

## Supplement 1

### Supplementary results incl. sensitivity analyses

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## S1.1 – Hydrodynamic model

MIKE 3 HD FM is based on a flexible mesh approach and a numerical solution of the three-dimensional (3D) incompressible Reynolds averaged Navier-Stokes equations invoking the assumptions of Boussinesq and of hydrostatic pressure. Thus, the model consists of continuity, momentum, temperature, salinity and density equations and it is closed by a turbulent closure scheme. The free surface is taken into account using a sigma-coordinate transformation approach. The scientific documentation of MIKE 3 HD FM is given in DHI (2017a).

The model bathymetry is based on a combination of C-Map navigation chart data and the Danish Coastal Authority survey data. The vertical datum of the bathymetry is DVR90. The vertical resolution consists of a combined sigma-z mesh, with 20 layers, of which the upper 5 layers are sigma-layers (sigma depth 5 meters) and the lower 15 are z-layers with a 1 m vertical grid spacing. The applied atmospheric data (wind speed and direction, air temperature and precipitation) are from StormGeo's WRF meteorological model covering the North Atlantic. The data are provided in a resolution of 0.1° x 0.1° in hourly time steps.

Measurements (from Denmark's national monitoring programme) or regional model results of water level, salinity and water temperature is applied as boundary data. Details on the model parametrisation are shown the table below.

*Summary of applied hydrodynamic model settings and constants in the Limfjord model.*

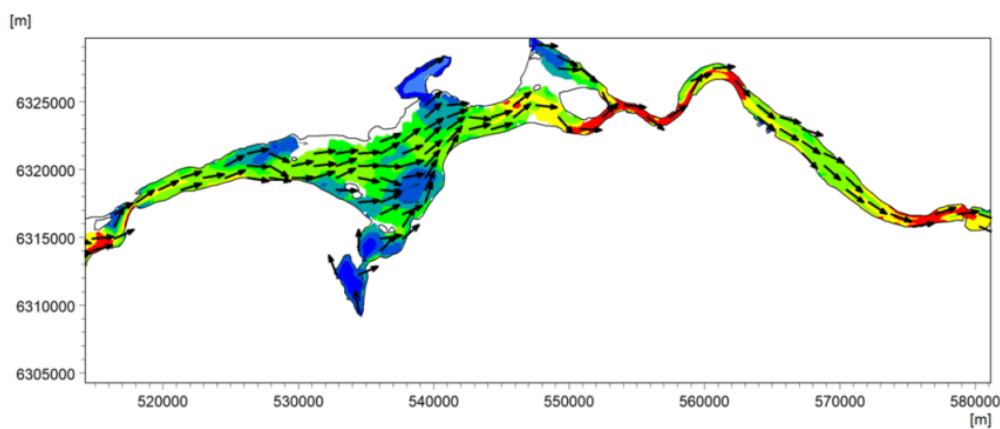
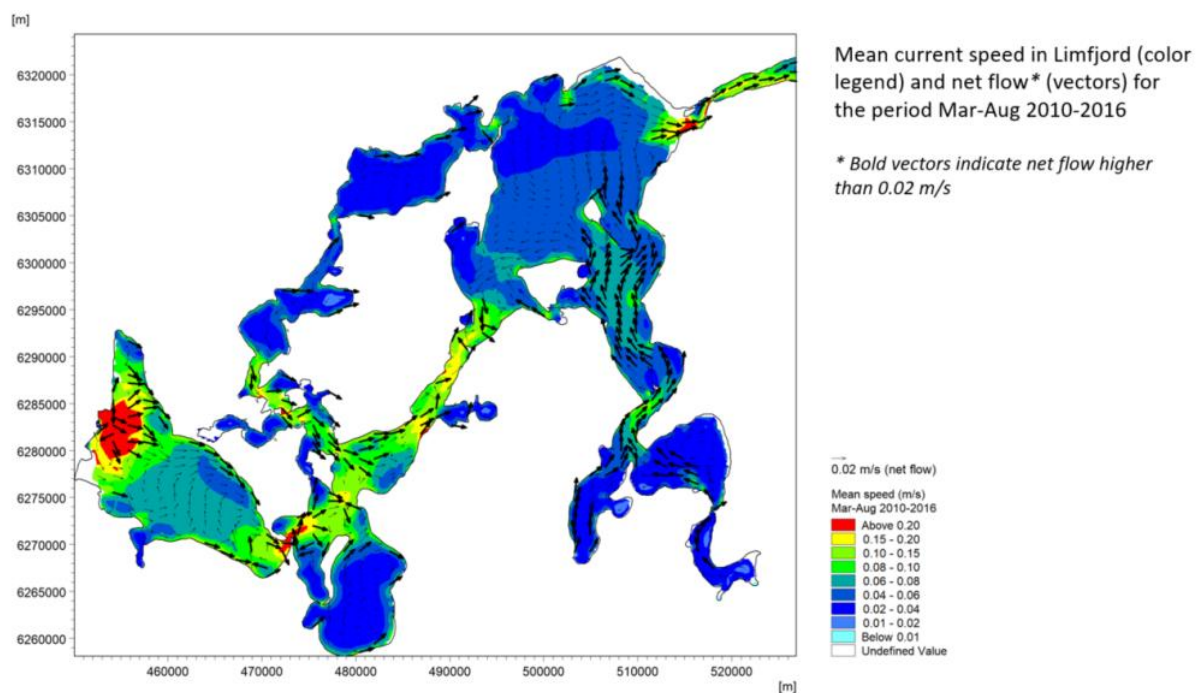
Feature/Parameter	Setting/Value
Flooding and drying	Included with parameters: 0.005m, 0.05m and 0.1m
Wind friction coefficient	Linearly varying between 0.001255 and 0.002425 for wind speeds between 7 and 25m/s
Bed roughness	Constant value 0.01m
Eddy viscosity	Horizontally: Smagorinsky formulation, $C_s=0.28$ Vertically: k- $\epsilon$ model with standard parameters and no damping
Solution technique	Shallow water equations: Low order Transport equations: Low order
Overall time-step	300s
Heat exchange	Light extinction coefficient 0.3, otherwise standard parameters Humidity: Constant = 88%
Dispersion (S/T)	Scaled to Eddy viscosity. Horizontal/vertical scaling factors = 1.0/0.01

Model output is saved in 2D (water level and water depth) and 3D (current speed and direction, salinity, and water temperature) every hour, and the model validation is reported in Erichsen & Birkeland (2019).

The ability of the spatial and temporal resolution of the model to resolve larval dispersal processes was not tested systematically. However, the spatial resolution is considered fine scale (<100 m – 500 m), and was adjusted iteratively during hydrodynamic model calibration to ensure optimal model performance regarding e.g., temperature and salinity against

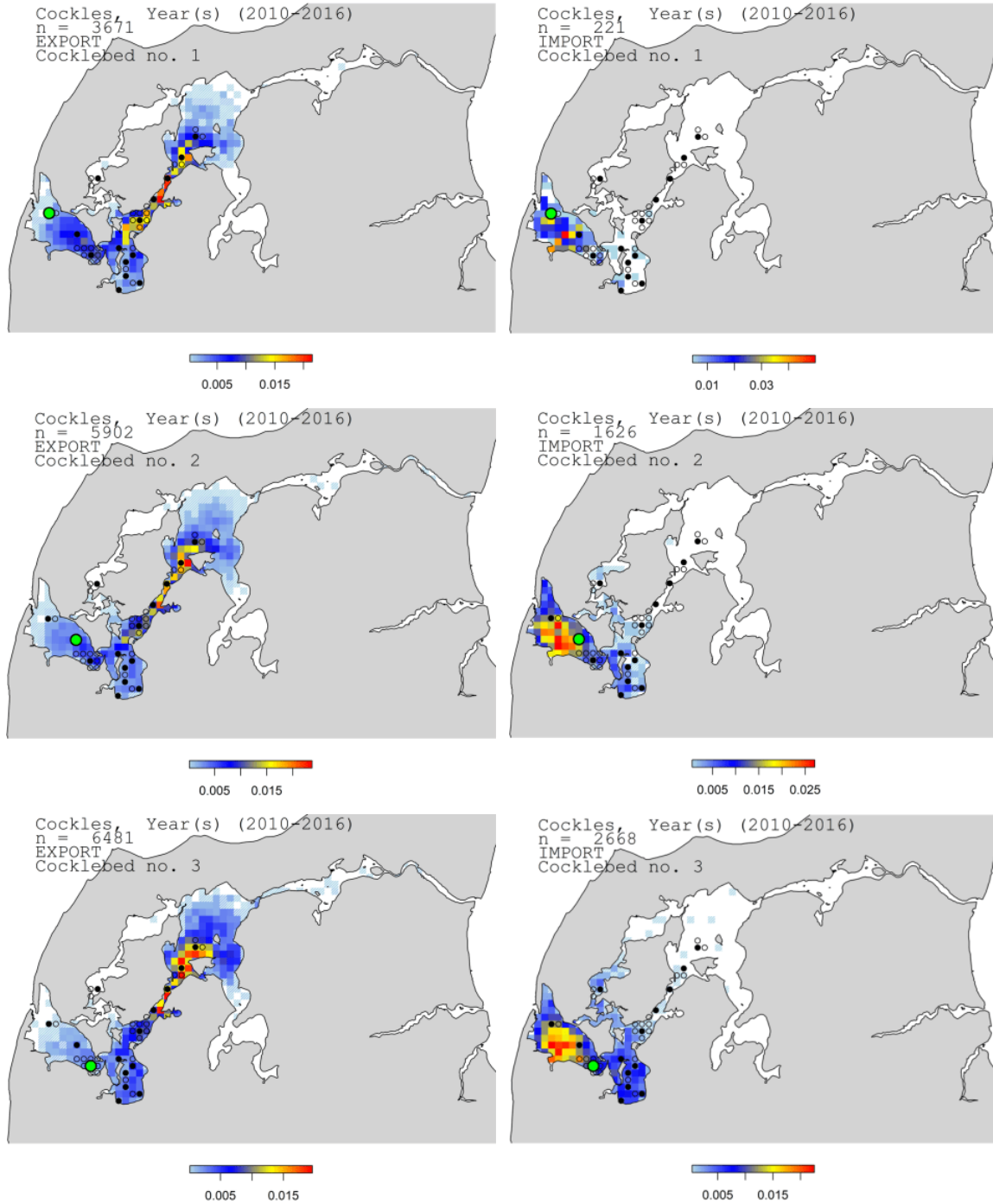
measurements at 33 stations (Erichsen and Birkeland 2019). Due to the use of salinity as a passive density and current driven calibration parameter, we consider the ability of the mesh resolution to resolve larval dispersal processes as sufficient, acknowledging that further reduction in mesh size (as well as time step) may improve model performance slightly. Downscaling of the computational mesh, in general, may lead to an increase of local retention of simulated larvae (Swearer et al 2019). The hydrodynamic model was originally developed to sustain biogeochemical modelling of Danish marine waters for the Danish Environmental Protection Agency and has been evaluated by an international evaluation committee (see: Implement 2017).

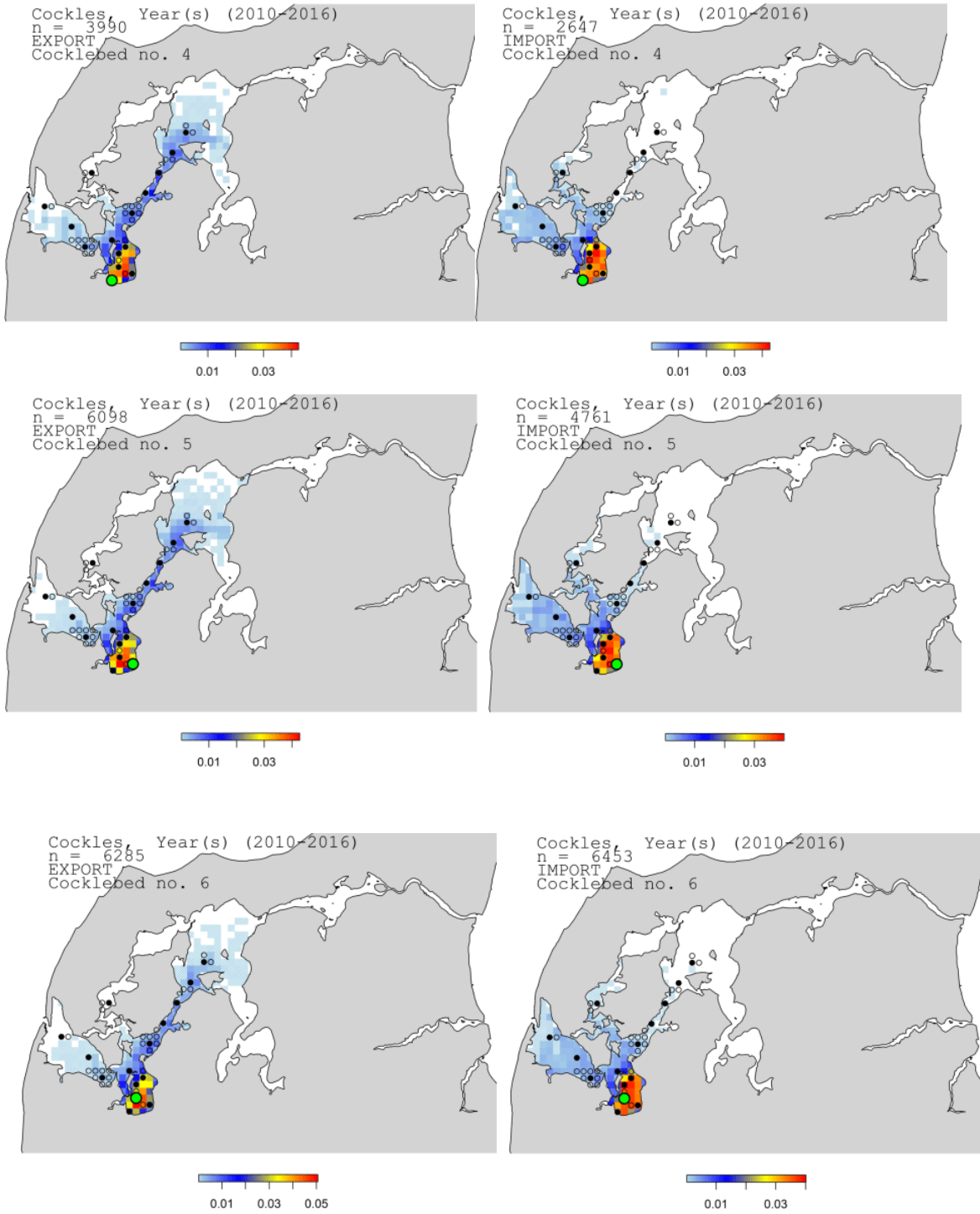
Residual current in Limfjorden extracted from the hydrodynamic model for march to august for 7 years 2010-2016 are shown in the figure below. Coordinates are in UTM.

