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Integrating structured and unstructured citizen science data to improve wildlife population monitoring

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7 Abstract

3

8 Accurate and robust population trend assessments are key to successful biodiversity

9 conservation. Citizen science surveys have provided good evidence of biodiversity declines

10 whilst engaging people with them. Citizen scientists are also collecting opportunistic biodiversity

11 records at unprecedented scales, vastly outnumbering records gathered through structured

12 surveys. Opportunistic records exhibit spatio-temporal biases and heterogeneity in observer

13 effort and skill, but their quantity offers a rich source of information. Data integration, the

14 combination of multiple information sources in a common analytical framework, can potentially

15 improve inferences about populations compared to analysing either in isolation. We combine

16 count data from a structured citizen science survey and detection-nondetection data from an

17 opportunistic citizen science programme. Population trends were modelled using dynamic N-

18 mixture models to integrate both data sources. We applied this approach to two different

inferential challenges arising from sparse data: (i) the estimation of population trends for an areasmaller than a structured survey stratum, and (ii) the estimation of national population trends for

21 a rare but widespread species. In both cases, data integration yielded population trajectories

similar to those estimated from structured survey data alone but had higher precision when the

23 density of opportunistic records was high. In some cases this allowed inferences about

24 population trends where indices derived from single data sources were too uncertain to assess

25 change. However, there were differences in the trend magnitude between the integrated and the

standard survey model.

27 We show that data integration of large-scale structured and unstructured data is feasible and

28 offers potential to improve national and regional wildlife trend estimates, although a need to

independently validate trends remains. Smaller gains are achieved in areas where uptake of

30 opportunistic recording is low. The integration of opportunistic records from volunteer-selected

31 locations alone may therefore not adequately address monitoring gaps for management and

32 policy applications. To achieve the latter, scheme organisers should consider providing

33 incentives for achieving representative coverage of target areas in both structured and

34 unstructured recording schemes.

35 Keywords: biodiversity monitoring; breeding bird survey; Citizen science; population trend;36 data integration;

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37 **1 Introduction**

38 The ability to accurately and robustly quantify species' population trajectories is key to 39 successful biodiversity conservation. Monitoring of changes in a species' population size or 40 range is essential to assess threat status; to act as an early-warning signal of population declines; 41 for conservation resource prioritization; and to assess the efficacy of environmental policies 42 (Lawton 1993; Johnston et al. 2015). Yet, most wildlife populations cannot be completely 43 enumerated, or even robustly surveyed, because resources for monitoring are finite. Large 44 geographic biases exist in monitoring effort even for well sampled taxa like birds (Meyer et al. 45 2015, 2016; Amano, Lamming & Sutherland 2016). This affects our knowledge of species 46 distributions, as well as our understanding of the processes underlying population dynamics 47 because potential drivers, such as climate or land-use change, can differ between surveyed and 48 unsurveyed regions (Pearce-Higgins et al. 2015). 49 National scale biodiversity monitoring schemes such as those that make up the Pan-European 50 Common Bird Monitoring Scheme (van Strien, Pannekoek & Gibbons 2001; Birdlife 51 International 2004) or the European Butterfly Monitoring Scheme (van Swaay et al. 2008, 2019) 52 are designed to provide coverage of a broad range of common species, allowing the derivation of 53 indicators of the state of nature while making the most of finite resources (Burns et al. 2018; 54 Havhow *et al.* 2019). Such high-level efforts have become closely intertwined with high-level 55 (i.e. national and supra-national) conservation legislation and policy. However, the 56 implementation of conservation policy on a legislative and executive level is increasingly 57 devolved within nations. For example, in the UK conservation is now devolved to sub-national 58 governments (NUTS 1 level) and their executive agencies, resulting in legislation and 59 implementation approaches, including e.g. red list assessments, that are specific to England,

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60	Scotland, Wales, and Northern Ireland (Bainbridge 2014; Kirsop-Taylor 2019); similarly, in
61	Germany federal conservation legislation provides an overarching legal framework but delegates
62	implementation to the states, and the executive agencies implementing state laws may be
63	devolved further to government regions (NUTS 2 level) or districts (NUTS 3 level) (Rose-
64	Ackerman 1994). There is also a shift from treating conservation and management as
65	jurisdictional issues towards more holistic approaches focussed on the maintenance of healthy
66	ecosystems and ecosystem services at the appropriate spatial scales (Kirsop-Taylor 2019). Apart
67	from individually designated large protected areas (e.g. national parks, protected landscapes),
68	such approaches are promoted e.g. through the European Landscape Convention and within
69	programmes of the EU common agricultural policy (Lomba et al. 2014). Again, the
70	implementation varies among signatory states. Within the UK such natural subdivisions are
71	reflected, for example, in the National Character Areas in England (Natural England 2014) or the
72	Area Statements in Wales (Welsh Government 2017), both of which are based on a combination
73	of landscape features, bio- and geodiversity, and socio-economic activity. The plethora of spatial
74	units that arise from jurisdictional devolution and landscape-centric approaches, creates an
75	increasing desire to repurpose data from national biodiversity monitoring schemes to provide
76	information at smaller spatial scales, not addressed by national trends and indicators.
77	Many national biodiversity monitoring schemes are based on long-term structured surveys,
78	which use predetermined monitoring sites and standardized survey methods. Structured surveys
79	provide robust estimates of population trends but require large and long-term commitments by
80	institutions – and where conducted as citizen science schemes, volunteers – and can be
81	challenging to organize and coordinate (Schmeller et al. 2009). Instead, projects which rely on
82	opportunistic records by interested members of the public may be a more effective means to

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83 increase the spatio-temporal coverage of distribution and abundance data (Dickinson, 84 Zuckerberg & Bonter 2010; Isaac & Pocock 2015). Although such projects may have primary 85 goals other than monitoring, e.g. raising awareness about focal taxa or facilitating personal 86 record keeping for naturalists, there is increasing interest in using such schemes to fill knowledge 87 gaps in regions that are poorly or not at all covered by structured surveys, and as a basis to obtain 88 indices of population trajectories that meaningfully capture true wildlife population trends (Kéry 89 et al. 2010; Isaac et al. 2014; Horns, Adler & Sekercioğlu 2018). Trend modelling based on such 90

data is challenging because of known biases in site selection, visit timing, survey effort, and/or

91 surveyor skill (Isaac & Pocock 2015; Johnston et al. 2018, 2020). Thus, there is usually a trade-

92 off between collecting a small amount of higher 'quality' data conforming to a defined common

93 structure or a larger amount of relatively heterogeneous (i.e. lower 'quality') data (Gardiner et al.

