

# Mapping Larval Connectivity for MPA-networks: – a Swedish case-study –

*Per-Olav Moksnes <sup>1,2</sup>, Per Jonsson <sup>1</sup>, Jonathan Havenhand <sup>1</sup>*

*<sup>1</sup>Department of Marine Sciences, University of Gothenburg*

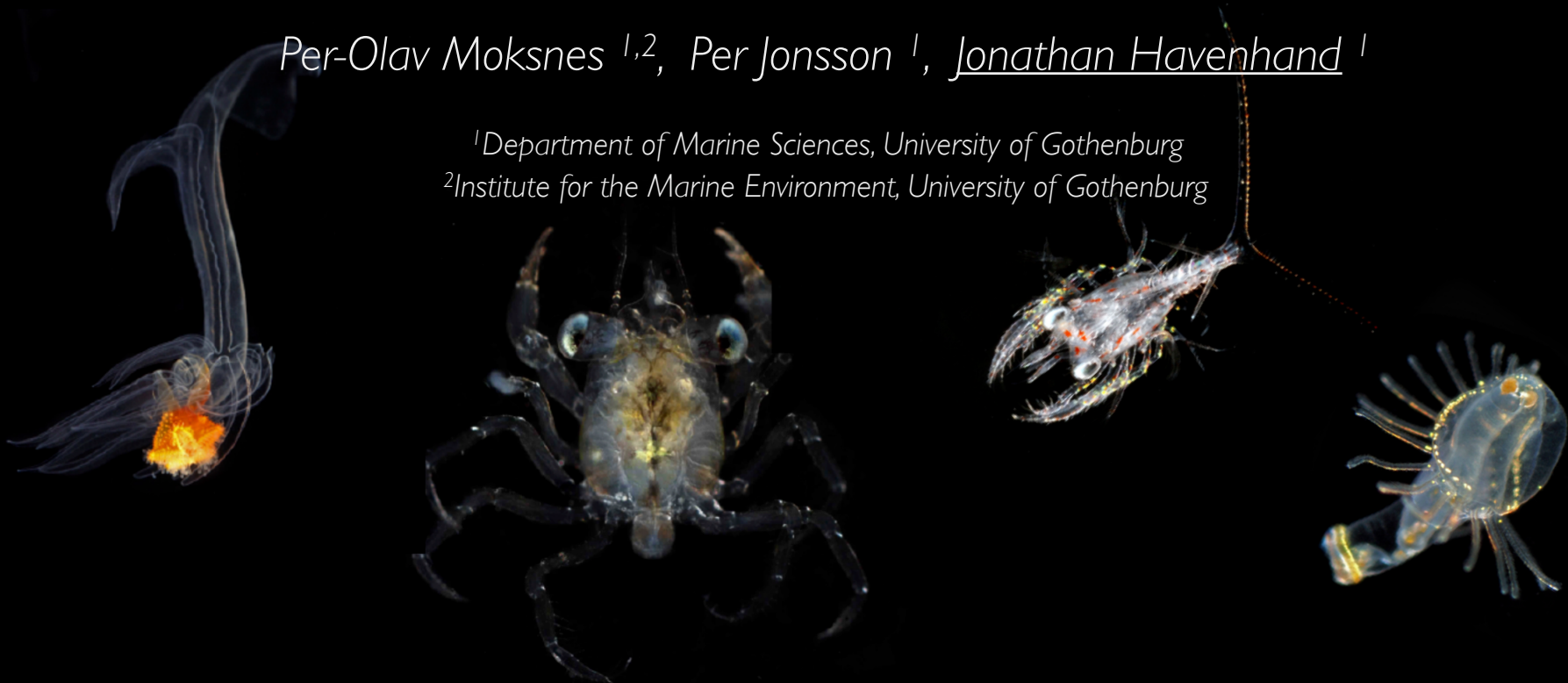
*<sup>2</sup>Institute for the Marine Environment, University of Gothenburg*

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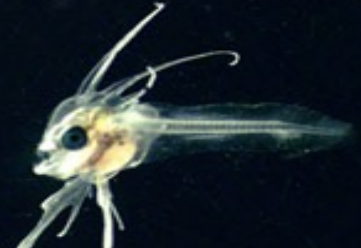
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# Most marine animals have planktonic larvae

Lobster larva



Anglerfish larva



Polychaete larva



Seastar larva



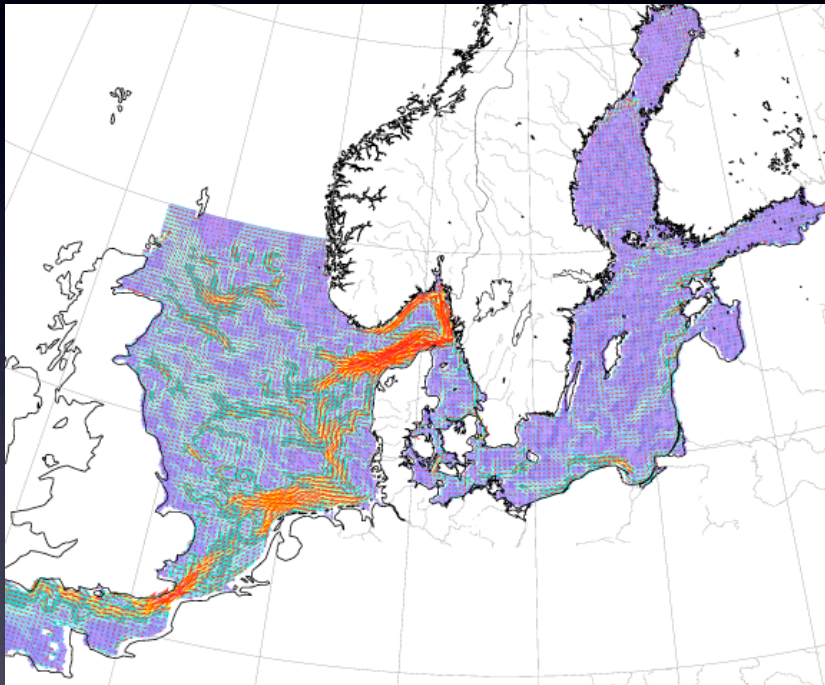
Barnacle larva



- potential for long-distance dispersal
- substantive effects on population dynamics and management

- create biophysical model
  - hydrodynamics (at relevant spatial and temporal scales)
  - larval dispersal trajectories
  - connectivity among sites (connectivity matrix)
- identify optimal MPA network (fancy mathematics)
  - *de novo*
  - as extension of existing network
- evaluate potential benefits of alternatives
- identify barriers to dispersal
  - biogeographic “units”

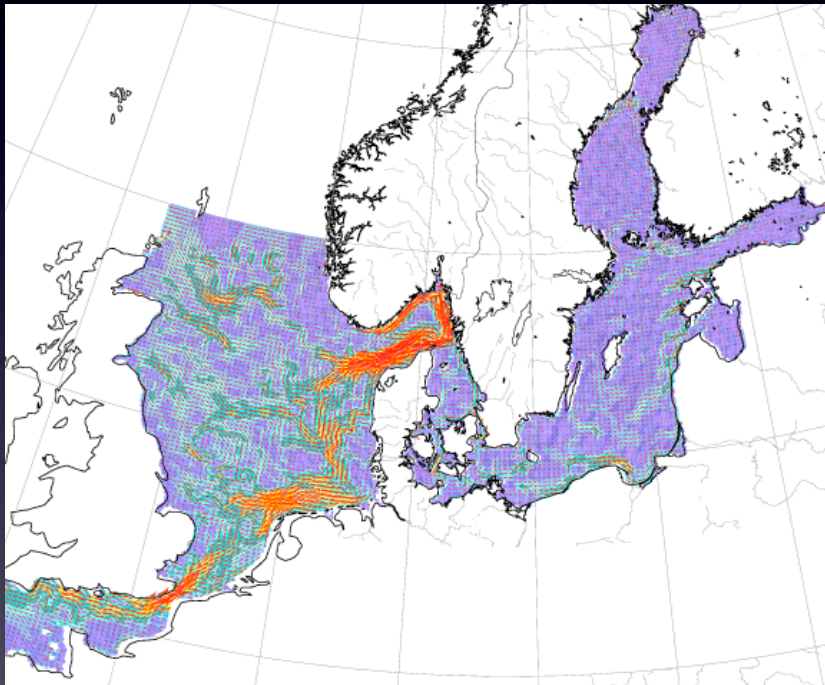
# Biophysical modeling



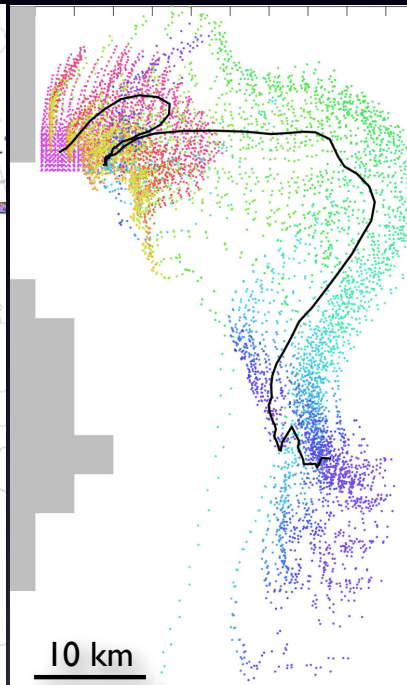
3D-circulation model

- BaltiX
  - circulation model
  - 120,000 km<sup>2</sup>
  - grid of 2 nm x 2 nm
  - 119 depth layers
  
  - run for 8 years (1995-2002)
  - data every 3h
    - transport vectors, T°, salinity
  - describes circulation

