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## State-space modeling of multi-decadal mark-recapture data reveals low adult dispersal in a nursery-dependent fish metapopulation

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### Abstract :

Quantifying connectivity within fish metapopulations is an important component in understanding population dynamics and providing an evidence base for assessment and management. We investigate meta-population connectivity of the common sole (*Solea solea* L.) in the Eastern English Channel (EEC). The EEC common sole stock is currently assessed as a single and spatially homogeneous population but connectivity induced through adult movements within this stock and with nearby stocks remains unknown. To fill this knowledge gap, we developed a state-space mark-recovery model, designed to estimate adult connectivity, using mark-recapture data from multiple release experiments from 1970 to 2018 across the EEC and adjacent management areas. The model estimates seasonal fish movements between five pre-defined areas, Western English Channel, Eastern English Channel (split into three discrete sub-areas) and North Sea. Over 32000 fish were tagged, 4036 of which were recovered via fisheries. Our results suggest minimal large-scale adult movements between these areas: movements among spatial units within the EEC were very low with even lower levels of immigration from areas adjoining the EEC. Our results support the hypothesis of segregated populations within the EEC. The importance of accommodating population substructure in the fisheries management is considered.

**Keywords :** Population structure, capture-mark-recovery, adult connectivity, multi-event modeling, *Solea solea* L., Eastern English Channel

## 35 1 INTRODUCTION

36 Movements of individuals determine connectivity between habitats, control meta-  
37 population dynamics (Hanski 1998; Benhamou 2014) and resilience of populations to  
38 natural and anthropic stressors. Understanding the movement and dispersal patterns of  
39 wild animals at every stage in their life cycle is therefore critical for a full understanding  
40 of population dynamics and the subsequent provision of an evidence base for population  
41 assessment and management.

42 In fisheries, an accurate definition of the spatial structure of fish populations is necessary  
43 for fish stock assessment and for setting appropriate fisheries management strategies  
44 (Kutkuhn 1981; Smith *et al.* 1990; Begg & Waldman 1999; Fogarty & Botsford 2007). A  
45 misspecification of the spatial limits of a stock can lead to biased estimates of population  
46 vital rates (Cadrin *et al.* 2014; Kerr *et al.* 2017). Dispersal process must be addressed at  
47 all life-history stages to accurately assess the spatial and temporal delineation of  
48 populations and to accurately specify spatial management measures that could  
49 potentially target specific areas and life stages (e.g. protecting nursery areas and  
50 spawning aggregations, Fogarty and Botsford 2007).

51 Recent studies have employed a wide variety of tools and methods to assess  
52 connectivity within populations (Le Bris *et al.* 2017; Rogers *et al.* 2017; Moreira *et al.*  
53 2018). Genetic studies using genetic markers such as microsatellites (Cuveliers *et al.*  
54 2012; Jasonowicz *et al.* 2016; Martinez *et al.* 2017) or single nucleotide polymorphism  
55 (Milano *et al.* 2014; Laconcha *et al.* 2015; Bekkevold *et al.* 2015) are often used to  
56 assess the spatial structure of a population and reproductive isolation within populations

57 (Östman *et al.* 2017; Marandel *et al.* 2017). Otoliths are also extensively used in  
58 connectivity studies, either through otolith morphology (Bacha *et al.* 2016; Hüsey *et al.*  
59 2016; Mahe *et al.* 2016) or otolith chemistry (Tanner *et al.* 2016; Callicó Fortunato *et al.*  
60 2017; Régnier *et al.* 2017; Moreira *et al.* 2018). Morphometry and meristics (Allaya *et al.*  
61 2016; Sley *et al.* 2016), parasites (Catalano *et al.* 2014; MacKenzie & Abaunza 2014)  
62 and life history traits (Begg *et al.* 1999; Erlandsson *et al.* 2017; Du Pontavice *et al.* 2018;  
63 Randon *et al.* 2018) have also been used to assess stock structure. In the past decade,  
64 stock delineation studies have resulted in revised stock boundaries for numerous stocks  
65 (e.g. blue whiting Mahe *et al.* 2007, Atlantic cod Zemeckis *et al.* 2014, and horse  
66 mackerel Abaunza *et al.* 2008).

67 Although the information derived from mark-recapture experiments is limited (e.g. they  
68 cannot be used to quantify gene flow, Cadrin *et al.* 2014), they have nevertheless  
69 proven useful for the investigation of fish movements and the spatial structure of  
70 populations (Howe & Coates 1975; Hilborn 1990; Gillanders *et al.* 2001; Patterson III *et*  
71 *al.* 2001; McGarvey & Feenstra 2002; Adlerstein *et al.* 2008; Cadrin *et al.* 2014;  
72 Hanselman *et al.* 2014; Le Bris *et al.* 2017; Liljestrand *et al.* 2019). When considering  
73 commercial fish stocks, tagging data generally consist of mark-release experiments  
74 conducted on scientific surveys, with tag-recovery facilitated via the fisheries, the latter  
75 largely dependent on volunteer reporting by the harvesters. A weakness of such data is  
76 that the detection probability is usually unknown, and non-reporting can be substantial  
77 (Henny & Burnham 1976; Frusher *et al.* 2001; Pollock *et al.* 2002; Cadigan & Bratley  
78 2003, 2006). However, ancillary information is often available (McGarvey & Feenstra  
79 2002). Catch and fishing-effort data are collected for most exploited stocks. Classical  
80 stock assessment models (e.g. Virtual Population Analysis or Statistical Catch-at-Age

81 Analysis) typically provide estimates of total and fishing mortality, and thereby total  
82 abundance. Such information can be used as input in the analysis of tagging data of  
83 harvested fish populations (McGarvey & Feenstra 2002).

84 The common sole (*Solea solea*, L.) is a flatfish substantively harvested in the Western  
85 English Channel to the North Sea (ICES 2017). Today, stock assessment is conducted  
86 separately for three ICES stock divisions (VIIe, VIId, IV; ICES 2017). The Eastern  
87 English Channel (EEC, ICES division VIId) stock, managed as one homogeneous  
88 population, has been overexploited over the last ten years (ICES 2017). Dispersal of the  
89 subadult components has been described: the larvae drift passively over short distances  
90 to local coastal nurseries (Rochette 2011), where the juveniles remain prior to migration  
91 offshore at maturity (Riou *et al.* 2001), where the fish reproduce and enter the fishery.  
92 Observed contrast in key life history traits (density-at-age and length-at-age data) have  
93 suggested potential spatial structuring within the adult component of the EEC common  
94 sole stock within three discrete spatial areas (Du Pontavice *et al.* 2018; Randon *et al.*  
95 2018). However, the movements of adult sole between these areas remain largely  
96 unknown. Here we have drawn on an extensive mark-recapture database collected over  
97 49 years to analyze fish movements and assess connectivity of the adult common sole  
98 population within the EEC and adjacent management areas. We tested the hypothesis  
99 of metapopulation structure within the EEC and estimated the level of mixing between  
100 sub-populations. For that purpose, we developed a capture-recapture model (Royle *et*  
101 *al.* 2013; McCrea & Morgan 2014) built in a state-space model framework (recently  
102 reviewed in Aeberhard *et al.* 2018 in the context of fisheries) to estimate adult and  
103 subadult movement probabilities. Finally, based on our observations, we consider the  
104 implications for management of the common sole stock in the EEC (and more widely) of

105 acknowledging and incorporating population substructure in management and  
106 assessment.

## 107 **2 MATERIALS AND METHODS**

### 108 **2.1 Spatial structure**

109 The spatial structure of the common sole population along the English Channel is  
110 analyzed using five areas (Figure 1): the Western Channel (WC), the North Sea (NS)  
111 and three areas for the EEC: English coast of the Eastern English Channel (UK),  
112 Southern French coast (FrW) and Northern French coast of the Eastern English Channel  
113 (FrE). The WC area is based on an existing spatial management unit (VIIe ICES 2017).  
114 The spatial management unit IV currently used for stock assessment in the North Sea  
115 (ICES 2017) is divided into three spatial subunits. Our study is restricted to the spatial  
116 subunit IVc (ICES 2017) which contains the major part of the common sole commercial  
117 catches in the North Sea. The division of the EEC into three areas (UK, FrW, FrE) is  
118 based on the occurrence of natural barriers of habitat unsuitable for common sole  
119 (Rochette *et al.* 2012). These natural barriers consist of deep gravel grounds, which  
120 occur centrally in the EEC (separating UK from FrW & FrE), and wide rocky reefs from  
121 the coasts out into deeper waters (separating FrW from FrE). These natural delineations  
122 could potentially define the spatial structure of the common sole population within the  
123 EEC and have recently been used to study its connectivity in the EEC (Du Pontavice *et*  
124 *al.* 2018; Randon *et al.* 2018).

