

Short Title: Abundance of Vinaceous-breasted Parrot (*Amazona vinacea*)

Title: Addressing multiple sources of uncertainty in the estimation of global parrot abundance from roost counts: a case study with the Vinaceous-breasted Parrot (*Amazona vinacea*)

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1 Abstract

2 Population size is a key predictor of extinction risk and is critical to listing species in IUCN
3 threat categories. Assessing population size can be particularly difficult for gregarious species,
4 such as parrots—one of the most threatened bird families—whose ecology and behavior generate
5 multiple sources of uncertainty that need to be addressed in monitoring efforts. To improve
6 estimates of abundance for the endangered Vinaceous-breasted Parrot (*Amazona vinacea*), we
7 combined extensive roost counts over the global range of the species (Argentina, Paraguay,
8 Brazil) with an intensive regional survey designed to address five sources of uncertainty about
9 parrot abundance in western Santa Catarina state (WSC), Brazil, in 2016 and 2017. We estimated
10 abundance at both regional and whole-range scales using N-mixture models of replicated count
11 data, which account for imperfect detection. The regional-scale estimate was $1,889 \pm 110$ and
12 $1,872 \pm 37$ individuals for 2016 and 2017, respectively; global abundance was estimated at $7,795$
13 ± 260 and $8,492 \pm 276$ individuals for the same two years. We found no statistical evidence of
14 population change at either scale of the analysis. Although our assessments of abundance and
15 geographic range are larger than those currently reported by the IUCN, we suggest the
16 Vinaceous-breasted Parrot should remain in the ‘Endangered’ IUCN threat category pending
17 further investigation of population trends. We recommend that roost-monitoring programs for
18 parrots consider and address sources of uncertainty through adequate field protocols and
19 statistical analyses, to better inform assessments of population size, trends, and threat status.

20 Key-words: endangered species, imperfect detection, N-mixture model, Psittacidae, roost count,
21 Vinaceous-breasted Parrot.

22

23 1. Introduction

24 Population size is arguably the most important state variable in population biology (Gaston,
25 1994); along with range size, it is the best predictor of extinction risk (Lawton, 1995) and plays a
26 central role in population management (Caughley, 1994; Norris, 2004). Abundance is directly
27 implicated in three of the five IUCN (International Union for the Conservation of Nature) criteria
28 for listing species in threat categories (Mace et al., 2008). Among the animal groups in most
29 urgent need of abundance information, parrots (Psittaciformes) stand out for having the highest
30 number of threatened species of all non-passerine bird orders (Olah et al., 2016). Of 394 extant
31 species of parrots, 117 (29%) are listed as threatened, and 81 of these are declining, according to
32 the IUCN (BirdLife International, 2020). The key causes of parrot population decline are habitat
33 loss—due to deforestation and agroindustrial expansion—, and nest poaching —due to the illegal
34 pet trade (Berkunsky et al., 2017; Olah et al., 2016; Wright et al., 2001). However, statistical
35 estimates of parrot population size remain difficult to obtain and are available for very few
36 species (Dénes et al. 2018; Marsden and Royle, 2015).

37 The globally endangered Vinaceous-breasted Parrot (VBP; *Amazona vinacea*) is
38 restricted to the Atlantic Forest biome, mostly within Brazil but with small areas of occurrence in
39 the Argentinian province of Misiones and in eastern Paraguay (Carrara et al., 2008; Cockle et al.,
40 2007; Prestes et al., 2014; Segovia and Cockle, 2012; Fig. 1). VBPs appear to be associated with
41 the ancient Paraná Pine (*Araucaria angustifolia*; Cockle et al. 2019; Collar et al., 2017; Tella et
42 al., 2016), but they also forage and nest in other trees (Bonaparte and Cockle, 2017; Cockle et
43 al., 2007; Prestes et al., 2014), and their incompletely known geographic range extends beyond
44 the current range of *Araucaria* forests (Carrara et al., 2008; Cockle et al., 2007; Collar et al.,
45 2017). As with many other parrot species, incomplete knowledge about the VBP geographic

46 range and population size results in part from movements associated with temporal variation in
47 food availability (Renton et al., 2015; Webb et al., 2014). Seasonal movements reportedly
48 coincide with the fruiting of *Ocotea puberula*, *Podocarpus lambertii*, *Vitex megapotamica*,
49 Juçara palms (*Euterpe edulis*), and *Araucaria* pines (Collar et al., 1992; Forshaw, 2010; Prestes
50 et al., 2014). Unpredictable movements make it difficult to anticipate where parrots will be, or
51 whether parrots seen in different places are the same or different individuals, presenting
52 interesting challenges to the estimation of population size. According to the IUCN, the extant
53 geographic range of the VBP covers approximately 145,700 km² (BirdLife International and
54 Handbook of the Birds of the World, 2016; Fig. 1). This range consists of five major patches
55 (>10,000 km²), and eleven relatively small patches (<1000 km²). Average distance between
56 major patch centroids is 834 ± 379 km, revealing a discontinuous VBP distribution. Such
57 discontinuity reflects not only the species' true range, but also the scarcity of information about
58 population structure and movements. Accordingly, the IUCN recently updated the range map
59 with a larger, 'possibly extant' layer that encloses all of the patches above (Fig. 1).

60 One traditional method to assess parrot abundance is to count individuals as they enter or
61 leave communal roosts, a technique used for VBP over the last two decades (Casagrande and
62 Beissinger, 1997; Abe, 2004; Coughill and Marsden, 2004; Cockle et al., 2007; Segovia and
63 Cockle, 2012). Our field observations prior to this work suggest that, as in many parrot species,
64 VBPs disperse in pairs across the species' range while courting and breeding (July–December),
65 begin congregating in communal roosts towards the end of the breeding season (December –
66 January), and may or may not continue to use these roosts throughout the entire non-breeding
67 period (until June). As a result, during the January-June non-breeding period, the number of
68 VBPs can vary from fewer than ten to hundreds of individuals, both among roosts and among

69 days at the same roost (Abe, 2004; name1, unpublished data). When August begins, there are
70 virtually no parrots left at communal roosts and the population is once again dispersed across
71 hundreds of nesting sites. Despite difficulties inherent to locating roosts and counting the number
72 of individuals, roost counts remain one of the most popular and cost-effective ways of assessing
73 the abundance of parrots (Matuzak and Brightsmith, 2007; Dénes et al., 2018).

74 Roost count design varies but always involves locating roosts, choosing the appropriate
75 time for counting, and actually counting a number that is as close as possible to the real number
76 of animals present (Casagrande and Beissinger, 1997). In order to improve knowledge of the
77 distribution and abundance of parrots from roost counts, one should approach the three tasks of
78 locating, timing, and counting in a way that minimizes the magnitude of five key sources of
79 uncertainty about the end result. Although we focus on one parrot species, the same sources of
80 uncertainty arise for researchers assessing the abundance of other gregarious species, such as
81 flamingos (Caziani et al., 2007) or bats (Mohd-Azlan et al., 2001; Walsh and Harris, 1996). The
82 first and second sources have to do with locating roosts. First, there is uncertainty about the
83 extent of the VBP's distribution. When does a gap in the range map represent true absence of the
84 species vs. absence of observations? This problem is well represented by the difference between
85 the IUCN 'Extant' and 'Possibly Extant' ranges in Figure 1. The second source is uncertainty
86 about density of roosts at the regional scale. At what point should one stop trying to find more
87 roosts to free time for studying known roosts in detail? The third source of uncertainty concerns
88 movement of individuals between roosts and constrains the timing of counts: if roosts correspond
89 to isolated local populations, different roosts could be counted at any time throughout a non-
90 breeding season. If, on the contrary, individuals move between roosts, researchers must account
91 for such movements or count parrots at multiple roosts simultaneously. The fourth and fifth

92 sources of uncertainty relate to the counting technique itself, and address, respectively, false
93 positive and false negative observations of individuals. A false positive happens when by
94 mistake a parrot is counted twice or more. A false negative happens when a parrot that is present
95 at a site is not counted because it was overlooked.

96 This paper offers an assessment of VBP abundance for the years 2016 and 2017. We
97 follow a two-pronged approach that combines data from two spatial scales, two counting
98 techniques, and two research teams. At the regional scale, we estimate the number of VBPs in
99 Western Santa Catarina/Brazil (WSC; Fig. 2) while seeking to address all five sources of
100 uncertainty listed above. We chose to focus the regional research on WSC because a) being an
101 area of intense agro-industrial activity with no previously published VBP observations, it has
102 been left out of the species' IUCN Extant map; b) it sits between two important VBP habitat
103 areas in different countries (Misiones, in Argentina, and the *Araucaria* forests of Eastern Santa
104 Catarina, in Brazil), and c) based on our previous experience, we expected to find roosts that
105 were not yet documented in WSC. At the whole-range scale, we provide a global statistical
106 estimate of the species based on counts of parrots observed in all VBP roosts known to us,
107 throughout the entire range of the species.

108

109 2. Methods

110 2.1. Whole-range sampling

111 Whole-range sampling took place over 98 sites spanning an area from northern Minas Gerais, in
112 the north, to northeastern Rio Grande do Sul, 1,500 km to the south. The area extends west to,
113 and includes eastern Paraguay, as well as the Argentinian province of Misiones (Figure 1).
114 Approximately one quarter (22) of the count sites are inside the IUCN Extant range of the VBP,

115 with the remaining three quarters (76) outside. Sites correspond to regularly-used roosts and to
116 points of frequent flyover by parrots at dawn and dusk (Supplemental Material Table S1). Our
117 research team and collaborators identified the count sites, sometimes over decades of VBP
118 observation (e.g. Cockle et al., 2007; Segovia and Cockle, 2012). All sites are located within the
119 Atlantic Forest, defined by the southeast Atlantic portion of the ‘tropical and subtropical moist
120 broadleaf forest’ eco-region of South America (Olson et al., 2001).

