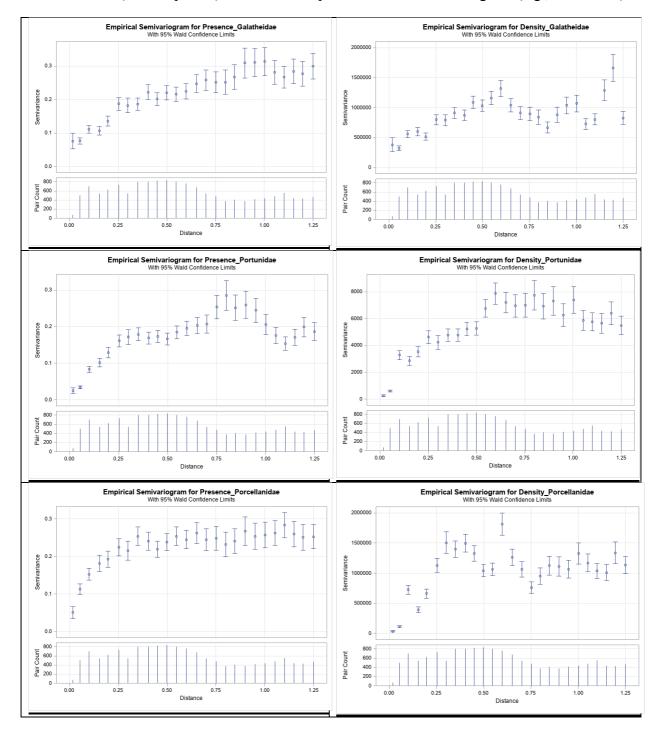
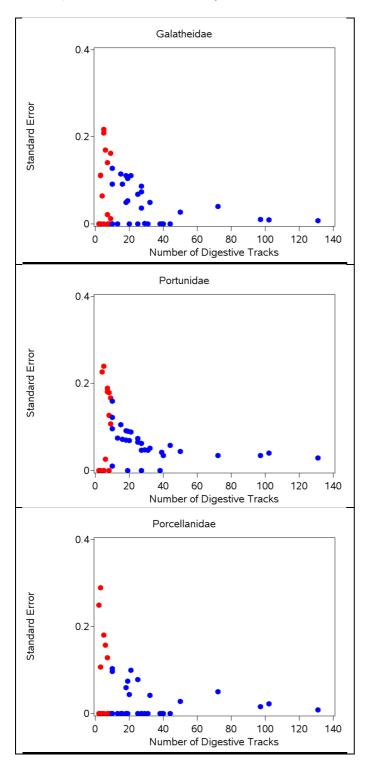
<u>Supplement 1.</u> Spatial structure of observed benthos occurrences and densities drawn from the Eastern English Channel Benthic Survey (ECBS)

Fig. S1. Empirical semi-variogram estimated for ECBS-based occurrences (left panels) and densities (right panels) of Galatheidae (top panels), Portunidae (middle panels) and Porcellanidae (bottom panels). Distance is expressed in fractions of degrees (e.g., 0.25 = 15').



<u>Supplement 2.</u> Standard error of the frequency of occurrence of each prey family found in fish digestive tracts (DTs) sampled from the Channel Groundfish Survey (CGFS)

Fig. S2. Standard error of bootstrapped frequencies of occurrence of Galatheidae (top panel), Portunidae (middle panel) and Porcellanidae (bottom panel) found in CGFS DTs (200 replicates), plotted against the sorted number of DT samples in each spatial unit (red: less than 9 DTs; blue: more than 9 DTs).



<u>Supplement 3.</u> Calculation of the maximal distance covered by fish before their prey are fully digested

The maximal distance that fish may cover before their prey are fully digested may be calculated as the maximal time needed to achieve a full digestion of their benthic prey (i.e., prey's residence time in fish digestive tracts (DTs)) times their maximal velocity (i.e., the maximal geographical range a fish could potentially cover before prey are digested).

Text S1. Calculation of prey residence time in fish digestive tracts

We estimated lower, upper and mean values of the prey residence time in each of the 16 fish species DTs building on DEB (Dynamic Energy Budget) equations.