### 125 **2.2 Data Collection**

126 The dataset collates four mark-recapture experiments carried out by (i) the Center for  
127 Environment Fisheries and Aquaculture Science (CEFAS, UK) from 1955 to 1985 and  
128 2002 to 2007 (Burt & Millner 2008) and (ii) the French Research Institute for Exploitation

129 of the Sea (IFREMER, France) from 1976 to 1980 and 2016 to 2018 (Table 1, Figure 2).  
130 For each release experiment, Petersen discs were used (Burt & Millner 2008). Discs are  
131 uniquely numbered and are securely attached to the dorsal flank of the fish. Adults and  
132 subadults were released close to the capture position as soon as was possible after  
133 capture. Recaptured marked fish were recovered by fishermen, who provided dates and  
134 spatial coordinates of the recaptures. To assess temporal variations in key model  
135 parameters (see below), the entire dataset was divided into four release experiments  
136 denoted (1) CEFAS<sub>1970</sub> from 1970 to 1985, (2) CEFAS<sub>2002</sub> from 2002 to 2007, (3)  
137 IFREMER<sub>1976</sub> from 1976 to 1980 and (4) IFREMER<sub>2016</sub> from 2016 to 2018 (Tables 1 and  
138 2). Data collected before 1970 were discarded, as information was not sufficient to  
139 estimate fish movements from mark-recovery data (i.e. no reliable estimate of fishing  
140 mortality, see section 2.4.2). Recaptured fish with no release or recovery position or date  
141 of recovery data were discarded. The mark-recapture dataset consists of 32739  
142 released and 7010 recovered fish with known dates and areas of release and recovery  
143 respectively.

### 144 **2.3 Time at liberty and time step**

145 A discrete 4 months time step was used in our modeling approach, based on the life  
146 cycle of the adult common sole (Rochette 2011): spawning (February to May), foraging  
147 (June to September) and overwintering (October to January). For each individual, the  
148 time at liberty (time elapsed between the date of release and the date of recapture) was  
149 recorded. The time at liberty was computed in a number of time steps (Table 1 and  
150 Figure 3). Individuals recovered within the time step of release were removed from the  
151 analysis (2974 fish, 7% of released fish).

## 152 2.4 Modeling approach

### 153 2.4.1 Core modeling structure

154 The final dataset used in the modeling approach consists of 32739 released and 4036  
 155 recovered fish with the following associated information (individual based): dates and  
 156 areas of release and recovery and release experiment. The dataset was analyzed  
 157 through a multi-event mark-recapture modeling approach (Pradel *et al.* 2005) built in a  
 158 state-space modeling framework that accounts for both processes and observation  
 159 errors. The process model tracks the history of each individual released fish on a  
 160 'seasonal' (4-month discrete time step) basis. The trajectory of each individual starts  
 161 with the release event, for which the date and areas are assumed to be recorded without  
 162 errors. In our multi-event model, we consider 15 potential states for the true fate of  
 163 individuals at each time step (Figure 4):

$$164 \quad \{A_{WC}, A_{UK}, A_{FrW}, A_{FrE}, A_{NS}, F_{WC}, F_{UK}, F_{FrW}, F_{FrE}, F_{NS}, M_{WC}, M_{UK}, M_{FrW}, M_{FrE}, M_{NS}\}$$

165 State  $A$  relates to live fish, state  $F$  relates to fish dying by fishing and state  $M$  relates to  
 166 fish dying of natural causes, all located respectively in areas WC, UK, FrW, FrE, NS,  
 167 Figure 1). At any time step  $t$ , a fish can be in one (and only one) of those 15 states. The  
 168 transition between time step  $t$  and  $t + 1$  consists of a three-step series of transitions  
 169 representing ecological and observation processes (Figure 4):

- 170 1. Movement process. Any alive fish at time  $t$  can remain in its current area  $i$  ( $i = 1, \dots, 5$ )  
 171 ) or move to another area  $j$  ( $j = 1, \dots, 5$ ) between  $t$  and  $t + 1$ . The dispersion of all fish  
 172 present in the area  $i$  at time  $t$  is modeled through a Multinomial distribution with  
 173 movement probabilities  $\phi_{(i,j)}$  and  $\sum_{j=1}^5 \phi_{(i,j)} = 1$  (see details hereafter).
- 174 2. Survival. The model assumes that mortality occurs after movements. After  
 175 movements, a fish can survive or die from either natural mortality or fishing mortality  
 176 between  $t$  and  $t + 1$ . For each individual, this transition is modeled as a Multinomial  
 177 distribution with survival rate, mortality rate by fishing or mortality rate by natural  
 178 causes as parameters (denoted  $r^s$ ,  $r^f$  and  $r^m$ , respectively; see details hereafter).



179 3. Observation process. The observation process (that ultimately defines the  
180 likelihood) links observation to the true biological state of each individual at time  $t$ .  
181 Only fish caught by the fishery can potentially be observed. Alive fish or fish dead  
182 from natural causes are unobservable. Once a marked fish is caught by the fishery,  
183 it can eventually be declared. The declaration of a marked fish caught is modeled  
184 through a Bernoulli distribution with declaration rate  $T$  (see details hereafter).

### 185 **2.4.2 Parameterization**

186 We tested several versions of the model accounting for different levels of spatial and  
187 temporal variations in the parameters. Below, we detail the parameterization used in the  
188 full model that accounts for seasonal movements, spatial heterogeneity and inter-annual  
189 variation of survival, and survey-specific declaration rate (model 1, Table 3). Other  
190 challenging models are detailed in section 2.4.3.

#### 191 *Movement process*

192 Probabilities of movement  $\phi_{(i,j,s)}$  are estimated separately for each pair of departure (  
193  $i = 1, \dots, 5$ ) and arrival areas ( $j = 1, \dots, 5$ ) and for each season  $s$  ( $s = 1, \dots, 4$ ). No variability  
194 between years is considered. Movement parameters from the WC to the NS, and from  
195 the NS to the WC are set to 0 and are not estimated (Figure 1). No fish were observed  
196 making these two migrations patterns in a single time step (i.e. 4 months). Therefore, it  
197 was assumed that the large distance separating the two areas does not allow for such  
198 movement in one time step.

#### 199 *Survival process*

200 Survival probabilities for each time step are fixed and assumed known without errors,  
201 defined as:

$$\begin{aligned}
 r^f &= \frac{f}{f+m}(1 - \exp(-(f+m))) \\
 r^m &= \frac{m}{f+m}(1 - \exp(-(f+m))) \\
 r^s &= 1 - (r^f + r^m)
 \end{aligned}$$

2022  
0  
2

203 where  $r^f$  is the probability of death by fishing,  $r^m$  is the probability of natural fish death  
204 and  $r^s$  is the probability of survival.  $m$  and  $f$  respectively are natural and fishing mortality  
205 (per time step of 4 months) as directly derived from published stock assessment  
206 evaluations (ICES 2017). For the three ICES areas (IVc, VIId and VIle) the spatially and  
207 temporally constant natural mortality was fixed to  $m = 0.1 \times timestep^{-1}$  (ICES 2017).  
208 Fishing mortality rate  $f$  was also considered known but with years and spatial variability.  
209 Available information from stock assessment differ among areas (ICES 2017): estimates  
210 of fishing mortality are available since 1955 for the NS area (ICES division IVc), from  
211 1969 for the WC area (ICES division VIle) and from 1982 for the UK, FrW, FrE areas  
212 jointly (ICES division VIId) (Figure 5). The data collected before 1970 were discarded  
213 because no reliable estimate of  $f$  in the EEC could be found before 1970. In order to use  
214 the longest time series of release data, we assumed that fishing mortality was equal in  
215 areas VIle and VIId between 1970 to 1981. Temporal variations were smoothed to limit  
216 the influence of uncertainty that surrounds short term (year-to-year) variations in  
217 estimates of fishing mortality (Figure 5). Preliminary analysis demonstrated that  
218 smoothed time series of  $f$  improve numerical stability of dispersal estimates. The  
219 mortality rates were allocated to each time step within the same year by considering that  
220  $m$  and  $f$  were homogeneous among seasons within a year.

### 221 *Declaration*

222 The probabilities that marked fish caught by the fishery are declared (and then  
223 observed) are estimated, and considered to be variable between release experiments  
224 (but spatially homogeneous and constant among seasons).

### 225 **2.4.3 Hypotheses testing and sensitivity analysis**

226 The full model (model 1, Table 3) accounts for (i) a movement process with parameters  
227 (estimated) that vary between seasons, (ii) yearly and spatially varying survival (fixed  
228 parameters), and (iii) declaration rates (estimated parameters) considered to be variable  
229 between release experiments. In all models, to avoid confusion between parameters and  
230 ensure stable numerical results in the maximum likelihood procedure, estimated  
231 parameters are the movement probabilities and the declaration rates, and all mortality  
232 rates (fishing and natural) are considered known.

