A multi-isotope (δ^{13}C, δ^{15}N, δ^2H) approach to connecting European breeding and African wintering populations of barn swallow (Hirundo rustica)

Abstract
Establishing links between breeding and wintering populations of long-distance migratory birds and other animals is fundamental to several aspects of migration research. However, severe limitations in our ability to track small-bodied migratory species still limits this field despite several recent technological breakthroughs. The measurement of naturally occurring stable isotopes of several elements in the tissues of migrants that travel across isotopic gradients or isoscapes has the potential to identify large scale migratory connectivity without some of the biases associated with the use of extrinsic markers. We investigated migratory connectivity between European breeding and African wintering populations of barn swallow (Hirundo rustica) by comparing feather isotope (δ^{13}C, δ^{15}N, δ^2H) values with those expected from previously established feather isotopic clusters for Africa. We used a likelihood approach to assigning individuals to molt origins that also made use of prior information provided by ring recoveries as part of the EURING and SAFRING ringing efforts. We found evidence for strong isotopic spatial structure in the dataset, supporting the notion of a migratory divide in Europe with birds breeding in the Netherlands, Denmark, Germany and Eastern Europe wintering in southern Africa and virtually all samples from Switzerland westward being assigned to clusters in the northern portion of the species’ winter range. Individuals from the United Kingdom were assigned to areas including Namibia, Botswana, northern South Africa, and along the coast of Mozambique and Tanzania. Birds wintering in the northernmost region of the wintering grounds tended to breed in the southernmost region of the breeding grounds, providing some evidence of leap-frog migration. We detected a strong latitudinal threshold in feather δ^{13}C in Europe for African-grown feathers, suggesting that birds breeding in southern Europe (< 50° Latitude) primarily used C3-dominated habitats in Africa, whereas birds in northern Europe (> 53° Latitude) primarily used C4-dominated habitats. Our results emphasize the power in using a multi-isotope approach to assign individuals and populations to known continental-scale isoscapes and the advantages of combining isotopic and conventional (ring recovery) information within a Bayesian assignment framework.

Keywords
Barn swallow • Isoscapes • Migratory connectivity • Stable-isotope

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Introduction
In the last few decades, there has been renewed interest in establishing connections between breeding and wintering populations of long-distance migratory birds [1,2]. Much of this interest is based on the clear recognition that factors occurring at one period of the annual cycle can influence events occurring at another [3-7]. Such seasonal interactions can reveal ultimate fitness consequences of the choice of wintering and stopover locations made by birds that travel to breed. For example, birds occupying favorable wintering habitats are more likely to achieve a suitable migratory body condition and arrive first on the breeding grounds where they subsequently raise more offspring [8]. Other factors influencing overwinter survival and arrival phenology of birds on the breeding grounds involve large-scale climatic events or trends experienced on the wintering grounds, or en route, and there is considerable evidence for differential vulnerability to such factors among species and subpopulations within species depending on degree of migratory connectivity [9,10].

Establishing migratory connectivity has benefited from several recent technological advances involving both extrinsic and intrinsic markers that can augment the more conventional but valuable long-term ring recovery programs [11]. Notably, the

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development of miniaturized light-sensitive geolocators suitable for deployment on relatively small passerines (> 18g) promises to provide provenance data accurate to within a few hundred kilometers [12,13], although significant fitness costs to birds from use of geolocators will require inclusion of untreated and sham-treated control groups, something that is rarely if ever done currently. These developments will undoubtedly revolutionize the field of migration research, although the lack of untreated controls may render any conclusions dependent on other approaches such as stable isotope and trace element analyses. However, there is still great need to better develop and refine our understanding of migratory connectivity through the use of intrinsic markers that require only a single capture and that are consequently unbiased by choice of initial marked population and which can be applied to many hundreds or thousands of individuals at relatively modest cost. Moreover, there is still concern that extrinsic markers can affect survivorship and behaviour of birds so equipped [14-16]. The use of stable isotope assays of the tissues from migratory animals provides a number of advantages over extrinsic markers, especially for small passerines. Although it is possible that sampling individual feathers and claws for such purposes may affect subsequent behavior or fitness of birds, such effects are expected to be minor and will not influence inferences of the movement history of individuals prior to capture which is the period of interest. The use of stable isotopes also opens up the possibility of cross-validation of studies of migratory connectivity based on geolocators and other tracking devices.

The stable isotope approach to establishing migratory connectivity between populations relies on the fact that the naturally occurring abundance of isotopes of several elements can be passed predictably from diet to consumer tissues and dietary values for several elements show geographically structured variation at multiple spatial scales. Birds are particularly amenable to this sort of research because their feathers can lock in isotopic information, and timing of feather molt is often relatively well known. Currently, there is a great deal of interest in being able to associate origins and movements of birds based on knowledge of the spatial pattern of foodweb isotope values that birds may encounter during their travels [17,18]. These patterns or “isoscaes” are in turn influenced by a variety of biogeochemical processes. Two important processes influencing foodweb isotope values, and consequently bird tissues, involve biogeochemical processes. Two important processes influencing patterns or “isoscapes” are in turn influenced by a variety of

barn swallow (Hirundo rustica) is one such species that breeds throughout Europe and winters throughout most of Africa where it undergoes an annual molt of flight feathers. Previous research based on extensive recoveries as a result of the European Union for Bird Ringing (EURING) Swallow Project [22] has shown evidence of population structure whereby barnswallows breeding in northern Europe generally winter in southern Africa and those breeding in southwestern Europe generally winter in west Africa [9,23,24]. There is evidence of heterogeneity in isotope profiles within breeding populations of barn swallows indicating differences in African winter quarters being associated with differences in phenology, reproduction and behavior [9]. Recently uncovered evidence within the EURING swallow dataset suggests a northward shift in African wintering grounds of barn swallows over the last 80 years due to global climate change [24]. This northward shift in wintering grounds was more pronounced for the southern populations wintering in southern Africa than in the populations wintering in the northern part of the winter range [24]. Barn swallows are known to be very specific in their choice of wintering site, as shown by the trace element profile of feathers allowing correct assignment of most individuals to a given roost [23]. Individual barn swallows are also highly philopatric to their chosen breeding sites and their winter quarters, with individuals often being captured in the same site year after year (e.g. [26]).

