

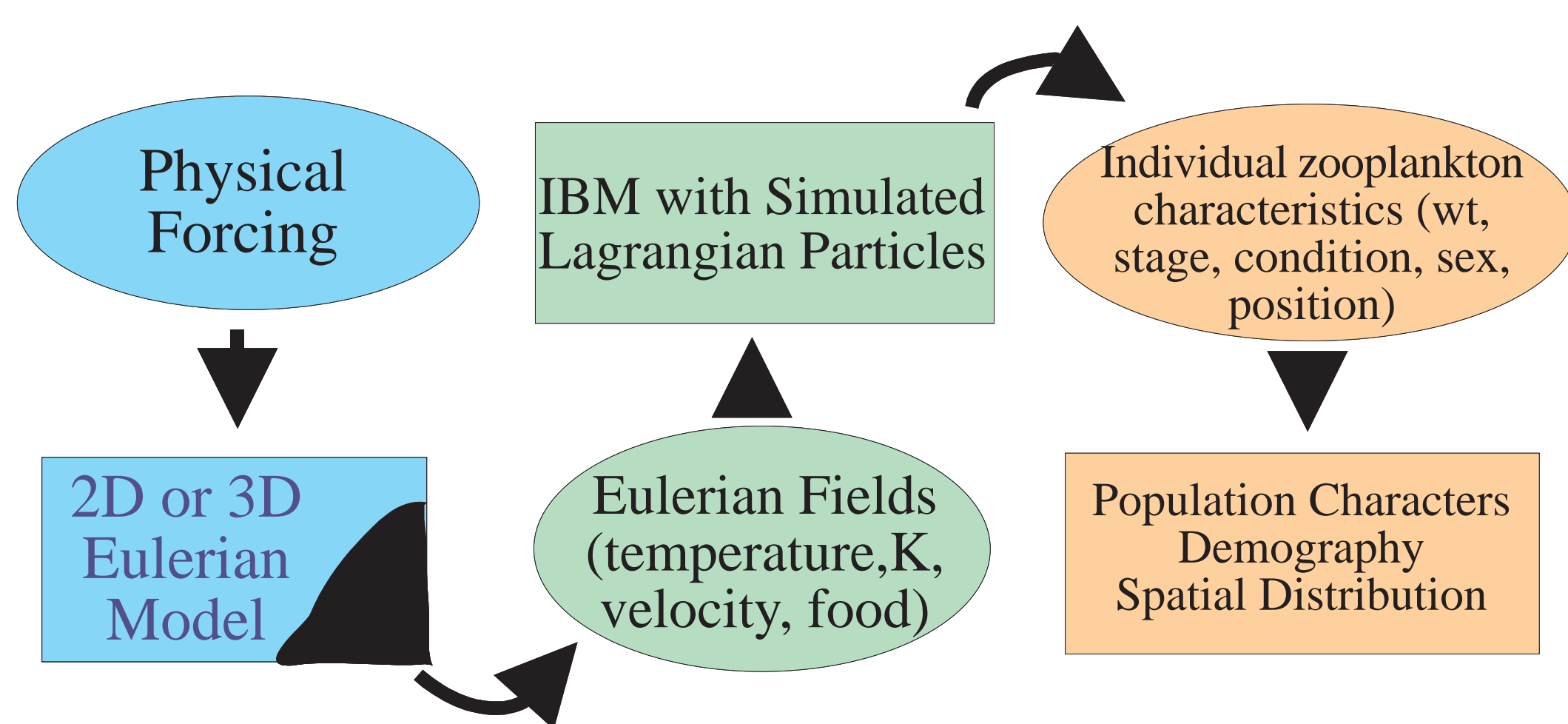
# Spatial and Temporal Distributions of Mesozooplankton in Idealized Models of Coastal Upwelling Ecosystems

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## Abstract

As part of a U.S. GLOBEC funded effort in the Northeast Pacific (NEP), we have been developing coupled biophysical models that link 1) physical circulation, 2) lower trophic level ecosystems, and 3) higher trophic levels, in wind-driven upwelling systems. Here we present results of some two and three dimensional simulations that use idealized coastal geometry and bathymetry, simple physical forcing, and relatively well understood lower trophic (NPZD) ecosystems models. We model the spatial and temporal distributions of higher trophic levels using individual based models (IBMs) in order to account for physiological and behavioral effects that cannot be easily modeled in the more traditional Eulerian framework. These idealized simulations are a crucial first step toward achieving more realistic simulations with fully coupled biophysical models using observed spatially and temporally varying forcing (wind, surface fluxes) and realistic coastal geometry and bathymetry.

