)
- Upper Newport Bay (benthic food web
- All Bay Sites (water column food web)
- All Bay Sites (benthic food web)

Table 9-1A

K_ds Used by Regional Water Board Staff in the Newport Bay Watershed Biodynamic Model[1]

Water Body	Median Kd	75th%ile Kd
Peters Canyon Wash	178	279
Lower San Diego Ck	136	238
IRWD wetlands	226	271
UCI wetlands	786	825
San Diego Ck- All Sites	159	279
Santa Ana Delhi Channel	74	127
Big Canyon Wash	1,469	1,803
Upper Bay water column*	139	188
Upper Bay benthic**	6,920	8,423
Lower Bay water column	359	401
Lower Bay benthic	18,513	23,750
All Bay Sites water column	212	353
All Bay Sites benthic	11,600	17,770

Table 9-1B

K_ds used in modeling by USGS[2] (Presser and Luoma, 2009; Tables 18-20)

SDC subwatershed (freshwater)	
Upper watershed	200
Lower San Diego Creek	320
IRWD wetlands	400
UCI wetlands	1,000
Newport Bay (saltwater)	
near mouth of estuary	200
upper bay	1,000
upper/lower bay	10,000
lower bay	20,000

- Most of the RB staff selected K_ds for the freshwater areas were within the same range as those recommended by USGS staff
- Biggest difference: K_ds for the saltwater areas
- RB staff divided data based on:
  - Location: UNB vs. LNB
  - Type: water column or benthic*

- * A substantial difference was observed between the water column particulate K_ds measured in the Bay and the benthic bed sediment K_ds estimated from data collected from several of the harbors in Newport Bay

Regional Board Staff Revisions to the Newport Bay Biodynamic Model

- The USGS model did not address BCW
  - Se problem in BCW not identified until June 2008
  - RB staff calculated K_ds and ran different model scenarios for Big Canyon
- Staff used a different TTF for birds
  - USGS: $TTF_{bird} = 1.8$
  - CH2M Hill: $TTF_{bird} = 1.4$

(Staff used CH2M Hill TTF for birds as it was based on field data including data collected from the NB watershed)

➢ *After reviewing recommendations from USGS and CH2M Hill, Regional Board staff selected the parameter values to be used in the final modeling runs*

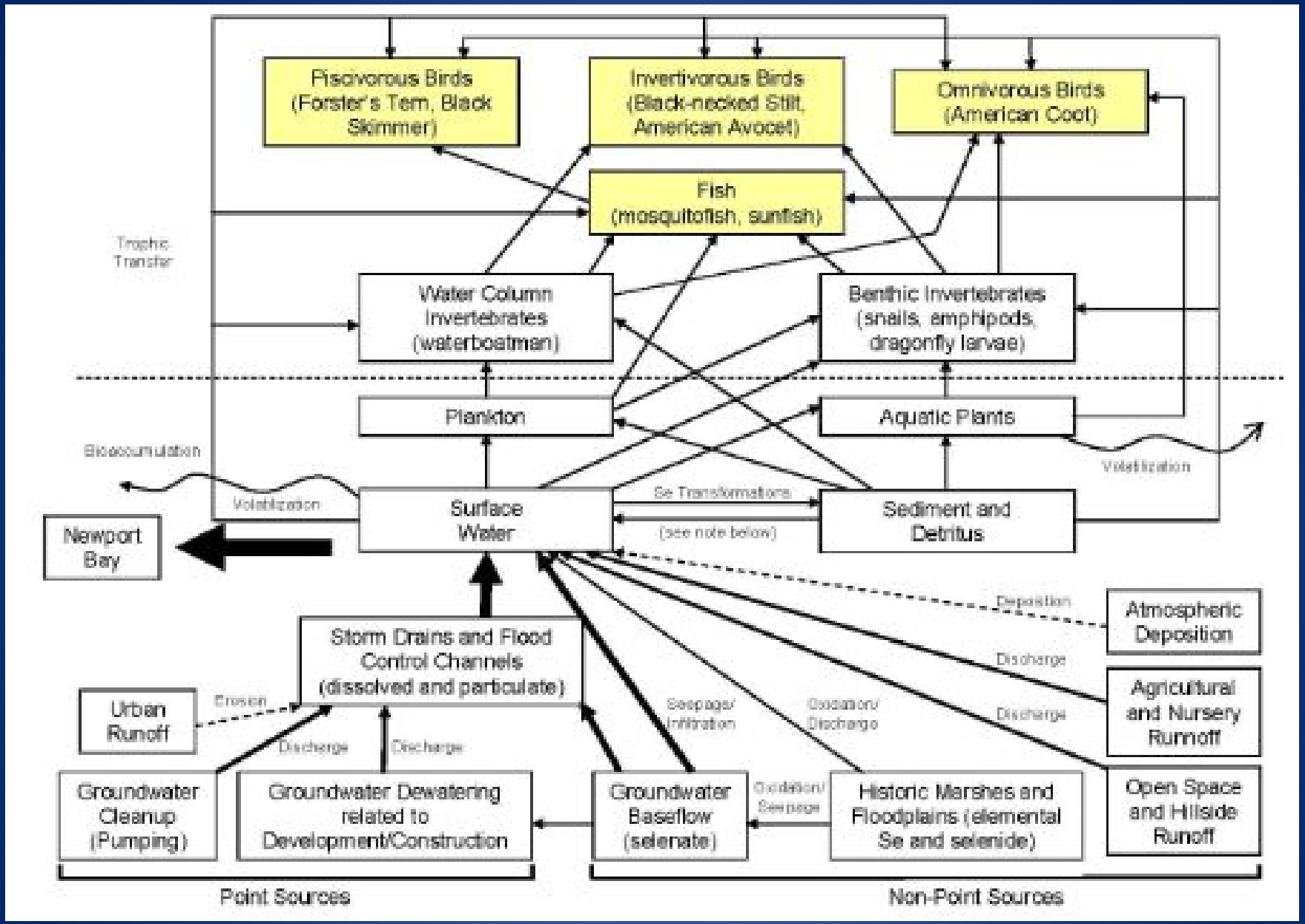


Figure 9-3: Conceptual Model, Exposure Pathways, and Food-Web Relationships for Freshwater Habitats in the Newport Bay Watershed (Source: CH2MHill, 2009b).