94 2012; Bayraktarov et al. 2018).

95 The consequences of this trade-off are a topic of active research (Aceves-Bueno *et al.* 2017; 96 Bayraktarov et al. 2018; Kelling et al. 2018; Specht & Lewandowski 2018; Boersch-Supan, 97 Trask & Baillie 2019; Johnston et al. 2020; Robinson et al. 2020), and there is a growing set of 98 modelling approaches to address the challenges of unstructured datasets using auxiliary 99 structured biodiversity data and/or observation models that account for preferential sampling, 100 usually at the cost of increased model complexity and computational demands (van Strien, van 101 Swaay & Termaat 2013; Fithian et al. 2015; Robinson, Ruiz-Gutierrez & Fink 2018; Isaac et al. 102 2019; Johnston et al. 2019, 2020).

103 Other recent work has investigated whether relatively simple models are sufficient to extract

104 population trend information from less structured data (Roberts, Donald & Green 2007; Roy et

105 al. 2012; Walker & Taylor 2017; Boersch-Supan et al. 2019). These simpler approaches

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- 106 generally rely on the assumption that the information gain from a larger quantity of records
- 107 outpaces potential biases from opportunistic sampling.
- 108 However, integrating these two data sources may help overcome some of these issues, by
- 109 combining the structure of survey data with the improved coverage of less structured schemes.
- 110 This has the potential to improve the precision of model parameters and the resulting inferences
- 111 (Fithian *et al.* 2015; Isaac *et al.* 2019), perhaps especially for species that are poorly covered by
- 112 structured monitoring programmes, as well as offering a route to gain a more mechanistic
- 113 understanding of the drivers of those population dynamics.
- 114 In the UK, biological recording by volunteers provides information on the occurrence or
- abundance of over 10000 taxa, although records are sparse for the vast majority of taxa (Roy et
- 116 *al.* 2014; Hayhow *et al.* 2019; Outhwaite *et al.* 2020). As part of these efforts, comprehensive
- 117 structured bird monitoring is undertaken through the Breeding Bird Survey (BBS; Figure 1)
- 118 which provides population trends for about 120 common and widespread bird species
- 119 (Greenwood et al. 1995; Freeman et al. 2007; Harris et al. 2018), but knowledge gaps remain for
- 120 rare and cryptic species (approximately 220 species are regular breeders (Robinson 2010)).
- 121 Opportunistic citizen science recording schemes such as BirdTrack (Figure 1;
- 122 www.birdtrack.net; Baillie et al. (2006); Newson et al. (2016)) provide greater coverage in space
- 123 and time, but lack the structured protocols and formal sampling design. A recent comparison of
- 124 these two datasets showed that national-scale annual reporting rate trends in BirdTrack were
- 125 broadly consistent with BBS abundance trends for common species, and those exhibiting marked
- 126 population changes (Boersch-Supan et al. 2019). However, the magnitude of reporting rate-
- 127 abundance relationships were inconsistent across species, and agreement in trends for rarer

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species could not be ascertained, in part because of high uncertainty about population change intrends from either dataset.

130 In this study, we leverage the spatio-temporal overlap of two citizen science schemes to 131 investigate the utility of joint analyses of structured and opportunistic datasets to derive 132 population trends for uncommon breeding birds at regional and local scales. This has the 133 potential to address a gap in currently available monitoring products with high relevance for 134 landscape management. In particular we evaluate integrated trend models for two different 135 inferential challenges: (i) the estimation of population trends for areas smaller than a BBS 136 stratum to improve small-area inferences about population trends for local managers and 137 decision makers, and (ii) the estimation of national population trends for a rare but widespread 138 species to assess the utility of data integration when a species is not widespread enough to fulfil 139 minimum sample size criteria for the structured survey model.

140 2 Materials and Methods

141 **2.1 Data sources**

142 We employed structured survey data from the Breeding Bird Survey (BBS) (Gregory, Baillie & 143 Bashford 2000; Harris et al. 2018), which follows a rigorous protocol in which skilled volunteers 144 count all birds heard or seen in three distance bands along two 1km transects within a 1km² site 145 on two annual morning visits during the breeding season. The two visits are not designed a priori 146 as replicates, but rather ensure coverage of both early breeding residents and later breeding 147 migrants. The early visit takes place April to mid May, and is followed by a late visit in mid May 148 to June. BBS provides a spatial coverage which is extremely high for a national monitoring 149 scheme (1.10-1.65% of the UK territory for the study period (Harris et al. 2018)), and sampling

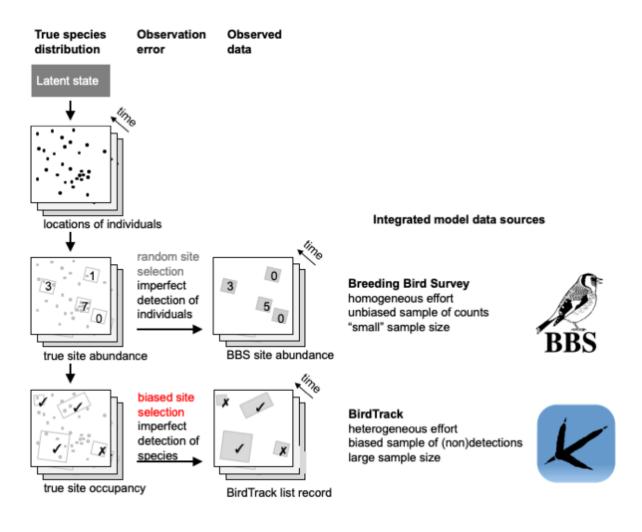
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150 is largely unbiased with respect to habitat types (with the exception of mountainous areas)

151 (Martay et al. 2018). The survey follows a stratified random design which aligns coverage with

- 152 variable volunteer availability. Coverage within strata ranges from 0.1% to 9%. This allows an
- 153 unbiased assessment of UK-wide and national trends for many common species, but the survey
- 154 was not designed to allow for inferences at sub-stratum level, or to provide reliable coverage of
- 155 rare species.