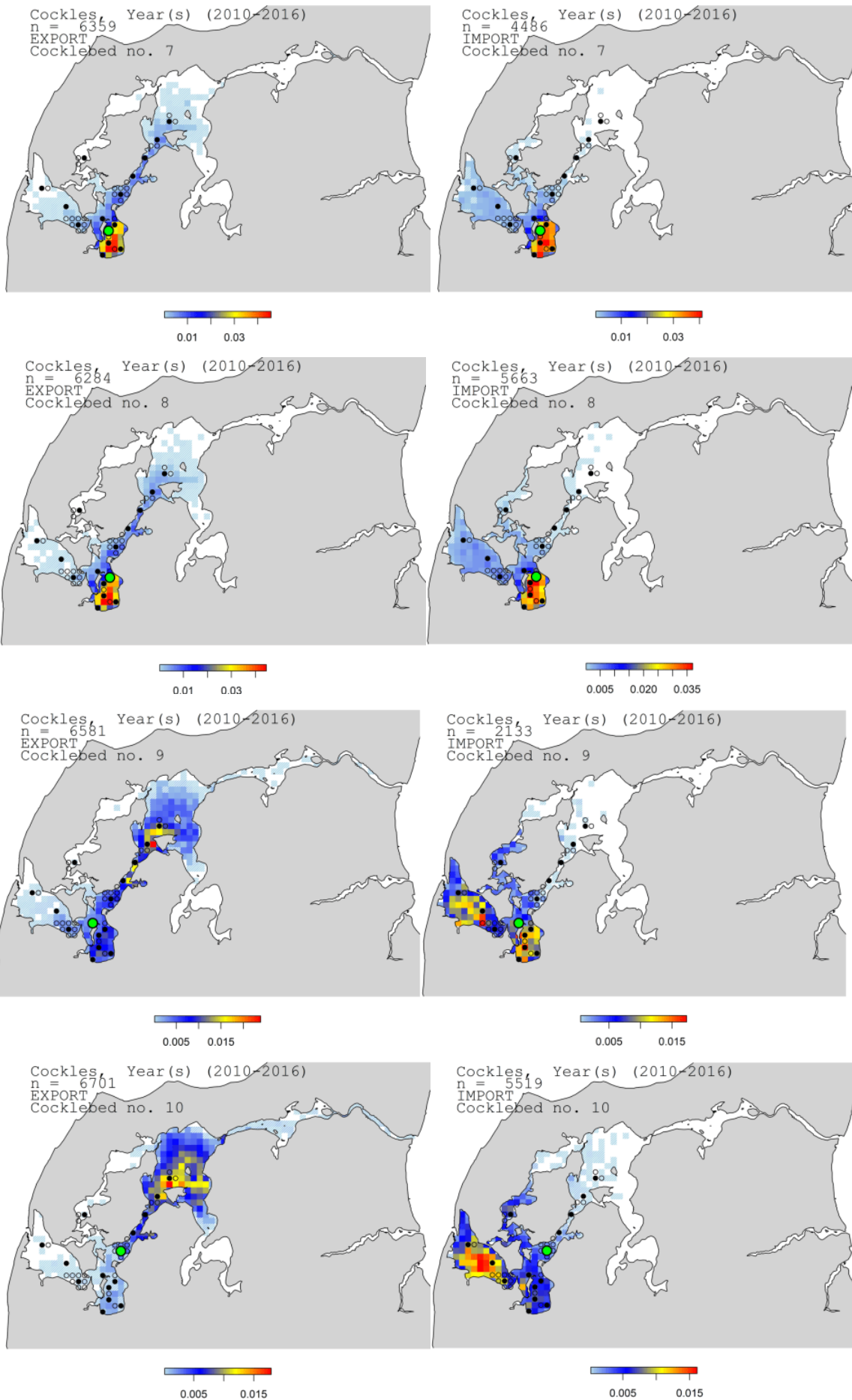


## S1.2 - Dispersal probabilities for major cockle beds (All years)

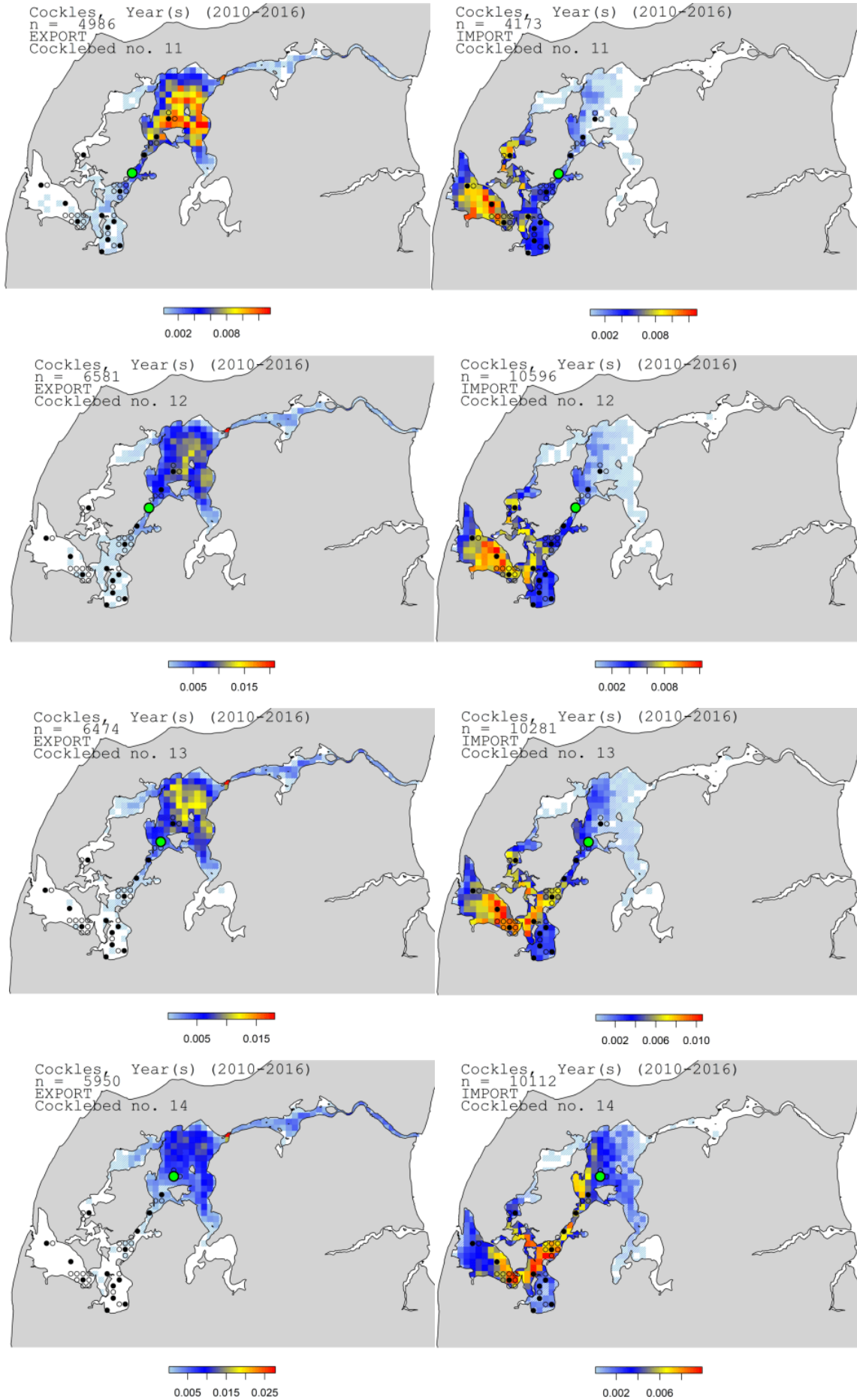
Connectivity probability maps were extracted for grid cells representing the 15 know major cockle beds within the connectivity grid representing agent export (incl. LR) and agent import (incl. SR) respectively.

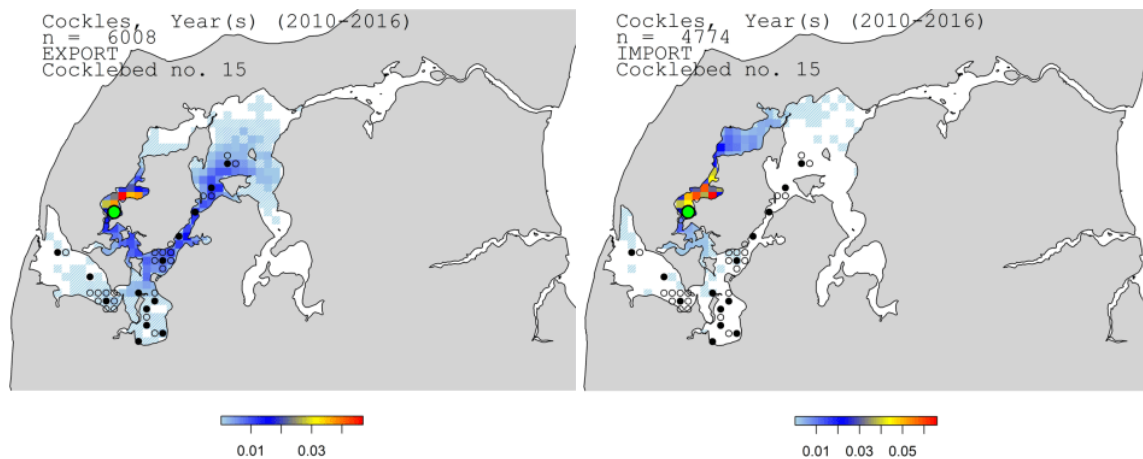












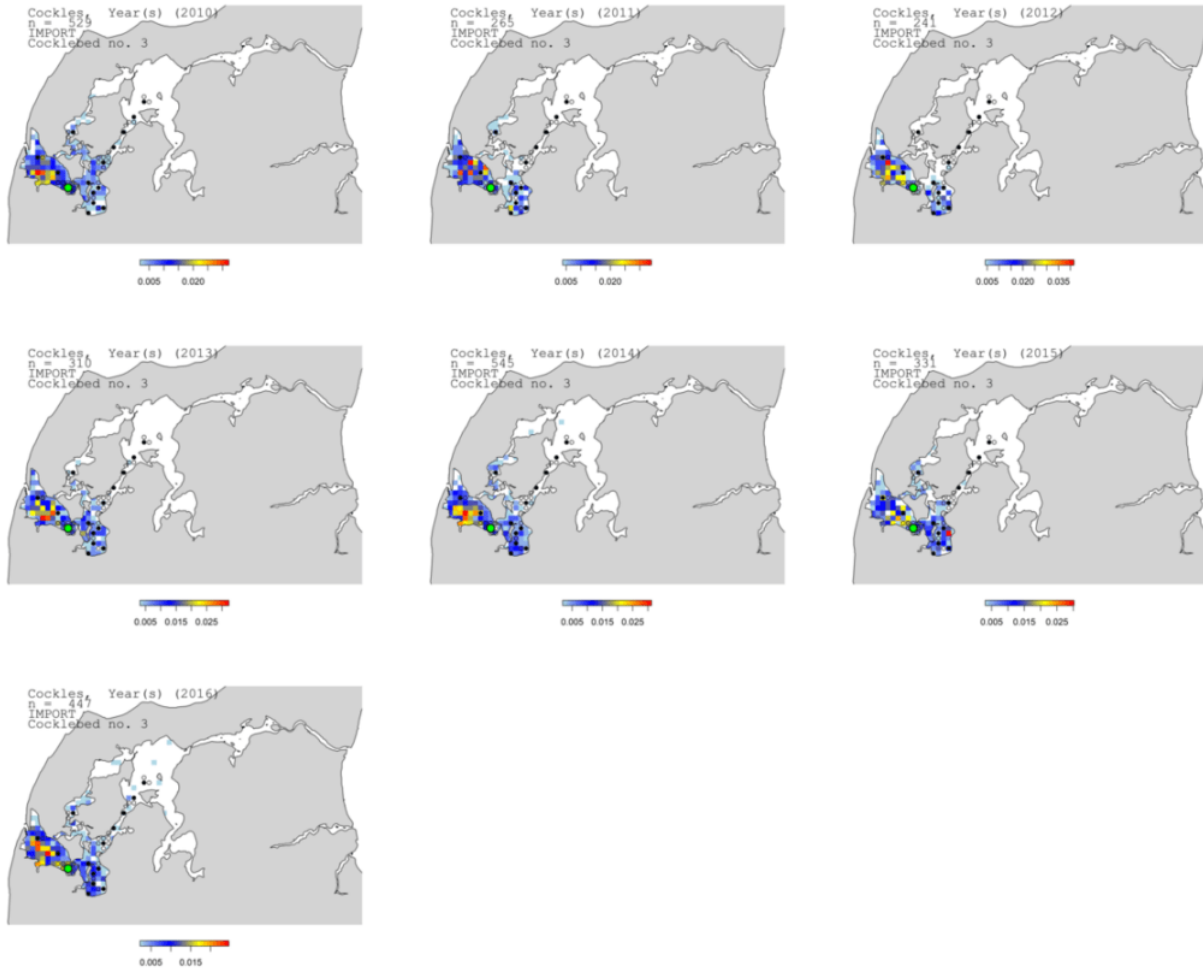
Export (left) and import (right) connectivity probability maps for selected positions in the connectivity grid (enlarged green dot) representing existing major cockle beds in Limfjorden (nos. 3, 6, 10, 13 and 15 - Figure 3) based on cockle larval dispersal simulation for seven years, 2010-2016. For export connectivity probability maps, colour legends represent dispersal probabilities calculated relative to the initial release of larvae in the ABM model including larvae exported out of the domain across the open boundaries but excluding agent stranded on dry cells (see methodology section). For import connectivity probability maps, colour legends represent dispersal probabilities calculated relative to the total number of larvae settled in each grid. “n” refers to the total number of larvae included in the analysis. Black dots (filled AND hollow) refer to connectivity grid (2x2 km) cells which coincide with high cockle densities from the 2018-19 survey, and/or from cockle fisheries data (black box data) from 2013-2021, see text for details.



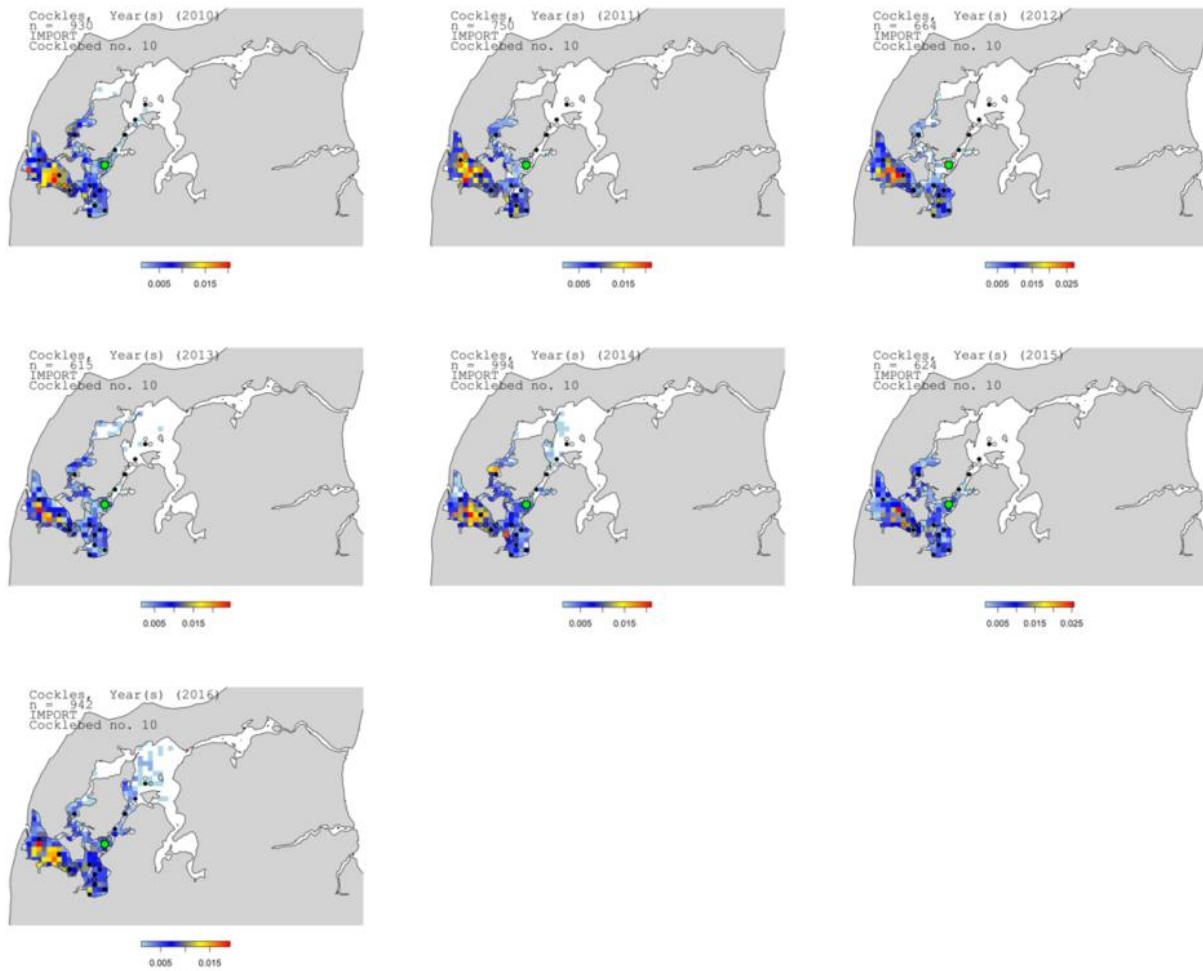
### S1.3 - Dispersal probabilities for major cockle beds (individual years)

Examples of between years variability in import dispersal probabilities for selected locations (green dot) including Nissum Bredning, Kås Bredning, Løgstør Bredning and Visby Bredning.