We assume that the mass of the digestive tract (M_{DT}) is proportional to the whole fish body mass (M) in isomorphs, and that it is length-invariant during the whole life cycle of one species. In fish, the ratio M_{DT}/M (hereafter p_{DT}) ranges between 4% (Hani et al. 2018) and 12% (German & Horn 2006). We could not, however, find the p_{DT} values specific to the 16 fish species under investigation in the literature, but, as the studied species are piscivorous, or omnivorous (while still carnivorous), it is expected that p_{DT} is in the lower range of the interval [4-12%] (Karachle & Stergiou 2010).

In DEB theory (Kooijman 2010), digestive tract residence time ($t_{\rm DT}$) is the ratio between, (i) the mass of the digestive tract at its maximum capacity $M_{\rm DTm}$ (mol C, mass quantified as C-moles) and, (ii) the ingestion rate ($J_{\rm XAm_20}$ in molC.d⁻¹) at 20°C, which needs to be further adjusted by a temperature correction factor ($T_{\rm cor}$):

$$t_{DT} = \frac{M_{DTm}}{J_{XAm_20}T_{cor}} \tag{1}$$

where

$$T_{cor} = exp\left(\frac{T_A}{T_{ref}} - \frac{T_A}{T}\right) \tag{2}$$

 T_A is the species-specific Arrhenius temperature, based on the Arrhenius relationship that accounts for the variation in the temperature dependence of metabolic rate across species (Gillooly et al. 2006), T_{ref} is the reference temperature of the process (here $20^{\circ}C = 293.15^{\circ}K$), and T is the average sea temperature recorded during the CGFS survey (here $17^{\circ}C = 290.15^{\circ}K$).

Equation (1) can be re-arranged as the ratio between:

- (i) the product shape-corrected length (L_{cor} in cm) and (volume) specific structural mass of the digestive tract ($[M_{DTm}]$ in mol.cm⁻³),
- (ii) the product of (surface) specific maximum ingestion rate ($\{J_{Xam}\}\$ in mol.d⁻¹.cm⁻²), temperature correction and the functional scaled response f.

$$t_{DT} = \frac{L_{cor}[M_{DTm}]}{f\{J_{XAm\ 20}\}T_{cor}} \tag{3}$$

 $[M_{DTm}] = [M]p_{DT}$, where [M] is the (volume) specific structural mass (in mol.cm⁻³). Note that [M] is equal to ca. 8.4 10^{-3} mol.cm⁻³ in fish (Kooijman and Lika 2014);

 $L_{cor} = \delta_M L$, where L is fish length (cm) and δ_M is the shape coefficient (in $g^{1/3} L^{-1}$) as defined by $W = (\delta_M L)^3$, where W is fish wet weight (in g);

f varies in principle between 0 and 1 depending on the feeding level (f=1 at satiety and f=0 when starving). In this study, f was considered not to drop below 0.8, which is the classical value used in DEB theory for individual fish living *in situ* (Kooijman & Lika 2014).

Data were retrieved from add-my-pet using AMPtool (Marques et al. 2018) under Matlab R2010b for 12 out of 16 species (Table S1). Four species (red mullet, *Mullus surmuletus*; red gurnard, *Aspitrigla cuculus*; starry smoothhound, *Mustellus asterias*; greater-spotted dogfish, *Scyliorhinus stellaris*) were undocumented. For these species, maximum length (L_{Max}) and δ_M values were retrieved from FishBase (https://www.fishbase.in), and J_{XAm_20} was estimated using closed taxonomic species assuming that J_{XAm_20} is linearly correlated to L_{Max} . Values for *Mullus surmelutus* and *Aspitrigla cuculus* were estimated using 34 species of Perciformes and for *Mustellus asterias* and *Scyliorhinus stellaris* using 11 species of Carcharhiniformes (Fig. S3).

Table S1. Values for the 16 species of the surface specific maximum ingestion rate ($\{J_{Xam}\}$ in mol.d⁻¹.cm⁻²), Arrhenius temperature (T_A in °K), the shape coefficient (δ_M in $g^{1/3}$ L⁻¹) and maximum physical length (L_{Max} in cm).