156

- 157 Figure 1: BBS surveys and BirdTrack lists are both observations of the true spatio-temporal distribution of birds.
- 158 Observations from each scheme differ in their information quality and quantity. BBS counts are collected with 159

known effort and spatially unbiased, but comparably sparse. BirdTrack lists are more numerous, but come from non-160

random locations and effort is heterogeneous. Figure adapted from Isaac et al. (2019).

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161 Structured data were supplemented with records from BirdTrack (Newson et al. 2016), which is 162 also a citizen science dataset, but with less stringent observation requirements and a wider range 163 of participants than the BBS: last year 2766 volunteers contributed to BBS whereas 6869 164 individuals submitted at least one BirdTrack list. BirdTrack participants contribute lists of 165 species they have detected during a self-selected time interval spent at a self-selected location. 166 Compared to the BBS there are about three times as many locations (i.e. 1km British National 167 Grid squares) in the UK that have at least one BirdTrack record during the breeding season in 168 recent years (Figure S1). However, the relative density of records for both schemes follows a 169 similar large-scale pattern: Coverage is higher near urban centres and lower in less populated and 170 more mountainous areas (Boersch-Supan et al. 2019; Darvill et al. 2020). On smaller spatial 171 scales the site-selection biases in BirdTrack are complex. Broadly speaking, sites fall into two 172 clusters: sites that are convenient to access, e.g. in the vicinity of participants' homes, and more 173 distant sites that offer more diverse bird assemblages (Johnston et al. 2020). 174 We only considered timed complete BirdTrack lists, i.e. lists for which birdwatchers recorded a 175 start and end time and reported that they had listed all detected species. To match the spatial 176 grain and temporal extent of the BBS data we only used lists with a location precision of 1km 177 collected from 01 April to 30 June of each year. The resulting dataset constitutes detection/non-178 detection data with biases associated with self-selection of sites and visit timings. Finally, we 179 filtered available data to retain only locations which had lists in three or more years, and within a 180 year we randomly sub-sampled lists from locations that had more than 25 visits.

181 **2.2 Modelling approach**

182 We used a state-space modelling approach to integrate data from BBS surveys and BirdTrack
183 lists [Isaac *et al.* (2019); Supplementary Materials]. The model assumes an underlying biological

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184	process describing species-specific abundances $N_{j,t}$ at a site j in every year t, and their changes
185	from year to year as a result of individuals that survive and remain at each site, and those that are
186	gained to a site by recruitment or immigration. Following Zipkin et al. (2017) we link this
187	process model to the count and detection-nondetection data with a separate observation model
188	for each data source: a dynamic N-mixture model for the count data and a dynamic occupancy
189	model for the detection-nondetection data (Figure S2).
190	Model parameters were estimated in a Bayesian framework using JAGS via the jagsUI package
191	in R (Plummer 2003; Kellner 2018; R Core Team 2018). Markov-chain Monte Carlo (MCMC)
192	estimation was run on four parallel chains until the Gelman-Rubin convergence diagnostic \hat{R}
193	indicated convergence, usually after 10,000-50,000 iterations.
194	We stratified the modelled sites based on prior information on site occupancy pre-dating the BBS
195	and BirdTrack data from the 1988-1991 Bird Atlas (Gibbons, Reid & Chapman 1993). Sites that
196	fell into occupied tetrads (2km x 2km squares) in the Atlas were assigned a positively-biased
197	normal prior truncated at zero for the initial abundance $N_+(5,10)$, and sites that fell into
198	unoccupied or unsurveyed tetrads were assigned a zero-biased normal prior, truncated at zero,
199	i.e. a half-normal prior $N_+(0,10)$.
200	Population trajectories from integrated models were compared to relative abundance indices
201	derived from BBS data alone using the standard BBS trend model, a survey weighted count
202	model with fixed additive site and year effects (Freeman et al. 2007) (Supplementary Methods)

and occupancy indices derived from dynamic occupancy models using BirdTrack data alone

which closely mirrored the structure of the integrated model (Kéry *et al.* 2010).

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205 **3 Case studies**

206 3.1 Improving small-area trends

207 The motivation for this case study was to assess the utility of data integration to draw inferences 208 about population trends areas smaller than a BBS stratum. We chose the Corn Bunting Miliaria 209 *calandra* as the focal species (Figure 2), a lowland farmland bird whose dramatic decline in 210 range and abundance in the UK has made it a red listed species of conservation concern (Eaton et 211 al. 2015) and the target of management interventions (Perkins et al. 2011). We fitted integrated 212 models for two areas to contrast different levels of recording coverage: the South Downs 213 National Character Area of southern England which has an expanse of c. 1.000 km ² (Figure 214 S3), and a similar sized area largely dominated by arable farmland in North East Scotland 215 (Figure S4). The South Downs are close to major conurbations and are well covered by 216 BirdTrack records from recreational birdwatchers; recording in North East Scotland occurs at 217 much lower rates (Figure 2).

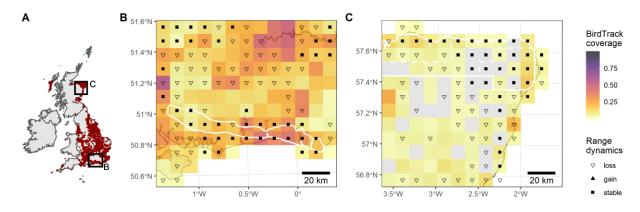


Figure 2: A: The range of Corn Bunting in Great Britain and Ireland 2007-2011. B: The South Downs NCA (white outline) is well covered by BirdTrack observations. C: Farmland in the NE of Scotland is poorly covered by BirdTrack observations. Coloured squares indicate BirdTrack list density. Grey squares lack BirdTrack lists.
 Symbols indicate Corn Bunting status based on the 2007-2011 Bird Atlas. White outlines show the spatial domain of the integrated models.