Our objectives were to evaluate isotopic evidence for migratory connectivity between European breeding grounds and African wintering grounds of barn swallows using an established theoretical multi-isotope (δ13C, δ15N, δ2H) feather isoscape for Africa [21]. Our approach was to sample feathers from swallows from known breeding colonies throughout Europe and to assign individuals to known isotopic clusters in Africa. We were also able to obtain growing feathers from adults and yet-to-be-molted feathers of juveniles in Africa providing African-grown and European-grown feathers, respectively. Thus, we were able to test our assumptions of migratory connectivity using isoscapes associated with both Europe and Africa. Importantly, using Bayesian assignment approaches, we used results from EURING as informative priors, thereby combining isotopic and conventional mark-recapture approaches to establish a best estimate of migratory connectivity in this species.

Methods

We made a concerted effort to collect feathers from barn swallows captured at breeding sites in Europe and North Africa and from the winter quarters in Africa. APM contacted national ringing schemes to obtain these samples. Barn swallows only make a single annual molt in the winter quarters [27]. All feather samples from Africa were separated into feathers of yearlings and older birds based on the wear of feathers, allowing us in several cases to simultaneously link a given wintering population to both the isotope profile of the winter quarters (feathers newly grown by adults in Africa) and the breeding grounds (feathers grown by juveniles in Europe when in the nest).
We obtained Barn swallow samples representing: 1) African grown feathers from adults sampled in Africa (n = 40), 2) African-grown feathers from adults sampled from European breeding sites (n = 159), 2) Yet-to-be-molted European-grown (natal) feathers sampled from juveniles captured in Africa (n = 30), and 4) European-grown (natal) feathers from nestlings sampled across the European breeding range (n = 75).

**Stable isotope analyses**

Feathers were stored in paper envelopes and kept dry prior to isotope analysis. All feathers were cleaned of surface oils in a 2:1 chloroform:methanol solvent soak overnight and subsequent rinsing before being dried for 72h in a fume hood. Samples were stored in equilibration with ambient water vapor for several months prior to further preparation. Samples were assayed for δH, δ13C and δ15N analyses at the Stable Isotope Laboratory of Environment Canada, Saskatoon, Canada. We determined the non-exchangeable δH value of feathers using the comparative equilibration method described by [23] and using three calibrated keratin hydrogen-isotope reference materials (mean ± sd) CBS: −197 ± 0.79 ‰, KHS: −54.1 ± 0.33 ‰, SKS: −121.6 ± 1.9 ‰). Hydrogen isotopic measurements were performed on H2 gas derived from high-temperature (1350°C) flash pyrolysis of 350±10 µg feather and keratin standard subsamples loaded into silver capsules using continuous-flow isotope-ratio mass spectrometry. Measurement of the keratin laboratory reference materials corrected for linear instrumental drift were both accurate and precise with typical within-run SD values of < 2 ‰ (n = 5). We report all results for non-exchangeable H expressed in the typical delta notation, in units of per mil (‰) normalized on the Vienna Standard Mean Ocean Water – Standard Light Antarctic Precipitation (VSMOW-SLAP) standard scale.

We used between 0.5 and 1.0 mg of feather material for δ13C and δ15N analyses, which were combusted online using a Eurovector 3000 (Milan, Italy - www.eurovector.it) elemental analyzer. The resulting CO2 and N2 was separated by Gas Chromatography (GC) and introduced into a Nu Horizon (Nu Instruments, Wrexham, UK - www.nu-ins.com) triple-collector isotope-ratio mass-spectrometer via an open split and compared to pure CO2 or N2 reference gasses respectively. Stable nitrogen (15N/14N) and carbon (13C/12C) isotope ratios were expressed in delta (δ) notation, as deviation in parts per thousand (‰) from the primary standards: atmospheric nitrogen (AIR) and Vienna Pee Dee Belemnitite carbonate (VPDB) standards, respectively. Using previously calibrated internal laboratory C and N standards (powdered keratin and gelatin), within-run precision for both δ15N and δ13C assays were better than ± 0.15 ‰.

**Geographic assignments**

We used likelihood-based assignment tests to infer molt origins of individual feathers. We conducted two types of assignment tests depending on the sample. Feathers that were grown on African wintering grounds (i.e. those sampled from returning adults to Europe or sampled from molting individuals in Africa) were assigned to multi-isotope clusters modified from those derived by [21]. Previously, [21] derived expected feather isoscapes for Africa based on plant physiology models (δ13C, δ15N) [29,30] and the growing-season precipitation δH isoscape of [19] and then determined regions of similar multi-isotope composition via cluster analysis. To these clusters, we applied assumed isotope discrimination factors linking plant biomass to feathers of insectivorous passerines (for the δ13C, δ15N data and an algorithm linking precipitation δH with feather δH [21]. We modified this feather isotopic cluster layer for Africa by first clipping the isoscape to the described barn swallow wintering range (BirdLife International and NatureServe, 2011). In addition, we split the isotopic clusters into northern (north of 6.7° S) versus southern (south of 6.7° S) Africa based on previous analysis of ring-recovery data [9], thus splitting the four isotopic clusters of [21] into eight (Figure 1). We subsequently calculated the mean expected isotopic composition for feathers grown in each cluster by summarizing cells within each isoscape falling within each isotopic cluster using an ArcGIS (ESRI, Redlands California) zonal statistics query on the underlying δH, δ13C, and δ15N isoscapes from which the multi-isotope isoscape was derived (Table 1). We then used multivariate normal probability density functions [31], to assess the likelihood that an isotopic cluster represented the origin for a sample given the expected (i.e. isoscape predictions

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**Figure 1.** Wintering range of barn swallows (Hirundo rustica) in Africa and the underlying isotopic gradients determined from cluster analysis of feather isoscapes for δH, δ13C, and δ15N (from Hobson et al. 2012a). The wintering range and isotopic clusters were split into northern (north of 6.7° S as indicated by the horizontal red line) versus southern Africa (south of 6.7° S) based on analysis of ring-recovery data (see Methods).
as per Table 1) and observed feather isotopic compositions. We estimated the covariance among all three isotopes in our sample using the ‘mvnmle’ package within R 2.13.0 (R Development Core Team, 2011). Using expected feather isotope means from the isoscapes and the covariance matrix between isotopes defined from our feather samples, we estimated the multivariate normal probability densities associated with each potential source population using the mvtnorm package [32] in R 2.13.0 (R Development Core Team, 2011). Previous analyses of ring-recovery data have identified distinct connectivity differences between south versus west Africa [9]). Thus, we used linear discriminant analysis (DFA) to analyze the ring-recovery data reported in [9], treating breeding ground latitude and longitude (and their interaction) as explanatory variables. The resulting discriminant function was applied to the approximate geographic co-ordinates where samples were collected on the breeding ground to estimate the probability that birds would winter north versus south of 6.7° S. The split of the wintering distribution and ring-recovery data into the dichotomous north versus south of 6.7° S was on the basis of previous cluster analysis of ring-recovery data [9] that showed two distinct wintering subpopulations divided along this axis. Thus, we subsequently treated DFA-derived likelihoods as prior probabilities, and used Bayes’ Theorem to estimate posterior probability of origin given the multivariate normal probability densities derived as per above (based upon the isotopic composition (δ²H, δ¹³C, and δ¹⁵N) of the feathers) and the prior probability of wintering north versus south of 6.7° S.

