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2 **Bovine tuberculosis model validation against a field study of**
3 **badger vaccination with selective culling**

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12

13 Abstract

14 Bovine tuberculosis (TB) is a costly disease in Britain and Ireland shared by cattle and badgers
15 (*Meles meles*), and to reduce the infection in cattle to low levels some form of badger
16 management is considered necessary. We compare the results of a badger field trial where test-
17 positive badgers are culled, and test-negative badgers vaccinated (a TVR approach) with the
18 results of the simulation model originally used to predict the effect of the trial in Northern
19 Ireland. Initial model results depended strongly on whether social perturbation occurred in the
20 badger population following culling, and the field study demonstrated no evidence for such
21 behavior. Here we re-run the model with the initial conditions of the TVR study and with no social
22 perturbation and predict a similar outcome in terms of number of badgers caught, number
23 testing positive, and the substantial decline in prevalence. These results validate our model and
24 demonstrate the utility of such predictive modelling for this disease system. This is particularly
25 important as the UK government moves away from widespread badger culling in England toward
26 more vaccination, as this combined approach gives a more robust method of disease
27 management than just vaccination on its own.

28

29 Introduction

30 In the British Isles, bovine tuberculosis (TB: caused by *Mycobacterium bovis*) remains a costly
31 disease shared by cattle and badgers (*Meles meles*), costing in excess of £150 million per year in
32 England alone [1]. In the absence of management, it appears that both species could sustain TB
33 [2-4] although the frequency of spread between the two species is highly variable in different

34 populations [5-8]. Thus some form of badger disease management would be required to reduce
35 and retain TB in cattle at very low levels. Various badger control strategies have been adopted:
36 from reactive and localised culling to large-scale culling in England with some vaccination,
37 vaccination in Wales, and culling and vaccination in Ireland. The relative efficacy of these
38 methods has been evaluated with simulation models [9-12], but culling approaches have
39 generally been non-selective. Such culling risks behavioural perturbation of the badger
40 population, which can induce increased ranging behaviour [13] and may increase disease
41 prevalence in badgers and possibly in cattle [14, 15].

42 Since 2010 an injectable vaccine, *Bacillus Calmette–Guérin* (BCG), has been available for use
43 in badgers that leads to a substantial reduction in disease in free-living badgers [16] and a degree
44 of herd protection for cubs [17]. Field trials have confirmed that badger vaccination is not inferior
45 to continuing culling [18]. Vaccination does not remove any (test positive) infected animals, so a
46 combined policy may be more effective. By using trap-side tests to diagnose TB (e.g. the dual
47 path platform test: DPP), leads to the possibility of selective culling of test-positive animals and
48 vaccination of test-negative animals. This is referred to as test and vaccinate or remove (TVR)
49 approach. Selective culling may also be more acceptable than widespread culling.

50 In Northern Ireland, where badger control had not previously been performed, an evaluation
51 of this TVR approach was conducted. Initial modelling before the trial started suggested that the
52 number of infected badgers remaining was very dependent on whether perturbation occurred:
53 in the absence of perturbation a decline of about 70% in the number of infected badgers was
54 seen, whereas with perturbation it was more modest [19]. Selective culling was also predicted
55 to result in an 83% reduction in the number of animals culled [20]. With the completion of the

56 subsequent five-year TVR study in Northern Ireland [21] we can re-examine these predicted
57 effects on the badger population, and use the exact initial conditions in the field to validate the
58 model output.

59

60 **Materials and Methods**

61 The TBi computer simulation model [12, 20, 22, 23] was used to model the TVR study site in
62 Northern Ireland. Input data included the initial population estimate, initial badger prevalence
63 and the number of badgers captured each year [21]. Based on this, the model simulated the
64 epidemiology, ecology and management of the badger population over the five-year course of
65 the study to determine the population size and number infected. Estimates of annual disease
66 prevalence during the trial, based on a Bayesian analysis combining multiple test methods [24],
67 were used to validate the model output.