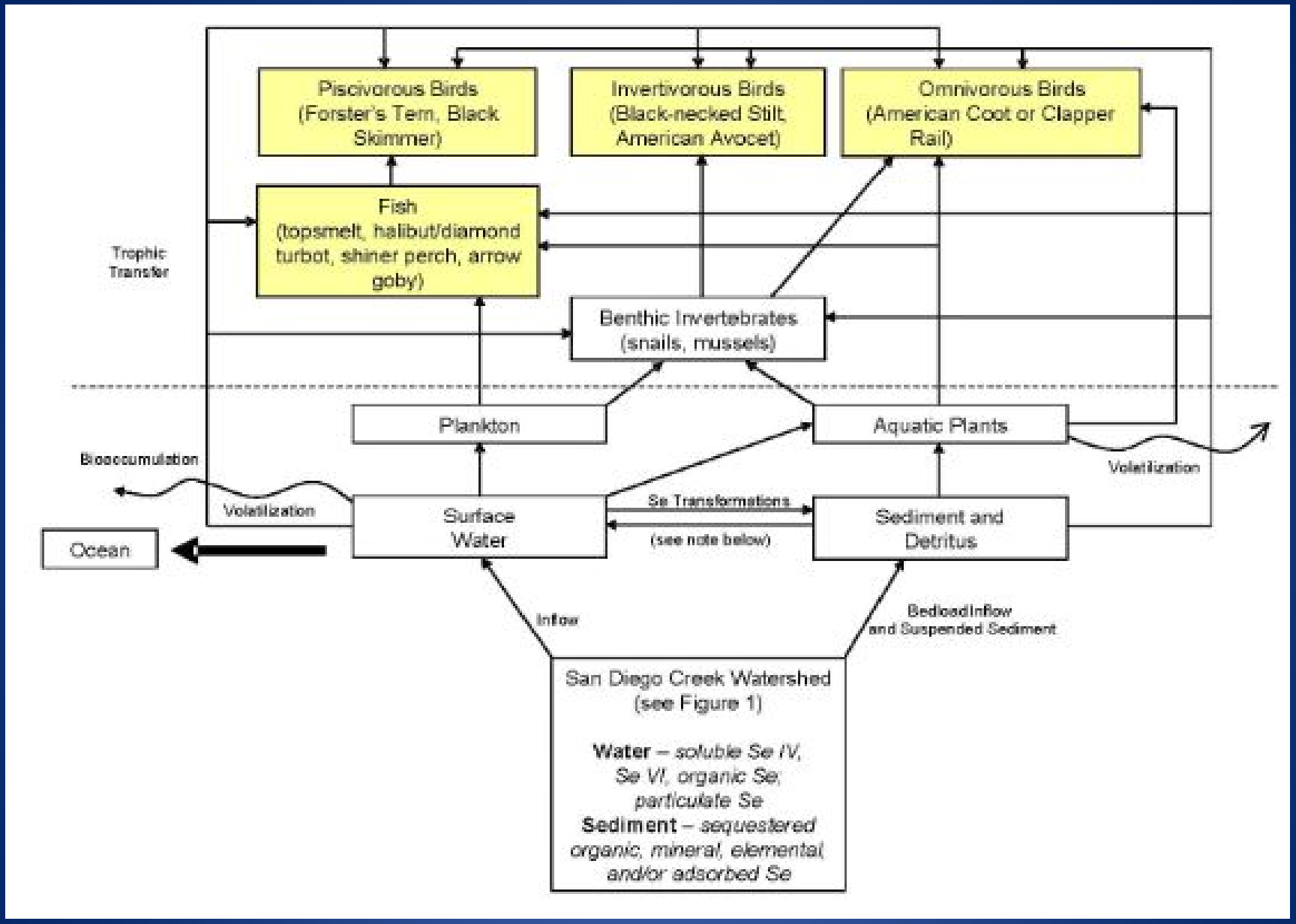


Figure 9-4: Conceptual Model, Exposure Pathways, and Food-Web Relationships for Saltwater Habitats in the Newport Bay Watershed (Source: CH2MHill, 2009b).

Newport Bay Biodynamic Model

Input parameters:

- K_ds (already discussed)
- Tissue targets/SSOs ($C_{organism}$)
  - Fish (whole body) = 5 µg Se/g dw
  - Bird egg (tissue only) = 8 µg Se/g dw
- Trophic transfer factors
  - Fish or invertebrate to bird eggs (TTF_{bird}) = 1.4*
  - Prey fish to predator fish (TTF_{fish}) = 1.1
  - Invertebrate to fish ($TTF_{preyfish}$ or TTF_{fish}) = 1.1
  - Particulate to freshwater invertebrate ($TTF_{invertebrate}$) = 2.8
  - Particulate to saltwater water column invertebrate ($TTF_{invertebrate}$) = 2.05
  - Particulate to saltwater benthic invertebrate ($TTF_{invertebrate}$) = 4.5

* As recommended by CH2M Hill