# Biophysical modeling



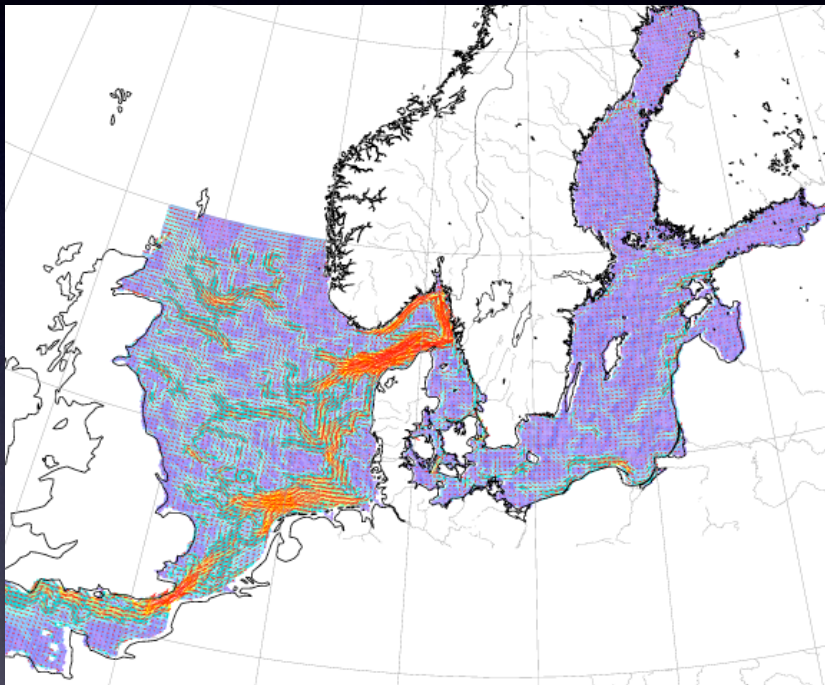
3D-circulation model



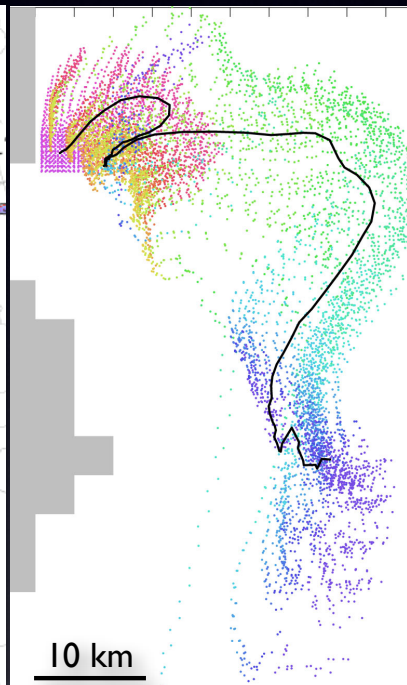
trajectory  
model

- TRACMASS model
  - uses BaltiX output “offline”
  - releases virtual larvae
    - reproductive season
    - planktonic duration
    - depth distribution
    - (no larval behaviour)
  - output:
    - start & end points

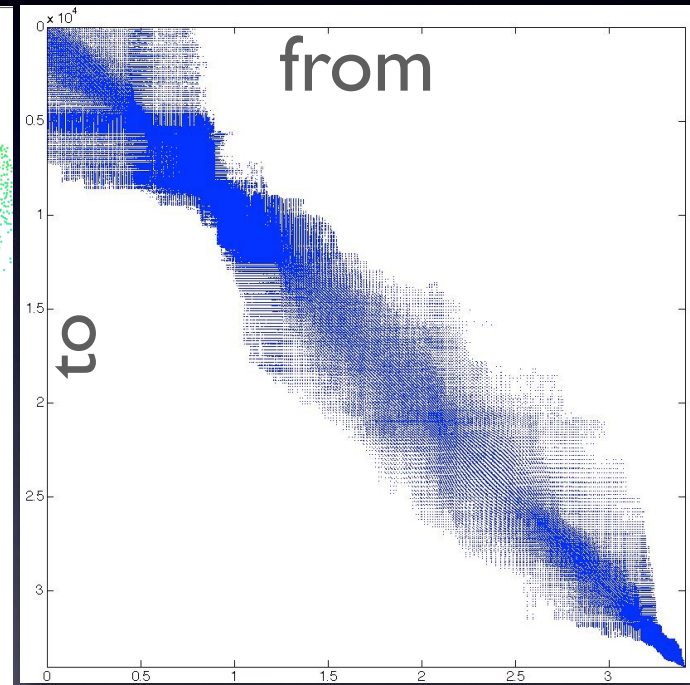
# Biophysical modeling



3D-circulation model



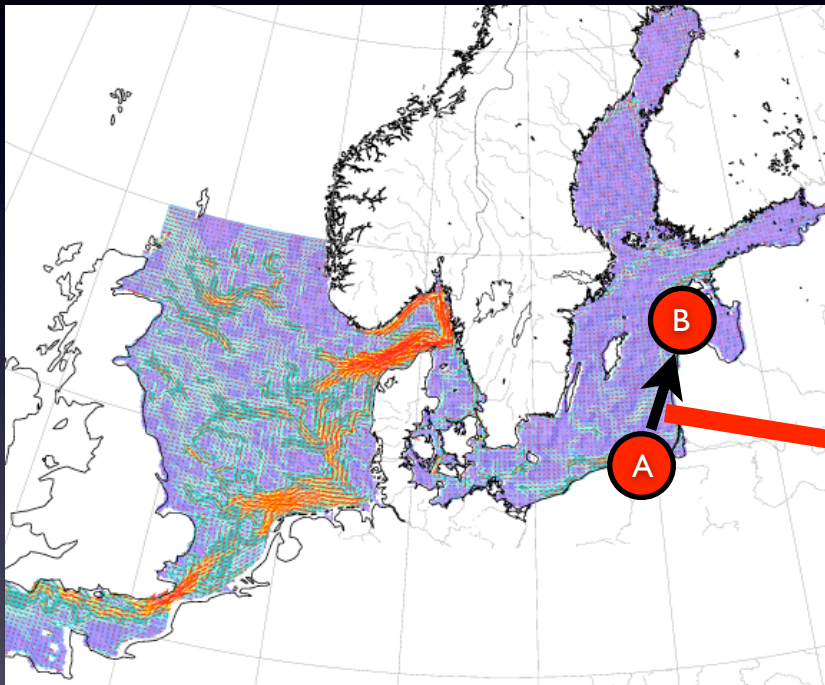
trajectory  
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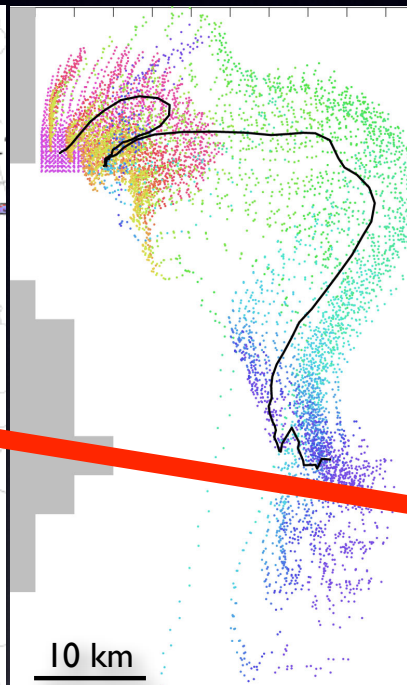
connectivity  
matrix



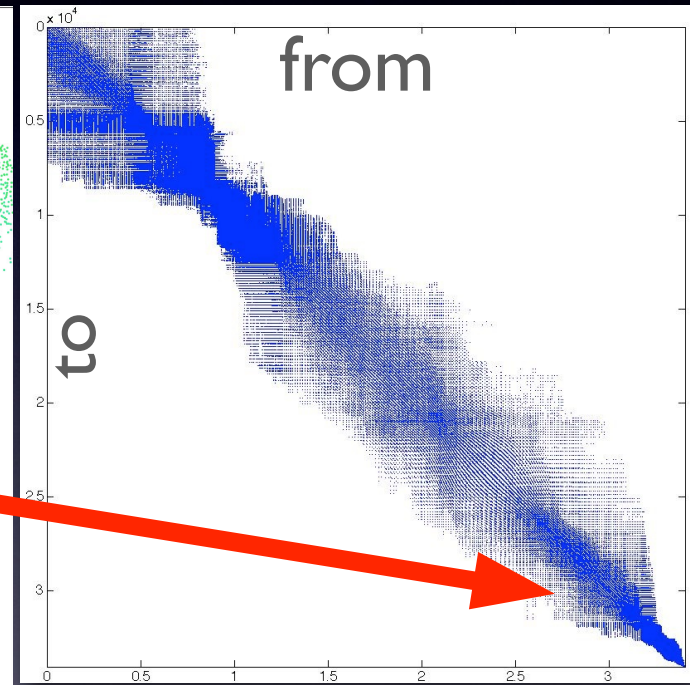
# Biophysical modeling



3D-circulation model



trajectory model

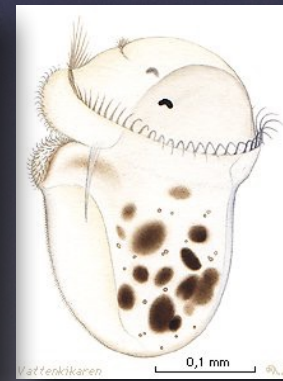
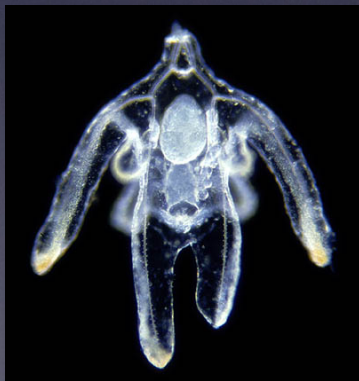


connectivity matrix

# Larval dispersal is difficult to study

Larvae (and algal spores) are typically:

- small (<1 mm)
- numerous ( $10^4 - 10^7$  per spawning)
- long-lived (weeks – months)
- display behaviour that can affect dispersal
- very little is known



?

