

Patterns of extirpation. II. The role of connectivity for the decline and recovery of elasmobranch populations in the German Bight as inferred from survey data

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Supplement. Additional information is provided on historical sampling intensity, the sensitivity of the incidence function in relation to changes of migration rate, distribution figures for species mentioned in the main article, and information on how the rarefied species numbers were calculated

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Supplement 1. Historical sampling

Fig. S1. Elasmobranch sampling locations (red dots) from 1902 to 1908. Q2, Q3: quarters of the year (April–June; July–September). Gray line: German EEZ; red line: 15 m depth contour

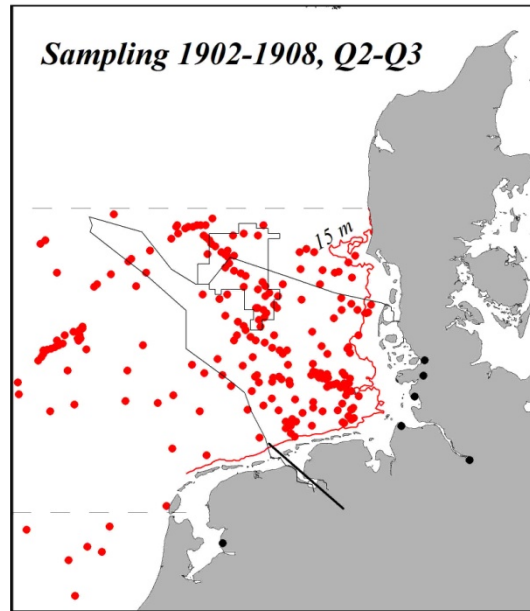
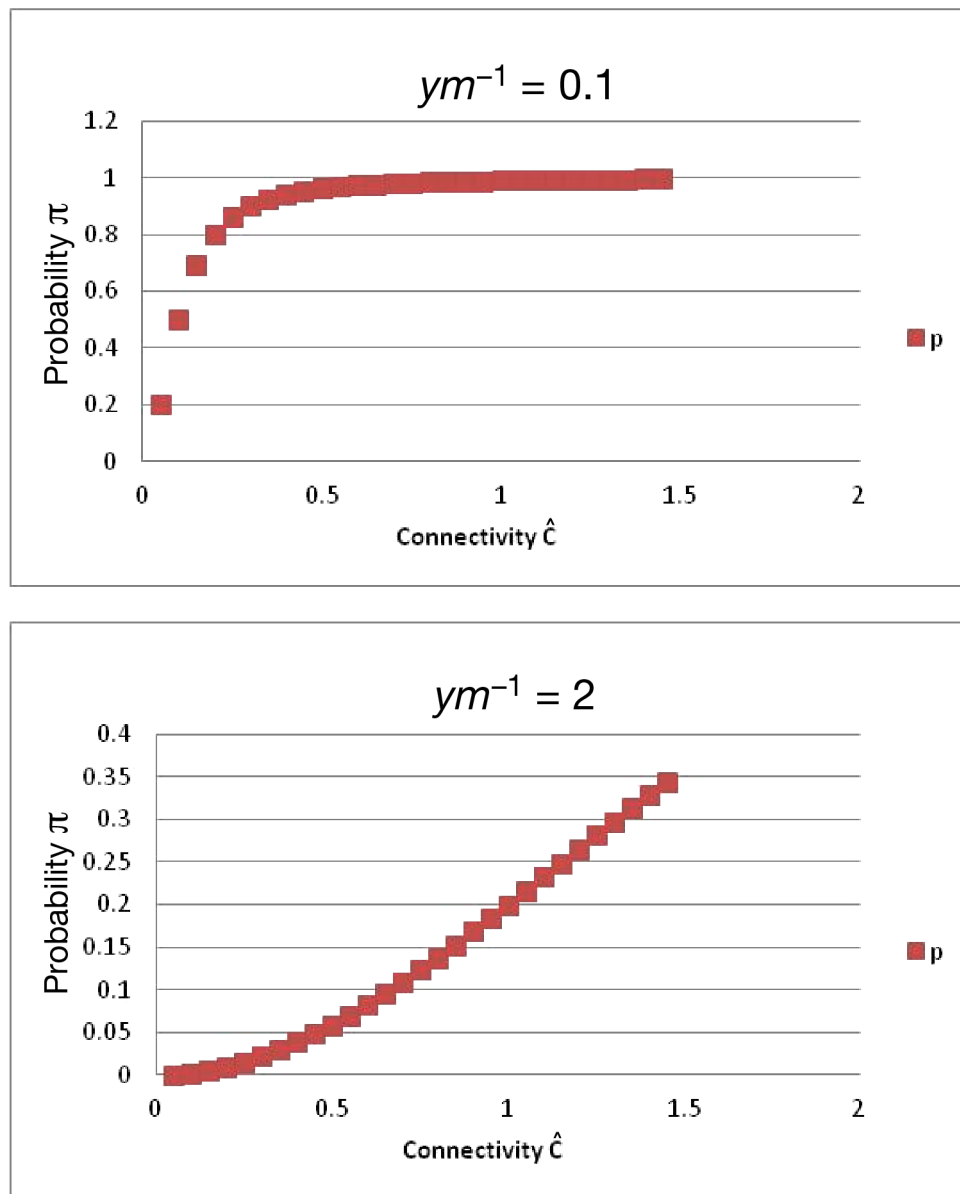


Table S1. Number of samples analyzed from Quarters 2 and 3. Samples in 1902 were only available from October onward. OT90 and OT115 refer to so-called 90 ft and 115 ft otter trawls.