We repeated the assignment of each individual feather to the isotopic clusters 1000 times via a simulation in which we specified the mean of the simulation to be equal to the observed feather δ²H, δ¹³C, and δ¹⁵N values. We specified a standard deviation of 12.2 ‰ for δ²H in our simulation based upon the distribution of residuals from the calibration equation linking δ²H in precipitation (δ²Hp) with feather δ²H (δ²Hf; 21). In contrast, we specified a standard deviation of 0.28 ‰ for both δ¹³C and δ¹⁵N feather values in our simulation based upon values reported in [33]. Within a given simulation, we assigned feather samples to an isotopic cluster by associating it with the cluster for which the highest likelihood was obtained. However, some samples were occasionally assigned to different clusters between simulations. Thus, we report mean number of birds (± SD) assigned to a given isotopic cluster across simulations.

In addition to multivariate geographic assignments to origin using clusters, we also conducted spatially explicit assignments to origin based upon feather δ²H alone. This was accomplished by clipping the δ²Hp isoscape provided by [19] and calibrating it to δ²Hf based upon regression of known-origin feathers against δ²Hp (δ²Hp = -6.77 + 1.42 * δ²Hf; 21). In contrast, we subsequently assigned samples to the resulting δ²Hp isoscapes using normal probability density functions to estimate the likelihood that cells within the isoscape could represent potential origins for the sample given the isoscape predicted δ²Hp and the observed δ²Hp [31,34-36].

### Table 1. Isoscape predicted isotopic composition (δ²H, δ¹³C, and δ¹⁵N in ‰) of feathers grown in Africa by geographic region and cluster (see Figure 1).

| Cluster | δ²H mean | δ²H SD | δ¹³C mean | δ¹³C SD | δ¹⁵N mean | δ¹⁵N SD |
|---------|----------|--------|-----------|--------|-----------|--------|
| North of 6.7° S | | | | | | |
| 1 | -18.2 | 9.9 | -21.2 | 2.2 | 9.5 | 0.6 |
| 2 | -29.3 | 5.1 | -14.9 | 1.7 | 9.5 | 0.3 |
| 3 | -17.2 | 7.1 | -13.9 | 1.7 | 10.2 | 0.4 |
| 4 | 13.6 | 8.2 | -11.3 | 2.1 | 11.4 | 0.8 |
| South of 6.7° S | | | | | | |
| 1 | -34.4 | 11.6 | -23.2 | 2.5 | 9.3 | 0.9 |
| 2 | -38.3 | 7.4 | -14.3 | 2.3 | 9.4 | 0.4 |
| 3 | -22.0 | 6.8 | -11.9 | 2.0 | 10.4 | 0.3 |
| 4 | -5.5 | 4.5 | -11.8 | 1.0 | 10.9 | 0.6 |
Results

Feathers sampled in Africa

Samples of barn swallows that were collected in Africa with feathers representing molt in Africa (n = 40), were obtained from Namibia (n=16), South Africa (n= 17) and Senegal (n= 7). Of these samples, 14 originated from regions in the isoscape classified as Cluster 1, two originated in regions classified as Cluster 2, and 24 originated in regions classified as Cluster 3. Eleven of the 14 samples (79%) originating from Cluster 1 were correctly assigned to Cluster 1 and one of the two samples originating from Cluster 2 were correctly assigned to Cluster 2. For the 24 samples originating from regions classified as Cluster 3, ten (42%) were correctly assigned. Another six samples from Cluster 3 were assigned to Cluster 2, which was also represented in the vicinity of the sampling location and is reasonably isotopically similar to Cluster 3; thus, ~67% of the sample collected in areas classified as Cluster 3 fit the isoscape well, which was expected from our chosen odds ratio of 2:1.

Feathers sampled in Europe

Of 24 barn swallows sampled in the United Kingdom, none were assigned to isotopic clusters in the northern portion of their African wintering range (Figure 2). The majority of birds sampled in the United Kingdom were assigned to Cluster 3 in southern Africa (i.e. south of 6.7°S), which falls largely within Namibia, Botswana, northern South Africa, and along the coast of Mozambique and Tanzania (Figures 1, 2). Several individuals were also associated with Cluster 2, consistent with central South Africa, Angola, Zambia, and the southern Congo (Figures 1, 2). Only a few were assigned to Cluster 4 in southern Africa (Figure 2), which is geographically associated with a small region of southern Mozambique (Figure 1).

Samples from Western Europe (other than the UK) were associated with both northern and southern Africa (Figure 2). However, our a priori grouping showed heterogeneity, with virtually all samples from Switzerland westward being assigned to clusters in the northern portion of the species’ winter distribution and samples from the Netherlands, Denmark, Germany and Eastern Europe assigned to clusters in southern Africa (Appendix 1). Of the samples from Western European countries assigned to northern Africa, the largest proportion were assigned to Cluster 2, however, substantial numbers were also assigned to Clusters 1 and 3 (Figure 2). In contrast, those samples that were associated with southern Africa (samples from Germany, Netherlands and Denmark, see Appendix 1).
were primarily assigned to Cluster 1, and secondarily to Cluster 2 (Figure 2).

Samples collected in Eastern Europe were almost exclusively associated with southern Africa (Figure 2). The exceptions were two samples from the Czech Republic that had the highest likelihood of coming from Cluster 1 in northern Africa (Appendix 1). The majority of samples from Eastern Europe were assigned to southern Africa, with the largest proportion of those being assigned to Cluster 2 and 3 and smaller numbers assigned to Clusters 1 and 4, respectively (Figure 2).