121 Sampling at the whole-range scale was carried out by 26 volunteer teams (Supplemental
122 Material Table S1) coordinated by name5 and name4. Counts took place in 2016 (24–26 March
123 in Argentina, 29 April to 15 May in Paraguay and Brazil) and 2017 (24 April to 15 May in
124 Paraguay and Brazil only). Each team worked in areas that were familiar to its members,
125 enabling us to cover most of the range in a short period and thus minimize the possibility of
126 double-counting between sites. Of the total 98 sites, 33 were sampled only in 2016, 30 only in
127 2017, and 35 in both years (Supplemental Material Table S1). We visited sites once per year,
128 counting parrots at the beginning or at the end of the day. Counts started at dawn (30 minutes
129 before sunrise) or dusk (90 minutes before sunset) and lasted until we could not detect parrot
130 movement into or out of the roost for 20 minutes—which always happened within two hours of
131 the beginning of the count. The number of counting posts at each site varied between one and
132 five, located at strategic points for observing movement of flying parrots in and out of the site
133 area. Each count was performed by a team of one to ten observers who registered the number of
134 parrots arriving or leaving the area, the flight direction, and the time. Whenever there was more
135 than one post in a count, observers from different posts met at the end of the count to compare
136 notes and agree on the minimum number of individual parrots seen.

137 2.2. Regional-scale sampling.

138 The regional-scale study area is the western part of the Brazilian state of Santa Catarina (WSC;
139 IBGE, 2015; Figure 2), with approximately 100 by 300 km extending West-East between the
140 Uruguay river (to the South) and the ridgeline that separates the Uruguay and Iguaçu watersheds
141 (to the North). Although mostly deforested, the area adjoins two large patches of forest habitat:
142 the Atlantic Forest of Misiones, to the west, and the *Araucaria* forests of Eastern Santa Catarina,
143 to the east (Figure 2). WSC is remarkable for having a high frequency of VBP sightings by
144 citizen scientists (Wikiaves, 2018) in an area that is almost entirely (88%) outside the IUCN
145 extant range of the species (Fig. 1). WSC falls within the *Araucaria* forest and the Interior forest
146 biogeographic sub-regions of the Atlantic Forest, which have lost, respectively, 87 and 93% of
147 their forest cover since the onset of European colonization (Ribeiro et al., 2009). Nowadays, the
148 remaining forest patches in WSC (Fig. 2) are surrounded by agro-industrial development,
149 consisting mostly of soybean (*Glycine max*), eucalyptus (*Eucalyptus* sp.), and pine (*Pinus* sp.)
150 plantations (Baptista and Rudel, 2006; Fearnside, 2001). The ten WSC sampling sites are a
151 subset of the whole-range sites. They comprise all known VBP roosts in WSC and they all
152 coincide with *Araucaria* forest patches >10 m tall. Four of the ten regional sites (*Guatambu*,
153 *Campo Erê*, *Abelardo Luz* and *Água Doce*) have very open to non-existent vegetation under the
154 *Araucaria* canopy (Fig. 2).

155 Fieldwork at the regional-scale was carried out by a single team coordinated by name1
156 and name2. Here, we performed monthly visits to each site, across two consecutive non-breeding
157 seasons: from December 2015 to July 2016, and from February to June 2017. By employing the
158 same team for all roost counts of the same month in WSC, we could control and coordinate field
159 technique much more tightly at the regional than at the whole-range scale. To avoid counting the
160 same parrots twice in different roosts during the same month, each visit was performed in the

161 shortest period possible—between four and ten days, depending on the number of roosts
162 sampled. Each roost was sampled at dusk and at dawn of the next day, allowing us to visit two
163 nearby roosts in the same twelve hour period. The shortest distance between roosts was 19 km
164 and the longest single-day displacement recorded for radio-tagged VBPs is 17 km (Prestes et al.,
165 2014). We moved between roosts at the average speed of 45 km per day; therefore, we find the
166 possibility of double counting between roosts to be sufficiently small. In all, we completed 13
167 visits to WSC, eight during 2015–2016 and five during 2017. To minimize uncertainty about
168 VBP distribution and roost density over the regional-scale, we spent one day per month
169 searching for roosts and interviewing WSC residents that we met in the field. As we discovered
170 new roosts, the number of roosts counted increased from four in December 2015 to five in
171 February 2016, eight in May 2016, and ten in May 2017 (Figure 2; Supplemental Material Table
172 S2). The *Lebon Régis* and *Entre Rios* sites, also located in WSC, were only visited during the
173 whole-range count of both years. In total, we completed 182 roost counts at the regional scale.

174 Regional-scale counts started at dusk (77) or dawn (105 counts), and lasted until we could
175 no longer detect parrot movements, following the same times and criteria as described for the
176 whole-range counts. We visited every roost before the first count to establish observation posts
177 in locations suitable for observing the arrival and departure of parrots. Each count was performed
178 by a team of three observers (one per observation post), each equipped with a roost area map, a
179 compass, an audio recorder, and a radio to communicate with team members about parrots going
180 their way. Every time an observer saw one or more VBPs, she recorded the number of
181 individuals, the time, and the direction of flight, as well as any other comments that could help
182 understand the movement of the birds. At the end of each count, the team of three observers met
183 to reconcile their notes and agree on one ‘most reasonable’ (MR) and one ‘highly conservative’

184 (HC) count result. The difference between MR and HC counts lies in how observers treat the
185 possibility of double counting. Suppose, for example, that an observer sees five parrots arriving
186 at a roost and a few minutes later sees another arrival of three individuals. Based on this
187 information, the MR count is eight individuals. Suppose further, however, that one of the
188 observers in the trio determined that there were unseen, but heard, parrots leaving the roost
189 during the time between the two observations above. In this case, the team might judge that there
190 was some, however small, possibility that the second group of three was a subset of the first
191 group of five, which had exited the roost, undetected, and returned within sight. If that were the
192 case, the HC count should be five and not eight, because five is the absolute minimum number of
193 birds that the team is sure to have seen arriving at the roost.

194 The consideration of MR and HC counts addresses one source of uncertainty about VBP
195 abundance estimates: the possibility that some animals may be counted more than once within
196 one count. A second source of uncertainty is imperfect detection, i.e. the possibility that some
197 animals are missed. To address imperfect detection, we replicated counts by working
198 simultaneously with two teams of three observers, at the same roost and time, in ten of the
199 thirteen sampling months. Simultaneous replication employed two observers (one from each
200 team of three) per post, keeping sufficient distance between observers to preclude overhearing
201 radio communications. Observers from different teams did not exchange any information about
202 their observations until each team had separately agreed on its count results. We thus treat every
203 team-specific count of a given roost and month, whether at dusk or dawn, as an independent
204 sample of that roost for that month. When working with two teams counting at dusk and dawn
205 we obtained the maximum of four replicate counts for one roost and month. Sometimes it rained
206 and other times we didn't have a second team, but we had more than one count in 90% of the

207 roost*month combinations. The crucial difference between sampling designs at the regional- and
208 whole-range scales was replication. At the regional-scale, we could afford and strove to replicate
209 counts of the same roost and month as much as possible.

210 2.3. Data analysis

211 We modeled both regional and whole-range data using an N-mixture model approach (Royle,
212 2004). N-mixture models account for imperfect detection and estimate the number of individuals
213 per site, given replicated count data. For each spatial scale, we summarized counts in an array C
214 with dimensions S by R by M , where S is the number of roost sites, R is the maximum number of
215 replicate counts per roost in any month, and M is the number of sampling months. Elements C_{ijk}
216 of this array give the number of parrots counted in the j^{th} count of the i^{th} roost in the k^{th} month,
217 with $i = 1, \dots, S$, $j = 1, \dots, R$, and $k = 1, \dots, M$. The N-mixture model represents the true number
218 N_{ik} of individuals in roost i and month k as drawn from a Poisson distribution with parameter λ_k .
219 That is, the number of individuals per roost varies according to a Poisson distribution with mean
220 λ_k , which itself varies through time. We account for imperfect detection by modeling the counts
221 C_{ijk} as the result of a binomial sample with N_{ik} independent trials and probability of success p_k .
222 In short, our models combine the biological variation of abundance among roosts with the
223 sampling process of parrot detection:

$$224 \quad N_{ik} \sim \text{Poisson}(\lambda_k)$$

$$225 \quad C_{ijk} \sim \text{Binomial}(N_{ik}, p_k).$$

226 When a roost i is not sampled in month k , we impute an estimate of N_{ik} based on the estimate of
227 λ_k for that month. Such imputation accounts for the temporal variation in effort and implies that
228 differences between abundance estimates from different months are not a result of variation in

229 the number of roosts counted. In the way we set up the analysis, this imputation is a by-product
230 of our Bayesian model fitting using MCMC methods (see below).

231 To analyze regional-scale data, we used two arrays C , of HC and MR counts, with
232 dimensions $S = 10$ sites, $R = 4$ counts, and $M = 13$ months. The first eight months correspond to
233 December 2015 through July 2016, while the last five correspond to February-June 2017.
234 Because our counts in WSC were often replicated at different times of the day, we modeled a
235 binary effect of time of day (dawn vs. dusk) on $\text{logit}(p)$, to account for possible differences in
236 visibility or parrot behavior or visibility between dawn and dusk counts. Models were fit in a
237 Bayesian framework using gamma-distributed vague priors for λ and p parameters. We
238 implemented models in the BUGS language (Lunn et al., 2000) running on JAGS (Plummer,
239 2003) with code adapted from Kéry and Royle (2016, chap. 6; Supplemental Material Appendix
240 A). Regional-scale inference is based on draws from the posterior probability distribution of
241 model parameters using an MCMC algorithm with three chains, 25,000 iterations and a burn-in
242 stage of 5,000 iterations.

243 Analysis of the whole-range data was based on the same model used for the regional
244 scale, with some adjustments to model and data structure. We organized data into an array C
245 with dimensions $S = 98$ sites, $R = 4$ counts, and $M = 2$ ‘months’. The first ‘month’ of whole-
246 range counts spans the period of late March to early May 2016, the second is May 2017. The
247 main limitation of the whole-range data is lack of replicated counts within the same site and
248 month outside WSC and one of the Misiones sites, i.e. in 87 out of 98 sites. While applying an
249 N-mixture model to such data, we rely on information from only a few sites to infer detection
250 probability everywhere else. This is not ideal but is the best we could do at present with the
251 available data. To avoid demanding too much from limited information on detection we took two

252 precautions. First, we simplified the detection model by estimating p as a constant value through
253 time, across ‘months’. Second, we included environmental information—area of remaining
254 *Araucaria* forest—as a covariate of λ . We measured *Araucaria* forest as standardized cover in a
255 circular buffer with 17 km radius around each roost, which amounts to an area of 907 km². We
256 also tried buffer radiuses of 5 and 50 km in exploratory analyses, but elected to use a 17-km
257 buffer because it corresponds to the longest single-day displacement recorded for radio-tagged
258 VBPs (Prestes et al., 2014), and indeed resulted in the highest (positive) slope for the relationship
259 between *Araucaria* cover and λ . *Araucaria* forest cover data resulted from the intersection of two
260 maps: a map of the potential range of South American *Araucaria* Forest drawn by Hueck (1966)
261 and georeferenced by Hasenack et al. (2017), and Ribeiro et al.’s (*in prep.*) map of existing
262 Atlantic Forest remnants that are larger than 30-by-30 meters in area. To explore the
263 consequences of the environmental covariate on our assessment of global population size, we
264 built two alternative models, one without (*Model 1*) and the other with (*Model 2*) a year-
265 dependent effect of *Araucaria* Forest cover on λ , the average roost population size. All regional-
266 scale counts used in the whole range analysis were MR counts. As at the regional scale, we fit
267 models in a Bayesian framework using vague priors. Whole-range scale inference was based on
268 an MCMC algorithm with three chains, 50,000 iterations and a burn-in of 1,000 iterations. At
269 both regional and whole-range scales, we ran the MCMC until obtaining a value of the
270 convergence criterion R-hat lower than 1.1 for all parameters.

