Genetic assignment with isotopes and habitat suitability (GAIAH), a migratory bird case study

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Summary

1. Identifying migratory connections across the annual cycle is important for studies of migrant ecology, evolution and conservation. While recent studies have demonstrated the utility of high-resolution SNP-based genetic markers for identifying population-specific migratory patterns, the accuracy of this approach relative to other intrinsic tagging techniques has not yet been assessed.

2. Here, using a straightforward application of Bayes' Rule, we develop a method for combining inferences from high-resolution genetic markers, stable isotopes and habitat suitability models, to spatially infer the breeding origin of migrants captured anywhere along their migratory pathway. Using leave-one-out cross validation, we compare the accuracy of this combined approach with the accuracy attained using each source of data independently.

3. Our results indicate that when each method is considered in isolation, the accuracy of genetic assignments far exceeded that of assignments based on stable isotopes or habitat suitability models. However, our joint assignment method consistently resulted in small, but informative increases in accuracy and did help to correct misassignments based on genetic data alone. We demonstrate the utility of the combined method by identifying previously undetectable patterns in the timing of migration in a North American migratory songbird, the Wilson's warbler.

4. Overall, our results support the idea that while genetic data provides the most accurate method for tracking animals using intrinsic markers when each method is considered independently, there is value in combining all three methods. The resulting methods are provided as part of a new computationally efficient R-package, GAIAH, allowing broad application of our statistical framework to other migratory animal systems.

Key-words: avian ecology, migratory connectivity, movement ecology, population assignment, Wilson's warbler

Introduction

The ecology and evolution of animals that undergo annual seasonal migration is shaped by events encountered across the entire annual cycle (Sillett, Holmes & Sherry 2000; Webster *et al.* 2002, 2005). It is now well established that habitat conditions during migratory or wintering phases can have significant carry-over effects on breeding ground productivity (Marra, Hobson & Holmes 1998; Sillett, Holmes & Sherry 2000; Norris & Taylor 2006). As a result, understanding patterns of migratory connectivity, or the geographic links between breeding,

wintering and stopover sites for a population over the course of an annual cycle, is a critical first step towards studies of migrant ecology, evolution and conservation.

Efforts to identify the strength of migratory connections have relied on a variety of methods for tracking animal movements (Marra, Hobson & Holmes 1998; Bonfil *et al.* 2005; Smith *et al.* 2005; Stutchbury *et al.* 2009). Extrinsic devices such as satellite transmitters and geo-locators have increased our knowledge of the movement patterns of individuals of a particular species (Stutchbury *et al.* 2009), but remain impractical for many large-scale (1000s of individuals) applications due to cost and weight restrictions, and the need to re-capture many individuals to collect the data (Arlt, Low & Pärt 2013; Bridge *et al.* 2013). An attractive alternative is the use of genetic and

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isotopic markers, that capture information contained within the tissue of an animal, to pinpoint an individual's population of origin. These methods have broad appeal because they are minimally invasive, cost-effective when applied at scale and do not require recapture of individuals (Rubenstein *et al.* 2002; Kelly, Ruegg & Smith 2005; Rundel *et al.* 2013). Furthermore, intrinsic methods make it possible to trace the origins of animals that have died from both natural and anthropogenic causes (i.e. poaching, collisions and disease), because genetic and isotopic samples can be collected from carcasses.

While some genetic approaches have been limited by a lack of resolution, advances in genome-wide sequencing have resulted in new technologies that can be applied to genetic tagging of wild populations (Allendorf, Hohenlohe & Luikart 2010; Metzker 2010; Davey *et al.* 2011). Even in species with high rates of dispersal, such as birds, fish and mammals it has been found that a small number ($n < 100$) of single-nucleotide polymorphisms (SNPs) found within, or linked to, genes under selection can be targeted to reveal population structure at spatial scales that are critical to regional conservation planning (Nielsen *et al.* 2009; Hess, Matala & Narum 2011; Nielsen *et al.* 2012; Ruegg *et al.* 2014). For example, Ruegg *et al.* (2014) found that 96 high-resolution SNPs could be used to identify six genetically distinct populations of a migratory songbird, the Wilson's warbler (*Cardellina pusilla*), whereas previous single-marker techniques found support for only two groups (Kimura *et al.* 2002). Furthermore, SNP assays that isolate short fragments of DNA specific to the taxa of interest make it possible to rapidly screen DNA from a variety of tissue types (i.e. bird feathers, fin clips, animal hair) that can be collected using non-invasive sampling techniques, making this method an attractive choice for conservation genomic studies (Ruegg *et al.* 2014; Kraus *et al.* 2015).

Despite their appeal, several questions remain as to how genetic tools compare with other intrinsic methods such as stable isotopes which are cost effective and have had broad applicability across many species (Hobson, Wassenaar & Taylor 1999; Brattström *et al.* 2008; Hobson, Barnett-Johnson & Cerling 2010; Hobson *et al.* 2012a,c; Cryan, Stricker & Wunder 2014), and habitat suitability models which can be used to refine isotopic- and genetic-based assignments (Hallworth *et al.* 2013; Pekarsky *et al.* 2015; Fournier *et al.* 2016). In contrast to stable isotope and habitat suitability model-based approaches, genomic methods require extensive expertise in laboratory and bioinformatic methods and therefore might not be appropriate in all situations. In addition, there are clear examples where genetic markers alone fall short of resolving populations across all or large parts of a species geographic range (Gagnaire *et al.* 2015; Toews *et al.* 2015). In such situations, the inclusion of stable isotopic data and/or habitat suitability models may increase the resolution of genetic markers on their own (Kelly, Ruegg & Smith 2005; Rundel *et al.* 2013; Pekarsky *et al.* 2015). For example, Rundel *et al.* (2013) showed that genetic and isotopic information can be combined to increase the assignment accuracy of individuals (birds) to their population of origin; however, this method was not designed to deal with disjunct patterns of genetic variation, like that observed in the Wilson's

warbler (Ruegg *et al.* 2014). More recently, several authors have used habitat suitability models to refine isotopic-based estimates of population assignment (Hallworth *et al.* 2013; Pekarsky *et al.* 2015; Fournier *et al.* 2016), but did not establish whether or not the use of habitat suitability as a prior actually led to improved estimates of the geographic origin of individuals and also did not establish how the resulting estimates compared in accuracy to genetic-based estimates.

Here, we combine genetic, stable isotope and habitat suitability data into a joint assignment procedure that infers the breeding origins of individuals collected anywhere along their migratory trajectory with greater resolution than can be attained using each method individually. We refine previously developed R-code (R Core Team 2016) for performing each type of assignment alone (Anderson, Waples & Kalinowski 2008; Bridge *et al.* 2013; Vander Zanden *et al.* 2014), making it computationally feasible to combine assignments and perform statistically rigorous leave-one-out cross validation. To assess the overall accuracy of our method in comparison to existing approaches we examine the results from each type of data – genetics, stable isotopes and habitat suitability – individually as well as jointly, in order to determine: (i) contributions of each data type to the accuracy of joint assignments, (ii) insights that might be gathered from the combined approach, and (iii) recommendations for future studies of migratory connectivity based on our results.