Data from African-grown feathers sampled in Europe displayed marked variation among sampling locations (Figure 3). There was some evidence for geographic structure in the variation in δ²H (Figure 3A), and substantial geographic variation in feather δ¹³C (Figure 3B), but variation in δ¹⁵N showed little pattern (Figure 3C). Linear modelling suggests approximately 11% of the variation in δ²H was attributable to variation along a longitudinal cline (F₁,₁₅₇ = 19.6, p < 0.001), with a decrease in δ²H of approximately 0.45 ‰ (SE= 0.10‰) per degree of longitude (Figure 4A). In contrast, graphical examination of the data suggested that δ¹³C showed non-linear variation with latitude (Figure 4B). A generalized additive model suggested a significant non-linear relationship (F₂,₈,₀ = 22.2, p < 0.001) which explained 30% of the variation in δ²H (Figure 4B), and suggests that birds breeding in southern Europe (< 50° Latitude) primarily used C₃-dominated habitats in Africa, whereas birds in northern Europe (> 53° Latitude) primarily used C₄-dominated habitats in Africa (Figure 4B). Thus, the birds from northern/eastern

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**Figure 3.** Boxplots representing the isotopic composition of African-grown barn swallow feather samples for A) δ²H, B) δ¹³C, and C) δ¹⁵N by country in which the sample was collected. Countries on X-axis are sorted in order of increasing latitude.
Europe assigned to Cluster 2 and 3 consistent with areas such as Botswana (see above), were isotopically consistent with C4-dominated areas surrounding Botswana (Figure 5).

In general, assignments of birds to the African δ2H isoscape resulted in similar results as the multi-isotope isoscape (Figure 6). Birds from the United Kingdom were primarily assigned to molt origins in Namibia, Botswana and South Africa (Figure 6A). There was also a significant likelihood that the sample had originated from northern Mozambique and southern Tanzania (Figure 6A). In contrast, birds from Western Europe (excluding the UK) were largely assigned to west Africa from Liberia west to Cameroon and into the Congo (Figure 6B). Some birds from the more northerly countries in the sample were assigned to southern Africa (south of 6.7° S), primarily to southern regions of the Democratic Republic of Congo, Namibia, Botswana and South Africa (Figure 6B). The eastern European barn swallow samples were similarly assigned to molt origins primarily associated with Namibia, Botswana and South Africa and perhaps northern Mozambique and southern Tanzania (Figure 6C).

Assigning birds sampled in Africa to the breeding ground δ2H isoscape based on analysis of retained breeding-ground feathers yielded fairly similar conclusions about connectivity between breeding ground and wintering ground populations (Figure 7). Samples from a breeding population in Algeria but of unknown origin were consistent with molt origins in the extreme southern portion of the breeding range (mean = -47 ‰, sd = 7.1) similar to those expected from Spain (predicted mean = -60 ‰, range = -85 to -37 ‰) or Algeria (predicted mean = -52 ‰, range = -63 to -37 ‰). In contrast, samples collected from South Africa (mean = -69.5 ‰, sd = 13.2 ‰) and Namibia (mean = -61.9 ‰, sd = 10.9 ‰), were assigned to regions of Europe well north of those from Algeria (Figure 7A and 7B, respectively), particularly for the South African sample, where likely origins include regions extending into Scandinavia, Germany, Poland and Russia for several individuals (Figure 7A).

Discussion

Our isotopic analysis of winter- and summer-grown feathers by barn swallows in Africa and Europe revealed considerable structure that could be used to associate birds with major isotopic clusters expected from plant- and water-based

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**Figure 4.** Geographic variation in the isotopic composition of Afro-tropical grown barn swallow feathers for A) δ2H and longitude and B) δ13C and latitude. Solid lines represents best fit A) linear model and B) generalized additive model, with 95% confidence intervals indicated by dashed lines (see text).

**Figure 5.** Predicted δ13C of passerine feathers grown in Africa, derived from applying a plant to tissue discrimination of 2‰ to the plant δ13C isoscape of Still and Powell (2010).
Barn swallow migratory connectivity

isoscapes, especially for Africa. This approach follows from a great deal of recent interest in using spatial assignment tools to infer origins of migratory species using isoscapes [20] that can in turn provide an independent means of inferring migratory connections between breeding and wintering grounds in this and other long-distance migrants. Our results are encouraging and while there are numerous assumptions inherent in the isoscape approach we advocate, our conclusions are largely in agreement with prior expectations of migratory patterns in barn swallows.

Our current knowledge of the wintering populations in Africa being separated into two major clusters in Western and Central Africa and in southern Africa, respectively [9], was used to inform our likelihood-based assignments to origin. Thus, it is not surprising that our assignments were directly consistent with previous ring-recovery analyses. However, the existence of geographically structured variation in δ2Hf and δ13C for African grown feathers collected on the breeding grounds provides independent support for a migratory divide, thus providing cross-validation between two different methods (banding recoveries and isotope profiles) that is rarely done in research on migratory connectivity. Clearly, more efforts to make cross-validations based on these two approaches, but also on others, are required to have confidence in our conclusions.

Figure 6. Geographic distribution of assigned molt origins to the African feather δ2H isoscape (see Methods) for barn swallows sampled in A) the United Kingdom (n = 24), B) western Europe (n = 101), and C) eastern Europe (n = 26). Samples for western Europe include Denmark (n = 8), Germany (n = 16), Italy (n = 16), the Netherlands (n = 16), Spain (n = 31), and Switzerland (n = 14). Samples for Eastern Europe include the Czech Republic (n = 8), Finland (n = 8), Poland (n = 10) and Lithuania (n = 8). Values depicted on maps represent the number of individuals in the sample that were isotopically consistent with the given cell representing a plausible origin at the selected odds ratio (see Methods).
We found evidence of considerable heterogeneity within populations in isotopic profiles. This suggests that local breeding populations are composed of individuals from multiple winter origins and or microhabitats. If it reflects multiple geographic origins, this finding appears to be in contrast with a high degree of both breeding and winter philopatry in the barn swallow [25,26,37,38]. For example, [37] has only found three out of more than 5000 adults ever moving to a new breeding colony after their first breeding event. Likewise [25] were able to assign most barn swallows correctly to their communal roost in the winter quarters simply based on trace element profiles of feathers. However, there is regular long-distance dispersal among barn swallows from their natal site to the first breeding ground, with dispersal distances exceeding 700 km [39]. Just a small number of such immigrants suffice for generating considerable heterogeneity. Populations from the UK and Eastern Europe were better segregated than populations from Western Europe (outside the UK). This suggests that there are greater limits to such dispersal in some parts of the European breeding range than in others.

Although there are currently great expectations linked to the study of migratory connectivity based on gelocators and other tracking devices [12], there is to the best of our knowledge no study investigating how control groups without tracking devices perform in terms of migration. Indeed, there is ample evidence for severe treatment effects in using a wide range of extrinsic markers including flipper tags in penguins [16], transmitter effects in birds [14] and geolocator effects in birds [15], D. Costantini and A. P. Møller, in preparation). This is problematic because a hallmark of experimental science since the discussions between Bohr and Heisenberg has been to test for treatment effects because we can only understand nature if our tools for such invesigations are not themselves the cause of the result. An approach for assessing such effects is simply to investigate the stable isotope profile or the trace element profile for treated and control individuals before and after the use of the geolocator. Given that migrants show a high degree of philopatry to their winter quarters [38], we should expect the chemical profiles of feathers to be the same in control individuals without tracking devices, while any burden experienced by experimental individuals should result in a difference in migration and winter quarters and hence a difference in feather isotope composition. A similar argument for a study of immigration to a sink population was provided by radioactive contamination due to the catastrophe at Chernobyl [40].

