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OPINION

Predicting the future of our oceans—Evaluating genomic forecasting approaches in marine species

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Abstract

Climate change is restructuring biodiversity on multiple scales and there is a pressing need to understand the downstream ecological and genomic consequences of this change. Recent advancements in the field of eco-evolutionary genomics have sought to include evolutionary processes in forecasting species' responses to climate change (e.g., genomic offset), but to date, much of this work has focused on terrestrial species. Coastal and offshore species, and the fisheries they support, may be even more vulnerable to climate change than their terrestrial counterparts, warranting a critical appraisal of these approaches in marine systems. First, we synthesize knowledge about the genomic basis of adaptation in marine species, and then we discuss the few examples where genomic forecasting has been applied in marine systems. Next, we identify the key challenges in validating genomic offset estimates in marine species, and we advocate for the inclusion of historical sampling data and hindcasting in the validation phase. Lastly, we describe a workflow to guide marine managers in incorporating these predictions into the decision-making process.

KEYWORDS
adaptation, climate change, genomic offset, marine species, validation

1 | INTRODUCTION

Climate change results in severe environmental fluctuation, with recent years being the warmest on record throughout the industrial period (Cheng et al., 2023). The global increase in average temperature is accompanied by a suite of environmental changes including increases in the frequency and intensity of extreme weather events, regional temperatures, atmospheric water vapor, and ocean heat, as well as decreases in pH, dissolved oxygen, and sea ice cover. For marine ecosystems, increased glacial runoff and rising sea temperatures pose significant challenges (He & Silliman, 2019). The consequences of these impacts are evidenced by distributional shifts in many taxa (e.g., Poloczanska et al., 2013), with populations at the trailing edge declining and populations at the leading edge shifting poleward or into deeper waters (Pinsky et al., 2020; Polyakov et al., 2020). In fact, marine species and the fisheries they sustain appear to be more vulnerable to climate change than their terrestrial counterparts (Pinsky, 2021). Given the global reliance on marine resources, these changes will undoubtedly impact food security and economic stability (Payne et al., 2021). Consequently, there is a need to "future-proof" marine ecosystems and conservation areas through proactive management based on a sound

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understanding of the ecological and genetic impacts of climate change (Tittensor et al., 2019).

There is a pressing necessity to predict climate change impacts in marine species and ecosystems to inform conservation planning and strategies. These predictions are particularly relevant to global fisheries and aquaculture, which provide a major source of nutrition to many countries (Béné et al., 2016). For instance, ocean warming has been linked to significant decreases in production capacity and shifts in the distribution of fisheries-targeted species (e.g., tuna, Monllor-Hurtado et al., 2017). Predicting range shifts in marine taxa remains a significant challenge and ultimately requires information on existing ranges, predictions of future environments, capacity for adaptive and plastic responses to environmental change, dispersal potential, and ecosystem structure and function. Marine species' ranges largely conform to their thermal limits (Sunday et al., 2012) and therefore even small changes in the thermal profile of a given marine region can have measurable consequences on population survival and subsequent extirpation.

A growing body of research has focused on developing tools to predict the impacts of climate change on wild populations. Ecological niche modelling—akin to species distribution modelling (SDM)—has been used in the last 20 years to map the probability of occurrence of a species across a landscape (Kearney & Porter, 2009). However, traditional SDMs do not consider adaptive responses of populations to environmental change, for instance, through multigenerational selection of advantageous genomic variants (e.g., standing genetic variation), or through the expression of epigenetic variants leading to acclimation via phenotypic plasticity. More recently, genomic offset—also termed genomic vulnerability (Bay et al., 2018)—has been applied to both terrestrial and marine taxa to predict potential future maladaptation driven by climate change (e.g., Fitzpatrick & Keller, 2015; Láruson et al., 2022; Layton et al., 2021). This approach maps the contemporary spatial turnover of adaptive alleles onto current environmental conditions and then calculates the offset between present and future climate-associated genomic composition as a measure of maladaptation to climate change. In other words, genomic offset is an estimate of the change in genomic composition that would be required to track predicted climate change. Despite some limitations and challenges, including validation and management buy-in (Rellstab et al., 2021), the approach seems to accurately estimate climate change vulnerability when compared to experimental predictions (e.g., Fitzpatrick et al., 2021). Bernatchez et al. (2023) provide a comprehensive overview of this method, among others, in their recent review of genomics-based monitoring approaches, but to date, no study has assessed these methods in specific ecological contexts. Given the potential of genomic offset estimates to inform climate change predictions, and the observation that marine species are already being impacted by climate change, an evaluation of the method's applicability to marine species is warranted.