We assess the accuracy of each method using data from a long-distance migratory bird, the Wilson's warbler (*Cardellina pusilla*), a particularly appropriate model for testing the efficacy of our approach because previous population-genetic/connectivity studies on this species provide a solid basis for comparison among methods (Kimura *et al.* 2002; Clegg *et al.* 2003; Paxton *et al.* 2007; Irwin, Irwin & Smith 2011; Paxton *et al.* 2013; Rundel *et al.* 2013). We start by deriving posterior probability rasters (or other scaled 'scores') for each method individually (genetics, stable isotopes and habitat suitability) and then combine those into a joint assignment probability. We then evaluate the gains in accuracy achieved by each method individually as well as by combining multiple data sources using leave-one-out cross-validation with a reference set of Wilson's warblers sampled from known locations during the breeding season. The combined approach is then applied to the assignment of migratory birds of unknown origin at a stopover site in Cibola, AZ during spring migration. Our methods have been implemented in the new R-package, GAIAH (**G**enetic **A**ssignment using **I**sotopes **A**nd **H**abitat suitability), available on CRAN (https://CRAN.R-project.org/package = gaiah). Our scripts for using GAIAH to replicate the results in this paper are available on GitHub (https://github.com/eriqande/gaiah-wiwa).

Materials and methods

SAMPLING

Sampling of Wilson's warblers is detailed in Ruegg *et al.* (2014). Briefly, a collection of 357 feathers from 30 locations (average of 12 individuals/site; range: 2–25) across the breeding range was made

possible through a large collaborative effort with bird banding stations both within and outside of the Monitoring Avian Productivity and Survivorship (MAPS) and the Landbird Monitoring of North America (LaMNA) networks. These samples became the foundation of the subsequent genetic and isotopic analysis of known-origin samples. Breeding samples were collected and categorized into groups based on collection date (June 1 to July 31), signs of breeding (presence/size of a cloacal protuberance) and life-history timetables for the Wilson's warbler. To illustrate the efficacy of the combined approach to the assessment of migratory stopover site use-through-time, 686 migrant samples were also collected from Cibola, AZ (31°18′N, 114°41′W), using consistent-effort, daily, passive mist-netting from 22 March to 24 May, in both 2008 and 2009.

GENETICS

The application of genetic markers to the assignment of Wilson's warblers is detailed in Ruegg *et al.* (2014). Briefly, genetic samples, consisting of the proximal end of one rectrix (breeding samples) and whole blood samples (migratory samples) were purified using a Qiagen DNeasy Blood and Tissue Kit and quantified using a NanoDrop™ Spectrophotometer (Thermo Scientific, Inc., Waltham, MA, USA). Genotyping was done using a panel of 96 high-resolution SNP markers ascertained from a genome-wide survey of genetic variation in the species using restriction-associated-digest, paired-end (RAD-PE) sequencing. Analyses using STRUCTURE 2.3.4 (Pritchard, Stephens & Donnelly 2000; Falush, Stephens & Pritchard 2003) and GENELAND 4.0.6 (Guillot, Mortier & Estoup 2005) indicated $G = 6$ spatially distinct population groups that could be reliably distinguished using the 96 SNPs. The spatial extent of these six groups identified by GENELAND was overlaid, and then clipped, by the known range of Wilson's warbler [downloaded from NatureServe, www.natureserve.org, (Ridgely *et al.* 2005)], to create a map of the occurrence of different population groups across the breeding range (see Fig. 1, Ruegg *et al.* 2014). Breeding birds collected from locales within each population group were included as reference samples for genetic population assignment to assign posterior probabilities across the six genetic groups using the program GSI_SIM (Anderson, Waples & Kalinowski 2008). For each bird, i, this program returns an estimate of the posterior probability,

$$P(\mathcal{G}_i = g | y_i^{\text{gen}}, B), \ g = 1, \ldots, G,$$

that i's genetic group ($\mathcal{G}_i$) is equal to g (g denotes one of the six genetic groups), given i's genotype y_i^{gen} and the reference or baseline samples, B.

These posterior probabilities refer to group membership of each bird; however, to combine these inferences with stable isotope data requires first converting group membership posteriors into posterior probabilities of spatial location. As the 96 SNPs provide only limited ability to resolve local origin of birds *within* each genetic group's geographic area, we converted the genetic posteriors for the ith bird to a grid, $\mathbf{M}_i^{\text{gen}}$, of spatially explicit posterior probabilities by distributing the posterior probability $P(\mathcal{G}_i = g | y_i^{\text{gen}}, B)$ uniformly across the raster grid representing the spatial range of group g, and ensuring that these are appropriately normalized to sum to one across the whole breeding range. Namely, within group g's range, posterior probability is distributed according to

$$\mathbf{M}_i^{\text{gen}}(g) = \frac{P(\mathcal{G}_i = g | y_i^{\text{gen}}, B)\mathbf{U}_g}{C_g}$$

where $\mathbf{U}_g$ is a matrix (raster) containing 1s in cells within genetic group g's region and 0's elsewhere, and C_g is the number of raster cells within

group g's region (i.e. the sum of the elements of $\mathbf{U}_g$). In most cases within the reference dataset, individuals were assigned with high probability to one genetic group and lower probability to other groups (see Fig. 1, Ruegg *et al.* 2014). To represent the uncertainty in the genetic assignments to different groups (which in most cases was very small, see Fig. S1, Supporting Information) we spread the posterior probability of assignment to each group across the geographic ranges of all the groups to which the bird was assigned and then weighted the values according to their likelihood so that the combined areas summed to 1.

Subsequently, the posterior probability of spatial assignment of birds based on genetics and assuming a uniform prior across space is

$$\mathbf{M}_i^{\text{gen}} = \sum_{g=1}^{G} \mathbf{M}_i^{\text{gen}}(g),$$

whose elements clearly sum to unity. $\mathbf{M}_i^{\text{gen}}$ is a raster of the same extent and resolution as $\mathbf{M}_i^{\text{iso}}$ (see next section).

