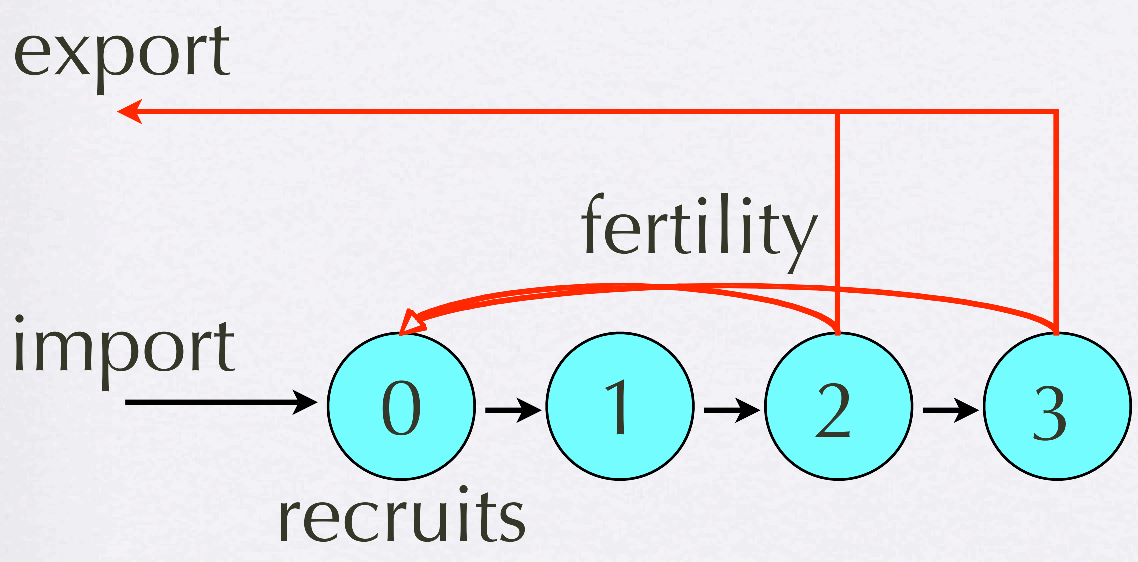
Dispersal and population connectivity

Per Jonsson
Tjärnö Marine Biological Laboratory
Göteborg University

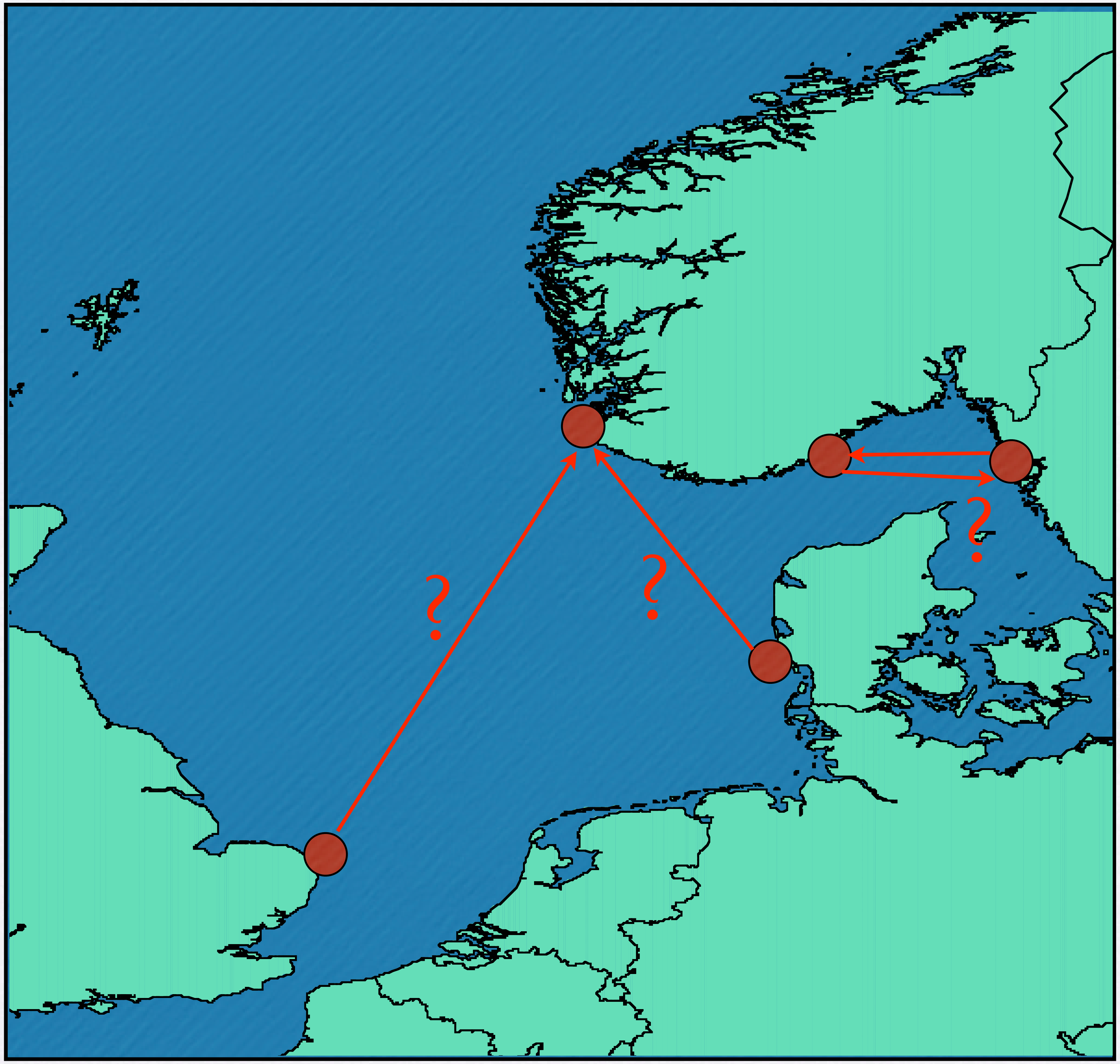
NMA course, Bergen 2005

Population dynamics

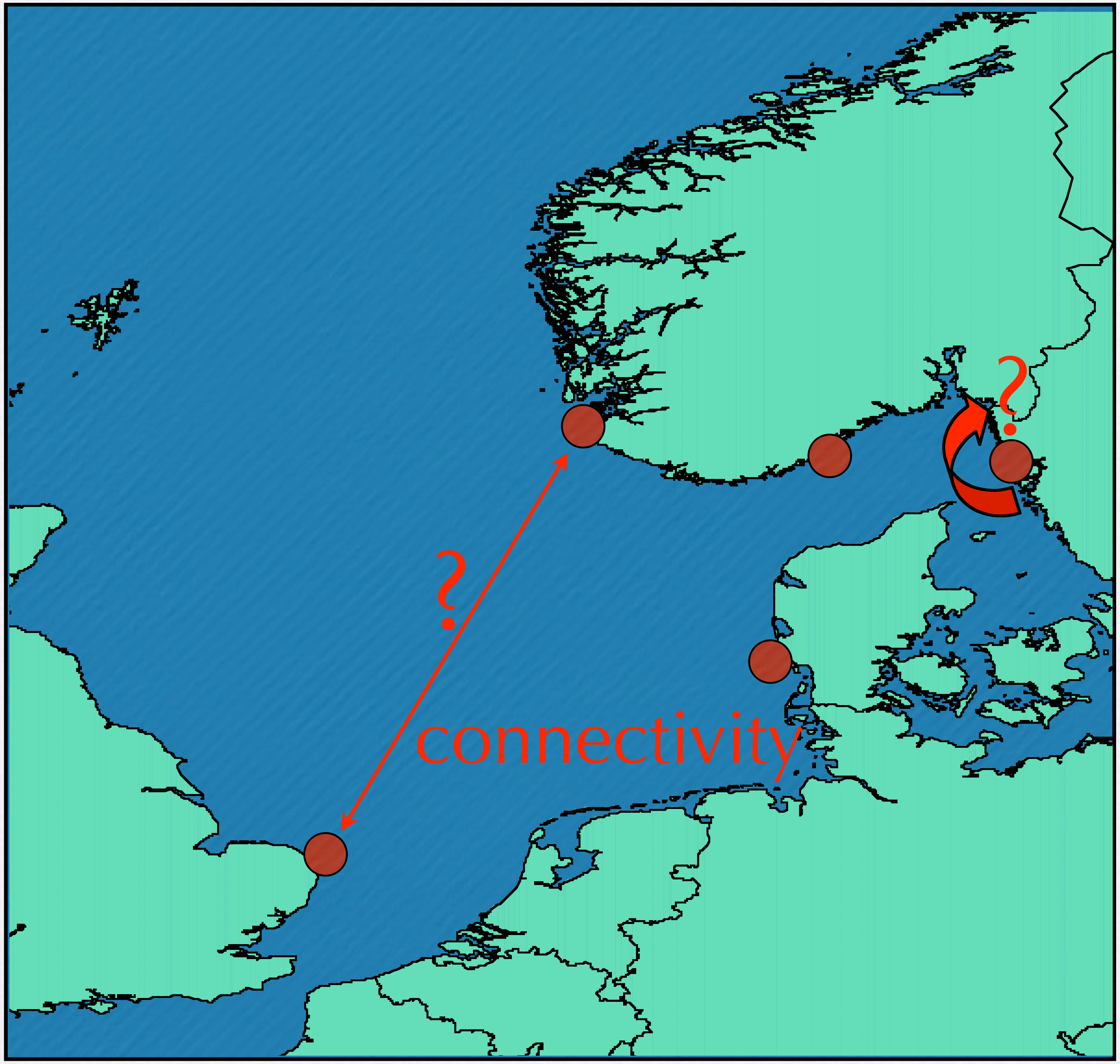
- Recruitment may depend on <u>local</u> demographic processes
- Or it can also depend on import from other sub-populations acting as a <u>meta-population</u>