Species	J_{XAm}	δ_{M}	$T_{\mathbf{A}}$	L _{Max}	Source
Clupea harengus	1.02E-03	0.19	6114	48.4 Ad	d my pet
Sardina pilchardus	4.09E-03	0.08	9800	27.5 Ad	d my pet
Sprattus sprattus	1.97E-04	0.19	9800	15.6 Ad	d my pet
Gadus morhua	2.15E-03	0.12	13500	251.4 Ad	d my pet
Merlangius merlangus	3.00E-03	0.18	7400	76.6 Ad	d my pet
Dicentrarchus labrax	1.31E-03	0.20	8433	77.7 Ad	d my pet
Trachurus trachurus	9.93E-04	0.16	8448	55.9 Ad	d my pet
Pleuronectes platessa	1.06E-02	0.18	6170	79.7 Ad	d my pet
Solea solea	7.92E-04	0.15	6114	72.3 Ad	d my pet
Trigla lucerna	8.86E-04	0.17	8000	80.3 Ad	d my pet
Raja clavata	1.96E-03	0.11	8000	109.4 Ad	d my pet
Scyliorhinus canicula	1.00E-03	0.06	8000	100.5 Ad	d my pet
Mullus surmuletus	1.06E-03	0.21	8000	40.0 Ad	d my pet+ Fish base
Aspitrigla cuculus	1.50E-03	0.20	8000	70.0 Ad	d my pet+ Fish base
Mustelus asterias	1.40E-03	0.12	8000	140.0 Ad	d my pet+ Fish base
Scyliorhinus stellaris	1.89E-03	0.15	8000	170.0 Ad	d my pet+ Fish base

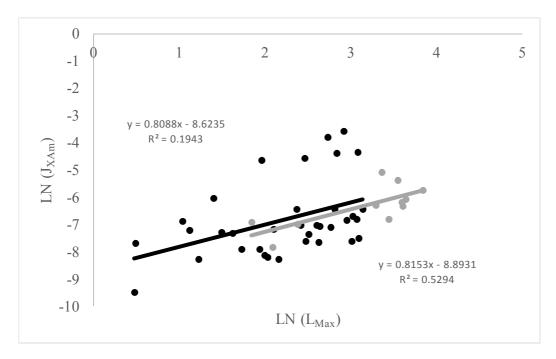


Fig. S3. Ln-Ln Linear regression of the surface specific maximum ingestion rate ($\{J_{Xam}\}$ in mol.d⁻¹.cm⁻²), as a function of the maximum physical length (L_{Max}) for Perciformes (black) and Carcharhiniformes (Grey).

We then estimated lower, upper and mean values of the prey residence time (t_{DT}) in each of the 16 fish species. The lower bound of t_{DT} was calculated assuming $p_{DT} = 4\%$ and f = 1, the upper bound was calculated assuming $p_{DT} = 12\%$ and f = 0.8, while the mean value was the average between the lower and upper bounds. Since the three benthic prey were consumed by the sixteen fish species in variable proportions, for each benthic prey family (Portunidae, Galatheidae, Porcellanidae) and each DT-based dataset (*comprehensive feeders dataset*, benthos-feeders dataset), we calculated the lower, upper and average residence time in an "average fish" DT. This was done by averaging the individual t_{DT} , weighted by the proportion of fish DT where a given prey was found, across fish species (Table S2).

Table S2. Residence time (days) of benthic prey in fish DTs (low range, top range, average values) calculated for 16 fish species (see Table S1). The DT residence time is also given for an average fish feeding on Portunidae, Galatheidae and Porcellanidae prey, when considering all fish predators and those feeding on benthos and endobenthos only (as defined in Table 1).

Functional group	Predator species	Prey species	DT residence	time (days)	
			Low range	Top range	Average
Benthos-feeding fish	Red gurnard	Aspitrigla cuculus	1.49	5.45	3.47
	Red mullet	Mullus surmuletus	1.72	6.30	4.01
	Starry smooth-hound	Mustelus asterias	1.80	6.77	4.29
	Thornback ray	Raja clavata	0.69	2.31	1.50
	Small-spotted catshark	Scyliorhinus canicula	1.51	5.05	3.28
	Large-spotted dogfish	Scyliorhinus stellaris	0.57	2.47	1.52
	Tub gurnard	Trigla lucerna	2.68	9.52	6.10
Endobenthos-feeding	Plaice	Pleuronectes platessa	0.29	0.87	0.58

