

Measuring dispersal as distance-dependent recruitment rates: testing the performance of DDRR on simulated data

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1	Measuring dispersal as Distance Dependent Recruitment Rates: Testing the
2	performance of DDRR on simulated data.
3	
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24	Abstract
25	Dispersal is an important process in ecology, but its measurement is difficult.

26 In particular natal dispersal, the net movement between site of birth and site of first 27 reproduction is important, since it determines population structure. Using simulated 28 data, I study the claim that measuring dispersal in terms of distance dependent 29 recruitment rates filters out many problems. Using several dispersal rules and several 30 spatial distributions of breeding sites, it is shown that distance dependent recruitment 31 rate (DDRR) estimates are independent of the spatial distribution of breeding sites and 32 are sensitive to differences in dispersal rules. These simulations were carried out with 33 sample sizes of 200 individuals, which is a number exceeded in many studies. 34 Variation in clumping of breeding sites (colony sizes) also has little effect on the 35 resulting DDRR estimates. The effects of individuals entering and leaving the study 36 area was simulated by assuming that only half the area was observed. Comparing the 37 'observed' movements with the total distribution of distances dispersed shows that the 38 shape of the DDRR is not affected, although the absolute values are, of course, lower. 39 Thus, DDRR estimates will allow us to start studying dispersal behaviour independent 40 of the peculiarities of the study area and independent of the distribution of observer 41 effort.

43 Introduction

44

45 Dispersal is an important process in ecology (Johnson and Gaines 1990; 46 Tinbergen 2005). In particular natal dispersal, the net displacement between site of 47 birth and site of first reproduction determines the spatial scale of population dynamics 48 and gene flow. In birds, large amounts of data have been collected where individuals 49 have been ringed in the nest and later been identified as breeding birds. Yet the 50 measurement of natal dispersal is quite problematic, because nearly always there are 51 important differences in the opportunity to observe movements over different 52 distances (Korner-Nievergelt et al. 2010). This heterogeneity in observability quickly 53 leads to discrepancies between the observed dispersal and the true dispersal distance 54 distribution (Baker et al. 1995; Kendall and Nichols 2004; Koenig et al. 1996; Nichols 55 and Kaiser 1999).

56 Two of the main problems in this respect are individuals that move out of the 57 study area and are thereby lost from observation (Barrowclough 1978) and the fact 58 that within a study the distribution of all possibly observed distances varies between 59 locations (van Noordwijk 1984; van Noordwijk 1995; Winkler et al. 2005). For 60 example the maximum distances are longer at the periphery than in the centre and the 61 number of sites at short distances are higher in the centre. It has been suggested that 62 this latter problem can largely be circumvented by expressing dispersal as distance 63 dependent recruitment rates DDRR In which observed dispersal movements are 64 expressed relative to the numbers ringed in that distance class (van Noordwijk 2006). 65 Here the performance of DDRR as a measure of dispersal is studied using 66 simulated data. There are many aspects of measuring dispersal that can be 67 investigated by means of simulations. Birds breed either in more or less evenly spaced

e	58	territor	ies or in colonies. Colonial breeding adds complications due to varaition in							
6	59	colony sizes. To include these problems the simulations are made in terms of breeding								
7	70	colonies. The results presented here are by no means exhaustive, but they illustrate								
-	71	several aspects of the method:								
7	72	1)	There should be a substantial reduction in the variation in results obtained							
-	73	from replicate studies with different distributions of breeding colonies.								
-	74	2)	Effects of variation in colony size should largely be eliminated.							
-	75	3)	The method should be sensitive to differences in dispersal rules used.							
-	76	4)	Effects of incomplete knowledge due to animals moving into and out of the							
-	77		study area should be largely eliminated from the results.							
7	78		These simulations also show that the resulting DDRR are easy to interpret,							
7	79	because	e they show the dispersal rules used in the simulation in a direct way.							
8	80									
8	81		Methods							
8	32		Calculation of Distance Dependent Recruitment Rates							
8	33		The basic data consist of observations on individuals that were born at a							
8	84	known	location and initiated reproduction at a known location. For each location,							
8	85	where a	a new breeding bird settled, it can be calculated how many individuals were							
8	86	ringed	at each distance in the birth year of the recruits. These data are summarised in							
8	87	distanc	e classes. These distributions of distances to ringing locations are then							
8	88	average	ed over all recruits. The resulting distribution describes the average numbers							
8	39	• 1								
C		ringed	in each distance class, which gives a complete description of what could							
2	90	-	in each distance class, which gives a complete description of what could y be observed. Dividing the frequencies of the actually observed number of							
	90 91	possibl								
Ç		possibl recruits	y be observed. Dividing the frequencies of the actually observed number of							