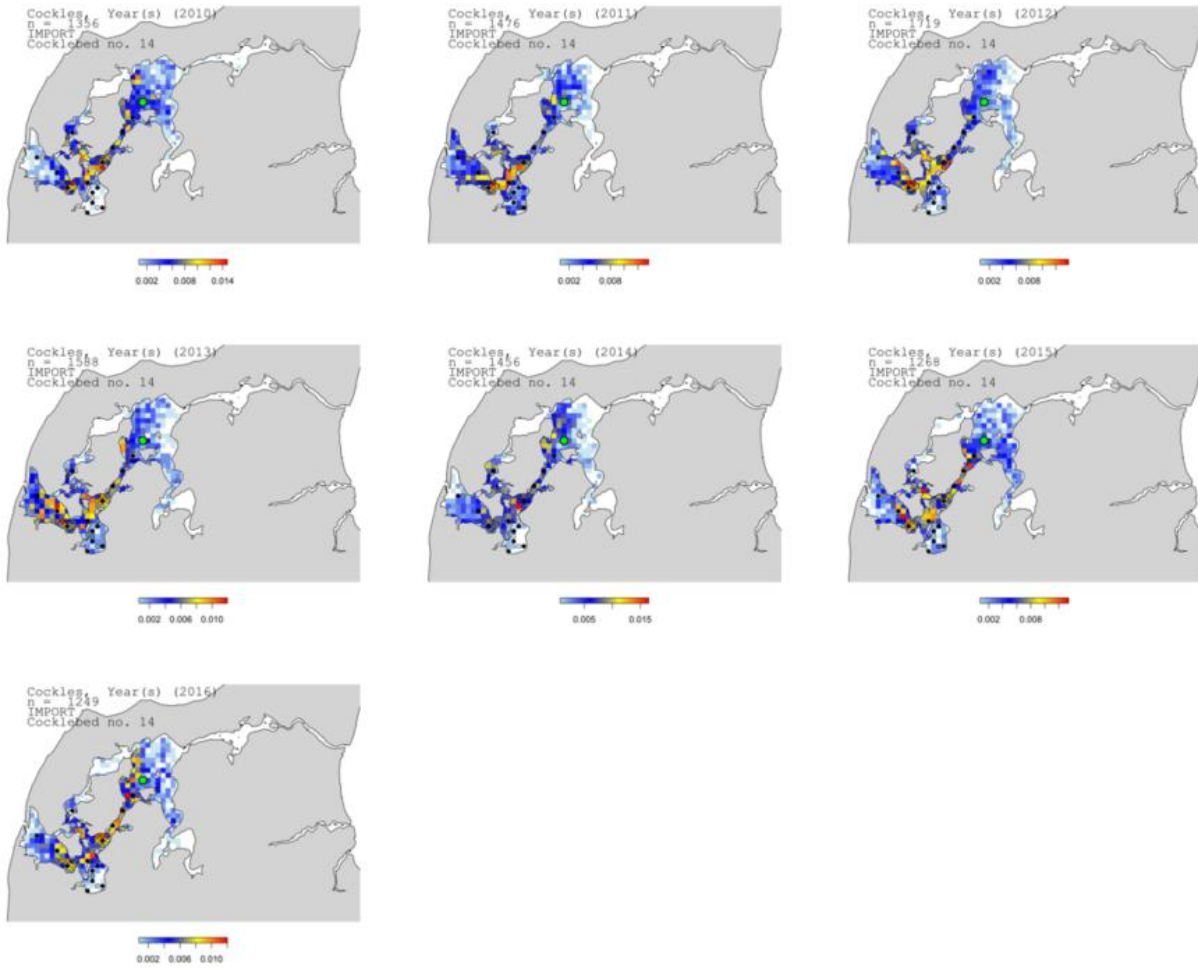
Nissum Bredning, Cocklebed no. 3:



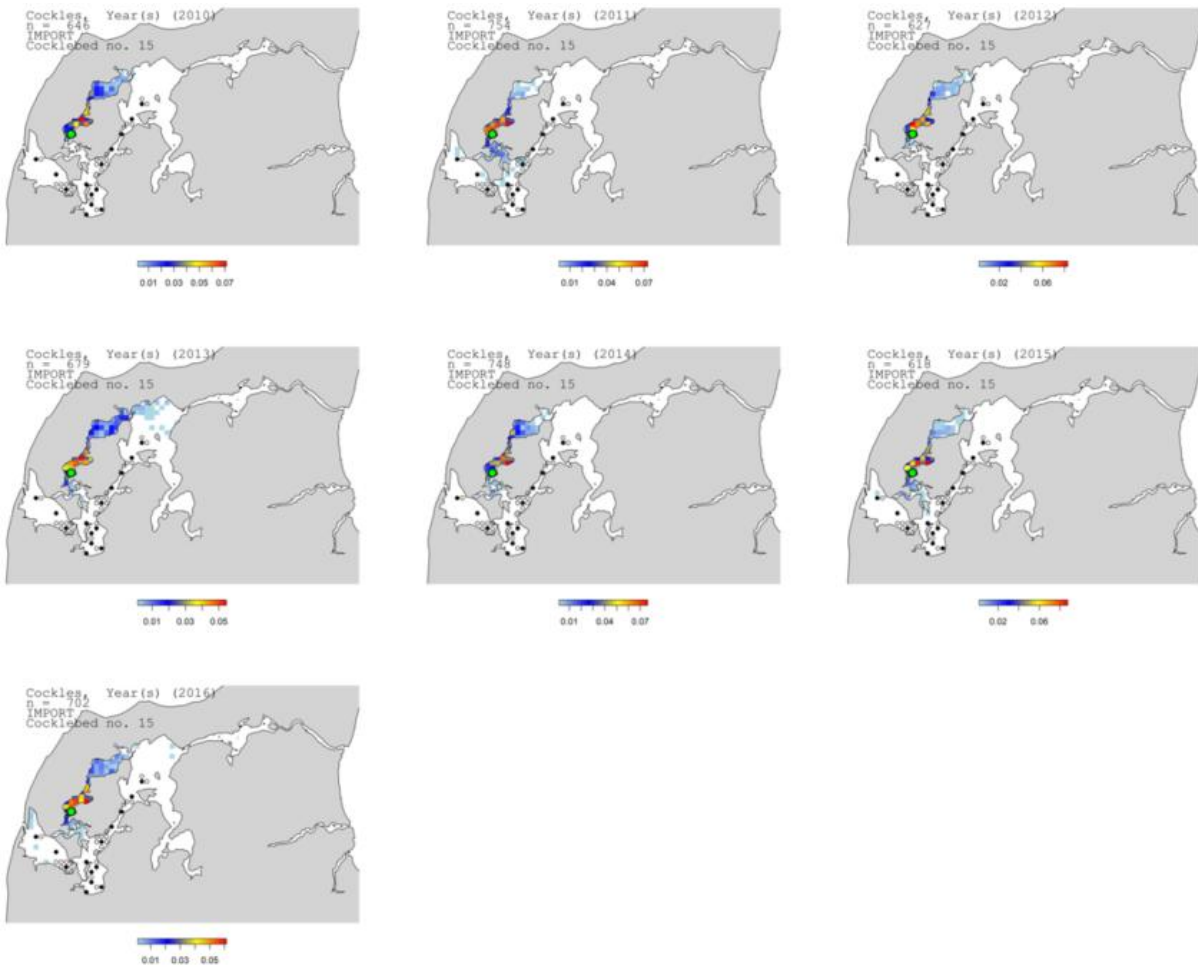
Kås Bredning, Cocklebed no. 10:



Løgstør Bredning, Cocklebed no. 14:

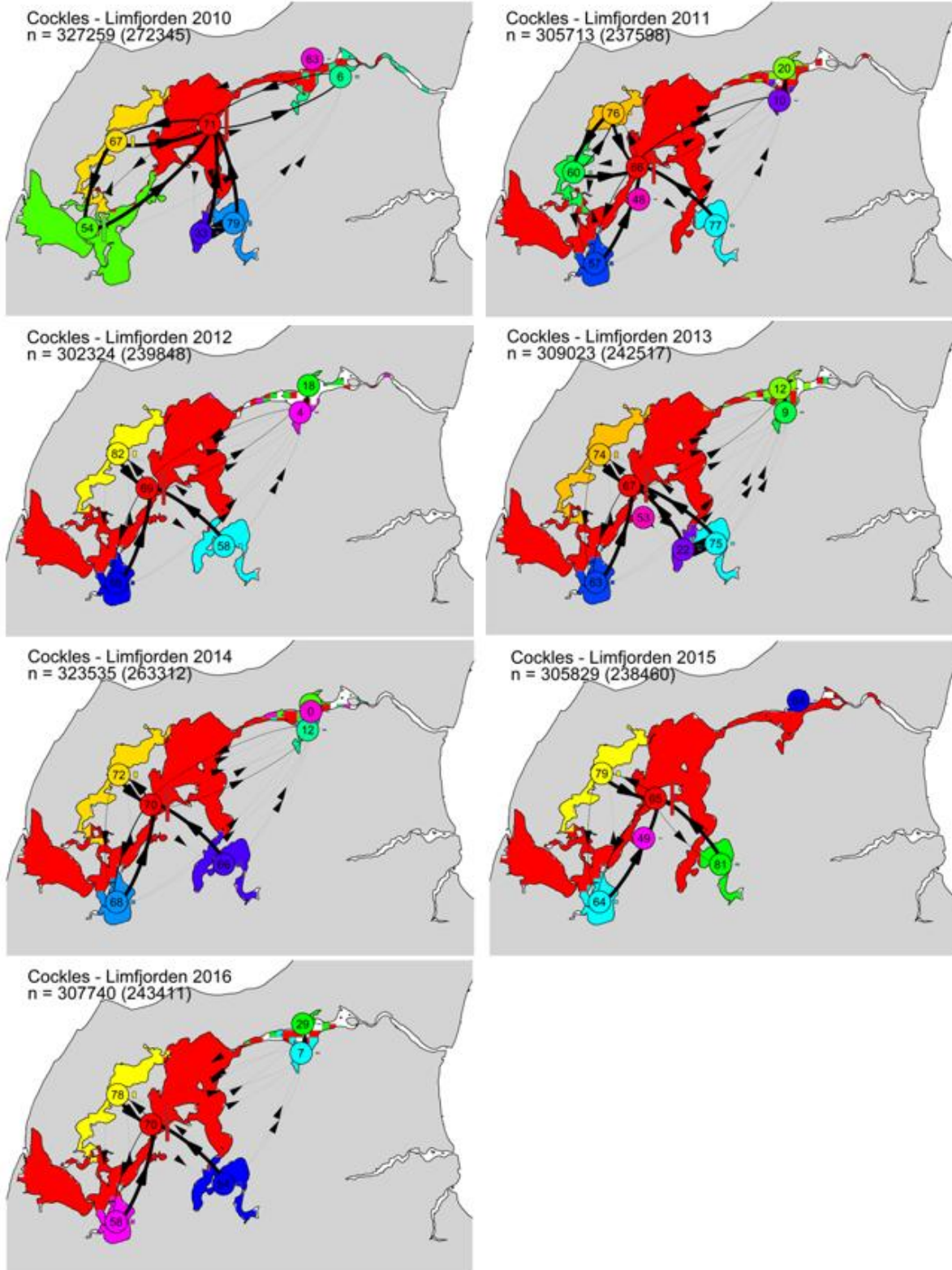


Visby Bredning, Cocklebed no. 15:



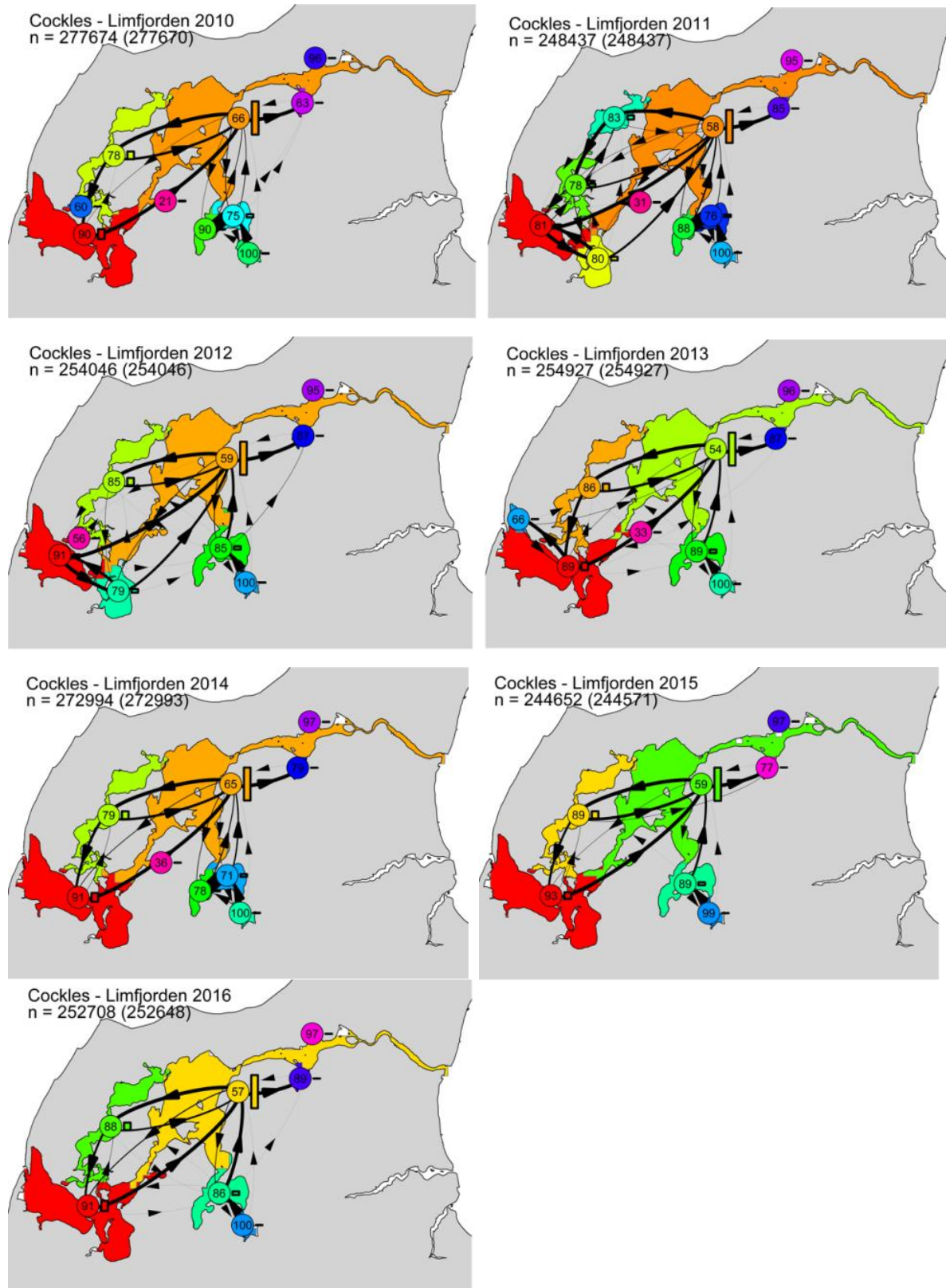
## S1.4 - Cluster analysis results for individual years

Cluster analysis for individual years 2010-2016 based on non-transposed connectivity matrices of absolute numbers of connections representing larval export and local retention:





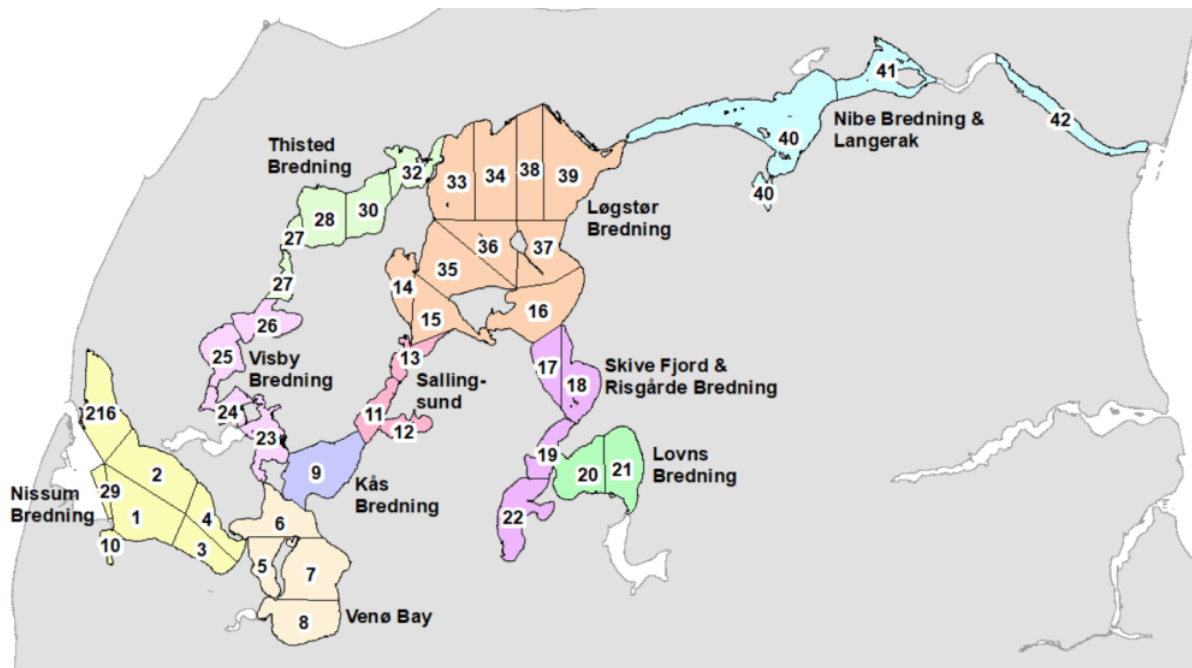
Cluster analysis for individual years 2010-2016 based on transposed connectivity matrices of absolute numbers of connections representing larval import and self-recruitment:





## S1.5 – Mussel Fisheries Administrative units of Limfjorden

Sub-basins of Limfjorden are shown in the below figure by colour and name, and “numbers” are the ID’s of the “mussel production areas” in Limfjorden referred to in the text as “Administrative units” as outlined by the Danish Fisheries Agency. Administrative units are included in the import and export probability connectivity matrices.