Future studies aimed at refining the isoscape approach to assignment of migratory birds to regions in Africa and elsewhere will require considerable efforts at ground truthing predictions made from our isotopic cluster analyses or the use of other multi-isotope assignment approaches. Currently, it is not well understood how plant- and water-based isoscape models truly reflect the isotopic composition of the prey base used by aerial

![Figure 7. Likelihood based assignment of barn swallows with retained (breeding ground) feathers to the precipitation δ2H isoscape of Bowen et al. (2005), for individuals sampled in A) South Africa (n=16), and B) Namibia (n=7). Assignments were conducted after recalibrating the precipitation isoscape to reflect δ2H in feathers via regression (see Methods). Values depicted on maps represent the number of individuals in the sample that were isotopically consistent with the given cell representing a plausible origin at the selected odds ratio (see Methods).](image-url)
insectivores like barn swallows. Nor is it clear how isotopic profiles can differ among insects produced from terrestrial and aquatic sources at a landscape level. Recent investigations on hydrogen and oxygen isotope composition of aquatic emergent insects suggest that these two insect groups can be encouragingly similar at continental scales [11], but further assays for the isotopes of carbon and nitrogen are now needed. Finally, our isoscape models are based largely on our knowledge of isotopic discrimination factors linking primary producers with tissues (feathers) of upper-trophic level consumers and these are generally imperfectly known (but see [21]).

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### Table S1. Distribution of likelihood-based assignments to multi-isotope clusters in Africa across 1000 simulations for 159 barn swallows sampled in Europe based on feather δ²H, δ¹³C, and δ¹⁵N (in ‰) and prior probability derived from ring-recoveries (see Methods).

| ID     | δ²H  | δ¹³C | δ¹⁵N | Location | 1 | 2 | 3 | 4 | 1 | 2 | 3 | 4 |
|--------|------|------|------|----------|---|---|---|---|---|---|---|---|---|
| 10473  | -36.5| -16.1| 11.8 | GBR      | 0 | 0 | 0 | 0 | 870| 107| 23 |
| 10474  | -27.8| -13.5| 11.4 | GBR      | 0 | 0 | 0 | 0 | 1000| 0 | 0 |
| 10475  | -31.2| -14.9| 11.7 | GBR      | 0 | 0 | 0 | 0 | 781 | 206| 13 |
| 10476  | -21.4| -12.6| 11.6 | GBR      | 0 | 0 | 0 | 0 | 1000| 0 | 0 |
| 10477  | -15.5| -15.3| 11.8 | GBR      | 0 | 0 | 0 | 0 | 1000| 0 | 0 |
| 10478  | -33.2| -17.5| 11.6 | GBR      | 0 | 0 | 0 | 0 | 133 | 749| 118|
| 10479  | -30.1| -15.6| 12.1 | GBR      | 0 | 0 | 0 | 0 | 989 | 0 | 0 |
| 10480  | -40.5| -16.3| 10.7 | GBR      | 0 | 0 | 0 | 0 | 7 | 775| 218|
| 10441  | -43.1| -13.7| 11.8 | GBR      | 0 | 0 | 0 | 0 | 410 | 582| 8 |
| 10442  | -29.0| -15.0| 11.8 | GBR      | 0 | 0 | 0 | 0 | 240 | 643| 117|
| 10443  | -26.1| -14.0| 11.8 | GBR      | 0 | 0 | 0 | 0 | 84  | 733| 183|
| 10444  | -22.8| -13.9| 12.4 | GBR      | 0 | 0 | 0 | 0 | 11  | 654| 335|
| 10445  | -23.0| -17.4| 13.4 | GBR      | 0 | 0 | 0 | 0 | 100 | 571| 329|
| 10446  | -22.0| -15.4| 11.4 | GBR      | 0 | 0 | 0 | 0 | 220 | 524| 256|
| 10447  | -31.0| -16.9| 12.6 | GBR      | 0 | 0 | 0 | 0 | 350 | 539| 111|
| 10448  | -14.9| -12.8| 11.4 | GBR      | 0 | 0 | 0 | 0 | 3   | 506| 491|
| 10449  | -57.6| -16.9| 11.8 | GBR      | 0 | 0 | 0 | 0 | 996 | 4  | 0  |
| 10450  | -33.8| -18.5| 11.4 | GBR      | 0 | 0 | 0 | 0 | 954 | 13 | 30 |
| 10451  | -33.8| -16.3| 12.9 | GBR      | 0 | 0 | 0 | 0 | 263 | 633| 104|
| 10452  | -47.0| -17.5| 13.6 | GBR      | 0 | 0 | 0 | 0 | 659 | 330| 11 |
| 10453  | -34.2| -12.9| 14.0 | GBR      | 0 | 0 | 0 | 0 | 819 | 181| 181|
| 10454  | -16.5| -17.5| 11.3 | GBR      | 0 | 0 | 0 | 0 | 456 | 187| 357|
| 10455  | -24.9| -13.9| 12.4 | GBR      | 0 | 0 | 0 | 0 | 13  | 716| 271|
| 10456  | -24.7| -15.6| 12.7 | GBR      | 0 | 0 | 0 | 0 | 66  | 687| 247|
| 10327  | -32.4| -22.2| 13.1 | Spain    | 61 | 774| 165| 0 | 0 | 0 | 0 | 0 |
| 10328  | -26.5| -21.9| 11.6 | Spain    | 809 | 190| 1 | 0 | 0 | 0 | 0 | 0 |
| 10329  | -12.8| -21.5| 13.9 | Spain    | 0 | 76 | 898| 26 | 0 | 0 | 0 | 0 | 0 |
| 10330  | -24.4| -20.6| 12.2 | Spain    | 25 | 613| 362| 0 | 0 | 0 | 0 | 0 |
| 10331  | -32.6| -21.4| 13.4 | Spain    | 0 | 680| 320| 0 | 0 | 0 | 0 | 0 | 0 |
| 10332  | -31.7| -21.9| 12.3 | Spain    | 270 | 679| 51 | 0 | 0 | 0 | 0 | 0 | 0 |
| 10333  | -5.5 | -21.0| 12.8 | Spain    | 11 | 74 | 876| 39 | 0 | 0 | 0 | 0 | 0 |
| 10334  | -10.7| -20.9| 13.0 | Spain    | 0 | 101| 882| 17 | 0 | 0 | 0 | 0 | 0 |
| 10335  | -8.1 | -17.6| 10.5 | Spain    | 1 | 218| 764| 17 | 0 | 0 | 0 | 0 | 0 |
| 10336  | -31.0| -21.2| 12.5 | Spain    | 28 | 779| 193| 0 | 0 | 0 | 0 | 0 | 0 |
| 10337  | -13.7| -17.4| 10.8 | Spain    | 0 | 298| 695| 7 | 0 | 0 | 0 | 0 | 0 |
| 10338  | -31.2| -22.7| 14.2 | Spain    | 1 | 546| 453| 0 | 0 | 0 | 0 | 0 | 0 |
| 10339  | -28.6| -14.5| 10.4 | Spain    | 0 | 546| 452| 2 | 0 | 0 | 0 | 0 | 0 |
| 10340  | -16.3| -18.7| 11.8 | Spain    | 0 | 276| 715| 9 | 0 | 0 | 0 | 0 | 0 |
| 10341  | -16.3| -20.3| 13.9 | Spain    | 0 | 54 | 905| 41 | 0 | 0 | 0 | 0 | 0 |
| 10342  | -37.8| -22.1| 12.8 | Spain    | 57 | 889| 54 | 0 | 0 | 0 | 0 | 0 | 0 |
| 10279  | -35.8| -20.7| 13.5 | Spain    | 0 | 669| 331| 0 | 0 | 0 | 0 | 0 | 0 |
Table S1. Distribution of likelihood-based assignments to multi-isotope clusters in Africa across 1000 simulations for 159 barn swallows sampled in Europe based on feather δ²H, δ¹³C, and δ¹⁵N (in ‰) and prior probability derived from ring-recoveries (see Methods).

