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Leveraging diverse datasets to assess imperilled species declines: the Sunflower Sea Star in Canada as a case study

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Abstract

Evaluating the extinction risk of species is critical for establishing conservation priorities, yet efforts to do so are often hindered by a lack of targeted scientific monitoring data. Since myriad new forms of data are available from community-sourced (or citizen) science, new analytical approaches are needed to incorporate these data types into the analysis of population trends. Here, we describe an adaptable statistical framework that uses a combination of Bayesian hierarchical and state–space analysis to overcome the challenges of using disparate data types to derive a single estimate of population change. We apply this method to a status assessment of the Sunflower Sea Star (*Pycnopodia helianthoides*) in Canada. By jointly analyzing quantitative observations from formal scientific surveys with semiquantitative observations from community-sourced surveys, we determined that *Pycnopodia* abundance in Canada declined by 82.1% (95% credible interval: 76.0%: 87.2%) following the onset of sea star wasting disease in 2013. Our approach substantially reduced uncertainty around the estimated decline relative to previous analytical frameworks and quadrupled the amount of data that could be used. Applying similar approaches to future species assessments will enable us to harness a greater diversity of data sources and reduce uncertainty in the conservation decision-making process.

Key words: Bayesian state-space model, citizen science, COSEWIC, IUCN Red List, threatened species, time series analysis

Introduction

Assessing long-term population changes accurately is a crucial component of identifying and prioritizing species at risk of extinction. Global and national threatened species assessment frameworks, such as the International Union for Conservation of Nature (IUCN) Red List of Threatened Species, rely on rigorous quantitative estimates of these changes to inform decision-making (Mace et al. 2008). Consequently, data deficiency poses a major barrier to assessing extinction risk (Bland et al. 2017). As many species are not intentionally targeted in long-term monitoring programs before an unexpected decline occurs (Moussy et al. 2022), robust empirical evidence for population declines is often sparse. Undoubtedly, investing in long-term monitoring programs is essential to addressing data deficiency (Schmeller et al. 2017; Scheele et al. 2019). However, at a time of rapid ecological change (Butchart et al. 2010), and with limited resources available to identify and stem population declines (McCarthy et al. 2012), collecting more "gold standard" data for many species is not always possible. Instead, there is an urgent need to develop creative solutions to make better use of the information that is already available, including data from less conventional sources (Edgar et al. 2016; Kindsvater et al. 2018; Johnston et al. 2022).

Community-sourced data (also referred to as "citizen science") initiatives are one such source of unconventional data. These programs have been expanding globally, increasing the amount of information available for many species otherwise lacking formal long-term scientific surveys (Dickinson et al. 2010). The unprecedented spatial and temporal monitoring capacity offered by these programs has begun to resolve issues of data deficiency for some species, but has simultaneously created new challenges for researchers (Dickinson et al. 2010; Johnston et al. 2022). For instance, while the proliferation of community-sourced data programs that record species presence opportunistically (e.g., iNaturalist, eBird) has supported a wealth of research, this type of presence-only data are often inadequate for assessing population trajectories over time (Neate-Clegg et al. 2020). Even in the case of more structured community-sourced surveys that record some measure of abundance (e.g., the Reef Environmental Education Foundation Volunteer Fish Survey Project, North

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American Breeding Bird Survey), data are often excluded from analyses due to concerns about sampling bias or analytical constraints with combining datasets with vastly different sampling methodologies or response metrics. Employing assessment tools that can address these challenges is critical to ensuring the inclusion of as much available data as possible.

Developing methods that can incorporate various data types (including community-sourced data) and generate robust estimates of change from sparse, uncertain, or qualitative information has been identified as a key goal for improving global species assessments (Collen et al. 2016). Advanced statistical models are widely considered an important tool for achieving this goal, as they enable us to overcome issues of bias and variability both in community-sourced datasets (Bird et al. 2014; Isaac et al. 2014) and more broadly (Kéry and Royle 2015). Indeed, there has been a recent push towards applying more advanced modelling approaches to assessments. For example, hierarchical models have been employed to reduce uncertainty in low-resolution monitoring datasets (Post et al. 2022) and a decision-support tool was recently developed to simplify the use of state–space models in IUCN Red List assessments (Sherley et al. 2020; Winker et al. 2020). Conservation practitioners are also increasingly recognizing the utility of probabilistic estimates of uncertainty around declines—such as those generated by Bayesian models—in evaluating risk (Sherley et al. 2020).

Despite these advances, most species-at-risk assessments still rely on relatively simple analyses (e.g., linear models, reductions calculated from two point estimates, etc. (IUCN Standards and Petitions Subcommittee 2022) that preclude the inclusion of unconventional data sources. This may be due in part to practical limitations (e.g., computing time, lack of advanced statistical training), case-by-case variations in data availability, or insufficient guidance on best practices (COSEWIC 2021; IUCN Standards and Petitions Subcommittee 2022). However, variability in survey effort within and among data sources, such as different survey techniques or varying temporal and spatial scales, can create massive uncertainties if analyzed using traditional approaches. For instance, a recent global assessment of the Sunflower Sea Star *Pycnopodia helianthoides* (hereafter *Pycnopodia*) found that the species' abundance had declined >90% across its eastern Pacific range from Mexico to Canada since 2012 (Gravem et al. 2020). The decline was caused by an epidemic of sea star wasting disease, which was first recorded in 2013 and began causing population crashes by 2014 (Hamilton et al. 2021*a*), driven by the bacterium *Vibrio pectenicida* strain FHCF-3 (Prentice et al. 2025). Despite this dramatic overall reduction in *Pycnopodia* abundance, regional analyses using linear models proved highly variable: in several regions, including the entirety of the Canadian range, the declines were not statistically significant under the analytical framework used by the assessors (Gravem et al. 2020; Hamilton et al. 2021*a*). This was due in part to difficulties in incorporating data from a wide range of sampling designs, since the standard density-based approach used in the IUCN population decline assessment required the exclusion of thousands of semiquantitative observations from opportunistic community-sourced surveys. Despite these challenges in regions like Canada and Alaska, the assessors estimated the global population decline of *Pycnopodia* as 90.6%, which met the threshold of "Critically Endangered" by IUCN Red List Criterion A2ae (Gravem et al. 2020). However, for a Canadian assessment of the species, evaluated by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC), the uncertainty within the Canadian range poses a much greater challenge for establishing a national classification for *Pycnopodia*. Analyzing the Canadian portion of this large and complex dataset requires more advanced modelling approaches that can incorporate disparate data sources in a rigorous manner.