68 TBi is a stochastic, individual-based, spatially explicit model which simulates the life histories
69 of a population of badgers at two-month timesteps. Life histories were generated using the
70 probabilities of reproduction, mortality, dispersal, disease progression and disease transmission
71 collected from the population at APHA's Woodchester Park research station in Gloucestershire.
72 Population density was taken from badger sett surveys conducted in County Down before the
73 trial, and the demographic makeup of social groups was matched to the local population. The
74 retention of some parameter values from the English model would have had minimal effect on
75 the simulated output as the epidemiology is driven by badger density and disease prevalence,
76 which were closely matched to the Northern Ireland study site. All model parameters and their

77 source are given in Table S1 and a full description of the model using the ODD protocol [25, 26]
78 is in a supplementary file (S2).

79 The model arena comprised of a 100 x100 grid, with each cell representing 200m x 200m;
80 the total grid representing a 400 km² landscape area. The population was 550 badgers in 85 social
81 groups. The arena comprised a central core of approximately 100 km² where badger
82 management was undertaken, and the boundary was defined by the extent of participating
83 farmland. Outside the core was a surrounding buffer two social groups wide where the possible
84 influence of control could be observed and outside this any effect of culling was expected to be
85 negligible. The grid was wrapped to form a torus to eliminate edge effects. Social groups were
86 randomly distributed across the arena and all badgers were members of a group and occupied a
87 territory which defined which social groups were neighbours.

88 **Characterisation of badgers**

89 Individual badgers were characterized by the variables: social group, sex, age, and health-
90 status. The age categories were cub, yearling (one-year old), and adult. The TB-status categories
91 were defined as: healthy, infected, single-site and multi-site excretor. Probability of disease
92 progression was based on field data from Woodchester Park [27]. Badger fecundity was density-
93 dependent based on an upper limit of litters in each social group. Births were simulated at the
94 start of the year, and litter size was modelled probabilistically from a distribution of known litter
95 sizes [28], with a mean of 2.94 cubs per litter, and a sex ratio of 1:1. State-dependent mortality
96 rates were based on field data from Woodchester Park [27]. Badgers up to two months of age
97 (i.e. while still underground) had a higher mortality rate than older badgers [29]. Animals in the

98 excretor disease classes also had higher mortality rates [27]. Badgers were allowed to disperse,
99 usually to smaller social groups if available [30], based on sex-dependent probabilities (males
100 more often than females) but independent of age and season. Badgers were also moved to
101 neighbouring social groups in response to any demographic imbalance. The probability of
102 transmission between individual badgers was adjusted so the population disease prevalence
103 matched the reported prevalence at the start of the study, estimated at 0.14 [24]. Disease
104 transmission occurred between animals of the same and neighbouring social groups. As badgers
105 interact more frequently with their own social group than with neighbouring groups, within-
106 group transmission was given a greater probability (20-fold) than between animals in
107 neighbouring groups [12]. Transmission probability increased as animals moved from excretor to
108 super excretor class.

109 **Simulation of management operations**

110 Prior to simulation of management operations, the model was run for 100 years to allow the
111 population and disease dynamics to stabilise after seeding. Management operations were
112 simulated by allocating badgers a probability of capture based on the proportion of accessible
113 land (0.94) supplied by DAERA (Menzies, F., pers. comm.) and trapping efficacy rates (0.54) [21].
114 Social groups were allocated to one of two trapping campaigns each year; territories not wholly
115 within accessible land could still be subject to some level of control as badgers could be trapped
116 away from the main sett. Badgers were individually marked during the study so recaptured
117 animals were identifiable and this information was also available in the model.

