

Additional material

A1 Timing of migration and geographic relations

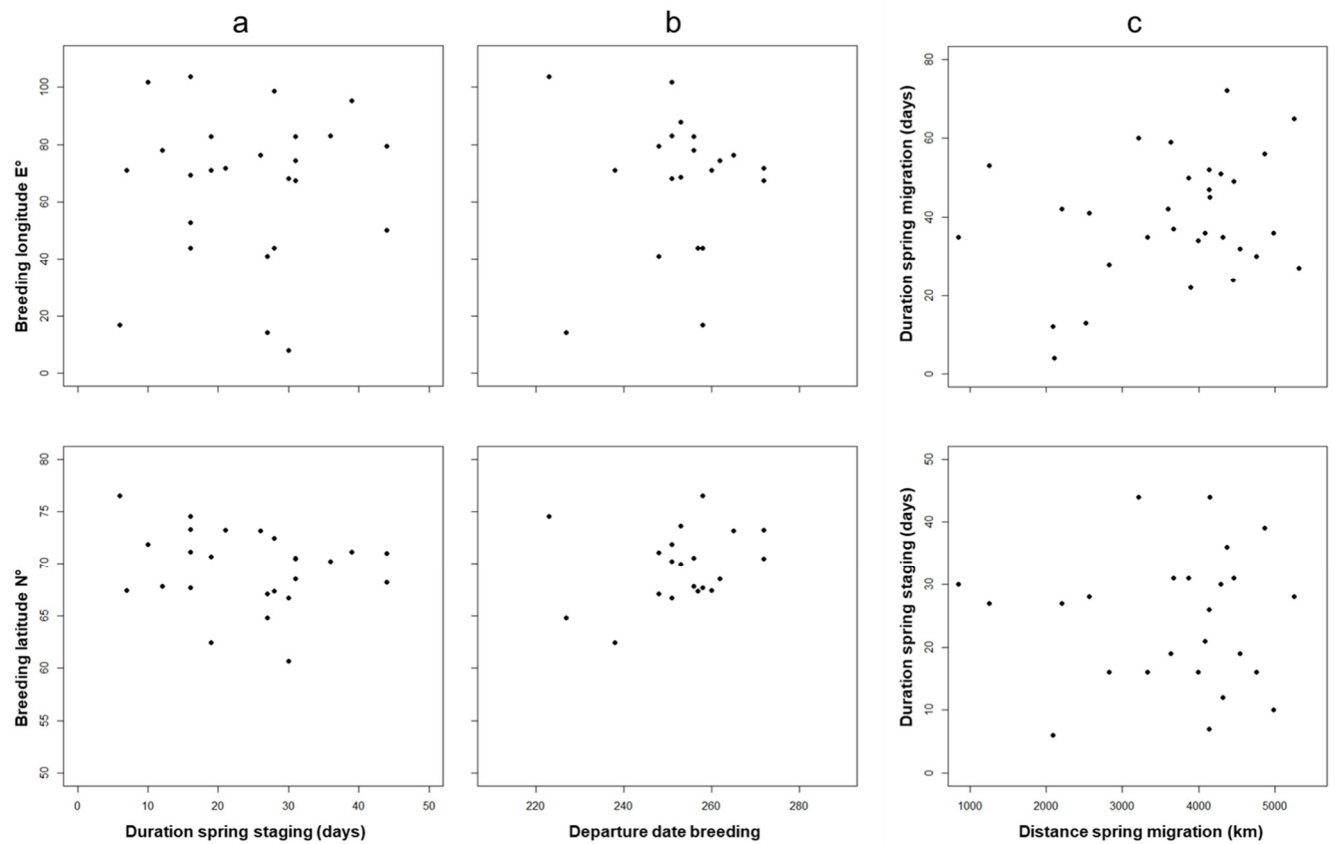


Fig. A1 Breeding location (longitude/latitude) and temporal patterns of NW European red-throated divers. Figure axes have been transposed for a better visualisation of geographical relations. (a) Duration spring staging in relation to breeding longitude ($r_s = 0.0974$ $n = 27$, $p = 0.629$) and latitude ($r = -0.158$ $n = 27$, $p = 0.431$), (b) Departure date from breeding grounds (day 1 = 1 January) (in north-eastern direction from capture site) in relation to breeding longitude ($r_s = -0.169$ $n = 20$, $P = 0.476$) and latitude ($r = 0.251$, $p = 0.285$), (c) Distance spring migration in relation to duration spring staging ($r = 0.297$, $n = 31$, $p = 0.111$) and duration spring migration ($r = 0.288$, $n = 31$, $p = 0.117$).

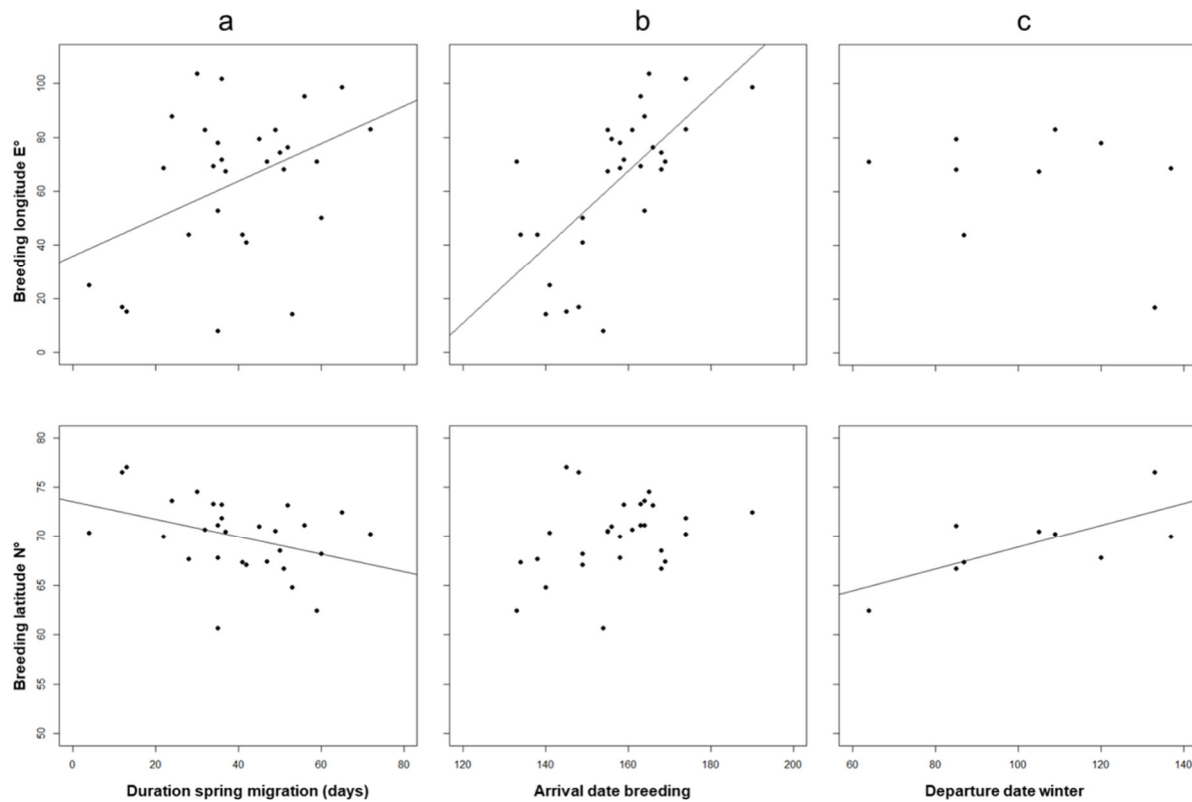


Fig. A2. Breeding location (longitude/latitude) and temporal patterns of NW European red-throated divers. Figure axes have been transposed for a better visualisation of geographical relations. (a) Traveling time in spring after capture (duration of spring migration) in relation to breeding longitude (longitude: $r = 0.407$, $n = 29$, $p = 0.027$; 8) and latitude (latitude: $r = 0.384$, $n = 29$, $p = 0.039$), (b) Date of arrival (day 1 = 1 January) on breeding grounds (in north-eastern direction from capture site) in relation to breeding longitude ($r_s = 0.695$, $n = 29$, $p < 0.001$) and latitude ($r = 0.373$, $n = 29$, $p = 0.078$), (c) Date of departure (day 1 = 1 January) from the wintering grounds in relation to breeding longitude ($r = 0.335$, $n = 9$, $p = 0.344$) and latitude ($r = 0.714$, $n = 9$, $p = 0.020$).