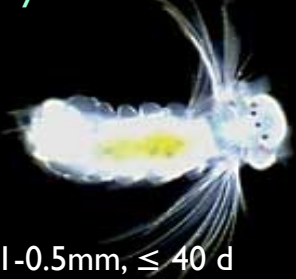
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Lobster larva



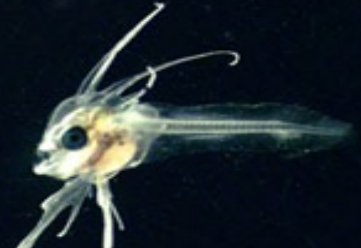
2-12 mm,  $\leq 30$  d

Polychaete larva



0.1-0.5mm,  $\leq 40$  d

Anglerfish larva



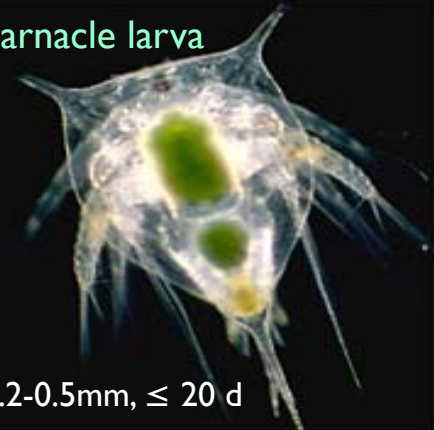
$\leq 20$  mm,  $\leq 50$  d

Seastar larva



0.5-5mm,  $\leq 4$  mo

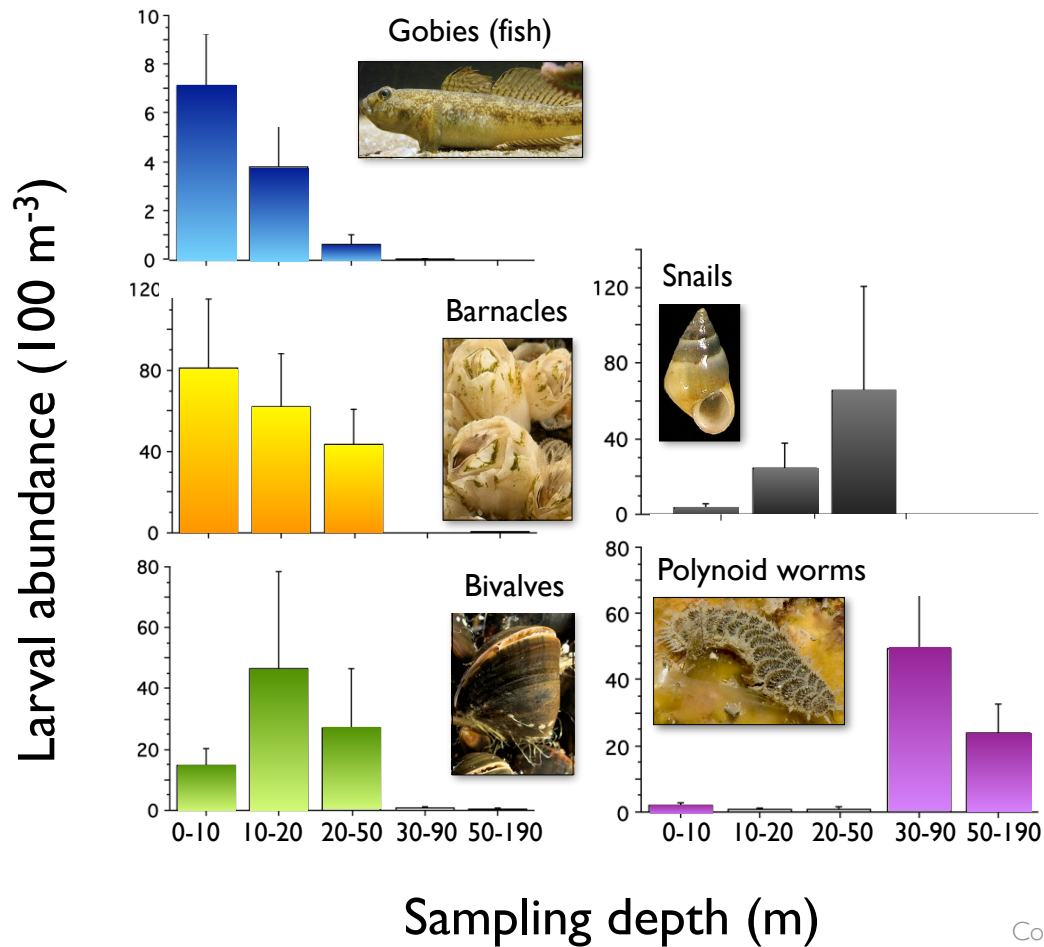
Barnacle larva



0.2-0.5mm,  $\leq 20$  d

- potential for long-distance dispersal
- substantive effects on population dynamics and management

# Depth distribution of larvae





# Scenarios of larval distribution & season

Larval release	PLD (d)	Depth (m)	Rocky-reef taxa	ID
April–August	10	0% 0–2	Anthozoa	B1
		20% 10–12	Crinoidea	
		40% 24–26		
		40% 48–50		
April–August	30	0% 0–2 m	Ophiurida	B2
		20% 10–12	<i>Galathea</i> sp	
		40% 24–26	<i>Pisidia longicornis</i>	
		40% 48–50	<i>Zeugopterus punctatus</i>	
April–August	30	10% 0–2 m	Echinoidea	B3
		40% 10–12	Mytilidae	
		40% 24–26	<i>Homarus gammarus</i>	
		10% 48–50	<i>Sabella</i> spp.	
April–August	60	10% 0–2	Gadidae	B4
		40% 10–12	Labridae	
		40% 24–26	<i>Cancer pagurus</i>	
		10% 48–50		
April–August	30	40% 0–2	Asteroidea	B5
		30% 10–12	<i>Liocarcinus</i> sp.	
		20% 24–26		
		10% 48–50		

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		20% 24–26		
		10% 48–50		

Jonsson et al. 2016 *Diversity & Distributions*

Larval release	PLD (days)	Drift depth (m)	ID
January–December	10	0–2	A1
January–December	10	24–26	A2
January–December	30	0–2	A3
January–December	30	24–26	A4

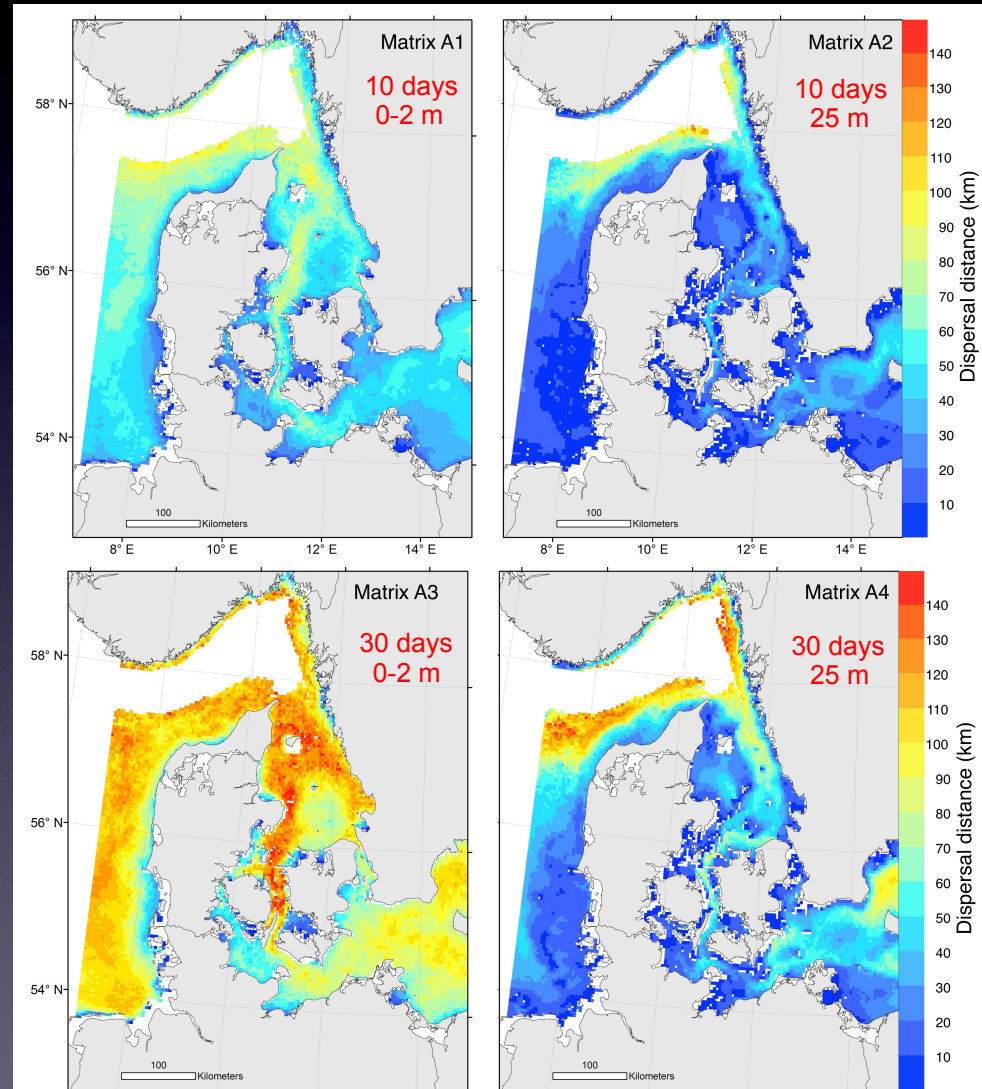
Jonsson et al. 2016 *Diversity & Distributions*



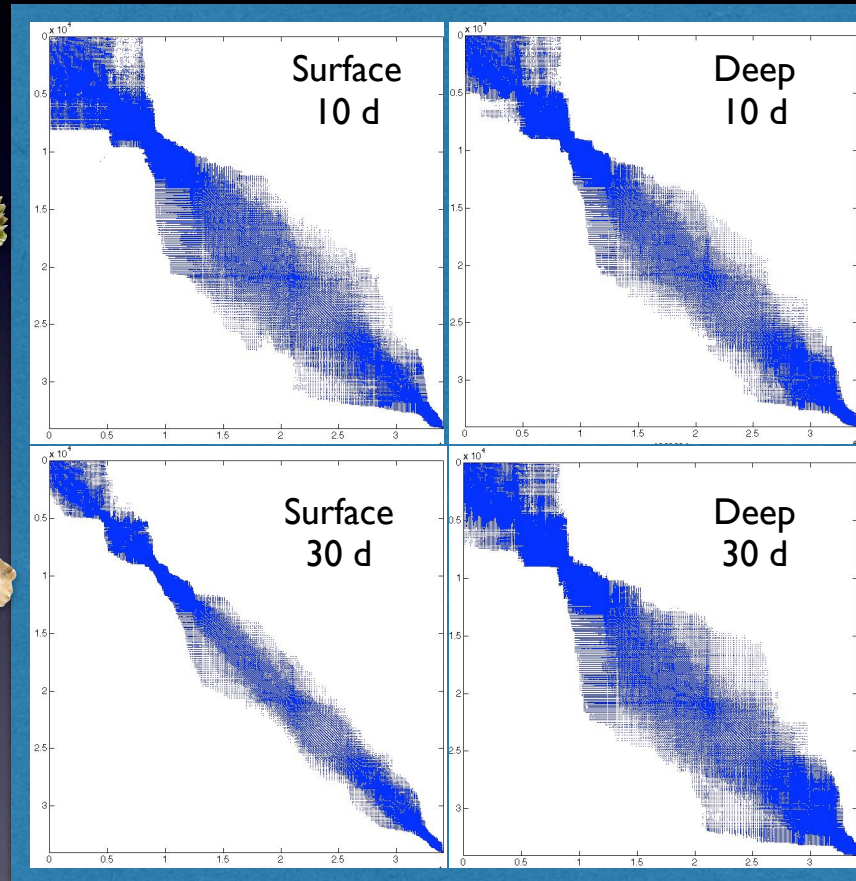
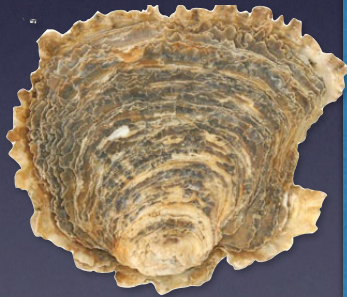
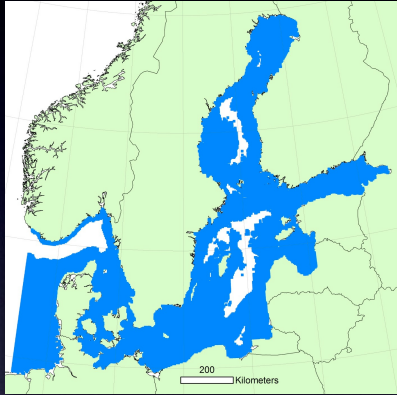
# Scenarios of larval distribution & season