271 To assess the Goodness of Fit (GoF) of our models, we applied leave-one-out cross-
272 validation (Conn et al. 2018) and a Bayesian p -value approach (Gelman et al. 1996) on a chi-
273 squared discrepancy statistic T . For both the regional and the whole-range analysis, the former
274 indicated that our models predicted the observed counts about right on average, but the latter

275 indicated severe overdispersion. The Bayesian p-value, reflecting the frequency with which
276 discrepancy is higher for replicated data (T_{rep}) than for observed data (T_{obs}), was zero for both
277 analyses. This was not unexpected, since parrots often travel in pairs, thus violating the
278 independence assumption of the model. To accommodate this, we had experimented with the
279 beta-binomial variant of the model developed by Martin et al. (2011) and Dorazio et al. (2013)
280 for group-living animals, which yielded acceptable GoF results, but completely unrealistic (too
281 high) abundance estimates. This 'good fit/bad prediction dilemma' (Kéry & Royle 2016) is
282 observed not rarely with N-mixture models and so far no formal remedy has been developed.

283 Thus, we had to decide between choosing an analysis that ignored detection error (e.g.,
284 some GLMM; Barker et al. 2018) and a simple N-mixture model that accommodates that key
285 consideration when estimating abundance, but resulting in lack of fit, or overdispersion. We
286 conducted a simple simulation (see Appendix 1), where we simulated replicated counts that
287 resembled our data in the regional analysis. Our simulation randomly varied the degree of
288 overdispersion at the site-level in both λ and p , and of site-by-occasion level in p . We then
289 analysed the data set using an intercepts-only N-mixture model that ignored the resulting lack of
290 fit and estimated the total population size. As an alternative, p -ignorant method we simply added
291 up the maximum count across sites. We simulated 1000 data sets and found that the root mean
292 squared error (RMSE) of the overdispersion-naive N-mixture model was 25% reduced compared
293 to the p -ignorant method of adding maximum counts. This led us to choose the formal estimation
294 method of the N-mixture model.

295 To accommodate the additional uncertainty stemming from the lack of fit or
296 overdispersion detected in the GoF test, we chose an *ad hoc* way of increasing the uncertainty in
297 our estimates by 'stretching' the posterior distributions around their mean. This was motivated by

298 the frequent adoption of variance inflation by some overdispersion factor c -hat in frequentist
299 analyses of count data, see e.g., Chapter 5 in Cooch and White (2020) for Cormack-Jolly-Seber
300 models. We estimated the degree of overdispersion c -hat by the ratio $T_{\text{obs}} / T_{\text{rep}}$, from above, at
301 5.6 for the regional and 5.8 for the whole-range scale. To make the posterior distributions more
302 dispersed, we first subtracted from all posterior samples of a parameter its mean, multiplied the
303 result by our estimate of c -hat and then added back the original mean. All uncertainty
304 assessments such as posterior SDs or credible intervals were then based on this 'stretched' sample
305 of the posterior of a parameter. In our simulation, the coverage of this approach for total
306 abundance summed across roosts was on average only 0.67 and thus considerably lower than the
307 nominal level of 0.95, but much better than the coverage of 'unstretched' CRIs would have been.
308 Therefore, to be conservative, we chose the stretching procedure despite its lack of theoretical
309 underpinning.

310

311 3. Results

312 Comparison of most reasonable (MR) and highly conservative (HC) results from the regional-
313 scale data suggest a small but consistent difference between counts. Whereas MR counts were
314 always greater than or equal to HC counts of the same roost and month, they were also less
315 variable between replicates within the same roost and month (Supplemental Material Table S2).
316 Accordingly, estimates of detection probability (p) tended to be higher for MR than for HC
317 results; this was true in nine out of thirteen months for the whole WSC region (Table 1).
318 Likewise, MR-based estimates of abundance tended to be more precise than their HC
319 counterparts: roost and month-specific estimates based on MR counts were as precise or more
320 precise than those based on HC counts in 95 of 130 cases (Supplemental Material Table S2).

321 Spatial and temporal variation is qualitatively similar between types of counts, with MR and HC
322 counts resulting in the same maximum-abundance month (March 2017) and the same maximum-
323 abundance roost (*Lebon Régis*). We also found a small but measurable effect of the time of day
324 on detection probability, with dusk counts having detection probability on average 0.03 above
325 dawn counts. The 95% credible interval of the negative ‘dawn’ coefficient excludes zero for both
326 MR and HC data. For simplicity, we focus on MR results for any WSC-related content in the
327 remainder of the paper.

328 Temporal variation in estimated abundance for WSC (summed across roosts) shows the
329 lowest number of individuals in the two extremes of the non-reproductive period (Table 1): in
330 December 2015, with an estimated 714 ± 92 individuals (posterior mean \pm standard deviation),
331 and in July 2016 with 655 ± 96 individuals. The highest aggregate WSC count (1,627
332 individuals) and N estimate ($1,896 \pm 105$ individuals) were obtained in May 2017. Spatial
333 variation among WSC roosts shows five of ten roosts – *Guatambu*, *Ipuacu*, *Abelardo Luz*, *Água*
334 *Doce* and *Lebon Régis* – reaching N estimates in excess of 200 at some point during the sampling
335 period. All roosts showed substantial variation in N between months in both years, but there was
336 no obvious synchrony in the temporal variation of the number of individuals at different roosts.
337 As with the highest estimates of N , the lowest were obtained in different months depending on
338 roost. For example, while *Água Doce* peaked in March 2016 and May 2017, *Guatambu* did so in
339 April 2016 and February 2017. *Abelardo Luz* was the only roost that peaked both years in the
340 same month, in June.

341 The posterior mean global abundance of VBPs varied slightly between models and years,
342 but was always smaller than 10,000 individuals. *Model 1* estimated $7,789 \pm 655$ individuals (95%
343 Bayesian credible interval 6,586–9,184) for 2016, and $8,483 \pm 693$ (7,181–9,977) for 2017. *Model*

344 2 estimated $8,012 \pm 714$ individuals (6,779–9,507) for 2016, and $9,039 \pm 779$ (7,641–10,677) for
345 2017. Estimates from *Model 2*, which includes a relationship between λ and *Araucaria* forest
346 cover, were slightly higher than those from *Model 1*, but the 95% credible intervals from
347 different models in the same year clearly overlap. Both counts and abundance estimates
348 increased from 2016 to 2017, but there was overlap between 95% credible intervals of estimates
349 from the same model in different years. The average probability of detecting a parrot that is
350 present at a visited roost was 0.70 ± 0.05 under *Model 1* and 0.67 ± 0.05 under *Model 2*. There was
351 a smaller difference between models within year than between years within model, but little
352 statistical support for temporal change in global abundance. The positive effect (a logit-scale
353 slope parameter) of *Araucaria* forest cover on λ , estimated by *Model 2*, differed between years
354 and was higher in 2016 (0.43 ± 0.04) than in 2017 (0.16 ± 0.04). Such effects amount to a
355 tripling of abundance as *Araucaria* cover increases from 20% to 80% of the buffer in 2016, but
356 only to a 1.3-factor increase accompanying the same cover change in 2017.

357 The spatial distribution of *Model 1* abundance estimates across regions of the whole
358 range (Table 2) reveals that Brazil accounted for more than 90% of the estimated population size
359 in both years. The Brazilian state of Santa Catarina had the highest number of roosts (41), as well
360 as the highest estimated population size of all Brazilian regions, accounting for 50% of the total
361 population in both years. Paraná had the second highest estimates among regions, accounting for
362 approximately 25% of the total population. Looking at the spatial variation of abundance
363 estimates per roost, Santa Catarina came out on top again, with an average of 94 to 102
364 individuals per roost. The highest number of individuals estimated at one site was 380 in 2016
365 and 390 in 2017. The two estimates came from sites approximately 180 km apart, both in Santa
366 Catarina and both in May, toward the end of the non-breeding season. The spatial distribution of

367 *Model 2* estimates was qualitatively similar to that of *Model 1*. We focus on *Model 1* for
368 simplicity and because it provides the most conservative abundance estimates.

369

370 4. Discussion

371 We developed a counting technique and associated statistical analysis to estimate VBP
372 abundance at two spatial scales: regional and whole-range. Our approach sought to address five
373 sources of uncertainty about parrot abundance related to range limits, roost density, movement
374 between roosts, false positive—these addressed by our count technique, and false negative
375 observations—addressed by our statistical analysis. Based on estimates of abundance for 2016
376 and 2017, we provide evidence that the global VBP population consists of a few thousand, but
377 definitely not more than ten thousand individuals. Comparison between global abundance
378 estimates from the two years reveals that even though average estimates were greater in 2017
379 than in 2016 under both models, there is no statistical evidence that such increase resulted from
380 population growth.

381 Global population estimates are approximately twice the maximum number of individuals
382 counted in whole-range counts (Table 2). Since never more than 70% of the total known roosts
383 were counted, these latter are bound to result in underestimates of the global population size.
384 Nonetheless, we strongly emphasize that these estimates do not warrant proposing a category
385 change for the species. The IUCN assigns threat levels based on a combination of five criteria
386 (Mace et al., 2008). In order to qualify for one level, a species must meet conditions from any of
387 the five criteria for that level. Thus, non-fulfillment of one criterion does not warrant category
388 change. More specifically, non-fulfillment of the conditions under criterion C (Small population
389 size and decline) would require examination of range and population dynamic conditions under

390 the other criteria, which are beyond the scope and possibilities of our two-year analysis of roost
391 counts. We suggest that the species should remain in the ‘Endangered’ IUCN threat category
392 pending demographic studies and analysis of the conditions under criteria A, B, D and E. Ideally,
393 given appropriate coverage of the species range and understanding of population dynamics, one
394 should be able to assess an extinction risk for the species, which is demanded by criterion E.