S1.6 - Connectivity probability matrices for sub-basins

		TO																																										SUM															
		Nissum					Venø				Salling					Lægstar					Visby				Thisted				Skive				Lovns		Nibe																								
Location	Location ID	1	2	3	4	10	29	216	5	6	7	8	9	11	12	13	14	15	16	33	34	35	36	37	38	39	23	24	25	26	27	28	30	32	17	18	19	22	20	21	40	41	42																
Nissum	1	5.14	3.99	2.70	3.98	0.32	0.37	0.55	0.89	5.00	2.08	1.86	11.23	6.70	2.95	3.52	0.52	8.45	1.42	0.57	0.65	7.23	1.51	1.73	0.50	0.33	0.34	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.08	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.01	74.2													
	2	3.43	2.67	1.82	2.56	0.18	0.20	0.38	0.91	4.13	2.31	2.22	9.97	7.05	3.69	4.15	0.70	10.40	2.16	0.79	1.09	9.72	2.43	2.75	0.84	0.53	0.31	0.01	0.00	0.01	0.00	0.00	0.00	0.03	0.14	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.01	0.01	77.7													
	3	2.57	1.95	1.88	1.77	0.17	0.20	0.24	1.10	4.17	3.24	3.23	9.55	7.24	4.33	4.21	1.20	12.15	3.97	1.40	2.02	13.16	3.89	4.45	1.74	1.43	0.33	0.02	0.01	0.00	0.00	0.00	0.01	0.02	0.32	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.04	0.03	92.4											
	4	1.68	1.18	1.14	1.34	0.07	0.09	0.19	0.91	3.08	2.97	3.34	8.03	6.31	4.67	4.12	1.24	12.46	4.97	1.74	2.65	14.57	4.84	5.89	2.34	1.75	0.39	0.02	0.02	0.01	0.00	0.01	0.01	0.02	0.46	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.29	0.03	0.09	93.2											
	10	5.11	3.36	3.12	3.43	0.48	0.54	0.60	0.99	5.02	2.50	3.39	11.67	7.74	3.01	4.01	0.60	9.25	1.40	0.72	0.94	8.45	1.57	1.75	0.57	0.24	0.30	0.03	0.02	0.02	0.00	0.00	0.02	0.00	0.08	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	81.0												
	29	4.63	3.65	2.28	2.89	0.30	0.37	0.57	0.69	4.33	1.51	1.36	9.77	5.10	1.97	2.56	0.36	6.16	0.77	0.31	0.95	5.10	0.94	0.97	0.22	0.04	0.29	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	57.7												
	216	1.71	1.65	0.90	1.43	0.08	0.10	0.16	0.37	2.19	1.01	0.80	5.49	3.91	1.71	1.88	0.35	4.86	0.77	0.37	0.49	4.18	1.12	1.04	0.24	0.13	0.15	0.01	0.02	0.01	0.00	0.00	0.00	0.00	0.01	0.04	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	39.3											
	Venø	5	1.50	1.02	1.38	1.45	0.16	0.13	0.08	2.24	4.27	7.53	9.25	9.21	6.98	4.67	4.17	1.08	11.16	3.55	1.34	1.90	12.20	3.80	4.40	1.57	1.10	0.36	0.01	0.00	0.00	0.00	0.00	0.01	0.02	0.35	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.01	0.04	97.3								
		6	0.72	0.39	0.74	0.68	0.06	0.05	0.03	1.27	2.57	6.16	7.88	5.84	5.20	4.68	3.45	1.38	11.11	6.05	2.14	3.14	14.18	5.31	6.96	3.18	2.73	0.34	0.05	0.03	0.03	0.00	0.00	0.02	0.07	0.67	0.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.41	0.08	0.09	96.0								
		7	0.61	0.29	0.95	0.63	0.05	0.03	0.03	3.86	5.18	27.13	35.43	5.93	3.15	2.12	1.67	0.23	3.49	0.74	0.25	0.30	3.08	0.71	0.83	0.28	0.19	0.13	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	96.3								
8		0.79	0.43	0.95	0.81	0.07	0.04	0.05	3.95	5.48	26.22	35.23	6.47	3.43	2.19	1.67	0.21	3.83	0.65	0.26	0.30	3.06	0.69	0.80	0.22	0.13	0.12	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	98.1							
Kås	9	0.25	0.10	0.26	0.20	0.01	0.02	0.01	0.42	0.97	1.51	1.92	2.76	3.45	5.15	2.55	1.68	9.83	9.56	4.16	5.67	14.57	7.08	10.72	5.99	5.76	0.17	0.02	0.02	0.05	0.00	0.01	0.07	0.23	1.21	0.73	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.113	0.26	0.33	98.9					
	11	0.05	0.01	0.05	0.04	0.00	0.01	0.00	0.10	0.31	0.32	0.31	1.10	1.83	3.14	1.77	1.63	6.83	10.50	5.33	9.19	11.38	7.31	11.50	8.36	9.41	0.08	0.01	0.00	0.01	0.00	0.03	0.19	0.46	1.61	1.09	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.38	0.66	0.99	98.2						
Salling	12	0.06	0.01	0.04	0.05	0.00	0.01	0.00	0.17	0.36	0.17	0.10	2.04	5.40	28.51	2.68	1.21	8.79	5.66	2.15	2.93	10.70	4.54	8.01	3.04	2.84	0.10	0.00	0.00	0.00	0.00	0.01	0.02	0.12	0.62	0.39	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.51	0.13	0.17	97.4					
	13	0.02	0.01	0.03	0.02	0.00	0.00	0.00	0.08	0.14	0.10	0.10	0.62	0.86	0.60	0.96	1.41	5.21	10.51	8.03	9.09	9.34	7.42	11.16	10.08	11.23	0.04	0.00	0.00	0.00	0.00	0.00	0.07	0.36	0.65	1.65	1.33	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.87	1.02	1.40	97.8		
Lægstar	14	0.01	0.01	0.02	0.02	0.00	0.00	0.00	0.04	0.16	0.06	0.04	0.79	1.07	0.31	1.38	2.74	7.44	7.89	9.22	10.83	12.07	8.77	9.25	9.41	8.99	0.06	0.01	0.00	0.01	0.02	0.15	0.47	0.71	1.07	0.67	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.83	0.91	1.08	97.8						
	15	0.01	0.00	0.02	0.02	0.00	0.00	0.00	0.02	0.09	0.04	0.06	0.43	0.68	0.24	0.81	1.43	4.87	9.64	9.58	9.59	9.26	7.29	10.29	9.98	11.53	0.04	0.00	0.00	0.00	0.02	0.14	0.47	0.78	1.69	1.43	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.19	1.37	1.86	96.3					
	16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.05	0.11	0.03	0.17	0.34	1.60	10.25	5.86	8.89	3.40	3.79	8.20	8.90	13.32	0.01	0.00	0.00	0.00	0.05	0.07	0.16	0.63	0.78	3.43	4.32	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.55	2.61	4.83	96.4	
	33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.07	0.01	0.01	0.33	0.52	0.03	0.63	1.84	3.21	3.89	11.07	9.33	7.17	6.82	4.90	7.78	8.04	0.07	0.01	0.08	0.29	1.30	3.95	5.91	2.31	0.64	0.45	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.93	1.62	2.98	99.0
	34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.01	0.00	0.15	0.27	0.01	0.33	1.22	1.82	2.51	9.65	7.74	4.60	4.78	3.40	7.50	8.16	0.03	0.01	0.09	0.22	0.81	2.52	4.24	2.16	0.50	0.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.94	2.12	4.77	74.3	
	35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.04	0.02	0.01	0.22	0.32	0.06	0.43	1.06	2.68	7.67	9.75	9.78	5.21	6.16	8.15	10.23	12.63	0.02	0.00	0.00	0.02	0.07	0.33	1.15	1.25	1.76	1.63	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.76	2.12	3.59	93.3
	36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.13	0.23	0.01	0.30	0.91	2.02	5.92	10.63	9.53	5.28	5.87	6.21	9.48	11.85	0.02	0.00	0.00	0.02	0.19	0.73	2.13	1.70	1.44	1.43	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.19	2.39	4.52	99.3
	37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.04	0.06	0.00	0.10	0.34	0.98	5.52	6.32	6.85	2.66	3.08	5.09	8.32	11.25	0.00	0.00	0.01	0.05	0.12	0.45	1.25	1.20	1.65	1.95	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.95	3.10	6.59	74.6
	38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.06	0.12	0.01	0.17	0.69	1.05	2.04	7.61	6.59	2.82	3.00	2.71	6.78	8.20	0.00	0.01	0.02	0.14	0.44	1.32	2.60	1.72	0.38	0.31	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.49	2.66	6.03	63.0
	39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.03	0.00	0.04	0.21</																																										

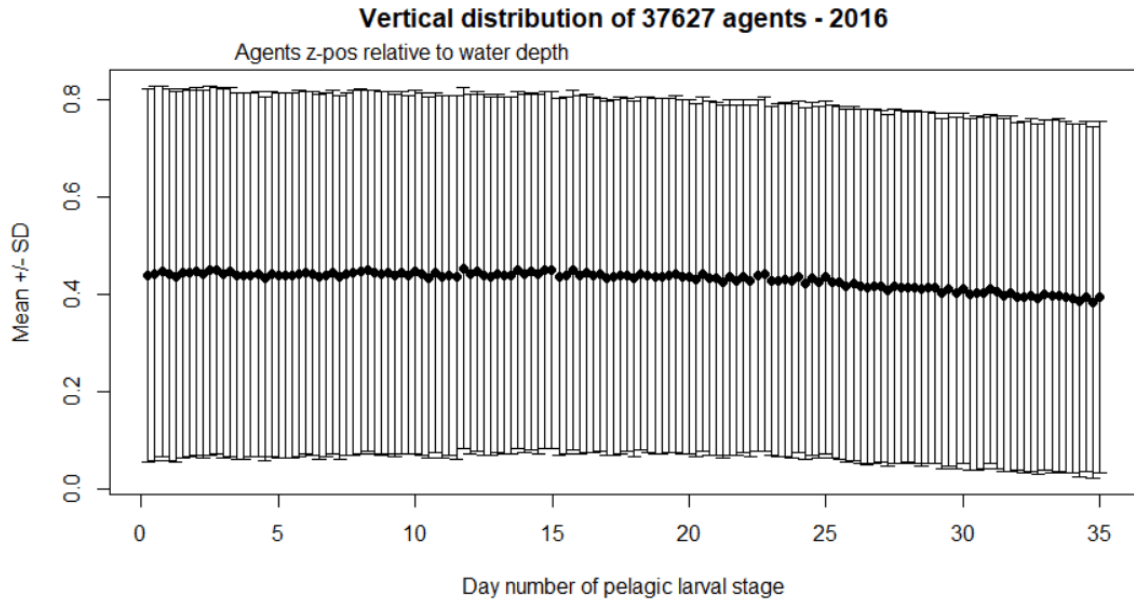


## S1.7 - Sensitivity analysis and tests - Vertical dispersion and mean vertical distribution

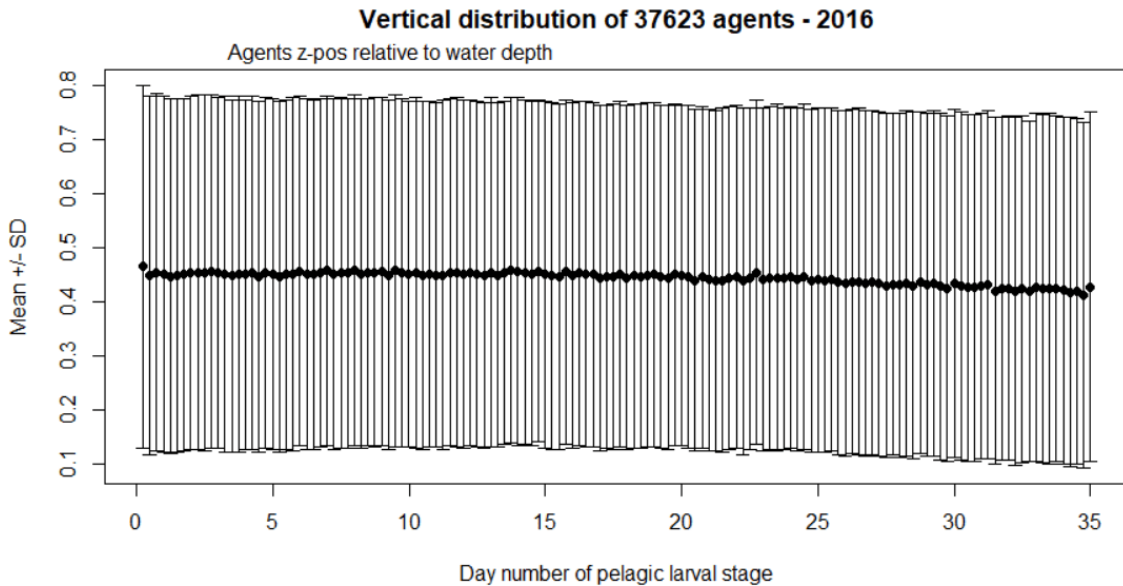
The mean vertical distribution depths (agent drift depth relative to total water depth) per larval “age” class (1 – 35 days) are shown for vertical dispersion constants of 0.01, 0.001, and 0.000 m<sup>2</sup>/s.

The difference in mean relative drift using a vertical dispersion constant of 0.001 (default) and 0.01 m<sup>2</sup>/s respectively is 0.01361135 (1.36 % of the mean depth range). In other words, agents on average are located 1.36 pct deeper (relative to the total water depth), when using 0.001 m<sup>2</sup>/s as a vertical dispersion factor instead of 0.01 m<sup>2</sup>/s. This corresponds to an average of ca. 6.5 cm. A vertical dispersion coefficient of 0 m<sup>2</sup>/s shows a clear difference in mean vertical positions, with larvae located closer to the bottom the first 1-5 days and gradually approaching a stable distribution that persist for the last 30 days. The mean relative depth distributions the last 30 days is 0.4005197. The difference relative to the 0.01 m<sup>2</sup>/s scenario is 0.03092 (3.09 % of the mean depth range) corresponding to an average of ca. 14.5 cm.