233 The existence of dispersal patterns that differ among seasons is tested by fitting models  
234 with no variability of movement probabilities between seasons (models 2, 5 and 7, Table  
235 3) and comparing the results obtained with the full model (model 1, Table 3). The  
236 variation of the declaration rates between release experiments is tested by fitting a  
237 model parameterized with a unique (but still estimated) declaration rate over the full time  
238 series (model 3, Table 3). The existence of inter-annual differences in movements  
239 during the time series is assessed by fitting separate models to the full time series of  
240 data (1970-2018; model 1, Table 3) and to the most recent (2002-2018; model 8, Table  
241 3) and historical time series only (1970-1998; model 9, Table 3). Hypotheses made on  
242 the fishing mortality (considered known in our model) are critical. We therefore also  
243 assessed the robustness of our results to the quantity of expertise on the spatio-  
244 temporal variability of fishing mortality brought into the model. Models with less refined  
245 hypotheses were fitted using: (i) fishing mortality constant over time but different  
246 between areas, computed as the mean of fishing mortality over time series per area  
247 (models 4 and 5, Table 3), and (ii) fishing mortality constant over time and

248 homogeneous in space, calculated as the mean over areas and times series (models 6  
249 and 7, Table 3).

#### 250 **2.4.4 Model fit and selection**

251 All models were built and fitted using the E-SURGE program (version 1.9.0, Choquet  
252 and Nogue 2010). Details about the implementation of the model in E-SURGE are given  
253 in Appendix A. Parameters (movement and declaration rates) were estimated in the  
254 maximum likelihood framework (MLE). The data consist in the sequence of observation  
255 events for all individuals, starting with  $i$  (the area of release,  $i = 1, \dots, 5$ ) at the tagging  
256 event, and ending with  $j$  (the area of recovery,  $j = 1, \dots, 5$ ) when the fish is recaptured and  
257 declared (with a series of 0 between the tagging and the recapture event as the fish can  
258 only be recaptured once) or ending with a series of 0 for fish that are never recaptured.  
259 The likelihood writes down as the product of Bernoulli distributions (declaration process)  
260 over all time steps and all fish (considered independent), marginalized over the  
261 probability distribution of all possible hidden states defined from the product of  
262 Multinomial distributions for the movement and mortality processes. The maximum  
263 likelihood is estimated using the Maximization-Expectation algorithm (Choquet and  
264 Nogue 2010).

265 A goodness-of-fit (GOF) test was conducted prior to model selection to check if our  
266 release and recapture data met the assumption of a general model (the Arnason-  
267 Schwarz Model, Pradel *et al.* 2003). We performed a GOF test using the U-CARE  
268 software (version 2.2, Choquet *et al.* 2009). GOF tests a 'trap-dependence' effect by  
269 comparing future recapture histories between individuals released on the current  
270 occasion versus individuals released on a previous occasion, for all individuals that are  
271 seen again (for more details on GOF test, see Appendix A).

272 Model selection was used to assess which model formulation in Table 3 was the best  
273 supported by the data. Model selection was based on the Akaike's information criterion  
274 corrected for overdispersion (QAIC). The model with the lowest score of QAIC is  
275 considered as the best model. Only models with the same dataset (same length of time  
276 series of data) were compared together.

#### 277 **2.4.5 Sensitivity to area boundaries**

278 A sensitivity analysis to the delineation of the areas was performed through a buffering  
279 method consisting in removing fish released and recovered at or near a border. Such  
280 individuals were potentially crossing the border using migration paths shorter than those  
281 for centrally-based fish, creating a potential edge effect and introducing bias  
282 (i.e. overestimation of movements among spatial areas) in estimates of movement  
283 probabilities. We computed a 30 km buffer around each boundary to remove a  
284 substantial amount (i.e. 10%) of released and recovered fish inside the buffer (3364 fish  
285 were removed).

### 286 **3 RESULTS**

287 The GOF test performed on the full dataset (from 1970 to 2018) revealed a lack of fit ( $\chi^2$   
2882 = 57.476,  $P = 0.000$  and  $df = 24$ ) when over-dispersion is not accounted for. An

8  
8

289 overdispersion coefficient ( $\hat{c}$ ) of 2.39 was applied to all models to account for  
290 overdispersion ( $\hat{c}$  superior to one, Burnham and Anderson 2003, Choquet *et al.* 2009).

291 Overall, the full model (model 1, Table 3) best explains the tagging-recovery data  
292 including seasonal movements, specific declaration rate for each release experiment,  
293 and fishing mortality varying across space and time.

294 The data also support the hypotheses of different detection rates per release  
295 experiments (QAIC model 1 < QAIC model 3, Table 3) with the lowest declaration rates  
296 estimated for the CEFAS<sub>2002</sub>, comparable detection rate between IFREMER<sub>1976</sub> and  
297 IFREMER<sub>2016</sub> experiments and a relatively high detection rate for the CEFAS<sub>1970</sub> release  
298 experiment. Declaration rate estimates presented in Figure 6 for model 1 were similar  
299 among models 1, 2 and 4-7 (Supplementary Files; Table S1).

300 Even if the estimated movement's probabilities between areas remain overall very low,  
301 the results support the existence of seasonal movements (Figure 7 and Figure S2 in  
302 Supplementary Files for a focus on movement between areas). Furthermore, the  
303 conclusion that the data support the existence of seasonal movements patterns is robust  
304 to changes in the time series of fishing mortality used as input to the model. Indeed,  
305 models with seasonal movements in general presented better QAIC scores when  
306 considering pairs of models with the same survival input (QAIC model 1 < QAIC model  
307 2; QAIC model 4 < QAIC model 5; Table 3).

308 Overall, the results support the hypothesis of very low connectivity between the different  
309 areas (model 1, Figure 7). For most areas and seasons, estimates of movement  
310 probability are very low, if not null (i.e. probabilities of staying in the areas of origin are  
311 close to one). Virtually no emigration is estimated from the NS and WC to the three  
312 areas of the EEC. This result highlights the primarily residential nature of the adult  
313 component of the common sole population, with only a very small proportion of adult fish  
314 migrating among areas. Low probabilities of movement are estimated ( $\Phi_{i,j} < 0.25$ ) for  
315 fish in the UK and FrE areas which move to WC and NS. Thus low to moderate exports  
316 outside of the EEC occur between the overwintering and spawning season. Low  
317 probabilities of emigration from the FrW to the WC is also estimated between spawning

318 and foraging seasons. Movement probabilities estimated with model 2 (no seasonal  
319 variability of movements) also support the hypothesis of very low dispersion of common  
320 sole between areas (Supplementary Files; Figure S2). Results are also robust to the  
321 delineation of the five areas. The analysis performed on a dataset without fish released  
322 and recovered near a border provided results (Supplementary Files; Figure S3)  
323 comparable to those obtained with no buffering (Supplementary Files; Tables S2, S3  
324 and S4).

325 Finally, the conclusion that very low connectivity exists between areas is robust to the  
326 time series of data considered. No strong differences exist between movement  
327 probability estimates obtained with the whole dataset (1970-2018), and with the shorter  
328 time series 1970-1998, corresponding to historical release experiments (CEFAS<sub>1970</sub> and  
329 IFREMER<sub>1976</sub>; Tables S2, S3 and S4 in Supplementary Files). Movement probability  
330 between the FrE and NS areas is an exception. Between these areas, higher  
331 movements are estimated when considering historical release experiments only.  
332 Between foraging and overwintering seasons, all fish from NS move to FrE (Table S3),  
333 whereas from spawning to foraging and overwintering to spawning seasons all fish from  
334 the FrE move to NS (Supplementary Files; Table S2). However, these estimated  
335 probabilities of movements can be explained by the small amount of fish released and  
336 recovered in the FrE area: 82 over the 1970-1998 period in comparison with the 1307  
337 fish released and recovered in the NS in the most recent period. Movement probabilities  
338 inferred from recent tagging data collected from 2002 to 2018 are similar to the ones  
339 estimated with the entire dataset (Supplementary Files; Tables S2, S3 and S4), with only  
340 small movements among areas. There are however small differences in estimates of  
341 movement probabilities between the recent tagging data and the full-time series, which

342 mostly concern the three areas of the EEC. Between the foraging and overwintering  
343 seasons, higher than average movement probability are estimated from the UK to the  
344 FrE areas, as well as from the FrW to the FrE areas (Supplementary Files; Table S2).  
345 Limited movements are also estimated from the FrE to the WC and FrW areas from  
346 spawning to foraging seasons (Supplementary Files; Table S2). Confidence intervals are  
347 greater for the more recent period than for 1970-2018 and 1970-1998 time series,  
348 because of the smaller amount of fish released during CEFAS<sub>2002</sub> and IFREMER<sub>2016</sub> in  
349 comparison with the CEFAS<sub>1970</sub> and IFREMER<sub>1976</sub> experiments (Table 3a).