Do populations show meta-population dynamics?



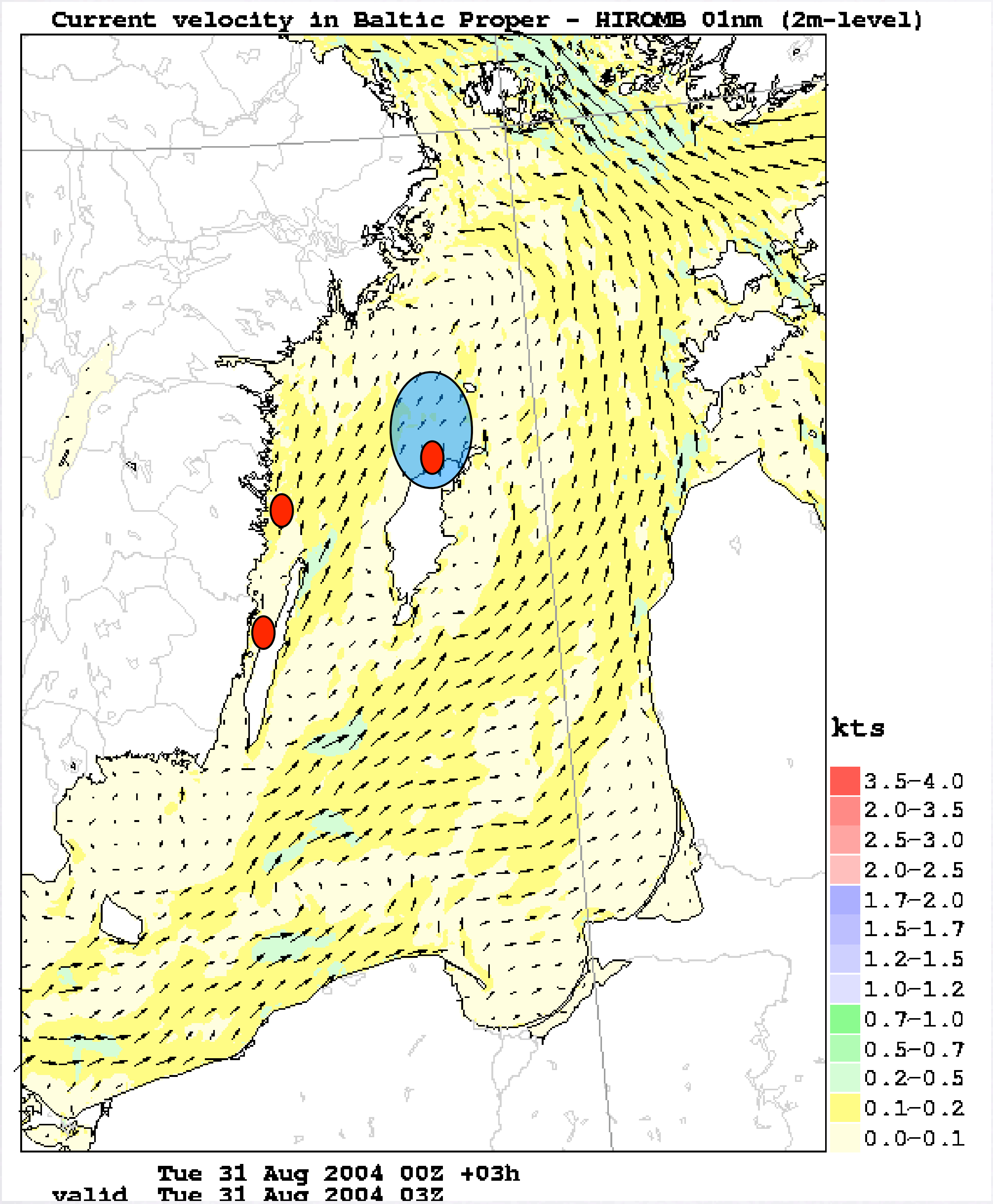
Open or closed populations?



Population connectivity has implications for:

- Population dynamics
- Community structure
- Genetic differentiation
- Evolution of local adaptations
- Speciation
- Management of exploited resources
- Design of Marine Protected Areas (MAP)