93	class, hence DDRR. Formal definitions are given in appendix 1 and a step by step
94	manual for calculating DDRR on real data is given in appendix 2.

- 95
- 96 **Basic simulations**

97 In each run, 25 points (studied colonies) were generated with coordinates 98 drawn from uniform distributions. Next, 200 individuals were generated that started at 99 one colony and moved to a second colony, according to one of the sets of dispersal 100 rules (see below). The distance between natal and breeding colony of each individual 101 was then calculated and these distances were grouped in a frequency distribution to be 102 presented as numbers observed. The same data were also analysed to generate DDRR 103 values. For each recruited individual, all distances to the starting colonies for all 104 individuals in that run were calculated to generate the average number of individuals 105 marked in each distance class. DDRR values are the number of individuals observed 106 per distance class, divided by the average number of individuals marked in that 107 distance class. All simulations were performed in PASCAL programs. 108 109 **Dispersal rules** 110 In all cases, the starting colony for each individual was drawn randomly from 111 the set of colonies. The following dispersal rules were used: 112 1) Random redistribution. One point was drawn randomly from the total set of 113 colonies. The probability that an individual moved to any colony (including 114 the colony of origin) is thus equal to one over the number of colonies. 115 2) Favouring short distances. Two colonies were drawn at random. The distances 116 from the starting colony were calculated and the colony with the smallest

117 distance was selected as destination.

- 3) *Strongly favouring short distances*. Similar to 2, but now the minimum
 distance from 5 randomly picked colonies was used instead of the minimum
 from 2.
- 4) *Favouring medium distances*. The median distance from 3 randomly picked
 colonies was used to determine the destination colony.
- 123
- 124

Extensions to the simulations.

125 In the real world colonies are unlikely to have the same size, the biggest

126 colonies may be evenly spaced and moreover study sites are limited, so that

127 individuals will be lost from sight by moving over the border of the study site. These

128 aspects were included in the analysis by three further extensions to the simulations.

129 First, colony sizes were made unequal. Instead of 25 colonies with equal sizes, 5

130 colonies were created with relative size 10, 5 with relative size 5, 10 with relative size

131 2 and 5 with relative size 1. This was achieved by using a list of 100 colonies, but

132 replicating the coordinates as many times as the relative size.

A second extension consisted of fixing the coordinates of the five biggest colonies at [200,200],[200,800],[800,200],[800,800] and [500,500] in a field of 1000 * 1000 creating an excess of movements of about 430 units and 600 units. The other colonies were still located at coordinates drawn randomly from uniform distributions and differed among runs.

138 The final complication added was that two quarters of the total area were 139 considered to be unobserved. Animals starting and/or finishing in these unobserved 140 areas were included in the 'total' dataset but excluded from the 'observed' dataset.

141 Numbers of replicate runs.

142 In all but the final analysis only five runs of the model are presented. This low 143 number was chosen, because in real datasets it is often possible to create a number of sub-sets of the data in this order of magnitude. Since standard errors depend to a large 144 145 extent on the number of replicates, the standard errors presented here are indicative of 146 what could be obtained with real data. Thus, when differences between dispersal rules are highly significant with these numbers, one can also expect them to be visible in 147 148 real data. The only exception is the final evaluation of how much better DDRR 149 performs when only partialdata are available. Here 100 runs are presented, which just 150 still allows to show the individual datapoints. 151

Results.