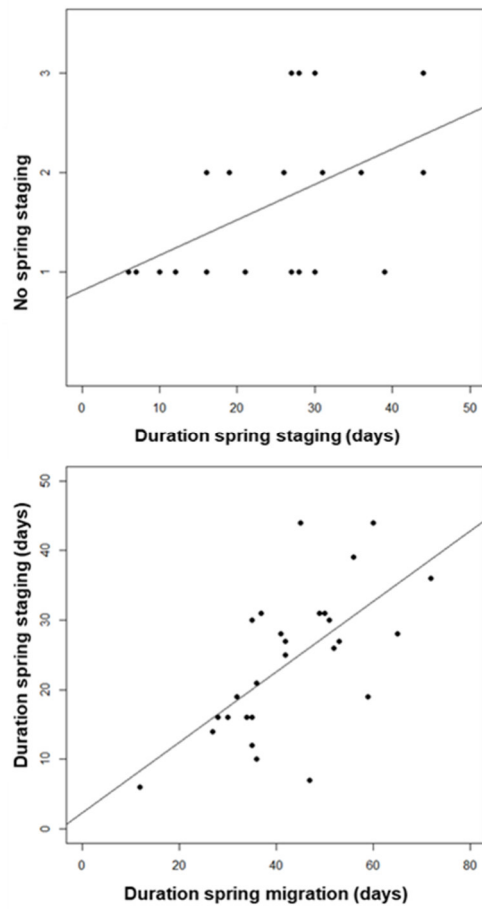


Fig. A3. Duration of spring staging of NW European red-throated divers migrating north-west. Above: Duration of spring staging in relation to traveling time in spring after capture (duration of spring migration) ($r = 0.643$, $n = 27$, $p < 0.001$); below: Duration of spring staging in relation to number of utilised fuelling sites (staging sites) ($\rho = 0.468$, $n = 27$, $p = 0.014$).

A2 Spring staging stops

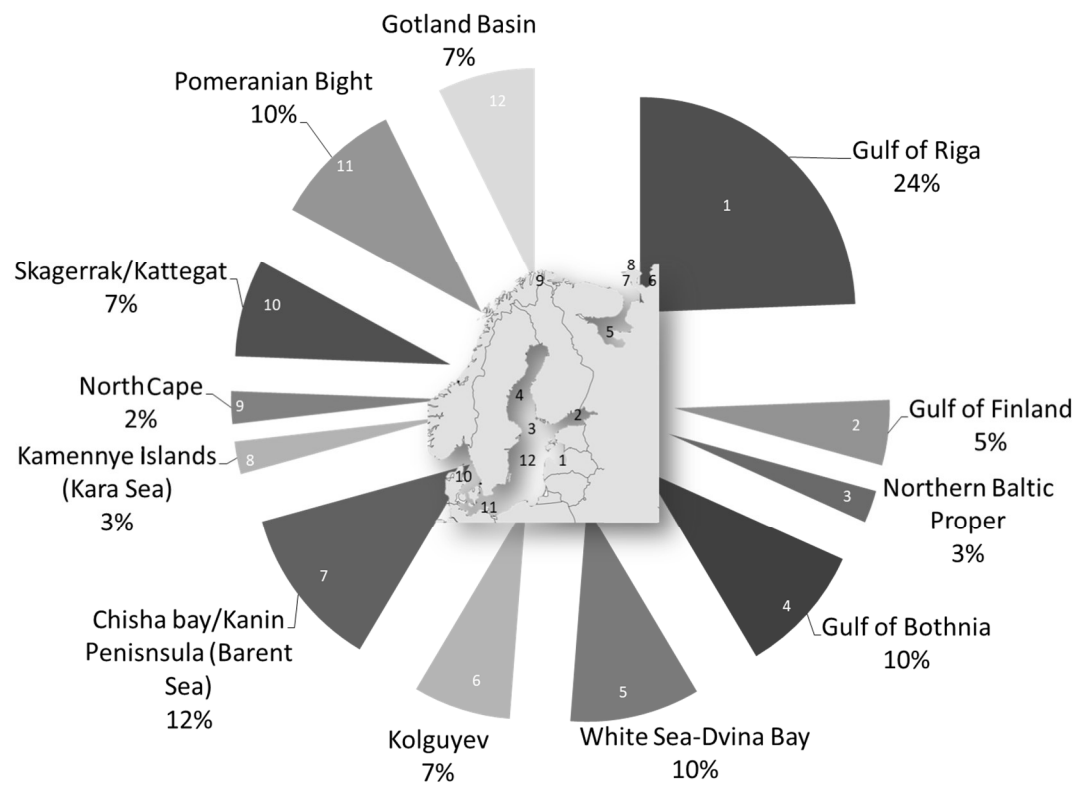


Fig. A4. Proportions of 41 spring staging stops (> 5 days) of red-throated divers migrating along the eastern route (n= 23) in per cent. Place names are indicated in a central map and labelled by numbers.

A3 Comparative methodological approach to calculate Repeatability

To critically examine the validity of the results a comparison of methods was conducted. The ANOVA-based methodology introduced by Lessels and Boag (1987) and reviewed by Nakagawa and Schielzeth (2010) was counter-tested using more recent approach and Linear mixed-effects model (LMM) based methods (Stoffel, Nakagawa and Schielzeth 2017, Ruthrauff et al. 2019, Kürten et al 2022) to test the validity of the results.

Repeatabilities (R), estimated by Linear mixed-effects models (LMM), were obtained using the rpt function of the rptR package (Stoffel, Nakagawa and Schielzeth 2017, Version 0.9.22), which provided the point estimate R, standard error (SE), confidence intervals and p-values. The statistical significance of the repeatability was tested by likelihood ratio tests (LRT). We used 1,000 bootstrap iterations and individual red-throated divers as random effects.

```
rep = rpt(trait1 ~ (1 | ARGOS_ID), grname = "ARGOS_ID", data = dat2,
nboot = 1000, npermut = 1000)
```

ANOVA-based repeatability estimates (R_A) were calculated as described in the main manuscript, using the F table of an ANOVA with the individual identities treated as factorial predictors. The repeatability (R_A) was calculated by the formula introduced by Lessels and Boag (1987), where the mean between individual sum of squares (MS_A), the mean within-individual (residual) sum of squares (MS_w) and the sample size for each individual (two years data) are considered. Further Information below in the section Calculation of Repeatability, method by Lessels & Boag (1987).

The results are shown in Fig. 5 and compared with those of the Anova based method in Table A1.