| ID     | δ²H  | δ¹³C | δ¹⁵N | Location | Northern Africa | Southern Africa |
|--------|------|------|------|----------|----------------|-----------------|
|        |      |      |      |          | 1   | 2   | 3   | 4   | 1   | 2   | 3   | 4   |
| 10280  | -32.0| -20.9| 13.7 | Spain    | 0   | 495 | 505 | 0   | 0   | 0   | 0   | 0   |
| 10281  | -33.8| -21.5| 12.3 | Spain    | 112 | 814 | 74  | 0   | 0   | 0   | 0   | 0   |
| 10282  | -43.2| -20.8| 12.2 | Spain    | 1   | 966 | 33  | 0   | 0   | 0   | 0   | 0   |
| 10283  | -40.1| -21.2| 11.7 | Spain    | 131 | 860 | 9   | 0   | 0   | 0   | 0   | 0   |
| 10284  | -34.7| -22.1| 12.9 | Spain    | 57  | 826 | 117 | 0   | 0   | 0   | 0   | 0   |
| 10285  | -42.8| -21.6| 13.0 | Spain    | 1   | 926 | 73  | 0   | 0   | 0   | 0   | 0   |
| 10286  | -32.4| -22.0| 10.7 | Spain    | 975 | 25  | 0   | 0   | 0   | 0   | 0   | 0   |
| 10289  | -48.1| -20.2| 11.5 | Spain    | 4   | 994 | 2   | 0   | 0   | 0   | 0   | 0   |
| 10290  | -17.5| -21.6| 12.8 | Spain    | 85  | 333 | 581 | 1   | 0   | 0   | 0   | 0   |
| 10291  | -30.9| -22.5| 11.5 | Spain    | 900 | 99  | 1   | 0   | 0   | 0   | 0   | 0   |
| 10292  | -35.2| -22.4| 11.7 | Spain    | 766 | 234 | 0   | 0   | 0   | 0   | 0   | 0   |
| 10293  | -40.1| -22.6| 10.4 | Spain    | 992 | 8   | 0   | 0   | 0   | 0   | 0   | 0   |
| 10294  | -41.7| -21.8| 11.4 | Spain    | 496 | 504 | 0   | 0   | 0   | 0   | 0   | 0   |
| 10295  | -41.8| -22.0| 10.4 | Spain    | 952 | 48  | 0   | 0   | 0   | 0   | 0   | 0   |
| 10539  | -33.8| -22.7| 12.7 | Netherlands | 0   | 0   | 0   | 0   | 1000 | 0   | 0   | 0   |
| 10540  | -28.9| -15.3| 9.8  | Netherlands | 0   | 0   | 0   | 0   | 0   | 883 | 73  | 44  |
| 10541  | -47.7| -18.0| 10.2 | Netherlands | 0   | 0   | 0   | 0   | 0   | 1000 | 0   | 0   |
| 10542  | -35.0| -20.9| 10.6 | Netherlands | 1   | 0   | 0   | 0   | 0   | 999  | 0   | 0   |
| 10543  | -22.8| -16.6| 13.6 | Netherlands | 0   | 0   | 0   | 0   | 0   | 31   | 600 | 369 |
| 10544  | -39.2| -21.1| 10.3 | Netherlands | 0   | 0   | 0   | 0   | 1000 | 0   | 0   | 0   |
| 10545  | -43.3| -16.9| 10.3 | Netherlands | 0   | 0   | 0   | 0   | 0   | 996  | 1   | 3   |
| 10546  | -38.6| -22.4| 13.3 | Netherlands | 0   | 0   | 0   | 0   | 1000 | 0   | 0   | 0   |
| 10547  | -46.3| -17.7| 10.8 | Netherlands | 0   | 0   | 0   | 0   | 0   | 996  | 0   | 4   |
| 10548  | -14.8| -19.7| 9.1  | Netherlands | 273 | 0   | 0   | 0   | 727  | 0   | 0   | 0   |
| 10549  | -56.7| -21.4| 11.6 | Netherlands | 0   | 0   | 0   | 0   | 1000 | 0   | 0   | 0   |
| 10550  | -36.5| -21.5| 10.9 | Netherlands | 0   | 0   | 0   | 0   | 1000 | 0   | 0   | 0   |
| 10551  | -30.4| -23.9| 13.8 | Netherlands | 0   | 0   | 0   | 0   | 1000 | 0   | 0   | 0   |
| 10552  | -29.2| -17.4| 13.4 | Netherlands | 0   | 0   | 0   | 0   | 0   | 193  | 628 | 179 |
| 10787  | -30.4| -22.7| 11.5 | Netherlands | 0   | 0   | 0   | 0   | 1000 | 0   | 0   | 0   |
| 10788  | -27.1| -18.6| 12.8 | Netherlands | 0   | 0   | 0   | 0   | 509  | 330 | 161 |
| 10249  | -25.1| -17.7| 10.8 | Switzerland | 0   | 651 | 349 | 0   | 0   | 0   | 0   | 0   |
| 10250  | -23.3| -22.6| 11.3 | Switzerland | 867 | 0   | 0   | 0   | 133  | 0   | 0   | 0   |
| 10251  | -24.2| -18.5| 10.7 | Switzerland | 7   | 705 | 288 | 0   | 0   | 0   | 0   | 0   |
| 10252  | -14.3| -23.2| 11.9 | Switzerland | 897 | 0   | 0   | 0   | 103  | 0   | 0   | 0   |
| 10253  | -34.3| -17.8| 11.1 | Switzerland | 0   | 847 | 153 | 0   | 0   | 0   | 0   | 0   |
| 10254  | -38.4| -20.4| 11.5 | Switzerland | 56  | 932 | 12  | 0   | 0   | 0   | 0   | 0   |
| 10255  | -42.2| -18.2| 11.6 | Switzerland | 0   | 920 | 80  | 0   | 0   | 0   | 0   | 0   |
| 10256  | -20.8| -21.7| 13.0 | Switzerland | 24  | 420 | 546 | 0   | 10  | 0   | 0   | 0   |
| 10257  | -11.1| -19.0| 10.8 | Switzerland | 76  | 352 | 562 | 10  | 0   | 0   | 0   | 0   |
| 10258  | -23.2| -20.4| 9.9  | Switzerland | 943 | 57  | 0   | 0   | 0   | 0   | 0   | 0   |
| 10259  | -15.3| -21.8| 10.9 | Switzerland | 986 | 2   | 0   | 12  | 0   | 0   | 0   | 0   |
| 10260  | -31.3| -19.1| 8.0  | Switzerland | 981 | 19  | 0   | 0   | 0   | 0   | 0   | 0   |
Table S1. Distribution of likelihood-based assignments to multi-isotope clusters in Africa across 1000 simulations for 159 barn swallows sampled in Europe based on feather δ²H, δ¹³C, and δ¹⁵N (in ‰) and prior probability derived from ring-recoveries (see Methods).