155	The results for four different dispersal rules are presented in Fig 1 in the form
156	of means and standard errors over 5 replicate runs. For random redistribution in the
157	study area, Fig 1a shows the numbers observed and Fig 1b shows the corresponding
158	DDRR estimates. Fig 1a illustrates how difficult it is to interpret raw data on
159	dispersal. The numbers observed in the 2^{nd} , 3^{rd} and 4^{th} distance classes are
160	considerably lower than in the next classes and numbers rapidly become lower after
161	distance class 13. The first of these two aspects is due to the relation between distance
162	and area. The area within a distance band increases linearly with the distance and thus
163	the number of possible destinations increases with distance (see van Noordwijk 1995).
164	The second aspect is due to the fact that at larger distances an increasing proportion of
165	the total area at that distance falls outside the study and thus there are few
166	observations of individuals moving over longer distances because there are few
167	opportunities to move long distances and be observed (only moving from one edge to
168	the opposite edge).
169	In contrast, the corresponding DDRR estimates (Fig 1b) are close (within 2
170	s.e.) to 1.0 for all distance classes. The dip in the distance classes 2, 3 and 4 is absent
171	and although the standard errors increase dramatically for the last few distance
172	classes, the results for distance classes 14 to 20 look interpretable in the DDRR,
173	whereas they are strongly affected by the limitations of the study area in the observed
174	numbers. One final aspect is that in the observed numbers, the standard errors
175	obtained from replicate simulation runs are high when the numbers observed are high
176	and low in the higher distances classes, whereas in the DDRR the standard errors are
177	high in the last distance classes. This latter pattern corresponds much better to the

greater imprecision of the estimates in the higher distance classes, which are based onsmall numbers.

180 The easiest way to create a dispersal pattern that is biased towards smaller 181 distances is to draw two random destinations and each time choose the shortest 182 distance (see van Noordwijk 1984). Results are presented in Fig 1c and 1d. The raw 183 data are again difficult to interpret. Although the relative dip in distance classes 2 and 184 3 is smaller than in Fig 1a, it is still present. In contrast, Fig 1d shows a gradual decline in DDRR with increasing distance. In this series of runs, the 2nd distance class 185 186 has a lower value than the first and third, but the difference is only about two s.e., 187 instead of five in the corresponding raw data. In Fig 1e-h, two more dispersal rules 188 are shown, strongly favouring small distances and favouring intermediate distances. 189 In all cases the DDRR is easily interpretable and peculiar aspects in the raw data have 190 been eliminated.

191

192 Unequal colony sizes

193 Randomly distributed colonies of equal size is a rather artificial situation, in 194 practice, it is more likely that colony sizes are unequal. With unequal colony sizes 195 (see methods) the standard errors increased, both in the raw numbers and in the 196 DDRR, but the dispersal rule used is still easily seen in the DDRR (Fig 2). In a next 197 step, the five big colonies were given fixed regularly distributed coordinates (see Fig 198 3) that were the same in replicate runs. This has the effect that the distances between 199 these colonies will be overrepresented in the raw data, (Fig 4a & 4c). This effect was 200 not present in the DDRR estimates derived from the same data (Fig 4b & 4d).

201

203

Evaluation.

204 How can we measure how much better the DDRR performs than the raw data? 205 There are two things that we want. First, the same dispersal rules in different settings 206 should give us similar results and second, different dispersal rules in the same setting 207 should give us different results. Here we compare the raw data and the corresponding 208 DDRR values for two dispersal rules (random redistribution and favouring short 209 distances) in two settings (randomly distributed colonies of equal size versus big 210 colonies at fixed locations plus randomly distributed small colonies). 211 For each distance class, we have a value and a standard error over 5 runs,

which allows us to do a t-test for each distance class. This gives us the probability that

the two values for the same distance class obtained for the different configurations of

the study area come from the same distribution. We can then combine the

215 probabilities for each point using Fisher's combination test ($Chi^2_{[2n]} = -2\Sigma InP$) to give

an overall statement on the similarity of the curves (for the raw data: Random

redistribution: $\operatorname{Chi}^2_{[40]} = 72.52$; P = 0.00125, Favouring small distances: $\operatorname{Chi}^2_{[40]} =$

218 88.91; P = 0.000014). We can do the same for the DDRR estimates (Random

219 redistribution: $\operatorname{Chi}^2_{[38]} = 28.75$; P = 0.86, Favouring small distances: $\operatorname{Chi}^2_{[38]} = 28.74$;

220 P = 0.86). Thus the raw numbers are quite different between the two different colony

221 configurations, but the DDRR measures are very similar for both dispersal rules used.