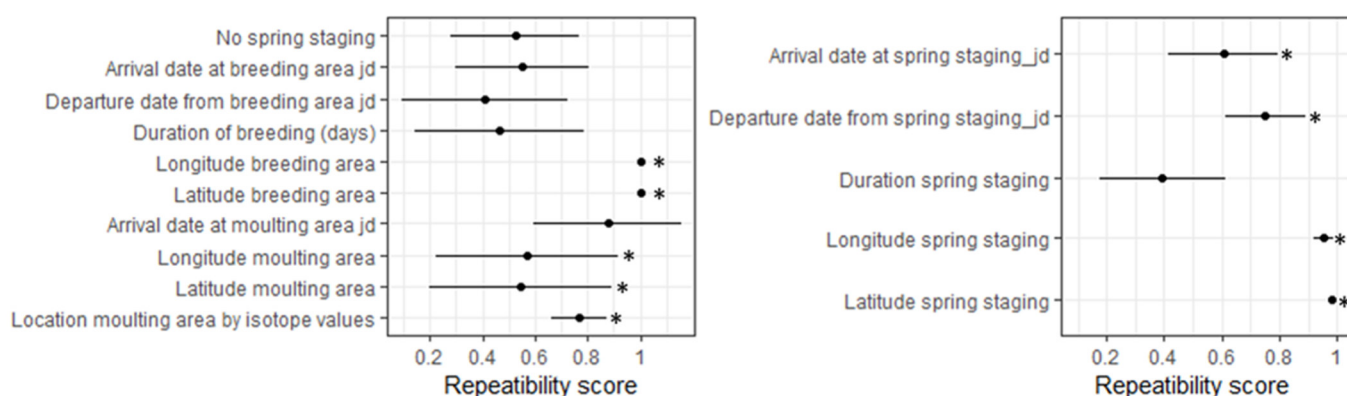


Fig. A5: Estimates ($\pm$ SE) of repeatability (R) of phenology and locations utilised by red-throated divers in successive years. Asteriks indicate significant R values.

The two methodological approaches showed comparable results (Table A1) with almost consistent results repeatabilities, which allows to conclude that the results are comparable and the repeatabilities obtained by both methods are reliable.

Table A1: Individual repeatability (R , R_A) of red-throated diver phenology and visited locations between two successive years, obtained by two comparative methodical approaches. On the left repeatability results (R) obtained by the LMM based approach and on the right repeatability results (R_A) obtained by the Anova based approach.

Trait	R	$\pm$ SE	97.5% CI	p_lrt	p_permut	n_tracks	n_indiv	R_A	$\pm$ SE	F	p	Total sample size	n=Ind
Arrival date at breeding Jd	0.552	0.260	0-0.890	0.053	0.080	14	7	0.552	0.273	3.5	0.064	14	n=7
Departure date from breeding Jd	0.408	0.317	0-0.925	0.105	0.283	8	4	0.408	0.450	2.4	0.211	8	n=4
Duration of breeding	0.463	0.311	0-0.923	0.124	0.240	8	4	0.463	0.424	2.7	0.179	8	n=4
Longitude breeding	1.000	0.000	1.000-1.000	0.001	0.000	14	7	1.000	0.000	24945	0.000	14	n=7
Latitude breeding	1.000	0.000	0.9991.000	0.001	0.000	14	7	1.000	0.000	9125	0.000	14	n=7
Arrival at moult Jd	0.876	0.278	0-0.992	0.152	0.034	6	3	0.876	0.150	15.11	0.027	6	n=3
Longitude moult	0.571	0.348	0-0.970	0.040	0.223	6	3	0.571	0.435	3.664	0.157	6	n=3
Latitude moult	0.547	0.343	0-0.968	0.053	0.241	6	3	0.547	0.452	3.418	0.168	6	n=3
Moult location identified by isotopes	0.770	0.108	0.485-0.906	0.003	0.000	38	19	0.785	0.089	8.278	0.000	38	n=19
No of spring staging stops (n ^a)	0.524	0.233	0-0.853	0.072	0.062	18	9	0.407	0.287	3.2	0.051	18	n=9
Arrival date at staging site JD (n ^b)	0.604	0.191	0.076-0.849	0.019	0.011	26	13	0.604	0.172	4.1	0.009	26	n=13
Departure date from staging site JD (n ^b)	0.751	0.141	0.380-0.906	0.001	0.001	26	13	0.751	0.123	7.0	0.001	26	n=13
Duration of staging stop (n ^b)	0.392	0.218	0.000-0.760	0.079	0.091	26	13	0.642	0.174	4.6	0.007	26	n=13
Longitude staging stop (n ^b)	0.954	0.034	0.855-0.985	0.001	0.000	26	13	0.954	0.025	42.9	0.000	26	n=13
Latitude staging stop (n ^b)	0.982	0.015	0.947-0.994	0.001	0.000	26	13	0.982	0.010	107.8	0.000	26	n=13

Significant results (< 0.05) are indicated in bold

n^a = Number of spring staging stops per individual compared between individuals

n^b = Individual staging stops that appeared in both years

A6 Data output after applying filter algorithms

Table A2: Defined ARGOS position quality classes (CLS 2013) and distribution of received data to the different classes before and after data filtering.

Class	Estimated error (m)	Number of positions in the unfiltered dataset	Number of positions in the filtered dataset	%
3	< 250	4,970	4,210	18.5
2	250–500	3,353	2,806	12.3
1	500–1,500	2,451	1,946	8.6
0	> 1,500	1,698	1,118	4.9
A	No accuracy information	4,878	3,746	16.5
B	No accuracy information	11,629	8,918	39.2
Z	Invalid location	74	0	0.0
TOTAL		29,053	22,744	100

A7 Kernel density estimates

Table A2: List of bird ID (Argos ID), home range size, calculation characteristics, region and time spent when and where home ranges were calculated. Home ranges were calculated using utilisation density estimation (grid=100 cells) and seasons in this analysis includes the full period a bird stayed in the area.

Season	ID	Breeding location	Area (km ²) of kernel 95 % (UTM-format)	Area (km ²) of kernel 50% (UTM-format)	Information of ud-estimation	Time of stay	No of locations (Argos 1 best per day)	Location
Winter	146438	Northern Russia	5462	1308	h="LSCV" =0.1	113	41	Eastern German Bight
	146440	Northern Russia	7072	1588	h="LSCV"=0.1	113	39	Southern Bight
	146442	Northern Russia	3477	1007	h="LSCV"=0.1	62	23	Irish Sea
	146443	Northern Russia	15667	880	h="LSCV"=0.01	102	11	Baltic Sea
	146444	Northern Russia	4802	1226	h="LSCV"=0.1	76	27	Eastern German Bight
	158324	Northern Russia	10545	1503	h="LSCV"=0.1	102	84	Southern Bight
	158328	Northern Russia	19001	2061	h="href", no results with h="LSCV"=0.5	133	105	Eastern German Bight-Western Baltic Sea
	57331	Svalbard	5712	921	h="href", no results with h="LSCV"=0.5	165	77	Eastern German Bight
	57339	No settlement during breeding	9880	819	h="LSCV"=0.5	101	50	Eastern German Bight
	57345	Northern Russia	9776	1536	h="LSCV"=0.1	130	70	Eastern German Bight
	Mean		9139 ± 4980	1285 +/- 394		109.7 ± 29.1		
Moult	146438	Northern Russia	4437	981	h="LSCV"=0.5	47	18	Baltic Sea-Gulf of Riga

14644 0	Northern Russia	742	134	h="LSCV"=0.03	52	18	Southern Bight
14644 2	Northern Russia	7660	1862	h="LSCV"=0.1	70	26	Baltic Sea-Gulf of Riga
14644 3	Northern Russia	1862	206	h="LSCV"=0.1	55	7	Baltic Sea-Gulf of Riga
14644 4	Northern Russia	4764	1122	h="LSCV"=0.1	55	21	Baltic Sea-Gulf of Riga
15832 4	Northern Russia	7950	2166	h="LSCV"=0.1	40	32	Baltic Sea-Northern Baltic
15832 7	Northern Russia	3395	896	h="LSCV"=0.1	31	21	Eastern German Bight
15832 8	Northern Russia	14349	3392	h="LSCV"=0.2	31	14	Baltic Sea-Gulf of Bothnia
15833 4	Northern Russia	33411	9205	h="LSCV"=0.2	60	34	Baltic Sea-Gulf of Bothnia
57331	Svalbard	3616	845	h="LSCV"=0.1	43	22	Eastern German Bight
57339	No settlement during breeding	2154	517	h="LSCV"=0.1	81	42	Baltic Sea-Gulf of Riga
57345	Northern Russia	2145	611	h="LSCV"=0.1	62	31	Eastern German Bight
57346	Northern Russia	4317.97	1134.885	h="LSCV"=0.1	60	43	Baltic Sea-Bay of Riga
Mean		6984.90 ± 8702.1	1774.8 +/- 2400.9		52.85 ± 14.5		