## Modeling Approach (Eulerian-Lagrangian Coupling)



## Conclusions

- 1) It is rare that individual members of populations can be justifiably aggregated into a single state variable representing abundance.
- 2) To accurately describe population dynamics we need to consider the specific processes and histories of individuals. For coupled physical-biological processes in the ocean, this means particle tracking models (PTMs) forced by Eulerian fields (from models or observations). Feedback to Eulerian fields is difficult and simulating realistic densities and density-dependence is awkward and expensive.
- 3) Need to consider diffusive processes in PTMs. Advective transport alone gives only a part of the story, and often gets it wrong.
- 4) Individual behavior-physics interaction can be as important in determining transports as advection and diffusion.

### i-State Distribution and i-State Configuration Models

- fundamental tool of demographic theory
- produce differential or difference equations
- examples:
  - NPZ+ models
  - Lotka-Volterra predator-prey models
- Assumes: global mixing, and few dimensions (e.g., age, size) control dynamics

- aka Individual Based Models
- Each individual has a vector of characteristics associated with it
- Examples:
  - \* Body Size (wt, length)
  - \* Age
  - \* Reproductive Condition
  - \* Nutritional Status
  - \* Behavior

**System State = History + Present Environment**

**= f (history)**

**“The past of the system affects its response to the present.”**  
 Caswell and John (1992)

#### i-State Configuration Advantages

- Biology is **mechanistically explicit** (not hidden in differential eqns)
- Biol-Chem-Physical interactions are clearly detailed
- Individual is the fundamental biological unit; **natural and intuitive** to model at that level, rather than at the population level
- Permits explicit inclusion of an individual's **history and behavior**
- **Spatial heterogeneity** interactions ‘easily’ handled

#### i-State Configuration Disadvantages

- Difficult to implement **feedback** (e.g., across multiple trophic levels, prey depletion)
- Difficult to simulate **realistic abundances** (large numbers of individuals)
- Difficult (impossible?) to simulate **density dependence**
- Many and complex biological/biochemical processes for individuals impose an extensive **computation penalty**