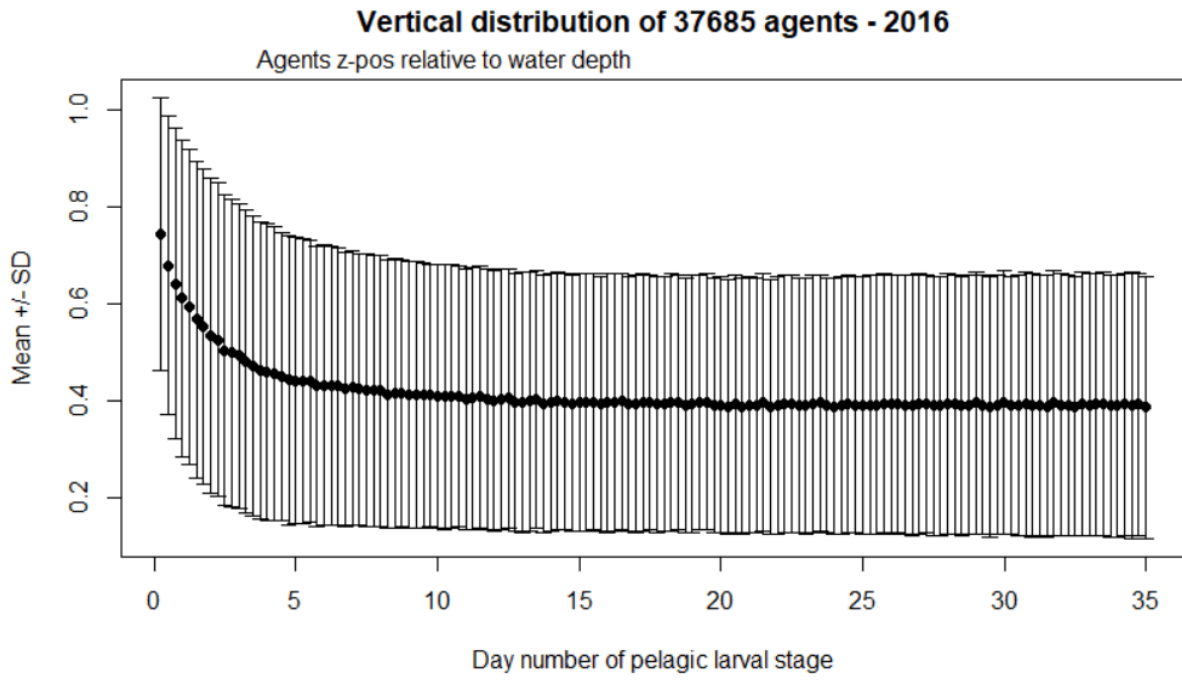
The vertical dispersion is expected to vary with a range of between 0.001 and 0.01 depending on the water currents, the wind conditions and the water depth (e.g. see Visser 1997)



*Caption: Plot of the vertical distribution (agent z-positions relative to the simulated water depth), plotted for each day number of the pelagic larval duration (1-35). The plot is based on a simulation for 2016, where 381 424 agents were released. To minimize the size of the result file, the plot includes a subsample of agents (every 10<sup>th</sup> agent) and time steps (every 24<sup>th</sup> hour) for the 101 days simulation. Agents where z-pos/water\_depth produced inf or NaN values were discarded. Most of these are related to agent positions on "dry" elements in the Hydrodynamic model. The vertical dispersion set for the simulation was **0.01 m<sup>2</sup>/s**. (mean relative depth = 0.431)*



*Caption: Same as previous, except vertical dispersion factor **0.001 m<sup>2</sup>/s**. (mean relative depth = 0.445)*



*Caption: Same as previous, except vertical dispersion factor  $0 \text{ m}^2/\text{s}$  (mean relative depth = 0.422)*

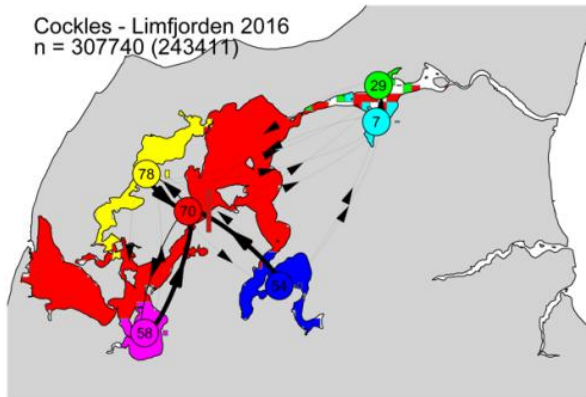


## S1.8 - Sensitivity analysis and tests - Vertical dispersion and cluster analysis results

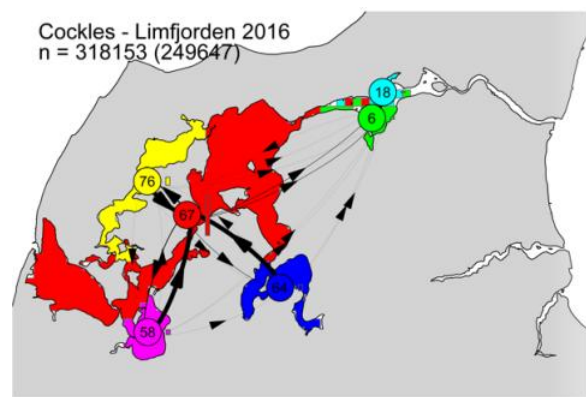
Model runs for all years were using a vertical dispersion factor of 0.01 m<sup>2</sup>/s. Sensitivity run for 2016 using 0.001 m<sup>2</sup>/s, show marginal changes to the cluster analysis results, with no effect on the cluster boundaries, and marginal changes to the within and between cluster connectivity.

Cluster analysis results for non-transposed matrices representing *larval export and local retention*:

0.01 m<sup>2</sup>/s:

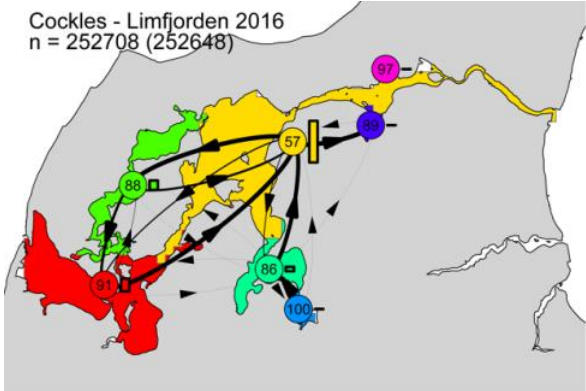


0.001 m<sup>2</sup>/s:

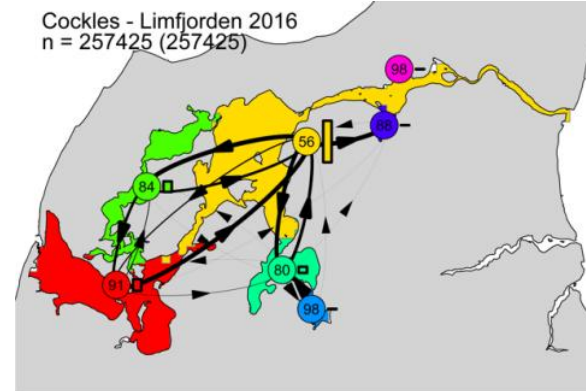


Cluster analysis results for transposed matrices representing *larval import and self-recruitment*:

0.01 m<sup>2</sup>/s:



0.001 m<sup>2</sup>/s:

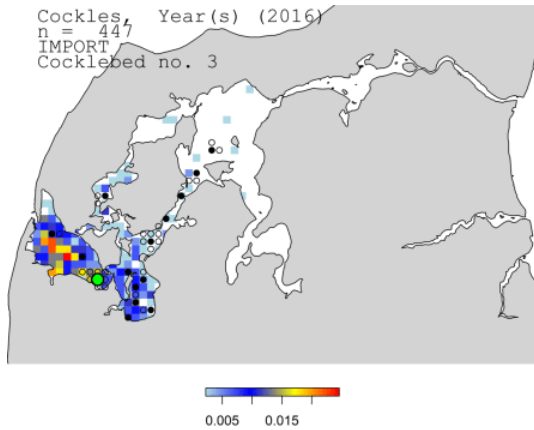


### S1.9 - Sensitivity analysis and tests - Vertical dispersion and dispersal probability

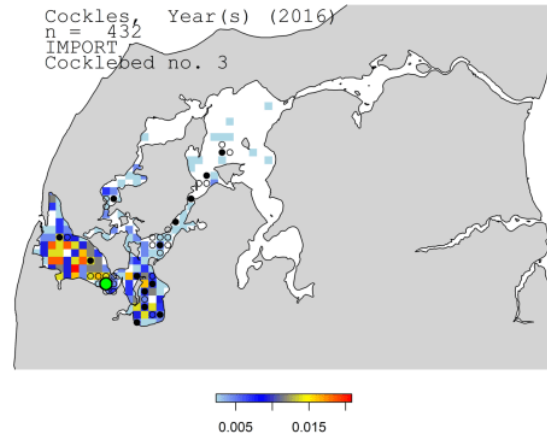
Dispersal probabilities in terms of larval import for selected locations (green dot) including Nissum Bredning, Kås Bredning, Løgstør Bredning and Visby Bredning.

#### Nissum Bredning

Ver. Disp. Coef. 0.010 m<sup>2</sup>/s:

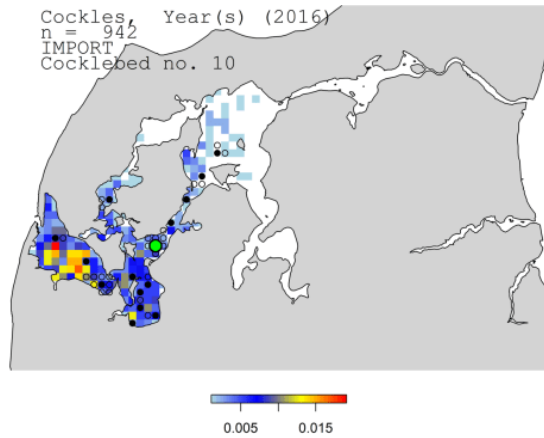


Ver. Disp. Coef. 0.001 m<sup>2</sup>/s:

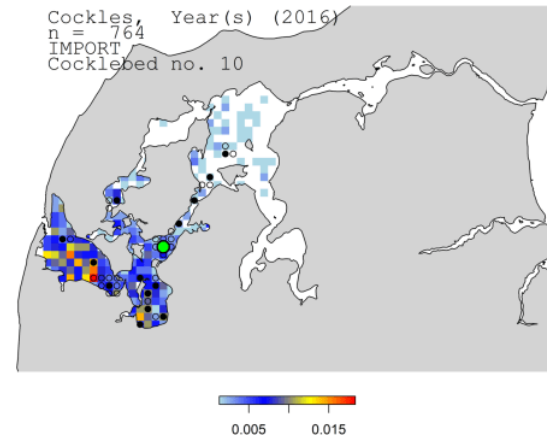


#### Kås Bredning

Ver. Disp. Coef. 0.010 m<sup>2</sup>/s:

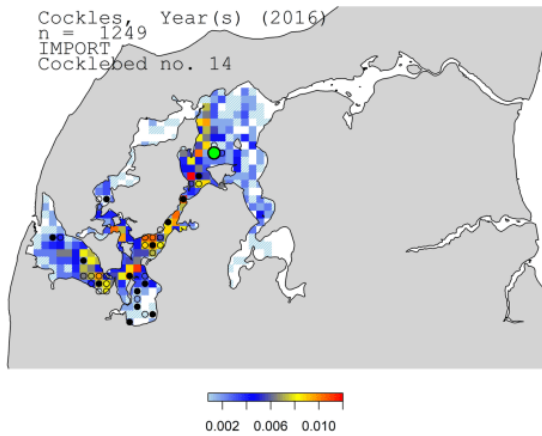


Ver. Disp. Coef. 0.001 m<sup>2</sup>/s:

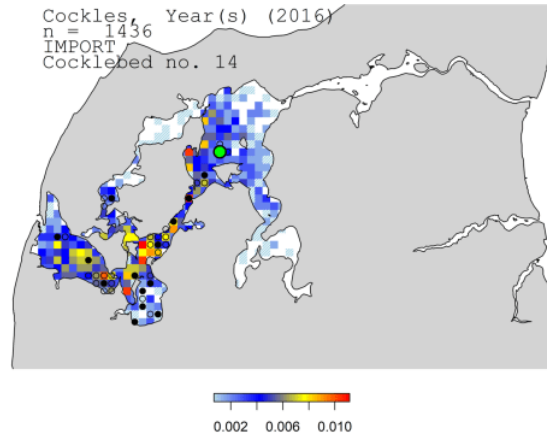


### Løgstør Bredning

Ver. Disp. Coef. 0.010 m<sup>2</sup>/s:

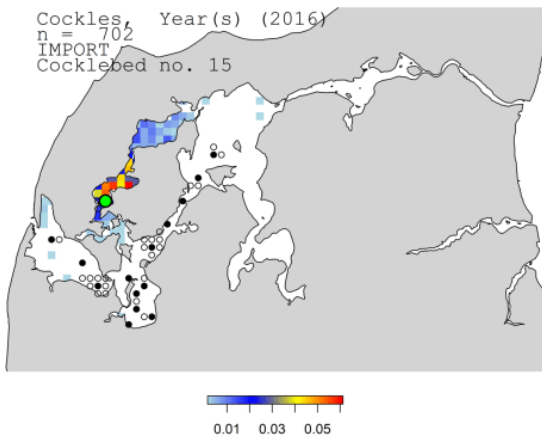


Ver. Disp. Coef. 0.001 m<sup>2</sup>/s:

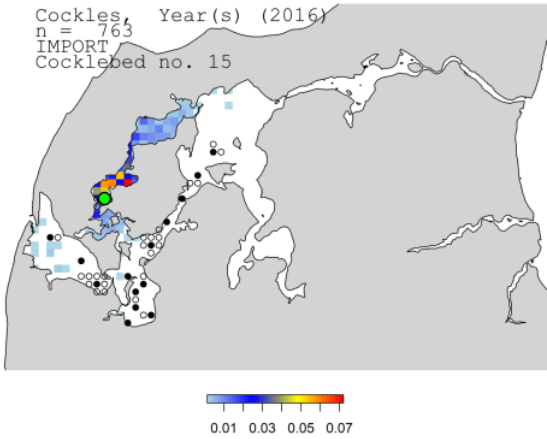


### Visby Bredning

Ver. Disp. Coef. 0.010 m<sup>2</sup>/s:



Ver. Disp. Coef. 0.001 m<sup>2</sup>/s:

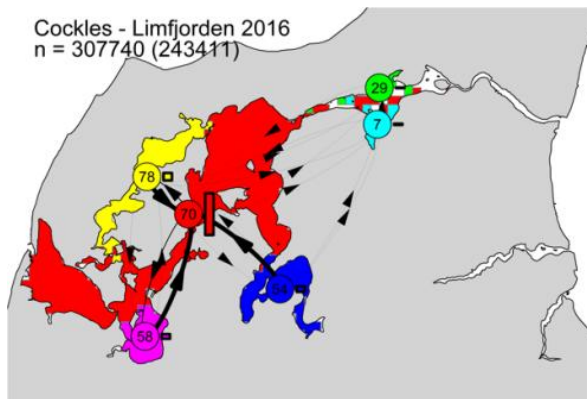


## S1.10 - Sensitivity analysis and tests - Horizontal dispersal and cluster analysis results

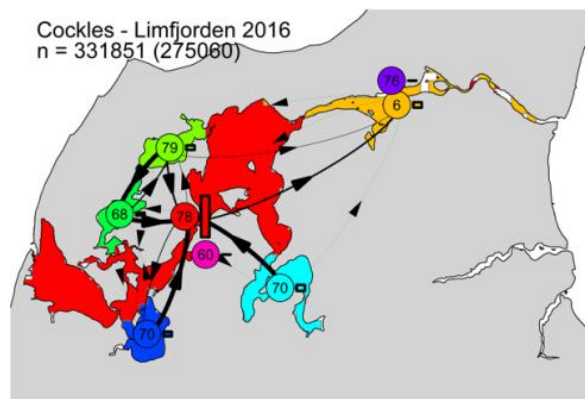
We used horizontal dispersion coefficient of  $1 \text{ m}^2/\text{s}$  (Rossi et al. 2014, Brennan et al. 2019) to represent the hydrodynamic processes such as small eddies not resolved in the computational mesh in the hydrodynamic model. We tested this assumption using a coefficient of  $10 \text{ m}^2/\text{s}$  and increasing the horizontal dispersion showed a reduction in dispersal between clusters (and thus, an increase in local retention and self-recruitment) in general, and an increase in the number of clusters in parts of the most isolated parts of Limfjorden.

