

The Role of Simulation Tools

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Why use simulation models?

Description

"...the study of the patterns of nature...

Dynamics

...how they change in space and time...

Processes

...how those patterns came to be..."

Sharon E. Kingsland (1985) "Modelling Nature

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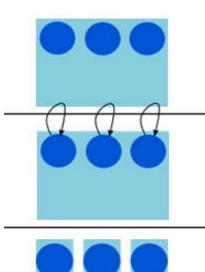
Simulation models as assumption busters

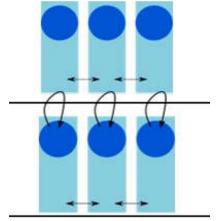
Using simulation tools to explore

"...how those patterns came to be..."

as

- Opaque thought experiments
- Assumption analysers
- Create quantitative scenarios
- Design experiments/monitoring programmes
- Guide further research







Models of adult tuna movement

Many of the observed patterns in the data we have are a function of movement

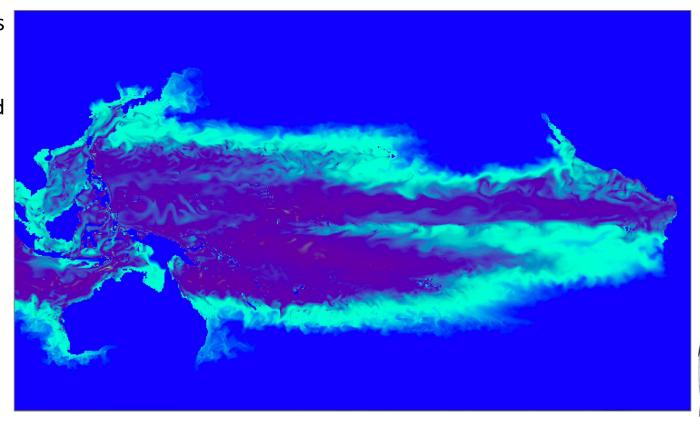
Two examples of models that can potentially help us understand the effect of movement on stock structure

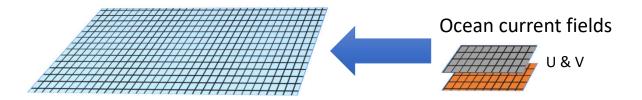
- SEAPODYM Ecosystem and population dynamics model
- Ikamoana Individual-based movement model



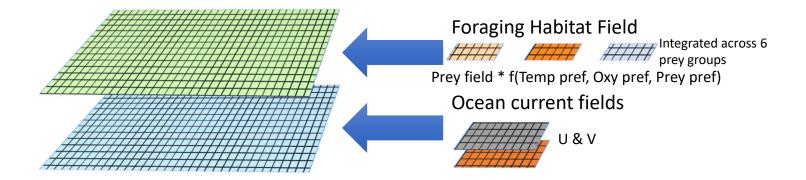
Advection-Diffusion-Reaction Ecosystem Model

- Simulates population dynamics of marine species
- Density of animals represented by tracer
- Regular grid spatial structure
- Equations govern the change in density/biomass
- Estimated using tagging and fisheries data