A8 Specific Information about treatment of stable isotope samples and running the analysis

After collection, feather samples were stored in individual plastic bags until analysis. To remove surface contaminants, feathers were individually cleaned in a chloroform/methanol solution (2/1, v/v), dried in an oven at 50°C for 48h and then cut into small fragments with stainless steel scissors. One feather per individual was analysed. To perform stable isotope analysis, a subsample of 0.3 to 0.5 mg was placed into tin cups. Samples were analysed at LIENSs Stable Isotope Facility at the University of La Rochelle. Carbon and nitrogen ratios were determined with a continuous-flow mass spectrometer (Delta V Advantage or Delta V Plus, Thermo Scientific, Bremen, Germany) coupled to an elemental analyser (Flash EA 1112 or Flash 2000, Thermo Scientific, Milan Italy). Measurements of internal laboratory standards were conducted using acetanilide (Thermo Scientific) and peptone (Sigma-Aldrich), and indicated an experimental precision of $\pm 0.15\%$ for both elements. Results are expressed in parts per thousand (‰), in the usual δ notation relative to Vienna Pee Dee Belemnite for $\delta^{13}\text{C}$ and atmospheric N_2 for $\delta^{15}\text{N}$, following the formula: $\delta^{13}\text{C}$ or $\delta^{15}\text{N} = ((R_{\text{sample}}/R_{\text{standard}}) - 1) \times 103$, where R is $^{13}\text{C}/^{12}\text{C}$ or $^{15}\text{N}/^{14}\text{N}$, respectively.

A9 Genetical sexing of captured birds

We followed Fridolfsson and Ellegren (2000) to identify the gender of each captured bird using molecular methods. PCR amplifications were performed in single reactions in a 20 μ L (20 μ l/ng) PCR reaction volume. Thermal cycling conditions were 95 °C for 5 min followed by 35 cycles of: 95 °C for 30 s, 47° do 30s, 72 °C for 60 s, followed by a final extension for 5 min. We determined mainly females (79%) in our sample set and further statistical testing between sexes was not possible due to small sample size of males. Therefore, we combined male and female satellite data for further analysis.

A10: Additional information Data analysis and Statistics

Filtering tracking data

```
Bird_ID<- subset(birds, birds$tagID==" Bird_ID ")  
Bird_ID <- as.data.frame(Bird_ID)  
  
lat<-Bird_ID$lat  
long<-Bird_ID$long  
dtime<-Bird_ID$dtime  
lc<-Bird_ID$lc  
  
lat1<-Bird_ID$lat1  
lat2<-Bird_ID$lat2  
lon1<-Bird_ID$lon1  
lon2<-Bird_ID$lon2  
  
freitas<-sdafilter(lat, long, dtime, lc, vmax=20)  
f_ Bird_ID <- cbind(Bird_ID,freitas)
```

Test for stable isotope differences

```
wilk's lambda Test
x<-as.matrix(subset(rovers, select=c(d13C, d15N)))
grp<-subset(rovers, select=area_IS)
wilks.test(x, grouping=grp, method="c")
```

Calculation correlations between timing of migration and geographic relations

Breeding Longitude versus arrival date (Julian date) Breeding

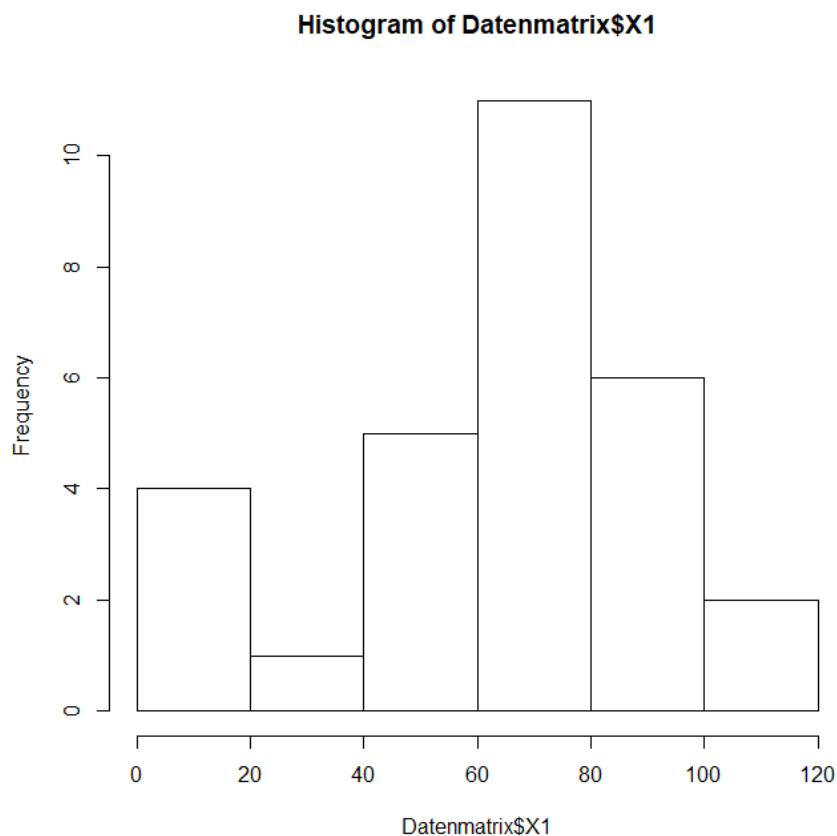
```
#Arrival date (Julian Date) Breeding
```

```
shapiro.test(Datenmatrix$Y)
Shapiro-wilk normality test
data:  Datenmatrix$Y
W = 0.97345, p-value = 0.6562
```

```
#Breeding Longitude
```

```
shapiro.test(Datenmatrix$X1)
Shapiro-wilk normality test
data:  Datenmatrix$X1
W = 0.92194, p-value = 0.03415
```

```
hist(Datenmatrix$X1)
```



```

cor.test(Datenmatrix$X1,Datenmatrix$Y,method="spearman")
#Spearman's rank correlation rho
#data:  Datenmatrix$X1 and Datenmatrix$Y
#S = 1237.6, p-value = 2.846e-05
#alternative hypothesis: true rho is not equal to 0
#sample estimates:
# rho #0.6951808

plot(Datenmatrix, xlim = c(0, 110), ylim = c(120, 200), pch = 19,
xlab="Breeding Longitude",ylab="Arrival Date breeding")

abline(lm(Datenmatrix$Y~Datenmatrix$X1)$coef)

```

Breeding latitude versus arrival date (Julian date) Breeding

```

#Breeding latitude

shapiro.test(Datenmatrix$X2)
Shapiro-wilk normality test
data:  Datenmatrix$X2
W = 0.97223, p-value = 0.6216

cor.test(Datenmatrix$X2,Datenmatrix$Y,method="pearson")
#output
#Pearson's product-moment correlation
#data:  Datenmatrix$X2 and Datenmatrix$Y
#t = 1.83, df = 27, p-value = 0.07831
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
#-0.03907375  0.62286187
#sample estimates:
#cor  #0.373

plot(Datenmatrix, xlim = c(50, 80), ylim = c(120, 200), pch = 19,
xlab="Breeding Latitude",ylab="Arrival Date breeding")