| ID    | δ²H  | δ¹³C | δ¹⁵N | Location     | 1   | 2   | 3   | 4   | 1   | 2   | 3   | 4   |
|-------|------|------|------|--------------|-----|-----|-----|-----|-----|-----|-----|-----|
| 10261 | -39.4| -17.4| 11.8 | Switzerland  | 0   | 793 | 207 | 0   | 0   | 0   | 0   | 0   |
| 10262 | -41.2| -23.0| 11.2 | Switzerland  | 348 | 0   | 0   | 0   | 652 | 0   | 0   | 0   |
| 10407 | -33.0| -23.2| 11.6 | Italy        | 821 | 0   | 0   | 0   | 179 | 0   | 0   | 0   |
| 10408 | -24.6| -23.5| 12.1 | Italy        | 859 | 0   | 0   | 0   | 141 | 0   | 0   | 0   |
| 10409 | -31.1| -22.8| 12.0 | Italy        | 770 | 40  | 1   | 0   | 189 | 0   | 0   | 0   |
| 10410 | -31.1| -18.2| 8.6  | Italy        | 592 | 408 | 0   | 0   | 0   | 0   | 0   | 0   |
| 10411 | -38.7| -20.0| 11.7 | Italy        | 3   | 950 | 47  | 0   | 0   | 0   | 0   | 0   |
| 10412 | -21.1| -19.2| 13.1 | Italy        | 0   | 172 | 819 | 9   | 0   | 0   | 0   | 0   |
| 10413 | -18.1| -19.1| 10.2 | Italy        | 467 | 469 | 64  | 0   | 0   | 0   | 0   | 0   |
| 10414 | -24.4| -22.4| 11.0 | Italy        | 981 | 4   | 0   | 0   | 15  | 0   | 0   | 0   |
| 10415 | -26.5| -21.8| 13.1 | Italy        | 22  | 581 | 397 | 0   | 0   | 0   | 0   | 0   |
| 10416 | -20.0| -20.3| 11.4 | Italy        | 296 | 503 | 201 | 0   | 0   | 0   | 0   | 0   |
| 10417 | -31.9| -20.5| 10.9 | Italy        | 382 | 612 | 6   | 0   | 0   | 0   | 0   | 0   |
| 10418 | -53.4| -15.0| 10.9 | Italy        | 0   | 974 | 26  | 0   | 0   | 0   | 0   | 0   |
| 10419 | -37.6| -23.0| 14.1 | Italy        | 2   | 574 | 226 | 0   | 198 | 0   | 0   | 0   |
| 10420 | -52.6| -14.6| 13.3 | Italy        | 0   | 576 | 424 | 0   | 0   | 0   | 0   | 0   |
| 10421 | -34.8| -21.8| 12.7 | Italy        | 70  | 838 | 90  | 0   | 2   | 0   | 0   | 0   |
| 10422 | -25.7| -18.7| 11.0 | Italy        | 1   | 762 | 237 | 0   | 0   | 0   | 0   | 0   |
| 10515 | -51.7| -22.8| 13.1 | Denmark      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10516 | -26.4| -21.4| 11.1 | Denmark      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10517 | -35.8| -16.1| 14.5 | Denmark      | 0   | 0   | 0   | 0   | 37  | 844 | 119 |
| 10518 | -38.6| -17.4| 11.6 | Denmark      | 0   | 0   | 0   | 0   | 0   | 919 | 64  | 17  |
| 10519 | -38.9| -15.2| 13.7 | Denmark      | 0   | 0   | 0   | 0   | 0   | 87  | 854 | 59  |
| 10520 | -33.2| -17.5| 10.8 | Denmark      | 0   | 0   | 0   | 0   | 0   | 951 | 18  | 31  |
| 10521 | -31.0| -20.7| 11.6 | Denmark      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10522 | -42.8| -17.0| 10.5 | Denmark      | 0   | 0   | 0   | 0   | 0   | 990 | 1   | 9   |
| 10383 | -46.9| -22.5| 10.9 | Germany      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10384 | -36.1| -19.2| 12.1 | Germany      | 0   | 0   | 10  | 0   | 86  | 864 | 15  | 25  |
| 10385 | -24.1| -20.9| 11.3 | Germany      | 3   | 0   | 0   | 0   | 996 | 0   | 0   | 1   |
| 10386 | -31.4| -21.4| 12.3 | Germany      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10387 | -47.0| -18.3| 11.0 | Germany      | 0   | 0   | 1   | 0   | 0   | 997 | 0   | 1   |
| 10388 | -38.6| -22.0| 12.9 | Germany      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10389 | -24.6| -20.5| 10.3 | Germany      | 40  | 0   | 0   | 0   | 960 | 0   | 0   | 0   |
| 10390 | -31.4| -21.1| 12.0 | Germany      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10391 | -18.9| -22.6| 11.8 | Germany      | 1   | 0   | 0   | 0   | 999 | 0   | 0   | 0   |
| 10392 | -23.0| -12.4| Germany      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10393 | -22.1| -21.3| 13.0 | Germany      | 0   | 0   | 0   | 0   | 975 | 0   | 0   | 25  |
| 10394 | -49.6| -18.4| 10.4 | Germany      | 0   | 0   | 1   | 0   | 8   | 991 | 0   | 0   |
| 10395 | -44.3| -16.3| 10.6 | Germany      | 0   | 0   | 0   | 0   | 975 | 22  | 3   |
| 10396 | -36.4| -22.4| 12.2 | Germany      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10397 | -61.0| -18.3| 10.8 | Germany      | 0   | 0   | 0   | 0   | 1000| 0   | 0   | 0   |
| 10398 | -22.2| -21.0| 12.6 | Germany      | 0   | 0   | 0   | 0   | 982 | 0   | 0   | 18  |
Table S1. Distribution of likelihood-based assignments to multi-isotope clusters in Africa across 1000 simulations for 159 barn swallows sampled in Europe based on feather δ²H, δ¹³C, and δ¹⁵N (in ‰) and prior probability derived from ring-recoveries (see Methods).