Design of MAP may be critical



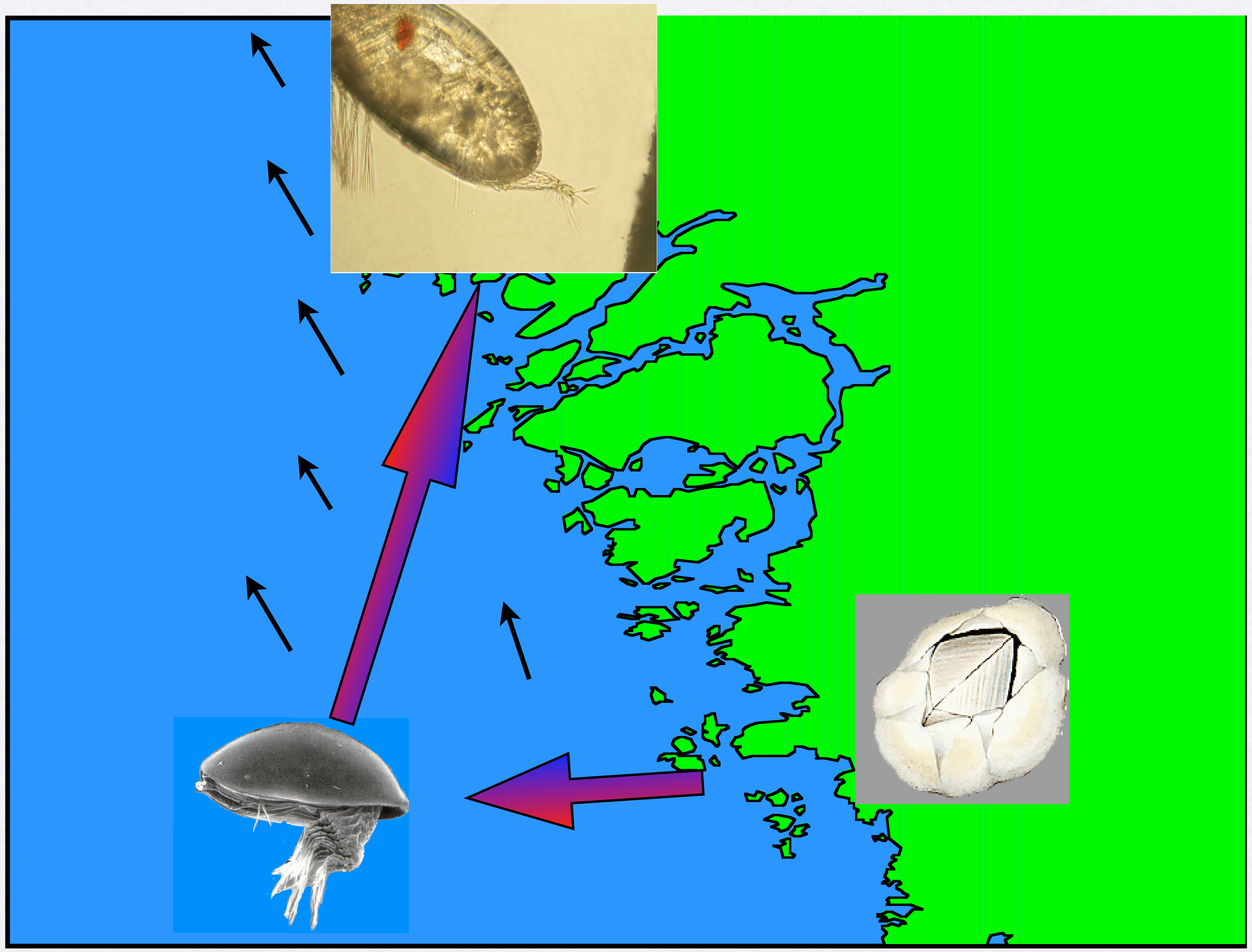
- Local recruitment
- Regional effect

What determines connectivity

- Coastal circulation (also small scale)
- Spawning (timing, duration, fertilization)
- Larval duration
- Larval behaviour (swimming and settling)
- Mortality

Dispersal

larval stage: hours - weeks



Traditional view of dispersal

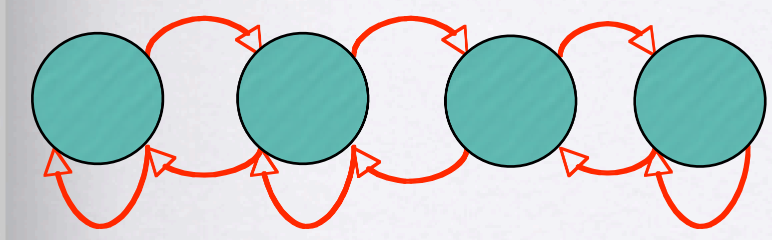
- Long-range dispersal ≈ larval duration x off-coast flow speed
- Limited local recruitment
- Open populations
- Low potential for genetic differentiation
- Low potential for local adaptations

Populations may be more closed

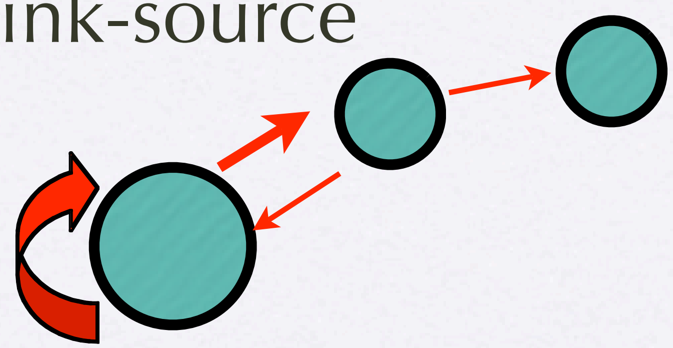
- Unexpected genetic structure (blue mussels)
- Local recruitment (marking of larval fish)
- Local adaptations (macro-algae)

Populations acting as sources or sinks

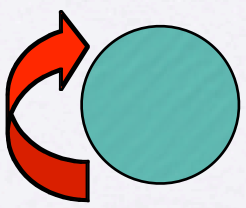
isolation by distance



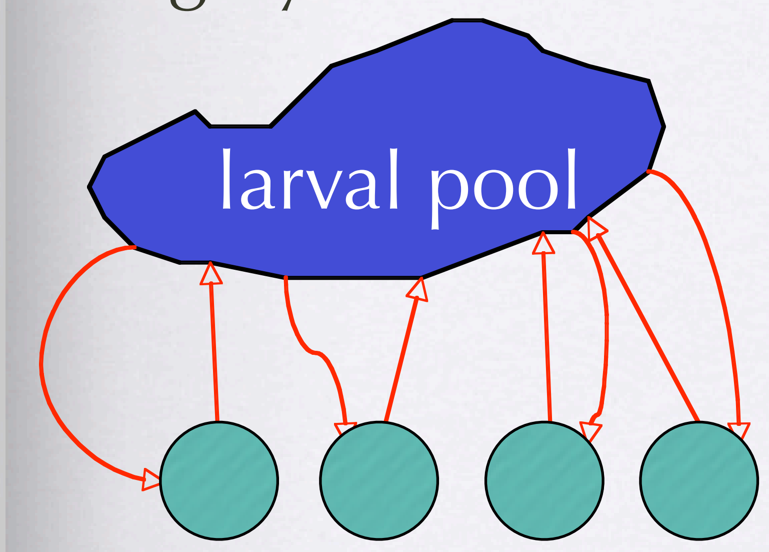
sink-source



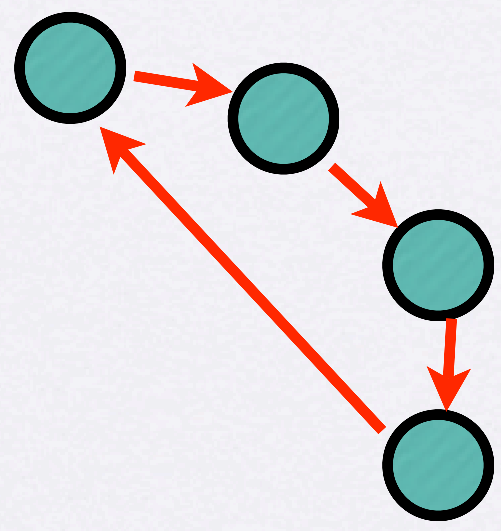
closed



highly connected



“stepping stones”



How can connectivity be predicted?

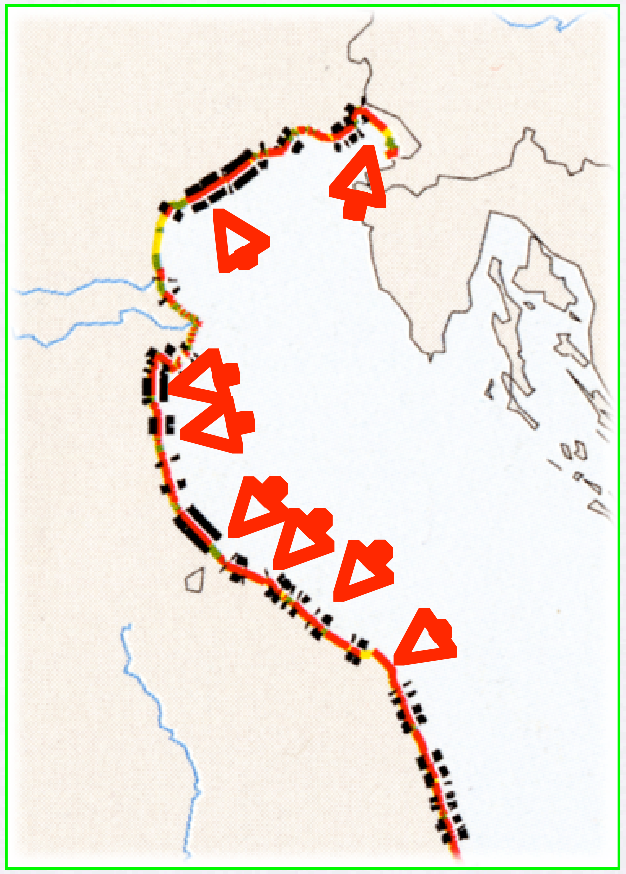
- Marking - recapture (fish larvae)
- Genetic differentiation (barnacles)
- Drift drouges (e.g. coupled to GPS)
- Model coastal circulation (with flow measurements)

Spatially explicit modeling

- Model the coastal circulation in space and time
- Use the velocity field to move virtual larvae from release to settlement

Case study: a set of breakwaters in a simple hydrodynamic setting?