```

Breeding longitude versus departure date (Julian date) Breeding

```

#Breeding longitude

shapiro.test(Datenmatrix$X1)
Shapiro-wilk normality test
data:  Datenmatrix$X1
W = 0.90196, p-value = 0.04489

#Departure date from breeding

shapiro.test(Datenmatrix$Y)
Shapiro-wilk normality test
data:  Datenmatrix$Y
W = 0.91029, p-value = 0.06455

cor.test(Datenmatrix$X1,Datenmatrix$Y,method="spearman")
#Spearman's rank correlation rho
#data:  Datenmatrix$X1 and Datenmatrix$Y
#S = 1554.8, p-value = 0.4763

```

```
#alternative hypothesis: true rho is not equal to 0
#sample estimates:
#rho #-0.1689938
```

```
plot(Datenmatrix, xlim = c(0, 110), ylim = c(210, 290), pch = 19,
xlab="Breeding Longitude",ylab="Departure Date breeding")
```

Breeding latitude versus departure date (Julian date) Breeding

```
#Breeding latitude
```

```
shapiro.test(Datenmatrix$X2)
Shapiro-wilk normality test
data:  Datenmatrix$X2
W = 0.98367, p-value = 0.9723
```

```
cor.test(Datenmatrix$X2,Datenmatrix$Y,method="pearson")
#Pearson's product-moment correlation
#data:  Datenmatrix$X2 and Datenmatrix$Y
#t = 1.1014, df = 18, p-value = 0.2852
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
# -0.2151677  0.6243719
#sample estimates:
# cor
#0.2512789
```

```
plot(Datenmatrix, xlim = c(50, 80), ylim = c(210, 290), pch = 19, xlab="
Breeding Latitude",ylab="Departure Date breeding")
```

Breeding longitude versus departure (Julian date) winter

```
#Breeding longitude
```

```
shapiro.test(Datenmatrix$X1)
Shapiro-wilk normality test
data:  Datenmatrix$X1
W = 0.91305, p-value = 0.3026
```

```
#Departure date (Julian date) winter
```

```
shapiro.test(Datenmatrix$Y)
Shapiro-wilk normality test
data:  Datenmatrix$Y
W = 0.95564, p-value = 0.7352
```

```
cor.test(Datenmatrix$X2,Datenmatrix$Y,method="pearson")
#data:  Datenmatrix$X1 and Datenmatrix$Y
#t = 1.0061, df = 8, p-value = 0.3438
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
# -0.3732570  0.7966559
#sample estimates:
#cor #0.335
```

```
plot(Datenmatrix, xlim = c(0, 110), ylim = c(60, 140), pch = 19,
xlab="Breeding Longitude",ylab="Departure Date winter")
```

```
summary(lm(Datenmatrix$Y~Datenmatrix$X1))
```

Breeding latitude versus departure date (Julian date) winter

```
#Breeding latitude
```

```
shapiro.test(Datenmatrix$X2)
Shapiro-wilk normality test
data:  Datenmatrix$X2
W = 0.9731, p-value = 0.918
```

```
cor.test(Datenmatrix$X2,Datenmatrix$Y,method="pearson")
#Pearson's product-moment correlation
#data:  Datenmatrix$X2 and Datenmatrix$Y
#t = 2.881, df = 8, p-value = 0.02048
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
#0.1524596 0.9268058
#sample estimates:
#cor #0.7135869
```

```
plot(Datenmatrix, xlim = c(50, 80), ylim = c(60, 140), pch = 19,
xlab="Breeding Latitude",ylab="Departure Date winter")
```

```
abline(lm(Datenmatrix$Y~Datenmatrix$X2)$coef)
```

```
summary(lm(Datenmatrix$Y~Datenmatrix$X2))
```

Breeding longitude versus travelling time (duration migration)

```
#Breeding longitude
```

```
shapiro.test(Datenmatrix$X1)
Shapiro-wilk normality test
data:  Datenmatrix$X1
W = 0.92194, p-value = 0.03415
```

```
#Duration migration (days)
```

```
shapiro.test(Datenmatrix$Y)
Shapiro-wilk normality test
data:  Datenmatrix$Y
W = 0.98541, p-value = 0.9492
```

```
cor.test(Datenmatrix$X1,Datenmatrix$Y,method="pearson")
#Pearson's product-moment correlation
#data:  Datenmatrix$X1 and Datenmatrix$Y
#t = 2.3121, df = 27, p-value = 0.02864
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
#0.04703071 0.67279195
#sample estimates:
#cor #0.406529
```

```
plot(Datenmatrix, xlim = c(0, 110), ylim = c(0, 80), pch = 19,
xlab="Breeding Longitude",ylab="Duration spring migration (days)")
```

```
abline(lm(Datenmatrix$Y~Datenmatrix$X1)$coef)

summary(lm(Datenmatrix$Y~Datenmatrix$X1))
```

Breeding latitude versus travelling time (duration migration)

```
#Breeding latitude

shapiro.test(Datenmatrix$X2)
Shapiro-wilk normality test
data:  Datenmatrix$X2
W = 0.97223, p-value = 0.6216
cor.test(Datenmatrix$X2,Datenmatrix$Y,method="pearson")
#Pearson's product-moment correlation
#data:  Datenmatrix$X2 and Datenmatrix$Y
#t = -2.1633, df = 27, p-value = 0.03954
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
#-0.6581442 -0.0207685
#sample estimates:
#cor #-0.3843486

plot(Datenmatrix, xlim = c(50, 80), ylim = c(0, 80), pch = 19,
xlab="Breeding Latitude",ylab="Duration spring migration (days)")

abline(lm(Datenmatrix$Y~Datenmatrix$X2)$coef)

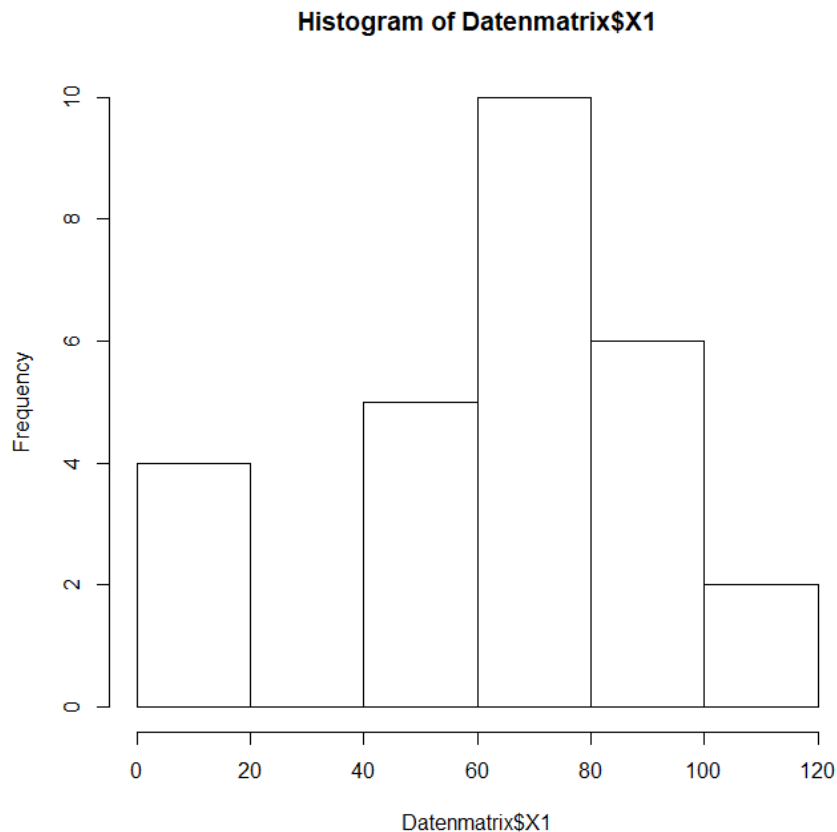
summary(lm(Datenmatrix$Y~Datenmatrix$X2))
```