At the same time, in both configurations the DDRR results were very different for the

223 two dispersal rules (both $P < 10^{-8}$). Thus DDRR performed as required.

224

225

The effects of partial observations.

In practice, study areas are nearly always limited and thus individuals will move into and out of the study area. The extent to which conclusions are affected by these movements is another aspect to be investigated. This was simulated by limiting the observations to two quarters of the total. Thus the simulations were carried out as before, but only when both the starting and end point were within the observed part, was the individual added to the observations.

232 One can now compare the total data-set with the observed sub-set (Fig 5). 233 Using the setting with the big colonies with fixed co-ordinates (two of which are now 234 hidden) and favouring short distances as the dispersal rule, the DDRR estimates are 235 proportional, while the raw data have quite differently shaped distributions. The 236 effects of the fixed big colonies are clearly visible in the raw data and these 237 irregularities have disappeared from the DDRR estimates. It is obvious that the 238 recruitment rates for the observed dataset are lower than the full data-set. DDRR 239 estimates are relative measures and not absolute measures. In this case, half the 240 individuals marked at birth disappear out of sight, so that the observed recruitment is 241 half as high (see discussion).

242 In this case, the performance of DDRR can be evaluated by considering the 243 correlation between the numbers observed per distance class with those in the total 244 data and to do the same for the DDRR estimates. In Fig 6 the results are presented for 245 100 runs. If one excludes DDRR estimates which are based on less than 5 individuals 246 ringed in that distance class, the correlations between the DDRR estimates of the 247 observed sub-set and the total are quite high, (mean 0.90, median 0.93), and higher 248 than for the raw numbers (mean 0.78, median 0.79). We are particularly interested in the quantity $1-r^2$ as a measure of the unexplained variance. Over the 100 runs, this 249 250 was smaller for the DDRR than for the raw numbers in 93 % of the runs (on average 51 % (of the $1-r^2$ in the numbers) smaller). In the few cases where DDRR did not 251 252 perform better, either the correlation was high for both the raw numbers and the

- 253 DDRR estimates or the number of datapoints in the observed set was very low. Thus,
- 254 DDRR allows us to draw better conclusions about the dispersal behaviour when (a
- substantial) part of the movements are unobserved then the raw numbers.

257 **Discussion**

258

The simulations described here demonstrate that DDRR estimates are easier to interpret than raw data. Moreover, changes in the lay-out of the study have no effect on the resulting DDRR estimates, while different dispersal rules used can easily be distinguished. Furthermore, hiding data from observation has little effect on the shape of the obtained DDRR estimates. DDRR estimates are not absolute numbers, they tell us how recruitment varies with distance. They clearly reach their limits at distances near the size of the area studied.

In calculating DDRR estimates, no assumptions are made about any sort of underlying distribution. The only two assumptions made are that dispersal can be summarised in terms of distances (see below) and that averages can be made over the data. This is equivalent to the assumption that there no heterogeneities in the dispersal rules use by the birds in space and time. Whenever there are sufficient data available, this last assumption can be checked by subdividing the data and checking whether the resulting DDRR values are different.

In situations where it is reasonable to make assumptions about equality of immigration and emigration, one could estimate the proportion of the dispersal process that has been lost from view from the proportion of immigrant first breeders. There are other advantages in studying dispersal in terms of recruitment. Whereas it is not possible to tell where emigrants went to, it is sometimes possible to obtain some information on where immigrants came from, based on isotope ratios in their feathers(Clark et al. 2004; Hobson et al. 2004).