#### 350 **4 DISCUSSION**

351 In the present study, we have analyzed for the first time a substantive database of mark-  
352 recapture data, with 32739 subadult and adult common sole being released over a  
353 period of 49 years. Our results suggest minimal movements of sole among areas in the  
354 EEC, and even lower immigration from adjacent areas, but low to moderate emigration  
355 to the NS and to the WC, mainly between the overwinter and spawning seasons. Our  
356 results provide evidence of low connectivity among common sole subpopulations within  
357 the EEC, and no inputs from the adjacent spatial management areas. This evidence of  
358 local segregation is consistent with recent studies using patterns in key life history traits  
359 (Du Pontavice *et al.* 2018; Randon *et al.* 2018) for the common sole in the EEC.

##### 360 *Reliability of the estimates of movement*

361 Commercially exploited fish populations are often widely monitored, which offers the  
362 opportunity to use survey-generated estimates of population vital rates, expert  
363 knowledge and/or stock assessment (McGarvey & Feenstra 2002). In our study, we  
364 used estimates of fishing and natural mortality from published stock assessments (ICES



365 2017) as input fixed a priori in our state-space capture-mark-recapture modeling  
366 approach. Models incorporating all data available on the survival process (e.g. yearly  
367 and spatially varying fishing mortality) best explain the data.

368 Seasonal movement probabilities estimated in our study revealed low movements, with  
369 small variations when considering different periods within the time series. However, the  
370 historical release experiments (CEFAS<sub>1970</sub> and IFREMER<sub>1976</sub>) were not designed  
371 specifically to study movement patterns at the scale of the English Channel, and  
372 relatively little tagging effort was expended in the two areas along the French coast (FrW  
373 and FrE). This deficit of data in the oldest release experiments can explain the difference  
374 in movement parameters estimated for the 1970 to 1998 time series with regards to the  
375 full time series or to the recent release experiment. Only the recent release experiments  
376 (CEFAS<sub>2002</sub> and IFREMER<sub>2016</sub>) sampled all three EEC areas more evenly. Jointly  
377 analyzing all four tagging experiments allowed for a more balanced dataset, and  
378 reduced singularities and potential bias incorporated by the spatial locations of fish  
379 releases between release experiments.

380 We recognize, however, some weaknesses in our approach, some of which open up  
381 exciting opportunities for future research. Our model is structured on a seasonal time  
382 step of 4-months that reflect biological seasons of the life cycle of the sole in the Eastern  
383 Channel. Although this is justified from a biological point of view, this choice excludes  
384 data from fish that were released and recovered within the same seasonal time step.  
385 The percentage of fish removed because of the chosen time step remains low (7% of  
386 released fish). For those removed fish, 94% were recovered in their zone of release, in  
387 accordance with the results obtained on a 4-monthly basis. In all models, mortality rates  
388 (fishing and natural) were considered known and estimated parameters are the

389 movement and declaration probabilities. Estimating movement, mortality and  
390 detectability is possible in certain configuration of mark-recapture models (Royle *et al.*  
391 2013) but separating temporal and spatial variations in those parameters is still difficult  
392 overall. In our model, attempts to estimate both natural mortality and declaration rates  
393 from our data have shown unstable numerical results and estimates that were non-  
394 robust to small changes in hypotheses, revealing some statistical confusion between  
395 mortality and declaration rates. In other terms, different combinations of mortality and  
396 declaration rates provide the same likelihood for the data. Because the total mortality  
397 estimated from statistical catch-at-age stock assessment models is robust (Quinn &  
398 Deriso 1999; ICES 2017), and because no expertize exists on the declaration rate, our  
399 choice here was to consider mortality as known, and to estimate declaration rates from  
400 the data. Although stock assessment results provide some measure of uncertainty about  
401  $f$  (confidence intervals), only point estimates were considered in our approach. This  
402 simplification answers practical considerations as no methods exist to account for  
403 uncertainty in  $f$  using the E-SURGE software. However, we carefully assessed the  
404 sensitivity of our results to the hypothesis made on the temporal and spatial variation of  
405 the fishing mortality. Because temporal and spatial variation in  $f$  are much higher than  
406 estimation uncertainty (ICES 2017), the robustness of our results to those changes in  $f$   
407 demonstrates the robustness of our inferences on movements to uncertainty about  $f$ .

408 However, estimates from stock assessment models (and especially fishing mortality) can  
409 be sensitive to hypotheses made on the spatial structure of the population (see for  
410 instance results by Archambault *et al.* 2016 on the same case study), and make  
411 inferences on dispersion by using fixed  $f$  from previous assessments that do not  
412 consider dispersion to be an issue. This paper is an important step toward the

413 construction of an integrated model to simultaneously estimate fishing mortality and  
414 dispersion by integrating tagging data within the stock assessment model. Tagging data,  
415 however, can have a complex structure, which when coupled with a poorly balanced  
416 sampling design, can provide further challenge to obtaining robust statistical inferences  
417 from tagging-integrated models (Maunder & Punt 2013). Consequently, we attempted  
418 here to develop a first analysis of the tagging data before integrating them in a more  
419 complex structure.

420 Our approach also considers natural mortality to be constant in space and in time. In  
421 stock assessment evaluations, natural mortality is usually fixed and the fishing mortality  
422 is estimated relative to the fixed value of natural mortality (ICES 2017). Preliminary  
423 exploration of the data (not shown) suggested that consideration of a higher value of  $m$   
424 (but still considering  $m$  to be constant in time and space) has a simple and intuitive  
425 impact on estimates of declaration rates. Considering a higher value of  $m$  leads to lower  
426 estimates of declaration rates, as the same number of recorded marked fish must be  
427 explained by a lower actual number of marked fish in the sea due to higher  $m$ . On the  
428 opposite, considering a smaller value of  $m$  leads to higher estimates of declaration rates.  
429 The effect of introducing spatial heterogeneity in  $m$  which is operationally challenging  
430 was not tested here. However, there is no evidence of a spatially varying natural  
431 mortality for the common sole in the English Channel. Consequently, our assumption of  
432 constant natural mortality among areas was considered to be a realistic and  
433 parsimonious modeling approach for the estimation of fish movement.

434 Although Du Pontavice et al. (2018) and Archambault et al. (2016) suggested  
435 heterogeneity of fishing mortality within the EEC, with the fishing pressure in FrE being  
436 higher than in the UK and FrW areas, no spatial variability of fishing mortality within the

437 three EEC areas was considered in our approach. However, because the EEC common  
438 sole stock is considered homogeneous, no stock assessment results were available for  
439 the individual 'sub-stock' areas (UK, FrW, FrE), and no spatialized catch data were  
440 available in the time series. Furthermore, although the fishery is strongly seasonal  
441 (Vermard and Savina, com. pers.), available times series of within-year fishing effort  
442 distribution were too short to be considered in our analysis (2000-2016 for French and  
443 2004-2016 for foreign fleets), precluding the application of varying fishing mortality  
444 between the 4-month 'seasons'. However, given (i) the very low level of dispersal  
445 estimated among the different areas in the EEC and (ii) the high robustness of these  
446 results to hypotheses on spatial and temporal variations in the fishing mortality that were  
447 tested, it is unlikely that using more refined data would have dramatically altered the  
448 conclusions. Furthermore, recapture probability in our approach depends only on  $m$  and  
449  $f$ . However because the fleet and associated gear is not routinely recorded for mark  
450 recovery, heterogeneity due to the use of different fishing gears, which could have  
451 introduced further realism to our model, was unable to be considered. Finally, we found  
452 strong statistical evidence in favor of different declaration rates between the tagging  
453 periods. Unfortunately, we were not able to find definitive explanations for those  
454 differences. One potential explanation might be haphazard levels of communication with  
455 the fishermen to publicize the tagging programs and associated rewards at different  
456 periods in time. We considered the declaration rate to be homogeneous in time and  
457 space within a period, which might have been a source of bias, in that different fleets  
458 operating in different zones may not have had equivalent information, interest or  
459 motivation to participate in scientific tagging programs. As a result, our estimated  
460 movement probabilities may have been biased by reducing the number of declarations

461 of marked fish caught in a particular area. We have assumed that the aggregation of  
462 several tagging surveys from both UK and French research institutes in the present  
463 modeling approach should limit the overall related biases.