fish	Sole	Solea solea	2.09	7.85	4.97
Demersal piscivorous	Bass	Bass Dicentrarchus labrax		11.24	7.13
fish	Cod Gadus morhua			6.00	3.82
	Whiting	Merlangius merlangus	0.51	1.70	1.11
Planktivorous fish	Herring	Clupea harengus	0.96	3.48	2.22
	Sardine	Sardina pilchardus	0.26	1.03	0.64
	Sprat	Sprattus sprattus	5.64	21.19	13.41
Pelagic piscivorous fish	lagic piscivorous fish Horse mackerel Trachurus trachurus			6.86	4.29
	All predators		1.91	7.02	4.46
Average fish feeding on Portunidae					
Portunidae	Benthos- and endobenth	os-feeding predators	1.49	5.38	3.44
	All predators		1.45	5.31	3.38
Average fish feeding on Galatheidae					
Galatheldae	Benthos- and endobenth	1.61	5.89	3.75	
A C: 1 C 1:	All predators		1.62	5.93	3.77
Average fish feeding on Porcellanidae					
rorcenamade	Benthos- and endobenth	os-feeding predators	1.66	6.08	3.87

Considering all predators, it can be shown (Table S2) that the longest average residence time is found for an average fish consuming Portunidae (4.5 days), compared to average fish consuming Porcellanidae (3.8 days), or Galatheidae (3.4 days). Considering benthos and endobenthos-feeding predators only, the longest average residence time is found for an average fish consuming Porcellanidae (3.9 days), compared to average fish consuming Galatheidae (3.8 days), or Portunidae (3.4 days). The sharp decrease in average residence time for the average fish consuming Portunidae is due to the fact that seabass, which has a high average residence time (7.1 days) and represents 19% of the DTs where Portunidae were found (Table 1), were excluded when considering the benthos- and endobenthos-feeding predators group.

<u>Text S2. Calculation of the maximal geographical range fish could cover before full digestion of prey</u>

The next step is to estimate the maximal geographical range a fish could potentially cover before prey are digested (i.e., during their maximal residence time in DT). Tagging surveys may provide information on average fish velocity, i.e., the distance covered by fish between the time they are tagged and released, and the time they are re-captured. Extensive tagging programmes have thus been carried out in the North Sea and the English Channel for over 100 years (Burt et al. 2006). These allow derivation of basic fish movement parameters for some of the most important benthic feeders considered in our study: sole, cod, whiting, bass, thornback ray, starry smooth-hound and small-spotted catshark (Table S3).

The maximal distance that fish belonging to these species may cover before their prey are fully digested may be calculated as the maximal time needed to achieve full digestion of their benthic prey (Table S2, top range value) multiplied by their maximal velocity (drawn from Table S3). The geographical range values obtained for whiting (<1 km), thornback ray (2.0 km), sole (2.4 km), cod (8.4 km) and bass (5.7 km) would allow these fish species to visit a maximum of two 15'x15' (~27 km x 27 km) spatial units before their prey are fully digested. The tagging information available for small-spotted catshark and starry smooth-hound (Table S3) was sparse and more difficult to interpret. Sims et al. (2001) suggested that small-spotted catshark shows sex-based philopatry and may be resident in an area in both the short and the long term (Sims et al., 2001), while Walker et al. (1980) found individuals covering up to 24 km in less than 1 day after being released (59 km/day on average). Extrapolating this value to the maximal time needed to achieve full prey digestion (5.1 days) would suggest a 301 km geographical range, which should be interpreted cautiously for the reasons given above. No starry smooth-hound velocity estimate could be found in Brevé et al. (2016). This study reported, however, that many of the 80 recaptured specimens had travelled more than 300 km (Fig. 1 in Brevé et al. 2016). This information suggests that small-spotted catshark and starry smooth-hound might potentially visit more than two spatial units before their prey are fully digested. No tagging information was available for the other three important benthic feeders considered in this study: red gurnard, red mullet and tub gurnard. However, even with a medium velocity of 1 km/day, which is likely a top range given their benthic behaviour, these fish species could only cover a maximum of 9.5 km and hence two spatial units before their prey are fully digested, similar to sole, cod, whiting, bass and thornback ray.

Table S3. Fish movement parameters drawn and/or estimated from a variety of tagging studies carried out in the North Sea, the English Channel, and South West Ireland: mean distance covered (km), no. days at liberty, velocity (km/day) between the time fish have been tagged and released, and the time they have been re-captured. Whenever possible, Quarter 4 recapture results are presented to better align with the CGFS survey period.