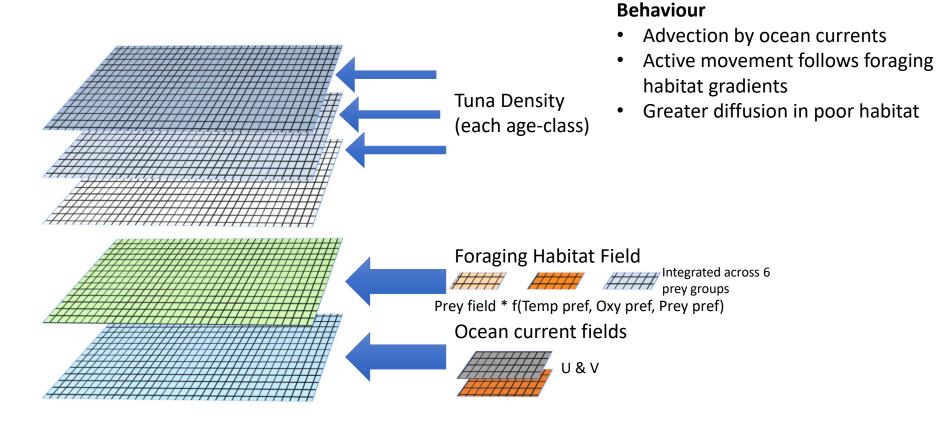




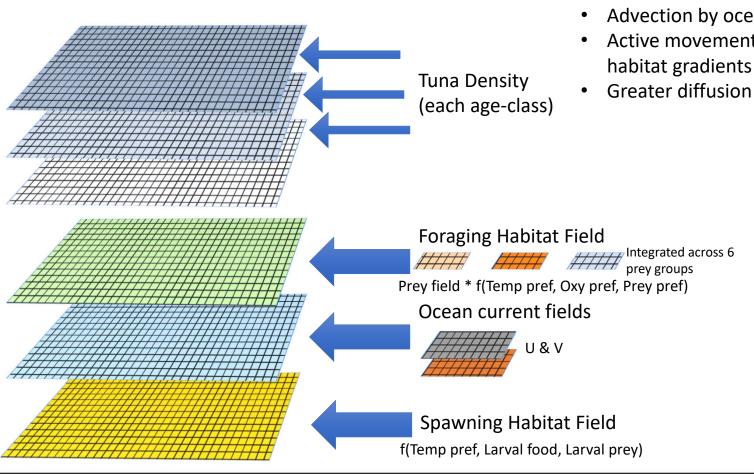








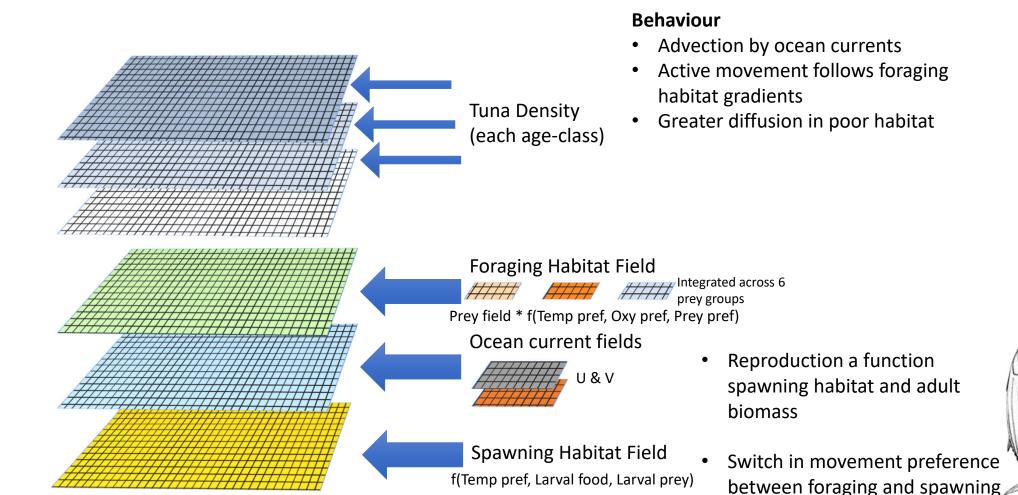




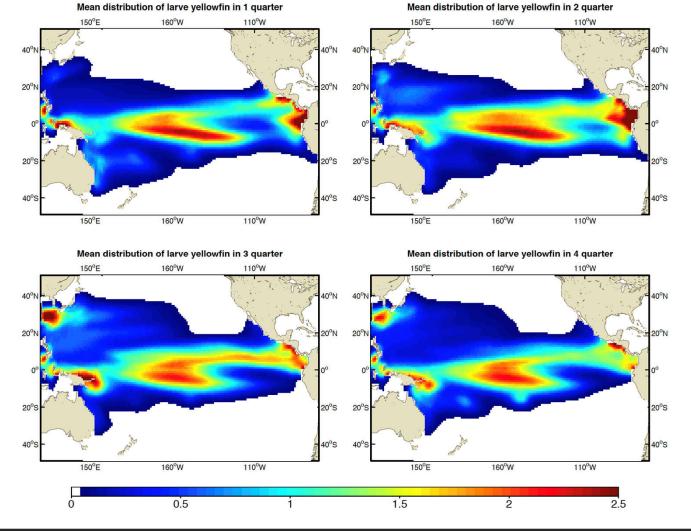


- Advection by ocean currents
- Active movement follows foraging habitat gradients
- Greater diffusion in poor habitat