### A Simple i-state Distribution Model

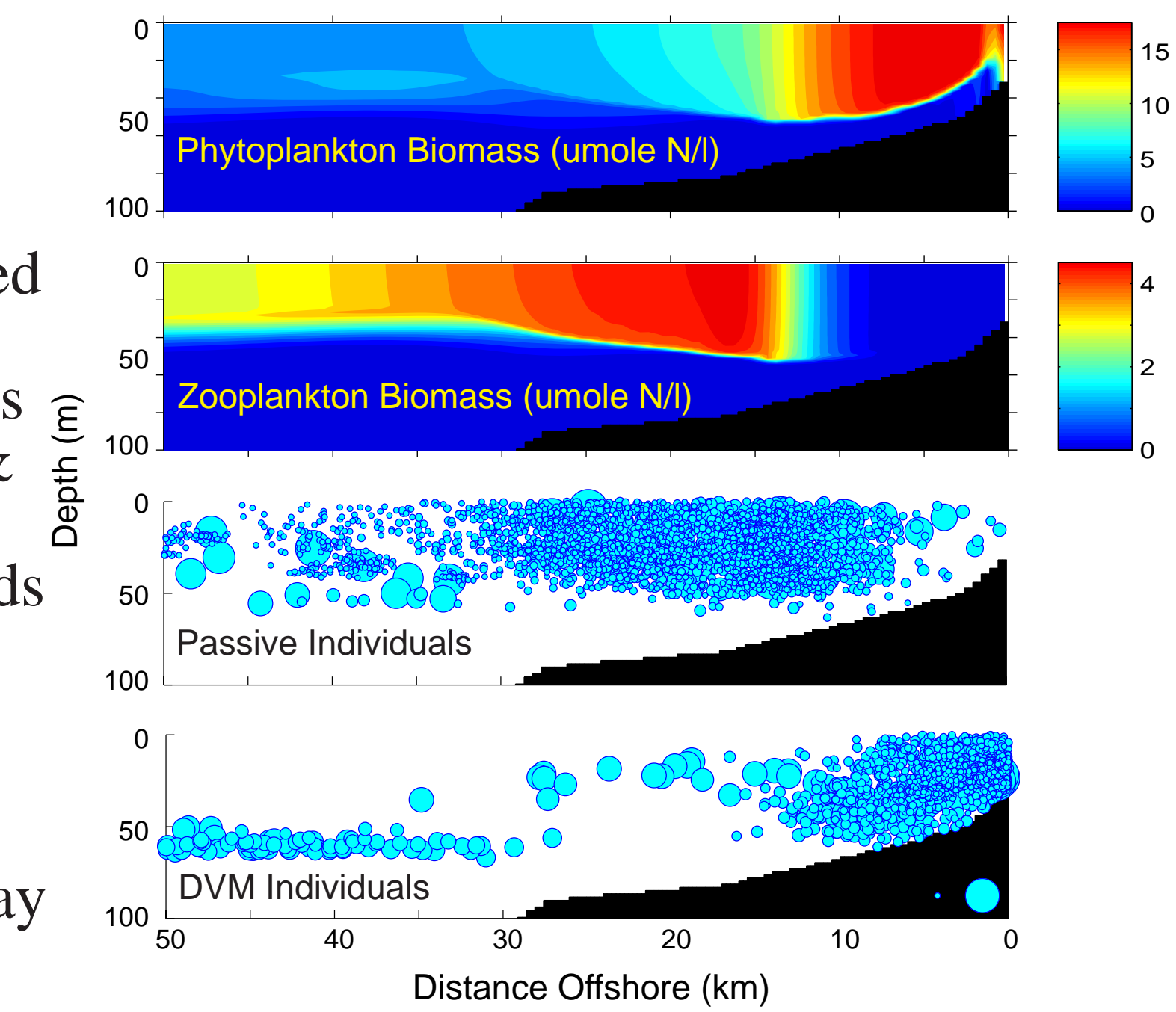
#### Nutrient - Phytoplankton - Zooplankton Model (after Franks et al. 1986)

Uptake (U) = f(N, light)  
 Grazing (G) = Ivlev w/o threshold  
 Egestion (E) = fraction not assim.  
 Mz = Mortality of Z; immediate remineralization  
 Mp = Mortality of P; immediate remineralization