STABLE ISOTOPES

Predictable continental patterns of stable hydrogen isotopes in precipitation ($\delta^2 H_p$) are highly correlated with stable hydrogen isotopes of animal tissues ($\delta^2 H_f$), allowing for inferences about the origin of where tissues were grown (Hobson & Wassenaar 2008). When the breeding and moulting locations are the same, as is the case for Wilson's warblers, then stable isotope values provide an assessment of the breeding origin of a bird that is independent of a genetic assessment. We expressed all isotope ratios in standard delta notation ($\delta^2 H$) where

$$\delta = \frac{\text{isotope ratio of sample}}{\text{isotope ratio of standard}} - 1,$$

with ratios shown as parts per thousand (‰) deviation from Vienna Standard Mean Ocean Water for hydrogen. Prior to analysis, all feathers (breeding and migratory samples) were cleaned with dilute detergent followed by a 2:1 chloroform:methanol solution (Paritte & Kelly 2009). For $\delta^2 H$ analyses, a 0·1–0·2 mg piece of feather was packed into a silver capsule and loaded into an auto-sampling tray. Isotope ratio measurements were performed at the University of Oklahoma with a ThermoFinnigan Delta V isotope ratio mass spectrometer connected to an elemental analyzer (H analyses: TC/EA, Thermo-Finnigan, Ringoes, NJ, USA). To control for exchangeable hydrogen, hydrogen isotope ratios were normalized according to Wassenaar & Hobson (2003), using established keratin standards: chicken feathers (−147·4‰), cow (*Bos taurus*) hooves (−187‰) and bowhead whale (*Balaena mysticetus*) baleen (−108‰). For additional details on our analysis methods, see Kelly *et al.* (2009) and Paritte & Kelly (2009).

We created an isoscape of $\delta^2 H_p$ and its associated variance using IsoMAP (Job Key 54152), an online resource to generate region- and time-specific isoscapes for geographic assignments (Bowen *et al.* 2014, www.isomap.org). In IsoMAP, a geospatial isoscape was generated using precipitation data from 120 stations collected during the time period of 1960–2009, and included CRU-derived climatic variables such as elevation, precipitation and minimum precipitation in the model (Mitchell & Jones 2005; similar to Hobson *et al.* 2012d). Using a parametric bootstrapping approach (Supporting Information 3) we converted the isoscape of $\delta^2 H_p$ values to an isoscape of $\delta^2 H_f$ values based on the relationship between $\delta^2 H_p$ and $\delta^2 H_f$ collected from the 357 known-origin, breeding Wilson's warblers sampled across the breeding range. We then computed the posterior probability of breeding origin given a feather $\delta^2 H_f$ ratio and three sources of variance following the methods used in Vander Zanden *et al.* (2014). The three sources of variance included variance associated with; (i) the original $\delta^2 H_p$ isoscape
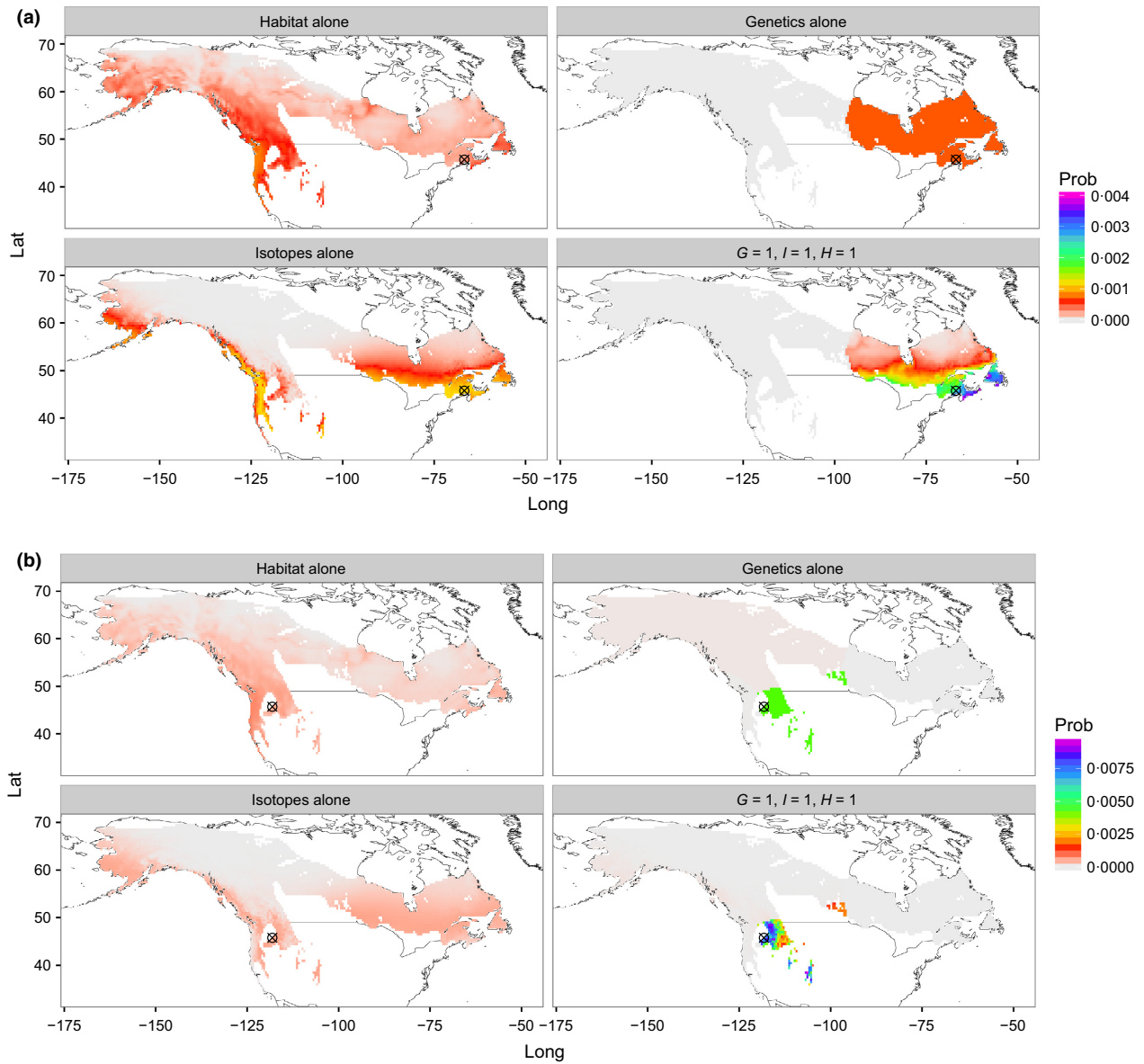
Fig. 1. Representative posterior probability surfaces for two birds: (a) a bird from the Eastern region, and (b) a bird from the Rocky Mountains region. Each of the four panels shows the result using a different type of data. The first three ('Habitat alone', 'Genetics Alone', and 'Isotopes alone', show results for each data type applied separately. '$G = 1, I = 1, H = 1$' shows the results from the combined approach with $\beta_{iso} = \beta_{hab} = 1$. Maps which showed particularly strong examples of the combined approach are shown here, while maps for all 367 reference birds can be found in Supporting Information 2, to which we refer those interested in the variability in assignments across methods and individuals. In general, the maps support the idea that combining methods provides the most accurate assignment probabilities.

generated in IsoMAP, (ii) the rescaled precipitation to feather δ^2H isoscape, and (iii) individual variation in δ^2H_f among birds sampled at the same breeding location.