78 breakwaters



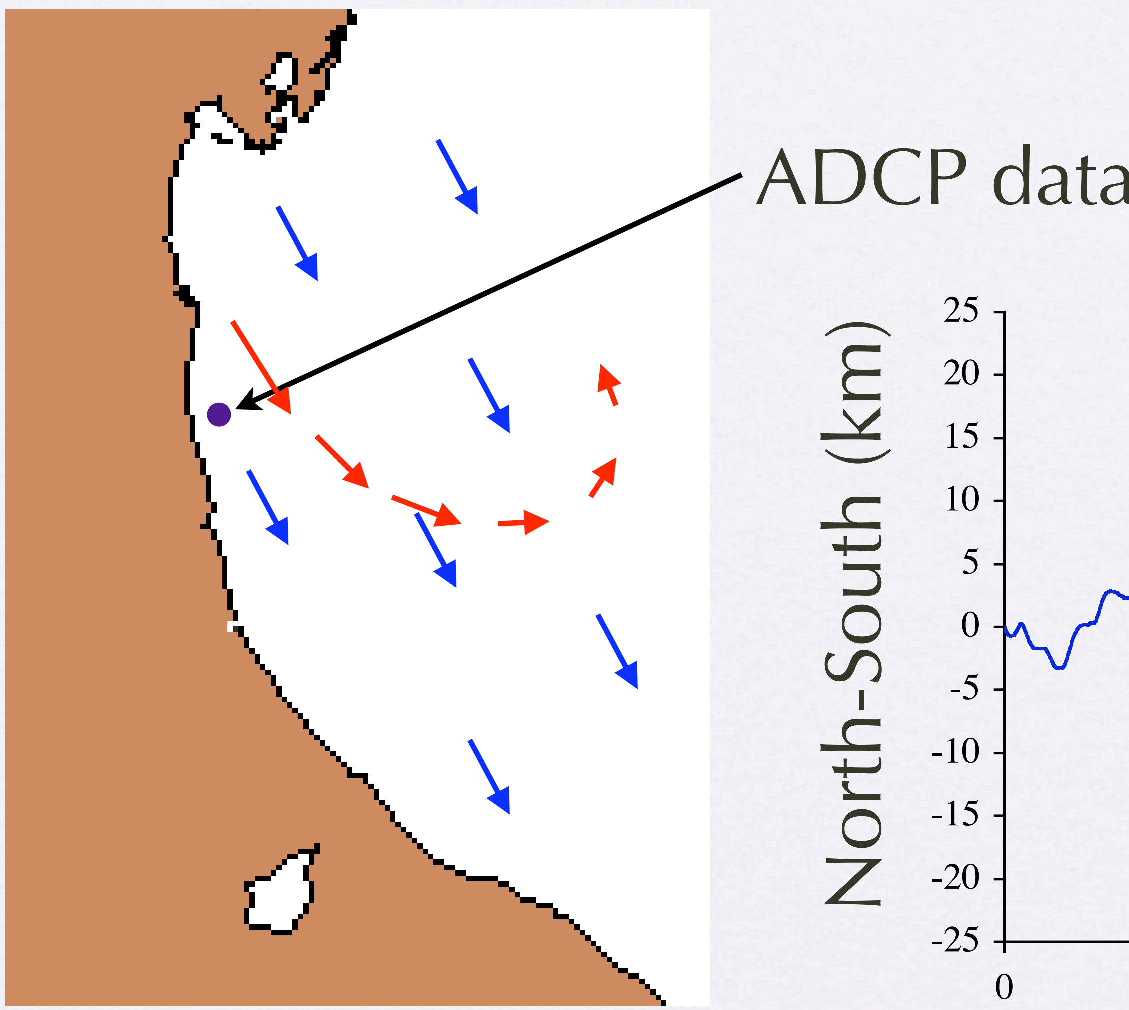
Objectives

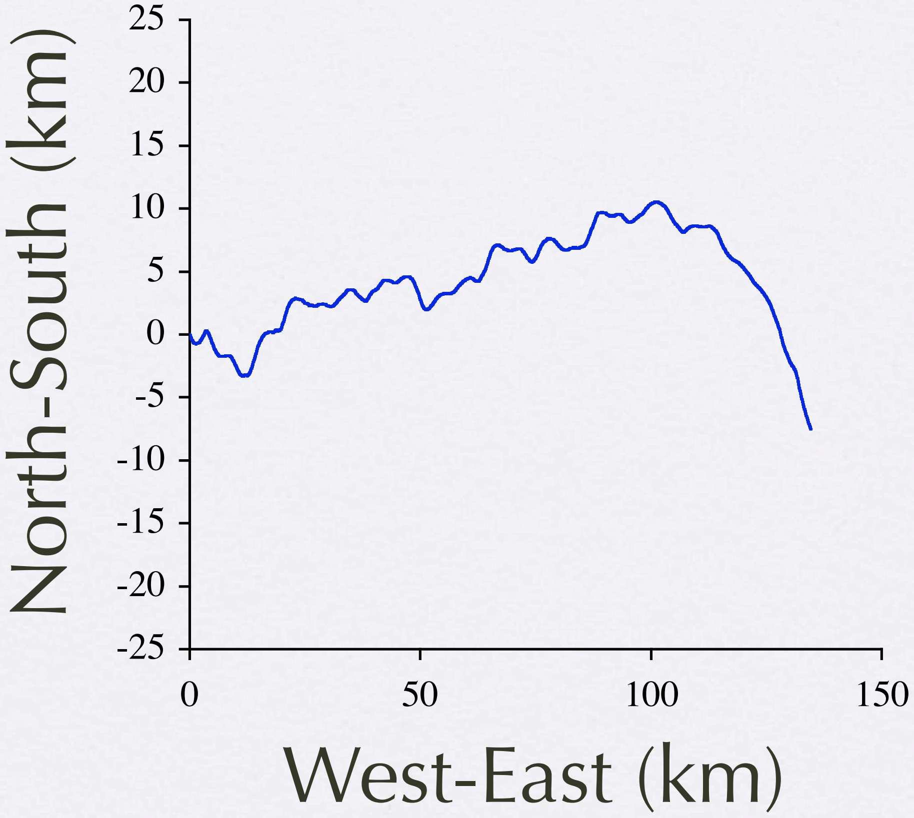
- Test dispersal models of different complexity
- Expore effects of larval vertical behaviour
- Compare predictions of connectivity with distribution patterns and genetic differentiation

Naive model

- Model organism: *Patella caerulea*
- Length of free-swimming larval period: 12 days
- Typical north/south current velocity: 6 cm/s
- Potential north/south dispersal: ca 60 km