395 The assessment of extinction risk can only be as good as the underlying estimates of
396 population size. Our regional and global estimates point out some of the ways in which
397 researchers can address sources of uncertainty when monitoring VBP and other parrots. At the
398 broadest level, there is uncertainty about species’ ranges. We tried to reduce uncertainty about
399 the VBP range by searching for new roosts 8 days/year in WSC, which returned a 150% increase
400 in the number of sampling sites over the 2 years of the study. We covered the northern half of
401 WSC in more detail than the southern half, which has only one known roost (*Guatambu*; Figure
402 2), because it has more *Araucaria* forest and a higher density of large ($\geq 5 \text{ km}^2$) forest patches;
403 yet, judging from verbal reports and the distribution of sightings in WikiAves (Wikiaves, 2018)
404 we believe there are more roosts to be found in the southern part of WSC. Only one-quarter of
405 the counting sites in the whole-range counts were inside the IUCN range, showing that range
406 uncertainty extends well beyond the limits of WSC (Figure 1). The small areas suggestive of
407 isolated populations in the IUCN Extant range (e.g., Figure 1) may be part of larger areas of
408 continuous use and may be useful starting points for improving knowledge about the species’
409 distributions.

410 From the abundance estimates and the spatial distribution of roosts, it appears that the
411 number of both roosts and individuals per unit area increases towards the interior of the
412 distribution range (Figure 1). Roosts with more than one hundred individuals counted are located

413 in the three southernmost states of Brazil, in agreement with the pattern of higher densities
414 towards the center of species' ranges reported by Brown et al. (1995) and Gaston (2009). The
415 non-homogenous density of individuals also appears related to the distribution of *Araucaria*
416 forest cover, which is centered in southern Brazil (Figure 1) and offers VBPs an important food
417 source during the autumn and winter months (Collar et al., 2017; Prestes et al., 2014; Tella et al.,
418 2016). *Model 2* results suggest that the relationship between *Araucaria* forest cover and parrot
419 abundance may change substantially through time, as it decreased by more than 50% from 2016
420 to 2017. Such change is likely due to variability in the amount, spatial distribution and temporal
421 distribution of *Araucaria angustifolia* seed production (Mantovani et al., 2004). When *Araucaria*
422 seed production coincides with winter-scarcity of alternative resources, *Araucaria* could become
423 a more important food source and a stronger driver of VBP distribution.

424 Spatiotemporal variability in environment and demography necessarily lead to temporal
425 variation in VBP distribution. Such dynamism is evident in WSC from the disappearance of
426 VBPs from roost sites during the breeding season, and from the variation in roost estimates
427 throughout the study (Supplemental Material Table S2). We estimated the lowest numbers of
428 VBPs during December 2015 and July 2016 (Table 1)—the first and last months of the sampling
429 period of 2016. Nonetheless, temporal variation of abundance was far from synchronous across
430 roosts (Supplemental Material Table S2). Indeed, estimates for *São Domingos* and *Abelardo Luz*
431 were lowest in January and March of 2016, respectively, neither month being the first or last of
432 the sampling period. If individuals were breeding in surrounding areas and aggregating at
433 centrally-located roosts for the non-breeding season, we would expect a gradual accumulation of
434 individuals at all roosts with a peak in the middle of the non-breeding season. Instead, we
435 observed irregular temporal variation in roost size, suggesting that VBPs move well beyond the

436 immediate surroundings of one roost as they track resources during the non-breeding season (see
437 also Forshaw, 2010; Prestes et al., 2014). As a result, individuals counted at one roost in a given
438 month may very well be present at a different roost in another month. This is why we based our
439 WSC estimate on the month with the highest estimate of each year (February 2016 and May
440 2017) and not on a sum of each roost's highest monthly estimate. Uncertainty about movement is
441 also the reason behind concentrating monthly counts in as short a period as possible. We cannot
442 be certain that VBPs don't move further than the reported maximum daily displacement of 17
443 km (Prestes et al. 2014); nonetheless, our own displacement between roosts was 2.6 times faster.
444 Only two of the ten roosts (Ipuacu and São Domingos) have two neighboring roosts within 30
445 km of distance, and these were always sampled on consecutive days minimizing the possibility
446 of parrot movement between counts. Ideally, one would have different observers counting all the
447 roosts at the same time, but barring that possibility we believe that our design is one acceptable
448 compromise.

449 Two further sources of uncertainty originate within counts. These are double counting
450 (false positive) and imperfect detection (false negative). They are more methodological in nature,
451 but should also guide decisions of study design and data analysis for estimating population sizes.
452 In parrot roost counts, double counting happens when observers overestimate the number of
453 parrots in a flock, and when parrots move out of sight and are mistakenly counted as different
454 individuals when they reappear. Our comparison of MR and HC results was an attempt to
455 evaluate the consequences of being less or more conservative about the possibility of double
456 counting. The consequences were negligible: 95% credible intervals of the MR and HC-based
457 estimates for WSC overlapped in all but one month (May 2017). In this month, the difference
458 was 197 individuals. The tendency for higher precision in MR than HC estimates stems from a

459 greater agreement among MR, than among HC results for the same roost and month. All else
460 being equal, greater similarity of counts fed into an N-mixture model result in higher estimates of
461 detection probability and therefore greater precision of the abundance estimate. This is no proof
462 that MR counts are indeed closer to the true value, but it does support our reliance on the MR
463 estimates. We suggest that by including MR and HC estimates in monitoring efforts for other
464 parrots, researchers can assess the potential effects of double-counting on population estimates.

465 Despite all our efforts to surround the roosts, work with three-observer teams, and
466 connect each team's observers by radio, the WSC counts taken by different teams at the same
467 place and time still differed. This problem of imperfect detection cannot be completely
468 eradicated, but it should be accounted for. Detection probability (p) was always estimated to be
469 greater than 0.6 on MR estimates, which is reassuring; however, its variation through time makes
470 it clear that p can't be estimated once and subsequently used to correct all counts from then on.
471 Researchers can address imperfect detection by replicating counts and estimating p during every
472 time period for which they want to estimate N . Furthermore, the temporal variation in estimated
473 p suggests that it is more than a simple function of observer experience. Part of the field team
474 gained experience with the species, the sites, and the logistics over the course of the study in
475 WSC, but p did not increase monotonically from the beginning to the end of the sampling period.
476 Instead, p varied from month to month without any apparent trend, reaching its maximum in
477 March 2016 and its minimum in April 2016 (Table 1). Detection at dawn was slightly (though
478 measurably) lower than at dusk, likely due to mist forming more frequently during the morning
479 than in the afternoon, but such intra-day variation was an order of magnitude lower than the
480 variation between months. We conclude that failure to detect parrots at roost counts is largely a

481 matter of chance, weather, and unpredictable parrot movements—not a matter of observer
482 experience.

483 The difference between the number of parrots estimated and counted over the whole
484 range is not just due to the failure to detect some parrots at roosts that were visited. Only 69% of
485 known roosts were visited in 2016 and 66% in 2017. The Bayesian MCMC-based
486 implementation of our model accounts for this incomplete coverage by imputing values of N for
487 each roost that was not visited, in agreement with the value of λ estimated across roosts for the
488 corresponding year. Multiplying the coverage of 0.66–0.69 by the average detection probability
489 of 0.67–0.70 estimated by models 1 and 2, one obtains products of 0.45–0.47, which
490 approximate the ratios of counted to estimated individuals in Table 2. We thus conclude that the
491 improvement of data quality for whole-range estimates should benefit more from increasing the
492 number of sites surveyed than from attempting to increase detection at each roost, which may be
493 beyond our control.

494 Habitat loss and nest poaching have caused alarming but poorly documented declines of
495 many Neotropical parrot populations, including VBPs (Berkunsky et al., 2017; Ribeiro et al.,
496 2009; Wright et al., 2001). Any efforts to protect these species will benefit from improved
497 knowledge of population size and structure. We hope that our approach to estimating population
498 size of VBPs in WSC and beyond will motivate others to obtain replicated counts of parrot roosts
499 for this and other species and improve on both our survey design and analyses. In an attempt to
500 coordinate observers and gather count information for VBPs, we set up an online count-reporting
501 tool where users can access existing data and contribute their own. The current version is
502 available in Portuguese at: <http://name1.azurewebsites.net>. The uncertainty surrounding regional-
503 and whole-range population estimates, however, is still high enough to justify employing a wide

504 variety of observation techniques in monitoring Vinaceous-breasted, and other Neotropical
505 parrots. On one front, citizen science networks such as WikiAves, Xeno-Canto, and eBird can
506 offer valuable information for mapping species ranges and reproductive areas. On the other,
507 molecular analysis of parrots across their range would help understand seasonal movements and
508 the spatial structure of populations. Progress will require formal integration of different types of
509 data into one statistical model of species distribution and abundance. Molecular data collection
510 will require effective and safe techniques for obtaining parrot DNA without endangering the
511 sampled individuals. Our study illustrates key sources of uncertainty about parrot abundance
512 estimates, and how they can be addressed through monitoring protocols and statistical analysis.
513 Critically, by addressing and estimating uncertainty, parrot monitoring efforts can move beyond
514 minimum or average roost counts to a broader understanding of what we do and do not know
515 about parrot numbers. On that basis, one can produce reliable assessments of population trends
516 over time.

517

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528

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665 **Figure 1.** Estimated number of Vinaceous-breasted Parrots per roost (circles), hypothetical
666 IUCN range areas (dashed polygons), and potential extent of *Araucaria angustifolia* forests (gray
667 polygon). Concentric circles show estimates from 2016 (gray) and 2017 (empty), with sizes
668 corresponding to the abundance classes shown in the legend. When the estimates from both years
669 fall in the same class, the superimposed circles appear as a single gray circle. The set of short-
670 dash polygons represent the IUCN ‘Extant’ range, while the single, larger, long-dash polygon
671 represents the IUCN ‘Possibly Extant’ range. Gray, upper-case labels indicate Paraguay (PY),
672 the Argentinian province of Misiones (AR), and the six Brazilian states mentioned in the text:
673 Espírito Santo (ES), Minas Gerais (MG), São Paulo (SP), Paraná (PR), Santa Catarina (SC), and
674 Rio Grande do Sul (RS).