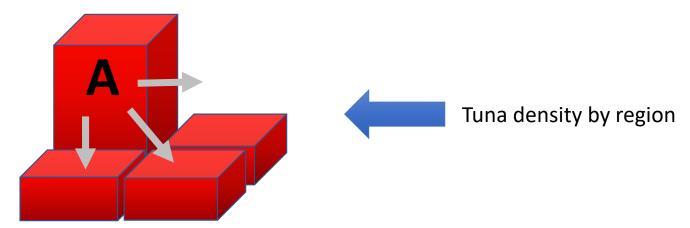
Simulate potential spawning grounds/successful spawning areas





Tracking the movement of biomass in SEAPODYM

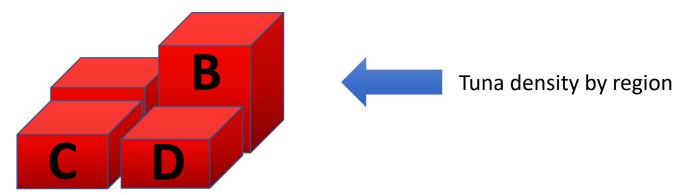
Broad scale connectivity





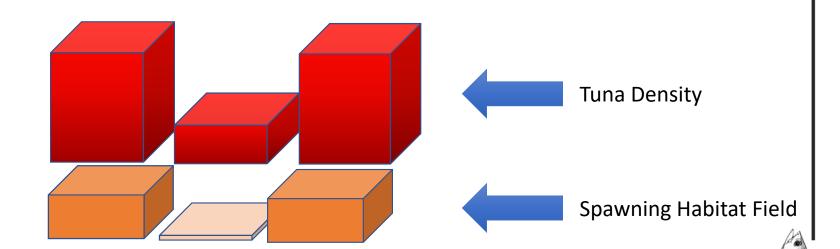
Tracking the movement of biomass in SEAPODYM

- Broad scale connectivity
- Where do fish move over some time-period?



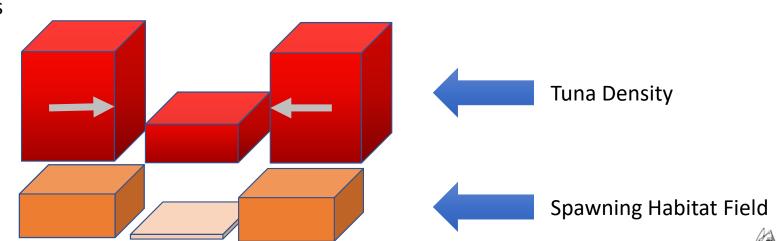


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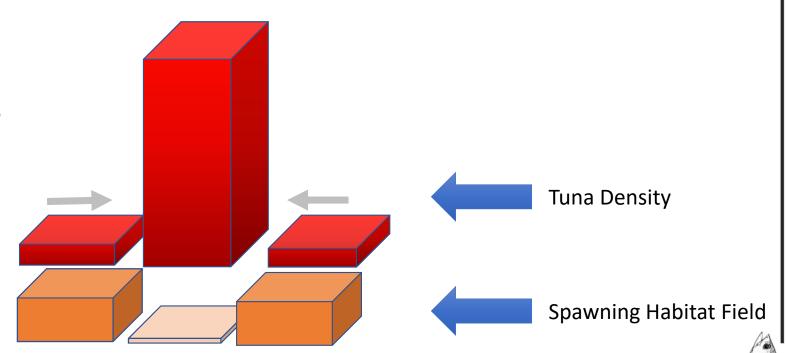
Tracking the movement of biomass in SEAPODYM