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224 **3.1.1** Species-specific model details

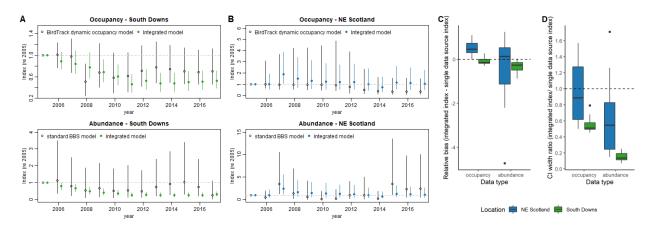
- 225 Survival and colonisation rates were separately estimated within each stratum (occupied,
- unoccupied, unsurveyed) as a yearly random effect, using an informative Beta prior (mean 0.58,
- variance 0.24) based on a mark-recapture estimate of survival probability (Luebcke 1977).

228 **3.1.2 Results**

- 229 Single data source trend models and the integrated trend could be derived for the South Downs
- 230 NCA. Because of the lower density of records in both schemes in north east Scotland, some or
- all trend models failed to fit for the two areas with the highest density of BirdTrack lists that
- were of equal size to the South Downs NCA. Model fitting was successful when using records
- from an area spanning Elgin to Peterhead, approximately three times the size of the South Downs
- NCA (Figure 2, Figure S4).
- 235 For both areas the trend estimates from the joint model did not differ substantially from
- 236 occupancy changes derived from BirdTrack or abundance changes derived from BBS alone,
- respectively. All models for the South Downs NCA showed a range and abundance decline
- between 2005 and 2011 followed by a period of relative stability (Figure 3A), and the models for
- 239 North East Scotland yielded highly uncertain abundance and occupancy trends, neither of which
- 240 provided statistically significant evidence of change since 2005 (Figure 3B).

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242 Figure 3: Occupancy and abundance trend estimates for Corn Bunting in the South Downs (A, green) and NE 243 Scotland (B, blue) based on single data sources (BBS or BirdTrack; open symbols) and the integrated model (BBS 244 and BirdTrack; solid symbols). Error bars show posterior 95% credible intervals. Boxplots aggregate relative bias 245 (C) and precision (D) of annual index values comparing the integrated and single data source models. 246 The integrated trend was negatively biased compared to both reference trends at both locations, 247 although point estimates for yearly index values from the integrated model were within the 248 credible intervals of each reference trend. In the South Downs credible intervals for the 249 integrated occupancy trend were about 50% as wide as those of the BirdTrack occupancy trend 250 model, and integrated abundance trend credible intervals were even narrower at about 20% of 251 those of the BBS trend (Figure 3C,D). The integrated model predicts a significant decline of 252 Corn Bunting range and abundance in the study area between 2005 and 2011. In contrast, models 253 based on either dataset alone do not allow inferences about population change given the large 254 uncertainty about annual index values. In Scotland inferential gains from data integration were 255 much more modest. The nominal precision of the integrated model results was on par with the 256 BirdTrack occupancy trend, and the credible intervals of the integrated abundance trend were 257 about half as wide as those for the BBS standard model (Figure 3C,D). 258 Aside from the inferences about range and abundance changes the integrated model also

259 provides estimates of detection parameters such as the influence of time spent recording on the

260 probability of detecting a given species (Figure 4). This is a crucial feature to assess the

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- 261 properties of unstructured observations, as observation protocols for these data are less stringent
- 262 leading to substantial heterogeneity in observer effort.

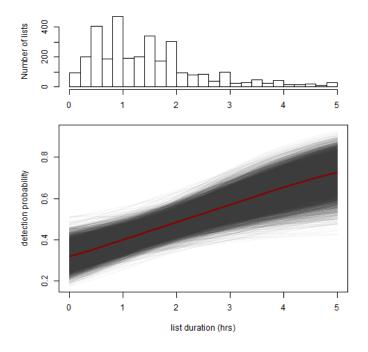


Figure 4: Detection probability of Corn Bunting in the South Downs increases with recording duration. Top:
 Distribution of BirdTrack list durations (in hours). Bottom: Estimated effect of list duration on the probability of
 detecting at least one individual. Red line shows median, grey lines show realisations from the detection model
 posterior.

268 **3.2** A rare but widespread species

- 269 The second case study assessed the utility of data integration to draw inferences about population
- trends for a species that is not widespread enough to fulfil the minimum sample size criterion for
- standard BBS reporting at the country level. We chose the Pied Flycatcher *Ficedula hypoleuca* in
- 272 Wales as the focal species (Figure S5). It is a migratory woodland bird with a distribution
- 273 restricted to upland deciduous woods in parts of western and northern Britain. It is red listed,
- both in Wales and UK wide, due to its breeding population decline over the last 25 years (Eaton
- 275 *et al.* 2015; Johnstone & Bladwell 2016).

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276 3.2.1 Results

- 277 In the relative comparison the occupancy change estimates from the joint model did not differ
- substantially from occupancy changes derived from BirdTrack alone (Figure 5).

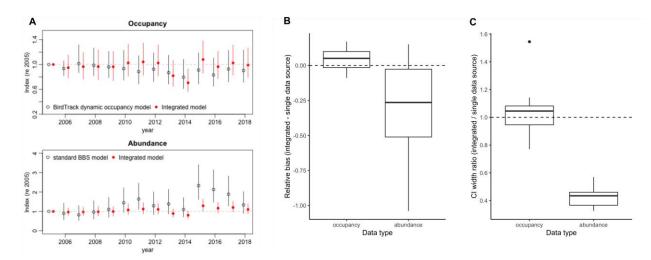




Figure 5: A: Occupancy and abundance trend estimates for Pied Flycatcher in Wales based on single data sources
(BBS *or* BirdTrack; open symbols) and the integrated model (BBS *and* BirdTrack; red solid symbols). Error bars
show posterior 95% credible intervals. B,C: Relative bias and precision of annual index values comparing the
integrated and single data source models..

The integrated abundance trend was more precise with credible intervals about 40% the width of 284 285 those of the BBS trend, however, the integrated trend was negatively biased compared to the 286 BBS trend (Figure 5 B,C). This bias was strong enough in recent years to result in diverging 287 inferences between the two models. The BBS model indicates that the Welsh Pied Flycatcher 288 population is growing, with significant gains in 2011 and 2015-2017 compared to the reference 289 year 2005. Population fluctuations indicated by the integrated trend model followed a similar 290 pattern of gains and losses but with overall smaller magnitudes of change, resulting in a 291 prediction of a stable population with no statistically significant gains or losses in any year since 292 2005 (Figure 5 A). Despite their discrepancy both of these findings are more optimistic than 293 trends observed for other humid-zone migrants in England (Morrison et al. 2013).