Species	Period	Area	No. Fish	Days at liberty	Distance	Velocity	Reference
Sole / juveniles	1955-2004 / Q4	Greater Thames Estuary	79	287	87	0.30	Burt & Millner (2008)
Sole / mature	1955-2004 / Q4	Greater Thames Estuary	342	599	127	0.21	
Sole / all	1955-2004 / Q4	UK coast betwenn Flamborough and The Wash	60	1096	113	0.10	
Sole / all	1955-2004 / Q4	Dutch offshore area	39	572	96	0.17	
Sole / juveniles	1955-2004 / Q4	Eastern English Channel	89	203	34	0.17	
Sole / mature	1955-2004 / Q4	Eastern English Channel	143	466	81	0.17	
Sole / juveniles	1955-2004 / Q4	UK coast between Brighton and Poole Harbour	133	231	30	0.13	
Sole / mature	1955-2004 / Q4	UK coast between Brighton and Poole Harbour	181	771	92	0.12	
Sole / all	1955-2004 / Q4	French coast	23	502	70	0.14	
Cod < 50	2004-2005 / Q1&Q4	ICES area IVc (North-West)	118	-	90	0.38	Righton (2005)
Cod > 50	2004-2005 / Q1&Q4	ICES area IVc (North-West)	80	-	98	0.25	

Species	Period	Area	No. Fish	Days at liberty	Distance	Velocity	Reference
Cod < 50	2004-2005 / Q1&Q4	ICES area IVc (East)	40	-	52	0.18	
Cod > 50	2004-2005 / Q1&Q4	ICES area IVc (East)	106	-	109	0.22	
Cod < 50	2004-2005 / Q1&Q4	ICES area IVc (South)	161	-	83	0.28	
Cod > 50	2004-2005 / Q1&Q4	ICES area IVc (South)	163	-	124	0.30	
Cod < 50	2004-2005 / Q1&Q4	Eastern English Channel	67	-	54	0.21	
Cod > 50	2004-2005 / Q1&Q4	Eastern English Channel	86	-	151	0.26	
Cod	2010 Q1	North Thames Estuary	12	29	40	1.40	Bendall & Randall (2010).
Whiting	1965-1972	Northern North Sea	0-48	-	-	0.03-0.50	Hislop & MacKenzie (1976)
Seabass	1970-1971	SW England	59	-	-	1.40	Holden & Williams (1974)
Starry smooth- hound	2011-2014	Dutch delta	80	Up to 746 days	Up to 1400 km	-	Brevé et al. (2016).
Small- spotted catshark	1976 Q4	East Anglian coast	3	0.38	16	59	Walker et al. (1980)
	1995-1996 / Q3	SW Ireland	11	Up to 365 days	<1	-	Sims et al. (2001)
Thornback ray	2008-2013	Western English Channel	43	-	-	0.43	Humphries et al. (2017)

Species	Period	Area	No. Fish	Days at liberty	Distance	Velocity	Reference
Thornback ray	2000 / Q4 (oct-dec) / conventional tagging)	Thames Estuary	2-4	186-343	12-39	0.04-0.06	Hunter et al. (2005)
Thornback ray	2000-2001 / Q4 (oct-dec) / electronic tagging)	Thames Estuary	4-16	28-251	81-105	0.28-0.85	

Supplement 4.

<u>Text S3.</u> Structure of the system of equations used to estimate probability of occurrence of benthic prev

Finding a prey is in a DT collected in square i (with probability q_i) assumes that: (1) this prey actually occurs in square i (with probability p_i) and that it has been eaten in square i (with probability $1 - \alpha$), or (2) the prey actually occurs in square j, which refers to any of the N_i spatial units directly neighbouring square i (with probability p_j) and that it has been eaten in square j by a fish that subsequently moved to square i where it was caught (with probability α/N_i):

$$q_i = (1 - \alpha)p_i + \left(\frac{\alpha}{N_i}\right) \sum_{j=1}^{N_i} p_j \tag{1}$$

We aim to derive all p_i by solving the system of linear equations obtained when varying i between 1 and the total number of spatial units being surveyed (1). To explore some of the theoretical properties of this system of equations, we considered a simple case with 9 spatial units represented below (white cells provide DT information; grey cells are void or uninformed):