 Adult biomass contributes to larval recruitment



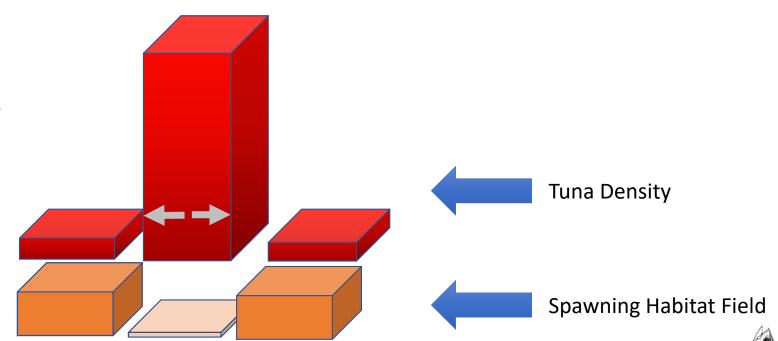
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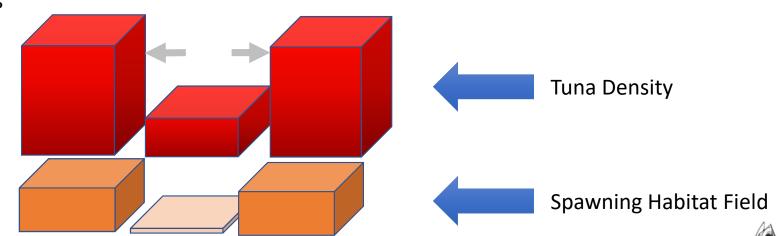
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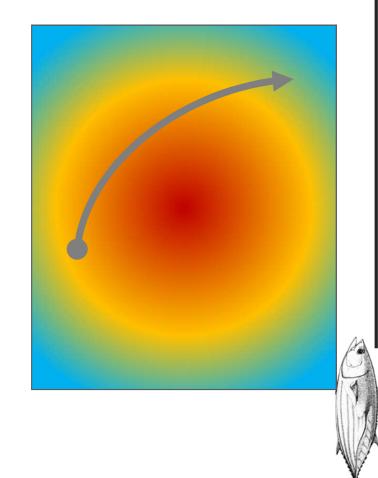
Tracking the movement of biomass in SEAPODYM

- Adult biomass contributes to larval recruitment
- Biomass advects/diffuses through domain
- Cannot track conditional pathway of tracer representing the biomass



Questions regarding the tracking of biomass at the individual level

- Connectivity between regions- source/sink dynamics?
- Differing growth rates of larvae and young fish
- Where might sampled YOY have come from at time-of-spawning?
- Mixing of tagged fish with the untagged population
- Mixing of genetically distinct sub-populations
- Accretion of isotopes/trace metals during lifetime of an individual



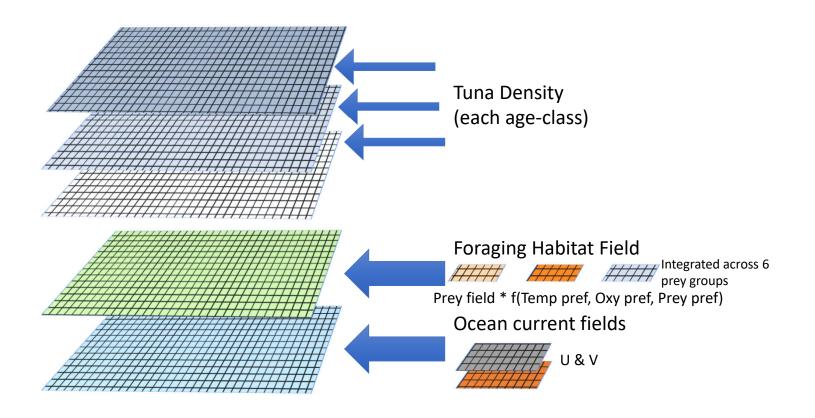


Individual-based Kinesis, Advection and Movement of Ocean ANimAls

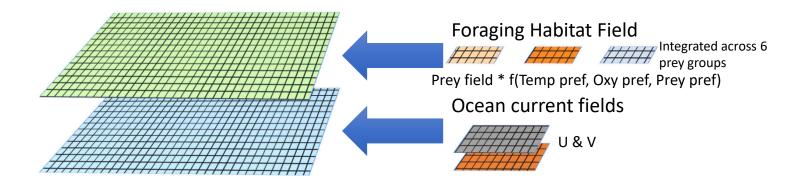
- Extends a recently developed Lagrangian particle simulator (Parcels) which **advects** individuals using physical forcing
- —Adds non-directional **kinesis** movements, such as Lagrangian diffusion, random walks, internal states of individuals etc.