It is an open question whether summarising dispersal in terms of physicaldistances is biologically the most relevant. For a forest bird, a distance of 1 km over

open landscape or over water is probably quite different from the same distance
through forest or along hedgerows. In principle, there is no limitation to the different
distance measures that could be used when calculating DDRR (Heinz et al. 2005). At
present, too little is known about for example the relation between dispersal and
density (Kim et al. 2009; Matthysen 2005) to evaluate whether expressing distance in
terms of number of territories moved is biologically relevant.

Among the dispersal rules tested in these simulations, it is easy to interpret the resulting DDRR measures. This should facilitate the connection between dispersal patterns observed and the behaviour of the individuals moving (Bowler and Benton 2005; Dingemanse et al. 2003; Greenwood 1980; Hawkes 2009; Russell and Rowley 1993).

293 A first step to take the limitations on dispersal observations into account has 294 been to compare the observed movements with a random redistribution of the animals 295 over the observed natal and observed breeding sites (van Noordwijk 1995; Winkler et 296 al. 2005). DDRR estimates are different in a number of ways. Whereas the reference 297 distribution under random redistribution changes if e.g. the study area is enlarged, 298 DDRR estimates should not change, unless the dispersal behaviour or the density is 299 different in the added area. The unit of movements observed per nestling ringed at 300 that distance also does not imply any null assumption about dispersal.

The dispersal rules used in these simulations, such as favouring short distances are not formulated in terms of the actual behaviour. In terms of the behaviour, two processes can be distinguished. First there is the location, size and shape of the area that an individual is familiar with, which depends on how individuals learn about the world. Second, there is the decision to settle somewhere within this area. The dispersal rules used in the simulations with random

307 redistribution or favouring short distances are equivalent to familiar areas centred 308 around the site of birth but differing in size. The rule of random redistribution implies 309 that individuals move up to the borders of the study area. This could happen either 310 when the study area is smaller than the area with which individuals are familiar, or 311 when the study area is a (habitat) island with reflective boundaries. The dispersal rule 312 of favouring intermediate distances could come about by individuals first moving 313 away from the natal site and then having a limited home range. In some cases, this 314 move away from the natal site or part of it may come about before independence, 315 which then leads to correlations of dispersal distances by siblings (Massot et al. 1994; 316 Matthysen et al. 2010). Thus, although the dispersal rules used were formulated in 317 terms of the resulting pattern, there are plausible mechanisms underlying them. 318 The unit used to describe dispersal is observed recruit per nestling ringed as a 319 function of distance. This unit is easy to understand and should facilitate the 320 incorporation of dispersal in models of populations or metapopulations (Reed and 321 Levine 2005). The interpretability of results in terms of the dispersal rules, the 322 filtering out of specific properties of the study area and the resulting robustness 323 should therefore make DDRR a very attractive way to describe dispersal. 324 The simulations reported here are by no means exhaustive. They show that 325 DDRR is a step forward in isolating the dispersal behaviour from peculiarities of the

study area. This should allow us to start analysing variation in dispersal that is due to
biologically interesting processes.

328

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333

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Figure legends:

402	Fig 1. A comparison of raw data and resulting DDRR estimates for four dispersal
403	rules. The means and se per distance class over five runs are given. In each run 25
404	randomly distributed colonies and 200 individuals were generated. a) raw data and b)
405	DDRR estimates for random redistribution, c) raw data and d) DDRR estimates for
406	favouring short distances, e) raw data and f) DDRR estimates for strong favouring
407	short distances and g) raw data and h) DDRR estimates for favouring intermediate
408	distances.
409	
410	Fig 2. A comparison of raw data and resulting DDRR estimates for colonies of
411	unequal size. a) raw data and b) DDRR estimates for random redistribution, c) raw
412	data and d) DDRR estimates for favouring short distances. Otherwise similar to fig 1.
413	
414	Fig 3. Set-up of "Regular" and incomplete observations. The five big colonies are in
414 415	Fig 3. Set-up of "Regular" and incomplete observations. The five big colonies are in fixed positions as indicated and the co-ordinates of the other colonies are drawn
415	fixed positions as indicated and the co-ordinates of the other colonies are drawn
415 416	fixed positions as indicated and the co-ordinates of the other colonies are drawn independently from uniform distributions separately in each run. In the simulations
415 416 417	fixed positions as indicated and the co-ordinates of the other colonies are drawn independently from uniform distributions separately in each run. In the simulations with incomplete observations, all movements starting or ending in the stippled areas
415 416 417 418	fixed positions as indicated and the co-ordinates of the other colonies are drawn independently from uniform distributions separately in each run. In the simulations with incomplete observations, all movements starting or ending in the stippled areas
415 416 417 418 419	fixed positions as indicated and the co-ordinates of the other colonies are drawn independently from uniform distributions separately in each run. In the simulations with incomplete observations, all movements starting or ending in the stippled areas are included in the total, but not in the observed dataset.
 415 416 417 418 419 420 	fixed positions as indicated and the co-ordinates of the other colonies are drawn independently from uniform distributions separately in each run. In the simulations with incomplete observations, all movements starting or ending in the stippled areas are included in the total, but not in the observed dataset. Fig 4. A comparison of two dispersal rules (random redistribution a,b) and favouring
 415 416 417 418 419 420 421 	fixed positions as indicated and the co-ordinates of the other colonies are drawn independently from uniform distributions separately in each run. In the simulations with incomplete observations, all movements starting or ending in the stippled areas are included in the total, but not in the observed dataset. Fig 4. A comparison of two dispersal rules (random redistribution a,b) and favouring short distances (c,d) in two different colony lay-outs (randomly distributed colonies of
 415 416 417 418 419 420 421 422 	fixed positions as indicated and the co-ordinates of the other colonies are drawn independently from uniform distributions separately in each run. In the simulations with incomplete observations, all movements starting or ending in the stippled areas are included in the total, but not in the observed dataset. Fig 4. A comparison of two dispersal rules (random redistribution a,b) and favouring short distances (c,d) in two different colony lay-outs (randomly distributed colonies of equal size (continuous blue line) and fixed big colonies with random small colonies

426	Fig 5. Comparison of the 'observed' with the 'total' dataset when half the area is
427	hidden from view (see fig 3). Means and se over 5 runs using the dispersal rule
428	favouring short distances. a) numbers observed, b) corresponding DDRR values.
429	
430	Fig 6. A scatterplot of the correlation between the 'total' and 'observed' dataset in raw

- 431 numbers per distance class (horizontal axis) and as DDRR estimates per distance class
- 432 (verticalaxis). The diagonal indicates equality of the correlations (see text).

433 Appendix 1. Formal definitions.

434

435 Let A_i be the ith (potential) breeding location with co-ordinates x_i and y_i .

- 436 Let B_i be the jth breeding location where N_i individuals were marked in year t-1. B is
- a sub-set of A.
- 438 Let C_k be the kth breeding location where a recruit was observed in year t. C is a sub-
- 439 set of A and k is the total number of recruits observed.

440
$$D_{jk} = \sqrt{((x_j - x_k)^2 + (y_j - y_k)^2)}$$

441 The distribution of all possible observations is then given by

442 { $N_j * D_{jk}$ } for all j and all k.

443

444 Let
$$N_p = \text{Count} \left(\{ N_j * D_{jk} \mid D_p - 1 \le D_{jk} < D_p \} \text{ where } D_p \text{ is the maximum distance of} \right)$$

445 the pth distance class and $D_0 = 0$.

446 Then N_p / k gives the average number of nestlings ringed at distances between D_{p-1}

447 and D_p , measured from the locations where recruits were observed in year t.