Less naive model

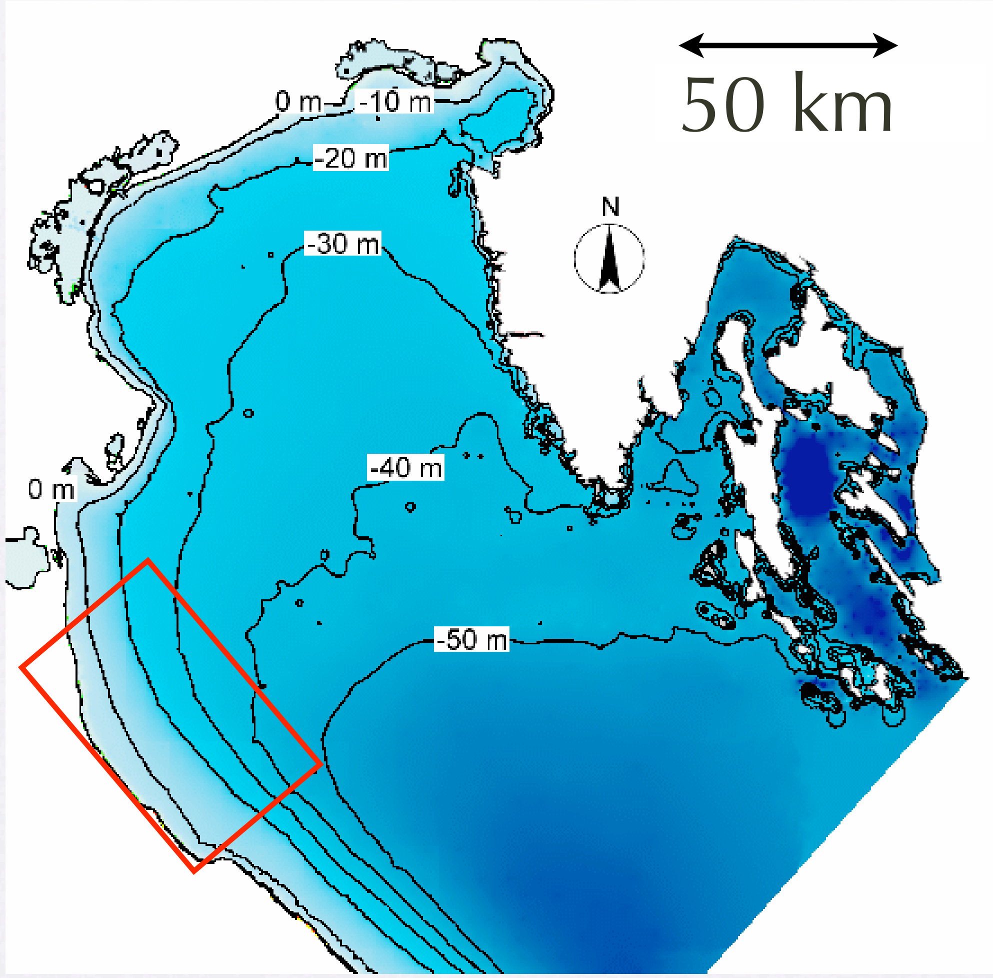




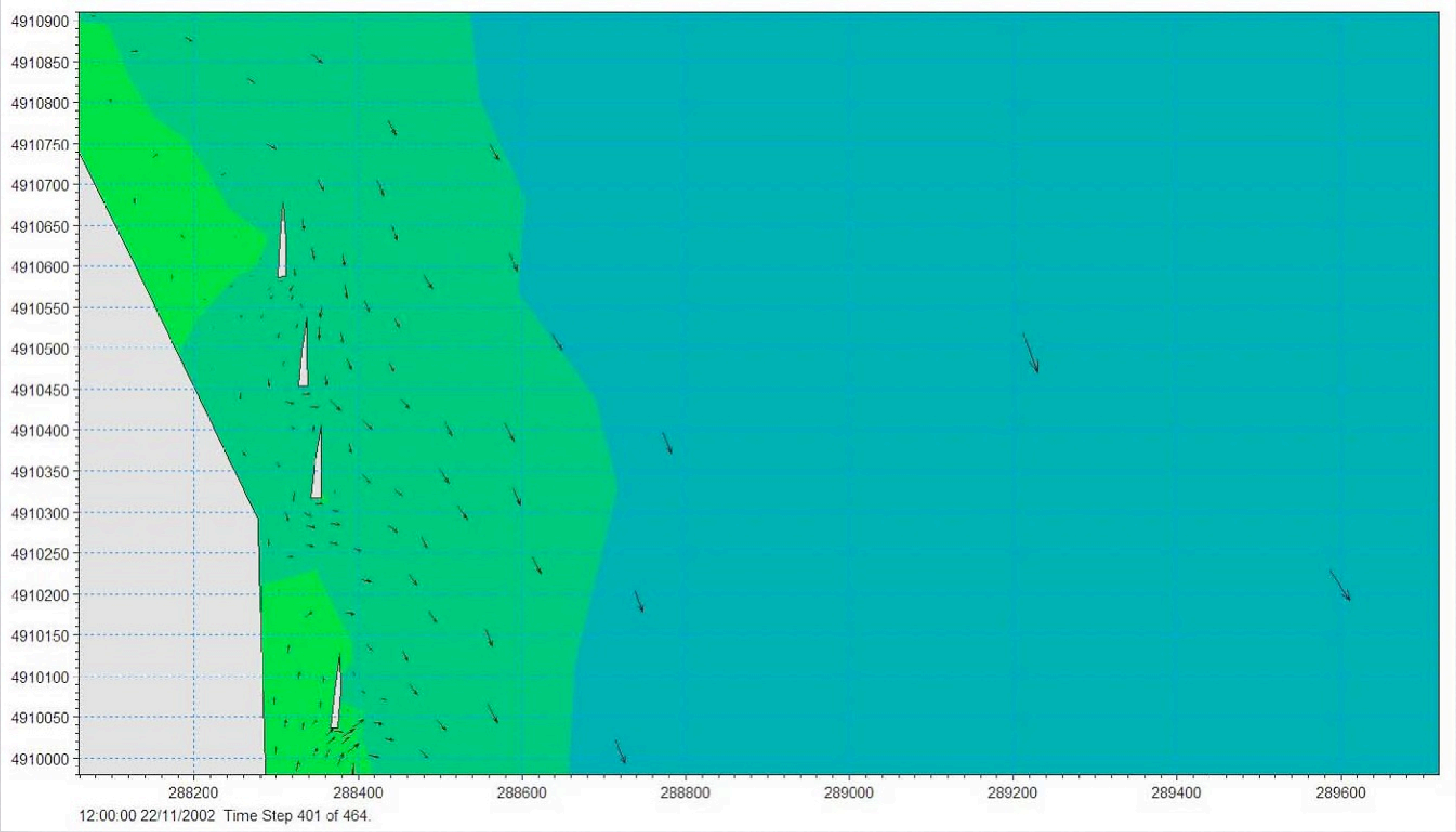
Building a circulation model

- Hydrodynamic model solving time-dependent non-linear equations of continuity and momentum conservation (MIKE, DHI)
- Model requires:
  - bathymetry
  - driving data (wind, tide)
  - boundary conditions (net flux, freshwater etc)
  - calibration and validation (current measurements)