464 *Combining different approaches to improve estimates of connectivity*

465 Several authors have recently highlighted the importance of combining multiple  
466 approaches to study stock delineation (Pita *et al.* 2016). Indeed, individual methods  
467 each have their own strengths and weaknesses, and combining results of different  
468 methods generally improves the overall reliability of the results (Cadrin *et al.* 2014; Izzo  
469 *et al.* 2017). For marine fish in particular, high mortality in early life stages (eggs, larvae  
470 and juveniles, Le Pape and Bonhommeau 2015) and the lack of barriers in the ocean  
471 often rend the genetic signal of segregation relatively weak (Selkoe *et al.* 2008). Only a  
472 very small proportion of fish dispersing at each generation will erase genetics  
473 differences between populations (Palmer *et al.* 2014), which can result in a mismatch  
474 between ecological and genetic connectivity (Hawkins *et al.* 2016).

475 The common sole stocks in the English Channel and North Sea are recognized as  
476 genetically distinct populations (Diopere *et al.* 2017) and have been managed separately  
477 for decades. While common sole in the EEC has been managed as a single  
478 homogeneous stock unit thus far, evidence from different approaches is now  
479 accumulating in support of considering spatial structure at a finer scale. Here we  
480 demonstrate very low exchanges between the three delineated EEC areas, and virtually  
481 no immigration from adjacent stocks. This demographic isolation is consistent with the  
482 marked discrepancies in growth between the areas (Du Pontavice *et al.* 2018; Randon  
483 *et al.* 2018) and the lasting synchrony among density-at-age time series inside each  
484 area (Randon *et al.* 2018).

485 *From low adult-mediated connectivity to segregation in EEC areas*

486 In the EEC, larval connectivity of the common sole is low, since spawning areas directly  
487 feed adjacent coastal nursery grounds (Rochette *et al.* 2012). After metamorphosis,  
488 juveniles grow on shallow nursery grounds (Riou *et al.* 2001; Rochette *et al.* 2010).  
489 Limited movements of juvenile flatfish (Le Pape & Cognez 2016), and the dependence  
490 of the juvenile common sole upon shallow nursery habitats (Riou *et al.* 2001) result in  
491 low juvenile connectivity (Coggan & Dando 1988). After about two years on nursery  
492 grounds, the common sole move to deeper offshore adult foraging grounds. In addition  
493 to premature segregation, the lack of connectivity during the adult phase is a potentially  
494 important driver of segregation (Frisk *et al.* 2014). However, estimated levels of  
495 dispersal demonstrate that at subadult and adult stages, EEC export a low fraction of  
496 individuals to the NS and a very low fraction to the WC. The EEC may act as a limited  
497 source of fish for these adjacent stocks. These movements occur mainly during the  
498 overwintering period of movements of subadults (Dorel *et al.* 1991) and adults (Horwood  
499 1993; Burt & Millner 2008) when common sole move out towards deeper sea areas.

500 *Management implications*

501 Ignoring the spatial structure of exploited fish population dynamics may induce  
502 mismatches between the stock units considered for stock assessment and management  
503 and the biological population structure (Carson *et al.* 2011; Frisk *et al.* 2014; Kerr *et al.*  
504 2017). A better consideration of the spatial structure of populations and of  
505 metapopulation dynamics is critical for sound evidence-based decision-making (Heino *et*  
506 *al.* 1997; Porch *et al.* 1998; Ulrich *et al.* 2017). Inconsistencies between the spatial  
507 structure of populations and delineation of stock units could impede effectiveness and  
508 appropriateness of management measures (Kerr *et al.* 2017), resulting in the

509 overexploitation of the less productive subunits (Cadrin & Secor 2009; Ying *et al.* 2011;  
510 Goethel & Berger 2017). Adults' movements play a critical role in population connectivity  
511 (Frisk *et al.* 2014), especially for species with a low level of connectivity at previous life  
512 stages. Failure to appropriately consider the role of adults' movements (or local  
513 segregation) can lead to bias in assessment of stock status and the proposal of  
514 management non-adapted to the true dynamics and productivity of stocks (Punt &  
515 Restrepo 1995; Porch *et al.* 1998).

516 Rochette *et al.* (2013) and Archambault *et al.* (2016) have developed an integrated life  
517 cycle Bayesian model of the EEC common sole stock. The life cycle sequentially  
518 considers the production of eggs by adults, larval survival and drift, survival and  
519 settlements in coastal nurseries, habitat-dependent survival of juveniles on nurseries  
520 and finally natural and fishing mortality of the adult population. Archambault *et al.* (2016)  
521 consider two contrasted hypotheses: (i) one single homogeneous adult population  
522 supplemented by all coastal nurseries; (ii) three isolated subpopulation supplemented by  
523 separated pools of coastal nurseries. Results show that accounting for spatial  
524 segregation markedly influences stock assessment results (Archambault *et al.* 2016).  
525 Results, from both this and the previous study, show that estimates of fishing mortality  
526 and management reference points such as MSY of the common sole in the EEC  
527 strongly depend upon the underpinning hypothesis of adult connectivity. Further  
528 extension of the integrated life cycle modeling framework of Archambault *et al.* (2016) to  
529 integrate the analysis of tagging data within the integrated life cycle model would allow  
530 the simultaneous estimation of fishing mortality in the different areas of the EEC and  
531 connectivity between those areas. We suggest that such an exercise would contribute to

532 improving scientific advice for the spatial management of the fishery (Methot 2009;  
533 Goethel *et al.* 2011; Griffiths *et al.* 2018).

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544 fisheries “Direction des Pêches Maritimes et de l’Aquaculture”.



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547 *Table 1: Number of marked and recovered fish, used in the analysis, per release*  
 548 *experiment and associated average time at liberty in number of 4-month periods and*  
 549 *recapture rates.*

Experiment	Marked	Recovered	Average time at liberty	Recapture rate
CEFAS <sub>1970</sub>	3627	3627	6.26	1
IFREMER <sub>1976</sub>	305	305	4.07	1
CEFAS <sub>2002</sub>	29	29	5.59	1
IFREMER <sub>2016</sub>	85	85	3.07	1
Total	4046	4046	6.02	1

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551 *Table 2: Number of fish released per area and time series and in parentheses the*  
 552 *number of recovered fish per area and time series.*

	Areas	1970-1998	2002-2018	1970-2018
1	WC	5025 (949)	250 (10)	5275 (959)
2	UK	6897 (1298)	1861 (13)	8758 (1311)
3	FrW	1448 (90)	1048 (7)	2496 (97)
4	FrE	1143 (93)	2148 (55)	3291 (148)
5	NS	12509 (1505)	410 (16)	12919 (1521)
6	Total	27022 (3935)	5717 (101)	32739 (4036)

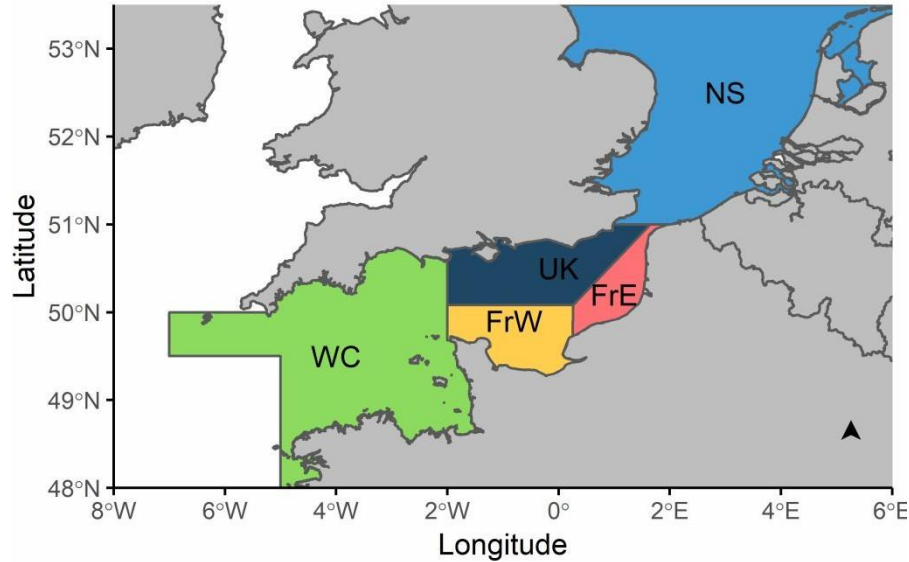
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555 *Table 3: Model definition. Models 1 to model 7 are fitted to the full time series. Model 1 is*  
 556 *the most complex model. Model selection is performed on the full dataset (1970 to 2018)*  
 557 *from model 1 to less complex alternatives in the dispersal, fishing mortality inputs and*  
 558 *detection rates.  $\Delta$ QAIC represents the difference in QAIC in comparison to model 1.*  
 559 *Models 8 and 9 have the same structure as model 1, but are fitted to truncated time*  
 560 *series and hence are not considered in the model selection process.*

