First citizen-science population abundance and growth rate estimates for green sea turtles *Chelonia mydas* foraging in the northern Great Barrier Reef, Australia

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Supplement 1: Assumptions of Capture Mark Recapture Models

Given that 12 years of data were analysed, the population was treated as open because losses and gains are expected, which was confirmed by formal tests of closure following Cooch and White (2017). A model with unconstrained apparent survival (ϕ) had lower AICc (second-order bias corrected Akaike's information criterion) than a model assuming 100% survival ($\phi =1$). Similarly, a model with unconstrained recruitment (f) had lower AICc than the no recruitment model ($f = 0$). Data were therefore modelled with open Capture Mark Recapture (CMR models). Demographic estimates from CMR modelling can be strongly biased if the basic assumptions are violated (Williams et al 2002). For open population models, these assumptions are usually expressed as (after Pollock et al., 1990; Williams et al., 2002):

1) every animal present in the population at time (i) has the same probability of recapture (homogenous catchability),
2) all individuals have equal probability of survival (homogeneous survival),
3) sampling is instantaneous, and
4) marks are unique, retained throughout the study period and identified correctly.

Here, we addressed Assumptions 1 and 2 (homogeneity of rate parameters) using the program U-CARE (version 2.2), based on the fully time-dependent CJS model (Choquet et al., 2009). There was no significant difference in the probability of recapture at $i+1$ between those captured and not captured at occasion i, conditional on presence at both occasions (TEST 2.CT, 'trap dependence' test: $G^2 = 7.21$, $p = 0.301$). Similarly, there was no significant difference in catchability between previously and newly marked individuals (TEST3.SR 'transience' test: $G^2= 1.23$, $p =0.996$), or in the expected time of first recapture between new and old individuals captured at occasion i and seen again at least once (TEST3.SM: $G^2= 1.78$, $p =0.776$). Test component TEST2.CL does not have a simple interpretation in itself (Cooch and White, 2017), and indicated a significant difference in the expected time of next recapture between individuals captured and not captured at occasion i conditional of being present at both occasions i and $i + 2$ ($G^2= 23.933$, $p =0.003$). This was because a large number of animals captured in 2009 were not subsequently seen again (Table S1). Overall, the global goodness of fit test indicated adequate fit (Quadratic $X^2 = 30.489$, $p = 0.248$) and the global estimate of $\hat{c}$ was 1.173, indicating slight over dispersion.

Annual sampling periods in this study were very short in relation to the lifespan of a green turtle (no evidence for violation of Assumption 3, instantaneous sampling). Finally, by using two flipper tags and a standard placement, the rate of tag loss was considered very low (Limpus, 1992) (no evidence for violation of Assumption 4, permanent, unique tags).

A further assumption for JS recruitment and Pradel λ models is that the study area remained constant. This is because an increase in the size of the study area can result in a positive bias in the recruitment parameter (Williams et al., 2002). Although search transects were not recorded (e.g. using a global positioning system) in this study, the area searched during each annual sampling period did not change over time.

Table S1: reduced *m*-array which represents recaptures (columns) from a given release batch (rows). Indices for recapture occasions along the first row are given in the first column. For example, of the 39 green turtles caught in 2006 (capture occasion 4), one was recaptured in 2008 and one was recaptured in 2011.

Year	Released	2	3	4	5	6	7	8	9	10	11	12	Recaptured
2003 (1)	115	1	8	2	0	0	1	0	1	5	1	0	19
2004 (2)	34		0	0	0	0	0	0	0	0	0	0	0
2005 (3)	81			3	0	1	2	0	1	1	3	0	11
2006 (4)	39				0	0	1	0	0	1	0	0	2
2007 (5)	0					0	0	0	0	0	0	0	0
2008 (6)	97						4	0	2	4	6	0	16
2009 (7)	276							3	4	0	18	1	26
2010 (8)	55								5	2	2	0	9
2011 (9)	79									3	6	0	9
2012 (10)	94										18	0	18
2013 (11)	376											5	5
2014 (12)	25												

Supplement 2: Model selection and goodness-of-fit criteria

We initially explored the fit of candidate models based on all combinations of biologically relevant parameters using CJS models, because they have fewer parameters than Jolly-Seber (JS) recruitment models and allow the calculation of deviance as a measure of goodness-of-fit (Williams et al., 2002; Cooch and White, 2017). An information theoretic approach (based on AICc) was then used to select the best models from the candidate models (following Burnham and Anderson, 2002). Where the variance inflation parameter ($\hat{c}$) of the global model indicated over-dispersion, the quasi AIC (QAIC) approach was used to select the best model (Cooch and White, 2017). Models with the highest support from the Akaike weight of evidence (w_i) were then assessed for identifiability errors by parameter counting and examining parameter estimates (following Cooch and White, 2017). Finally, we tested the goodness-of-fit of the final model using a parametric bootstrap (following Amstrup et al., 2005). This estimated $\hat{c}$ as the observed deviance for the model divided by the mean of 1000 simulated deviances (Amstrup et al., 2005). The goodness of fit was then evaluated as the proportion of simulated deviances that exceeded the observed value (Amstrup et al., 2005). Capture histories were simulated in R using the same number of encounters and estimated parameters as the final model.

