

# Individual-based Models

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- What do we need models for?
- What classes of models exist?
- What are individual-based models (IBM's)?
- Single-species population models for zooplankton:
  - General principles
  - Examples

# What do we need models for?

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Interpretation of current status of a population:  
*Hindcasting.*

Prediction of future development: *Forecasting.*

Identification of critical processes within the system. - Consideration of possible outcomes of changed environmental conditions: *physical forcing*, climate change.

# What classes of models exist?

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## Transport models (Circulation models):

Aspect physical oceanography dominates; current effects, water mass transport in detail. Biological oceanography in less detail if included.

## Population models:

Biological questions analyzed in detail. Physical oceanography in less detail if included.

## Ecosystem models of physical-biological interactions:

Combine physics and biology.

# What classes of models exist?

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Aspect physical oceanography dominates; current effects, water mass transport in detail. Biological oceanography in less detail if included.

## Population models:

Biological questions analyzed in detail. Physical oceanography in less detail if included.

## Ecosystem models of physical-biological interactions:

Combine physics and biology: E.g. current fields (advection), vertical mixing, horizontal mixing, fronts (T/S gradients), gradients in light intensity. Growth of the individual, life history, reproductive rates, mortality (incl. predation), behavior.

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# Three types of single-species zooplankton population models

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## (1) NPZ models

*Strengths:* One or few variables, useful for flux studies

*Weaknesses:* Not useful for questions related to single populations

## (2) Structured population models, Eulerian approach

(concentration based, spatially explicit)

*Strengths:* Includes specific stage- and size-dependent biol. processes

*Weaknesses:* Many variables. Lack of information on functional responses, mortality/ predation processes, behavior

## (3) Lagrangian approach: individual-based models

*Strengths:* Integration of biol. Processes in detail, of individual variability. 'Easy' coupling with physical models

*Weaknesses:* Validation needed for many biological parameters,.  
Weak in representing entire trophic environment, complex models.

# What are individual-based models?

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Simulations based on the overall consequences of processes involving individuals of a population. In an IBM, the characteristics of each individual are tracked through time. This stands in contrast to modeling techniques where characteristics of the population are averaged, and changes in these averages are being compared.

(SGPBI report 2002)

# IBM's

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(Van Winkle et al. 1993:) Benefit of an IBM is that it provides a framework within which researchers conceptualize the natural processes, design their research, analyze results, and combine empirical studies and modeling in a synergistic manner.



# Elements of an IBM:

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**Variables** - Two kinds of pertinent variables in a model, i.e. quantities that vary in time and space:

- 1) *Internal variable = state variables*, related to governing processes within system: e.g. developmental stage, trophic level.
- 2) *External forcing variables*, e.g. light, temperature, food concentration.

# Elements of an IBM:

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**Functions** - Identify mathematical functions of interactions, e.g. functional response curves.

Mathematical description of the system. If the system is specified by the values of  $n$  state variables, the mathematical model of the system requires  $n$  equations. Equations are built by introducing rules for the interactions between the variables of the system (state variables) and variables outside the system (forcing variables).

# Elements of an IBM:

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Many models consist of time-dependent differential equations. The state of the system at time  $t$  depends on the state at a previous time  $t-dt$  and upon the conditions that prevailed and determined the change since  $t-dt$  up to but not including the instant  $t$ .

# What does single-species population model (IBM) for zooplankton require?

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The model is to provide a link between individual processes and demographic processes.

What do you need to characterize a population?

# What does single-species population model (IBM) for zooplankton require?

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## Demographic information (Pop.)

### Processes (Pop.)

- Population growth rate
- natural mortality
- predation

### Variables (Pop.)

- Age structure; number of individuals within a developmental stage

# What does single-species population model (IBM) for zooplankton require?

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## Information on the individual (Ind.)

### Processes (Ind.)

- Ingestion, assimilation, excretion
- Respiration
- Growth rate

### Variables (Ind.)

- Body size, body weight
- Developmental stage/ gonad development
- Nutritional state (e.g. lipid content)

# Example of a life cycle: *Calanus finmarchicus* on Georges Bank

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## **Diel seasonal migration:**

Late winter: Overwintering *Calanus* ascend from depth to surface.

Over spring and summer, two generations on the bank.