675 **Figure 2.** Regional-scale study area of Western Santa Catarina (light gray). Dark gray indicates
676 every patch of forest (excluding tree plantations) > 5 km² in area, according to the Brazilian
677 Ministry of the Environment’s *Mapa de Cobertura Vegetal dos Biomas Brasileiros* (MMA,
678 2007). Circles show the location of all presently known WSC roosts with their name
679 abbreviations: PS (*Palma Sola*), CE (*Campo Erê*), GT (*Guatambu*), QU (*Quilombo*), SD (*São*
680 *Domingos*), IP (*Ipuacu*), AL (*Abelardo Luz*), ER (*Entre Rios*), AG (*Água Doce*) and LR (*Lebon*
681 *Régis*).

682 **Table 1.** Western Santa Catarina estimates of the number of Vinaceous-breasted Parrots (N) in
683 all known roosts and the average probability (p_{dawn}) of detecting one parrot present at those
684 roosts that were visited, at dawn, by month. Values preceded by the ‘ \pm ’ sign are standard
685 deviations of the posterior distribution of the parameter in question. Numbers in parentheses
686 show the sum of the highest counts from each roost sampled in the corresponding month. MR
687 and HC indicate estimates based on, respectively, ‘most reasonable’ and ‘highly conservative’
688 count results. Boldface numbers identify the highest N estimate of each year.

Month	2015 – 2016		2017	
	N	p_{dawn}	N	p_{dawn}
December (MR)	714±92 (265)	0.87±0.06		
(HC)	686±106 (244)	0.78±0.08		
January (MR)	1,091±190 (335)	0.69±0.10		
(HC)	956±183 (297)	0.68±0.12		
February (MR)	1,826±236 (696)	0.67±0.08	893±90 (426)	0.68±0.06
(HC)	1,825±270 (670)	0.63±0.09	754±87 (374)	0.70±0.07
March (MR)	1,364±100 (639)	0.87±0.03	1,151±121 (587)	0.78±0.08
(HC)	1,229±99 (588)	0.91±0.03	1,175±176 (529)	0.62±0.10
April (MR)	1,482±173 (562)	0.61±0.06	940±98 (493)	0.79±0.08
(HC)	1,546±218 (538)	0.53±0.07	859±131 (418)	0.70±0.11
May (MR)	1,522±166 (997)	0.72±0.10	1,896±105 (1,627)	0.76±0.06
(HC)	1,755±336 (965)	0.55±0.13	1,693±74 (1,517)	0.82±0.05
June (MR)	1,397±89 (761)	0.80±0.04	1,109±121 (639)	0.64±0.07
(HC)	1,329±91 (724)	0.78±0.04	1,100±161 (588)	0.53±0.09
July (MR)	655±96 (321)	0.73±0.09		
(HC)	580±90 (286)	0.74±0.10		

689

690 **Table 2.** Roosts visited, total number counted and Model 1 estimates of the number of
691 Vinaceous-breasted Parrots in Argentina, Brazil, and Paraguay during the whole-range counts of
692 2016 and 2017. Estimates are given as mean \pm standard deviation of the posterior distribution.
693 Dashes denote absence of counts in the corresponding location and year.

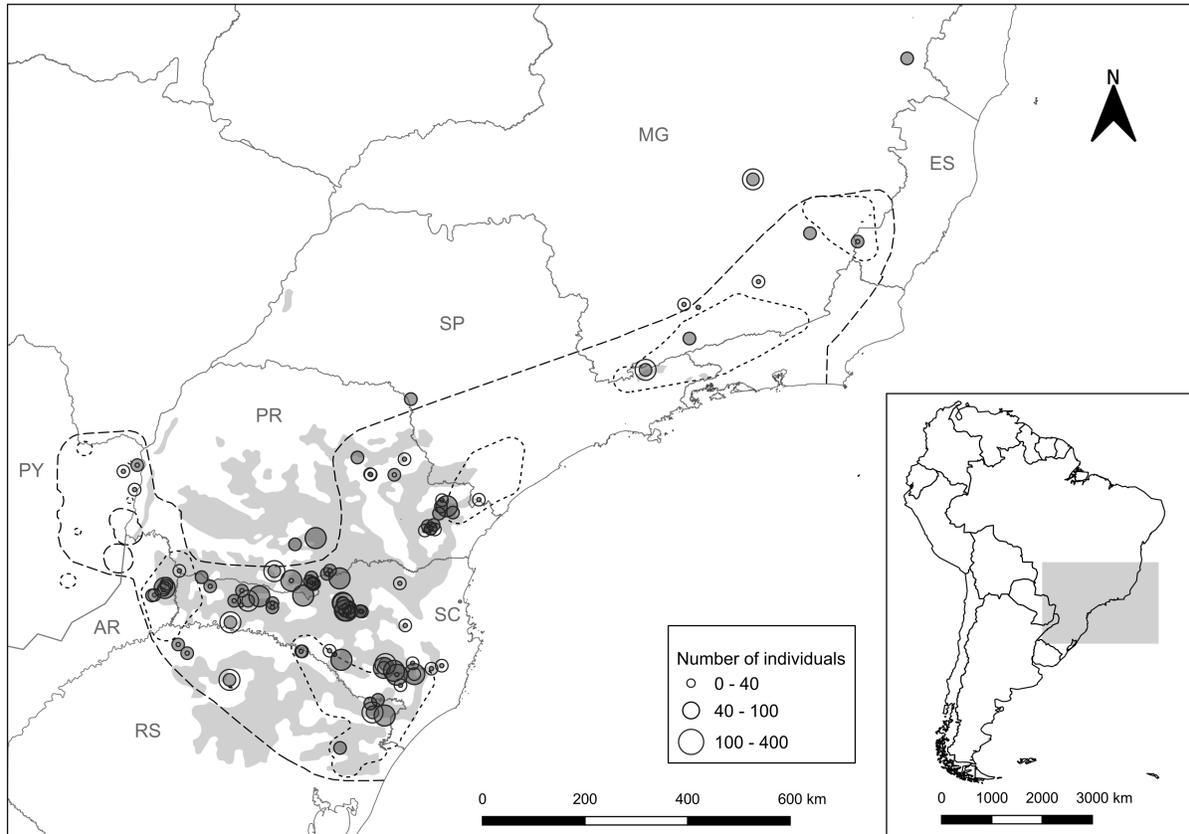
694

Country	Region	2016			2017		
		Roosts visited	Count	M1 estimate	Roosts visited	Count	M1 estimate
Argentina	Misiones	7	252	426 \pm 56	0	–	605 \pm 78
Brazil	Espírito Santo	0	–	80 \pm 23	1	2	28 \pm 14
	Minas Gerais	5	58	336 \pm 60	3	135	558 \pm 70
	Paraná	16	803	2,112 \pm 198	17	805	2,050 \pm 205
	Rio Grande do Sul	6	335	717 \pm 75	9	409	642 \pm 71
	Santa Catarina	28	2,324	3,860 \pm 285	31	2,606	4,197 \pm 296
	São Paulo	3	93	164 \pm 27	2	109	247 \pm 35
Paraguay	Alto Paraná	3	23	94 \pm 27	2	18	156 \pm 36
TOTAL		68	3,888	7,789 \pm 655	65	4,084	8,483 \pm 693

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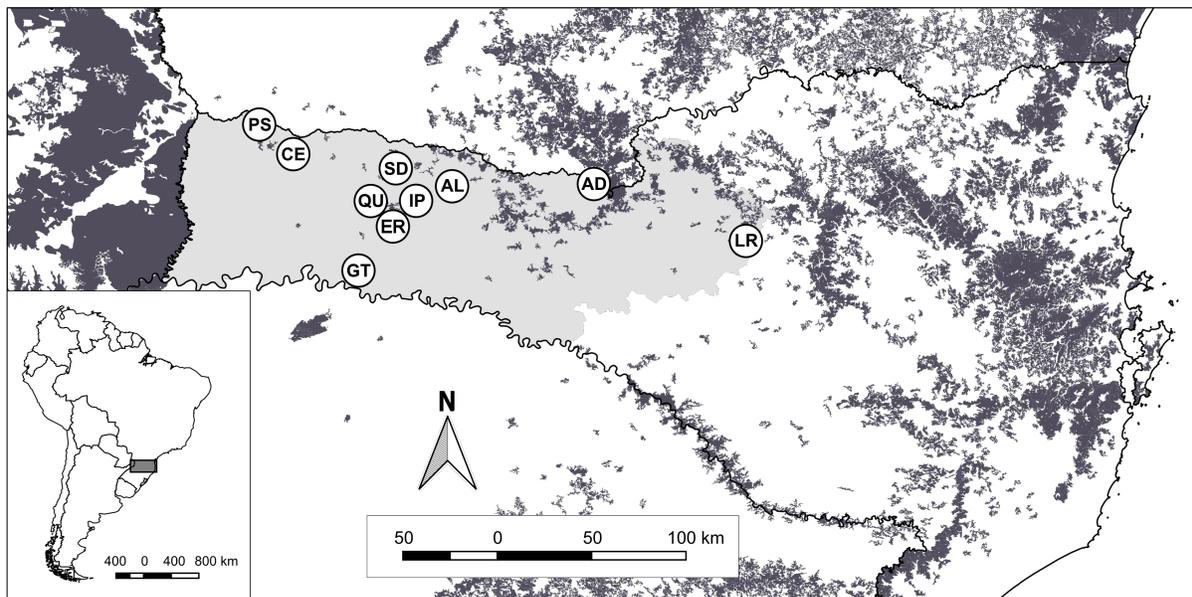


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Figure 1

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Figure 2

Supplemental Material Table S1. Whole-range count sites by country and region, with contact observer, and the year sampled. Contacts given with initials are co-authors of this paper.