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294 **4 Discussion**

295 Integrated models of BBS and BirdTrack data provided realistic estimates of the regional 296 population trajectories of both bird species. In all cases the integrated trends had higher nominal 297 precision for the abundance trajectory compared to models based on structured count data alone. 298 Integrated occupancy trends were at least as precise as, or more precise than occupancy trends 299 based on unstructured detection-nondetection data alone. Bias in the trends for both species was 300 harder to assess. Population trajectories followed similar shapes, but overall effect sizes differed 301 between models. Further work is required to validate integrated trend models against existing 302 independent survey data, and to develop cross-validation strategies for evaluating integrated 303 models in the absence of independent reference data. The availability of independent reference 304 data is limited to a small number of species and regions (e.g. Stevens, Murn & Hennessey 305 (2019), Stevens, Murn & Hennessey (2020)). In part this is due to the relative recent 306 development of BirdTrack, which means that, as yet, temporal overlap with several established 307 national surveys for rare bird species (e.g. Cirl Bunting (Stanbury et al. 2010), Dotterel (Hayhow 308 et al. 2015), Hen Harrier (Wotton et al. 2018)) is insufficient for formal comparisons - a situation 309 that should improve in the future.

310 Although the BBS collects detectability data using distance sampling, this information is

311 currently not included in the calculation of routine BBS trends, as the effects of heterogeneous

312 detection on trend estimates are deemed small (Newson *et al.* 2013). However, this assumption is

313 less likely to hold for rare species. The integrated model therefore attempted to capture

- 314 observation uncertainty in structured data using an N-mixture model. Although this type of
- 315 observation model has been shown to be robust under certain field conditions (Bötsch, Jenni &
- 316 Kéry 2019), N-mixture models are known to be sensitive to violations of their assumptions,

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317 including the closure assumption (i.e. that there is no change in occupancy between survey visits) 318 (Barker et al. 2018). Given the two BBS visits are not designed as replicates this assumption 319 only holds for species with relatively unchanged detectability within the survey window. Using 320 the distance sampling data to model detectability in the BBS data would be preferable (Farr, 321 Green & Zipkin 2020), however, the corresponding observation model is computationally much 322 more demanding than the N-mixture model. Computational effort for the estimation of 323 integrated model parameters was high with the larger case study requiring model fitting times in 324 the order of 5-24 hours on dedicated scientific computing hardware with Intel Xeon E5 325 processors and ample memory. This makes model development and checking slow and may limit 326 the roll-out of this model type for routine reporting across many species and regions. 327 The expected gains from data integration will vary both depending on the target species and 328 target area. Target areas are an important consideration because sampling coverage for both 329 structured and unstructured data are not evenly distributed (Figure 6). The modelling approach 330 used for the Corn Bunting case study performed well in the South Downs because this area has 331 good BBS coverage and exceptional BirdTrack coverage. In North East Scotland low coverage 332 from BBS and very low coverage from BirdTrack made it impossible to fit some or all trend 333 models for an area equivalent to the South Downs NCA (c. 1,000 km⁻²). Model fitting did succeed when increasing the spatial domain to about 3,000 km 2 , but even then gains in 334 335 precision from the integrated approach were modest. In fact, for much of Scotland the target 336 species range does not overlap with the distribution of opportunistic sampling effort (Figure 2), 337 making it impossible to gain information from opportunistic observations e.g. about the efficacy 338 of agri-environment schemes and indicating the lower limit at which such data might inform 339 policy.

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340 Similarly, the modelling strategy used here would likely not provide gains for country-level 341 trends in Northern Ireland at the current level of BirdTrack coverage (Figure S1). Integration of 342 opportunistic records is thus not a silver bullet for closing gaps in biodiversity monitoring on 343 sub-national scales. At current levels of recording in the UK precision gains in bird trends from 344 data integration can be expected at most NUTS 1 units (e.g. countries, statistical regions of 345 England), densely settled NUTS 2 units (e.g. counties) or similarly sized landscape units such as 346 NCAs, but likely only few NUTS 3 units (e.g. unitary authorities, districts, council areas). 347 In summary, we demonstrate that integration of structured and unstructured biodiversity records 348 is in principle feasible for trend reporting at national and sub-national scale. Given the growing 349 popularity of recreational biodiversity recording, opportunistic records are available in many 350 countries which also maintain structured survey schemes, making our approach transferable 351 beyond the UK and to non-avian taxa. However our findings also highlight that addressing 352 monitoring gaps at these scales can not be solved with statistical models alone, but requires a 353 careful consideration of the most promising survey approaches: In densely populated areas 354 existing opportunistic citizen science schemes may provide a relatively easy solution to fill 355 information gaps, but elsewhere information gains require steering the observation efforts in both 356 opportunistic (see e.g. Callaghan et al. (2019b), Callaghan et al. (2019a)) and structured 357 schemes, as is done e.g. for the BBS by targeted efforts to increase observer coverage of 358 mountainous survey strata (Darvill et al. 2020). Birds are disproportionally well covered by both 359 structured and unstructured schemes within the UK and globally (Amano et al. 2016; Sorte & 360 Somveille 2020). Given the generally lower coverage of non-avian taxa by structured surveys, 361 the potential for relative information gain from opportunistic schemes is expected to be much 362 larger. At the same time, our findings imply that scheme design considerations are likely even

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more important for these taxa to ensure that spatially biased and/or heterogenous coverage from
opportunistic observations at national and sub-national scales does not affect the representativity
of derived trends.

366 **5** Author contributions

367 PHBS and RAR conceived the study; PHBS led data analysis and writing with input from RAR.

368 Both contributed critically to the manuscript and gave final approval for publication.

369 6 Data availability statement

370 The BTO is committed to making data and information readily available. Data underlying this

371 study are available by making a direct request to datarequests@bto.org, or through our website

372 https://www.bto.org/our-science/data/data-request-system.