Specifically, this approach assumes that y_i^{iso}, the isotope ratio measured in the feather of the ith bird, is a normal random variable with mean and variance determined by its location in space. If these means and variances, denoted by the matrices $\mathbf{T}^{(\mu)}$ and $\mathbf{T}^{(\sigma^2)}$, respectively, were known across a regular grid of possible origin locations, then it would be straightforward to compute the posterior probability of breeding location. Namely, assuming a uniform prior on spatial origin, the posterior that bird i originated from the (r, c)th cell in the grid is proportional to the density of observing y_i^{iso} given it was drawn from a normal density with mean $T_{r,c}^{(\mu)}$ and variance $T_{r,c}^{(\sigma^2)}$ (the (r, c)th elements of $\mathbf{T}^{(\mu)}$ and $\mathbf{T}^{(\sigma^2)}$ respectively).

It should be noted that $\mathbf{T}^{(\mu)}$ and $\mathbf{T}^{(\sigma^2)}$ are not known, so we follow Vander Zanden *et al.* (2014) by using $\widetilde{\mathbf{T}}^{(\mu)}$ and $\widetilde{\mathbf{T}}^{(\sigma^2)}$ in their place, computed as

$$\widetilde{\mathbf{T}}^{(\mu)} = \bar{a}\mathbf{P}^{(\mu)} + \bar{b} \qquad \text{eqn 1}$$

$$\widetilde{\mathbf{T}}^{(\sigma^2)} = \mathbf{R}^{(\sigma^2)} + \mathbf{P}^{(\sigma^2)} + \sigma_{indiv}^2\mathbf{J}, \qquad \text{eqn 2}$$

where $\mathbf{P}^{(\mu)}$ and $\mathbf{P}^{(\sigma^2)}$ are the predictions and associated variances, respectively, for the precipitation isotope ratios from IsoMAP made on the same grid as $\widetilde{\mathbf{T}}^{(\mu)}$ and $\widetilde{\mathbf{T}}^{(\sigma^2)}$; $\mathbf{J}$ is a matrix of 1's of the same dimension as $\widetilde{\mathbf{T}}^{(\sigma^2)}$; $\mathbf{R}^{(\sigma^2)}$, $\bar{a}$ and $\bar{b}$, are determined by a parametric bootstrapping approach described in Supporting Information 3; and σ_{indiv}^2 is a term accounting for individual variation in isotope ratios which was set to the square of the mean of the standard deviation of y_i^{iso} among birds

sampled at common locations across the breeding range during the breeding season. Posterior probabilities derived in this manner for bird *i* are a set of values over a spatial grid. Setting values outside of the known breeding range to zero and normalizing to sum to one gives the matrix, $\mathbf{M}_i^{\mathrm{iso}}$.

HABITAT SUITABILITY

In order for subspecies ranges to be further classified in terms of their utilization by breeding individuals, habitat suitability models were constructed for Wilson's warblers across their breeding range. This was performed by identifying the geographical locations of Wilson's warblers during the breeding season, and then modelling the relationship of these occurrences to the environmental conditions at those sites. This model was then used to predict the probability of occurrence of individuals across the species range.

Locations of individuals were extracted from the eBird website (www.ebird.org). To ensure that we used only those birds that were breeding (or at least were located on breeding grounds), we filtered the nearly 450 000 records of Wilson's warblers available to include only those sighted on or after 10 June, but before 1 August, of any given calender year. To avoid redundant observations at the same site artificially influencing models, we used each unique geographic location only once. The final dataset contained 9984 unique locations of Wilson's warblers on breeding grounds.

We used the machine learning algorithm MAXENT 3.3.3 (Phillips, Anderson & Schapire 2006) to model Wilson's warbler distributions. As this method relies only on presence data (i.e. it does not require records of Wilson's warbler *absence*), it is particularly well-suited for the use of eBird occurrence records to capture complex biological responses to environment (Elith *et al.* 2011), and has performed well in previous statistical comparisons with other species distribution modelling techniques (Harrigan *et al.* 2014). Environmental variables were chosen to best reflect unique predictive ability, and variables were removed from final analyses when a Pearson's correlation coefficient was >0·7 among the variable and any other predictor. We ran three replicates of a MAXENT model using the Wilson's warbler records as a response variable and 14 climate and landscape variables as predictors. These included eight (among 19 available) bio-climatic layers (Bio 1, 2, 4–6, 12, 15, 19, downloaded from www.worldclim.org) as well as variables representing landcover, tree cover, elevation and vegetation characteristics and heterogeneity [Normalized Difference Vegetation Index (NDVI) mean and standard deviation] downloaded from the Global Land Cover Facility (www.landcover.org). Default parameters were used for all MAXENT runs except for the following: clamping turned off, a maximum of 100 000 background points selected and 20% of data withheld for subsequent testing. In addition, both predictor response curves, as well as jackknifing to assess variable importance, were created as part of the output.

Once final models were evaluated and found to converge on similar response curves and probability estimates, the mean output ascii file was exported to ArcGIS and was clipped to the extent of the breeding range of Wilson's warbler, as determined using digital range maps provided by NatureServe (www.natureserve.org; Ridgely *et al.* 2005). These final probability estimates were then downsampled in resolution to yield a raster $\mathbf{M}^{\mathrm{hab}}$ with the same extent and resolution as $\mathbf{M}_i^{\mathrm{gen}}$ and $\mathbf{M}_i^{\mathrm{iso}}$.

COMBINING DATA TYPES

The above approaches yield $\mathbf{M}_i^{\mathrm{gen}}$ and $\mathbf{M}_i^{\mathrm{iso}}$ for the *i*th bird, as well as a prior probability of occurrence of a Wilson's warbler in any location,

$\mathbf{M}^{\mathrm{hab}}$. Treated as matrices of probabilities, these rasters can be combined using Bayes' rule to obtain a combined estimate of probability of spatial origin for each bird. In order to explore weighting the different sources of information (genetics, stable isotopes and habitat) differently, we considered incorporating the parameter $\beta = (\beta_{\mathrm{iso}}, \beta_{\mathrm{hab}})$ that determines the relative amount of weight given to the stable isotope and habitat data, and hence compute the combined probability as

$$\mathbf{M}_i^{\mathrm{comb}}(\beta) = \frac{1}{C(\beta)} \mathbf{M}_i^{\mathrm{gen}} (\mathbf{M}_i^{\mathrm{iso}})^{\beta_{\mathrm{iso}}} (\mathbf{M}^{\mathrm{hab}})^{\beta_{\mathrm{hab}}}, \qquad \text{eqn 3}$$

where $(\mathbf{M})^{\beta}$ denotes the matrix $\mathbf{M}$ with every element raised to the power β. $C(\beta)$ is a normalizing constant that ensures that the elements of $\mathbf{M}_i^{\mathrm{comb}}(\beta)$ sum to one. It can be easily found for any $\beta = (\beta_{\mathrm{iso}}, \beta_{\mathrm{hab}})$ by simply summing over all the elements of the unnormalized matrix.