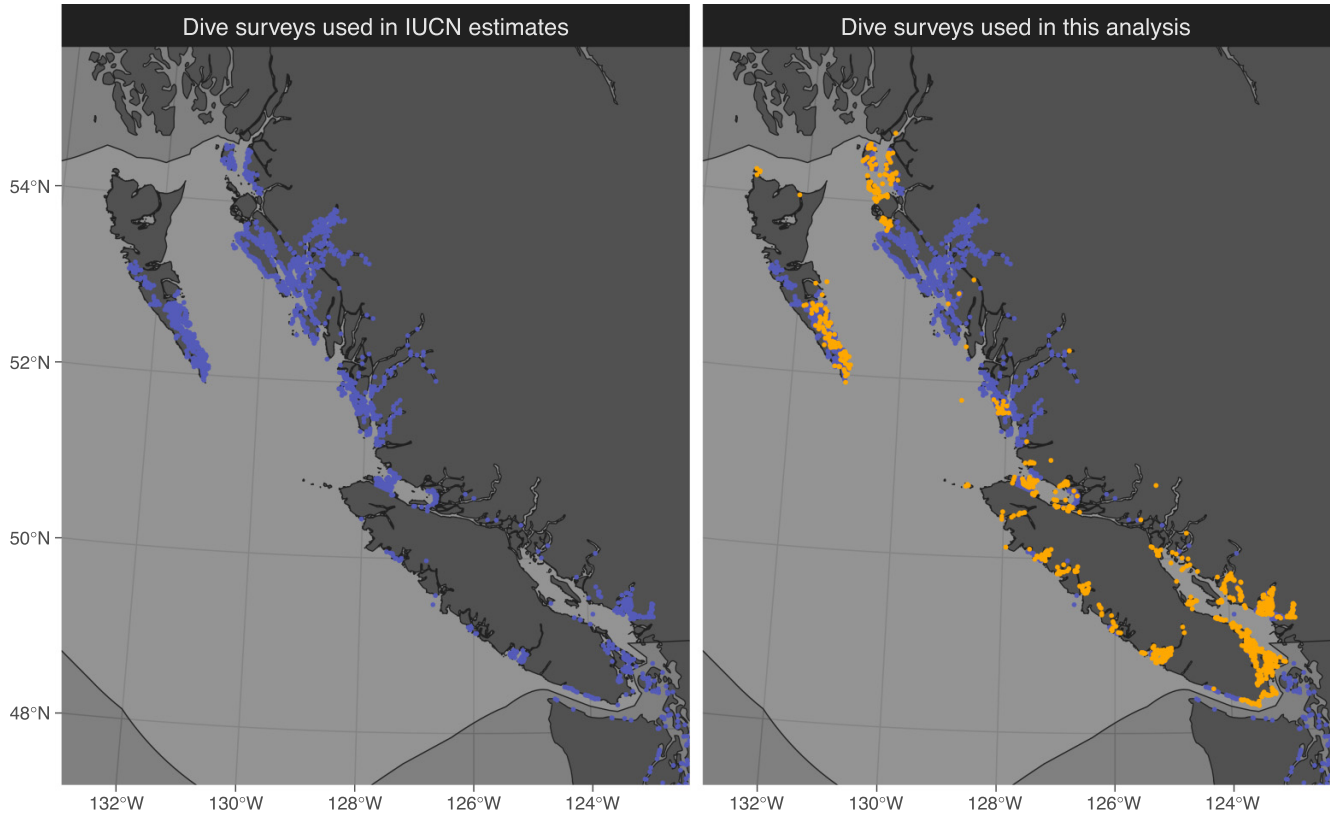
Here, we demonstrate how an easily adaptable population assessment methodology can be applied to integrate quantitative observations from structured scientific surveys with semiquantitative observations from opportunistic community-sourced surveys. As a case study, we employed this framework in a national, Canadian-focused assessment of *Pycnopodia*. We reanalyzed the entire Canadian subset of the dive survey data collected for the IUCN Red List assessment of *Pycnopodia* (Gravem et al. 2020; Hamilton et al. 2021*a*, 2021*b*), including newly available data, together with the thousands of semiquantitative abundance records from community-sourced surveys that were omitted from the global assessment. Our approach draws on recently developed methods for estimating global population declines for the IUCN Red List (Sherley et al. 2020; Winker et al. 2020) and for comparing community-sourced data to structured scientific surveys (Greenberg et al. 2024). Specifically, we addressed three challenges in developing this methodology for species-at-risk assessments: (1) accounting for variability in sampling methods and survey design among data sources, (2) integrating data with different response metrics into a unified analysis, and (3) differentiating between observation error and true population changes over time. Our approach is easily adaptable to a diverse range of data types, making it a useful tool for assessing species that are currently monitored through unconventional, semiquantitative methods.