373 7 Acknowledgements

374 We thank the thousands of volunteers who contribute records to BirdTrack and the BBS and past 375 and present survey organizers and staff, particularly Sarah Harris, Scott Mayson, Steve Pritchard, 376 and Andy Musgrove. BirdTrack is operated by the BTO, and supported by the RSPB, BirdWatch 377 Ireland, Scottish Ornithologists' Club, and the Welsh Ornithological Society. The 378 BTO/JNCC/RSPB Breeding Bird Survey is a partnership jointly funded by the BTO, RSPB, and 379 JNCC. This study was part funded by JNCC through the Terrestrial Surveillance Development 380 and Analysis partnership. Computations for this study used JASMIN, the UK's collaborative 381 data analysis environment (http://jasmin.ac.uk). We thank David Allen, Stephen Baillie, Alison 382 Eyres, Simon Gillings, and Paula Lightfoot for comments on earlier versions of this manuscript.

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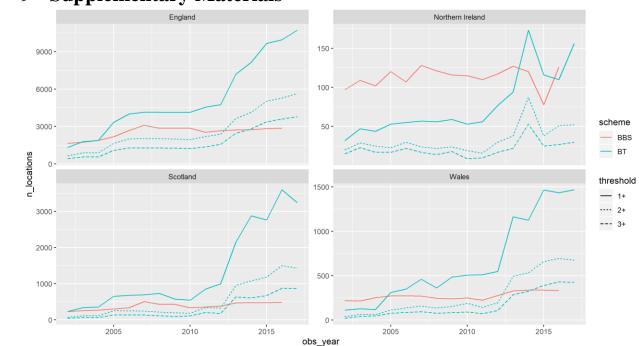
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575 9 Supplementary Materials

576

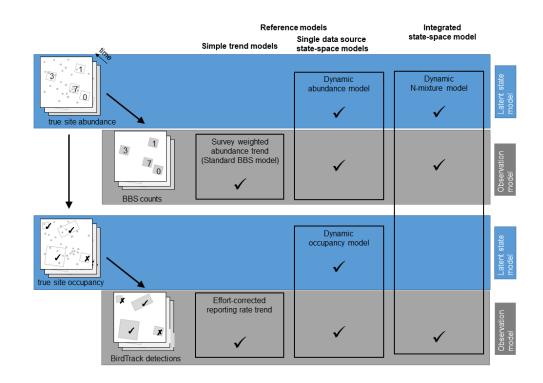
Figure S1: Opportunistic sampling coverage (measured here as annual locations with lists, solid blue line) has
greatly increased since the inception of the BirdTrack scheme and now exceeds the number of BBS plots (solid red
line) in all four countries. Revisits of locations by BirdTrack participants are relatively rare, however, with only
about half of the sites having lists in two or more years (dotted blue line), and even fewer in three or more years
(dashed blue line).

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582 9.1 Integrated Model details

- 583 We used a state-space modelling approach which models the latent biological processes of
- 584 population persistence and growth and links them to the observed data using an observation
- 585 model that accounts for imperfect detection to integrate data from BBS surveys and BirdTrack
- 586 lists (Figure S2:). This integrated model is compared to trends derived from each of the two data
- 587 sources separately. For the structured BBS data we use the statistical model that is used in the
- 588 official reporting of this survey (Freeman *et al.* 2007) as a reference model.
- 589 This is a simple trend model in that it relies on the randomised nature of the survey and does not
- 590 explicitly model the observation process. For the unstructured BirdTrack data the reference
- 591 model we use is a dynamic occupancy model which explicitly models the observation process
- 592 (van Strien *et al.* 2013). This class of models has been shown to be reasonably robust for
- 593 opportunistic biological records (Kéry et al. 2010; van Strien et al. 2013), unlike simpler trend
- 594 models (Boersch-Supan *et al.* 2019).



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Figure S2: An overview of the modelling approaches used in his study. Reference models cover a single dataset at a time and serve as a comparison with the integrated model. There are two types of reference models, simple regression models of the observations and hierarchical models that explicitly separate the biological state process (i.e. the latent population dynamics) from the observation process. Data integration relies on this conceptual separation and link the two different data sources via a common process model.

601 9.1.1 Biological process model

- 602 The state process for this model assumes there is a population abundance $N_{i,t}$ at a site j in every
- 603 time step t, which is imperfectly observed. $N_{i,t}$ changes between successive timesteps as a result
- 604 of individuals that survive and remain at each site $S_{i,t}$, and those that are gained to a site by
- 605 recruitment or immigration $G_{i,t}$. These sub-processes are expressed as

$$S_{i,t} \sim \operatorname{Bin}(N_{i,t-1},\omega)$$

$$G_{i,t} \sim \text{Pois}(\gamma)$$

- 606 where ω is the apparent annual survival probability of individuals, and γ is the expected number
- 607 of individuals that are gained at site *j* by recruitment or immigration between t 1 and *t*.
- 608 For every time step t > 1 the total population abundance at site *j* is

$$N_{j,t} = S_{j,t} + G_{j,t}$$

For the first year (t = 1), the state process is initialized by modelling abundance at each site

610 according to a Poisson distribution with an expected count λ

$$N_{j,1} \sim \text{Pois}(\lambda)$$

611 From the state model we can further derive the colonisation probability $\phi_{j,t}$ of an unoccupied 612 site as

$$\phi_{i,t} = 1 - e^{-\gamma}$$

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613 as well as the extinction probability $\epsilon_{j,t}$ as

$$\epsilon_{j,t} = (1-\omega)^{N_{j,t}} \cdot e^{-\gamma}$$

614 9.1.2 Observation model

615 The true population abundance $N_{i,t}$ in the survey area was linked to the data according to two

616 sampling processes, counts of individuals in the case of BBS data and detection of at least one

617 individual or non-detection in the case of BirdTrack lists. In both cases repeat visits to a site

618 between April and the end of June were treated as replicates, implying the assumption of a

- 619 closed population over this period, which we deemed reasonable for the species covered.
- 620 We assumed detection was imperfect for both sampling approaches, i.e. for count data the

621 number of individuals encountered during a survey visit $n_{j,t,k} \le N_{j,t}$ and similarly, an occurrence

622 record $y_{i,t,k}$ could be a nondetection if none of the $N_{i,t}$ individuals was seen or heard during a

623 site visit. We modelled the count data as arising from a binomial process

$$n_{j,t,k} \sim \operatorname{Bin}(N_{j,t},p)$$

with an individual detection probability *p*. Detection-nondetection data were modelled as arisingfrom a Bernoulli trial

$$y_{j,t,k} \sim \text{Bern}(1 - (1 - p_{occ})^{N_{j,t}})$$

626 with a separate detection probability p_{occ} , to take into account potential differences in survey 627 methodology and/or observer skill between BBS and BirdTrack records.