118 In the field trial, animals were tested trap-side using the Dual-Path Platform VetTB test (DPP)
119 on whole blood samples. In year one (2014), regardless of test result all badgers were vaccinated
120 and released. In years two to five (2015-2018), test positive badgers were culled and test negative
121 badgers vaccinated and released [21]. Field trial methods were replicated in the model with the
122 simulation of one year of vaccination only, followed by four years of TVR. The model simulated
123 DPP testing using a test sensitivity of 0.63 and specificity of 0.94 [24], based on the use of lines 1
124 or 2 in the DPP test under field conditions. In the study, animals were vaccinated with BCG Danish
125 in years 1-3 and BCG Sophia in years 4-5 due to supply issues. It was assumed in the model that
126 both vaccines gave a 0.6 probability of providing full protection from infection for susceptible
127 badgers. Protection was for the lifetime of the badger, with further opportunity for full protection
128 at subsequent capture for animals for which vaccination had previously been unsuccessful. A
129 simulation of the same population with no control was also undertaken to provide a baseline. A
130 total of 100 simulations was run for each model scenario.

131 Field results suggest limited social perturbation resulted from badger removal operations
132 [31, 32]. Therefore, effects of perturbation were not simulated beyond the filling of demographic
133 vacancies in neighbouring social groups described above. Although TVR does result in additional
134 vacancies, there are many fewer than with non-selective culling and this demographic
135 rebalancing contributes little additional transmission compared to the increased ranging
136 behaviour seen in removal operations such as the Randomised Badger Culling Trial (RBCT) in
137 England [33].

138

139 Results

140 Model output is reported for the number of unique badger captures and the number of
141 badgers testing positive using the simulated DPP test; these are compared to results from the
142 study. Model output is also recorded for disease prevalence in the core, buffer, outer area of the
143 arena and mean of the whole arena under TVR and no control; prevalence in the core is compared
144 to the empirical estimate of prevalence from a Bayesian model combining three test methods
145 used in the field trial [24].

146 The number of unique badger captures did not vary substantially over the course of the study
147 as relatively few were removed, and the population recovered before the following year. The
148 model produced a similar result, although the number reported by the model was highest in the
149 first year whereas in the field study the maximum occurred in the second year (Fig1).

150

151 **Fig 1. Comparison between model results and data from the field trial for number of unique**
152 **badger captures in each year of the trial.** Points indicate results from the TVR trial and violin
153 plots show the distribution of model predictions.

154

155 The simulated proportion of captured badgers that tested positive using the cage-side DPP
156 test was in line with the general trend in population prevalence. The number testing positive in
157 the model was in reasonable agreement with the study in each year except 2016, where the field
158 results were unusually low, but even in that year there was overlap between model results and
159 the 95% confidence limits of the empirical estimate (Fig 2). Since in year one (2014), all badgers

160 were vaccinated and released regardless of test result, and in years 2-5 (2015-2018) test positive
161 badgers were removed, for these later years the proportion testing positive is equal to the
162 proportion of captured badgers removed.

163

164 **Fig 2. Comparison between model results and data from the field trial for proportion of**
165 **captures testing positive using the cage-side DPP test in each year of the trial.** Points indicate
166 results from the TVR trial with error bars showing 95% binomial confidence interval, and violin
167 plots show the distribution of model predictions.

168

169 A large benefit of control was seen in the core where population level disease prevalence
170 was predicted to reduce from the initial value of 0.14 to about 0.02, which closely matched the
171 empirical estimate for change in annual prevalence [24] (Fig 3). The simulation was continued to
172 year 2035 assuming no further control was applied (Fig 4). The model predicted prevalence in
173 the core would slowly increase to about 0.05 some 15 years after control ended, although long-
174 term model projections are always less reliable than short-term ones. The outcome when no
175 control was applied was an unchanging population prevalence. A small benefit was seen in the
176 buffer because some groups there may have partly overlapped with participating farms and
177 therefore experienced some removal. There would also have been a small effect over the course
178 of the study as some diseased animals in the higher prevalence buffer will have moved to the
179 core, slightly reducing the benefit of control seen there and also some animals emigrated from

180 the lower prevalence population in the core to the buffer, reducing the level of disease in the
181 buffer.

182

183 **Fig 3. Model results for median annual prevalence in the core area during the control period,**
184 **with the no control scenario shown for comparison.** Shading indicates the inter-quartile range
185 for the model predictions. The dashed line represents the estimated population-level prevalence
186 from each year of the trial [24].