Larval dispersal under “simple scenarios”:

- large effects of larval duration, drift depth and release location
- typical dispersal distance is much larger than most MPA's



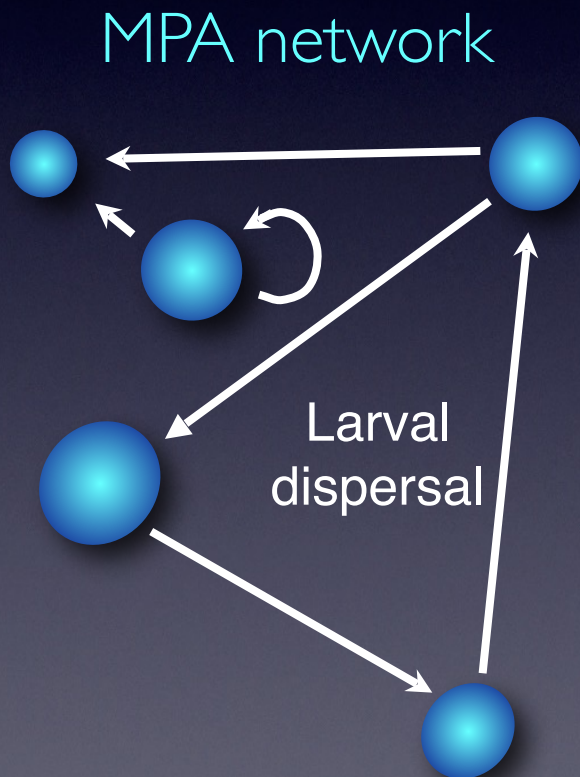
# Connectivity matrix for each scenario



Each dispersal strategy produces a unique connectivity matrix

- create biophysical model
  - hydrodynamics (at relevant spatial and temporal scales)
  - larval dispersal trajectories
  - connectivity among sites (connectivity matrix)
- identify optimal MPA network (fancy mathematics)
  - *de novo*
  - as extension of existing network
- evaluate potential benefits of alternatives
- identify barriers to dispersal
  - biogeographic “units”

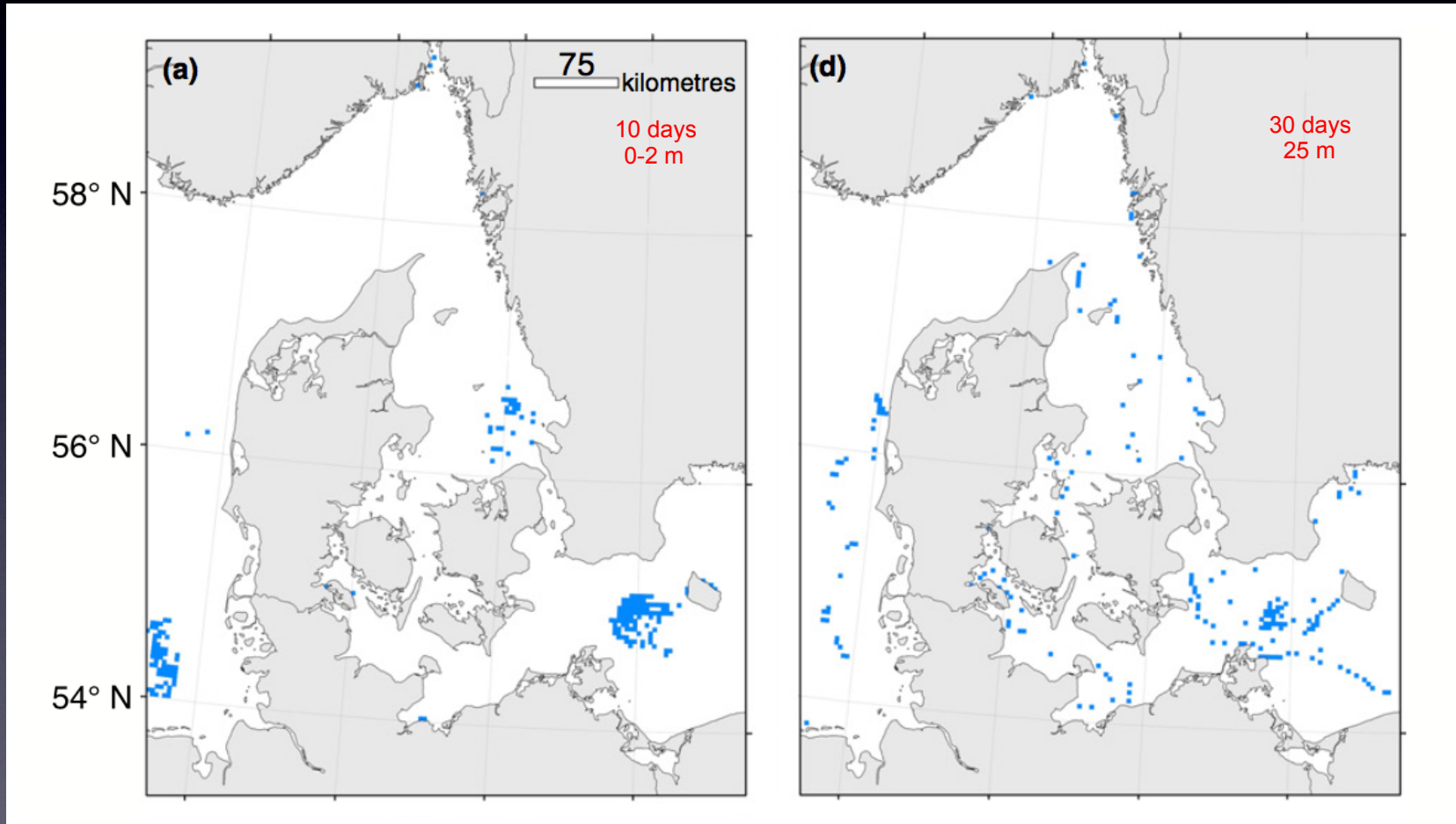
# Identifying the optimal MPA-network



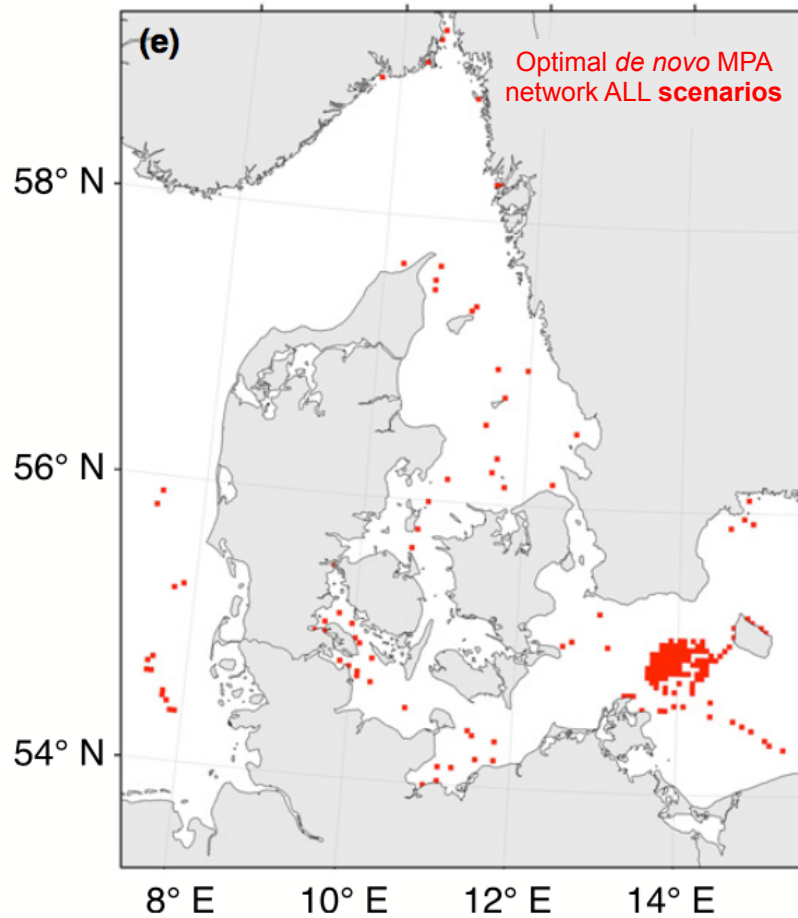
- “Eigenvalue Perturbation Theory”

- selects areas that both deliver (sources) and receive (sinks) high numbers of larvae
- identifies the optimal areas for the maximal overall connectivity
- ranks all areas based on their contribution