Year	Hauls OT90 Single codend	Hauls OT90 Double codend	Hauls OT115 Single codend	Hauls OT115 Double codend
1902	4			
1903	19			
1904	11		24	
1905	7			
1906	2	1	5	
1907				17
1908			25	21
1919			12	24
1920			3	51
1921			40	2
1923			42	
1930			37	
1931			9	49
1932			1	51

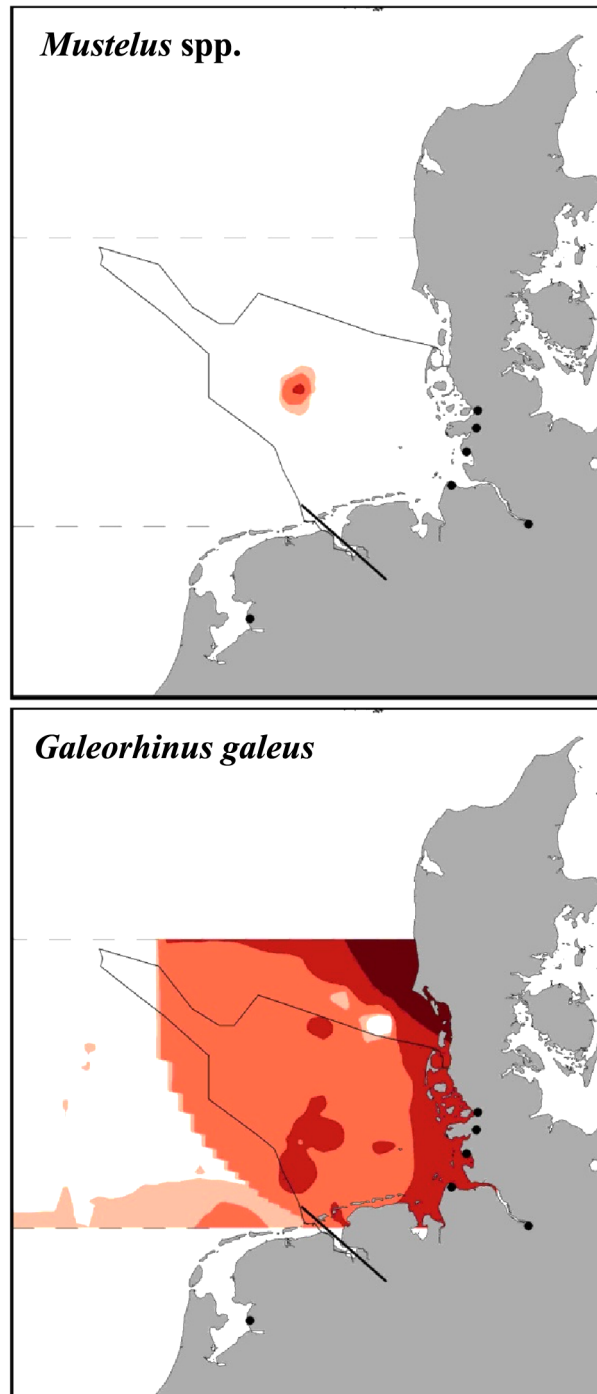
Supplement 2. Sensitivity of the connectivity function to migration rate

Fig. S2. Sensitivity of the connectivity function in relation to migration rate. With increasing m , probability π , of immigration increases



Supplement 3. Additional distribution figures

Fig. S3. Smoothhound *Mustelus* spp. and tope shark *Galeorhinus galeus* distributions in 1902–1908. Biomass contours in kg per 30 min trawling (survey catch per unit effort); contour levels 0-0.05-0.25-1-5 kg/30 min. Dashed lines: area for which kriging was applied; thin gray line: German EEZ; bold black line: border to The Netherlands; dots: coastal harbour sites



Supplement 4. Rarefaction correction for sample size/trawl duration

Correction for sample size was calculated as the individual-based rarefaction proportion scaled to the abundance of specimens caught in 30 min (see Colwell et al. 2012):

$$S_{i,l} = 1 - \frac{\binom{m_l}{a_l}}{\binom{N_l}{a_l}} \quad (S1)$$

where m_l is the abundance of all species other than i in sample l for which total abundance is N_l , i.e. $m_l = N_l - n_{i,l}$, and a_l is the subsample from N_l that is obtained in 30 min of trawling. Rarefaction requires a fully random distribution of specimens (Smith et al. 1985).

LITERATURE CITED

Colwell RK, Chao A, Gotelli NJ, Lin SY, Mao CX, Chazdon RL, Longino JT (2012) Models and estimators linking individual-based and sample-based rarefaction, extrapolation and comparison of assemblages. *J Plant Ecol* 5:3–21

Smith EP, Stewart PM, Cairns J Jr (1985) Similarities between rarefaction methods. *Hydrobiologia* 120:167–170