187 **Fig 4. Model results for median annual prevalence in each zone and overall simulated area**
188 **(Arena), predicted to year 2035.** Vertical dotted lines indicate start and end of TVR trial. Shading
189 indicates inter-quartile range for model predictions.

190

191 Discussion

192 In recent decades there has been an increasing reliance on using computer models to predict
193 the consequences of disease outbreaks or disease control. Such models can rarely be validated
194 prior to any control in the field. Here we take the original model used to evaluate a TVR badger
195 control study for bovine TB in Northern Ireland and uniquely validate it against the data from the
196 field trial. Such validation increases support for its use in other locations, or other scenarios.

197 During the five-year field trial a total of 824 badgers were caught, with between 271 and 341
198 unique captures each year [21]. This agrees well with the simulation, although the numbers
199 caught in 2015 were higher than in 2014, whereas in the model the reverse was expected. Each

200 year between 4% and 16% of badgers were removed: i.e., were DPP test positive [21]. This also
201 agrees with our initial expectation of an 83% reduction in the number of badgers culled compared
202 to a proactive cull: i.e., all trapped badgers would have been removed.

203 However, the most important prediction of the model was a substantial reduction in disease
204 prevalence if social perturbation did not occur. During the trial a total of 105 individual badgers
205 were followed using GPS collars, and there was no evidence of a change in home range size,
206 neither annually, nor monthly, between the years of the study [31]. This strongly suggests that
207 social perturbation did not occur in this population during the study. The field trial demonstrated
208 a substantial decline in prevalence during the trial [24], with the last years having a slightly lower
209 prevalence than the simulated results, when we also assumed no social perturbation (Fig 3).
210 Therefore, the model may be slightly conservative about the level of disease reduction. It is also
211 worth noting that we predicted a slow recover of disease in the badger population, but it would
212 require a repeated field study on this site to confirm or deny this longer-term prediction, and in
213 general longer-term model predictions are less reliable as other factors may well occur in the
214 interim.

215 Overall, this points to the success of the model in predicting the effects of the TVR approach
216 in Northern Ireland. Since the simulated output depends most heavily on the badger social
217 groups size and density, it therefore seems likely that the TVR approach would have similar
218 outcomes across Ireland or other areas where badger dynamics are similar, but we cannot
219 immediately extrapolate these results to England and Wales where social group size and density
220 are both higher. However, in many areas in England badgers have been subjected to recent
221 culling, and the density and social group size may now be more similar to the field study. We also

222 did not account for any ongoing transmission from cattle to badgers throughout the trial and this
223 would be expected to ‘seed’ the badger population with more *M. bovis*. Longer term model
224 predictions are always less reliable than short term predictions, due to stochastic drift, changes
225 in populations dynamics, habitat and farming, and the additional seeding that may occur from
226 cattle would further erode the accuracy over time. Thus, we do not place any reliance on the
227 longer-term dynamics of disease in the badger population at this stage. To gain more accurate
228 longer-term dynamics would require linking this model to a cattle TB model, and including cattle
229 management.

230

231 Conclusions

232 Models are often used to evaluate disease management scenarios in both animals and man.
233 Such models are often fitted to field data to help parameterize them, but validation against
234 unrelated field data is uncommon. We used an established simulation model of badgers and
235 bovine tuberculosis and adjusted it to the local situation in Northern Ireland to predict the
236 outcome of a proposed field study of a selective cull/vaccinate strategy. In this paper we report
237 on the output of that model, after parameter changes to exactly fit the start of the field trial. The
238 field study confirmed that no substantial social perturbation was apparent, and the revised
239 model used to make retro-predictions that closely matched the real-world data. This is the first
240 time that the simulation model was validated against badger vaccination and means that the use
241 of the model for badger vaccination in other circumstances, such as in England where the focus
242 is changing from culling to vaccination, should be reliable.

243

244 Acknowledgments

245 The authors would like to acknowledge the help of Fraser Menzies for helpful discussion on both
246 the original modelling for the TVR study, and the start conditions for this follow up analysis.