- 448 Let {D} be the set of distances between site of birth and site of recruitment for all
- 449 recruits with known birth locations.
- 450 Let $M_p = Count(\{ D \mid D_p 1 \le D \le D_p \} \}$
- 451 $DDRR_p = M_p / (N_p / k).$
- 452

453 Note 1.

- 454 It is assumed here that individuals recruit one year after birth. The set B should
- 455 always be taken from the appropriate year

456 Note 2.

- 457 There is a choice to either use the set C over all recruits irrespective of whether these
- 458 recruits have a known origin or not, or alternatively to restrict the set to recruits with
- 459 known origin. This will make a difference (only) when immigrants (recruits with
- 460 unknown origin) settle in different places from local recruits. This could happen for
- 461 example when the study area is very large relative to dispersal distances and more
- 462 immigrants are expected in the periphery.
- 463 Note 3.
- 464 When data are collected over several years, it is recommended to calculate an average
- 465 distribution weighted by the number of recruits per year:
- 466 $N_p = (\sum N_{pt}) / \sum k_t$ where N_{pt} and k_t are the quantities for year t.
- 467

468 Appendix 2. A step-by-step guide to calculate distance dependent recruitment rates. 469

470 Step 1. Ingredients.

471 We need the following data:

472 a) A list of all nests where nestlings were ringed with their co-ordinates and the

473 numbers ringed at each location. Using UTM co-ordinates or national grid co-

474 ordinates makes the calculation of distances a bit easier, but this is not essential.

475 b) A list of all locations where recruits (first-time breeders) were observed with their

476 co-ordinates. Here one has a choice of either using only recruits whose birth location

477 is known or also including recruits with unknown birth locations. This will make a

478 difference if immigrants settle at different locations compared to local recruits.

479 c) A list with the distances for the observed recruits, i.e. individuals for which both

480 the birth and the recruitment location are known.

481

482 Step 2. Calculating distances between all locations.

483 This is the first step in describing all possible observations. For most data sets one 484 will want to make these calculations separately for each year and the amount of data 485 will then be manageable within a spreadsheet programme. In the example in Table 1, 486 the numbers ringed and the co-ordinates of the nestboxes where birds fledged are

487 given in columns A, B and C, and the co-ordinates of recruited birds in the next year

488 are given in rows 1 and 2, starting in column E. The distances between each

489 combination of fledging and recruiting are given in the cells E4:I15. The formulas for

- 490 the first three elements on the diagonal are given below the table. Through the use of
- 491 the dollar sign, a single formula can be copied for the whole table. In cell A1 is the

492 number of recruits. Finally, in cell A16 is given the sum of all nestlings ringed, to be

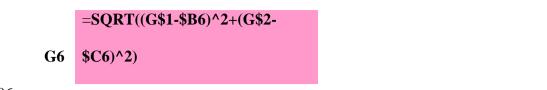
493 used for checking for calculation errors.

494

	A	В	С	D	Ε	F	G	н	Ι
1	5				5983	6217	7044	7082	5891
2					7803	7624	7843	8041	7794
3									
4	6	7371	7941		1395	1197	341	306	1487
5	6	7180	8011		1215	1038	216	102	1307
6	6	6958	7571		1002	743	285	486	1090
7	7	7212	7636		1240	995	267	425	1330
8	7	6043	7922		133	345	1004	1046	199
9	7	5891	7794		92	368	1154	1216	0
10	6	5935	7770		58	318	1111	1179	50
11	7	5922	7737		90	316	1127	1199	65
12	4	5887	7268		544	485	1292	1423	526
13	8	5963	7321		482	395	1200	1331	478
14	4	5940	7620		188	277	1126	1217	181
15	6	6317	7557		415	120	781	905	487
16	74								

495 Table 1. Calculation of distances, see text.

	=SQRT((E\$1-\$B4)^2+(E\$2-
E4	\$C4)^2)
	=SQRT((F\$1-\$B5)^2+(F\$2-
F5	\$C5)^2)