- —Active **movements** that cause individuals to follow habitat gradients, or move in response to other individuals, environment etc.
- Not a population dynamics model!

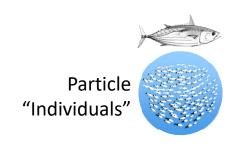




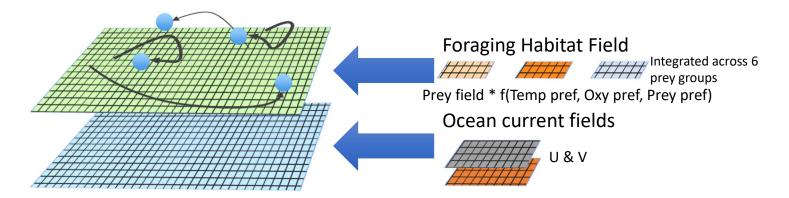




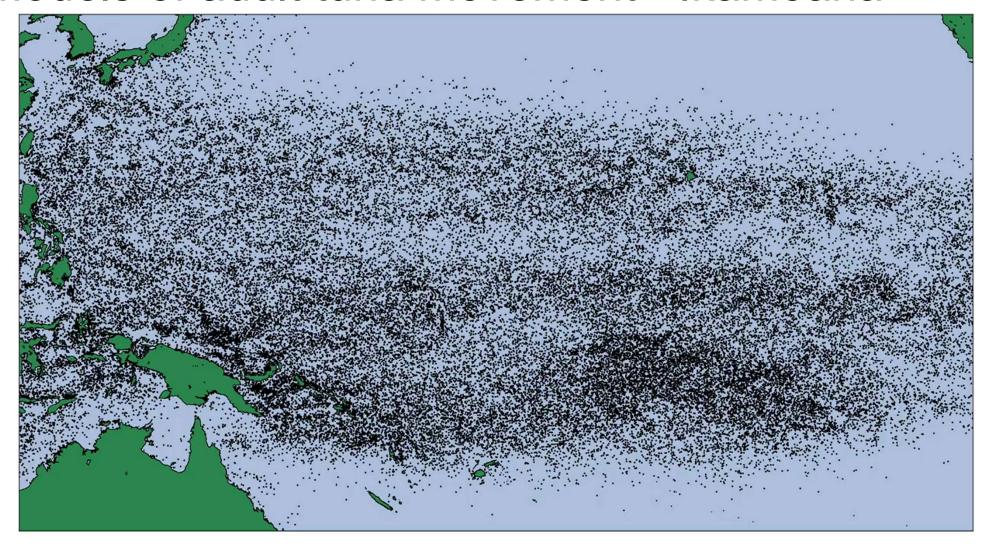




- Number of individuals in school
- Continuous age (and mortality)
- Continuous position
- Recorded trajectories
- Memory of fields sampled (e.g. spawning habitat index)
- Variable behaviours (e.g. those estimated by SEAPODYM)









Quantifying connectivity through stock assessment regions

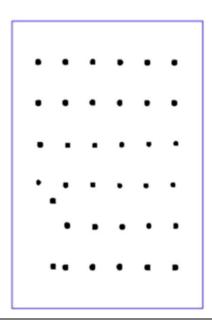
- Transfer rates under a given behavioural scenario
- Use individual-scale pathways

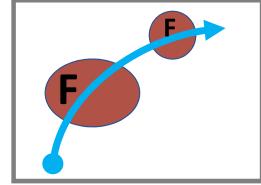
 Early origins of fish recruiting into purse seine fishery in each stock assessment regions