247

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251 [0414/bovine-tb-strategy-review-government-response.pdf](https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/870414/bovine-tb-strategy-review-government-response.pdf): Defra. Accessed 15/9/2022
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351

352 Supporting Information

353 **S1 Table. Input model parameters.**

354 **S2 File. Model ODD protocol.**

355

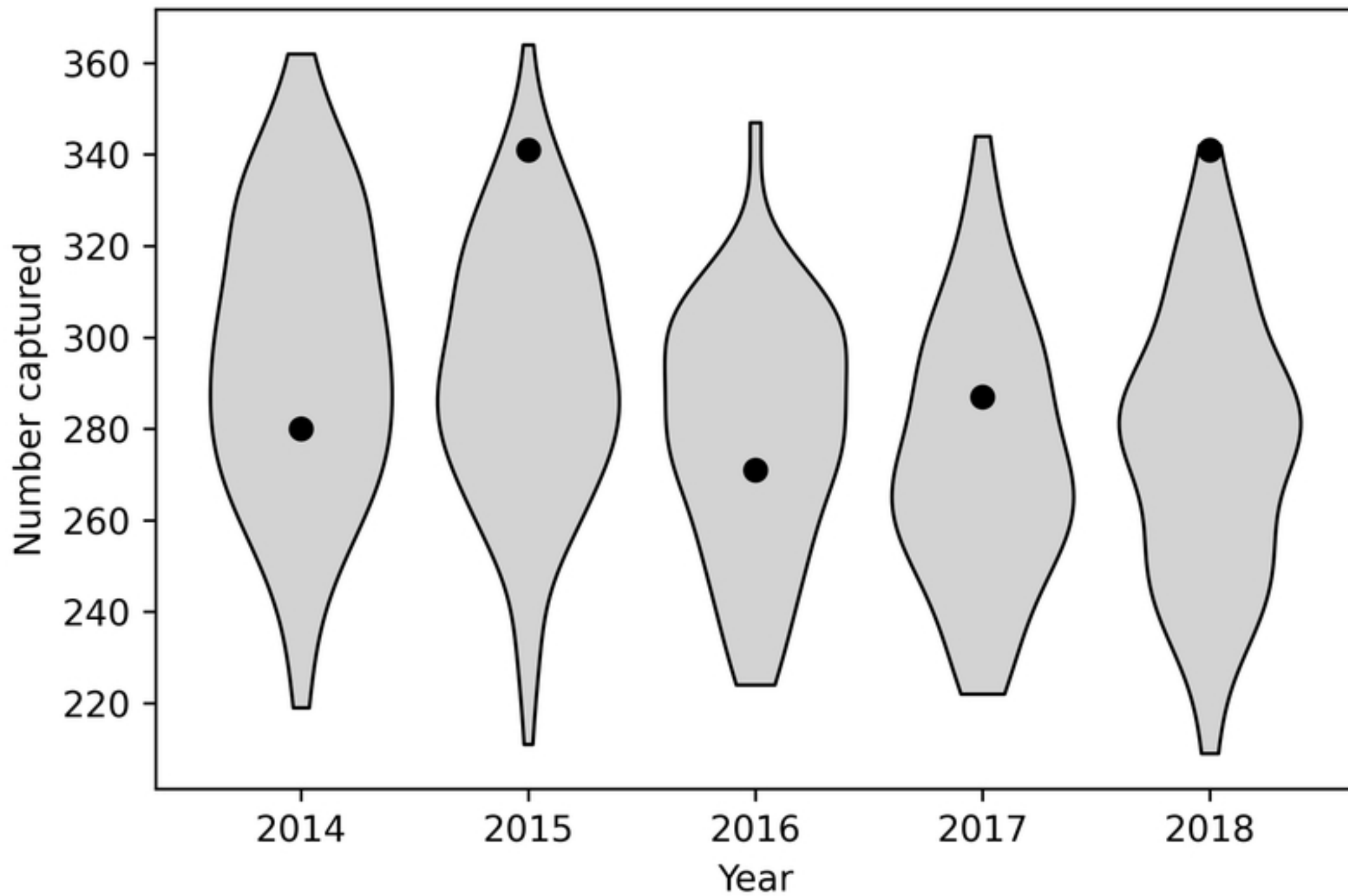


Figure 1