497 Step 3. Aggregating distances into frequencies per class.

498 Given the distances between all points calculated in the previous step, we should now 499 calculate the frequencies of distances within each distance class. The easiest way of 500 doing this is first to calculate the cumulative numbers, because this requires only one 501 criterion at a time. In table 2, the criterion applied for each column is given in row 1. 502 For example in row 4 in table 1, we find two distances between 300 and 400 m. and 503 three distances between 1000 and 1500 m. In each case we multiply the frequency by 504 the number ringed from that box (See formulas for cells L4 and M5 below the table). 505 Row 16 gives us the sums in each column. In row 17 we transform the cumulative 506 distribution into numbers per class, by subtracting the sum of the previous classes (see 507 example formula for cell M17) below the table. In row 18, the last step is to divide 508 these total numbers of possible observations by the number of recruits, which gives us 509 the average numbers of nestlings ringed in each distance class, averaged over the 510 points where recruits were observed. One important check is that the sum of these 511 nestling densities (in cell V18) must be equal to the total number of nestlings ringed 512 from cell A16 in Table 1. Errors in copying formulas are easily made, in particular 513 when the size of the table has changed. One advantage of specifying the criteria in 514 row 1 is that it becomes very easy to redo the calculations with different class 515 boundaries.

516

	K	L	Μ	Ν	0	Р	Q	R	S	Т	U	V
1		<100	<200	<300	<400	<600	<800	<1000	<1500	<2000	<20000	
2												
3												
4		0	0	0	12	12	12	12	30	30	30	
5		0	6	12	12	12	12	12	30	30	30	
6		0	0	6	6	12	18	18	30	30	30	
7		0	0	7	7	14	14	21	35	35	35	
8		0	14	14	21	21	21	21	35	35	35	
9		14	14	14	21	21	21	21	35	35	35	
10		12	12	12	18	18	18	18	30	30	30	
11		14	14	14	21	21	21	21	35	35	35	
12		0	0	0	0	12	12	12	20	20	20	
13		0	0	0	8	24	24	24	40	40	40	
14		0	8	12	12	12	12	12	20	20	20	
15		0	6	6	6	18	24	30	30	30	30	
16	sums 1.	40	74	97	144	197	209	222	370	370	370	
17	sums 2.	40	34	23	47	53	12	13	148	0	0	370
	densitie											
18	S	8	6.8	4.6	9.4	10.6	2.4	2.6	29.6	0	0	74
19												
20												
L4	=\$A4*CC)UNTIF	F(\$E4:\$ J	14,L\$1)								
M5	=\$A5*COUNTIF(\$E5:\$J5,M\$1)											
M17	=M16-L16											
P18	=P17/\$A\$	51										

Table 2. Aggregating distances and calculating densities of nestlings ringed.

520 Step 4. Calculating averages over years.

521 In step 3, we calculated the average densities of nestlings ringed in each distance class 522 relative to the positions where new breeding birds were recruited for one single year, 523 or rather one specific combination with a year of birth and a year of recruiting. We 524 will normally have such data for a number of years and it is straightforward to 525 calculate the average per distance class over the years. However, there are a number 526 of choices to be made. One choice is the number of different (replicate) estimates we 527 can make, another choice is whether or not to weight the average densities of 528 nestlings ringed by the numbers of recruits whose dispersal distances were observed. 529 When there is little variation in the densities and or the numbers recruited per year, 530 weighted and unweighted averages will give the same results. When there is 531 substantial variation among years, then weighting is a good idea, since the limitations 532 on what can be observed should be related to the observations made.

533

534 Step 5. Evaluating the number of classes.

535 If it is possible to make replicate estimates, keeping the variation in densities within 536 each estimate low is a secondary criterion. Most important are the numbers observed 537 in each distance/time period class. Given the number of observations, we can either 538 choose a finer resolution in space by choosing more distance classes, or in time by 539 calculating more replicate estimates. As a rule of thumb, I would recommend that the 540 average number of actual observations per class is on average at least 5 and that not 541 more than 25 % of the cells has less than 5 observations. Given a spatial scale, the 542 optimal number of replicates can also be determined by searching for the minimum in the standard errors of the recruitment estimates per distance class. 543

544

545 **Step 6. Calculating the recruitment rates.**

- 546 The recruitment rates are obtained by dividing the actual number of observations of
- 547 individuals that have moved a particular distance by the average density of nestlings
- 548 ringed in that class. The unit is thus observed recruit per nestling ringed.
- 549
- 550