Methods

Data collection and compilation

The IUCN assessors compiled a dataset of field surveys (including SCUBA dives, submersible (remotely operated vehicle) dives, trawls, and intertidal surveys) from 31 sources that sampled across the global range of *Pycnopodia*, i.e., along the west coast of North America (Gravem et al. 2020). They have since published an updated version of their analyses and made the dataset publicly available (Hamilton et al. 2021*a*, 2021*b*). Ten of these sources contained data from the Canadian range (all from SCUBA dives) and were retained for this assessment (Table S1; Fig. 1), including data collected by First Nations (the CCIRA and Gwaii Haanas datasets), academics (the Simon Fraser-Lee, Simon Fraser-Salomon, Simon Fraser-Schultz, and VIU datasets), governmental and nongovernmental scientists (the Gwaii Haanas and Hakai datasets), and community-sourced data initiatives (the REEF, Pacific Marine Life Surveys, and MARINe datasets). We supplemented the

Fig. 1. Sampling locations of all dive surveys within Canada used in the (*a*) International Union for Conservation of Nature (IUCN) *Pycnopodia helianthoides* population assessment and (*b*) the current analysis. Each point represents a single dive survey. The blue points represent data used in both reports and the yellow points representing additional data used in the current analysis (i.e., the community-sourced data and DFO data). Base map obtained from Flanders Marine Institute (2023).



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IUCN data with government dive surveys conducted by Fisheries and Oceans Canada (DFO; Fig. 1).

All dive surveys used for population decline estimates in the IUCN assessment (as well as the newly incorporated DFO data) employed a belt transect technique, in which divers lay out a line and record all *Pycnopodia* observed in a predetermined area. The other surveys employed a transect-free roving technique, in which divers were able to move freely and record all *Pycnopodia* they encountered, while recording the length of time spent searching. The roving surveys were not included in the IUCN population decline model, as they could not be used to directly estimate densities of *Pycnopodia*; they were, however, retained for an additional analysis in the report examining the probability of occurrence on surveys. Most surveys were intended to census multiple species rather than exclusively *Pycnopodia*, but all surveys retained in our analysis included instructions to record any *Pycnopodia* observed. Thus, any zero included in these datasets represents the absence of *Pycnopodia* on surveys, rather than a lack of data. In total, we retained 9124 dive surveys. Several differences between the datasets make them challenging to combine into a single traditional analysis: some survey programs recorded true counts of *Pycnopodia* as a response variable, while others recorded abundance scores representing a range of numbers of individuals, there was variability in the type of search effort recorded (i.e., time or area), and each survey program differed in its level of spatial and temporal replication.

Statistical analysis

The modelling approach used in this assessment has two major components: (1) generalized linear mixed-effects models (GLMMs) to model dataset-specific population changes and (2) a state–space model (Ward et al. 2010; Holmes et al. 2012; Greenberg et al. 2024), which allows an integrated population estimate to be made from the trends in the dataset-specific GLMMs (see Fig. S1 for simplified schematic of these components).

1. Dataset-specific models (GLMMS)

Each dataset-specific model is a GLMM estimating a time-varying intercept for each year of survey data (i.e., α_t) that tracks mean abundance through time. We included a combination of random (e.g., dive site) and fixed (e.g., log-transformed time or area surveyed, depth) effects in each model, depending on the available data for each dataset. While most of the datasets recorded counts of individual *Pycnopodia* as a response variable, two of the largest datasets (i.e., the Reef Environmental Education Foundation (REEF) and the OceanWise Pacific Marine Life Database (OW)) used discrete abundance scores instead, with REEF data allocated into $K = 5$

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categories (i.e., 0, 1, 2–10, 11–100, >100 individuals observed on a single survey), and OW data allocated into $K = 7$ categories (i.e., 0, 1–10, 11–25, 26–50, 51–100, 101–1000, >1000 individuals). We therefore used two separate approaches for the dataset-specific GLMMs: ordinal logistic regressions for the datasets with abundance scores, and negative binomial regressions for the datasets with counts.

1a. Ordinal logistic regressions

For each dataset i (where i = [REEF, OW]) with abundance scores (w), we developed an ordinal logistic regression, in which an underlying linear predictor η of dive site s, and year t (where t = 2001–2021), is a function of the individual year- (α_t) and site-specific (α_s) abundances, as well as survey-specific covariates for each dataset (β) that may influence detection ability, such as dive time, maximum survey depth, diver experience, visibility, and current:

$$(1)\quad \text{OrderedLogistic}\left(w_{s,t} \middle| \eta_{s,t}, c_{1:K-1}\right)$$

$$(2)\quad \eta_{s,t} = \alpha_t + \alpha_s + \beta X$$

The estimated cut points ($c_{1:K-1}$) categorize the latent linear predictor η into probability intervals for each score bin (k):

$$(3)\quad \begin{matrix} \Pr(k=1) \\ \Pr(k=2) \\ \dots \\ \Pr(k=K-1) \\ \Pr(k=K) \end{matrix} = \begin{cases} \text{logit}^{-1}(c_1 - \eta) \\ \text{logit}^{-1}(c_2 - \eta) - \text{logit}^{-1}(c_1 - \eta) \\ \dots \\ \text{logit}^{-1}(c_{K-1} - \eta) - \text{logit}^{-1}(c_{K-2} - \eta) \\ 1 - \text{logit}^{-1}(c_{K-1} - \eta) \end{cases}$$