Bathymetry

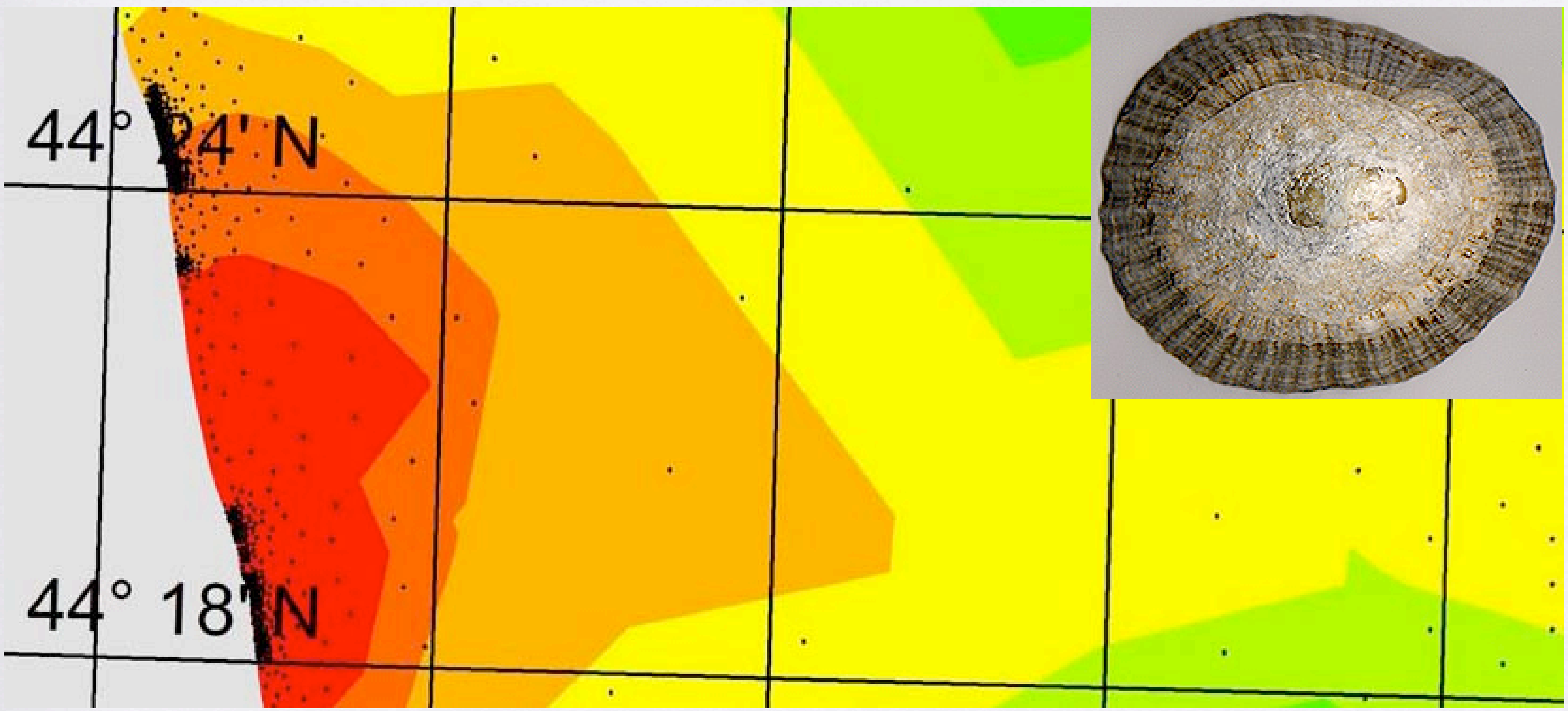


Output from hydrodynamic model

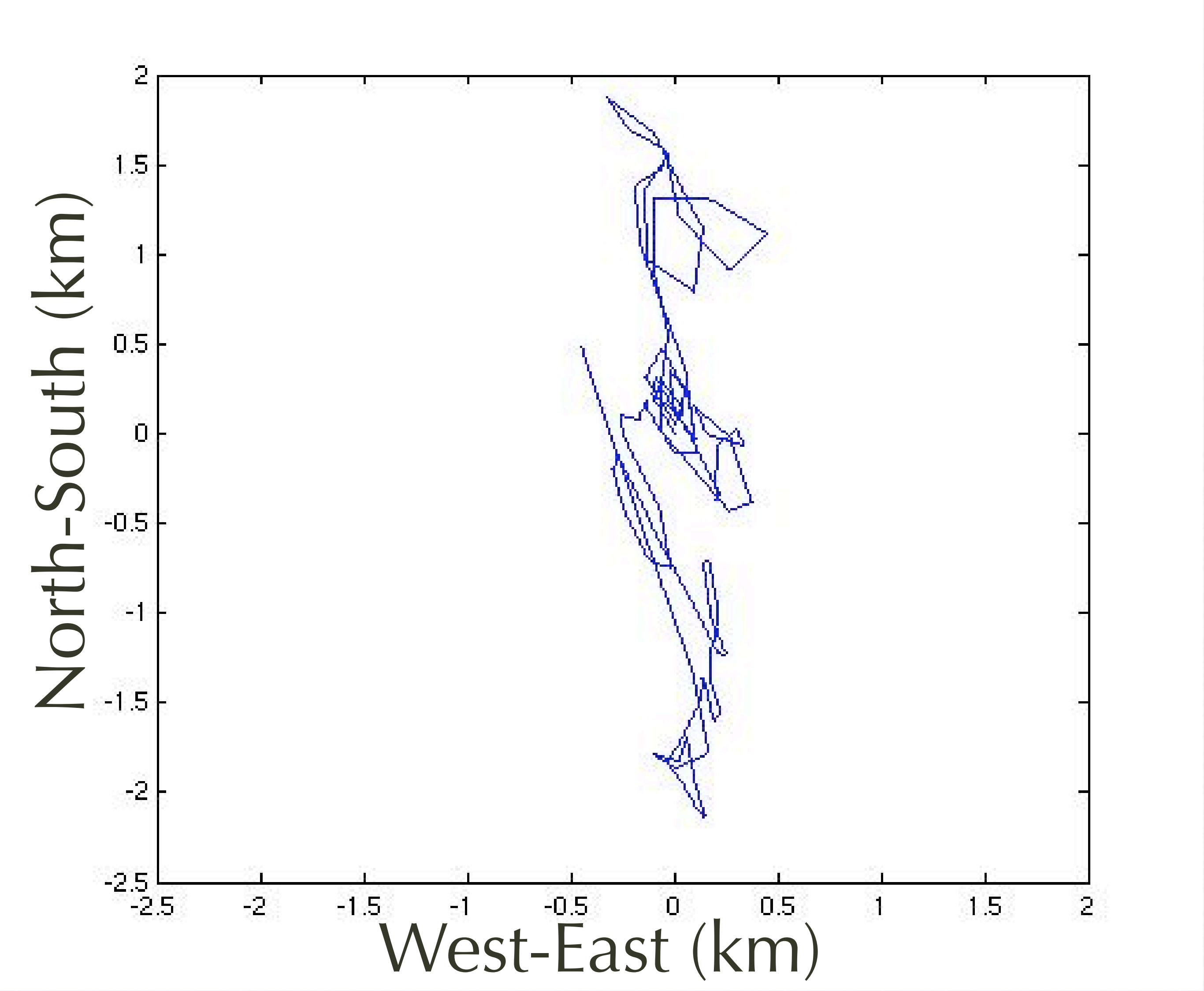


Dispersal model

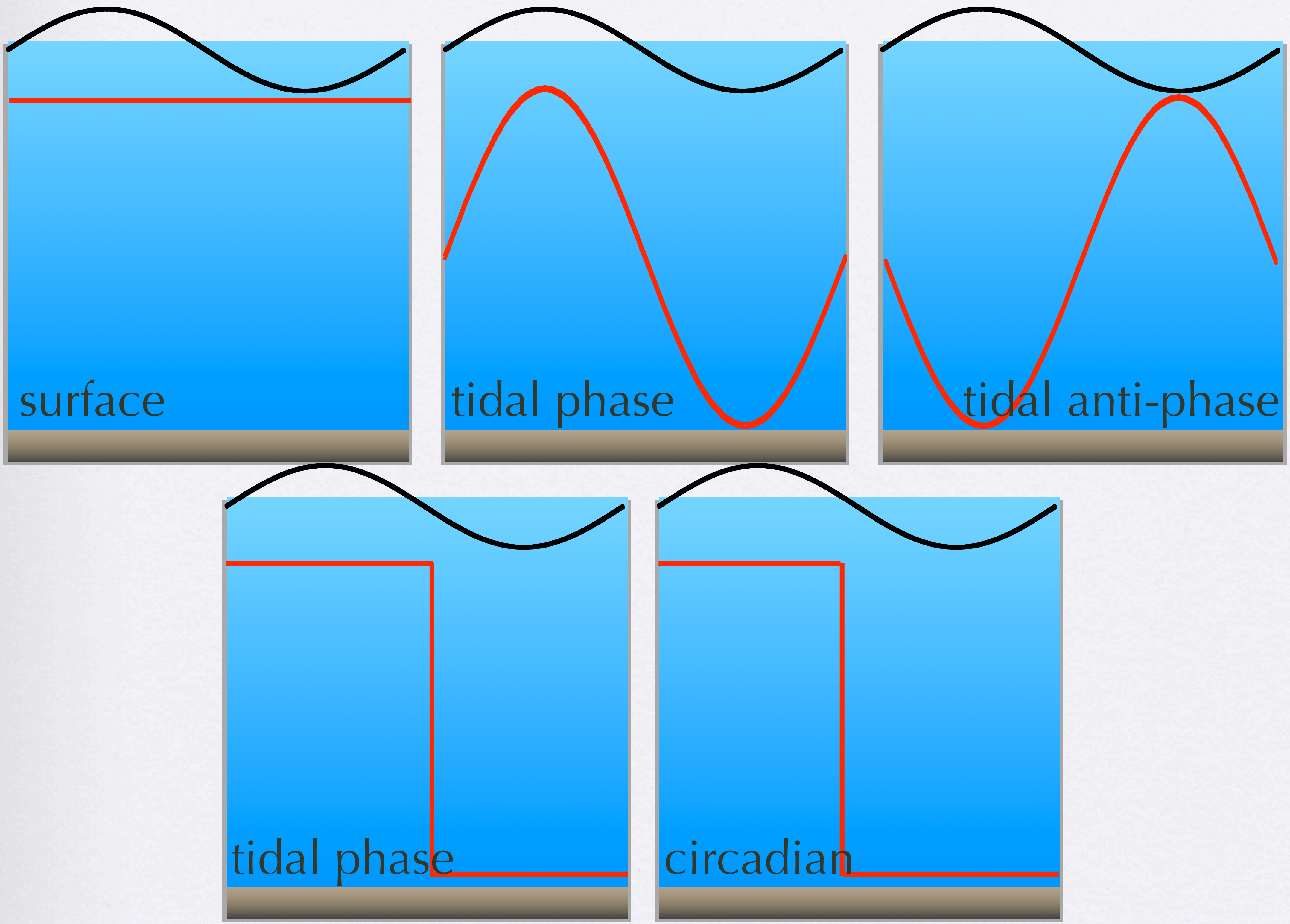
- Virtual larvae of *Patella caerulea* are released from each breakwater