Among the different genetic groups of birds, the relative utility of isotopic data vs. habitat suitability may vary. In theory, one could leverage this to advantage by choosing different values of β_{iso} and β_{hab} for birds that are assigned with genetics to particular genetic groups. However, doing so accurately would require sampling of reference birds proportionally with respect to their true density on the landscape, which may not be the case with the genetic samples used herein, which were obtained opportunistically from bird banding stations. Accordingly, while we explored a range of values of $(\beta_{\mathrm{iso}}, \beta_{\mathrm{hab}})$, for all results in the paper we used values of $\beta_{\mathrm{iso}} = \beta_{\mathrm{hab}} = 1$.

ASSESSMENT OF ACCURACY

To assess the extent to which the inclusion of stable isotope and habitat data improve the spatial localization of birds on the breeding grounds we test how well birds of known breeding location (those in the reference dataset) can be inferred using genetics alone, stable isotopes alone, habitat suitability alone or a combination of each. When doing so with the reference birds, we use a leave-one-out procedure, removing individual *i* from the reference dataset when computing $\mathbf{M}_i^{\mathrm{gen}}$ and $\mathbf{M}_i^{\mathrm{iso}}$.

To assess accuracy we develop an easily interpreted metric, S_i^{pm}, the posterior mean of great circle distance between the true location of *i* and inferred locations. This is found by averaging the distance between *i*'s true location and the centre of every cell in the breeding range, weighted by $\mathbf{M}_i$. In order to assess the accuracy of genetics, stable isotopes or habitat used separately or together, we compute S_i^{pm} with $\mathbf{M}_i^{\mathrm{iso}}$, $\mathbf{M}_i^{\mathrm{gen}}$, $\mathbf{M}^{\mathrm{hab}}$ or $\mathbf{M}_i^{\mathrm{comb}}(\beta)$ respectively.

ASSIGNMENT OF UNKNOWN MIGRATORY BIRDS – EXAMPLE DATASET

To illustrate the efficacy of the combined approach we applied the combined approach to a set of migratory birds of unknown origin captured at a stopover site in Cibola, AZ during spring migration. For each bird, we determined the combined probability of origin using eqn (3), creating a matrix of probability assignments, $\mathbf{M}_i^{\mathrm{comb}}$, for each migrant. We then calculated the posterior mean migration distance remaining from the stopover site by averaging the distance between the stopover site and the centre of every cell in the breeding range, weighted by $\mathbf{M}_i^{\mathrm{comb}}$.

Results

GENETICS

As previously reported (Ruegg *et al.* 2014), the *maximum-a-posteriori* self-assignments of the reference birds using

genetic data showed that a high fraction (88·2%) of birds are correctly assigned to their true region of origin. The rate of correct assignment varied across regions, with the lowest rate of correct assignment occurring in Coastal California (78%), followed by Rocky Mountain (81%), Pacific Northwest (85%), California Sierra (86%), Alaska to Alberta (95%) and Eastern North America (100%). Of the birds that are assigned correctly, their average maximum posterior is 96% and when birds are incorrectly assigned to their true region of origin, the average maximum posterior is 74%. This confirms that when genetic assignments are incorrect, isotopes and suitability have the potential to increase posteriors, and thereby improve localizations in joint assignments.

STABLE ISOTOPES

Across the Wilson's warbler breeding range, δ^2H_p values range from $-14\cdot3‰$ to $-190\cdot6‰$ with uncertainty across the δ^2H_p isoscape varying (SD: 8·5‰ to 21·6‰) as a result of the uneven distribution of precipitation stations used to model δ^2H_p. Regions with the greatest uncertainty in δ^2H_p values included coastal Alaska, Northwest Territories and Newfoundland. The rescaling equation used to convert the δ^2H_p isoscape to a δ^2H_f isoscape was $\delta^2H_f = 0\cdot74(\delta^2H_p) - 38\cdot01$; that is, in eqn (1), $\bar{a} = 0\cdot74$ and $\bar{b} = -38\cdot01$. The standard deviation associated with the rescaled precipitation to feather δ^2H isoscape, $\mathbf{R}^{(\sigma)}$, ranged from 0·6‰ to 6·6‰, while the mean, within-site standard deviation of δ^2H_f from the 357 Wilson's warblers of known breeding origin sampled across 30 locations was $\sigma_{indiv} = 12\cdot5‰$ (Table S1). The total variability, $\mathbf{T}^{(\sigma)}$, including the three sources of uncertainty, contained standard deviation values ranging between 15·2‰ and 24·9‰, depending on the geographic region of assignment.

HABITAT SUITABILITY

Habitat suitability model runs yielded accurate species probability of occurrence maps according to several criteria. First, the mean score of all replicates using only data withheld for testing was high, with an AUC = 0·938. Standard deviations in AUC between each replicate run were minimal (lowest AUC = 0·937, highest AUC = 0·939). Additionally, environmental predictors deemed most important in explaining presence of Wilson's Warblers were consistent across all replicate runs, with Bio 19 (Precipitation of the coldest quarter), Bio 5 (Maximum temperature of the warmest month) and Bio 4 (Temperature Seasonality) contributing to over 70% of the variation in occurrence explained by the MAXENT model. Finally, our final map displaying the point-wise mean probability of occurrence (Fig. S2) closely matched previously published maps of the species distribution of Wilson's Warbler [for instance, probability of occurrence was consistently <0·23 in regions outside of the species range, and habitat suitability generally identified regions that were also found to harbour high abundance of Wilson's warblers according to previously published data (Status of Birds in Canada, Peter Blancher, based on BBS abundance map estimates)].

From predictor response curves, we found that increases in precipitation in the coldest quarter (Bio19) and temperature in the warmest month (Bio5) led to increases in the probability of Wilson's warbler occurrence, whereas increases in temperature seasonality (Bio4) led to decreases in probability of occurrence (Fig. S2). These relationships resulted in several regions of high habitat suitability being identified within the Wilson's warbler range, including much of the Pacific coastline, the Sierra Nevada Mountain range, parts of the Rocky Mountain range and the Canadian Maritimes for eastern breeding populations.

COMPARISON OF DATA TYPES

Overall, combining genetics, isotopes and habitat suitability improved the inference of breeding origin of Wilson's warblers. The posterior mean great circle distance between the true location and inferred location for nearly every bird in the reference dataset was decreased by combining all three sources of data (Fig. 2). Of the three individual data sources, genetic data provided the most accurate localization of individuals, while stable isotope assignments and the habitat suitability prior used alone resulted in significantly less accurate localization. There were also significant differences in the accuracy of assignments of the reference birds to breeding location based upon geographic region (Fig. 3): genetic assignments performed best in all regions; for birds originating from the Pacific Northwest, the Sierras and the Rocky Mountains, more accurate assignments were achieved by using the prior information from habitat suitability than using data on stable isotopes alone; and conversely isotope-only assignments outperformed assignments using just the habitat suitability prior in Coastal California and the Eastern United States.