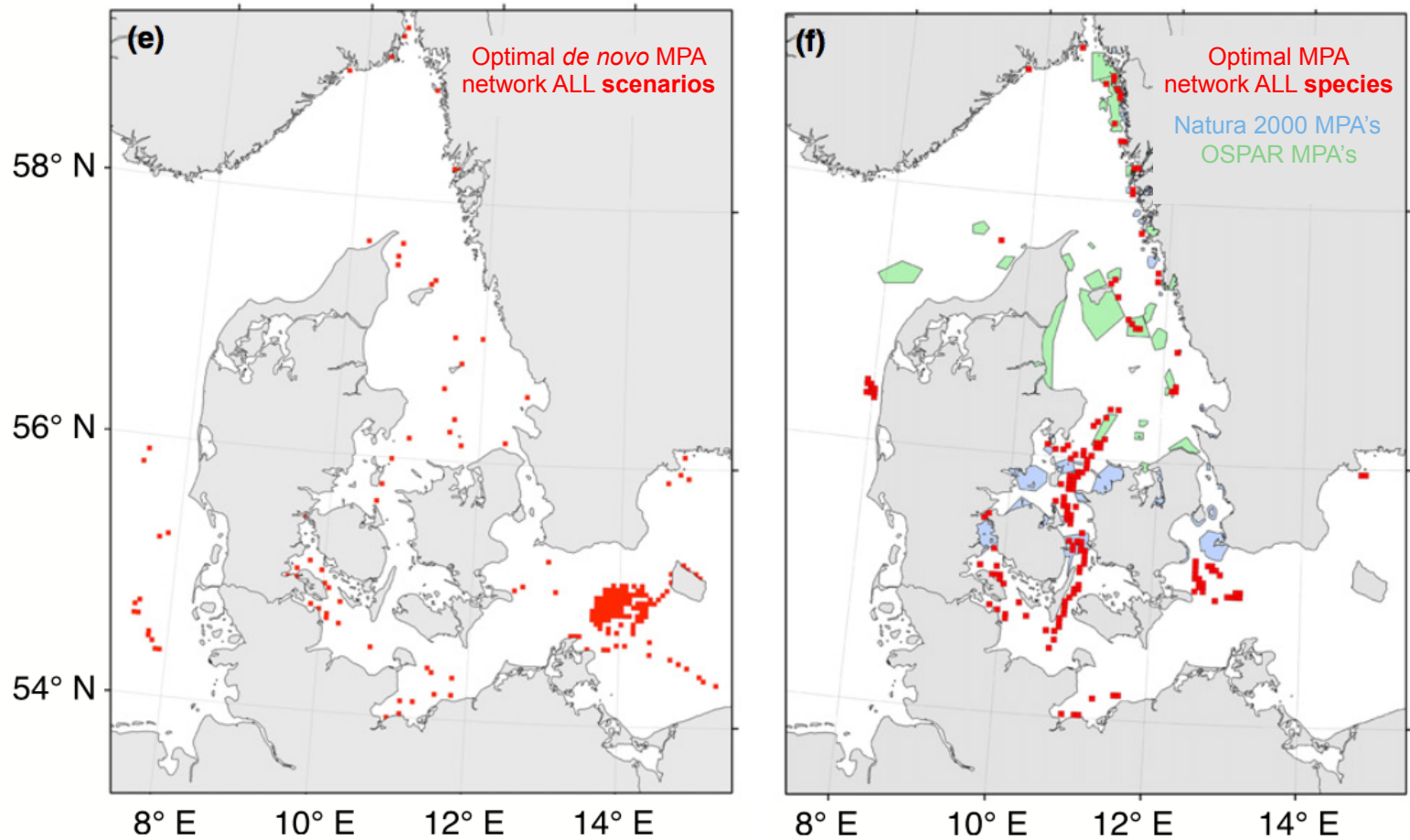
# Identifying the optimal MPA-network



# Identifying the optimal *multi-species* MPA-network



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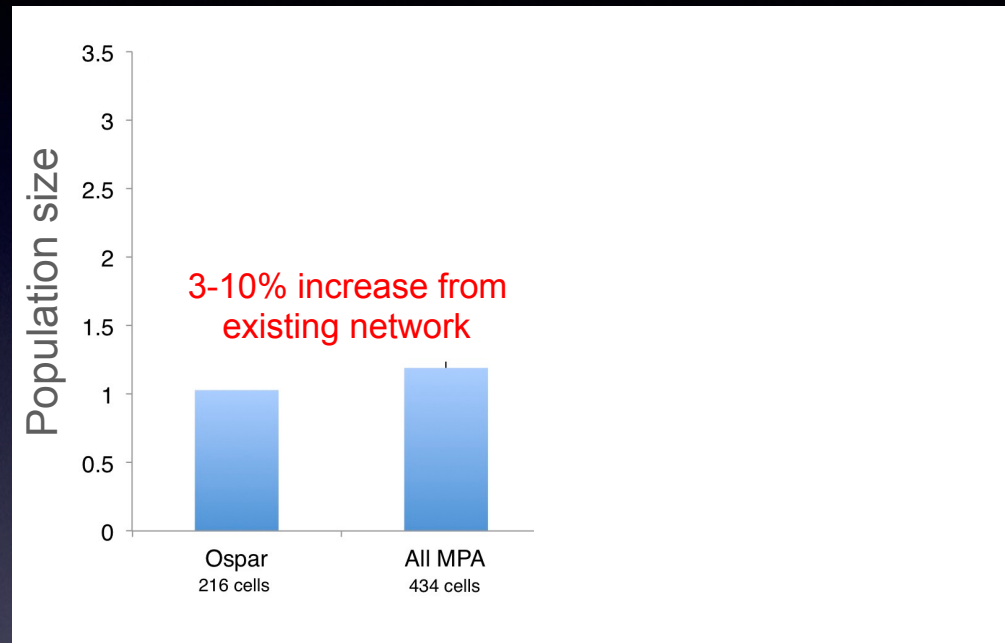
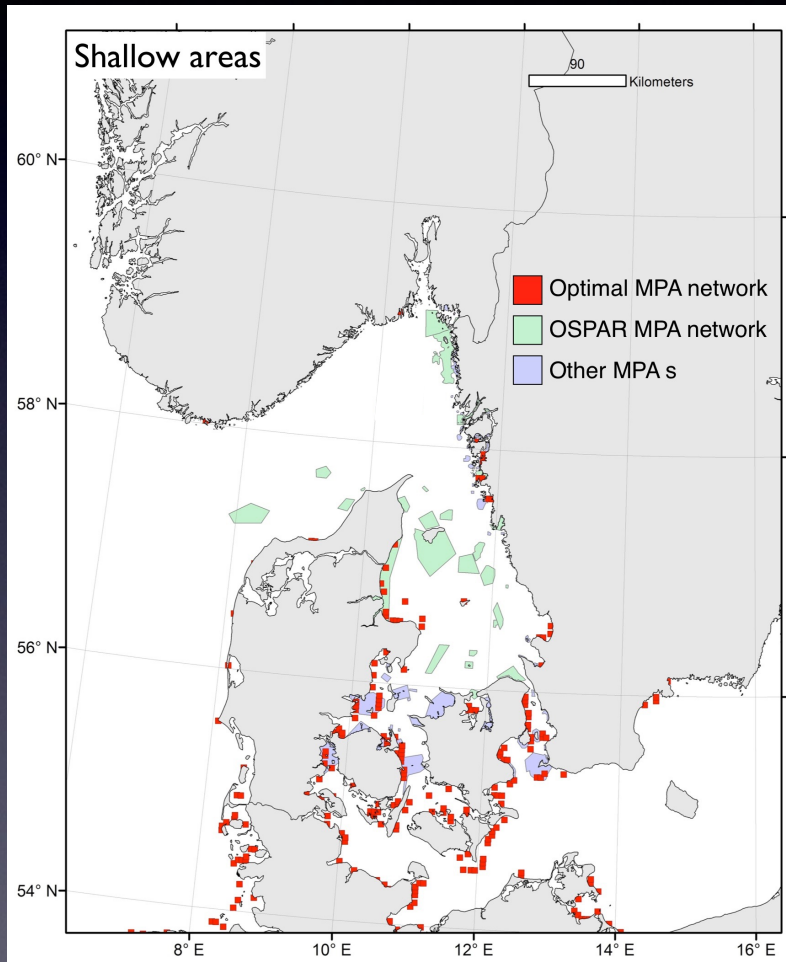
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# Evaluating alternate model MPA-networks

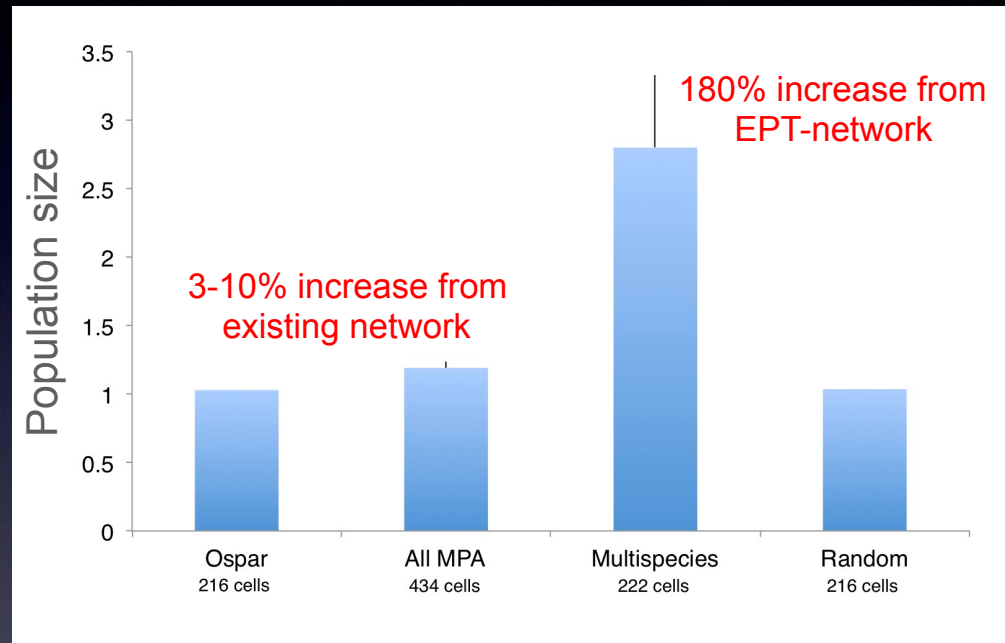
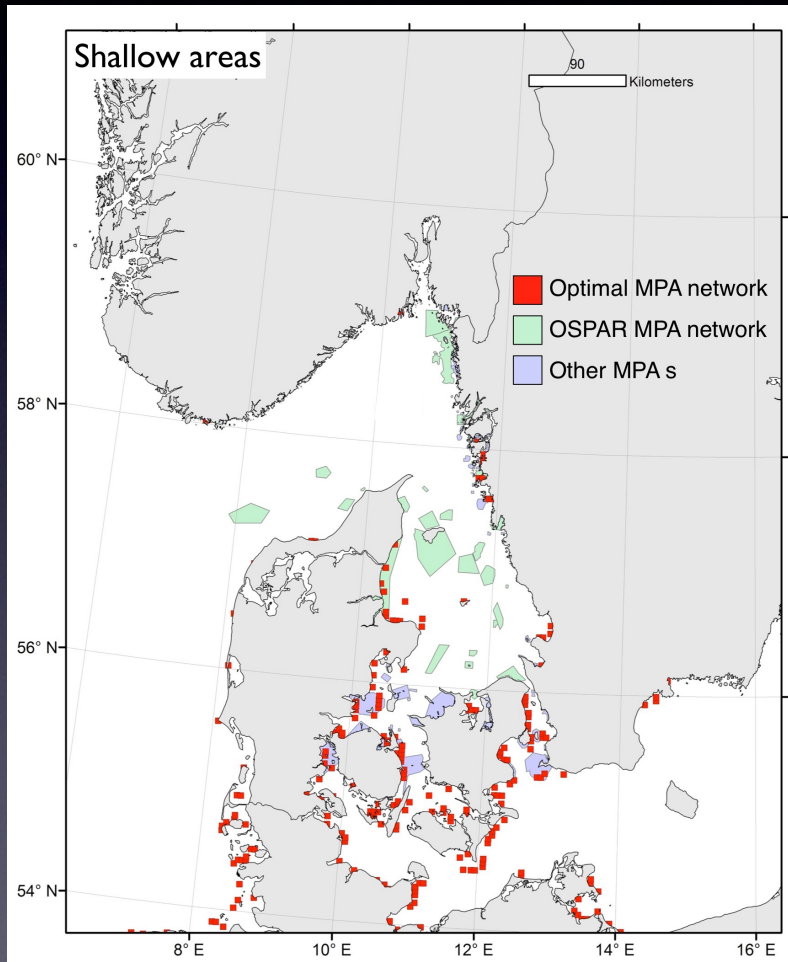
- model dispersal & growth in each meta-population
  - do this for 100 years
- simulate positive effects of MPA's
  - 20% higher growth rate
- simulate random disturbances
  - 95% reduction in population size every 8<sup>th</sup> year
- evaluate networks
  - compare size of populations after disturbance