Country and Region	Site	Contact	Year Sampled	
			2016	2017
ARGENTINA				
Misiones	1. San Pedro – Centro	N3* and Bianca Bonaparte	X	
	2. San Pedro – Siete Estellas	N3 and Bianca Bonaparte	X	
	3. Cruce Caballero	N3 and Bianca Bonaparte	X	
	4. Alegría	N3 and Bianca Bonaparte	X	
	5. Tobuna	N3 and Bianca Bonaparte	X	
	6. Santa Rosa	N3 and Bianca Bonaparte	X	
	7. Irigoyen	N3 and Bianca Bonaparte	X	
BRAZIL				
Espírito Santo	8. Dores do Rio Preto	Tatiane Pongiluppi		X
Minas Gerais	9. Minas Gerais	Sérgio Carvalho	X	
	10. Carrancas e Minduri	Kassius Santos	X	X
	11. Baipendi	Emanuel Ladroz	X	
	12. Santo Antônio do Grama	Leonardo Miranda	X	
	13. Luminárias	Kassius Santos	X	
	14. Serra do Cipó	Lucas Carrara		X
	15. Crisólita	Marina Somenzari		X
Paraná	16. General Carneiro A	N4†, N5§ and N7¶	X	X
	17. General Carneiro B	N4, N5 and N7	X	
	18. General Carneiro C	N4, N5 and N7		X
	19. General Carneiro D	N4, N5 and N7		X
	20. General Carneiro E	N4, N5 and N7		X
	21. Bituruna	N4, N5 and N7		X
	22. Curitiba A	Roberto Boçon	X	
	23. Curitiba B	Romulo da Silva	X	
	24. Curitiba C	Rafael Sezerban	X	
	25. Curitiba D	Roberto Boçon		X
	26. Curitiba E	Roberto Boçon		X
	27. Curitiba F	Rafael Sezerban		X

Supplemental Material Table S1: (cont.)

Country and Region	Site	Contact	Year Sampled	
			2016	2017
	28. Bocaiúva do Sul A	Elenise Sipinski	X	X
	29. Bocaiúva do Sul B	Romulo da Silva	X	
	30. Tunas do Paraná	Roberta Boss	X	
	31. Bocaiúva do Sul/Tunas do PR	Pedro Scherer-Neto		X
	32. Bocaiúva do Sul C	Patricia Serafini	X	
	33. Castro/Pirai do Sul/Jaguariaíva	Tony Teixeira		X
	34. Jaguariaíva	Tony A. Bichinky	X	
	35. Tibagi A	Romulo da Silva	X	
	36. Tibagi B	Romulo da Silva	X	
	37. Coronel Domingos Soares	N4, N5 and N7		X
	38. Inácio Martins	N4, N5 and N7	X	X
	39. Palmas	N4, N5 and N7	X	X
	40. Pinhão	N4, N5 and N7	X	X
	41. Telêmaco Borba	Roberto Boçon	X	X
	42. União da Vitória	N4, N5 and N7		X
Rio Grande do Sul	43. Barracão	N4, N5 and N7	X	X
	44. Sarandi	N4, N5 and N7	X	X
	45. Coqueiros do Sul	N4, N5 and N7		X
	46. Canela	N4, N5 and N7	X	X
	47. Bom Jesus	N4, N5 and N7	X	X
	48. Bom Jesus B	N4, N5 and N7	X	X
	49. São José dos Ausentes	N4, N5 and N7	X	X
	50. Miraguaí	N4, N5 and N7		X
	51. Dois Irmãos da Missão	N4, N5 and N7		X
Santa Catarina	52. Cerro Negro	N4, N5 and N7	X	X
	53. Abdon Batista	N4, N5 and N7		X
	54. Abelardo Luz	N1** and N2††	X	X
	55. Passos Maia	Vanessa Kanaan		X
	56. Ponte Serrada	Vanessa Kanaan		X

Supplemental Material Table S1: (cont.)

Country and Region	Site	Contact	Year Sampled	
			2016	2017
	57. Água Doce	N1 and N2	X	X
	58. Anitápolis	N4, N5 and N7	X	
	59. Anitápolis B	N4, N5 and N7	X	
	60. Bom Retiro	N4, N5 and N7	X	
	61. Campo Belo do Sul	N4, N5 and N7	X	X
	62. Campo Erê	N1 and N2	X	X
	63. Ipuaçu	N1 and N2		X
	64. Entre Rios	N1 and N2	X	X
	65. Guatambu	N1 and N2	X	X
	66. Irineópolis	N4, N5 and N7	X	X
	67. Itaiópolis	N4, N5 and N7	X	
	68. Lebon Régis	N4, N5 and N7	X	X
	69. Lebon Régis B	N4, N5 and N7	X	X
	70. Lebon Régis C	N4, N5 and N7	X	
	71. Lebon Régis D	N4, N5 and N7	X	
	72. Lebon Régis E	N4, N5 and N7	X	
	73. Lebon Régis F	N4, N5 and N7		X
	74. Lebon Régis G	N4, N5 and N7		X
	75. Lebon Régis H	N4, N5 and N7		X
	76. Lebon Régis I	N4, N5 and N7		X
	77. Lorentino	Miguel Angelo Biz	X	
	78. Palma Sola	Paulo A. Neto, N1 e N2	X	X
	79. Urupema	N4, N5 and N7	X	X
	80. Urupema	N4, N5 and N7	X	X
	81. Painei	N4, N5 and N7	X	X
	82. São Joaquim	N4, N5 and N7	X	X
	83. São Joaquim	N4, N5 and N7	X	X
	84. Painei	N4, N5 and N7	X	X
	85. Quilombo	N1 and N2		X
	86. Santa Cecília A	N4, N5 and N7		X

Supplemental Material Table S1: (cont.)

Country and Region	Site	Contact	Year Sampled	
			2016	2017
	87 Santa Cecília B	N4, N5 and N7		X
	88. Santa Cecília C	N4, N5 and N7		X
	89. São Domingos	N1 and N2	X	X
	90. Urubici	N4, N5 and N7	X	
	91. Porto União	N4, N5 and N7		X
	92. Urubici	N4, N5 and N7	X	
São Paulo	93. Timburi	Fernando Zurdo	X	
	94. São Paulo	Fernando Zurdo	X	X
	95. Campos do Jordão	Luís Fábio Silveira	X	X
PARAGUAY				
Canindeyú	96. Refúgio Biológico Carapá	N8§§	X	X
	97. Reserva Privada Itabó Rivas	N8	X	
Alto Paraná	98. Reserva Biológica de Limoy	N8	X	X

* N3 = name3

† N4 = name4

§ N5 = name5

¶ N7 = name7

** N1 = name1

†† N2 = name2

§§ N8 = name8

Supplemental Material Table S2. Monthly counts and estimates \pm standard deviation of the local abundance for each WSC (regional-scale) roost throughout the study period, based on ‘highly conservative’ (HC) and ‘most reasonable’ (MR) count results. Numbers in parentheses show the highest count for the corresponding roost and month. Roosts with NA in parentheses do not have counts in the corresponding month; their estimates for those months are derived from Model 1. Roost order in the table is longitudinal from West to East.

Year	Month\Roost	Palma Sola	Campo Erê	Guatambu	Quilombo	São Domingos	
2016	December	(MR)	12 \pm 4 (10)	71 \pm 24 (NA)	165 \pm 10 (155)	71 \pm 23 (NA)	83 \pm 8 (75)
		(HC)	13 \pm 6 (8)	69 \pm 24 (NA)	157 \pm 13 (143)	69 \pm 24 (NA)	81 \pm 10 (71)
	January	(MR)	86 \pm 18 (65)	110 \pm 14 (NA)	221 \pm 26 (175)	109 \pm 32 (NA)	27 \pm 13 (10)
		(HC)	72 \pm 17 (53)	96 \pm 31 (NA)	192 \pm 25 (158)	96 \pm 31 (NA)	25 \pm 14 (10)
	February	(MR)	129 \pm 19 (101)	182 \pm 41 (NA)	191 \pm 26 (141)	183 \pm 41 (NA)	100 \pm 17 (77)
		(HC)	126 \pm 21 (94)	182 \pm 46 (NA)	192 \pm 30 (137)	182 \pm 45 (NA)	102 \pm 19 (75)
	March	(MR)	76 \pm 7 (68)	136 \pm 31 (NA)	61 \pm 7 (51)	136 \pm 31 (NA)	32 \pm 6 (25)
		(HC)	67 \pm 5 (63)	123 \pm 30 (NA)	51 \pm 5 (47)	123 \pm 31 (NA)	27 \pm 5 (24)
	April	(MR)	32 \pm 15 (5)	148 \pm 35 (NA)	246 \pm 22 (197)	148 \pm 35 (NA)	59 \pm 11 (39)
		(HC)	43 \pm 21 (5)	154 \pm 39 (NA)	255 \pm 29 (191)	155 \pm 39 (NA)	65 \pm 14 (35)
	May	(MR)	48 \pm 16 (25)	47 \pm 16 (25)	63 \pm 15 (40)	152 \pm 35 (NA)	83 \pm 18 (58)
		(HC)	72 \pm 34 (21)	74 \pm 35 (24)	81 \pm 30 (36)	175 \pm 48 (NA)	96 \pm 36 (45)
	June	(MR)	6 \pm 6 (0)	4 \pm 4 (0)	40 \pm 7 (29)	139 \pm 31 (NA)	35 \pm 8 (24)
		(HC)	6 \pm 6 (0)	4 \pm 4 (0)	37 \pm 8 (26)	132 \pm 31 (NA)	33 \pm 8 (22)
July	(MR)	38 \pm 8 (31)	55 \pm 9 (46)	18 \pm 7 (12)	65 \pm 23 (NA)	58 \pm 10 (45)	
	(HC)	35 \pm 7 (30)	44 \pm 8 (37)	13 \pm 6 (8)	58 \pm 22 (NA)	54 \pm 11 (42)	
2017	February	(MR)	173 \pm 15 (131)	23 \pm 5 (17)	200 \pm 12 (184)	89 \pm 25 (NA)	51 \pm 10 (32)
		(HC)	151 \pm 14 (124)	21 \pm 4 (17)	164 \pm 12 (150)	75 \pm 25 (NA)	38 \pm 8 (25)
	March	(MR)	202 \pm 17 (177)	27 \pm 8 (18)	152 \pm 15 (125)	115 \pm 29 (NA)	67 \pm 11 (54)
		(HC)	193 \pm 22 (162)	36 \pm 15 (18)	163 \pm 23 (118)	118 \pm 33 (NA)	63 \pm 17 (41)
	April	(MR)	154 \pm 13 (135)	29 \pm 5 (23)	178 \pm 15 (157)	94 \pm 26 (NA)	44 \pm 9 (35)
		(HC)	145 \pm 16 (126)	31 \pm 8 (22)	137 \pm 19 (113)	86 \pm 27 (NA)	40 \pm 13 (23)
	May	(MR)	49 \pm 11 (34)	34 \pm 10 (20)	183 \pm 17 (147)	38 \pm 10 (25)	42 \pm 11 (27)
		(HC)	42 \pm 8 (34)	27 \pm 8 (20)	153 \pm 12 (135)	26 \pm 7 (19)	30 \pm 8 (22)
	June	(MR)	121 \pm 17 (84)	40 \pm 18 (5)	117 \pm 16 (84)	33 \pm 12 (12)	76 \pm 15 (45)
		(HC)	110 \pm 19 (81)	49 \pm 23 (5)	122 \pm 22 (77)	35 \pm 17 (8)	82 \pm 20 (41)

Supplemental Material Table S2. (cont.)