We standardized (i.e., centered and scaled) all continuous variables such that the year-specific abundances (α_t) represent an index of abundance at the mean level of survey effort and typical survey conditions. We accounted for some of the potential bias that could be introduced into the estimate of the population trajectory by the overrepresentation of consistently high or low abundance sites in postcrash years by modelling a random effect of site (α_s), such that the annual abundance estimates are reflective of an average-abundance site rather than the sites sampled most frequently in a given year. Thus, α_t functions as an index of abundance that is comparable across years, even when sampling effort varies, and can be used to determine the probability of an individual survey falling into each score (k) in a given year by setting $\eta = \alpha_t$ in eq. 3.

These probabilities can then be multiplied by a chosen count in each category to generate a conservative estimate of the index of abundance for each year (Table S2; Fig. S2). Since most observations in these datasets fell into the lower score bins (i.e., those with the least variability in possible true counts), the choice of which value to use (e.g., the median or the highest count in each category) did not change the estimated rate of decline across years by more than 2% (Table S2). Similarly, simulating a potential count from within each bin for each iteration of the model yielded results nearly identical to that obtained by using the median count within each bin. Throughout this paper, we present the results using the lowest count in each bin, since this yields the most conservative possible estimate of decline. In some cases, it may be more appropriate to choose one of the other approaches, and in all cases, we recommend assessing the sensitivity of this decision.

1b. Negative binomial regressions

We modeled each of the remaining datasets (i = DFO-Abalone, DFO-Multispecies, and the combined small datasets from the original IUCN analysis), that report true counts of *Pycnopodia* (y), with a GLMM with a negative binomial distribution using a quadratic parameterization with an expected mean count (μ), inverse shape parameter (ϕ), and a log link function:

$$(4)\quad \text{NegativeBinomial}\left(y_{s,t} \middle| \mu_{s,t}, \phi\right)$$

$$(5)\quad \mu_{s,t} = e^{(\alpha_t + \alpha_s + \beta X)}$$

$$(6)\quad Var\left(y_{s,t}\right) = \mu_{s,t} + \frac{\mu_{s,t}}{\phi}$$

or a zero-inflated negative binomial regression if the posterior predictive check of the standard negative binomial model substantially underpredicted the number of zeros in the data (Kéry and Royle 2015):

$$(7)\quad ZI - \text{NegBin}\left(y_{s,t} \middle| \theta, \mu_{s,t}, \phi\right) = \begin{cases} \theta + (1-\theta) * \text{NegBin}\left(0 \middle| \mu_{s,t}, \phi\right) & \text{if } y_{s,t} = 0 \\ (1-\theta) * \text{NegBin}\left(y_{s,t} \middle| \mu_{s,t}, \phi\right) & \text{if } y_{s,t} > 0 \end{cases}$$

As with the ordinal logistic regressions, α_t functions as an index of abundance that is comparable across years, even when sampling effort varies.

2. State–space model

The annual abundance estimates from the GLMMs ($\alpha_{i,t}$) reflect an underlying population state x_t (i.e., the estimated index of the true population) with varying degrees of observation error within each survey. We chose to model a single underlying population state, as *Pycnopodia* in Canada are considered to belong to a single designatable unit (i.e., a discrete and evolutionarily significant unit of biodiversity; COSEWIC 2020), with no evidence for large-scale genetic structure. Each dataset has its own estimate of independent annual observation errors ($v_{t,i}$, which accounts for sources of variation such as missed observations or targeting sites that are unrepresentative of the true population), which are assumed to be drawn from a normal distribution centered on 0 with variance r_i. This underlying population state itself is derived from a first-order autoregressive process, in which the population index at a given year t (i.e., x_t) differs from the previous year's population index (i.e., x_{t-1}) by an average annual change, u_{period} (which represents the long-term, consistent trend across a given time period), and an annual process noise w_t (which represents year-specific demographic fluctuations). This annual process noise is assumed to be drawn from a normal distri-

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bution centered around 0 with variance q. The average annual change, u_{period}, represents a vector of three different values: one for years prior to the start of the sea star population crash in 2014, one during the years of the crash in Canada from 2014 to 2015, and one after the crash ended from 2015 to 2021, the last year of surveys considered here. We selected these time periods based on the well-documented timeline of the onset of SSWD (Hamilton et al. 2021*a*) and the fact that the estimated process noise in these years is nearly four times greater than the next highest year if the periods are not modelled. By modelling each period separately, we ensure that the extreme declines observed during the crash years do not artificially inflate the estimate of the process noise variance and therefore do not lead to an underestimation of observation error. This also allows for assessments of how stable the population was prior to the crash as well as of any signs of recovery or further decline following the crash:

$$x_t = x_{t-1} + u_{\text{period}} + w_t \quad w_t \sim N(0, q) \tag{8}$$

$$\begin{bmatrix} \alpha_{t,\text{REEF}} \\ \alpha_{t,\text{OW}} \\ \alpha_{t,\text{small}} \\ \alpha_{t,\text{DFO}a} \\ \alpha_{t,\text{DFO}m} \end{bmatrix} = x_t + \begin{bmatrix} 0 \\ d_{\text{OW}} \\ d_{\text{small}} \\ d_{\text{DFO}a} \\ d_{\text{DFO}m} \end{bmatrix} + \begin{bmatrix} v_{t,\text{REEF}} \\ v_{t,\text{OW}} \\ v_{t,\text{small}} \\ v_{t,\text{DFO}a} \\ v_{t,\text{DFO}m} \end{bmatrix} \quad v_{t,i} \sim N(0,\ r_i) \tag{9}$$