Breeding longitude versus duration spring staging

```
#Breeding longitude

shapiro.test(Datenmatrix$X1)
Shapiro-wilk normality test
data:  Datenmatrix$X1
W = 0.912, p-value = 0.02543

hist(Datenmatrix$X1)
```



#Duration spring staging

```
shapiro.test(Datenmatrix$Y)
Shapiro-wilk normality test
data:  Datenmatrix$Y
W = 0.96532, p-value = 0.4841
```

```
cor.test(Datenmatrix$X1,Datenmatrix$Y,method="spearman")
#Spearman's rank correlation rho
#data:  Datenmatrix$X1 and Datenmatrix$Y
#S = 2956.9, p-value = 0.6289
#alternative hypothesis: true rho is not equal to 0
#sample estimates:
#rho #0.09739718
```

```
plot(Datenmatrix, xlim = c(0, 110), ylim = c(0, 50), pch = 19,
xlab="Breeding Longitude",ylab="Duration spring staging (days)")
summary(lm(Datenmatrix$Y~Datenmatrix$X1))
```

Breeding latitude versus duration staging

#Breeding latitude

```
shapiro.test(Datenmatrix$X2)
Shapiro-wilk normality test
data:  Datenmatrix$X2
W = 0.97493, p-value = 0.7346
```

```
cor.test(Datenmatrix$X2,Datenmatrix$Y,method="pearson")
#Pearson's product-moment correlation
```

```
#data: Datenmatrix$X2 and Datenmatrix$Y
#t = -0.80037, df = 25, p-value = 0.431
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
#-0.5075871 0.2361359
#sample estimates:
#cor #-0.1580617

plot(Datenmatrix, xlim = c(50, 80), ylim = c(0, 50), pch = 19,
      xlab="Breeding Latitude", ylab="Duration spring staging (days)")

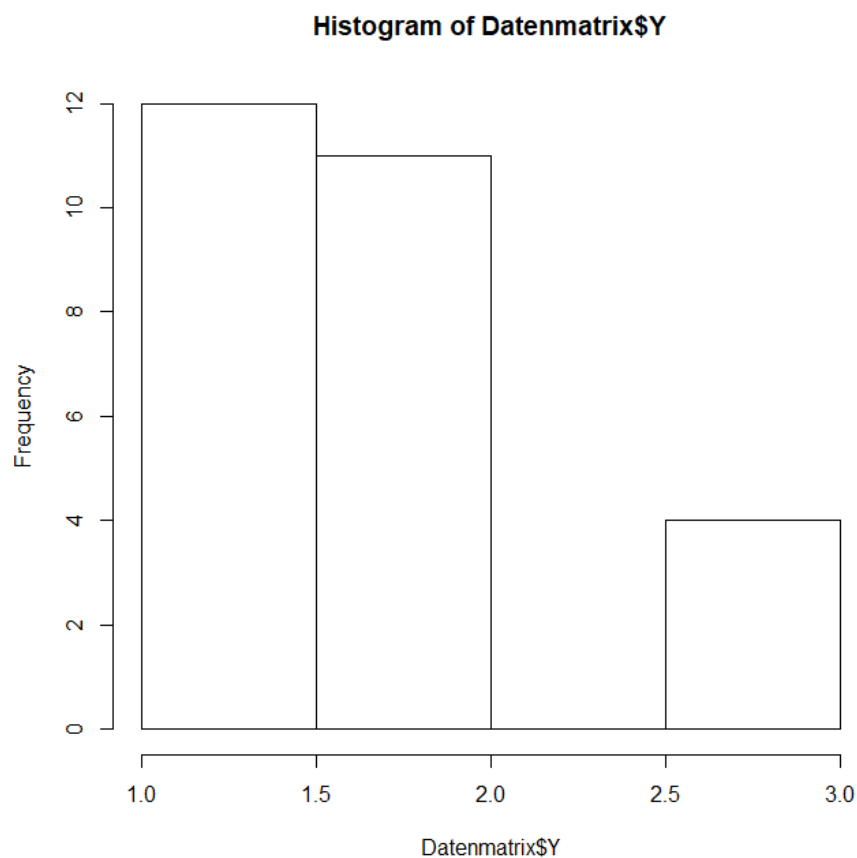
summary(lm(Datenmatrix$Y~Datenmatrix$X2))
```

Duration staging versus No stagings

#No of stagings

```
shapiro.test(Datenmatrix$Y)
Shapiro-wilk normality test
data: Datenmatrix$Y
W = 0.78126, p-value = 6.594e-05
```

```
hist(Datenmatrix$Y)
```



#Duration spring staging

```
shapiro.test(Datenmatrix$X)
Shapiro-wilk normality test
```

```

data: Datenmatrix$X
W = 0.96584, p-value = 0.4965

cor.test(Datenmatrix$X,Datenmatrix$Y,method="spearman")
#Spearman's rank correlation rho
#data: Datenmatrix$X and Datenmatrix$Y
#S = 1743, p-value = 0.01384
#alternative hypothesis: true rho is not equal to 0
#sample estimates:
#rho #0.4679444

plot(Datenmatrix, xlim = c(0, 3), ylim = c(0, 50), xaxp = c(1,3,2), pch =
19, xlab="No spring stagings",ylab="Duration spring staging (days)")

abline(lm(Datenmatrix$Y~Datenmatrix$X1)$coef)

```

Duration migration versus duration staging

```

#Duration migration

shapiro.test(Datenmatrix$Y)
Shapiro-Wilk normality test
data: Datenmatrix$Y
W = 0.98172, p-value = 0.899

cor.test(Datenmatrix$X1,Datenmatrix$Y,method="pearson")
#Pearson's product-moment correlation
#data: Datenmatrix$X1 and Datenmatrix$Y
#t = 4.1994, df = 25, p-value = 0.0002965
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
# 0.3482312 0.8222036
#sample estimates:
#cor #0.6431371

plot(Datenmatrix, xlim = c(0, 80), ylim = c(0, 50), pch = 19,
xlab="Duration spring migration (days)",ylab="Duration spring staging
(days)")

abline(lm(Datenmatrix$Y~Datenmatrix$X1)$coef)

summary(lm(Datenmatrix$Y~Datenmatrix$X1))

```

Distance spring migration versus duration spring migration

```

#Distance spring migration

shapiro.test(Datenmatrix$Y)
Shapiro-Wilk normality test
data: Datenmatrix$Y
W = 0.9435, p-value = 0.113

cor.test(Datenmatrix$X1,Datenmatrix$Y,method="pearson")
#Pearson's product-moment correlation
#data: Datenmatrix$X1 and Datenmatrix$Y
#t = 1.6167, df = 29, p-value = 0.1168
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:

```

```
#-0.07437729  0.58252877
#sample estimates:
#cor #0.2875409
```

```
plot(Datenmatrix, xlim = c(900, 5500), ylim = c(0, 80), pch = 19,
xlab="Distance spring migration (km)",ylab="Duration spring migration
(days)")
```

Distance spring migration versus duration spring staging

```
plot(Datenmatrix, xlim = c(900, 5500), ylim = c(0, 50), pch = 19,
xlab="Distance spring migration (km)",ylab="Duration spring staging
(days)")
```

```
cor.test(Datenmatrix$X1,Datenmatrix$Y,method="pearson")
#Pearson's product-moment correlation
#data:  Datenmatrix$X1 and Datenmatrix$Y
#t = 1.646, df = 28, p-value = 0.111
#alternative hypothesis: true correlation is not equal to 0
#95 percent confidence interval:
# -0.07082928  0.59375276
#sample estimates:
# cor #0.2970192
```

Migratory connectivity: Calculating Mantel Correlation coefficient

Capture site to breeding sites

```
wil.dists <- dist(cbind(Datenmatrix$Long_wil, Datenmatrix$Lat_wil))  
Breed.dists <- dist(cbind(Datenmatrix$Breed_Long, Datenmatrix$Breed_Lat))
```

```
mantel.rtest(wil.dists, Breed.dists, nrepet = 9999)
```