Assumes: all Z at a given locale are identical

## 2D Simulations

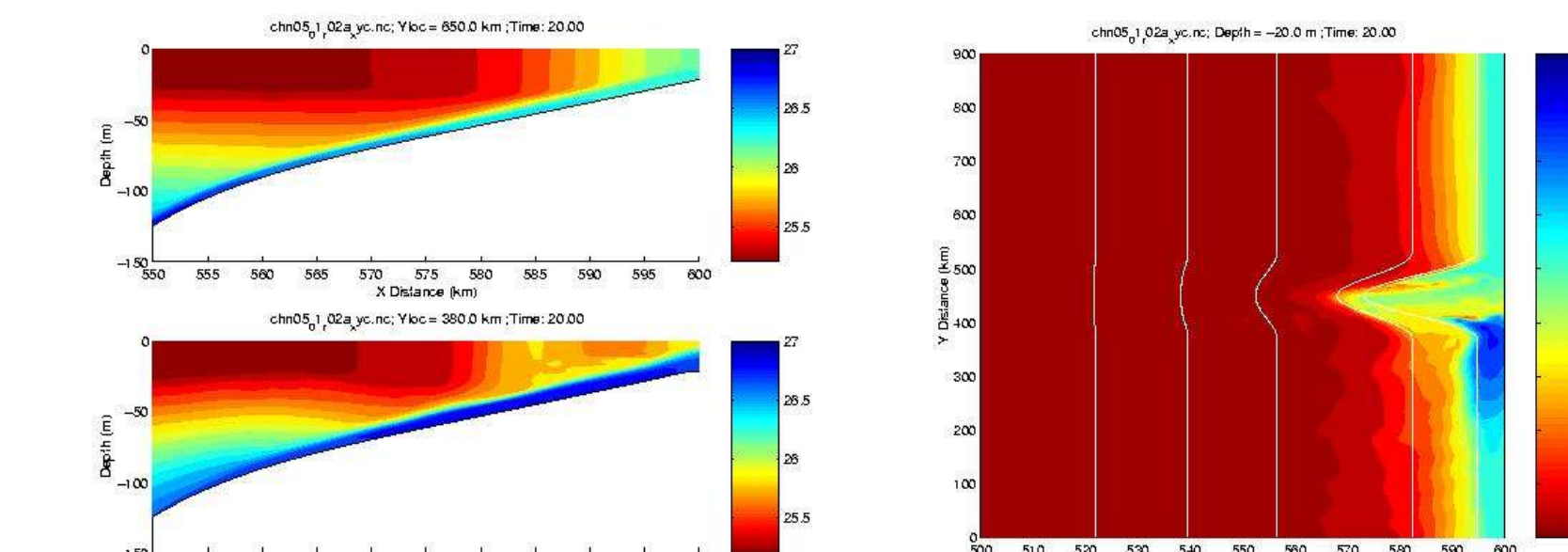
- Physical Model includes KPP surface mixing, bottom mixing; forcing by temporally varying idealized winds.
- Franks et al. NPZ model; 120 day simulation
- Stored snapshots of physics and ecosystem used as input to a PTM-IBM simulation of passive and ontogenetically dependent DVM copepods
- IBM is bioenergetics based model of growth & reproduction; mortality is stage specific, but location independent; swimming speed depends on light, ambient food, satiation.