# Evaluating an optimal *multi-species* MPA-network



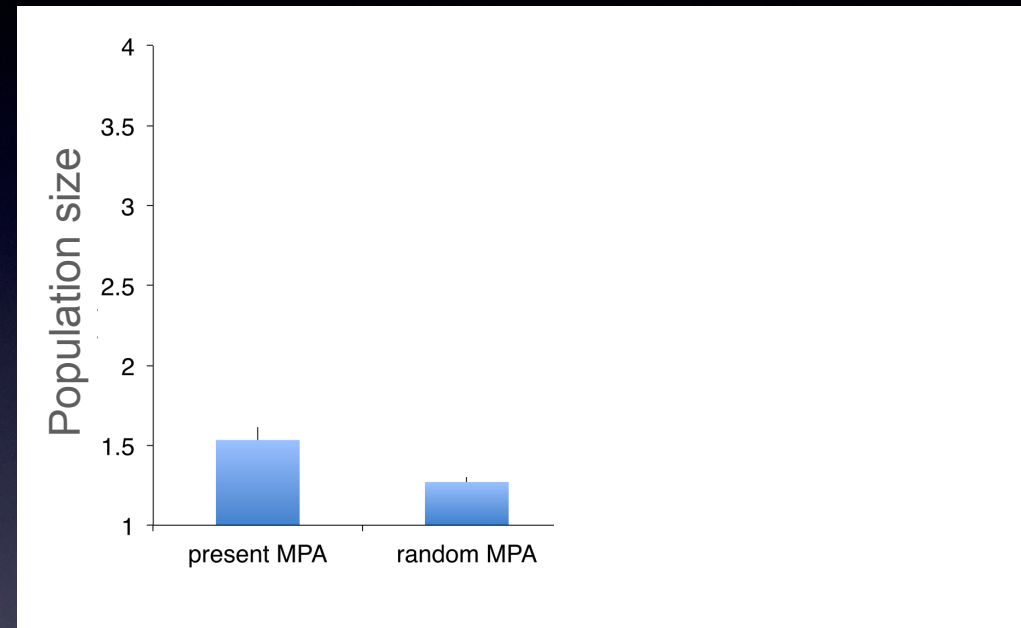
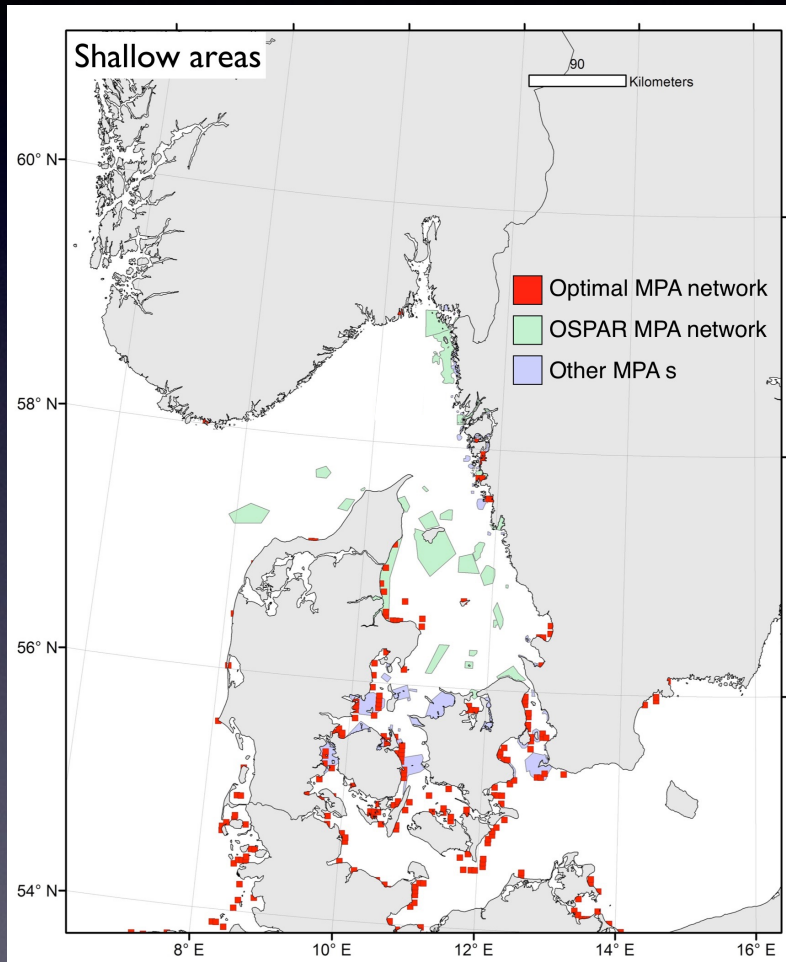
Moksnes et al. 2014. *Larval connectivity and ecological coherence of MPAs in the Kattegat-Skagerrak region.*  
Swedish Institute for the Marine Environment report 2014:2

# Evaluating an optimal *multi-species* MPA-network



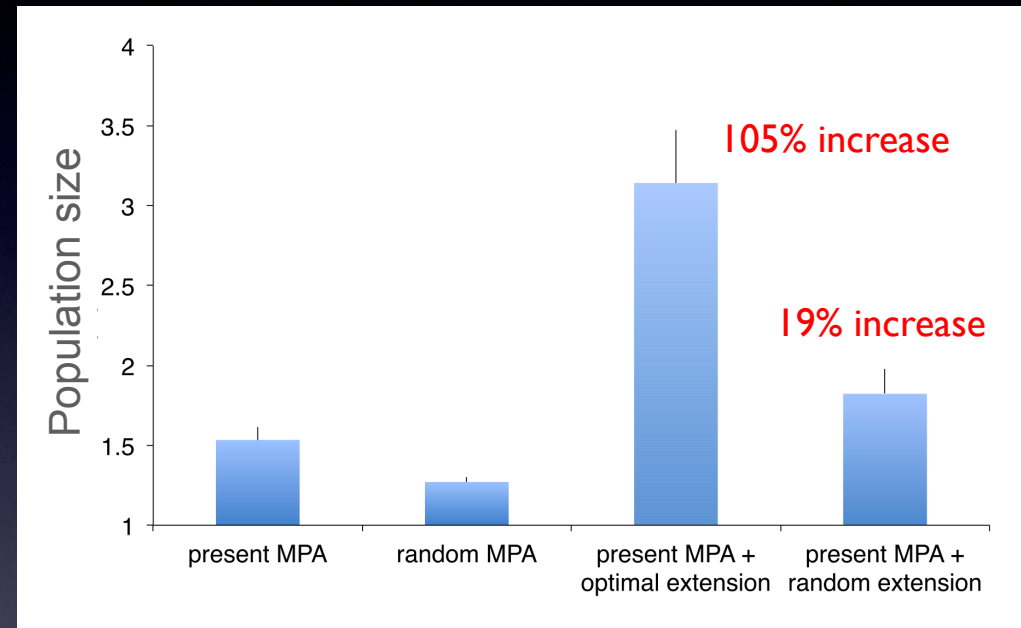
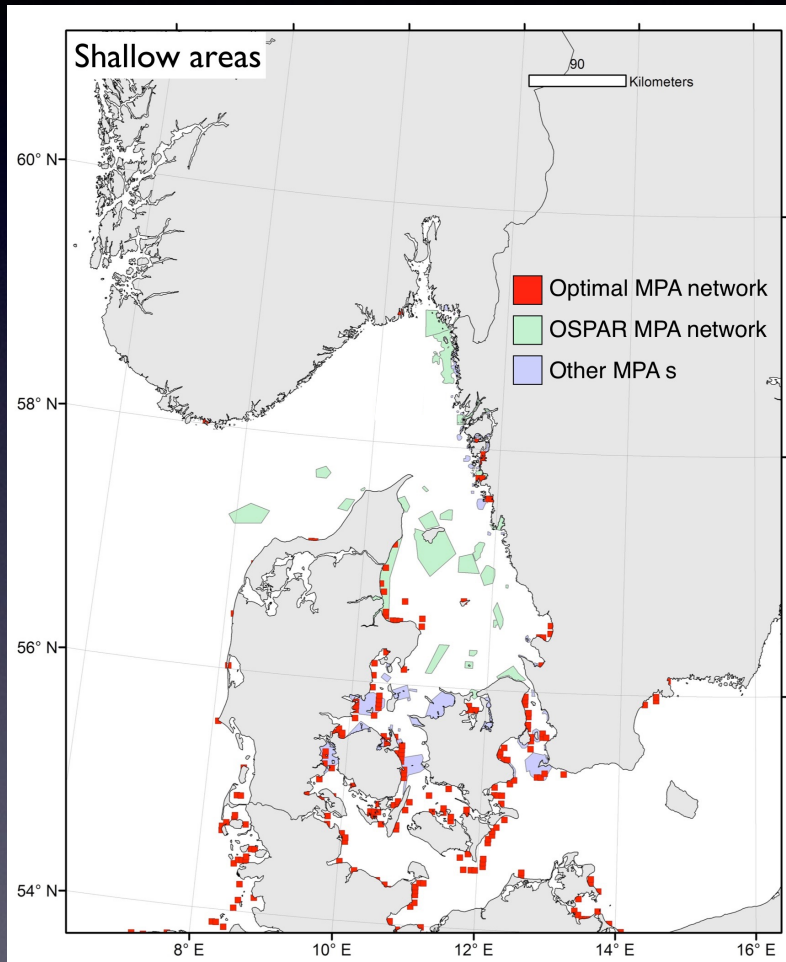
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# Evaluating expansion of an existing MPA-network