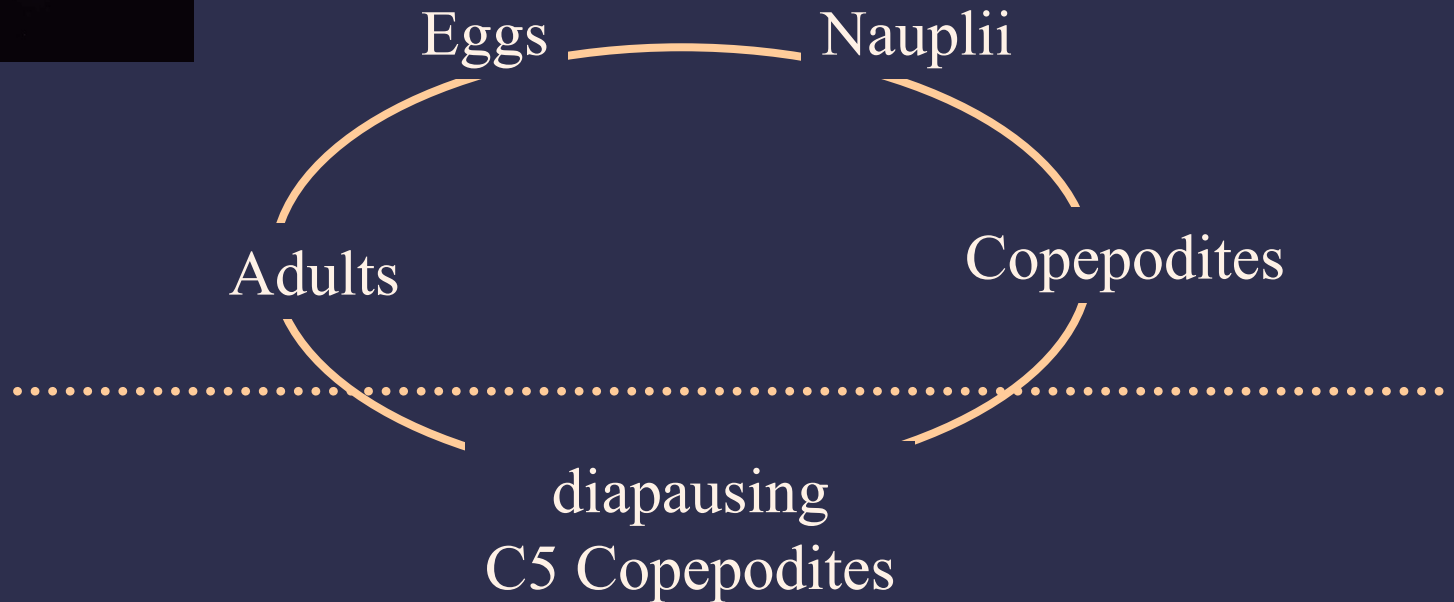
Late summer/ fall: *Calanus* C5 (5. copepodite stage) descend to depths > 200 m and enter diapause, a resting stage.

Fall/winter: diapause.

# Life cycle of *Calanus finmarchicus*:



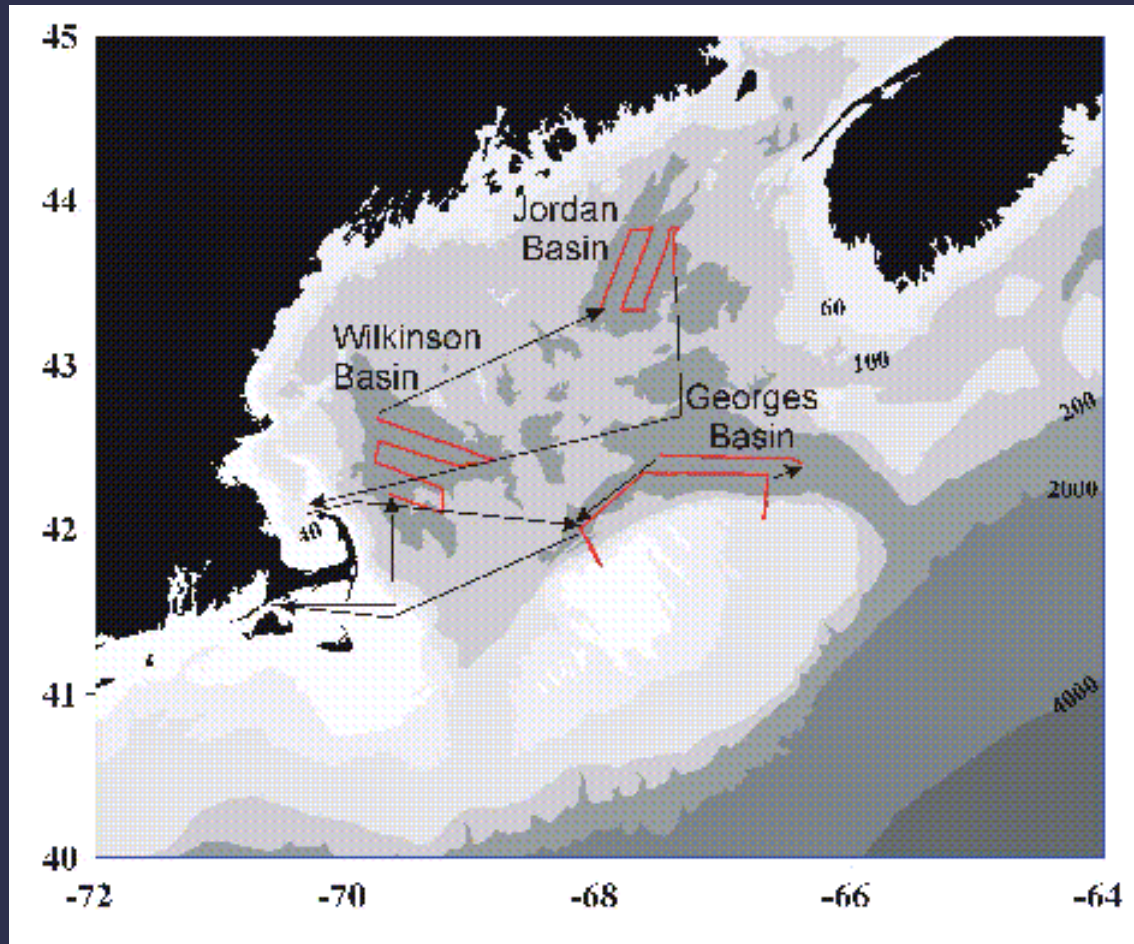
**Gulf of Maine / Georges Bank  
(Early spring through early summer)**