- IBM IC's: 5000 randomly located individuals, all identical in weight (usually 10 ug C)



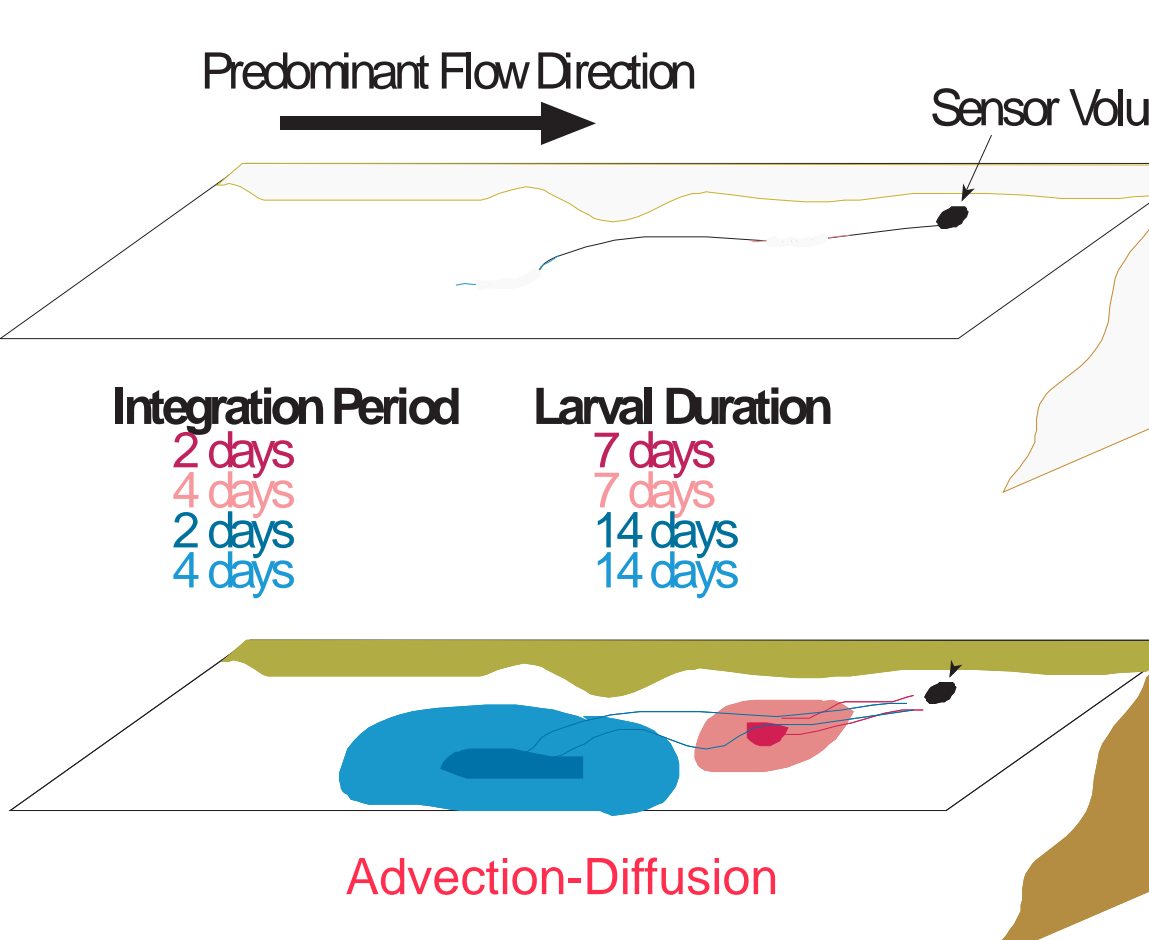
Shown at right are Eulerian P and Z fields for day 30, and IBM particle locations and weights for day 40 from a run with passive particles and a run with DVM particles. Z in Eulerian model are “passive” and have similar spatial pattern (low nearshore, higher offshore) as the IBM simulation with passive particles. Ontogenetically dependent DVM in the IBM results in a completely opposite spatial pattern (high nearshore, rare offshore).