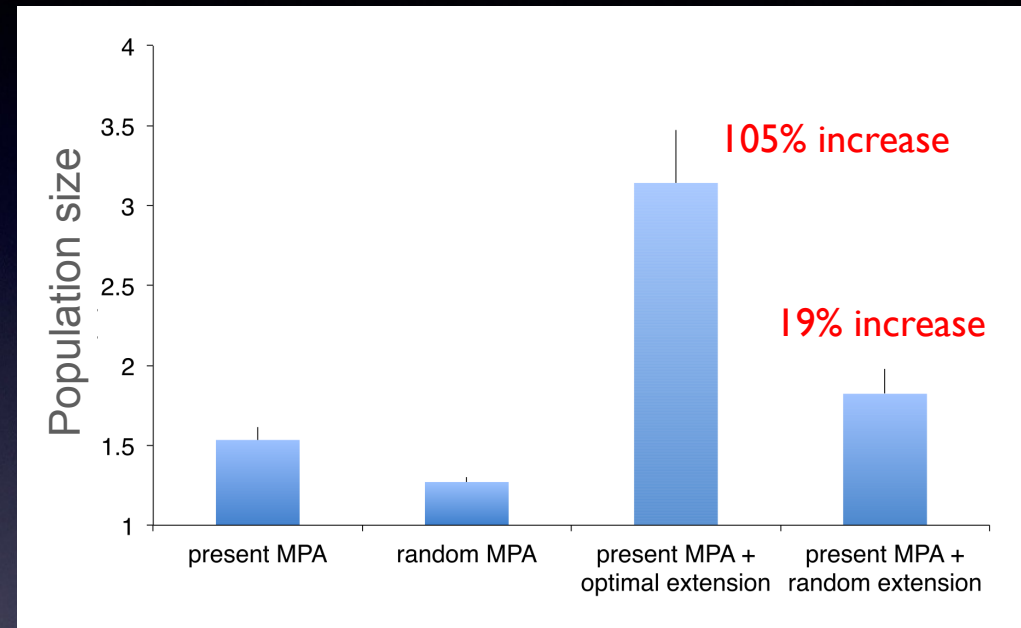
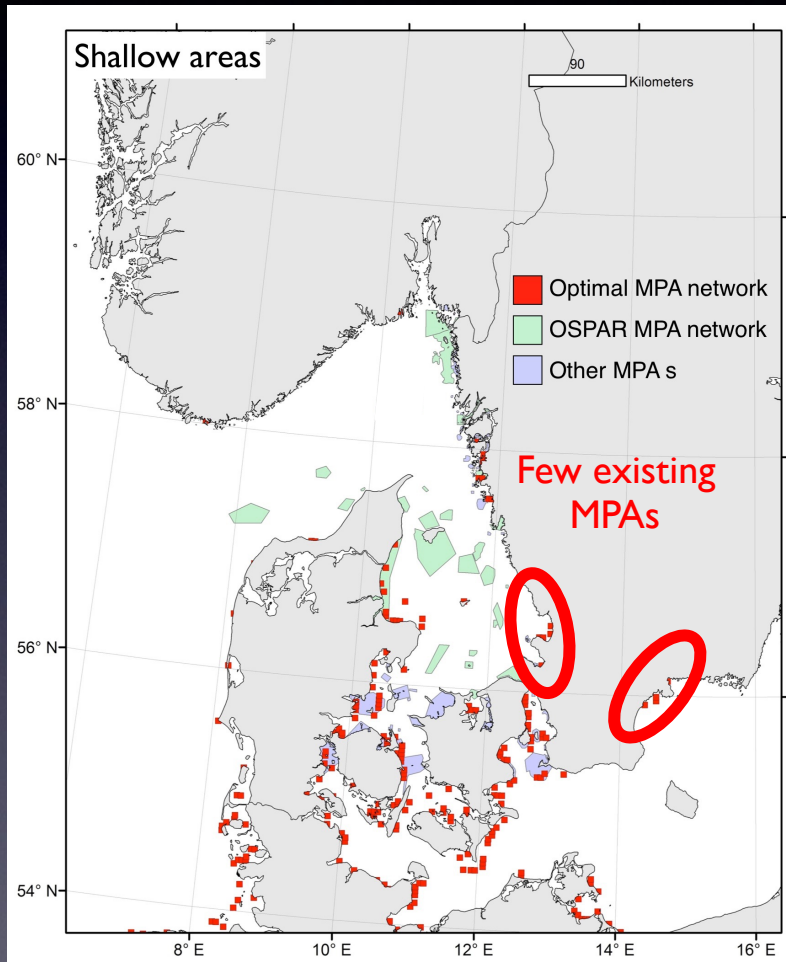
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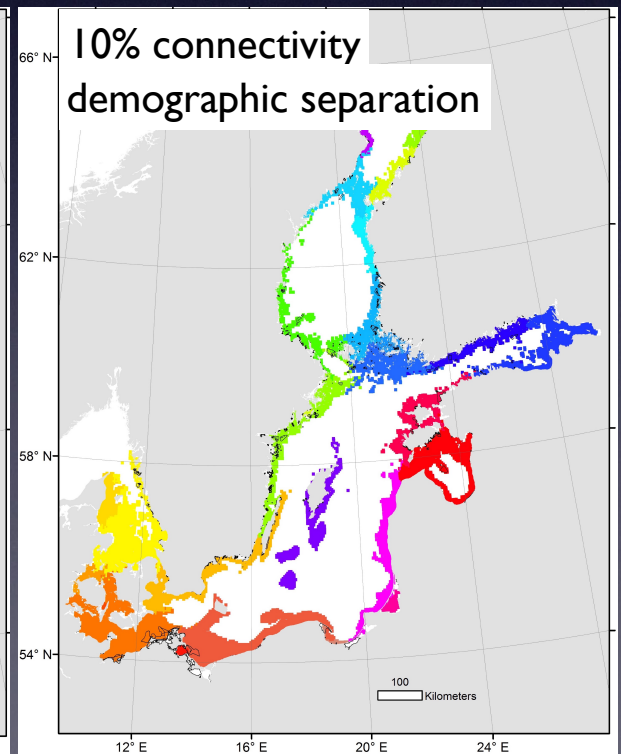
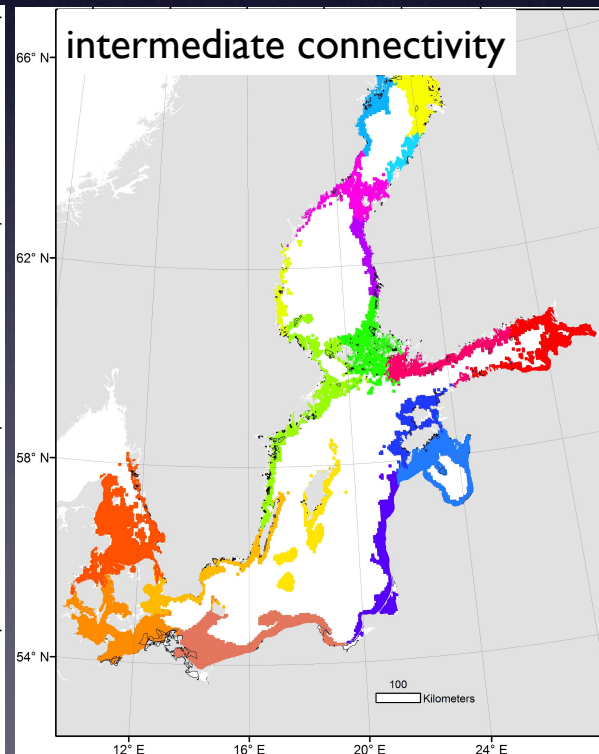
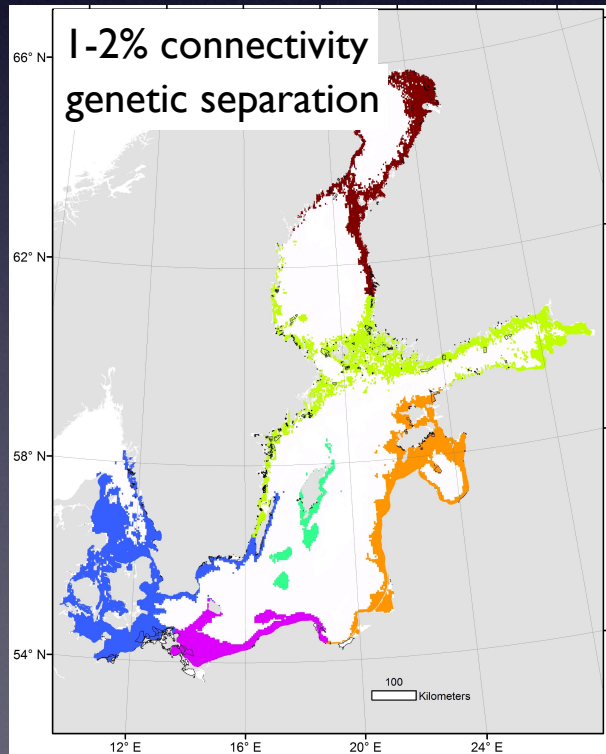


Moksnes et al. 2014. *Larval connectivity and ecological coherence of MPAs in the Kattegat-Skagerrak region*. Swedish Institute for the Marine Environment report 2014:2

- create biophysical model
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  - *de novo*
  - as addition to existing network
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# Dispersal barriers & Management units

- 0-10 m
- 60 day duration
- dispersal at surface
- patterns vary with:
  - release depth
  - larval duration
  - dispersal profile





# Limitations of the approach

- large spatial resolution (2 nm) cannot model coastal circulation well  
larval retention in bays underestimated
- species distribution data, and habitat types, are not included  
these influence locations of larval release as well as growth of populations:  
KEY aspect of MPA specification!
- selection only operates on larval connectivity  
habitat quality, adult dispersal, targeted fishing/disturbance also important