Cluster analysis results based on non-transposed matrix representing larval export and local retention:

Hor. Disp. Coef. -  $1 \text{ m}^2/\text{s}$ :

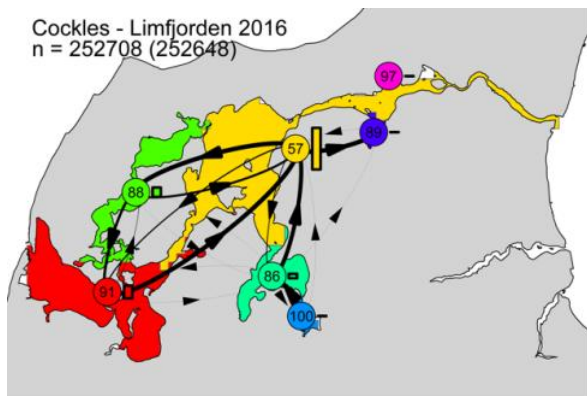


Hor. Disp. Coef. -  $10 \text{ m}^2/\text{s}$ :

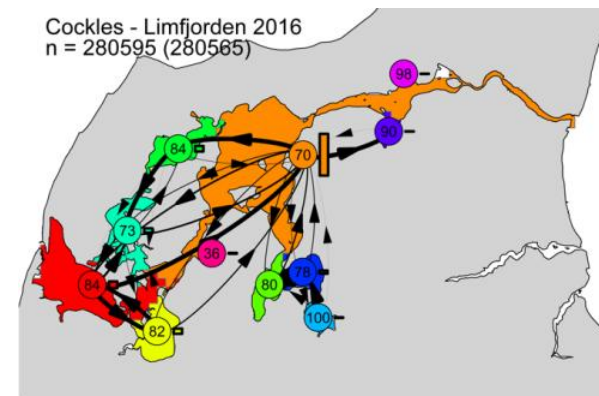


Cluster analysis results based on transposed matrix representing larval imports and self-recruitment:

Hor. Disp. Coef. -  $1 \text{ m}^2/\text{s}$ :



Hor. Disp. Coef. -  $10 \text{ m}^2/\text{s}$ :

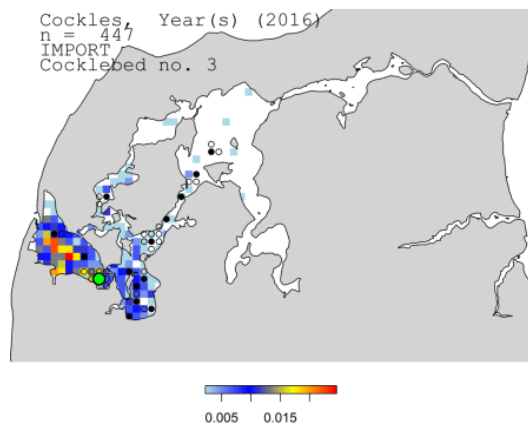


## S1.11 - Sensitivity analysis and tests - Horizontal dispersal and larval dispersal probability

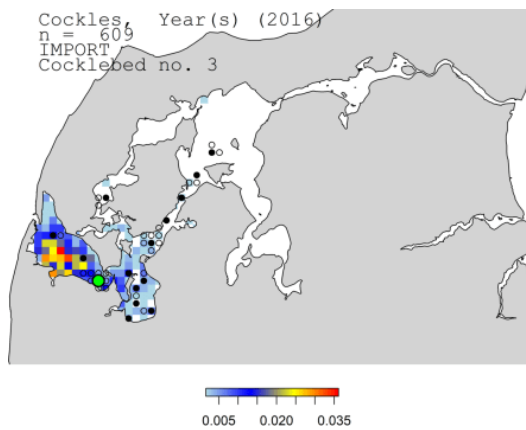
Dispersal probabilities in terms for larval import for selected major cockle beds (green dot) including Nissum Bredning (3), Kås Bredning (10), Løgstør Bredning (14) and Visby Bredning (15). Dispersal probabilities were only marginally affected for cockle bed no. 3 and 10. However, for both cockle beds 14 and 15 an increase in horizontal dispersal coefficient from 1 to 10 m<sup>2</sup>/s show a clear decrease in the areal extent of the donor area. Thus a higher dispersion representing hydrodynamic processes such as eddies not resolved by the computational grid may potentially affect the dispersal of larvae reducing the connectivity between sub-basins.

### Nissum Bredning

Hor. Disp. Coef. - 1 m<sup>2</sup>/s:

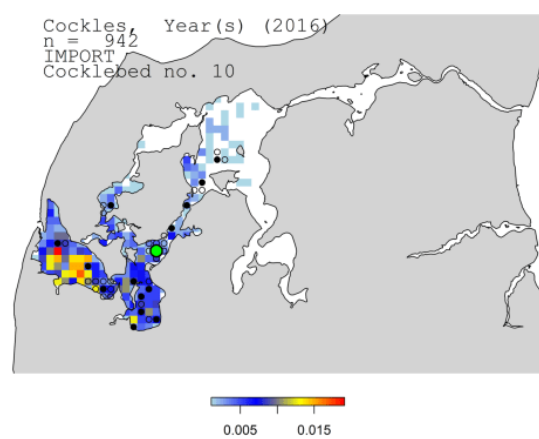


Hor. Disp. Coef. - 10 m<sup>2</sup>/s:

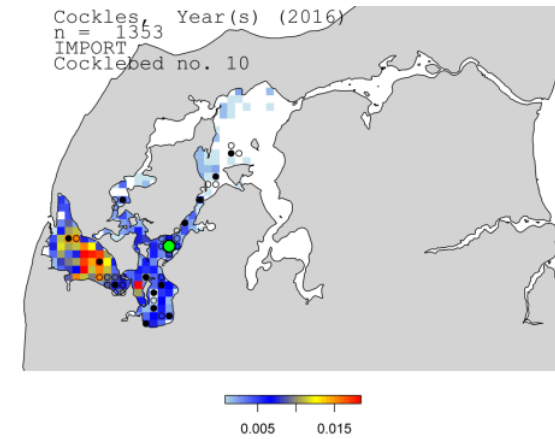


### Kås Bredning

Hor. Disp. Coef. - 1 m<sup>2</sup>/s:

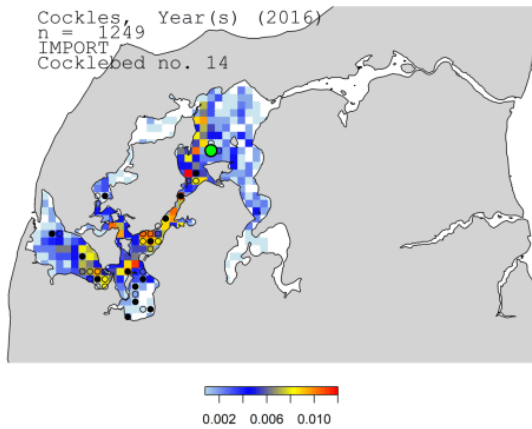


Hor. Disp. Coef. - 10 m<sup>2</sup>/s:

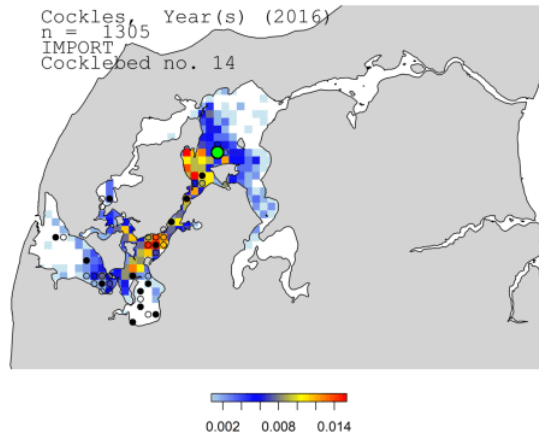


### Løgstør Bredning

Hor. Disp. Coef. -  $1 \text{ m}^2/\text{s}$ :

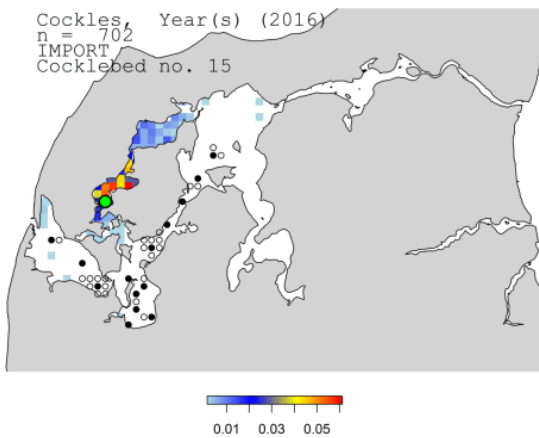


Hor. Disp. Coef. -  $10 \text{ m}^2/\text{s}$ :

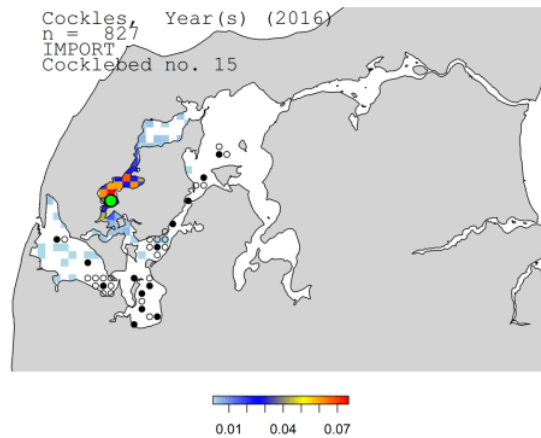


### Visby Bredning

Hor. Disp. Coef. -  $1 \text{ m}^2/\text{s}$ :



Hor. Disp. Coef. -  $10 \text{ m}^2/\text{s}$ :





## S1.12 - Sensitivity analysis and tests - Pelagic larval duration and cluster analysis results

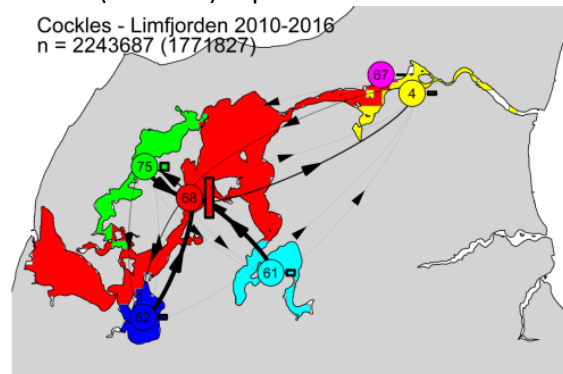
A rerun of all 7 years using a pelagic larval duration of between 30 and 40 days, sampled randomly from a uniform distribution, not identical but comparable to the approach by Coscia et al. 2020. Here they simulated larvae duration of 40 days, and included larval durations from 30 to 40 days as input to the connectivity matrices.

Below we compare results from the cluster analysis of a PLD of 35 days with a PLD of 30-40 days based on simulations for seven years 2010 – 2016.

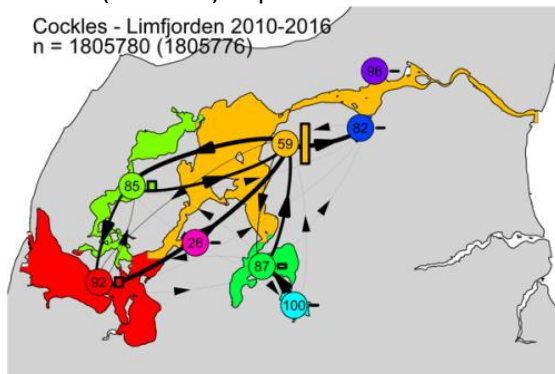
We also tested a broader range of PLD values including 21, 25, 30, 35, 40 and 50 days based on simulations for 2016.

Changing the PLD from a fixed 35 days to a random PLD between 30-40 days, only showed marginal differences in cluster analysis results and dispersal probability maps based on all seven years simulation results. A larger range of PLD values were compared for 2016 including 21, 25, 30, 35, 40 and 50 days with 30, 35, 40 and 50 days showing almost identical results. Number of cluster increased when analyses were based on 25 and 21 days. The location of boundaries between clusters can be interpreted as uni- or bi-directional dispersal barriers and these remained more or less unchanged across tested PLDs. Proportions of local retention and self-recruitment, however, in general decreased with increasing PLD indicating an increase in larval exchange between clusters.

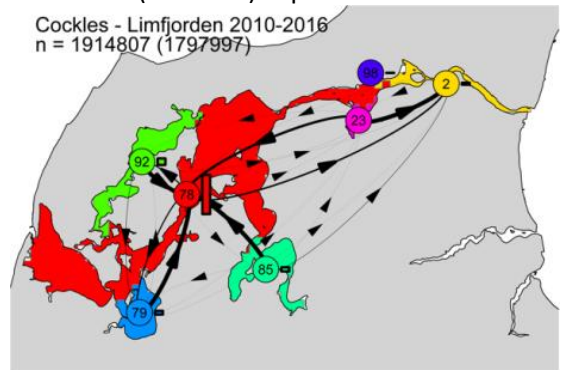
PLD 35 (All Years) Export and local retention:



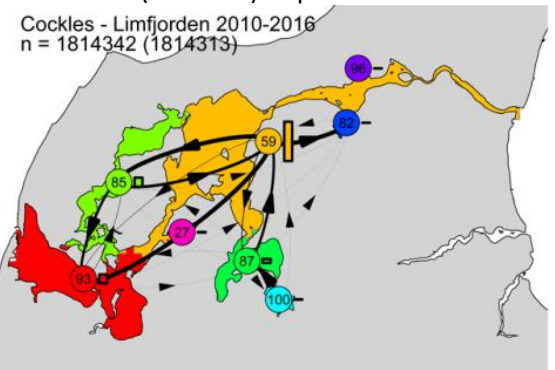
PLD 35 (All Years) Import and self-recruitment:



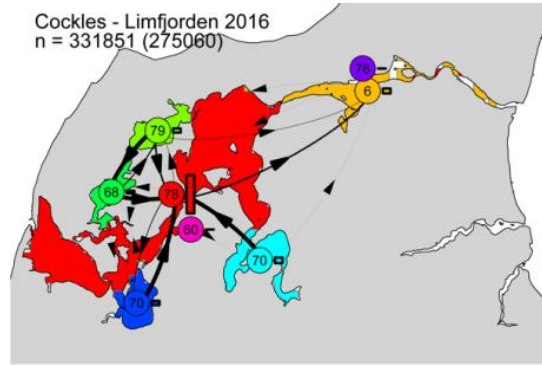
PLD 30-40 (All Years) Export + local retention:



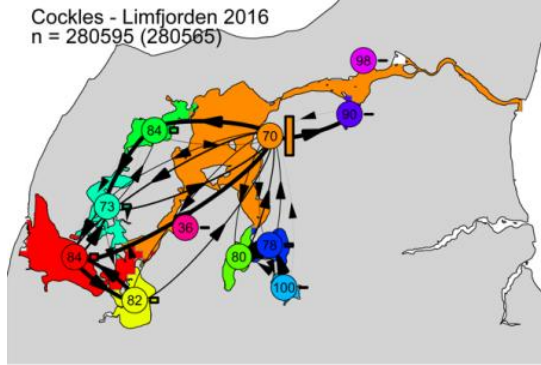
PLD 30-40 (All Years) Import + self-recruitment:



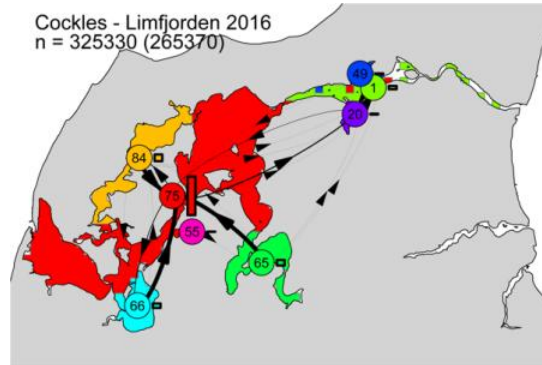
PLD 21 (2016) Export + local retention:



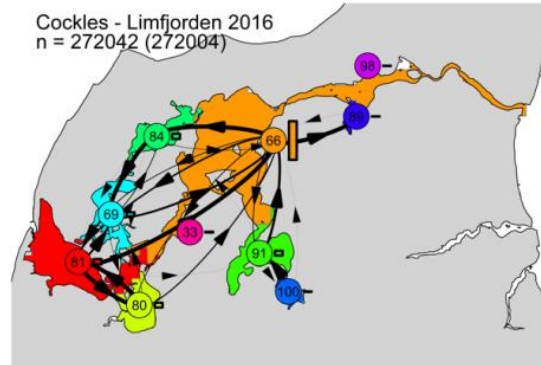
PLD 21 (2016) Import + self-recruitment:



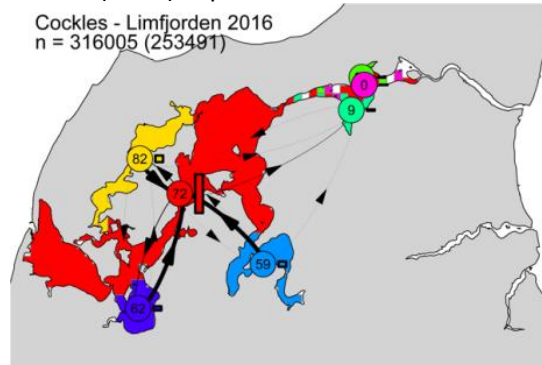
PLD 25 (2016) Export + local retention:



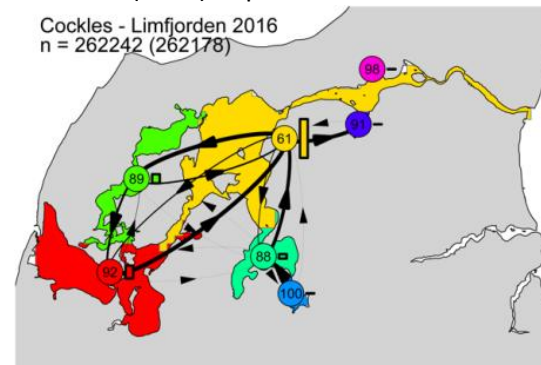
PLD 25 (2016) Import + self-recruitment:



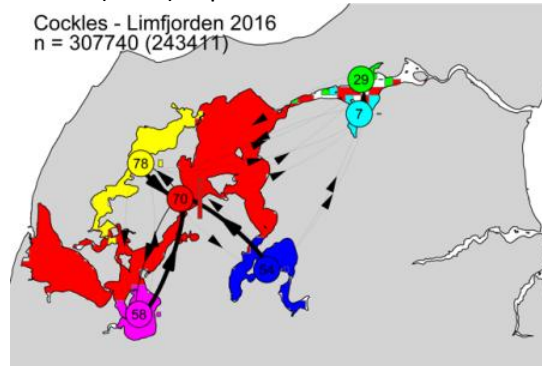
PLD 30 (2016) Export + local retention:



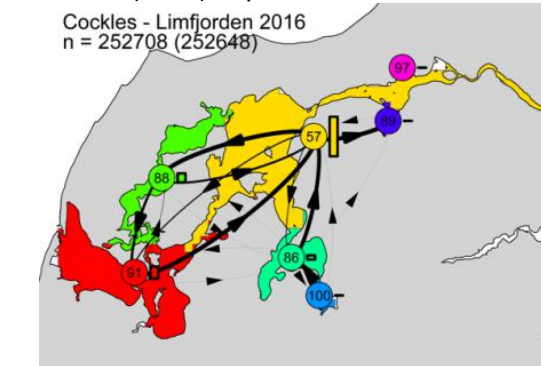
PLD 30 (2016) Import + self-recruitment:



PLD 35 (2016) Export + local retention:

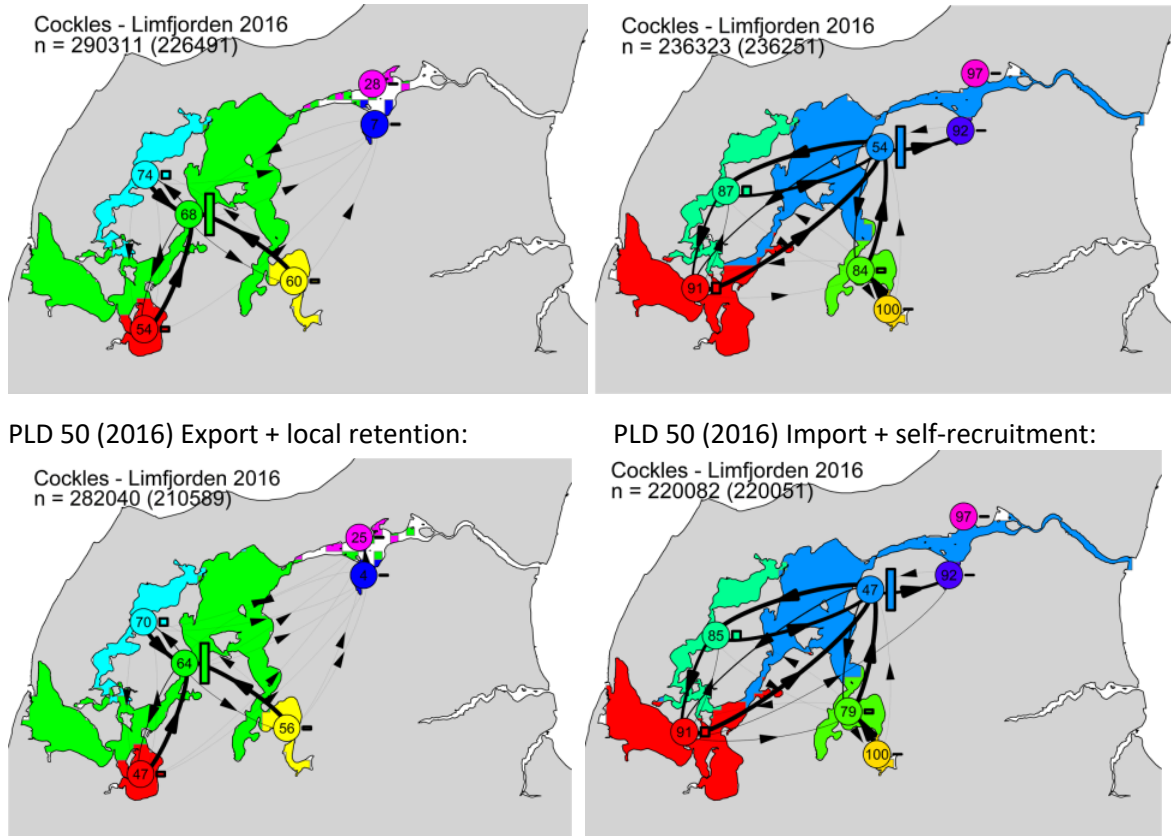


PLD 35 (2016) Import + self-recruitment:



PLD 40 (2016) Export + local retention:

PLD 40 (2016) Import + self-recruitment:



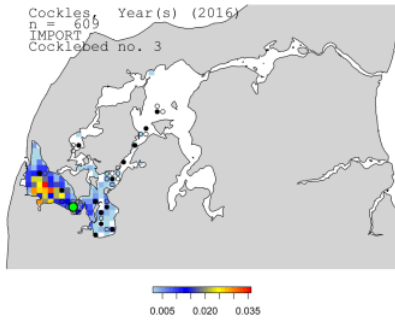
### S1.13 - Sensitivity analysis and tests - Pelagic larval duration and larval dispersal probability.

Dispersal probabilities in terms of larval import and export for selected locations (green dot) including Nissum Bredning, Kås Bredning, Løgstør Bredning and Visby Bredning.

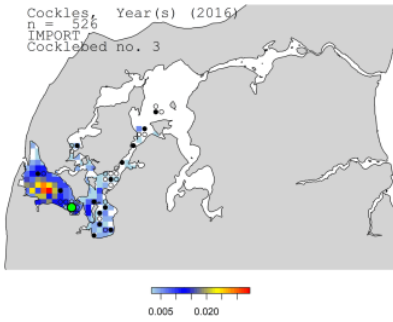
The areal extent of the main donor areas of the 3 of the 4 selected major cockle beds (cockle beds nos. 3, 10 and 13) showed a slight increase with increasing PLD, although disproportional to the relative change in PLD, i.e. increasing the PLD from 25 to 50 days did not result in a 100% increase in the extent of the donor areas. This is partly due to the areal confinement of the donor areas to the west and the vicinity of the model boundary to the North Sea. The total number of imported larvae did however show a proportional decrease indicating that a larger proportion of released larvae in donor areas to these 3 cockle beds are transported further east to the central and eastern parts of the Limfjorden. This is supported by the export dispersal probability maps. For major cockle bed no. 10 in Kås Bredning as for major cockle bed no. 15 in Visby Bredning, the locations of the core donor areas in Nissum Bredning and within Visby Bredning itself respectively (red and yellow colors in the import probability maps), showed only a limited displacement using a PLD of 25, 30, 35, 40 or 50 days. For major cockle bed no. 13 in Løgstør Bredning, some of the core donor areas in e.g. Nissum Bredning showed displacements of up to approximately 10 km to the east with decreasing PLD.

### Import - Nissum Bredning

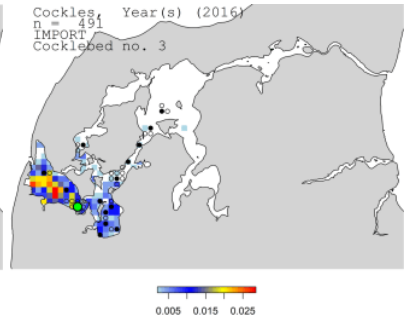
PLD 21 - 2016:



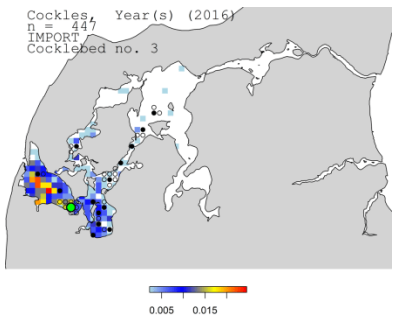
PLD 25 - 2016:



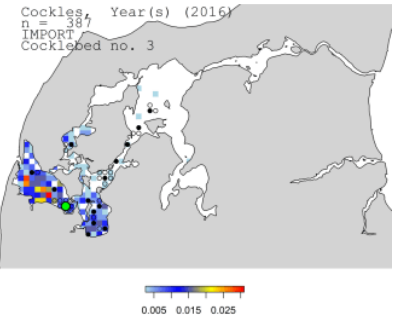
PLD 30 - 2016:



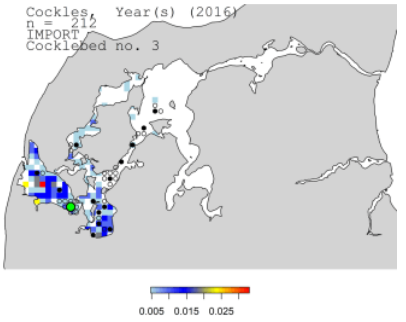
PLD 35 - 2016:



PLD 40 - 2016:

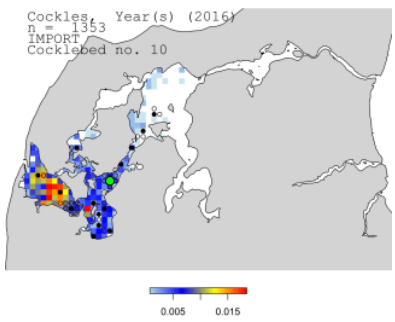


PLD 50 - 2016:

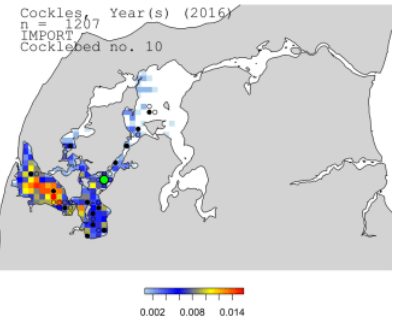


### Import - Kås Bredning

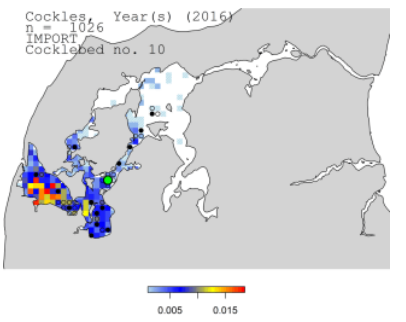
PLD 21 - 2016:



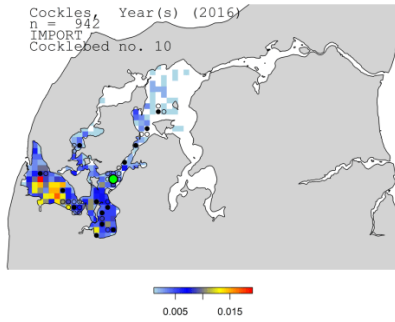
PLD 25 - 2016:



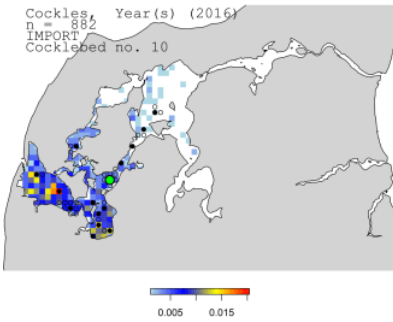
PLD 30 - 2016:



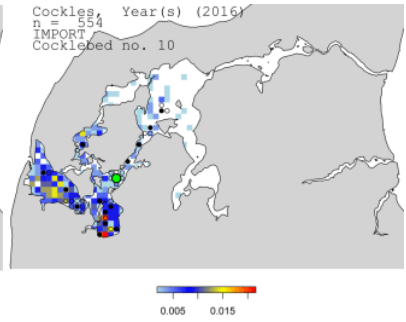
PLD 35 - 2016:



PLD 40 - 2016:



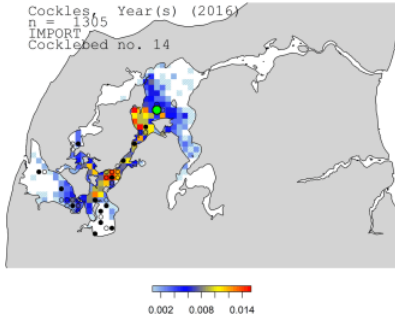
PLD 50 - 2016:



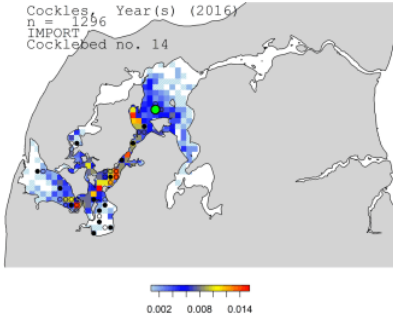


### Import - Løgstør Bredning

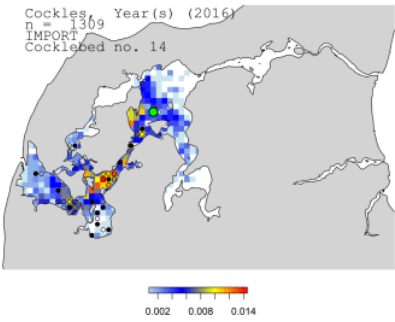
PLD 21 - 2016:



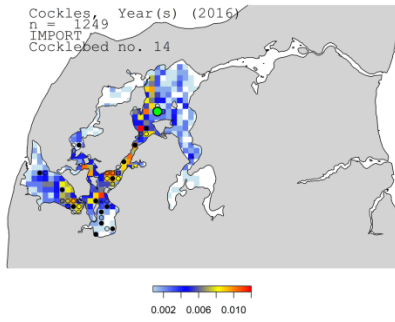
PLD 25 - 2016:



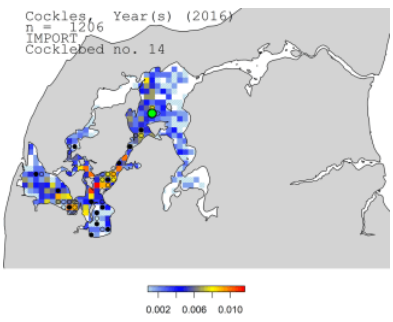
PLD 30 - 2016:



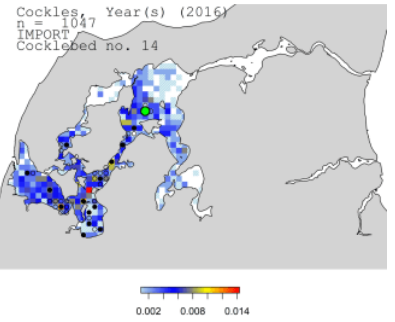
PLD 35 - 2016:



PLD 40 - 2016:

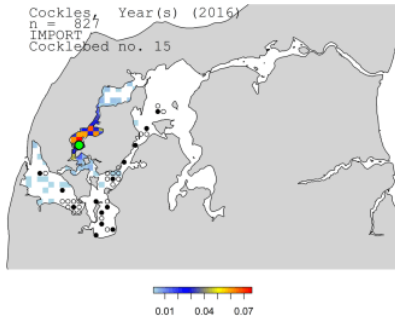


PLD 50 - 2016:

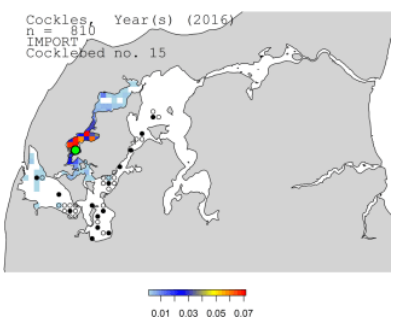


### Import - Visby Bredning

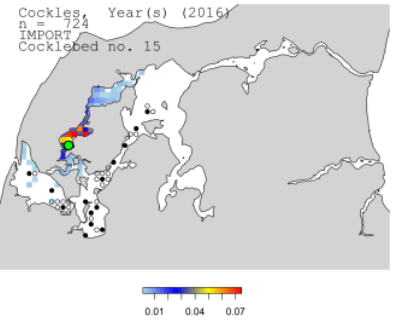
PLD 21 - 2016:



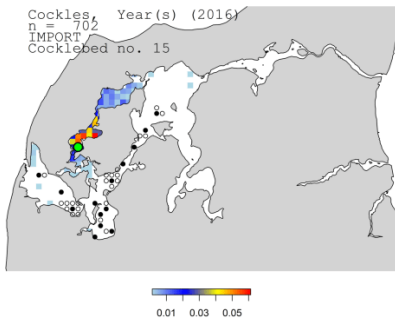
PLD 25 - 2016:



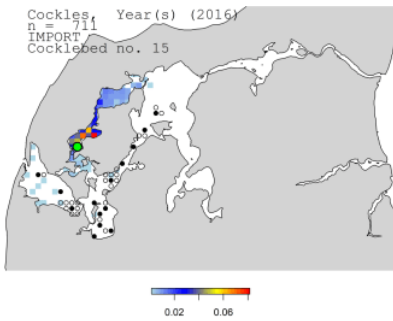
PLD 30 - 2016:



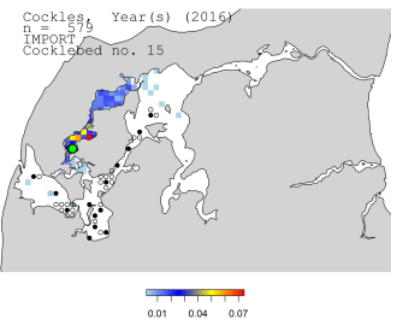
PLD 35 - 2016:



PLD 40 - 2016:



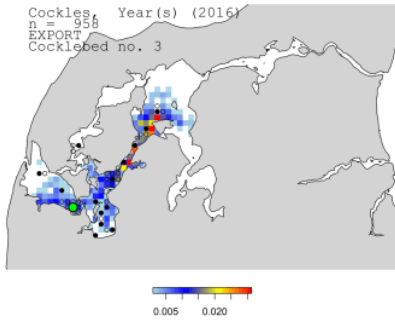
PLD 50 - 2016:



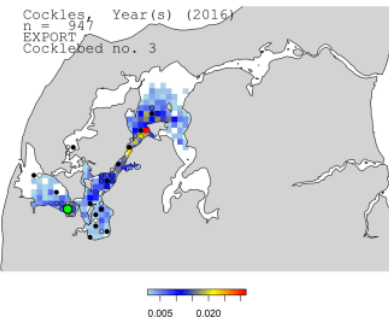


**Export – Nissum Bredning:**

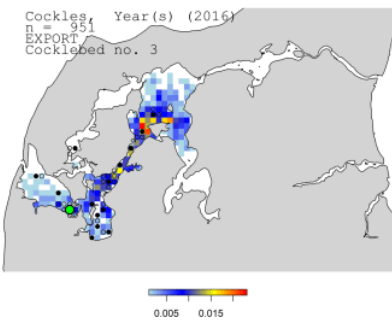
PLD 21 - 2016:



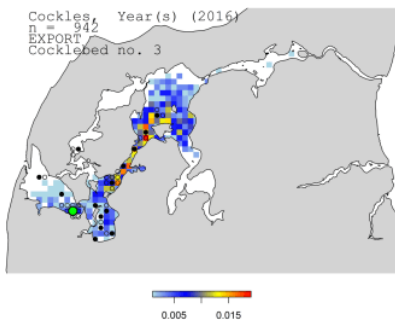
PLD 25 - 2016:



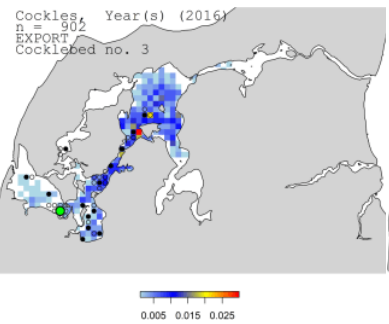
PLD 30 - 2016:



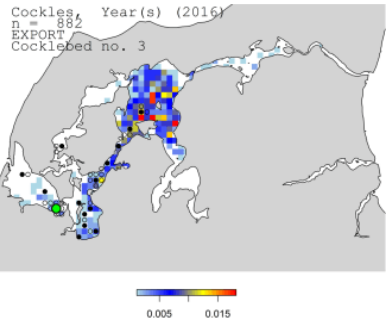
PLD 35 - 2016:



PLD 40 - 2016:

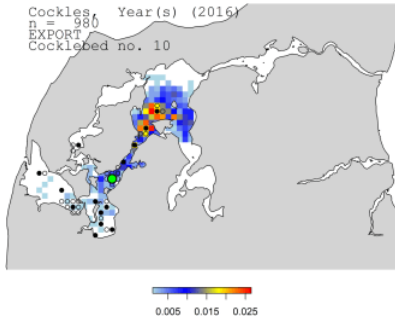


PLD 50 - 2016:

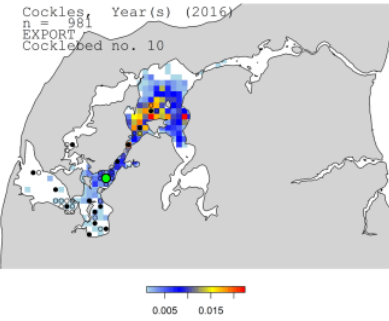


**Export – Kaas Bredning:**

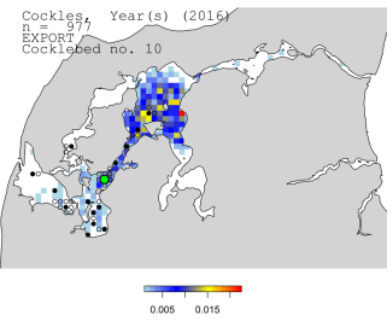
PLD 21 - 2016:



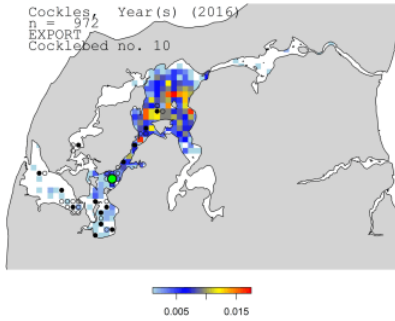
PLD 25 - 2016:



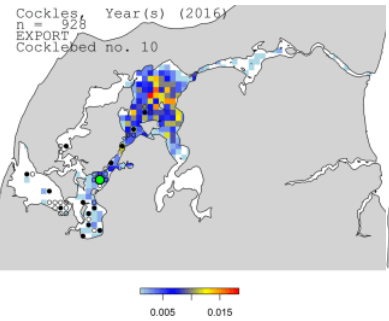
PLD 30 - 2016:



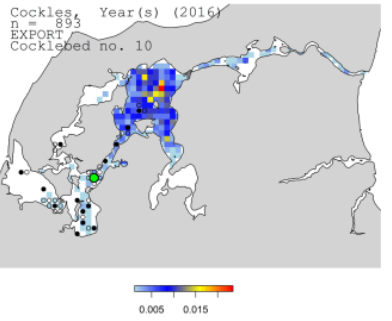
PLD 35 - 2016:



PLD 40 - 2016:



PLD 50 - 2016:

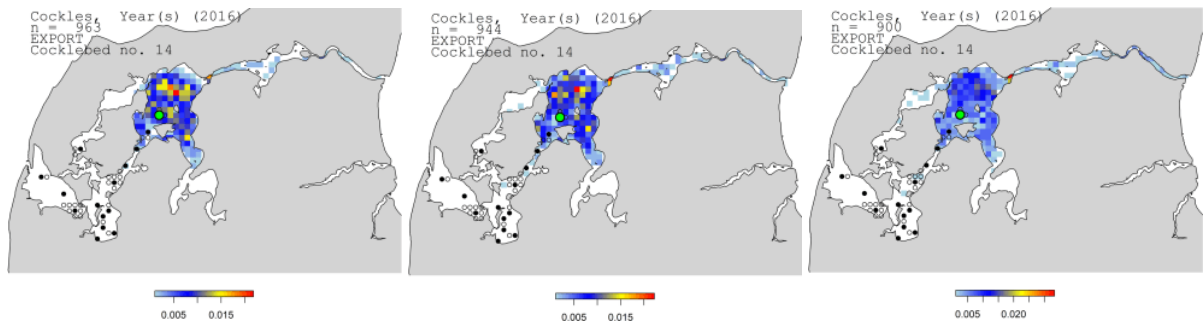


**Export – Løgstør Bredning:**

PLD 21 - 2016:

PLD 25 - 2016:

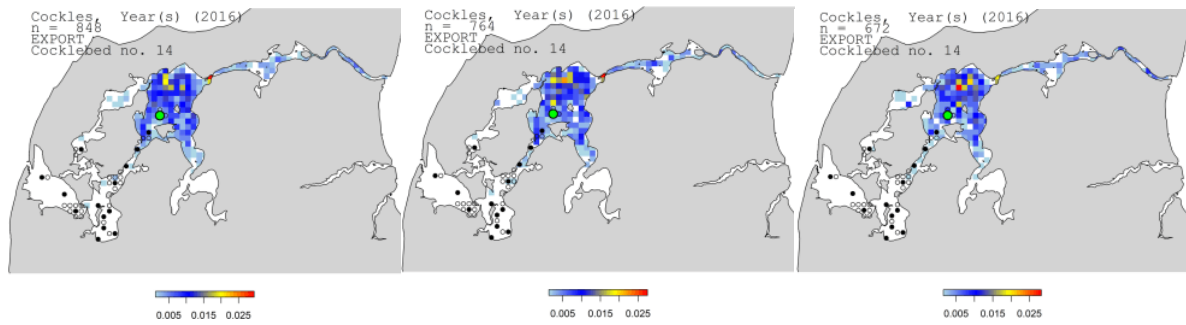
PLD 30 - 2016:



PLD 35 - 2016:

PLD 40 - 2016:

PLD 50 - 2016:

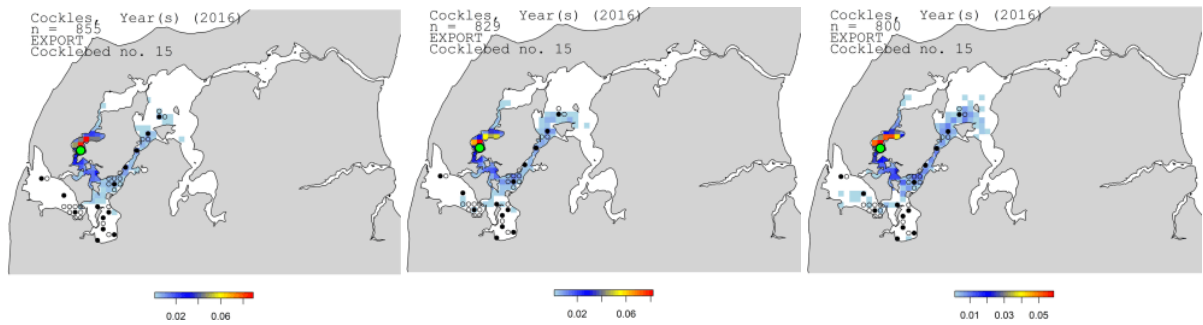


**Export – Visby Bredning:**

PLD 21 - 2016:

PLD 25 - 2016:

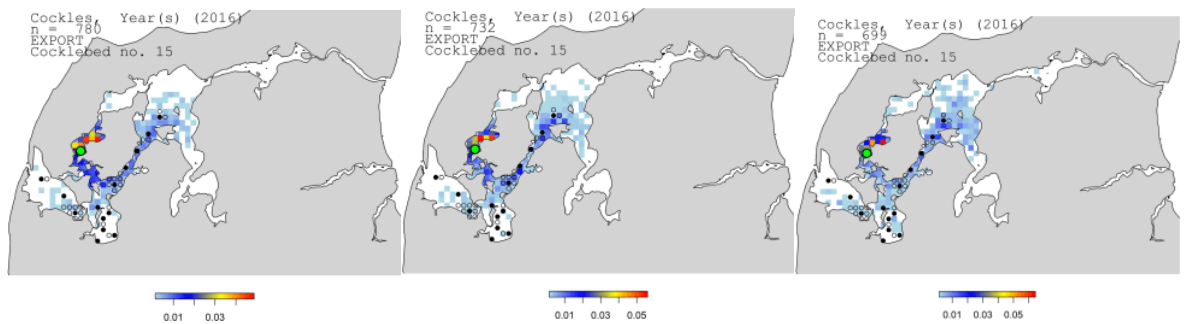
PLD 30 - 2016:



PLD 35 - 2016:

PLD 40 - 2016:

PLD 50 - 2016:



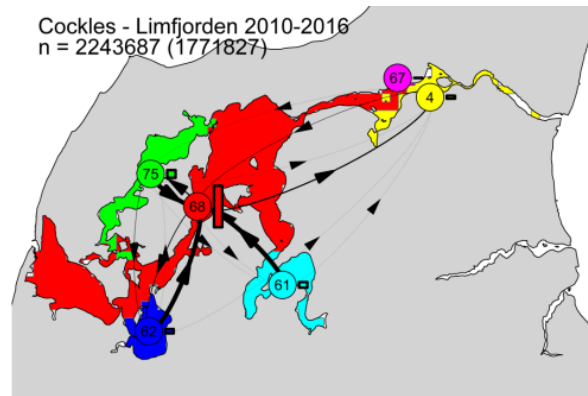
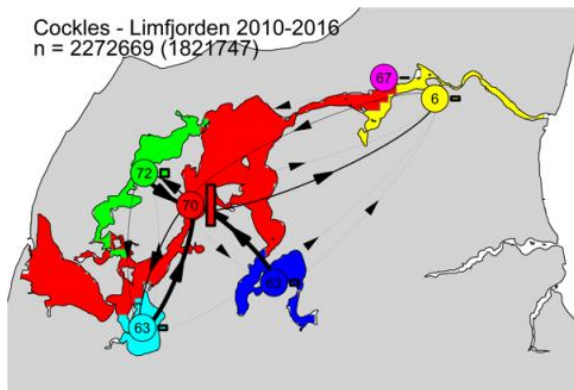
S1.14 - Sensitivity analysis and tests - Spawning period and cluster analysis results

To test for the selected spawning period we compared results from the simulations based on the chosen spawning period May-June with simulations using an earlier period from April-May. Based on seven years of simulations, the results showed almost no differences between the two scenarios.

Non-transposed matrices (Export and local retention):

Spawning April – May

Spawning May – June



Transposed matrices (Import and self-recruitment):

Spawning April – May

Spawning May – June