EXAMPLE DATA – TIMING OF MIGRATION IN PACIFIC NORTHWEST WILSON'S WARBLERS

In order to illustrate our combined approach on real-world migratory data, we calculated the posterior mean remaining migratory distance of birds sampled from Cibola, AZ during the spring migrations of 2008 and 2009. A general pattern, previously suggested in Ruegg *et al.* (2014), of birds en route to Coastal California migrating through before birds en route to the Pacific Northwest, the Sierras and Alaska to Alberta, was reinforced using our combined-data approach (Fig. 4a). In addition, we found previously undetected patterns in the timing of migrants en route to the Pacific Northwest, with migrants headed to the southern Pacific Northwest arriving earlier than migrants en route to northern Pacific Northwest. These results were concordant across both years (Fig. 4b).

Discussion

Tracking the origins of migratory animals using non-invasive, intrinsic marking techniques has been a particularly challenging endeavour for movement ecologists. Here we develop a streamlined method for combining three independent data sources (genetics, stable isotopes and habitat suitability
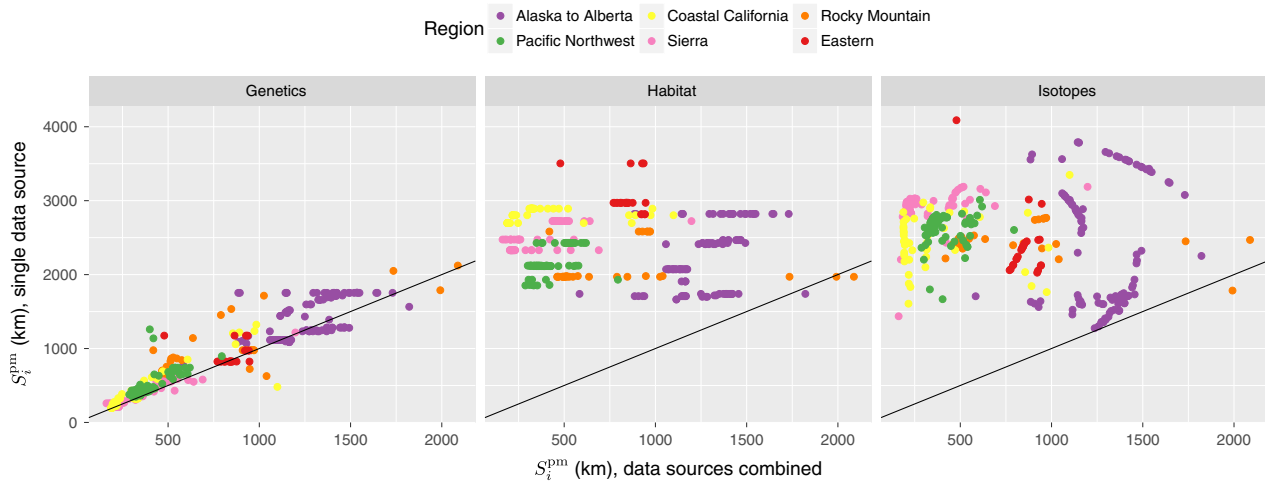
Fig. 2. A comparison of the posterior mean great circle distances, S_i^{pm}, between individual data types and the combined approach. Each point represents one bird. In all panels the x-axis shows S_i^{pm} using all data sources combined and the y-axis shows S_i^{pm} when using a single data source. The proximity of the points to the $y = x$ line shows how well each method does compared to the combined approach. The results clearly demonstrate that genetic data provide the most accurate inference of the true origin, while habitat suitability and stable isotope data provide more modest improvements. Nonetheless the fact that the majority of points lie above the $y = x$ line in the 'genetics' plot confirms that the addition of habitat and stable isotope data improves the inference of breeding origin (as all the points would fall on the $y = x$ line if the inclusion of stable isotopes and habitat did not change the inferences made with genetics alone).
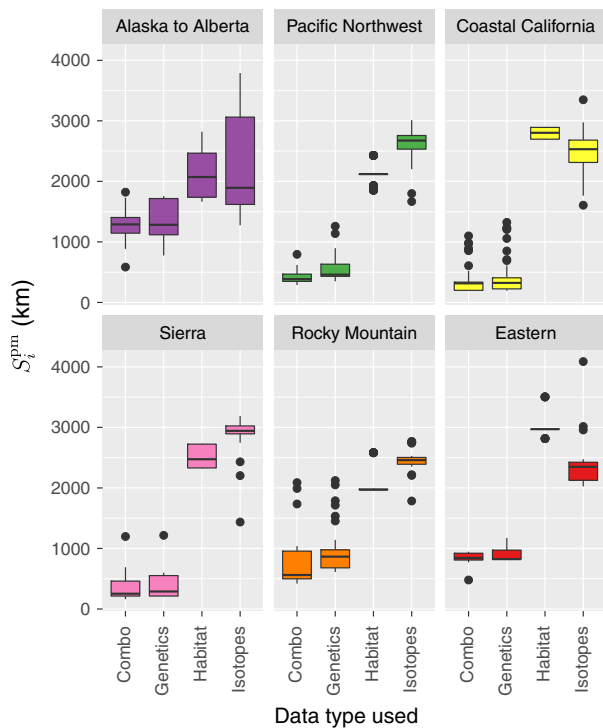

Fig. 3. The accuracy of each type of data as estimated by the posterior mean great circle distance to the true location by region. The figure demonstrates that genetic data alone contributes the most to the accuracy of assignments to the true breeding location across all regions, while isotopic and habitat suitability data provide more modest improvements that differ in strength by region.

models) that improves upon the accuracy of each method when used on its own. Using leave-one-out cross validation to compare the relative accuracy of each method independently,

we find that genetic data alone provide the most accurate estimation of the true origin of our reference birds, consistently outperforming assignments based upon stable isotopes and habitat suitability models (Figs 1 and 3). Improvements to the R-code for batch isotopic and genetic assignments initially developed by Vander Zanden *et al.* (2014) and Anderson, Waples & Kalinowski (2008), respectively, were compiled into an R-package called GAIAH in an effort to make future implementations of the resulting combined approach for generating joint Bayesian probability surfaces feasible across a broad range of migratory systems. Below we discuss region- and data type-specific differences in the assignments, illustrate the utility of our combined method for uncovering new patterns of connectivity across time in birds captured during spring migration, and discuss the implications of our results for future studies considering limitations in both time and resources.