Monte-Carlo test

```
Call: mantel.rtest(m1 = wil.dists, m2 = Breed.dists, nrepet = 9999)
```

Observation: 0.06978909

Based on 9999 replicates

Simulated p-value: 0.2026

Alternative hypothesis: greater

Std.Obs	Expectation	Variance
0.4908121500	0.0003623148	0.0200089103

Breeding (Siberian arctic) to moult (tracking data)

```
Breed.dists <- dist(cbind(Datenmatrix$Breed_Long, Datenmatrix$Breed_Lat))  
Moult.dists <- dist(cbind(Datenmatrix$Moult_Long, Datenmatrix$Moult_Lat))
```

```
mantel.rtest(Breed.dists, Moult.dists, nrepet = 9999)
```

output Monte-Carlo test

Monte-Carlo test

```
Call: mantel.rtest(m1 = Breed.dists, m2 = Moult.dists, nrepet = 9999)
```

Observation: 0.1356365

Based on 9999 replicates

Simulated p-value: 0.2153

Alternative hypothesis: greater

Std.Obs	Expectation	Variance
0.8247494206	0.0004045423	0.0268852669

Breeding (Siberian arctic) to moult, (isotope values)

```
Breed.dists <- dist(cbind(Datenmatrix$BreedLong, Datenmatrix$BreedLat))  
MoultIso.dists2 <- dist(Datenmatrix$d13C_12C)
```

```
mantel.rtest(Breed.dists, MoultIso.dists2, nrepet = 9999)
```

Monte-Carlo test

```
Call: mantel.rtest(m1 = Breed.dists, m2 = MoultIso.dists2, nrepet = 9999)
```

Observation: 0.03813477

Based on 9999 replicates

Simulated p-value: 0.2235

Alternative hypothesis: greater

Std.Obs	Expectation	Variance
0.5263460075	0.0002617669	0.0051774602

Breeding (Siberian arctic) to winter

```
Breed.dists <- dist(cbind(Datenmatrix$Breed_Long, Datenmatrix$Breed_Lat))  
Winter.dists <- dist(cbind(Datenmatrix$Winter_Long,  
Datenmatrix$Winter_Lat))
```

```
mantel.rtest(Breed.dists, winter.dists, nrepet = 9999)
```

Monte-Carlo test

```
Call: mantel.rtest(m1 = Breed.dists, m2 = winter.dists, nrepet = 9999)
```

Observation: 0.2742247

Based on 9999 replicates

Simulated p-value: 0.1035

Alternative hypothesis: greater

Std.Obs	Expectation	Variance
1.452722471	0.002000939	0.035114517

Calculation of Kernel densities

```
#Load packages
```

```
library(maps)
library(mapdata)
library(sp)
library(lattice)
require(MASS)
require(PBSmapping)
library(ggplot2)
data(worldLLhigh)
library(fields)
library(adehabitatHR)
library(geosphere)
library(rgeos)
library(oceanmap)
library(maptools)
library(rgdal)
library(readxl)
```

```
tmpdata<-Datenmatrix
coords<-tmpdata[,c(4,5)]
coords<-SpatialPoints(coords)
```

```
#create utilisation distribution
```

```
#Smoothing parameter estimated with href parameter o LSCV
#If h is set to "href", the ad hoc method is used for the smoothing
parameter.
#If h is set to "LSCV", the least-square cross validation method is used.
#If an Epanechnikov Kernel is used kern is set to epa
K1<-kernelUD(coords,h="href",grid=100)
K1<-kernelUD(coords,h="LSCV",grid=100)
K1<-kernelUD(coords,h="href",kern="epa",grid=200, extent=2)
```

```
#Define the kernel
```

```
kernel95<-getverticeshr(K1,percent=95)
plot(coords,pch=1);plot(kernel95,lwd=2,add=TRUE)
kernel75<-getverticeshr(K1,percent=75)
plot(coords,pch=1);plot(kernel75,lwd=2,add=TRUE)
kernel50<-getverticeshr(K1,percent=50)
plot(coords,pch=1);plot(kernel50,lwd=2,add=TRUE)
```

```
#check the kernel plus observations onto an existing map
```

```
# xlim = longitude range; ylim = Latitude range, modified for each
individual
```

```
map( "worldHires", xlim=c(5, 10), ylim=c(53, 58),resolution=-
5,fill=TRUE,col = "gray64",plot=TRUE)
plot(coords,add=TRUE,pch=1,cex=0.5)
plot(kernel95,lwd=2,add=TRUE,col=2)
plot(kernel50,lwd=2,add=TRUE,col=3)
```

```
###make shape file
```

```
writeOGR(kernel50,
dsn="C:/Users/Documents/R/HomeRange_KDE/shapes_KDE",layer="birdid_50_2",dri
ver="ESRI Shapefile")
```

```

writeOGR(kernel97,
dsn="C:/Users/Documents/R/HomeRange_KDE/shapes_KDE",layer="birdid_97_2",driver="ESRI Shapefile")

writeOGR(kernel95,
dsn="C:/Users/Documents/R/HomeRange_KDE/shapes_KDE",layer="birdid_95_2",driver="ESRI Shapefile")

# Estimate/calculate size of area
# convert kernels to km2,

coords<-tmpdata[,c(4,5)]
colnames(coords)<-c("X","Y")
summary(coords)

#Specify that the current dataframe has the attribute Latitude-Longitude
("LL")

attr(coords,"projection")<-"LL"

#convert the dataframe to UTM units (Km)
converted<-convUL(coords,km=TRUE)

#R gives for each calculation the individual detected projection in UTM
summary(converted)

#Re-define the "converted" dataframe as a "Spatial Points" format dataframe
XY<-converted[,c("X","Y")]

UTMcoords<-SpatialPoints(XY)

#create a new kernel based on UTM coordinates
#create a utilisation distribution

K1<-kernelUD(UTMcoords,h="LSCV",grid=100)

#create a kernel with specified percentage 95%, input/output in km
UTMkernel<-getverticeshr(K1,percent=95,unin="km",unout="km")

#Request the area of the UTM-format kernel
UTMkernel

#create a kernel with specified percentage 50%, input/output in km
UTMkernel<-getverticeshr(K1,percent=50,unin="km",unout="km")
UTMkernel

```

Calculation of Repeatability, method by Lessels & Boag (1987)

Test for repeatability of performance across double determinations

1. Run ANOVAS

2. Calculate repeatability

```
# MSa = Mean Square ID (Group, Individuals, Identifiers)
# MSw = Mean Square Residuals
# NO = No of repetitions (2)
```

Variance between groups = $s^2_A = (MS_a - MS_w) / NO$

$s^2_A = (MS_a - MS_w) / NO$

Repeatability $r^2 = s^2_A / (MS_w + s^2_A)$

$s^2_A / (MS_w + s^2_A)$

No of spring staging

1. Run ANOVAS

```
AnovaModel1.1 <- aov(No_stagings ~ ID_b, data=Datenmatrix)
```

```
summary(AnovaModel1.1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID_b	8	7.111	0.8889	3.2	0.0513.
Residuals	9	2.500	0.2778		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
16 observations deleted due to missingness

2. Calculate repeatability

Variance between groups $s^2_A = (MS_a - MS_w) / NO$

$(0.8889 - 0.2778) / 2$

[1] 0.30555

Repeatability $r = s^2_A / (MS_w + s^2_A)$

$0.30555 / (0.4444 + 0.30555)$

[1] 0.4074272

Arrival in staging sites between 2 years

Tests with only sites that appeared in both years

1. Run ANOVAS

```
AnovaModel1.1 <- aov(Date_arriv_JD_year_ind ~ ID, data=Datenmatrix)
```

```
summary(AnovaModel1.1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID	12	10575	881.3	4.054	0.00905 **
Residuals	13	2826	217.4		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2. Calculate repeatability:

Variance between groups $s^2_A = (MS_a - MS_w) / NO$

$(881.3 - 217.4) / 2$

[1] 331.95

Repeatability $r = s^2_A / (MS_w + s^2_A)$

$331.95 / (217.4 + 331.95)$

[1] 0.6042596

Repeatability of departure date from staging sites between 2 years

1. Run ANOVAS

```
AnovaModel.1 <- aov(Date_dep_JD_year_ind ~ ID, data=Datenmatrix)
summary(AnovaModel.1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID	12	6559	546.6	7.045	0.000677 ***
Residuals	13	1009	77.6		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2. Calculate repeatability:

```
Variance between groups s2A = (MSa - MSw) / N0
(546.6-77.6)/2
[1] 234.5
```

```
Repeatability r = s2A / (MSw + s2A)
234.5/(77.6+234.5)
[1] 0.7513617
```

Repeatability of utilisation of staging sites (Lon) between 2 years

1. Run ANOVAS

```
AnovaModel.TL <- aov(Lon ~ ID, data=Datenmatrix)
summary(AnovaModel.TL)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID	12	2377	198.08	42.88	1.92e-08 ***
Residuals	13	60	4.62		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2. Calculate repeatability

```
Variance between groups s2A = (MSa - MSw) / N0
(198.08-4.62)/2
[1] 96.73
```

```
Repeatability r = s2A / (MSw + s2A)
96.73/(4.62+96.73)
[1] 0.9544154
```

Repeatability of utilisation of staging sites (Lat) between 2 years

1. Run ANOVAS

```
AnovaModel.TL <- aov(Lat ~ ID, data=Datenmatrix)
summary(AnovaModel.TL)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID	12	660.8	55.06	107.8	5.63e-11 ***
Residuals	13	6.6	0.51		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2. Calculate repeatability

```
Variance between groups s2A = (MSa - MSw) / N0
(55.06-0.51)/2
[1] 27.275
```

```
Repeatability r = s2A / (MSw + s2A)
27.275/(0.51+27.275)
#[1] 0.9816448
```

Repeatability of time of stay in staging sites between 2 years

1. Run ANOVAS

```
AnovaModel.TL <- aov(Time_of_stay_b ~ ID_b, data=Datenmatrix)
summary(AnovaModel.TL)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID_b	11	1186.5	107.86	4.582	0.00715 **
Residuals	12	282.5	23.54		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2. Calculate repeatability

Variance between groups $s^2_A = (MS_A - MS_W) / N_0$
(107.86-23.54)/2

[1] 42.16

Repeatability $r = s^2_A / (MS_W + s^2_A)$

42.16/(23.54+42.16)

[1] 0.6417047

Repeatability of arrival in breeding areas between 2 years

1. Run ANOVAS

```
AnovaModel.1 <- aov(Date_arriv_JD_year_indep ~ ID_a, data=Datenmatrix)
summary(AnovaModel.1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID_a	6	2008.7	334.8	3.464	0.0644 .
Residuals	7	676.5	96.6		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2. Calculate repeatability:

Variance between groups $s^2_A = (MS_A - MS_W) / N_0$
(334.8-96.6)/2

[1] 119.1

Repeatability $r = s^2_A / (MS_W + s^2_A)$

119.1/(96.6+119.1)

[1] 0.55215582

Repeatability of departure date from breeding areas between 2 years

1. run ANOVAS

```
AnovaModel.1 <- aov(Date_dep_JD_year_indep ~ ID_b, data=Datenmatrix)
summary(AnovaModel.1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID_b	3	153.5	51.17	2.38	0.211
Residuals	4	86.0	21.50		

2. Calculate repeatability:

Variance between groups $s^2_A = (MS_A - MS_W) / N_0$
(51.17-21.50)/2

[1] 14.835

Repeatability $r = s^2_A / (MS_W + s^2_A)$

14.835/(21.50+14.835)

[1] 0.4082841

Repeatability of utilisation of breeding sites (Lon) between 2 years

```
AnovaModel.TL <- aov(Lon ~ ID_a, data=Datenmatrix)
summary(AnovaModel.TL)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
--	----	--------	---------	---------	--------

```
ID_a      6  6149    1025    24945 8.66e-15 ***
Residuals 7      0      0
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
2. Calculate repeatability
Variance between groups s2A = (MSa - MSw) / N0
(1025-0)/2
[1] 512.5
```

```
Repeatability r = s2A / (MSw + s2A)
512.5/(0+512.5)
#[1] 1
```

Repeatability of utilisation of breeding sites (Lat) between 2 years

```
AnovaModel.TL <- aov(Lat ~ ID_a, data=Datenmatrix)
summary(AnovaModel.TL)
      Df Sum Sq Mean Sq F value    Pr(>F)
ID_a     6  228.26   38.04    9125 2.92e-13 ***
Residuals 7    0.03    0.00
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
2. Calculate repeatability
Variance between groups s2A = (MSa - MSw) / N0
(38.04-0.00)/2
[1] 19.02
```

```
Repeatability r = s2A / (MSw + s2A)
19.02/(0.00+19.02)
[1] 1
```

Repeatability of Time of stay in sites between 2 years

```
1. Run ANOVAS
AnovaModel.TL <- aov(Time_of_stay ~ ID_b, data=Datenmatrix)
summary(AnovaModel.TL)
      Df Sum Sq Mean Sq F value    Pr(>F)
ID_b     3    925   308.3    2.723  0.179
Residuals 4    453   113.2
```

```
2. Calculate repeatability
Variance between groups s2A = (MSa - MSw) / N0
(308.3-113.2)/2
[1] 97.55
```

```
Repeatability r = s2A / (MSw + s2A)
97.55/(113.2+97.55)
[1] 0.4628707
```

Repeatability of moulting sites by isotopes and tracking data

```
1. Run ANOVAS
AnovaModel.1 <- aov(categorised ~ ID, data=Datenmatrix)
summary(AnovaModel.1)
      Df Sum Sq Mean Sq F value    Pr(>F)
ID      18  7.842   0.4357    8.278 1.41e-05 ***
Residuals 19  1.000   0.0526
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 Df Sum Sq
Mean Sq F value Pr(>F)

2. Calculate repeatability:

Variance between groups $s^2_A = (MS_A - MS_W) / N_0$
 $(0.4357 - 0.0526) / 2$
 [1] 0.19155

Repeatability $r = s^2_A / (MS_W + s^2_A)$
 $0.19155 / (0.0526 + 0.19155)$
 [1] 0.7845587

Repeatability of arrival in moulting areas between 2 years

1. run ANOVAS

```
AnovaModel.1 <- aov(Date_arriv_JD_year_indep ~ ID_a, data=Datenmatrix)
summary(AnovaModel.1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ID_a	2	549.0	274.50	15.11	0.0271 *
Residuals	3	54.5	18.17		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2. Calculate repeatability:

Variance between groups $s^2_A = (MS_A - MS_W) / N_0$
 $(274.50 - 18.17) / 2$
 [1] 128.165

Repeatability $r = s^2_A / (MS_W + s^2_A)$
 $128.165 / (18.17 + 128.165)$
 [1] 0.8758328

Calculation of standard error (SER_A)

Formula taken from Nakagawa S, Schielzeth H (2010) Repeatability for Gaussian and non-Gaussian data: a practical guide for biologists. Biological Reviews 85(4):935-956.

$$SER_A = 2 \cdot (N - 1) \cdot (1 - RA)^2 [1 + (n_0 - 1) \cdot RA] / n^2 \cdot 0 \cdot (N - k) \cdot (k - 1)$$

- k is the number of individuals,
- N is the total sample size
- N_i is the sample size for the i th individual.
- The correction term n_0 is equal to the sample size per individual if sample sizes are equal for all groups