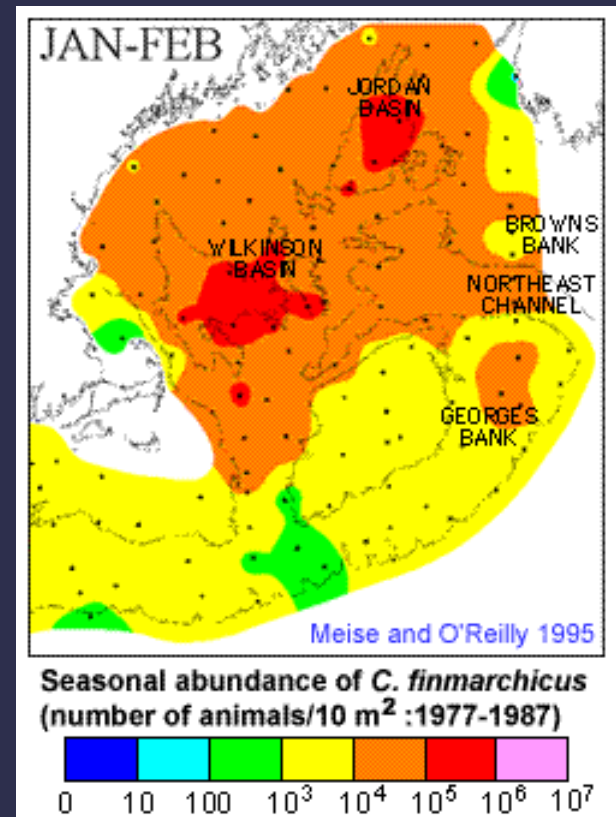
**Deep Basins, Continental Slope and Offshore  
(Late summer through winter)**



# *Calanus finmarchicus* on Georges Bank



An Eulerian model:



(This movie is not based on an IBM)

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# Building an IBM

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Populations are treated as collections of individuals, each of which is represented by a set of variables that stores its “*i*-state” (e.g. age, size, weight, reserves, etc.).

These variables are grouped in a data structure that either represents a single individual, or they are grouped in arrays (e.g. one array with all the ages of the individuals).

The *i*-state of an individual changes as a function of its current *i*-state, the interaction with other individuals, and the state of the local environment.

# Building an IBM

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Processes on the level of the population as a whole are inferred by the combined contributions from the individuals.

The model starts with a given number of defined individuals in the initial population within the initial environmental stage. It then monitors the changes in each individual that occur through internal processes (biological) or external forcing (biological or physical).

# Example of a copepod IBM

(without behavior, without physics)

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## Purpose of the model:

To examine biases in estimating production from copepod cohorts.

## Three variables for each individual:

(1) Weight, (2) Developmental stage, (3) Specification dead / alive.

50,000 ind.– each with initial weight drawn from a lognormal distribution.

Weight:  $W_i(t) = (1 + G_i) W_i(t-1) ,$

with  $G_i$  = growth rate from random normal distribution.