Year	Month\Roost	Ipuaçu	Entre Rios	Abelardo Luz	Água Doce	Lebon Régis	
2016	December	(MR)	72±23 (NA)	71±23 (NA)	71±22 (NA)	26±2 (25)	71±23 (NA)
		(HC)	69±24 (NA)	68±24 (NA)	68±24 (NA)	25±4 (22)	68±24 (NA)
	January	(MR)	109±32 (NA)	109±32 (NA)	110±33 (NA)	103±17 (85)	109±32 (NA)
		(HC)	95±32 (NA)	96±32 (NA)	96±31 (NA)	94±17 (76)	96±32 (NA)
	February	(MR)	183±41 (NA)	182±41 (NA)	129±27 (77)	366±34 (300)	182±41 (NA)
		(HC)	183±44 (NA)	182±44 (NA)	134±31 (77)	360±38 (287)	182±44 (NA)
	March	(MR)	136±30 (NA)	136±30 (NA)	19±5 (14)	495±12 (481)	136±30 (NA)
		(HC)	123±31 (NA)	123±32 (NA)	17±4 (14)	453±11 (440)	123±31 (NA)
	April	(MR)	148±35 (NA)	148±35 (NA)	82±17 (48)	323±25 (273)	148±35 (NA)
		(HC)	155±39 (NA)	154±39 (NA)	86±23 (42)	325±30 (265)	154±40 (NA)
	May	(MR)	152±35 (NA)	44±22 (8)	140±19 (114)	215±24 (184)	579±22 (543)
		(HC)	175±47 (NA)	75±39 (8)	164±38 (110)	233±44 (178)	610±40 (543)
	June	(MR)	139±31 (NA)	140±31 (NA)	450±12 (433)	304±12 (275)	140±30 (NA)
		(HC)	133±32 (NA)	133±31 (NA)	430±13 (409)	287±12 (267)	133±31 (NA)
July	(MR)	66±22 (NA)	65±23 (NA)	166±16 (143)	58±11 (44)	65±23 (NA)	
	(HC)	58±22 (NA)	58±22 (NA)	155±16 (131)	49±10 (38)	58±22 (NA)	
2017	February	(MR)	89±25 (NA)	89±25 (NA)	62±9 (42)	28±6 (20)	89±25 (NA)
		(HC)	75±25 (NA)	76±24 (NA)	57±9 (42)	22±5 (16)	75±24 (NA)
	March	(MR)	115±30 (NA)	115±29 (NA)	202±17 (174)	46±8 (39)	115±29 (NA)
		(HC)	117±33 (NA)	117±34 (NA)	198±24 (155)	53±15 (35)	118±34 (NA)
	April	(MR)	94±26 (NA)	94±25 (NA)	133±11 (122)	27±7 (21)	94±26 (NA)
		(HC)	86±28 (NA)	86±27 (NA)	134±16 (115)	29±11 (19)	86±28 (NA)
	May	(MR)	328±19 (289)	44±19 (6)	264±15 (242)	169±17 (132)	744±19 (705)
		(HC)	304±15 (280)	30±15 (6)	207±12 (193)	146±13 (122)	729±15 (705)
	June	(MR)	15±11 (2)	109±29 (NA)	349±18 (320)	122±18 (87)	109±29 (NA)
		(HC)	21±16 (0)	110±32 (NA)	336±24 (295)	125±23 (81)	110±32 (NA)

Supplemental Material Appendix A: BUGS language specification of the models used in estimating Vinaceous-breasted Parrot abundance. Model A is the model used for the regional scale analysis of Western Santa Catarina data. Models B and C correspond to Model 1 and Model 2, respectively, in the text; they were used for analyzing data at the whole-range scale. All models were based on Royle (2004) and Kéry and Royle (2016).

```
#Model A: Regional analysis with WSC data

#Data object
str(bdata <- list(counts = counts, month = month, site = site, n =
nrow(counts), visit = ncol(counts), nmonth = max(month), morning = COV2-
1))

# Specify model in BUGS language
cat(file = "modelA.txt", "
model {

# Priors
# for abundance
for(s in 1:nmonth){
  lambda[s] ~ dgamma(0.01, 0.01)
  beta0[s] ~ dunif(-10,10)
}
# for detection
beta1 ~ dunif(-10,10)

# Biological model for true abundance
for(i in 1:n){ # loop over sites
  N[i] ~ dpois(lambda[month[i]])
  # Observed data at replicated counts
  for(j in 1:visit){ #loop over visits in each site
    counts[i,j] ~ dbin(p[i,j], N[i])
    logit(p[i,j]) <- beta0[month[i]] + beta1*morning[i,j]

    ## Commands for computing Bayesian p-value
    eval[i,j] <- p[i,j]*N[i]
    E[i,j] <- pow((counts[i,j] - eval[i,j]),2) / (eval[i,j] + 0.5)
    # Generate replicate data and compute fit stats
    C.new[i,j] ~ dbin(p[i,j], N[i])
    E.new[i,j] <- pow((C.new[i,j] - eval[i,j]),2)/(eval[i,j]+0.5)
  } #counts
} #sites

fit <- sum(E)
fit.new <- sum(E.new)
c.hat <- fit / fit.new
# Total abundance across all sites
Ntotal[1] <- sum(N[1:10])
Ntotal[2] <- sum(N[11:20])
Ntotal[3] <- sum(N[21:30])
Ntotal[4] <- sum(N[31:40])
Ntotal[5] <- sum(N[41:50])
Ntotal[6] <- sum(N[51:60])
Ntotal[7] <- sum(N[61:70])
Ntotal[8] <- sum(N[71:80])
Ntotal[9] <- sum(N[81:90])
```

```

    Ntotal[10] <- sum(N[91:100])
    Ntotal[11] <- sum(N[101:110])
    Ntotal[12] <- sum(N[111:120])
    Ntotal[13] <- sum(N[121:130])
  }
  ")

# Initial Values
Nst <- apply(counts, 1, max, na.rm=TRUE) + 1
Nst[Nst == '-Inf'] <- 1
inits <- function(){list(N=Nst)}

##Params monitored
params <- c('lambda', 'p', 'N', "beta0", "beta1", "fit", "fit.new",
" c.hat", "Ntotal")

# MCMC settings
na <- 1000; nc <- 3; nb <- 10000; ni <- 25000; nt <- 20

# Call JAGS
fmA <- jags(bdata, inits, params, "modelA.txt", n.adapt = na, n.chains =
nc, n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)

```

```

#Model B: Whole-range analysis without covariates (Model 1 in manuscript)

#Data object
str(bdata <- list(counts = countsWR, month = monthWR, site = siteWR, n =
nrow(countsWR), visit = ncol(countsWR), nmonth = max(monthWR)))

#Specify model in BUGS language
cat(file = "modelB.txt", "
model {

  # Priors
  # for abundance
  for(s in 1:nmonth){
    lambda[s] ~ dgamma(0.01, 0.01)
  }
  # for detection
  p ~ dunif(0,1) #fixed for all sites and months

  # Biological model for true abundance
  for(i in 1:n){ # loop over sites
    N[i] ~ dpois(lambda[month[i]])
    # Observed data at replicated counts
    for(j in 1:visit){ #loop over visits in each site
      counts[i,j] ~ dbin(p, N[i])
      ## Commands for computing Bayesian p-value
      eval[i,j] <- p*N[i]
      E[i,j] <- pow((counts[i,j]-eval[i,j]),2) / (eval[i,j] + 0.5)
      # Generate replicate data and compute fit stats
      C.new[i,j] ~ dbin(p, N[i])
      E.new[i,j] <- pow((C.new[i,j] - eval[i,j]),2)/(eval[i,j]+0.5)
    } # reps
  } # sites

  fit <- sum(E)
  fit.new <- sum(E.new)
  c.hat <- fit / fit.new
  # Total abundance across all sites
  Ntotal[1] <- sum(N[1:98])
  Ntotal[2] <- sum(N[99:196])

}
")

# Initial Values
Nst <- apply(countsWR, 1, max, na.rm=TRUE) + 1
Nst[Nst == '-Inf'] <- 1
inits <- function(){list(N=Nst)}

# Parameters monitored
params <- c('lambda', 'p', 'N', 'fit', 'fit.new', 'c.hat', 'Ntotal')

# MCMC settings
na <- 1000; nc <- 3; nb <- 10000; ni <- 25000; nt <- 20

# Call JAGS
fmB <- jags(bdata, inits, params, "modelB.txt", n.adapt = na, n.chains =
nc, n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)

```

```

#Model C: Whole-range analysis with covariate on abundance(Model 2 in ms)

#Data object
str(bdata <- list(counts = countsWR, month = monthWR, site = siteWR, n =
nrow(countsWR), visit = ncol(countsWR), nmonth = max(monthWR), arauc =
rep(siteCovsWR[,5],2)))

# Specify model in BUGS language
cat(file = "modelC.txt", "
model {
  # Priors
  # for abundance
  for(s in 1:nmonth){
    beta0[s] ~ dunif(-10,10)
    betal[s] ~ dunif(-10,10)
  }
  p ~ dunif(0,1) #fixed p between sites and visits of the same month

  # Biological model for true abundance
  for(i in 1:n){ #loop over sites
    N[i] ~ dpois(lambda[i])
    log(lambda[i]) <- beta0[month[i]] + betal[month[i]]*arauc[i]
    #Observed data at replicated counts
    for(j in 1:visit){ #loop over visits in each site
      counts[i,j] ~ dbin(p, N[i])
      eval[i,j] <- p*N[i]
      E[i,j] <- pow((counts[i,j]-eval[i,j]),2) / (eval[i,j] + 0.5)
      # Generate replicate data and compute fit stats
      C.new[i,j] ~ dbin(p,N[i])
      E.new[i,j] <- pow((C.new[i,j] - eval[i,j]),2)/(eval[i,j]+0.5)
    } #reps

  } #sites

  fit <- sum(E)
  fit.new <- sum(E.new)
  c.hat <- fit / fit.new
  # Total abundance across all sites
  Ntotal[1] <- sum(N[1:98])
  Ntotal[2] <- sum(N[99:196])
}
")

#Initial Values
Nst <- apply(countsWR, 1, max, na.rm=TRUE) + 1
Nst[Nst == '-Inf'] <- 1
inits <- function(){list(N=Nst)}

#Parameters monitored
params <- c('lambda', 'p', 'N', 'beta0', 'betal', 'fit', 'fit.new',
'c.hat', 'Ntotal')

#MCMC settings
na <- 1000; nc <- 3; nb <- 10000; ni <- 25000; nt <- 20

#Call JAGS
fmD <- jags(bdata, inits, params, "modelC.txt", n.adapt = na, n.chains =
nc, n.thin = nt, n.iter = ni, n.burnin = nb, parallel = TRUE)

```

Supplemental Material Appendix B: Simulation assessment of (1) the coverage of the posterior-stretching procedure, and (2) the choice of an overdispersion-naïve binomial N-mixture model over a p -ignorant approach

We conducted a simple simulation with two goals:

- (1) To assess the coverage of credible intervals that are computed from a 'stretched' posterior distribution as described in the main text of the article. By 'coverage' we mean the extent to which estimation credible intervals cover the true values of parameters fed to the simulation.
- (2) To assess the estimation error associated with our use of an overdispersion-naïve binomial N-mixture model and compare it with a p -ignorant method that simply adds maximum counts across sites.