Each dataset may have a constant difference in expected abundance (d_i, e.g., in cases where certain datasets targeted consistently high-density sites or had consistently higher sampling effort). We chose to use the REEF dataset as the baseline to estimate these differences, as it had the largest number of surveys, encompassed the largest geographic range of survey sites, and was not solely targeting *Pycnopodia* (to avoid potential overestimates of decline caused by site-selection bias; Fournier et al. 2019; Table S1; Figs 1, S3). Consequently, the underlying population states and all annual estimates of abundance presented in this assessment are scaled to the REEF dataset for ease of visualization (but see Fig. S4 for unscaled results for each dataset). The choice of baseline dataset does not impact the relative annual changes in the population index, only the absolute values.

Due to the rapid and well-defined period of the population crash and the relative stability of the population before and after the crash (see *Results*), we then calculated the mean pre and postcrash indices of abundance and the percent reduction between them once for each iteration of the model sampler. The median, 2.5%, and 97.5% quantiles of the reduction were then extracted from the resulting distribution to determine the total estimated population reduction and the 95% credible interval. For populations exhibiting continuous declines over time, our approach can be adapted to calculate the percent change over time following the methods of Winker et al. (2020), i.e., calculating a 3-year median around the year three generations prior to the final year of data, and a 3-year median around the final year of data.

The entire model was run in the probabilistic programming language Stan version 2.32.2 (Stan Development Team 2023) using the cmdstanr package (Gabry et al. 2023) in R version 4.3.1 (R Core Team 2023). Regularizing priors were chosen for each parameter (Table S3) to constrain parameter estimates to realistic values and improve model convergence without providing information on assumed directionality of effects. We assessed model convergence using Gelman–Rubin statistics with a threshold of 1.01, visual inspection of traceplots, and effective sample sizes of >1000 (Gelman et al. 2013). We assessed model fit using posterior predictive checks from the bayesplot package (Gabry and Mahr 2022) and standardized residual checks from the DHARMa package (Hartig 2022).

Finally, in the original IUCN report, uncertainties around the declines were high enough to yield nonsignificant results but were not explicitly presented. We therefore reanalyzed the Canadian subset of the data used in the IUCN report using the methods originally employed (Gravem et al. 2020; Hamilton et al. 2021*a*) and our new model to directly compare our estimates of uncertainty. To repeat the IUCN analysis, we ran a linear model on the densities of *Pycnopodia*, using the interaction between the time period (i.e., pre- or post-crash) and the geographic region (i.e., the Salish Sea, $n = 331$, and the rest of British Columbia, $n = 1309$, as presented in the IUCN report) as fixed effects.

Results

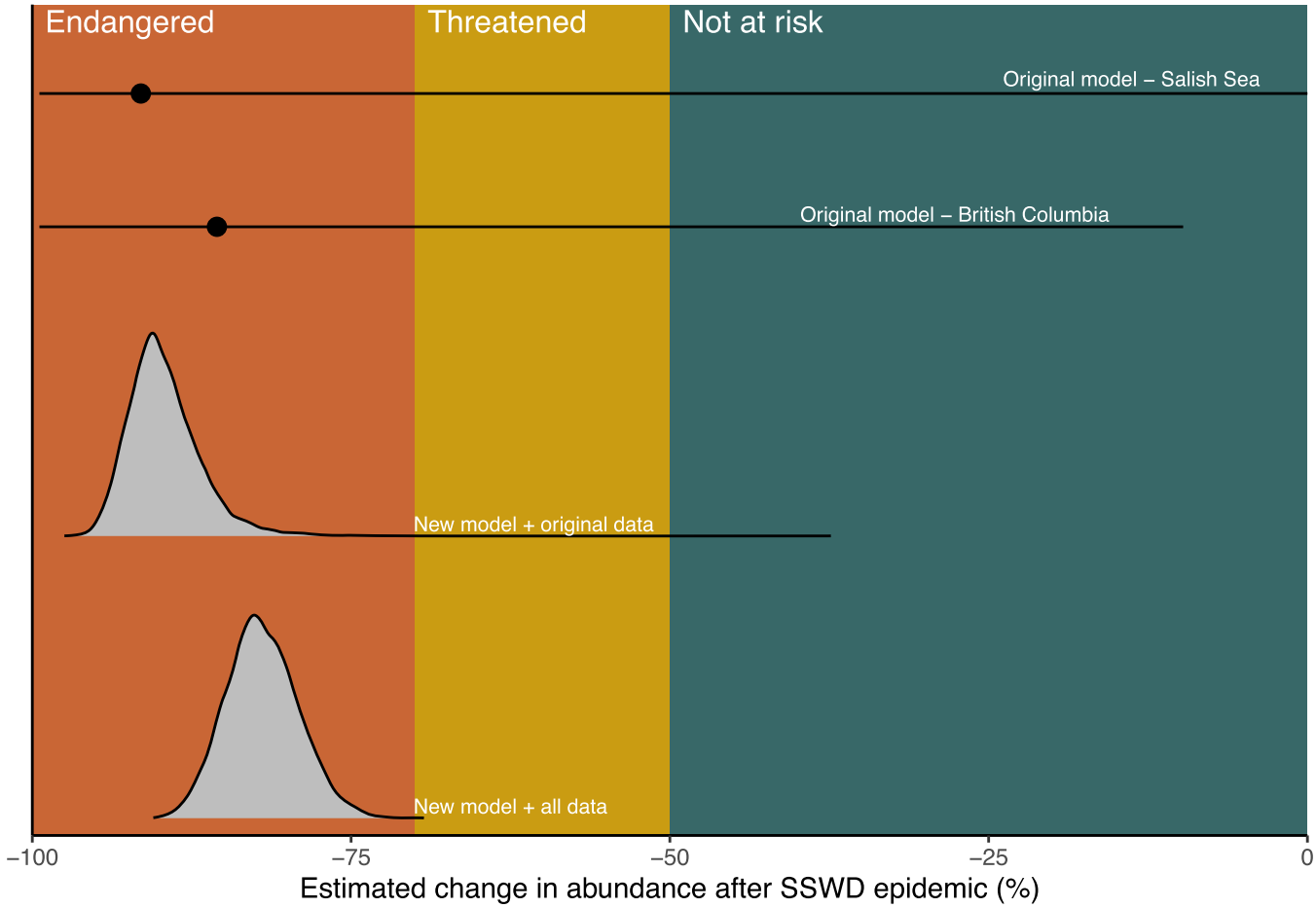
The estimated reduction in abundance of *Pycnopodia* in Canada between 2000 and 2021 was 82.1% (95% credible interval: −76.0%: −87.2%; Fig. 2), with most of the decline occurring over two years (i.e., 2014 and 2015; Fig. 3). Prior to 2014, the population appeared relatively stable ($u_{\text{prewasting}} = 0.02$, 95% credible interval −0.10 to 0.13; Table S4), and it has shown limited recovery since the crash ($u_{\text{postwasting}} = -0.08$, 95% credible interval −0.27 to 0.11).