ACCURACY OF EACH DATA TYPE RELATIVE TO THE COMBINED APPROACH

Our results indicate that while the joint assignment method consistently provided the best approximation of the true origin of birds in our reference sample (Figs 3 and 2), the accuracy of genetic assignments on their own far exceeded that of assignments based on stable isotopes or habitat suitability models. In general, the inclusion of habitat suitability and stable isotope data helped to localize assignments within regions identified by strong genetic assignment probabilities and, in some cases, helped correct misassignments based on genetic data alone. Surprisingly, for many birds originating from western regions (the Rocky Mountains, the Pacific Northwest and the Sierras), simply using the habitat suitability prior alone provided a better inference of the true origin of individuals than did stable
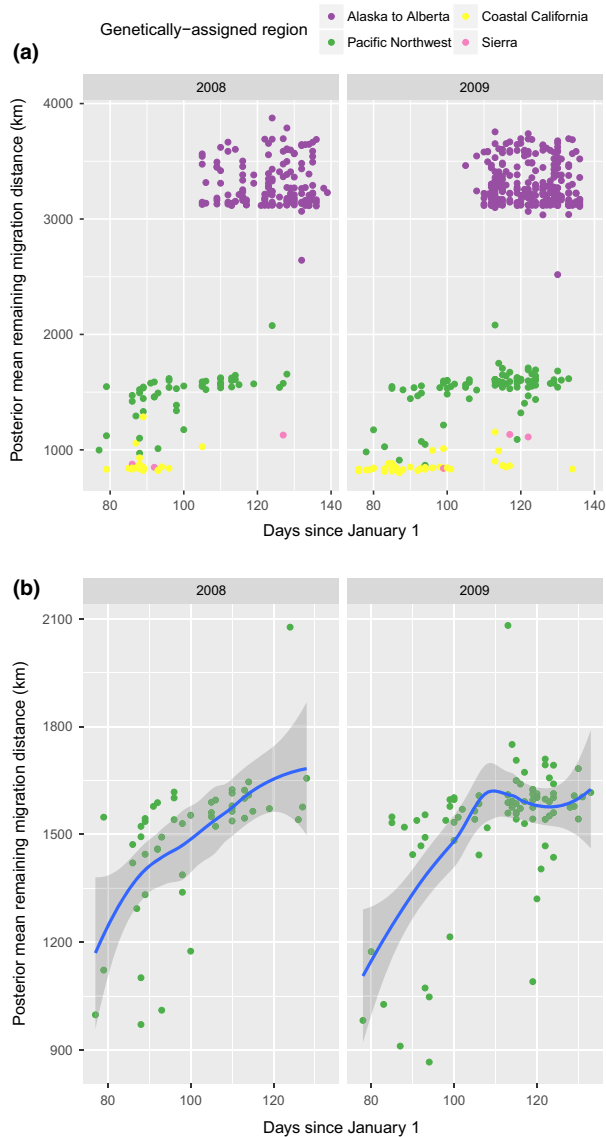
Fig. 4. Utility of the combined approach demonstrated with spring Wilson's warbler migrants stopping over in Cibola, AZ: (a) The posterior mean remaining migration distance by day of the year for all birds stopping over in Cibola AZ during spring migration across the years of 2008 and 2009. (b) The posterior mean remaining migration distance by day of the year for genetically assigned Pacific Northwest birds stopping over in Cibola, AZ during spring migration, demonstrating a previously undetected pattern of birds en route to more northern regions of the Pacific Northwest arriving later than birds en route to the southern portion of the Pacific Northwest. Blue line and gray area are a loess smooth and 95% confidence intervals, respectively, of the conditional mean over time.

hydrogen isotope data. We hypothesize that this result is largely driven by high environmental variability in Western North America, which contributes to the informativeness of the suitability models in this region, and to the similarity in stable hydrogen isotopes between eastern and western parts of North America at equivalent latitudes, which contributes to the reduction in accuracy of stable istope-based assignments in species with cross continental distributions (Hobson & Wassenaar 2008). We acknowledge that the differences in accuracy

between the methods assessed herein is in part a due to the cross-continent distribution of our study species, the Wilson's warbler, which poses particular challenges for stable istope-based analysis and that more data are needed to assess the genralizability of our accuracy findings across other migratory systems. Overall, our result supports the idea that while genetic data provide the most accurate method for tracing the origins of species with as much genetic diversity as the Wilson's warbler, there is value in combining all three methods.

While the development of our new R-package, GAIAH, has streamlined the process of data integration, there remain a number of ways to improve upon population assignment methods using intrinsic markers. For example, the power of genetics for population assignment demonstrated herein is part due to the fact that our genetic inferences are based upon 96 variables (corresponding to the 96 SNPs), while our isotope inferences are based on a single variable (hydrogen isotopes). In the future, the combination of multiple stable isotopes (e.g. carbon, nitrogen, sulphur) into a multivariate assignment framework could improve the accuracy of single isotope-based assignments as has been demonstrated in numerous other taxa (Sellick *et al.* 2009; Hobson, Møller & Van Wilgenburg 2012b; García-Pérez & Hobson 2014; Veen *et al.* 2014). At the same time, it is now routine to screen hundreds of thousands of SNP markers with similar levels of effort which could simultaneously increase the power of genetic-based assignments (Andrews *et al.* 2016).

In addition, our results indicate that it remains difficult to identify individuals originating from the region spanning from Alaska to Alberta. This may be due in part to the absence of precipitation stations needed for the construction of high-resolution isoscapes and habitat suitability models in this region and/or to the limited number of genetic samples from across the same area. Thus, in the future, all three methods could be improved with additional environmental and genetic sampling. Lastly, significant improvements to all three methods could be made by constraining assignments to smaller geographic areas within a species range using prior information from band returns or morphometrics (Hobson *et al.* 2009; Van Wilgenburg & Hobson 2011). For example, in the case of Wilson's warblers migrating through Cibola, AZ, assignments could be constrained to the western breeding region based upon an absence of eastern breeders in band return records from this region. While restricting assignments to the western region would significantly increase the accuracy of all three methods, it would have the biggest impact on stable isotope-based assignments because of similarity in stable hydrogen isotopes in eastern and western regions at the same latitude and the strong latitudinal effect on $\delta^2 H_p$.

It is important to note that our results are based upon a single species and one might wonder whether they are limited to Wilson's warblers or whether they will be applicable across other migratory systems. While we do not have the data herein to test the generality of the differences in accuracy between the three methods in species beyond Wilson's warblers, there are cases where assignments based on genetic data will not

perform as well, and cases where assignments based on stable isotopes and habitat suitability models will perform better. For example, genetic-based assignments will perform worse when genetic variation changes more gradually as a function of geographic distance (i.e. isolation-by-distance) rather than being separated into discrete groups as in the case of the Wilson's warbler. This may occur in species that underwent range expansions out of a single glacial refugium and are not under strong selection for local adaptation. In these cases, it would be possible to construct the genetic posterior matrices, $\mathbf{M}_i^{\text{gen}}$, by using an assignment approach designed to deal with continuous spatial data (Wasser *et al.* 2004; Rañola, Novembre & Lange 2014). Such an approach is implemented in the package IsoScat (Rundel *et al.* 2013), but could be improved by incorporating a genetic model that allows for allele frequencies to change non-linearly with geography (e.g. Rañola, Novembre & Lange 2014). There are also examples of situations where stable isotopes alone provided more accurate assignments than in the case of the Wilson's warbler. For example, stable isotopes have stronger power in delineating the origin of migratory species with geographic distributions that span large latitudinal gradients with little longitudinal variation. Examples of migratory birds in North America that have been shown to be particularly well suited to stable isotope analysis include, the black-throated blue warbler, *Setophaga caerulescens* Golden-winged Warblers, *Vermivora chrysoptera* and the black-and-white warbler, *Mniotilta varia* (Chamberlain *et al.* 1996; Rubenstein *et al.* 2002; Paxton & Moore 2015; Streby, Andersen & Buehler 2016). In conclusion, future work in will reveal the extent to which the genetic-based assignments in species without strong population structure can be used in combination with stable isotope and habitat suitability-based assignments in species whose ranges span regions of high stable isotope and environmental variability.