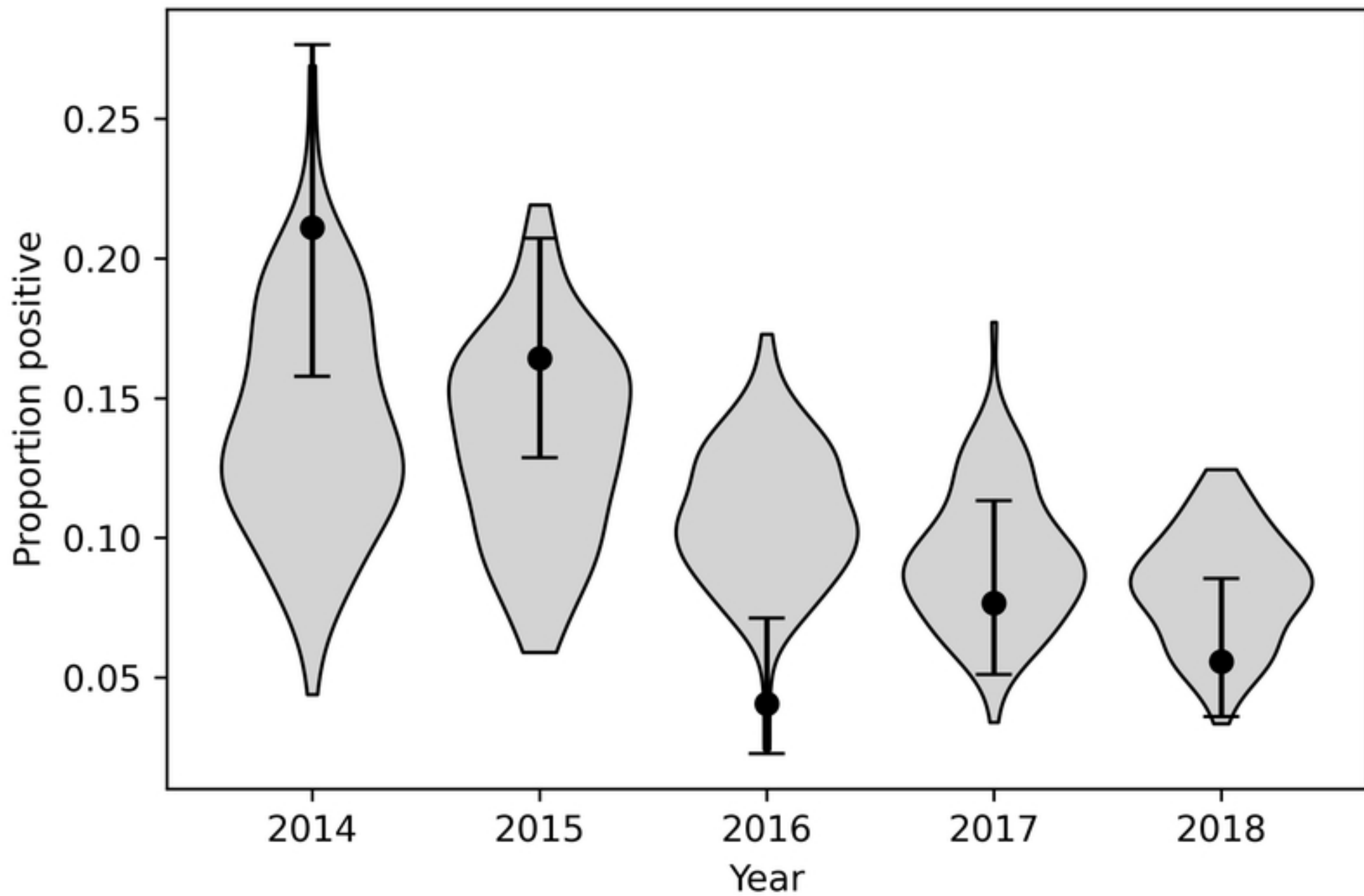


Figure 2

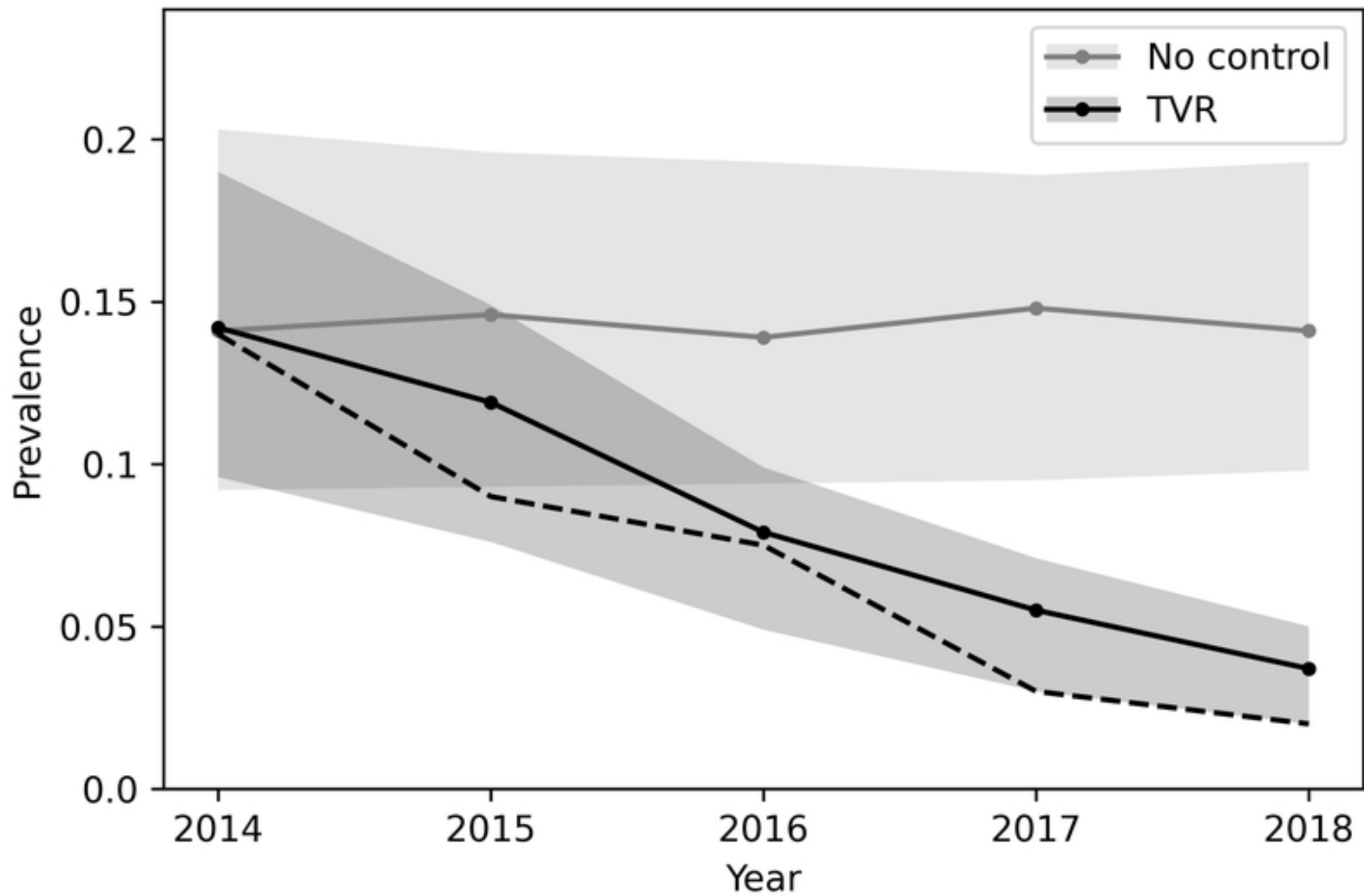


Figure 3

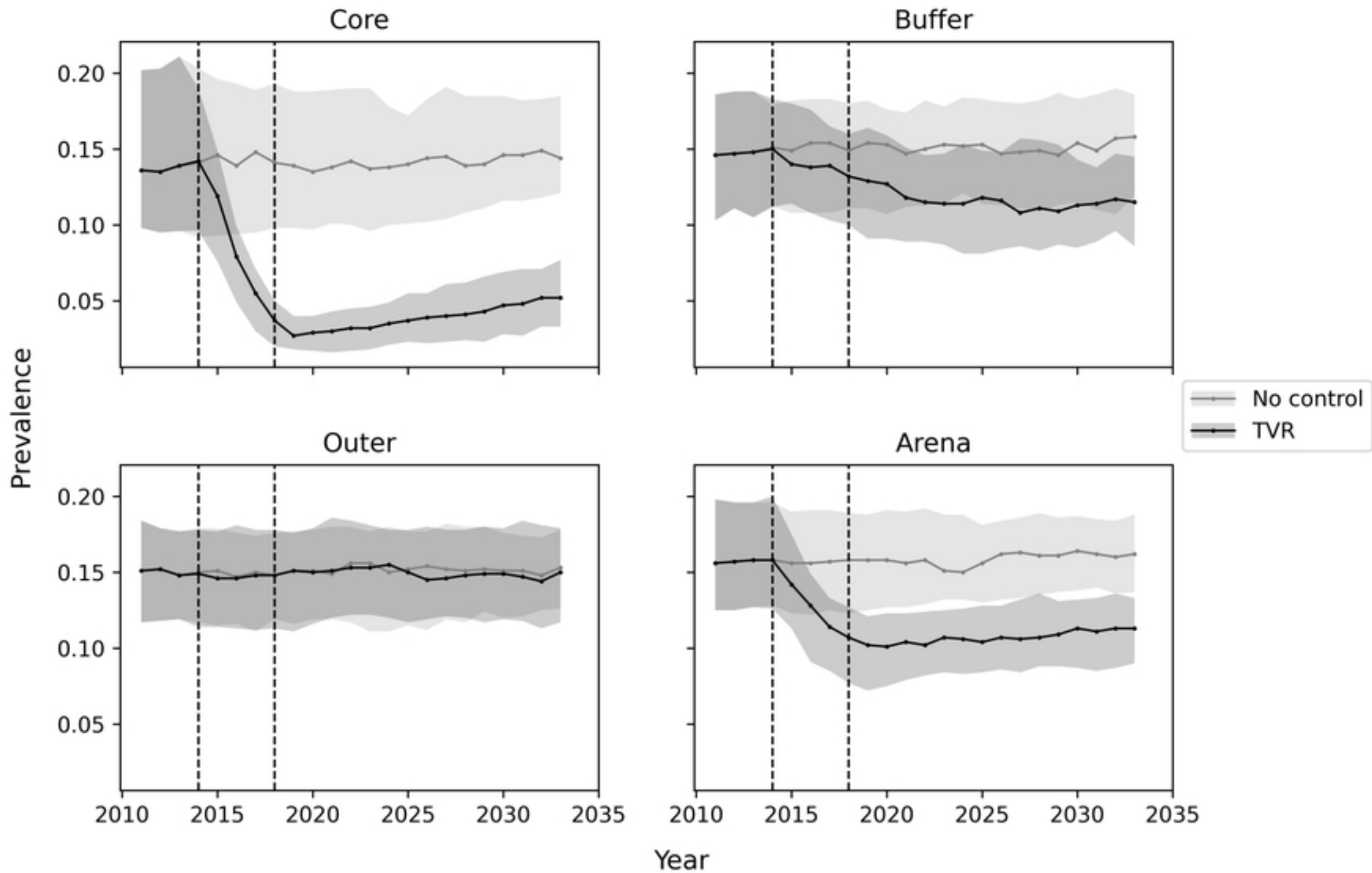


Figure 4