| ID     | δ²H  | δ¹³C | δ¹⁵N | Location    | 1  | 2  | 3  | 4  | 1  | 2  | 3  | 4  |
|--------|------|------|------|-------------|----|----|----|----|----|----|----|----|
| 10423  | -50.2| -14.0| 9.7  | Czech Rep.  | 0  | 0  | 2  | 0  | 0  | 984| 13 | 1  |
| 10424  | -33.1| -22.7| 12.3 | Czech Rep.  | 0  | 0  | 0  | 0  | 1000| 0  | 0  | 0  |
| 10425  | -44.3| -15.2| 10.2 | Czech Rep.  | 0  | 0  | 9  | 0  | 0  | 977| 14 | 0  |
| 10426  | -21.1| -19.7| 8.7  | Czech Rep.  | 719| 0  | 0  | 0  | 281| 0  | 0  | 0  |
| 10427  | -32.8| -21.2| 12.0 | Czech Rep.  | 2  | 0  | 1  | 0  | 997| 0  | 0  | 0  |
| 10428  | -27.0| -18.1| 12.0 | Czech Rep.  | 0  | 0  | 0  | 0  | 325| 0  | 0  | 0  |
| 10429  | -32.5| -21.5| 11.5 | Czech Rep.  | 0  | 0  | 0  | 0  | 1000 |0  | 0  | 0  |
| 10430  | -21.1| -20.4| 7.6  | Czech Rep.  | 860| 0  | 0  | 0  | 140| 0  | 0  | 0  |
| 10481  | -37.3| -16.6| 11.3 | Poland      | 0  | 0  | 0  | 0  | 0  | 14 | 858| 128|
| 10482  | -72.2| -16.5| 8.8  | Poland      | 0  | 0  | 0  | 0  | 0  | 999| 1  | 0  |
| 10499  | -40.9| -15.5| 11.4 | Poland      | 0  | 0  | 0  | 0  | 2  | 966| 2  | 10 |
| 10500  | -61.5| -17.6| 10.5 | Poland      | 0  | 0  | 0  | 0  | 84 | 821| 95 |
| 10501  | -65.7| -16.2| 9.3  | Poland      | 0  | 0  | 0  | 0  | 0  | 998| 2  | 0  |
| 10502  | -29.4| -13.8| 11.6 | Poland      | 0  | 0  | 0  | 0  | 0  | 1000|0  | 0  |
| 10503  | -21.5| -21.3| 12.6 | Poland      | 0  | 0  | 0  | 0  | 0  | 1  | 781| 218|
| 10504  | -30.8| -15.5| 14.5 | Poland      | 0  | 0  | 0  | 0  | 0  | 15 | 522| 463|
| 10505  | -29.1| -10.6| 11.1 | Poland      | 0  | 0  | 0  | 0  | 0  | 741| 175| 84 |
| 10506  | -57.8| -15.1| 9.9  | Poland      | 0  | 0  | 0  | 0  | 0  | 110| 631| 259|
| 10507  | -39.3| -18.6| 11.3 | Lithuania   | 0  | 0  | 0  | 0  | 0  | 660| 296| 44 |
| 10508  | -32.2| -13.2| 11.8 | Lithuania   | 0  | 0  | 0  | 0  | 0  | 118| 735| 147|
| 10509  | -59.3| -17.4| 11.8 | Lithuania   | 0  | 0  | 0  | 0  | 0  | 294| 600| 106|
| 10510  | -64.5| -17.1| 10.3 | Lithuania   | 0  | 0  | 0  | 0  | 0  | 12 | 661| 327|
| 10511  | -31.1| -14.1| 14.0 | Lithuania   | 0  | 0  | 0  | 0  | 0  | 40 | 475| 485|
| 10512  | -16.8| -14.4| 12.0 | Lithuania   | 0  | 0  | 0  | 0  | 0  | 832| 127| 41 |
| 10513  | -24.6| -15.3| 10.0 | Lithuania   | 0  | 0  | 0  | 0  | 0  | 299| 605| 96 |
| 10514  | -23.3| -15.4| 12.2 | Lithuania   | 0  | 0  | 0  | 0  | 0  | 966| 28 | 6  |
| 10351  | -38.1| -14.9| 13.6 | Finland     | 0  | 0  | 0  | 0  | 0  | 63 | 873| 64 |
| 10352  | -67.0| -17.4| 9.3  | Finland     | 0  | 0  | 0  | 0  | 0  | 1000|0  | 0  |
| 10353  | -38.6| -11.6| 12.4 | Finland     | 0  | 0  | 0  | 0  | 0  | 18 | 915| 67 |
| 10354  | -70.9| -16.2| 9.4  | Finland     | 0  | 0  | 0  | 0  | 0  | 1000|0  | 0  |
| 10355  | -23.6| -16.5| 14.2 | Finland     | 0  | 0  | 0  | 0  | 0  | 13 | 587| 400|
| 10356  | -94.5| -23.0| 9.3  | Finland     | 0  | 0  | 0  | 0  | 1000| 0  | 0  | 0  |
| 10357  | -27.5| -15.3| 12.2 | Finland     | 0  | 0  | 0  | 0  | 156| 686| 158|
| 10358  | -24.6| -16.5| 12.6 | Finland     | 0  | 0  | 0  | 0  | 149| 600| 251|