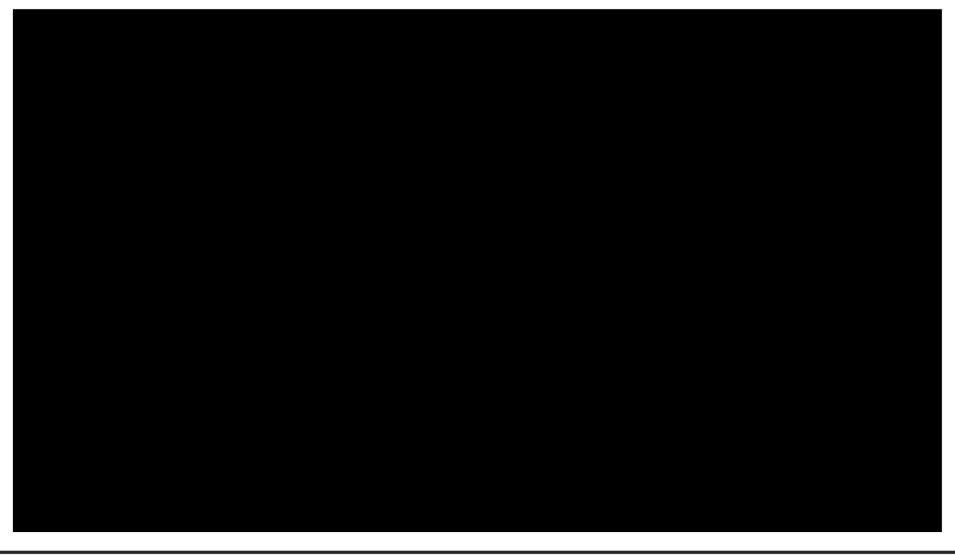
Quantifying tag mixing

- Probability of capture for tagged fish vs untagged fish
- Changes across release scenarios
 - Temporal
 - Location
 - Release size
- Examine spatially varying F along pathways of individuals
- Compare the F experienced by a whole cohort in a region with that of a 'tagged' subset





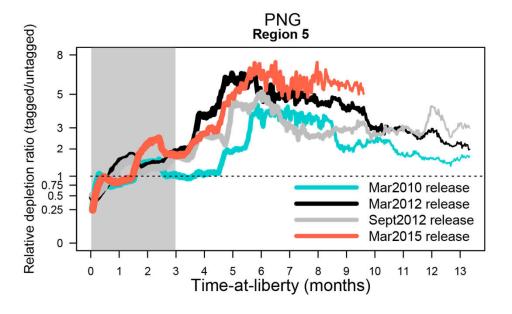


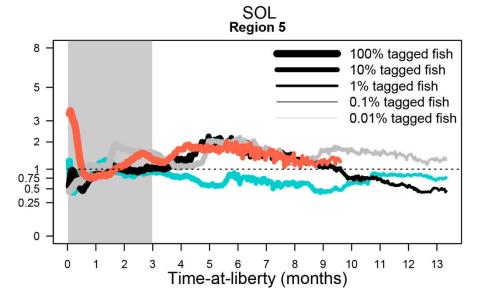




When we compare with a tagged subset, originating from a specific location

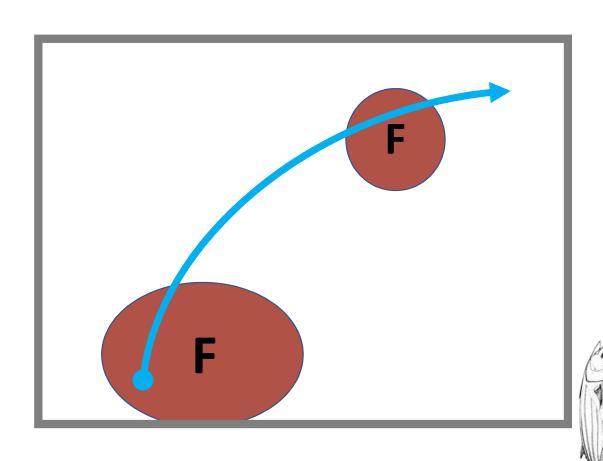
- Difference in depletion due to fishing highly variable through time
- Depends on time/location/region
- Suggests implications for how we might use tagging data from different releases







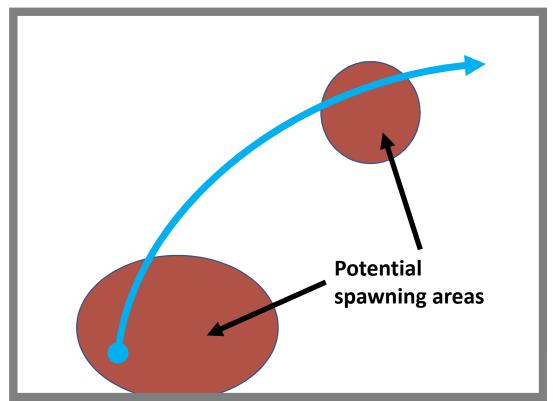
Tag mixing simulations an example of testing a movement hypothesis on capture probability