## 3D Simulations

- 3D Spectral Element Ocean Model (SEOM)
- Idealized bank and cape geometries
- No ecosystem model
- Stored snapshots of physical fields used to explore particle trajectories
- Advection-only; Advection-Diffusion; Advection-Diffusion-Reaction Cases



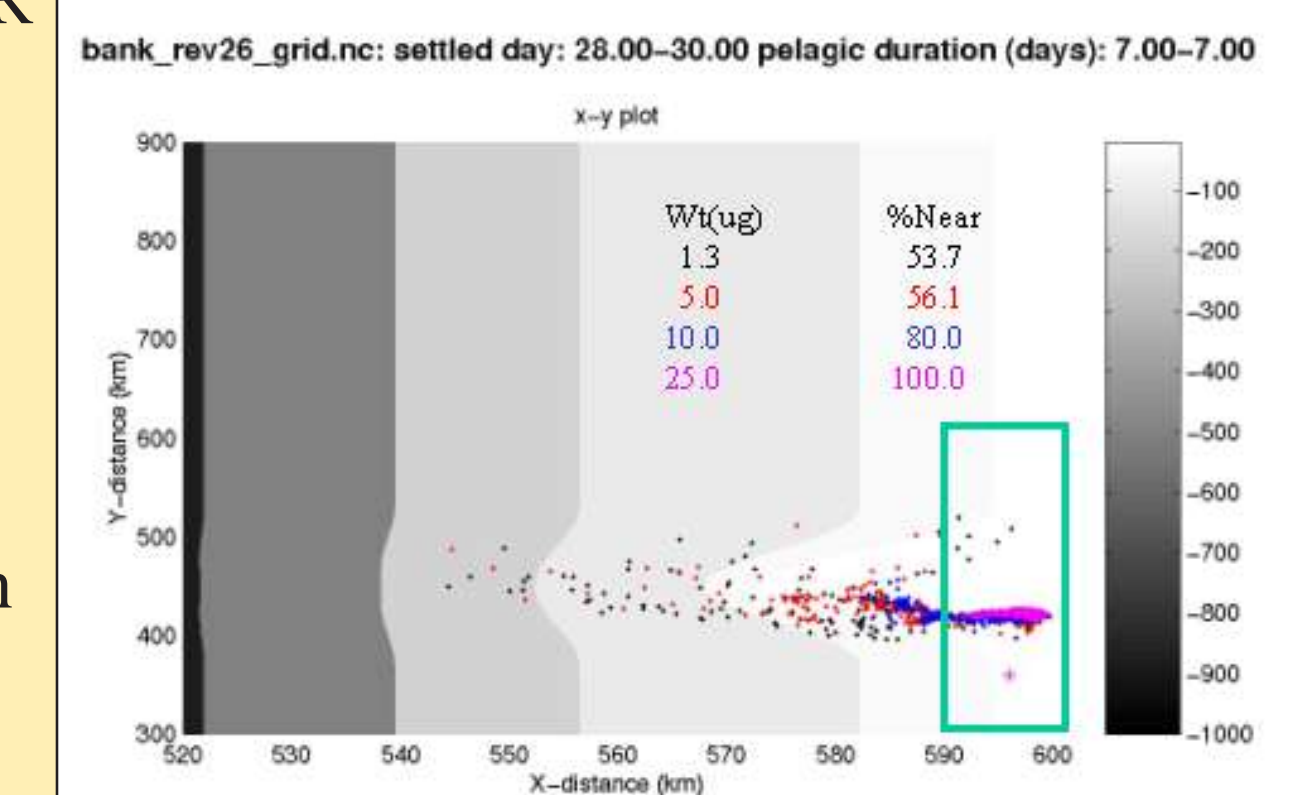
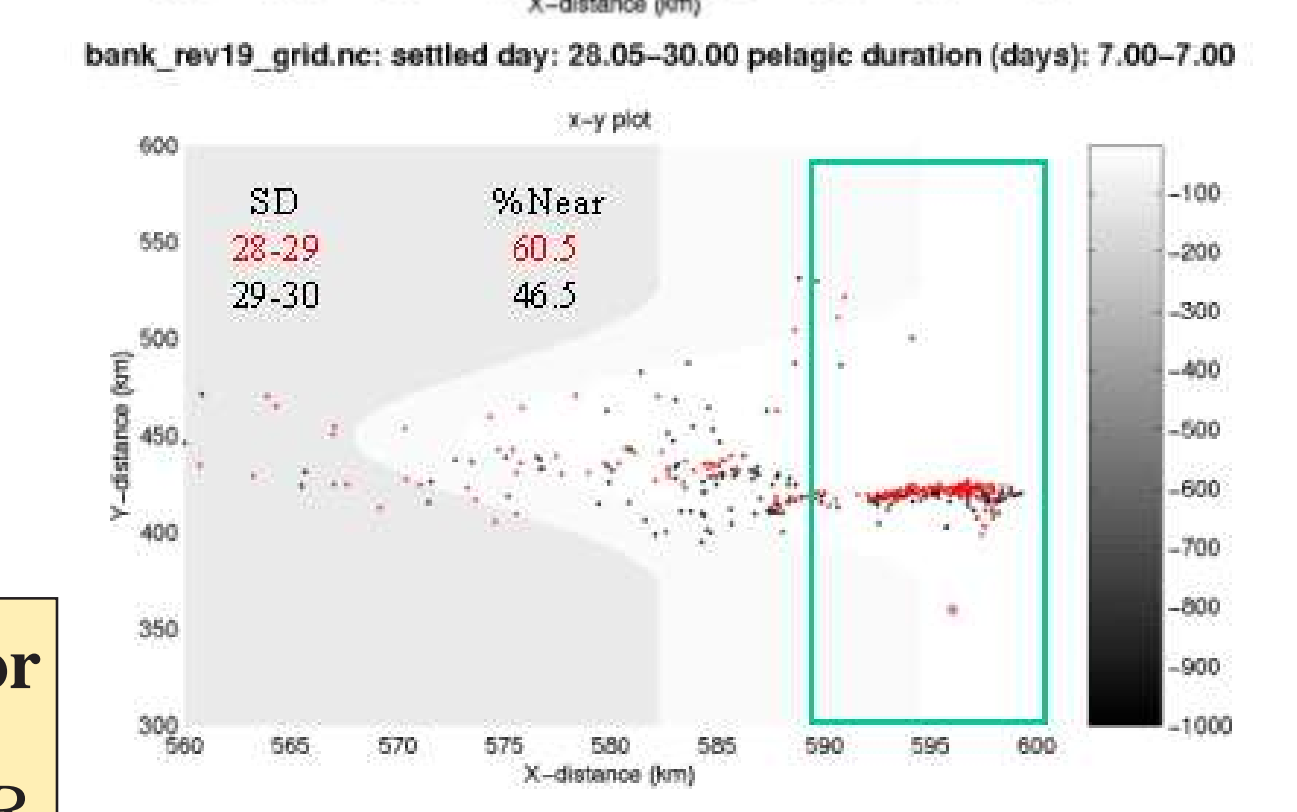
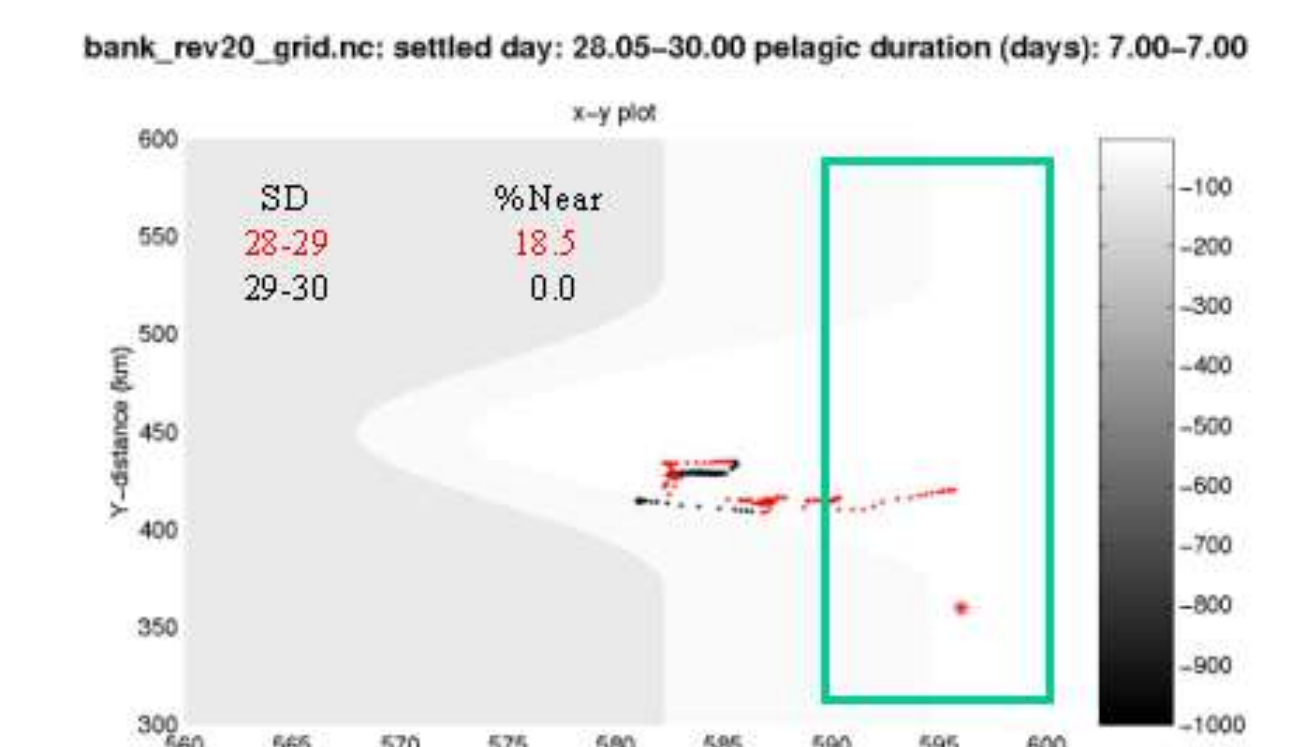
Schematic of Source Region Identification Assuming Fixed Sensor Location with Advection Only



### % Nearshore 7 Days Prior to Settlement

Wt	A	AD	AR	ADR
1.3	9	53	7.5	54
5.0			20	56
10			67	80
25			100	100

Wt in ug C/ind  
 A=Advection  
 AD = Advection-Diffusion  
 AR = Advection-Reaction  
 ADR = Adv.-Diff.-Rxn



Green box highlights region within 10 km of shore (=Nearshore)