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628 9.2 Reference Trends

629 9.2.1 BBS abundance trends

630 Abundance models for BBS data followed the Poisson GLM approach employed in the official

- BBS trend production (Freeman *et al.* 2007), which models the mean local count λ_{it} at site *i* and
- 632 year t based on the observed maximum counts $y_{obs,it}$ across the two survey visits as a function
- 633 of fixed additive site and year effects β_i and β_t , respectively.

$$y_{obs,it} \sim Poisson(\lambda_{it})$$

$$log(\lambda_{it}) = \beta_i + \beta_t.$$

- 634 Abundance indices are derived from the conditional year effects β_t . For BBS data we further
- 635 used sampling weights equal to the inverse inclusion probability of a site within a stratum for a

636 given year – to account for uneven monitoring coverage among BBS survey strata.

637 Parameter inference was conducted in a Bayesian framework using a weighted likelihood

- 638 approach as implemented in the brms package (Bürkner 2018), rather than following the
- 639 bootstrapping approach of Freeman *et al.* (2007).

640 9.2.2 BirdTrack Dynamic Occupancy models

641 Occupancy trends from BirdTrack data were modelled using a dynamic site occupancy model

642 (Kéry *et al.* 2010; van Strien *et al.* 2013) which closely mirrored the structure of the integrated

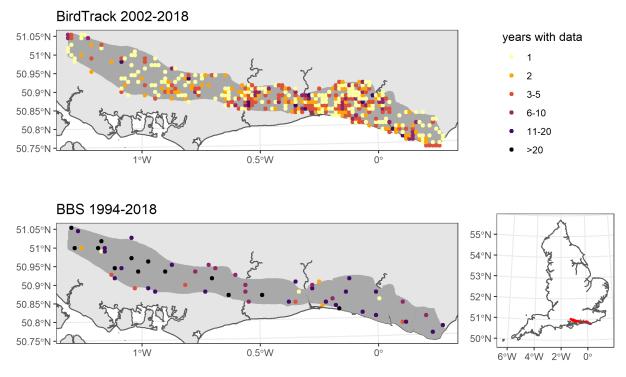
- 643 model. The latent state $N_{i,t}$ becomes a binary indicator of occupancy in these models, and initial
- 644 occupancy $N_{i,1}$ and the immigration/recruitment process $G_{i,t}$ were modelled as a Bernoulli

645 processes.

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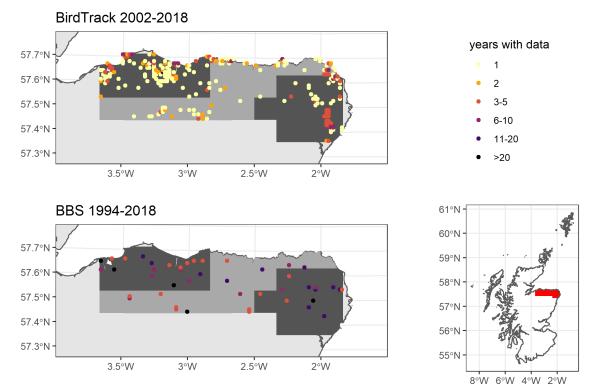
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646 9.3 Data details



647

648 Figure S3: The study area for the South Downs Corn Bunting case study and locations of BBS surveys and complete649 BirdTrack lists.

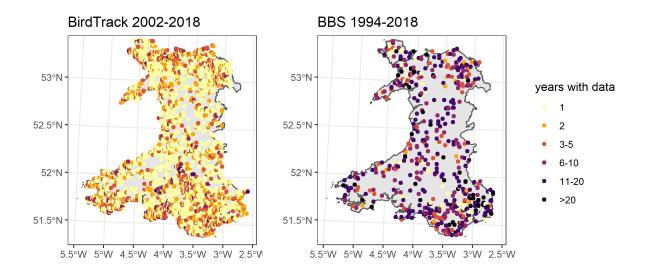


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651 Figure S4: The study area for the Scottish Corn Bunting case study and locations of BBS surveys and complete

652 BirdTrack lists. Both dark shaded areas are approximately the same size as the South Downs NCA (Fig. S3), but 653 data were to sparse in both to fit the integrated and/or references models. Model fitting succeeded when using 654 records from the dark and medium grey shaded areas.



655

656 Figure S5: Top: The study area for the Pied Flycatcher case study and locations of BBS surveys (n=519) and 657 locations of complete BirdTrack lists (n=1034). Bottom: Time-series of the number of locations with BBS surveys 658 and complete BirdTrack lists (solid) and locations with positive detections of the target species (dashed).

9.4 Model code examples 659

9.4.1 BBS survey weighted trend models 660

```
661
      #BBS survey trend using maximum likelihood estimation with survey weights
662
      library(survey)
663
      bbs_design <- svydesign(ids = ~1, weights = ~weight, data = bbs_counts)</pre>
664
      bbs trend <- syglm(count \sim year factor + square, design = bbs design,
665
      family=poisson)
666
667
      #BBS survey trend using Bayesian weighted likelihood approach
668
      library(brms)
669
      bbs trend brms <- brm(count weights(weight, scale = TRUE) ~ year factor +
670
      square - 1, data = bbs pf counts, family = poisson)
671
      9.4.2 BirdTrack dynamic occupancy model JAGS code
```

```
672
      model{
673
          #Priors
674
            lambda ~ dnorm(0,0.2)T(0,) # initial abundance -half normal prior
675
            p \sim dbeta(2, 2) # detection # use beta prior centred on 0.5 since
```