Using our model on the Canadian subset of data used in the global IUCN analysis yielded a similar median estimated reduction (−90.5%) to the published IUCN estimates for the Salish Sea and the rest of British Columbia (−92.4% and −87.9%, respectively; Fig. 2). However, our model reduced the uncertainty in these estimated declines from confidence intervals that spanned the entire range of possible threat categories (−100% : +137.4% and −100% : −9.8%) to a credible interval that only encompassed the Endangered category (−83.3% : −94.6%). The addition of the community-sourced data to our analysis yielded a similarly narrow credible interval (−76.0% : −87.2%), but reduced the median estimated magnitude of decline to 82.1%.

Discussion

Overall, using a combination of Bayesian hierarchical and state–space modelling approaches, we consolidated data from 12 disparate sources into a single, integrated estimate of population decline of the Sunflower Sea Star *P. helianthoides*. By using an approach capable of modelling integrated population trajectories from ordinal data alongside count data (Greenberg et al. 2024), we were able to incorporate into our analysis more than four times the number of dive sur-

Fig. 2. Estimated population reduction of *Pycnopodia helianthoides* following the onset of sea star wasting disease (SSWD) based on the original and current modelling frameworks. The points and error bars represent the mean estimates and 95% confidence intervals based on the linear models used in the initial IUCN report. The grey areas represent the posterior probability of the reduction (i.e., the distribution of estimated reductions from 12 000 iterations of the model) from the current modelling framework. Colour bands represent the threat classification thresholds applied over three generations of change by the Committee on the Status of Endangered Wildlife in Canada under Criterion A1.



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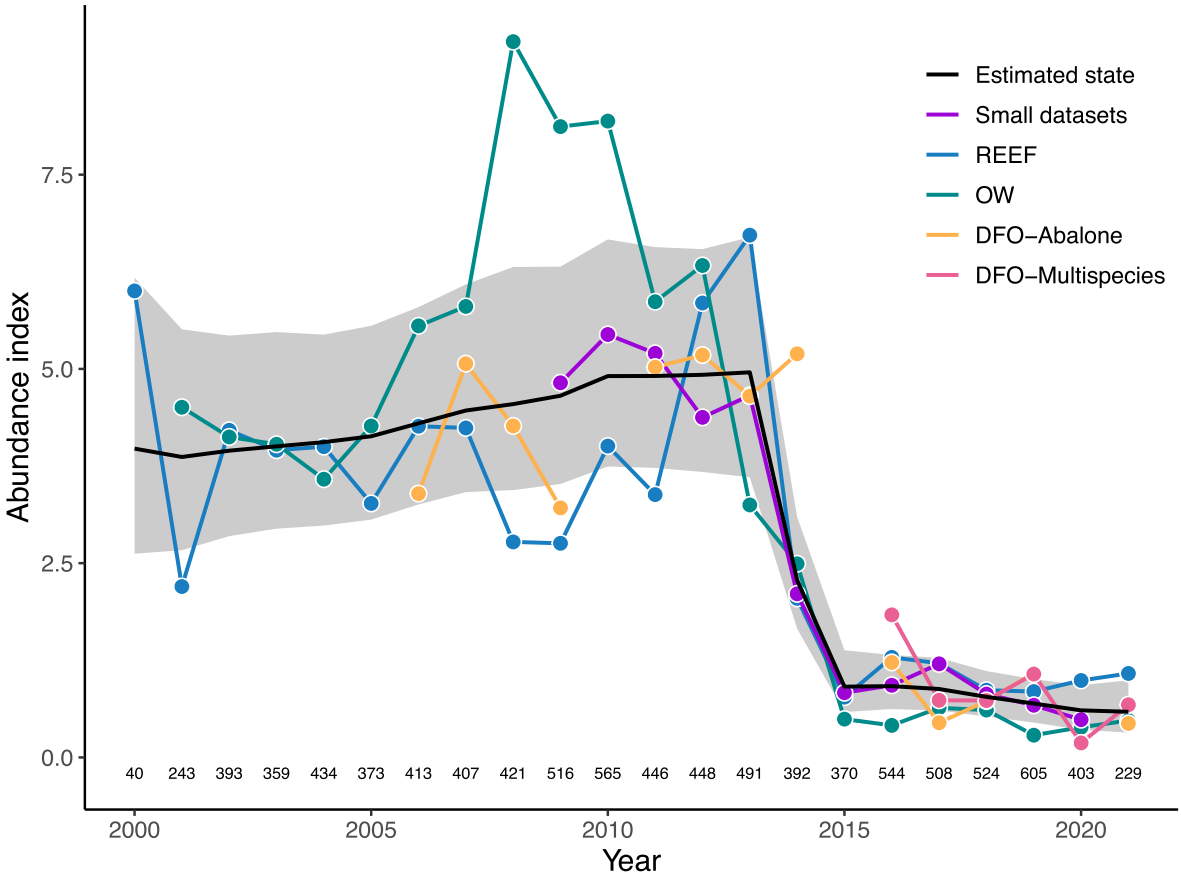
veys used for the Canadian range in the global IUCN assessment. Based on COSEWIC's quantitative criterion A2, *Pycnopodia* would be considered "Endangered" if there were a reduction of at least 50% of mature individuals over three generations and no known way to reverse the driver of decline. Our results suggest with 100% certainty that *Pycnopodia* in Canada meet this threshold. Even under the more restrictive criterion A1, our results suggest with 99.97% certainty that *Pycnopodia* meet the threshold of a reduction of at least 70% of mature individuals over three generations (Fig. 2).