- Settlement during competency on breakwaters is recorded



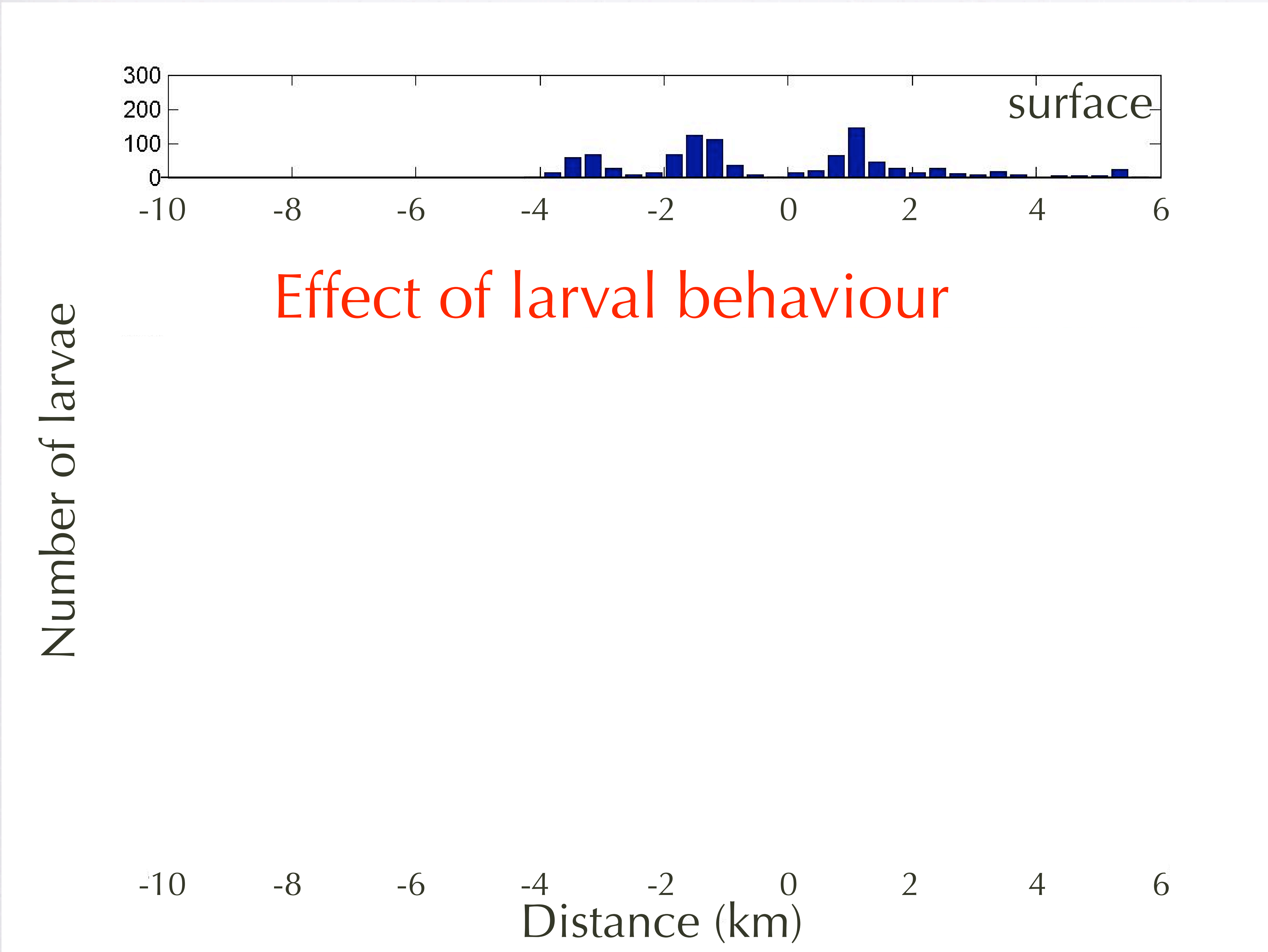
Dispersal tracks



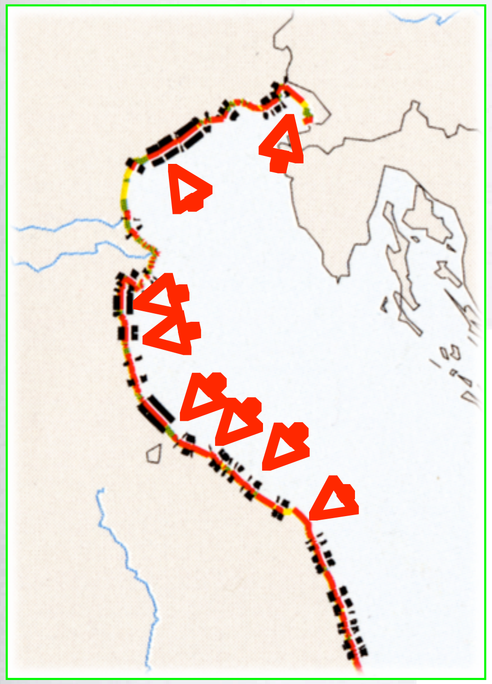
Dispersal distance and effects of behaviour