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```
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```

```
676
      we know detectability is ok
677
678
             omega intercept ~ dnorm(0,0.1)# survival intercept
679
             gamma intercept ~ dnorm(0, 0.1)# colonisation intercept
680
             tau <- 1/pow(sigma, 2)</pre>
681
             sigma ~ dt(0, pow(2.5,-2), 1)T(0,)#half-cauchy prior following
682
      https://arxiv.org/pdf/0901.4011.pdf
683
             tau_gamma <- 1/pow(sigma_gamma, 2)</pre>
684
             sigma_gamma ~ dt(0, pow(2.5, -2), 1)T(0,)#half-cauchy prior following
685
      https://arxiv.org/pdf/0901.4011.pdf
686
687
             for(t in 2:nYears){
688
               logit(omega[t-1]) <- omega_intercept + omega_raneff[t-1]</pre>
689
               omega raneff[t-1] ~ dnorm(0, tau)
690
               log(gamma[t-1]) <- gamma intercept + gamma raneff[t-1]</pre>
691
               gamma raneff[t-1] ~ dnorm(0, tau gamma)
692
             }
693
694
695
           #Likelihood - Biological process model
696
           for(i in 1:nSites) {
697
           #First year of sampling
698
           N[i,1] ~ dpois(lambda)
699
700
           #All other years of sampling
701
           for(t in 2:nYears) {
702
           S[i,t-1] ~ dbin(omega[t-1], N[i,t-1])
703
           G[i,t-1] ~ dpois(gamma[t-1])
704
           N[i,t] <- S[i,t-1] + G[i,t-1]
705
           }
706
           }
707
708
           #Detection process model for count data
709
           for (i in 1:nCount) {
710
           for (j in 1:nReps) {
711
           for (t in 1:nYears) {
712
           y_{2[i,t,j]} \sim dbin(p, N[i,t])
713
           }}}
714
715
             #derived quantities (track N total w/o using up memory for the entire N
716
      array)
717
           for (i in 1:nYears){
718
               N.total[i] <- sum(N[,i])</pre>
719
        }
720
      }
```

721 9.4.3 Joint model JAGS code for corn bunting case study

```
722 #joint model with observation covariates for corn bunting
723 model {
```

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```
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```

```
724
        #Priors
725
        lambda[1] \sim dnorm(0,0.1)T(0,) \# initial mean abundance for sites without
726
      Atlas presences
727
        lambda[2] \sim dnorm(5,0.1)T(0,) \# initial mean abundance for sites with Atlas
728
      presences
729
        lambda[3] ~ dnorm(0,0.1)T(0,) # initial mean abundance for sites not
730
      surveyed for 1990 Atlas
731
        #gamma ~ dunif(0,10) # gains
732
        for(j in 1:3){#set different baseline vital rates for different atlas
733
      categories
734
        mu_omega[j] ~ dbeta(57.4,41.2)# survival intercept using informative prior
735
      derived from Luebcke 1977
736
        gamma intercept[j] ~ dnorm(0,0.1)# colonisation intercept
737
        }
738
        p \sim dunif(0,1)
                             # detection probability prior
739
        p.occ intercept ~ dnorm(0,0.1)# intercept
740
        p.occ beta time ~ dnorm(0,0.1)# coefficient on list duration
741
        p.occ beta yday[1] \sim dnorm(0,0.1)# coefficient on list duration
742
        p.occ beta yday[2] \sim dnorm(0,0.1)# coefficient on list duration^2
743
744
        tau <- 1/pow(sigma, 2)</pre>
745
        sigma ~ dt(0, pow(2.5,-2), 1)T(0,)#half-cauchy prior following
746
      https://arxiv.org/pdf/0901.4011.pdf
747
        tau gamma <- 1/pow(sigma gamma, 2)</pre>
748
        sigma_gamma ~ dt(0, pow(2.5, -2), 1)T(0,)#half-cauchy prior following
749
      https://arxiv.org/pdf/0901.4011.pdf
750
751
752
        for(t in 2:nYears){
753
          for(j in 1:3){#site classes
754
          omega[j,t-1] ~ dnorm(mu omega[j], tau)T(0,1)
755
          gamma[j,t-1] <- gamma_intercept[j] + gamma_raneff[j,t-1]</pre>
756
          gamma_raneff[j,t-1] ~ dnorm(0, tau_gamma)
757
          }
758
        }
759
760
761
        #Likelihood - Biological process model
762
        for(i in 1:nSites) {
763
          #First year of sampling
764
          N[i,1] ~ dpois(lambda[SitePrior[i]])
765
          #All other years of sampling
766
          for(t in 2:nYears) {
767
            S[i,t-1] ~ dbin(omega[SitePrior[i],t-1], N[i,t-1])
768
            G[i,t-1] ~ dpois(exp(gamma[SitePrior[i],t-1]))
769
            N[i,t] <- S[i,t-1] + G[i,t-1]
770
          }
771
        }
772
```

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```
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```

773	
774	<pre>#Detection process model for sites with detection/nondetection data *only*</pre>
775	#dense array formulation, i.e. imputing NAs
776	<pre># for (i in 1:nSites){ # loop over state array to determine site-specific</pre>
777	Bernoulli parameters. This could be made more efficient by not calculating
778	this for all sites
779	<pre># for (t in 1:nYears){</pre>
780	<pre># p.site[i,t] <- 1-pow((1-p.occ[i,t]),N[i,t])</pre>
781	# }
782	# }
783	#loop over observations
784	for (j in 1:nOccObs) {
785	OccObs[j] ~ dbern(1-pow((1-p.occ[j]),N[OccSite[j],OccYear[j]]))
786	logit(p.occ[j]) <- p.occ_intercept + p.occ_beta_time*OccDuration[j] +
787	p.occ_beta_yday[1]*OccYday[j] + p.occ_beta_yday[2]*(OccYday[j]*OccYday[j])
788	}
789	
790	#Detection process model for sites with count data *only*
791	#looping over observations
792	for (j in 1:nCountObs) {
793	CountObs[j] ~ dbin(p, N[CountSite[j],CountYear[j]])
794	}
795	
796	
797	#derived quantities (so it's possible to track N total without using up
798	memory for the entire N array)
799	<pre>for (i in 1:nYears){</pre>
800	N.total[i] <- sum(N[,i])
801	N.occupied[i] <- sum(N[,i]>0)
802	<pre>mean_occ[i] <- mean(N[,i]>0)</pre>
803	}
804	
805	}