Recapture probability was too low to support age or sex-specific models. Similarly, even though the time-varying survival model (ϕ_t, p_{effort}) was the most supported by w_i, only 8 of 13 parameters were identifiable. The model with a constant apparent survival was therefore chosen ($\phi\bullet$, p_{effort}). The parametric bootstrap indicated slight overdispersion (observed deviance / mean simulated variance = $\hat{c}$ = 1.087), but that the observed data did not

significantly differ from expected ($p= 0.213$) (Figure S1). Based on these results, we then fitted the POPAN model: $\phi\bullet\ p_{effort}\ b\bullet$, because the low recapture probabilities resulted in identifiability issues with the more complex time-varying formulation ($\phi\bullet\ p_{effort}\ b_t$).

The temporal trend in the annual population estimates was modelled using a non-linear regression (R package nlme version 3.1; Pinheiro et al. 2016), which accounted for variance within years by weighting the fit by the inverse of the variance in annual population estimates. The following non-linear population growth model was fitted:

$$n_t = n_{t-1}\ \lambda_f^{\left(1-\frac{n_{t-1}}{K}\right)}$$

(Equation S1)

which is a conventional model for density-dependent population growth based on the Ricker model (Clark, 2007), where n_t is the number of animals in the population, n_{t-1} is the number of animals in the population in the previous year, k is the carrying capacity and λ_f is the finite rate of population growth. The estimates of λ_f and k were 1.325 (se: 0.0207) and 4448 (se: 118.5), respectively (Figure 4).

We then explored the sensitivity of the models by simulating capture histories for a 'superpopulation' size of 8,233 turtles (gross population estimate) and 12 capture occasions, but different values of ϕ, b and p. This exercise indicated that a recapture probability of 0.02 was sufficient for the POPAN ($\phi\bullet\ p_{effort}\ b\bullet$) and Pradel ($\phi\bullet\ p_{effort}\ \lambda\bullet$) models to detect a rebuilding trend of 8% per annum. The modelling also indicated that the dampening trend exhibited by the annual estimates from the $\phi\bullet\ p_{effort}\ b\bullet$ model was because of the combination of a high survival rate and constant recruitment.
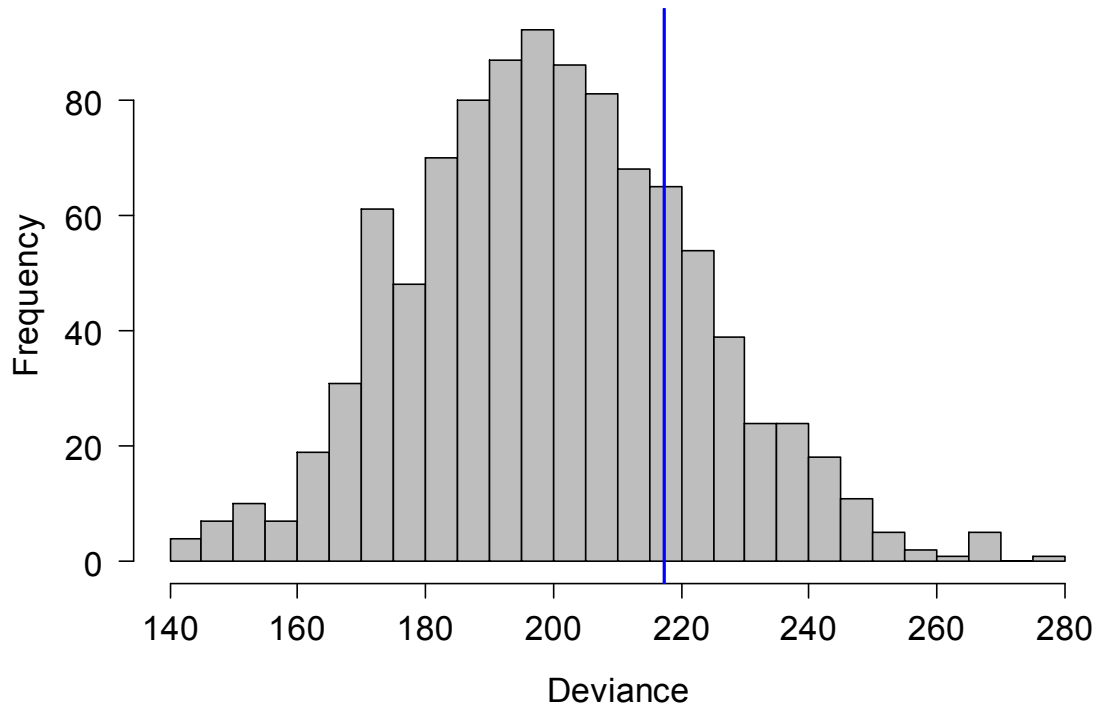

Figure S1: Goodness of fit of the CJS survival model {ϕ,p_{effort}}. The blue line is the deviance observed in the final fitted model compared to simulated deviance from the parametric bootstrap (1000 runs).

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