Tag mixing simulations an example of testing a movement hypothesis on capture probability

Could similarly use:

Spawning areas

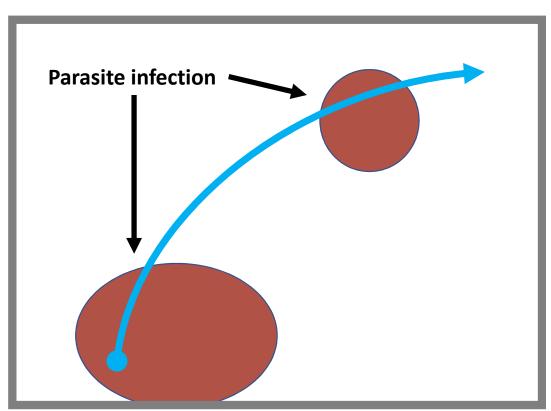




Tag mixing simulations an example of testing a movement hypothesis on capture probability

Could similarly use:

- Spawning areas
- Parasite infection sources

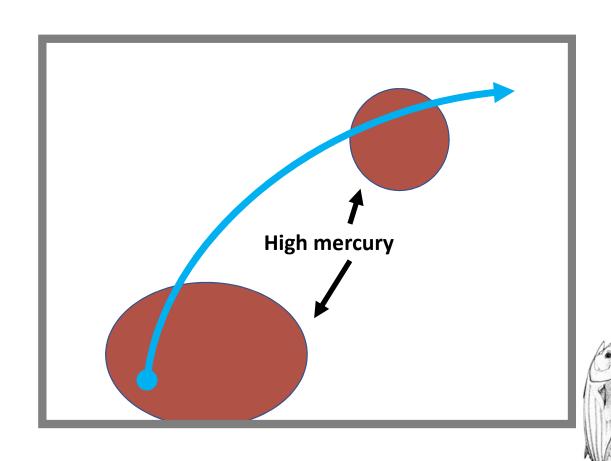




Tag mixing simulations an example of testing a movement hypothesis on capture probability

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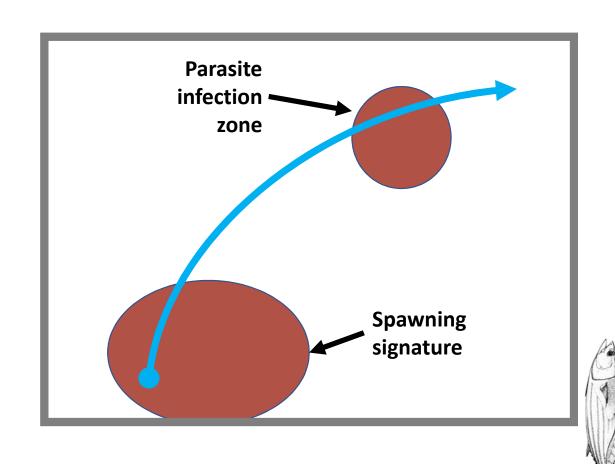
- Spawning areas
- Parasite infection sources
- Microchemistry accretion



Tag mixing simulations an example of testing a movement hypothesis on capture probability

Could similarly use:

- Spawning areas
- Parasite infection sources
- Microchemistry accretion
- Combine observed patterns



Points for discussion

- 1. Given these, and other tools, are there specific hypotheses we would like to test in a movement model?
 - Specific observations
 - What are your hunches?
- 2. Is there any consensus on bracketing the extremes of behavioural hypotheses?
 - All fish are random walkers one extreme
 - Strong, natal homing to fixed, discrete spawning areas another extreme
- 3. Where can we constrain hypotheses from multiple datasets/patterns?
 - Where do data overlap spatially and temporally?
 - Which patterns are most clear?
- 4. Are there simulation tools to test hypotheses regarding mechanisms other than movement?