# Conclusions

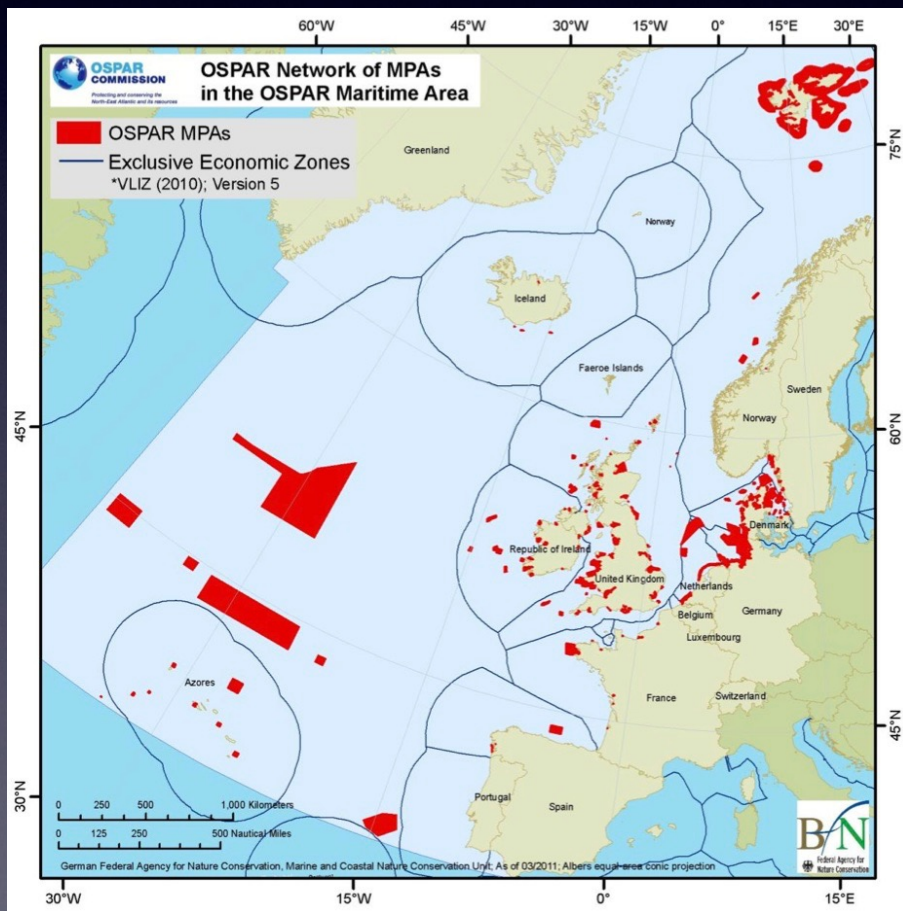
1. this is can be a very **powerful tool**
  - if the circulation model data are available
2. larval dispersal and connectivity **vary with location and larval strategies**
  - cannot be approximated with general dispersal distances
3. **modeling different larval strategies** can provide valuable information
4. existing MPA-networks are **not optimally designed** for larval connectivity
5. carefully chosen **small additions** (<20%) to existing networks can **double population size & resilience**
6. this modeling approach can identify **dispersal barriers that are important for management**

# Thank you!

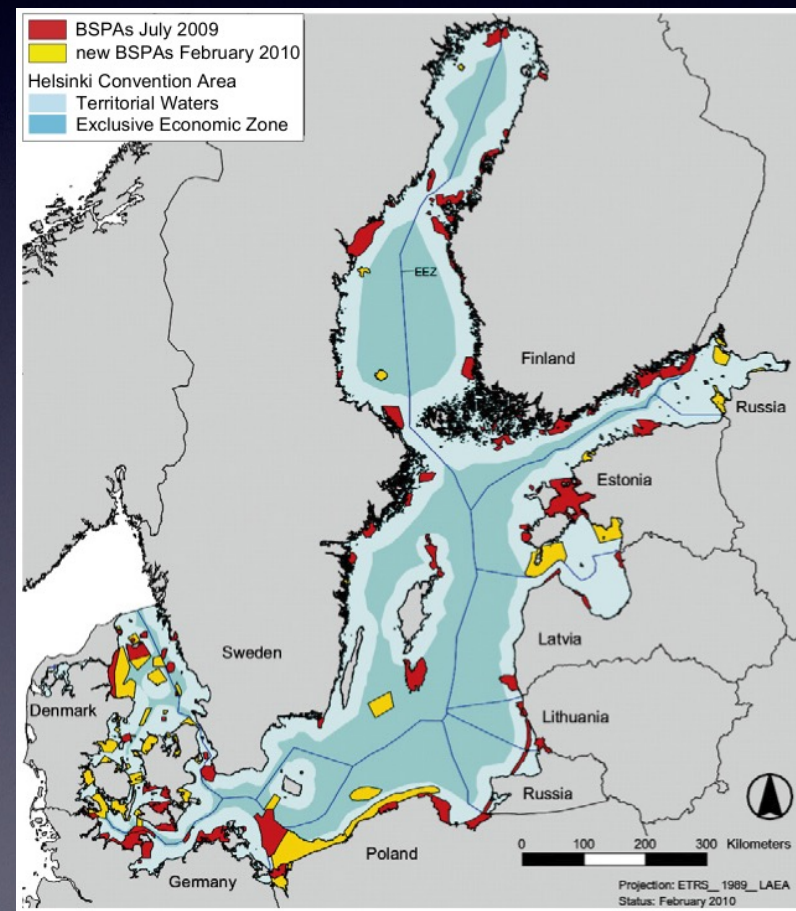
- Swedish Agency for Marine & Water Management
- Gothenburg University
- Swedish Research Council VR
- Swedish Environmental Research Council FORMAS

# Networks of marine protected areas (MPAs)

## North Atlantic (OSPAR)



## Baltic (HELCOM)



# Natura 2000 (EU)

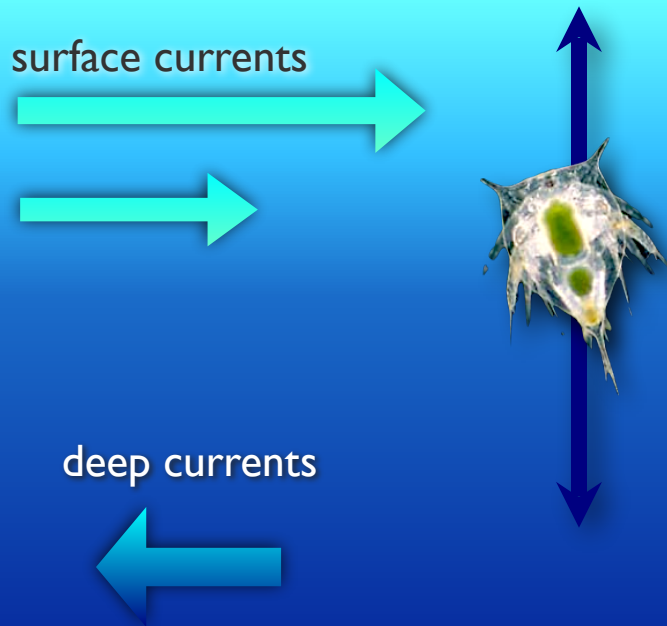
- 3000 sites covering ~ 6% of EU territorial waters
- “Ecological Coherence”
  1. Adequacy
  2. Representativity
  3. Replication
  4. Connectivity



# Larvae interact with ocean currents

don't disperse passively

- Planktonic Larval Duration (PLD)
- dispersal depth
- spawning time



## Comparison with earlier assessment of connectivity of MPA-networks

### OSPAR / HELCOM

1. Only between MPAs
2. Fixed general dispersal-distances (e.g. 250 km)
3. Methods to evaluate network connectivity and coherence missing

### The present method

Between all relevant areas

Area- and species-specific individually modeled dispersals

New method to identify optimal MPA-networks for multiple species (**consensus networks**)

Nilsson Jacobi & Jonsson. 2011. *Ecol. Appl.* 21:1861-1870

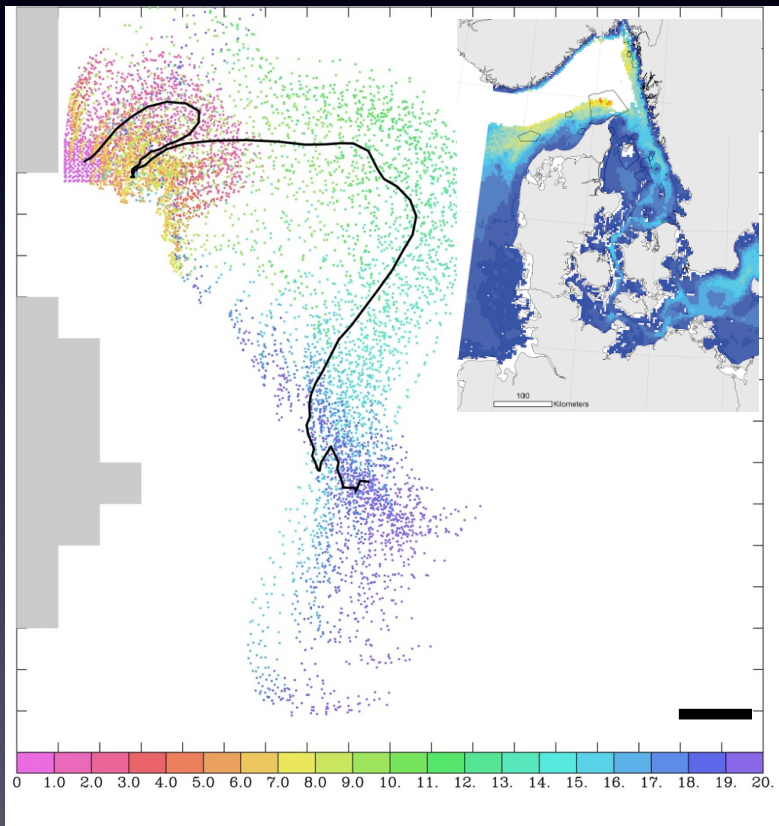
Nilsson Jacobi et al. 2012. *Ecography.* 35:1004-1016

Moksnes P-O et al. 2014. *Swedish Institute for the Marine Environment. Report no. 2014:2*

Moksnes P-O et al. 2015. *Swedish Agency for Marine and Water Management. Report. 2015:24*

Jonsson et al. 2016 *Diversity and distribution* 22:161-173

b. Particle tracking model simulating larval dispersal (**TRACMASS**)



Virtual larvae released from all grid cells 0-100 m (in total 34 000 cells).

20 different larval types (drift depths, larval duration) released from all cells once per month during 8 years.

In total, 3.2 million virtual larvae modeled.



# Estimates of connectivity

Connectivity matrix (probability estimates)  
*For each larval type*

		From				
		1	2	3	4	5
To	1	s	e <sub>21</sub>	e <sub>31</sub>	e <sub>41</sub>	e <sub>51</sub>
	2	e <sub>12</sub>	s	e <sub>32</sub>	e <sub>42</sub>	e <sub>52</sub>
	3	e <sub>13</sub>	e <sub>23</sub>	s	e <sub>43</sub>	e <sub>53</sub>
	4	e <sub>14</sub>	e <sub>24</sub>	e <sub>34</sub>	s	e <sub>54</sub>
	5	e <sub>15</sub>	e <sub>25</sub>	e <sub>35</sub>	e <sub>45</sub>	s