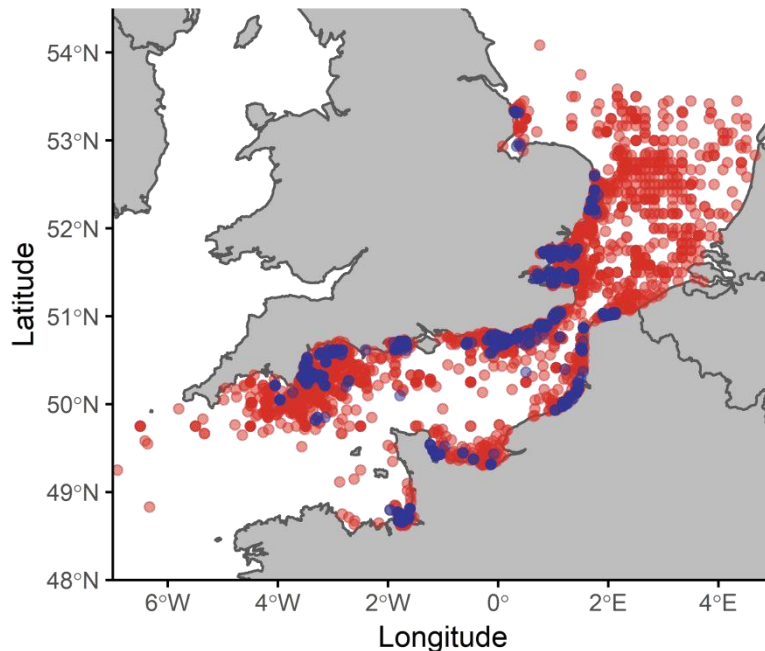
Model	Dispersal	Fishing mortality	Detection	Time Series	QAIC	$\Delta$ QAIC
1	Seasonal	Area x Years	Release experiments	1970-2018	144966	-
2	Constant	Area x Years	Release experiments	1970-2018	144976	10
3	Seasonal	Area x Years	Unique	1970-2018	145882	916
4	Seasonal	Area	Release experiments	1970-2018	145156	190
5	Constant	Area	Release experiments	1970-2018	145187	221
6	Seasonal	Homogeneous	Release experiments	1970-2018	145148	182
7	Constant	Homogeneous	Release experiments	1970-2018	145132	166
8	Seasonal	Area x Years	Release experiments	1970-1998	-	-
9	Seasonal	Area x Years	Release experiments	2002-2018	-	-

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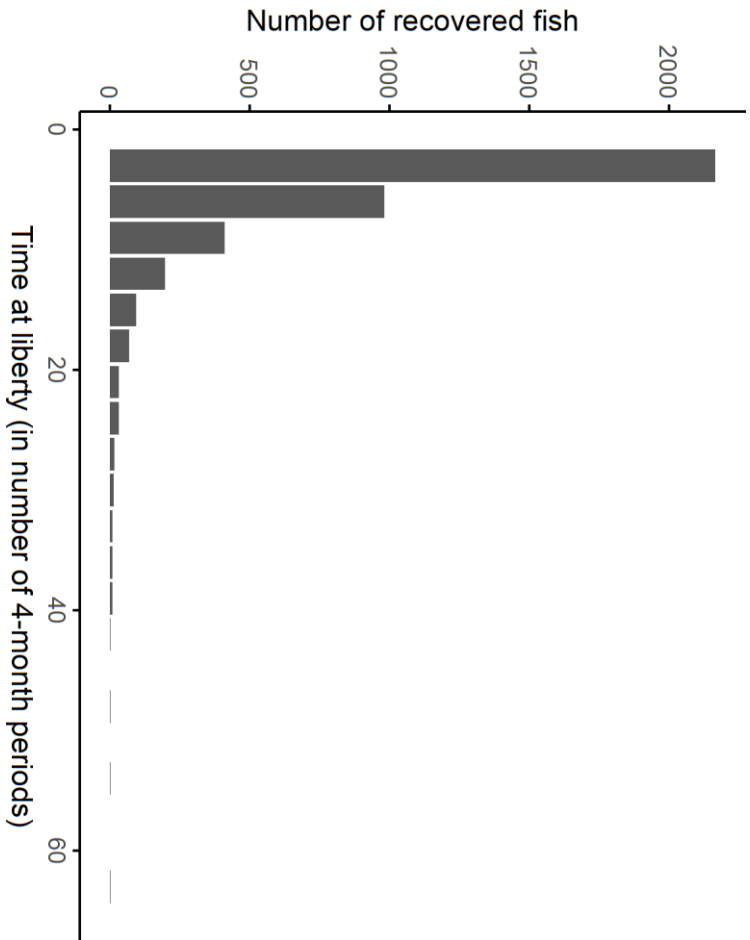


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563 *Figure 1: Map of the model geographical definition with the five areas potentially*  
 564 *structuring common sole stocks (ICES. 2017; IFREMER 2019): Western Channel (WC,*  
 565 *ICES division VIIe), English coast of the Eastern English Channel (UK, ICES division*  
 566 *VIIId), Southern French coast (FrW, ICES division VIIId), Northern French coast of the*  
 567 *Eastern English Channel (FrE, ICES division VIIId) and the southern part of the North*  
 568 *Sea (NS, ICES division IVc).*

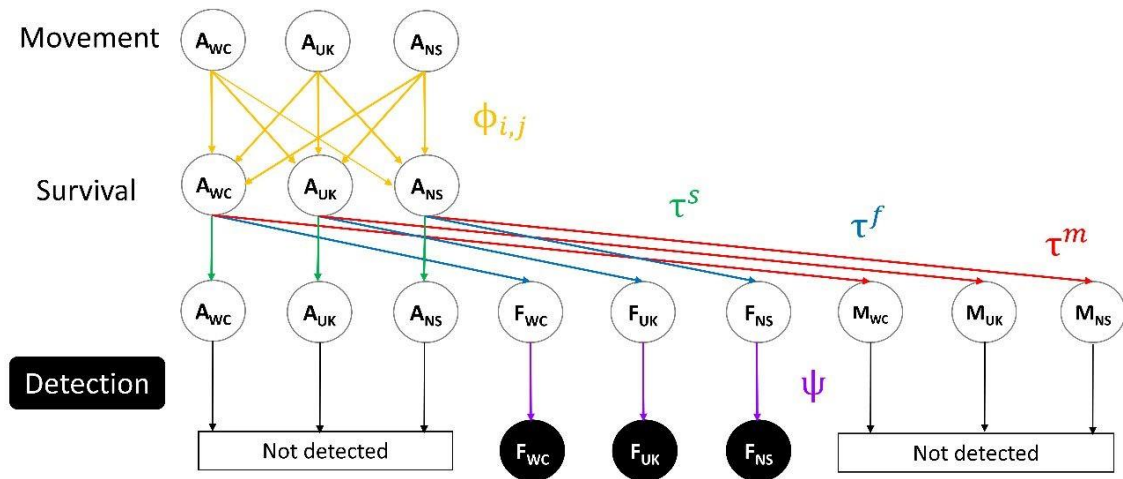


569 *Figure 2: Release locations (in blue) and recapture locations (in red) of tagged common*  
 570 *sole in the English Channel, east of the Western Channel and west of North Sea (Burt &*  
 571 *Millner 2008; IFREMER 2019).*  
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*Figure 3: Time at liberty in number of seasons (4-month periods) for the 4036 marked fish recovered between 1970 and 2018.*

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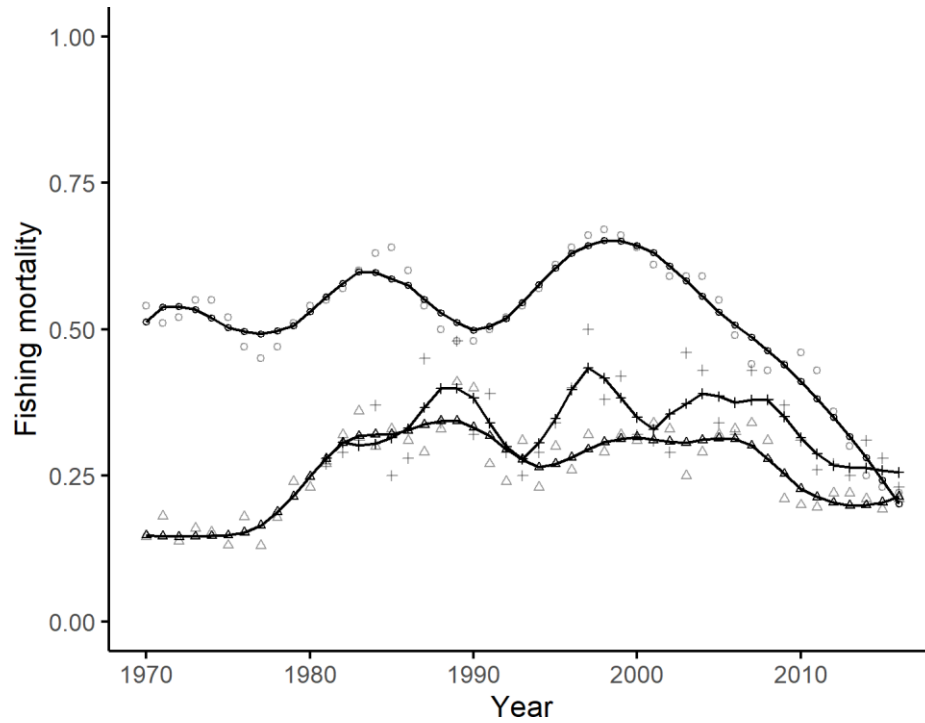