For this, we simulated 1000 data sets that contained heavy overdispersion in both abundance and detection. Sample sizes were 130 sites and 2 replicate counts, with average abundance of 120 and average detection 0.7; these resembled the constraints and estimates of our whole-range analysis. Then, we analyzed each simulated data set with a simple binomial N-mixture model that had only an intercept for abundance and another one for detection. Thus, this model was overdispersion-naïve in the sense that it did not take overdispersion into account by trying to estimate it. At the same time, for each data set, we took the maximum count simulated at each site and added this up across sites for a p -ignorant estimate of N_{total} , the total abundance across all 130 sites.

We simulated the overdispersed replicated count data sets using function `simNmix` in the AHMbook R package (Kéry, Royle & Meredith 2020). In this function, overdispersion can be simulated by adding Gaussian noise at the site level into the linear predictor for the log-linear model of abundance, or at the site, occasion, or site-by-occasion (= 'survey') level into the linear predictor for the logit-linear model of detection. The magnitude of each component of overdispersion is governed by the value of the standard deviation of a zero-mean Normal distribution from which the respective contributions are drawn as random numbers.

In both our regional and whole-range counts, we hypothesize that overdispersion may be present at the site-level in abundance and at the site-level as well as the survey- (i.e. site-by-occasion) level in detection. So, for each data set we first randomly picked a value for the standard deviation of each level of overdispersion from a Uniform distribution on (0, 1), where 0 denotes the absence of that component of overdispersion and 1 means a lot of overdispersion. Thus, we intend our simulation to represent a broad assessment of the two methods for assessing the regional total (N_{total}) under the p -ignorant and the overdispersion-naïve approaches against a very broad range of conditions in terms of the type of process that creates counts (i.e., coming from the abundance part of the data-generating processes or from the detection part or from both) and of the magnitude of the associated noise that is introduced into the counts.

This appendix contains the R and JAGS code to execute the full simulation and also, at the end, presents some brief results.

```

library(AHMbook)
?simNmix                                # Check how sim function works

# Create R objects to save results
# -----
simrep <- 1000                          # Number of simulation reps

# True values etc
sigma.vals <- array(NA, dim = c(simrep, 3))
colnames(sigma.vals) <- c('sigma.lam', 'sigma.p.site',
  'sigma.p.survey')
true.Nsite <- array(NA, dim = c(data$nsite, simrep))
true.Ntotal <- numeric(simrep)

# p-ignorant estimators for Nsite and Ntotal
maxCount <- array(NA, dim = c(data$nsite, simrep))
sumMaxCount <- numeric(simrep)

# posterior summaries of everything
# NOTE: this requires one to have fit the model below once before
# You have to manually pick some of the code below first to create
# a data set and analyse it
posterior.summaries <- array(NA, dim = c(dim(fm$summary), simrep))
dimnames(posterior.summaries) <- list(rownames(fm$summary),
  colnames(fm$summary), NULL)
STRETCH.CRI <- array(NA, dim = c(2, simrep))
dimnames(STRETCH.CRI) <- list(c(c('Stretch Lower', 'Stretch
Upper')), NULL)

# Launch simulation
for(i in 1:simrep){

  cat(paste('\n\n*** Simrep Number', i, '***\n\n\n'))

  # Simulate a data set with OD
  # -----
  # pick a random value for the three types of OD that make sense
  for the parrots
  ( sigma.lam <- runif(1, 0, 1) )
  ( sigma.p.site <- runif(1, 0, 1) )
  ( sigma.p.survey <- runif(1, 0, 1) )

  # Simulate a data set using these values
  data <- simNmix(nsites = 130, nvisits = 2, mean.lam = 120, mean.p
= 0.7,
    sigma.lam = sigma.lam, sigma.p.site = sigma.p.site,
    sigma.p.survey = sigma.p.survey, show.plot = FALSE)
  summary(c(data$C))      # summary of observed counts
  summary(exp(data$log.lam)) # summary of lambda

  # Now we fit the model to this data set,
  # ignoring the extra-sources of dispersion
  # -----

```

```

# Data object
str(bdata <- list(counts = data$C, nsites = nrow(data$C),
nsurveys = ncol(data$C))

# Specify model in BUGS language
cat(file = "model.txt", "
model {
  #Priors
  lambda ~ dgamma(0.001, 0.001)
  p ~ dunif(0,1)

  # Biological model for true abundance
  for(i in 1:nsites){
    N[i] ~ dpois(lambda)
    for(j in 1:nsurveys){
      #Observed data at replicated counts
      counts[i,j] ~ dbin(p, N[i]) #counts follow binomial
distribution
      ## Commands for computing Bayesian p-value
      eval[i,j] <- p * N[i]
      E[i,j] <- pow((counts[i,j] - eval[i,j]), 2) / (eval[i,j]
+ 0.001)
      # Pearson GoF statistic
      # Generate replicate data and compute fit stats
      C.new[i,j] ~ dbin(p, N[i])
      E.new[i,j] <- pow((C.new[i,j] - eval[i,j]),2) /
(eval[i,j] + 0.001) # Pearson GoF statistic
    }
  } #sites

  # Fit assessments
  fit <- sum(E)
  fit.new <- sum(E.new)
  c.hat <- fit / fit.new

  # Total abundance across all sites
  Ntotal <- sum(N[])
}
")

# Initial Values
Nst <- apply(data$C, 1, max, na.rm=TRUE) + 1
inits <- function(){list(N=Nst)}

# Parameters monitored
params <- c("N", "Ntotal", "lambda", "p", "fit", "fit.new",
"c.hat")

# MCMC settings
na <- 1000; nc <- 3; nb <- 3000; ni <- 10000; nt <- 7

# Call JAGS

```

```

fm <- jags(bdata, inits, params, "model.txt", n.adapt = na,
n.chains = nc,
          n.thin = nt, n.iter = ni, n.burnin = nb, parallel =
TRUE)

# Now stretch the posterior for Ntotal by sqrt(c.hat)
# And then check the coverage of the stretched CRIs

# Step 1: subtract the mean of the posterior draws
draws <- fm$sims.list$Ntotal # make a copy
cent.draws <- draws - fm$mean$Ntotal

# Step 2: stretch
cent.stretched.draws <- cent.draws * sqrt(fm$mean$c.hat)

# Step 3: put back the mean and compute stretched CRIs
stretch.draws <- cent.stretched.draws + fm$mean$Ntotal
stretch.CRI.Ntotal <- quantile(stretch.draws, prob = c(0.025,
0.975))

# Save all that we need
sigma.vals[i, ] <- c(sigma.lam, sigma.p.site, sigma.p.survey)
true.Ntotal[i] <- data$Ntotal

# p-ignorant estimators for Nsite and Ntotal
maxCount[,i] <- apply(data$C, 1, max)
sumMaxCount[i] <- data$summax

# posterior summaries of everything
posterior.summaries[, ,i] <- fm$summary
STRETCH.CRI[,i] <- stretch.CRI.Ntotal

} # simrep

## Present the results
# -----
# Quick and dirty check whether things have generally converged
hist(posterior.summaries[,8,]) # ... OK

# (1) Results for coverage of the stretched CRI ad-hoc procedure
# -----
inside <- numeric(simrep)
for(i in 1:simrep){
  inside[i] <- (true.Ntotal[i] > STRETCH.CRI[1,i]) *
(true.Ntotal[i] < STRETCH.CRI[2,i])
}

mean(inside)
[1] 0.633

```

Hence, the mean coverage of the stretched CRIs for Ntotal is only 0.633, which is a long way from 0.95, but it is without a doubt much better than what we would obtain without stretching the CRIs.

```
# (2) Results for estimation error of p-ignorant vs. OD-naive
Nmix:
#   Would we do better by simply taking the max counts ?
# -----
-

# For the total N across all sites: Ntotal
# -----
# Compare Mean total error for both approaches
(RMSE.total.counts <- sqrt(mean(sumMaxCount - true.Ntotal)^2) )
(RMSE.total.Nmix <- sqrt(mean(posterior.summaries[131,1,] -
true.Ntotal)^2) )

# [1] 4929.368          # max counts
# [1] 3720.835          # OD naive Nmix

round((3720.835 - 4929.368) / 4929.368, 4)      # minus 25% in
error when using Nmix over counts
```

Hence, averaged over all the overdispersion scenarios represented by the 1000 realizations from our data-simulation process, we expect to have 25% less total estimation error (in the root mean squared error sense) when using an overdispersion-naive binomial N-mixture model than when using a p-ignorant approach where we simply add up the maximum counts across sites.

This result was decisive for our choice to use an N-mixture model for inference about parrot total population size even when that model did not pass our Goodness of fit tests.

We do, however, not recommend such an approach in general and emphasize once more the ad hoc nature of our procedure. We believe this is the right approach for our data set and objectives, but that may not be true for other studies!

References

Kéry, M., Royle, J.A., Meredith, M., 2020. AHMbook: Functions and Data for the Book “Applied Hierarchical Modeling in Ecology” Vols. 1 and 2. Available at: <https://www.mbr-pwrc.usgs.gov/pubanalysis/keryroylebook/> and <https://sites.google.com/site/appliedhierarchicalmodeling/home>