<i>i</i> =1; N ₁ =3	<i>i</i> =2; N ₂ =5	<i>i</i> =3; N ₃ =3	
<i>i</i> =4; N ₄ =5	<i>i</i> =5; N ₅ =8	<i>i</i> =6; N ₆ =5	
<i>i</i> =7; N ₇ =3	<i>i</i> =8; N ₈ =5	<i>i</i> =9; N ₉ =3	

The system of linear equations to be solved is then:

$$\begin{cases} q_{1} = (1-\alpha)p_{1} + \frac{\alpha}{3}p_{2} + 0p_{3} + \frac{\alpha}{3}p_{4} + \frac{\alpha}{3}p_{5} + 0p_{6} + 0p_{7} + 0p_{8} + 0p_{9} \\ q_{2} = \frac{\alpha}{5}p_{1} + (1-\alpha)p_{2} + \frac{\alpha}{5}p_{3} + \frac{\alpha}{5}p_{4} + \frac{\alpha}{5}p_{5} + \frac{\alpha}{5}p_{6} + 0p_{7} + 0p_{8} + 0p_{9} \\ q_{3} = 0p_{1} + \frac{\alpha}{3}p_{2} + (1-\alpha)p_{3} + 0p_{4} + \frac{\alpha}{3}p_{5} + \frac{\alpha}{3}p_{6} + 0p_{7} + 0p_{8} + 0p_{9} \\ q_{4} = \frac{\alpha}{5}p_{1} + \frac{\alpha}{5}p_{2} + 0p_{3} + (1-\alpha)p_{4} + \frac{\alpha}{5}p_{5} + 0p_{6} + \frac{\alpha}{5}p_{7} + \frac{\alpha}{5}p_{8} + 0p_{9} \\ q_{5} = \frac{\alpha}{8}p_{1} + \frac{\alpha}{8}p_{2} + \frac{\alpha}{8}p_{3} + \frac{\alpha}{8}p_{4} + (1-\alpha)p_{5} + \frac{\alpha}{8}p_{6} + \frac{\alpha}{8}p_{7} + \frac{\alpha}{8}p_{8} + \frac{\alpha}{8}p_{9} \\ q_{6} = 0p_{1} + \frac{\alpha}{5}p_{2} + \frac{\alpha}{5}p_{3} + 0p_{4} + \frac{\alpha}{5}p_{5} + (1-\alpha)p_{6} + 0p_{7} + \frac{\alpha}{5}p_{8} + \frac{\alpha}{5}p_{9} \\ q_{7} = 0p_{1} + 0p_{2} + 0p_{3} + \frac{\alpha}{3}p_{4} + \frac{\alpha}{5}p_{5} + \frac{\alpha}{5}p_{6} + \frac{\alpha}{5}p_{7} + (1-\alpha)p_{8} + \frac{\alpha}{5}p_{9} \\ q_{8} = 0p_{1} + 0p_{2} + 0p_{3} + \frac{\alpha}{5}p_{4} + \frac{\alpha}{5}p_{5} + \frac{\alpha}{5}p_{6} + \frac{\alpha}{5}p_{7} + (1-\alpha)p_{8} + \frac{\alpha}{5}p_{9} \\ q_{9} = 0p_{1} + 0p_{2} + 0p_{3} + 0p_{4} + \frac{\alpha}{3}p_{5} + \frac{\alpha}{3}p_{6} + 0p_{7} + \frac{\alpha}{3}p_{8} + (1-\alpha)p_{9} \end{cases}$$

The system of linear equations (2) may for convenience be represented in a matrix form:

$Q = M \cdot P$

P is a (9 x 1) single-column matrix, the coefficients of which are:

p_1	n ₂	n ₂	n ₄	n ₅	n ₆	n ₇	no	n _o
P_{\perp}	P 2	1 2	P4	PJ	PU	Ρ/	Po	P

 \mathbf{Q} is a (9 x 1) single-column matrix, the coefficients of which are:

O1	Пэ	O3	Q4	O ₅	O ₆	O7	q_8	Пo
41	92	43	94	45	90	4/	98	49

M is a (9 x 9) square matrix, the coefficients of which are:

1-α	α/3	0	α/3	α/3	0	0	0	0
α/5	1-α	α/5	α/5	α/5	α/5	0	0	0
0	α/3	1-α	0	α/3	α/3	0	0	0
α/5	α/5	0	1-α	α/5	0	α/5	$\alpha/5$	0
α/8	α/8	α/8	α/8	1-α	α/8	α/8	α/8	α/8
0	α/5	α/5	0	α/5	1-α	0	$\alpha/5$	α/5
0	0	0	$\alpha/3$	α/3	0	1-α	α/3	0
0	0	0	α/5	α/5	α/5	α/5	1-α	α/5
0	0	0	0	α/3	α/3	0	α/3	1-α

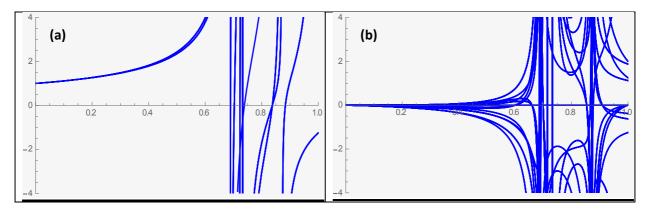
Solving (2) requires to inverse **M** and calculate **P**:

$$P = M^{-1} \cdot Q$$

Symbolic matrix calculus was performed using the Mathematica package (Wolfram Research Inc. 2019). Showing the full representation of \mathbf{M}^{-1} (and of \mathbf{P}) as a function of α would be possible but awkward, and beyond the scope of this study. It is here sufficient to indicate that \mathbf{M}^{-1} is a (9 x 9) square matrix, each coefficient of which is a ratio between two polynomials of degree 8, where the indeterminate is α .

Fig. S4 represents the variations of the different coefficients of \mathbf{M}^{-1} in relation to α , separating those positioned inside and outside the diagonal of the matrix.

Fig. S4. Variations of the different coefficients of M^{-1} in relation to α : (a) elements of the diagonal of matrix M^{-1} ; (b) all elements of matrix M^{-1} except the diagonal.

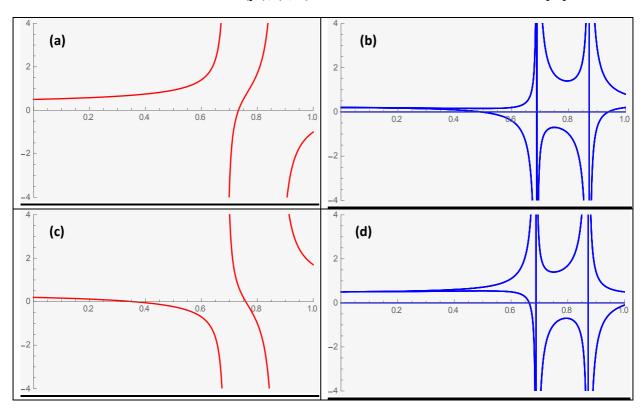


All coefficients of the diagonal, i.e., the coefficients which relate the observed and actual probabilities of occurrence from the same spatial unit, are greater than 1 and increase monotonically with α when $\alpha < \frac{1}{50}(39 - \sqrt{21})$ [~0.69]. The coefficients positioned outside of the diagonal exhibit various trends (increasing, decreasing, convex) and values (positive,

negative) when α < 0.69. When α exceeds 0.69, the variations of all \mathbf{M}^{-1} coefficients relative to α are non-monotonic, with several discontinuities, and take all possible positive and negative real values. This demonstrates that solving (S2) may lead to some \mathbf{P} coefficients being negative or greater than 1 for various combinations of \mathbf{Q} coefficients and α ranging between 0 and 1.

This is illustrated with two simple examples, where all \mathbf{Q} coefficients equate to 0.2 except the central element (q₅), which equates to 0.5 (Figs. S5a & S5b), and where all \mathbf{Q} coefficients equate to 0.5 except the central element (q₅), which equates to 0.2 (Figs. S5c & S5d). We show that values of the \mathbf{P} coefficients may be found beyond range [0, 1], and hence may not be interpreted as probabilities.

Fig. S5. Variations of the different coefficients of **P** in relation to α : (a, b) all elements of the **Q** vector matrix are set to 0.2 except the central element that equates to 0.5; (c, d) all elements of the **Q** vector matrix are set to 0.5 except the central element that equates to 0.2; (a, c) central element of vector matrix **P** (p₅); (b, d) all elements of vector matrix **P** except p₅.



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