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581 *Figure 4: Diagram representing the model structure used in the analysis. Each step*  
 582 *represents a different model parameter or transition probability. Only three (WC, UK,*  
 583 *NS) of the five areas are represented for ease of reading. Live fish ( $A_{WC}, A_{UK}, A_{NS}$ ) and*  
 584 *fish dying due to natural causes ( $M_{WC}, M_{UK}, M_{NS}$ ) cannot be seen and hence cannot be*  
 585 *detected.*

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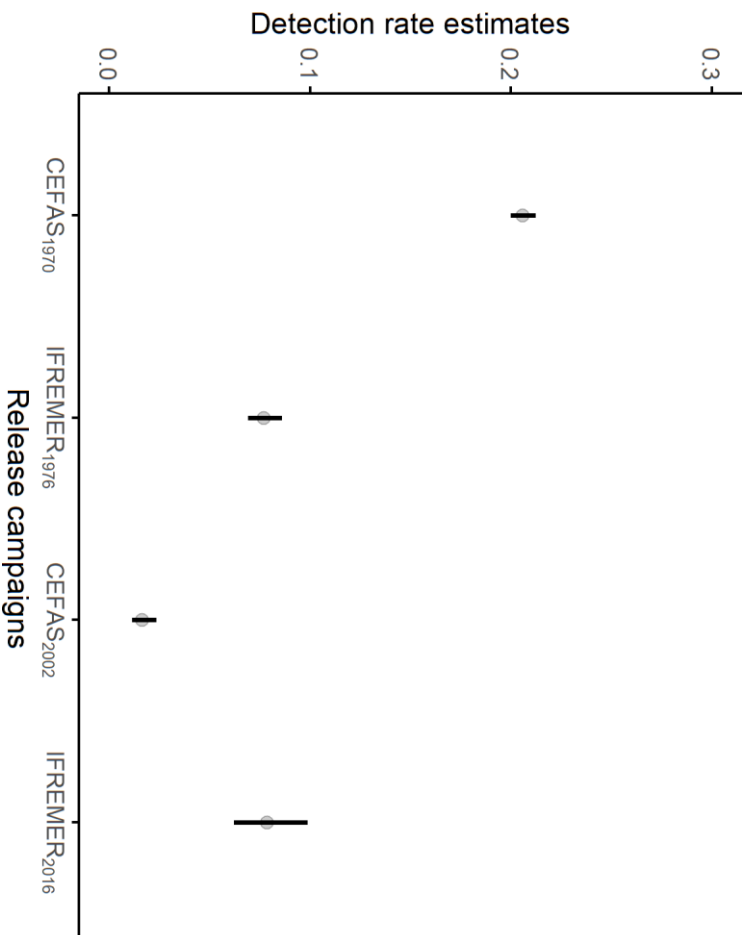
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589 *Figure 5: Annual fishing mortality rate estimated from stock assessments (ICES 2017).*  
 590 *Dotted line represents  $f$  for area IV, triangle line represents  $f$  for area VIId, and cross-*  
 591 *line is for area VIIe. Shaded triangle, dot and cross represent estimates from stock*  
 592 *assessment without smoothing. Locally weighted least squares regression was used to*  
 593 *perform smoothing with 30% of smoothing span.*

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*Figure 6: Detection rate ( $\psi$ ) estimates and their 95% confidence intervals per release experiments from model 1 with the full time series (1970 to 2018).*

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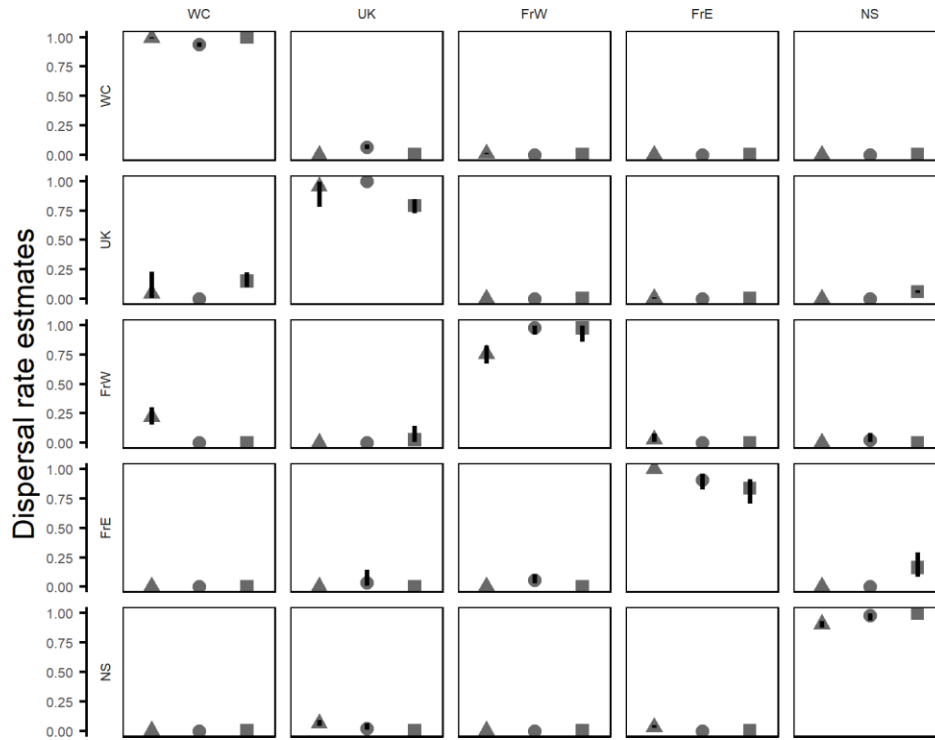
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 602 *Figure 7: Movement probability estimates and their 95% confidence intervals from model*  
 603 *1. Rows represent areas of departure and columns areas of arrival. Triangles are MLE*  
 604 *estimates of movement probabilities from spawning to foraging seasons. Circles from*  
 605 *foraging to overwintering seasons. Squares from overwintering to spawning season.*

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## APPENDIX A

### MODEL STRUCTURE AND E-SURGE SPECIFICATION

E-SURGE (Choquet & Nogue 2010) is used to implement multi-event models which are defined by steps representing biological and observation process. Each process is associated to a row-stochastic matrix for which each row corresponds to a multinomial distribution. All cells probability in the same row must sum to one and so one parameter is defined as the complement of the others (i.e.  $1 - \sum \text{others}$ ) and is denoted by the symbol  $\star$  in the following matrices. Cells with probabilities fixed at 0 are denoted with a dash (-). Matrices rows correspond to the starting state and columns correspond to the arrival state. In our multi-event model, we consider 16 biological states to inform on the true fate of individuals at each occasion:

$$\{A_{WC}, A_{UK}, A_{FrW}, A_{FrE}, A_{NS}, F_{WC}, F_{UK}, F_{FrW}, F_{FrE}, F_{NS}, M_{WC}, M_{UK}, M_{FrW}, M_{FrE}, M_{NS}, \dagger\}$$

State  $A$  relates to live fish, state  $F$  relates to fish killed by fishing and state  $M$  relates to fish dying of natural causes, all located respectively in areas WC, UK, FrW, FrE, NS (Figure 1). An extra state  $\dagger$  is introduced to represent an unobservable dead state which discriminates between the “newly dead” fish from the unobservable “long-time-dead” fish (Lebreton *et al.* 1999; Fernández-Chacón *et al.* 2016). This state is required to estimate the detection rate of fish caught by the fisheries and to distinguish the different causes of mortality. In practice, a fish, that died from fishing or natural causes at time step  $t$ , is assigned to the state “long time dead” at the time step  $t + 1$  and can not change of state afterwards.

#### *Initialization*

Table A1: Matrix I: initial state probabilities ( $\pi$ ) are assigned to alive state only, because tagging is performed on alive fish only.