The benefits of using our framework were twofold. First, the state–space model drastically reduced uncertainty in the estimated population reduction, even when using the same subset of data as in the IUCN assessment (Fig. 2). Second, the inclusion of the community-sourced data reduced the estimated population reduction from 90.1% to 82.2%, likely because of a reduction in site-selection bias. As formal scientific surveys often target sites with higher initial abundances of focal species (Pechmann et al. 1991; Palmer 1993; Fournier et al. 2019), estimates of decline generated from these surveys can often be biased simply due to regression to the mean (Barnett et al. 2005). Multispecies surveys are generally less prone to these site-selection biases (Fournier et al. 2019)—thus, modelling frameworks that allow for the inclusion of these nontargeted surveys can help solve, or at least reduce, issues of bias in estimates of decline. For *Pycnopodia* in Canada, these methodological advantages mean that we are as close to certain as can be that the species is endangered.

Despite their current limited use in species-at-risk assessments, the model components used in our analysis have been well developed for ecological time-series (Dennis et al. 2006; Auger-Méthé et al. 2021; Goodsell et al. 2021; Greenberg et al. 2024) and can address many of the issues that normally afflict species assessments based on the population decline criterion (Sherley et al. 2020). For instance, both process noise and observation error can lead to inaccurate estimates of population trends (Connors et al. 2014; Auger-Méthé et al. 2016; Rueda-Cediel et al. 2018). However, state–space models are less sensitive to outliers than classical regression approaches, and modelling replicated samples from the same population

Fig. 3. The observed population trajectory (solid black line, 95% credible interval: grey ribbon) of *Pycnopodia helianthoides* in Canada over the past two decades (2000–2021; $n = 9124$ surveys). Coloured points and lines represent the annual abundance estimate from each dataset-specific model. The number of surveys conducted each year across all datasets is shown at the bottom of the figure. All datasets have been scaled to the Reef Environmental Education Foundation (REEF) dataset for visualization (see Fig. S4 for unscaled results). The abundance index therefore represents the number of *Pycnopodia* expected to be observed on a typical REEF survey (i.e., a 47.6 min long roving survey) in a given year.



using a multivariate analysis allows for a more reliable estimation of parameters (Dennis et al. 2010). Additionally, the outputs of Bayesian state–space models can often improve conservation practitioners' understanding of uncertainties in risk relative to simpler model outputs (Sherley et al. 2020). For instance, while a 95% confidence interval around an estimate of decline can inform practitioners of the range of possible threat classifications, a Bayesian posterior distribution explicitly shows how the balance of probability is divided across each threat classification (e.g., Fig. 2).

Our approach also offers a potential avenue for more thoughtfully including Indigenous Knowledge Systems in species-at-risk assessments, an area on which there is currently little guidance (COSEWIC 2017; IUCN 2022). Processes that allow for separate consideration of Indigenous and Western Knowledge Systems through two distinct sets of assessment criteria (e.g., Northwest Territories Species at Risk Committee 2022; Singer et al. 2023) are arguably the most equitable approach to weaving knowledge systems together without engaging in knowledge extraction (McGregor 2021); however, most national and international species-at-risk assessment processes currently require a single, integrated assessment (COSEWIC 2021; IUCN Standards and Petitions Subcommittee 2022). Our model provides a format to treat data collected using disparate methodologies on more even footing within this context, by enabling data collected through interviews with Indigenous knowledge holders (e.g., descriptions of relative abundances over time) to directly inform population trend estimates alongside quantitative data. In our case, several First Nations shared data from formal scientific surveys with us for this analysis, which allowed for a straightforward inclusion of these data into both our model and the previous global assessment. In other cases where Indigenous communities have other forms of data or knowledge that they wish to be considered in status assessment models, our approach would provide the flexibility needed to analyze this information more equitably.