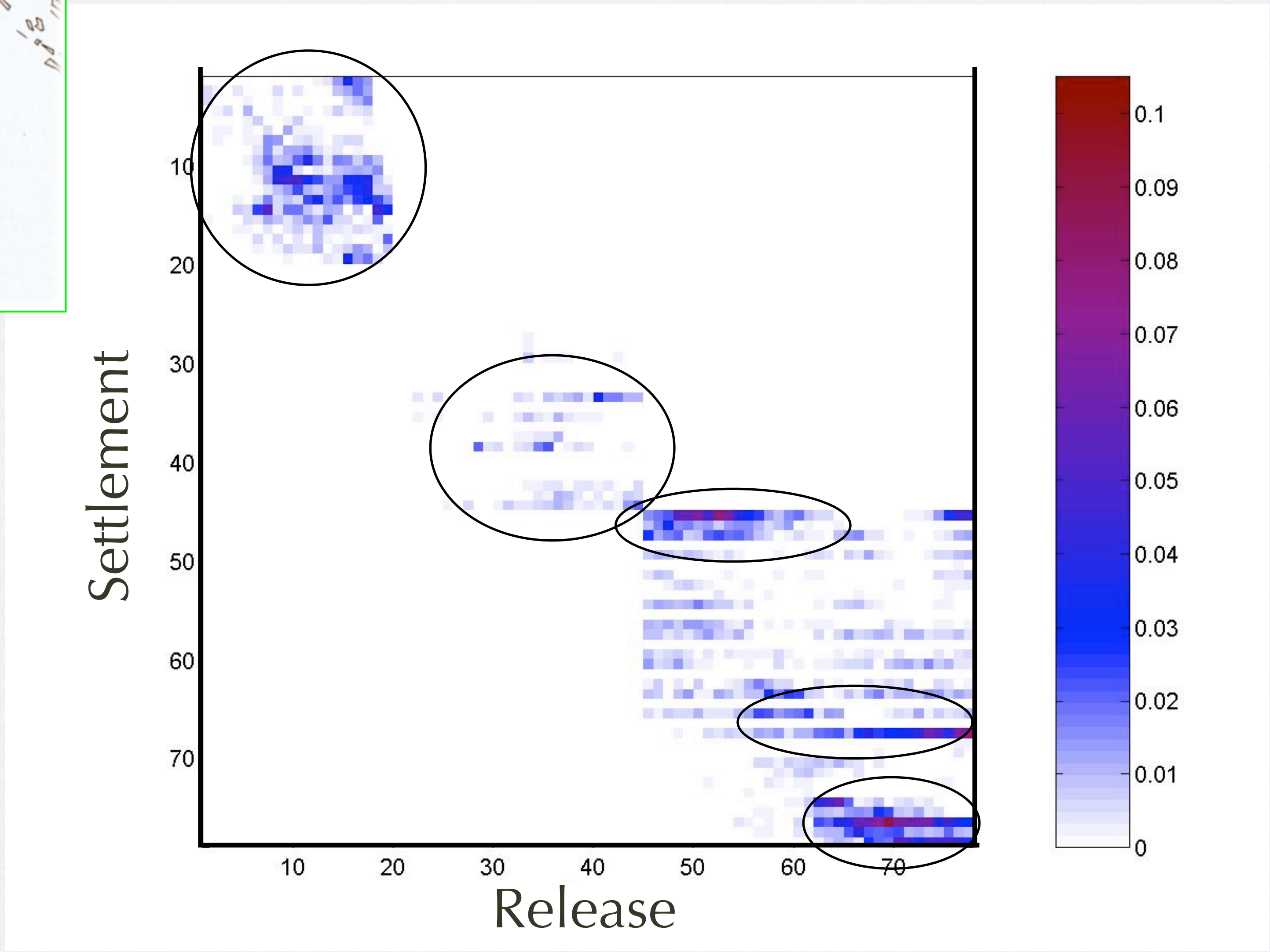


Dispersal distance

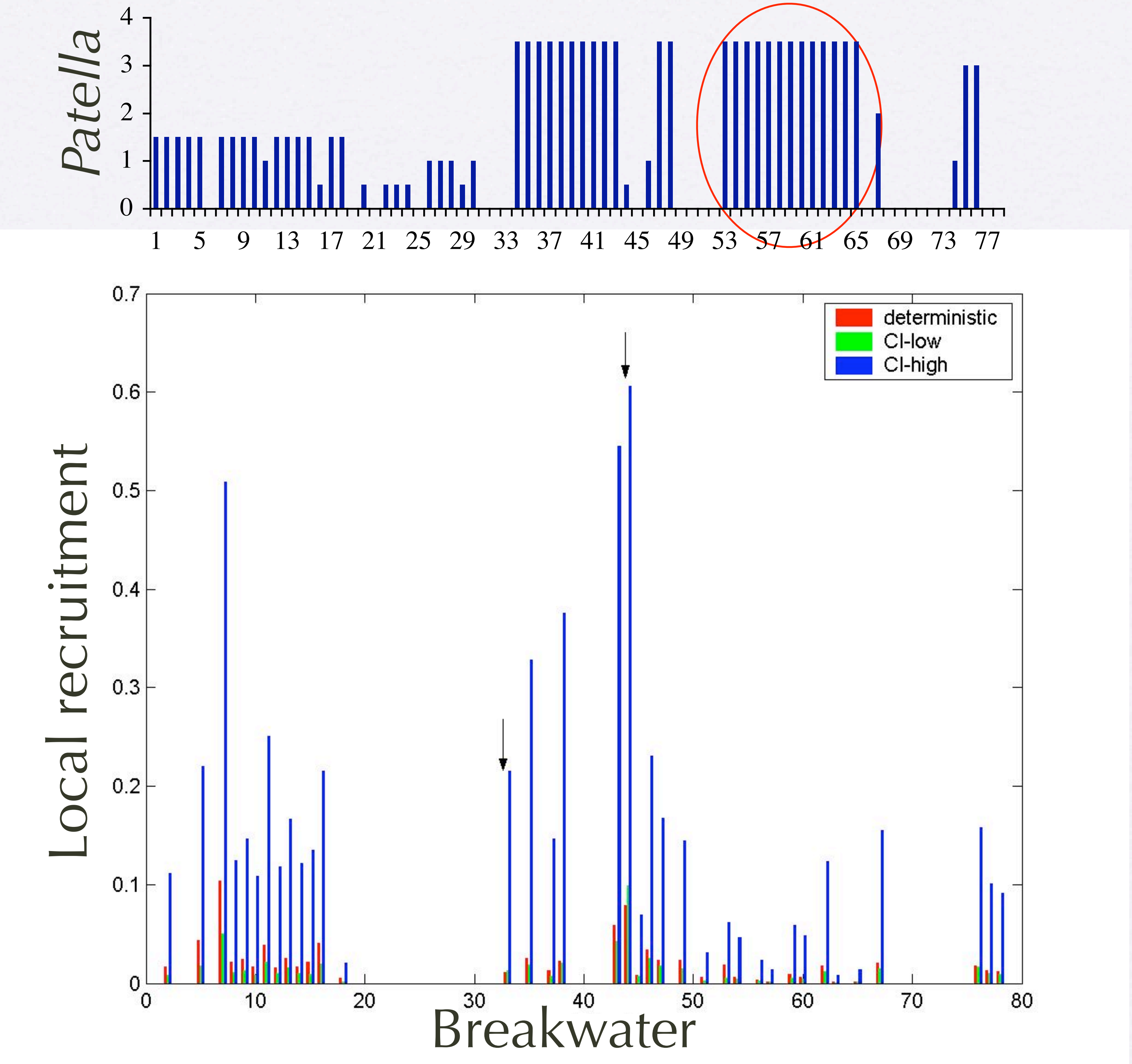


Connectivity matrix





Local recruitment



Conclusions

- Coastal circulation leads to asymmetric dispersal
- Larval behaviour may be important
- Temporal variability may be high
- Connectedness varied greatly for the studied breakwaters

Use of spatially explicit dispersal models

- Do they predict anything useful? Still a general lack of validation.
- Often complex models but may serve as benchmarking for simpler models
- Future hydrodynamic models can have finer spatial resolution
- A general lack of knowledge about larval biology

In collaboration with

- Andreas Sundelöf, Göteborg University
- Laura Airoldi, University of Bologna


Thank you!