$A_{WC}$	$A_{UK}$	$A_{FrW}$	$A_{FrE}$	$A_{NS}$	$F_{WC}$	$F_{UK}$	$F_{FrW}$	$F_{FrE}$	$F_{NS}$	$M_{WC}$	$M_{UK}$	$M_{FrW}$	$M_{FrE}$	$M_{NS}$	†
*	$\pi$	$\pi$	$\pi$	$\pi$	-	-	-	-	-	-	-	-	-	-	-

### Dispersal

The first five rows of matrix  $D$  corresponds to fish that are alive at time  $t$  and move (or not) during the transition to time  $t + 1$ . For instance,  $\phi_{WC,UK}$  is the probability for a fish in state  $A_{WC}$  at time  $t$  to move from the  $WC$  area to the  $UK$  area and be in state  $A_{UK}$  at time step  $t + 1$ . The last 10 rows correspond to fish that are dead and by definition cannot move to another area and hence cannot change state at time  $t + 1$ .

Table A2: Matrix D: migration probabilities ( $\Phi_{i,j}$ ).

	$A_{WC}$	$A_{UK}$	$A_{FrW}$	$A_{FrE}$	$A_{NS}$	$F_{WC}$	$F_{UK}$	$F_{FrW}$	$F_{FrE}$	$F_{NS}$	$M_{WC}$	$M_{UK}$	$M_{FrW}$	$M_{FrE}$	$M_{NS}$	†
$A_{WC}$	*	$\phi_{WC,UK}$	$\phi_{WC,FrW}$	$\phi_{WC,FrE}$	-	-	-	-	-	-	-	-	-	-	-	-
$A_{UK}$	$\phi_{UK,WC}$	*	$\phi_{UK,FrW}$	$\phi_{UK,FrE}$	$\phi_{UK,NS}$	-	-	-	-	-	-	-	-	-	-	-
$A_{FrW}$	$\phi_{FrW,W}$	$\phi_{FrW,U}$	*	$\phi_{FrW,Fr}$	$\phi_{FrW,NS}$	-	-	-	-	-	-	-	-	-	-	-
$A_{FrE}$	$\phi_{FrE,WC}$	$\phi_{FrE,UK}$	$\phi_{FrE,Fr}$	*	$\phi_{FrE,NS}$	-	-	-	-	-	-	-	-	-	-	-
$A_{NS}$	-	$\phi_{NS,UK}$	$\phi_{NS,FrW}$	$\phi_{NS,FrE}$	*	-	-	-	-	-	-	-	-	-	-	-
$F_{WC}$	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
$F_{UK}$	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
$F_{FrW}$	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
$F_{FrE}$	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
$F_{NS}$	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-
$M_{WC}$	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-
$M_{UK}$	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-
$M_{FrW}$	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
$M_{FrE}$	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
$M_{NS}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-
†	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1

### Survival

After movement, fish survive (or not) following the survival transition matrix  $S$ .  $r^f$  is the probability of dying from fishing and  $r^m$  from natural causes. The first five rows of matrix  $S$  corresponds to fish that are alive at time  $t$  and can survive or not during the transition to time  $t + 1$ . The last 10 rows correspond to fish that are ‘long-time-dead’.  $r^f$  and  $r^m$  are input from external knowledge (see section 2.4.2., ICES 2017) and are not estimated from the tagging data in E-SURGE.

*Table A3: Matrix S: calculation of survival probabilities with fishing mortality probabilities ( $r^f$ ) and natural mortality probabilities ( $r^m$ ). Survival probabilities are fixed parameters from stock assessment evaluation (ICES 2017).*

	$A_{WC}$	$A_{UK}$	$A_{FrW}$	$A_{FrE}$	$A_{NS}$	$F_{WC}$	$F_{UK}$	$F_{FrW}$	$F_{FrE}$	$F_{NS}$	$M_{WC}$	$M_{UK}$	$M_{FrW}$	$M_{FrE}$	$M_{NS}$	†
$A_{WC}$	*	-	-	-	-	$r^f$	-	-	-	-	$r^m$	-	-	-	-	-
$A_{UK}$	-	*	-	-	-	-	$r^f$	-	-	-	-	$r^m$	-	-	-	-
$A_{FrW}$	-	-	*	-	-	-	-	$r^f$	-	-	-	-	$r^m$	-	-	-
$A_{FrE}$	-	-	-	*	-	-	-	-	$r^f$	-	-	-	-	$r^m$	-	-
$A_{NS}$	-	-	-	-	*	-	-	-	-	$r^f$	-	-	-	-	$r^m$	-
$F_{WC}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$F_{UK}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$F_{FrW}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$F_{FrE}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$F_{NS}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$M_{WC}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$M_{UK}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$M_{FrW}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$M_{FrE}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
$M_{NS}$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
†	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1

*First encounter event*

This matrix is defined differently for the first encounter event (tag-release,  $k = 1$ ) than for the second encounter event (tag-recovery  $k = 2$ ).

*Table A4: Matrix B: events and corresponding model states for the first encounter. Fish are captured in their respective area without errors.*

	not seen	captured WC	in UK	captured FrW	in FrE	captured NS	in
$A_{WC}$	-	1	-	-	-	-	-
$A_{UK}$	-	-	1	-	-	-	-
$A_{FrW}$	-	-	-	1	-	-	-
$A_{FrE}$	-	-	-	-	1	-	-
$A_{NS}$	-	-	-	-	-	1	-
$F_{WC}$	1	-	-	-	-	-	-
$F_{UK}$	1	-	-	-	-	-	-
$F_{FrW}$	1	-	-	-	-	-	-
$F_{FrE}$	1	-	-	-	-	-	-
$F_{NS}$	1	-	-	-	-	-	-
$M_{WC}$	1	-	-	-	-	-	-
$M_{UK}$	1	-	-	-	-	-	-
$M_{FrW}$	1	-	-	-	-	-	-
$M_{FrE}$	1	-	-	-	-	-	-
$M_{NS}$	1	-	-	-	-	-	-
†	1	-	-	-	-	-	-

### Second encounter event

The second elementary matrix presents the probability of each state given the observation for the second and solely encounter ( $k = 2$ ). In the second encounter event, only fish caught by the fishery can be seen. The matrix contains the detection rates  $\psi$ :

*Table A5: Matrix B: events and corresponding model states for the second and solely encounter. Only fish captured by the fisheries can be recaptured. Detection rate  $\psi$  is estimated from the data.*

	not seen	captured WC	in captured UK	in captured FrW	in captured FrE	in captured NS
$A_{WC}$	1	-	-	-	-	-
$A_{UK}$	1	-	-	-	-	-
$A_{FrW}$	1	-	-	-	-	-
$A_{FrE}$	1	-	-	-	-	-
$A_{NS}$	1	-	-	-	-	-
$F_{WC}$	*	$\psi$	-	-	-	-
$F_{UK}$	*	-	$\psi$	-	-	-
$F_{FrW}$	*	-	-	$\psi$	-	-
$F_{FrE}$	*	-	-	-	$\psi$	-
$F_{NS}$	*	-	-	-	-	$\psi$
$M_{WC}$	1	-	-	-	-	-
$M_{UK}$	1	-	-	-	-	-
$M_{FrW}$	1	-	-	-	-	-
$M_{FrE}$	1	-	-	-	-	-
$M_{NS}$	1	-	-	-	-	-
†	1	-	-	-	-	-

### GOODNESS-OF-FIT TEST

Goodness-of-fit (GOF) tests are an important component of capture-recapture modeling: they are used to assess the accuracy of a model in capturing the variance of the data (Pradel *et al.* 2005). The GOF test is divided into two components the 3G test, which compares the capture histories of newly-tagged and previously-tagged individuals released at the same time, and the M component testing a trap-dependence effect by comparing future capture histories between individuals released on the current occasion versus individuals released on a previous occasion, for all individuals that are seen again. In our case study, the 3G test does not exist, because our datasets only includes dead recoveries (Gauthier & Lebreton 2008). The GOF test then relies on the M component only.

GOF is performed on a reduced model that considers parameters to be state and time-dependent with only six states 'dead' or 'alive' in each area (Pradel *et al.* 2003; Duriez *et al.* 2009; Fernández-Chacón *et al.* 2016). GOF cannot handle multiple unobservable states and models with more than 10 different events. We then pooled together subareas of the EEC and summarized observations in seven types of events (not encountered = 0, encountered alive in WC = 1, recovered dead in WC = 4, encountered alive in EEC = 2, recovered dead in ECC = 5, encountered alive in NS = 3, recovered dead in NS = 6). The GOF test was conducted prior to model selection using the U-CARE software (version 2.2, Choquet *et al.* 2009). The GOF test performed on our data was significant revealing a lack-of-fit ( $\chi^2 = 57.476$ ,  $P = 0.000$  and  $df = 24$ ) to the general Arnason-Schwarz model (Pradel *et al.* 2003). To address this  $\chi^2$  of the GOF test divided by the total number of degrees of freedom, to correct for potential lack of fit (Burnham & Anderson 2003; Choquet *et al.* 2009; Fernández-Chacón *et al.* 2016).