Data requirements and limitations

We recognize that data formats and availability will vary for any species undergoing assessment; we therefore offer

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our approach as a scaffolding for other assessments rather than a one-size-fits-all framework. Our approach is useful when quantitative (i.e., direct counts) or semiquantitative (e.g., scores relating to ranges of possible counts, relative abundances described in interviews) data that reflect relative abundances are available. Some measure of survey effort (e.g., time or area) and reports of absences of individuals are both necessary to make reasonable estimations of trends. Consequently, presence-only data (e.g., iNaturalist sightings) and presence–absence data are not amenable for this approach (though they can be valuable for assessments using alternative approaches such as occupancy modelling; Johnston et al. 2022).

Several key components of our model may need to be adjusted on a case-by-case basis. For instance, since *Pycnopodia* on the Pacific coast of Canada is considered a single population by COSEWIC, we chose to model a single underlying population state for all data. Modelling a shared population index allowed all of the data to inform the year-to-year changes in the underlying state, with datasets with higher sample sizes having a stronger influence on overall trends since they contribute more to the model likelihood. In other cases, it may be more appropriate to weight datasets equally, regardless of sample size (e.g., if a dataset with a relatively small sample size was known to have relatively low observation uncertainty). Additionally, if an assessed species spans multiple designatable units, multiple correlated processes could be modeled simultaneously to better reflect regional variability in population trends (Holmes et al. 2021)—and if there is evidence of spatial autocorrelation in a dataset, our model could be extended to include an explicit consideration of spatial structure, including through the addition of a Gaussian random field (e.g., Anderson et al. 2022) or a Gaussian process (e.g., Wright et al. 2021) on the site-specific effects. To test whether spatial variability in sampling biased our estimate of the decline, we reran our model with an additional time-varying effect of region within each dataset (see Supplementary Material). There were no consistent regional differences (i.e., no region showed consistently high or low counts across all datasets), and model comparison using leave-one-out cross-validation (Vehtari et al. 2017) showed that the model with a region effect did not outperform the base model.

Future simulation testing would be required to determine the full range of situations in which it is appropriate to integrate ordinal and count data into a single trend estimate. For species frequently observed in the highest abundance category, it would be challenging to detect any population changes over time using ordinal methods, which would likely cause a mismatch between count data and ordinal data in years of extremely high abundance. However, for most threatened species, observations of consistently high abundance across surveys are unlikely, making ordinal data more comparable to count data (Fig. S2). It should also be noted that the methods employed in community-sourced data collection may not always be sufficient to capture trends in rare or cryptic species that are difficult to identify (Callaghan et al. 2021). Observer skill is a relatively minor issue for conspicuous, slow-moving species such as *Pycnopodia*, and volunteer divers were unlikely to be disproportionately targeting sites with high initial *Pycnopodia* abundances, reducing potential biases in our data relative to some species.

Conclusion

Marine invertebrates such as *Pycnopodia* lack many of the characteristics that are generally considered high priority for the development of long-term monitoring programs (Possingham et al. 2002; Mammola et al. 2020): they are neither charismatic, commercially valuable, nor already listed under national species-at-risk legislation. This perpetuates their ineligibility for assessments through typical venues—without monitoring, it is nearly impossible to list a species, but without a listing, it is challenging to attain funding for the necessary monitoring. However, by leveraging diverse and less conventional data types, we were able to form a clear picture of the status of this species even in the absence of specific formal monitoring. By ensuring that all existing information, including that gathered by community-based scientists and shared local or Indigenous knowledge, is used, some of the biases in monitoring prioritization can be alleviated, which may ultimately contribute to a more balanced taxonomic representation in protected species lists.

In a time of accelerating ecological change, conservation practitioners are often charged with making management decisions amid great uncertainty (Polasky et al. 2011). Reducing some of this uncertainty in estimates of decline can relieve tensions that arise between evidentiary and precautionary approaches to listing species at risk of extinction (Akçakaya et al. 2000; Collen et al. 2016; Romeiras et al. 2016), and more accurately quantifying the remaining uncertainty compels practitioners to explicitly define their willingness to tolerate risk (Post et al. 2022). Our analytical approach for modelling species abundances over time achieves both of these aims by simultaneously increasing the number of data sources (e.g., from community-sourced data initiatives) that can be used in assessments, explicitly accounting for sampling biases and variability through hierarchical modelling, and generating continuous probabilistic estimates of population declines. The widespread application of advanced analytical techniques to better harness the diversity of existing data will be critical to effectively tackling major conservation issues.

Acknowledgements

We thank Fisheries and Oceans Canada for funding this assessment, as well as Jackie Hildering for initiating the assessment process. We thank the initial IUCN assessment team (Walter Heady, Vienna Saccomanno, Kristen Alvstad, Alyssa Gehman, and Taylor Frierson) for the immense amount of work they conducted to compile the datasets used in this manuscript, and Kyle Wilson and Colin Bailey for statistical advice. Finally, we are extremely grateful to the many data contributors, without whom the assessment and this manuscript would not have been possible. Our full list of ac-

knowledgments of individual data contributors can be found in the Supplementary Material.

Article information

Editor
Britt Dianne Hall

History dates
Received: 28 July 2025
Accepted: 16 December 2025
Version of record online: 27 April 2026

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Data availability
Code and data related to this publication are available on Zenodo: https://doi.org/10.5281/zenodo.18274840.

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Competing interests
The authors declare no competing interests.

Supplementary material

Supplementary data are available with the article at https://doi.org/10.1139/facets-2025-0245.

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