When the weight exceeded a critical value, advancement to new developmental stage:

Stage:  $Stage_i(t) = Stage_i(t-1) + 1$

# Example of a copepod IBM

(without behavior, without physics)

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Mortality  $M_i$  was assumed to be constant for each stage, but could vary between stages.  $M_i$  determined whether or not an individual survived to the next stage.

Any weight gained by individuals that were alive at the end of the simulation was accumulated into “growth production”, whereas any weight gain by individuals that died was combined into “lost production”. Total production was the sum of both.

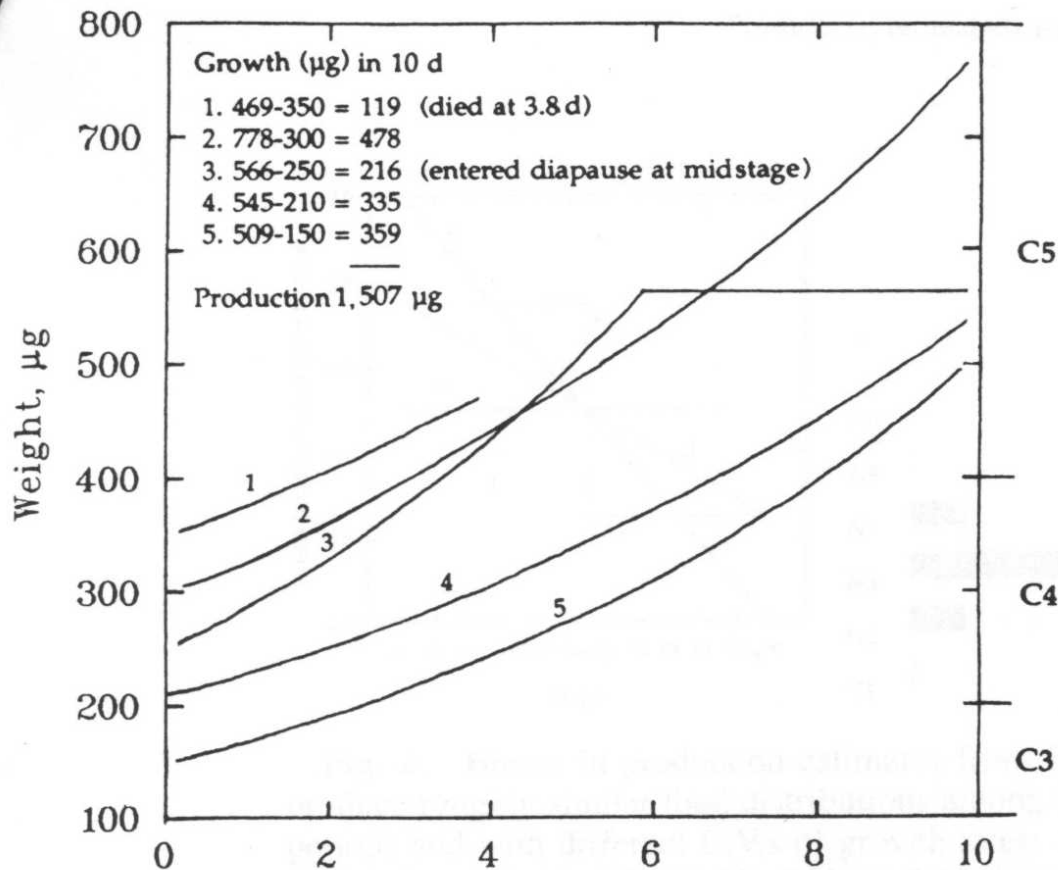


Fig. 1. The structure of the model used to simulate production.

Example of 5 individuals in the model. They move into a new stage once they reach twice the weight of the previous stage.

McLaren (1997)

With the model different simulations were run to investigate whether variances in the initial weights and growth rates of the individuals influenced the population's production. Only extreme size dependence of growth rates or mortality had an effect of biasing calculations based on cohorts.

# Example of a copepod IBM

(without behavior, without physics)

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IBM of *Metridia pacifica* with the basic equations like in McLaren (1997), but with greater detail on the physiological functions. Individual growth calculated as assimilation less respiration. With inter-individual variation in physiology.



# Introduction for part II

Comments on reading assignment:

Batchelder, H.P. & Miller, C.B. (1989), Ecological  
Modelling 48: 113-136

# Literature sources:

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Carlotti, F., Giske, J. & Werner, F. (2000). Modeling zooplankton dynamics. *In*: Harris, R.P. et al. (eds.) Zooplankton Methodology Manual. Academic Press, San Diego.

McLaren, I.A. (1997). Modeling biases in estimating production from copepod cohorts. *Limnol. Oceanogr.* 42: 584-589.

Report of the Second Meeting of the ICES Study Group on Modelling Physical/Biological Interactions (SGPBI), 2002.

End Part 1