DEMONSTRATION OF THE UTILITY OF THE COMBINED APPROACH

We demonstrated the utility of the combined method by assigning 686 Wilson's warblers migrating through Cibola, AZ during the spring of 2008 and 2009, back to their most probable breeding destination. The results identify previously undetected patterns in the timing of migrants en route to the Pacific Northwest, with Wilson's warblers en route to more southern locations in Northern California migrating through earlier than birds en route to more northern locations near the Washington, British Columbia boarder (Fig. 4b). These results were consistent across years and further corroborate similar patterns of leap-frog migration in western Wilson's warblers identified in previous work on a much coarser continental scale (Clegg *et al.* 2003; Paxton *et al.* 2007, 2013; Rundel *et al.* 2013). Interestingly, similar leapfrog patterns were not seen in migrants en route to breeding regions ranging from Alberta to Alaska (Fig. 4), but is not clear whether this is due to a lack of resolution in the markers or the lack of a leap-frog pattern in this region. In addition, similar leapfrog patterns were also not observed within the California population where genetic

resolution was high and stable isotopes provided the second most informative measure of the true location of reference birds. Overall these data illustrate the power of the combined approach for identifying fine-scale patterns in migratory behavior which have not been detected using any other methodology to date.

RECOMMENDATIONS FOR FUTURE MIGRATORY-CONNECTIVITY STUDIES

Our results suggest that if time and money is not a limiting factor then there is utility in combining all three approaches. However, because high-resolution genetic markers alone provide a nearly optimal estimation of assignment accuracy without the need for additional data sources, researchers that are working on species with as much population genetic structure as the Wilson's warbler and that have access to the necessary genetic tools should consider investing in genomic approaches. The utility of SNP-based approaches for population assignment will be most apparent when high volumes of samples are to be screened because at that point the per individual cost of screening becomes less. Furthermore, once a basemap of genetic variation across geographic space (i.e. a genoscape) has been produced, it can be used for many other purposes such as the identification of biologically meaningful population boundaries, studies of introgression, hybridization, parentage, kinship and effective population size (Andrews *et al.* 2016; Garner *et al.* 2016). That being said, it is important to recognize that the development of high-resolution genetic markers requires substantial initial investments in highly trained personnel able to process genome-wide data, as well as in sequencing and reagent costs. In contrast, there are a number of aspects of stable isotope and habitat suitability-based approaches that make them more widely applicable and cost effective. First, the technical expertise required to implement stable isotope-based methods is less because of the accessibility of reputable isotope labs that are able to routinely process samples using a comparative equilibrium approach (Wassenaar & Hobson 2003). Furthermore, the fact that habitat suitability models can be constructed using freely available records of animal locations (in this case from eBird) and associated environmental variables makes them the easiest to implement of all three methods and we recommend their incorporation whenever possible. Second, unlike genoscapes which will differ depending upon the natural history of the organism and must be created from scratch for each new species, isoscapes and habitat suitability models are more easily transferable across species because their construction is dependent upon known biogeochemical processes (temperature, relative humidity, rainfall, etc) common across landscapes. Lastly, as mentioned above, there are numerous examples were isotope-based methods will preform better than in the case of the Wilson's warbler and in these cases the combination of habitat suitability models and multiple stable isotopes analyzed in a multivariate framework may provide an appropriate level of resolution for the questions at hand. In conclusion, while it is hard to understate the power of SNP-based approaches for population

assignment in species with similar levels of population structure to the Wilson's warbler, researchers must consider the biology of the organism, the number of samples to be screened, and the other potential uses of the resulting genetic data when considering an investment in genome-wide methods for studies of migratory connectivity.

Conclusions

Identifying the population of origin of migratory animals using intrinsic-marker techniques is now feasible at increasingly small spatial scales. Here, we show that genetic assignments far outweigh the accuracy of assignments based on stable isotopes or habitat suitability models alone in species with similar levels of population structure to the Wilson's warbler. Thus, when logistically possible, the inclusion of all three data sources (genetics, stable isotopes and habitat suitability) can serve to refine genetic-only estimates. As in the case of the Wilson's warbler, the combination of all three sources of data can reveal previously undetected patterns in the timing of migratory events. Overall, initial (seemingly large) investments in developing high-resolution genetic markers must be weighed on a case-by-case basis, but undoubtedly provide a high return on investment for heavily managed species or species for which high volumes of samples are to be screened. Our results provide methodological recommendations and a framework for analysis that can be used to facilitate future advances in the field of movement ecology including the discovery of new migratory pathways and cryptic migratory species, as well as the tools necessary to manage declining taxa in the face of rapid ecological changes.

Authors' contributions

Acknowledgements

Data accessibility

The methods introduced in this paper are implemented in the R package GAIAH (https://CRAN.R-project.org/package=gaiah) which also includes the data. The R package and additional scripts to recreate all the results in this paper are archived with Dryad https://doi.org/10.5061/dryad.sv8n7 (Ruegg *et al.* 2017).

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Supporting Information

Details of electronic Supporting Information are provided below.

Supporting Information 1. A file that includes the following:

Fig. S1. Posterior probabilities of assignment of all individuals in the reference set of birds to regions based upon high-resolution SNP-based markers.

Fig. S2. Habitat suitability model for the Wilson's warbler based upon eBird data.

Fig. S3. The effect of different weighting schemes for isotopes and habitat suitability (values of β_{iso} and β_{hab}) on the posterior mean great circle distance (pmgcd) to the true location with and without genetics. Each point shows the average pmgcd over all birds from the indicated region.

Solid lines indicate inferences without genetic data. Dashed lines indicate the inclusion of the genetic data. The figure demonstrates that when genetic data are included, the accuracy is relatively unaffected by changing the weight schemes on isotopes and habitat suitability. Without genetics, the weighting schemes for isotopes and habitat suitability yield different pmgcd, but not consistently over the different regions.

Table S1. Environmental variables and their contribution to full species distribution model for Wilson's warbler.

Supporting Information 2. A file containing 367 figures like those in Fig. 1, one for every bird in the reference dataset.

Supporting Information 3. Equations describing the parametric bootstrap for calculation of isotope posterior probabilities.