There are several reasons why estimating genomic offset can be useful for managing and conserving marine ecosystems and species. The poikilothermic nature of most marine fish, invertebrates, and macrophytes means that temperature is often a dominant selective pressure driving adaptive genetic diversity across populations. The low genetic structure and generally large effective population sizes (N_e) often observed within marine species (Bradbury et al., 2008) means that the influence of genetic drift is typically minimal compared with that of natural selection. Moreover, many marine species occupy large latitudinal ranges and genomic approaches have repeatedly demonstrated putative adaptation across these variable environments. Taken together, our ability to resolve the genomic basis of climate-associated adaptation may be elevated in the marine environment compared with terrestrial, which can translate into improved power to predict population-level responses or vulnerability in these systems.

In this opinion piece, we review the literature on the genomic basis of climate adaptation in marine species (Section 2), evaluate current examples of genomic offset estimates in marine systems (Section 3), assess the potential for validation of these estimates (Section 4), and finally, we discuss the utility of these estimates in informing fisheries policy (Section 5). Here, we argue that the wealth of data available from long-term monitoring programs in exploited marine species provides an unprecedented opportunity for validating offset estimates in an otherwise logistically challenging environment. We also argue that implementing offset estimates in marine management will enable a more comprehensive assessment of the impacts of climate change on exploitation.

2 | GENOMIC BASIS OF ADAPTATION IN MARINE SPECIES

Accurate prediction of potential maladaptation requires an understanding of how species are adapted to their environments. The number of potential drivers of adaptation in the marine environment is broad and includes variables such as temperature, salinity, dissolved oxygen, pH, and depth. Although theory would predict that extensive gene flow facilitated by long pelagic larval durations in marine species would erode and prevent local adaptation, recent studies employing genome-wide data have provided strong evidence for climate-associated adaptation in several marine taxa (e.g., Drinan et al., 2018; Vranken et al., 2021). For some species with high connectivity and gene flow, like Atlantic cod (*Gadus morhua*), herring (*Clupea harengus*), horse mackerel (*Trachurus trachurus*), and northern sand lance (*Ammodytes dubius*), a few "large effect" chromosomal rearrangements seem to explain most of the climate-associated genomic variation (e.g., Barth et al., 2019; Fuentes-Pardo, Farrell, et al., 2023; Kess et al., 2020). For example, a large 10 Mb inversion on chromosome 21 discriminates northern and southern populations of horse mackerel in Europe (Fuentes-Pardo, Farrell, et al., 2023). In other cases, a signature of local adaptation is restricted to many regions of "small effect" in the genome, requiring dense genomic data for detection, as seen in Arctic charr (*S. alpinus*), Atlantic silversides (*Menidia menidia*), and the Baltic copepod (*Eurytemora affinis*) (Kess et al., 2021; Stern et al., 2022; Wilder et al., 2020). Here, adaptive SNPs are dispersed across most of the genome, rather than being concentrated in one particular region, constituting a signature of polygenic adaptation. The genomic underpinnings of local adaptation can vary not only across species but also across environmental gradients, and this is especially complex in marine systems where species are distributed across both geographic and bathymetric clines.

Genomic signatures of thermal adaptation have repeatedly been reported and appear to be more prevalent in marine systems than in terrestrial or freshwater systems (Sasaki et al., 2022). For example, temperature-driven structure has been observed in sea scallop (*Placopecten magellanicus*) (Van Wyngaarden et al., 2017), northern shrimp (*Pandalus borealis*) (Stanley et al., 2018), capelin (*Mallotus villosus*) (Cayuela et al., 2021), and Atlantic herring (*Clupea harengus*) (Fuentes-Pardo, Bourne, et al., 2023). Extreme thermal events can also result in a reshuffling of genetic clusters leading to local adaptation. For example, Coleman et al. (2020) demonstrated that an extreme marine heatwave caused a significant poleward shift in populations of kelp forests along the coast of western Australia, whereby “cool water” alleles were replaced by “warm water” alleles, resulting in a genetic tropicalization of the populations. While within a species, the same adaptive alleles can be selected multiple times in distinct geographic areas, resulting in parallel evolution of thermal adaptation (Bradbury et al., 2010), the universality of the molecular processes involved in thermal adaptation is largely unknown in marine systems, partly due to the lack of genomic resources and functional validation of the markers under selection in published studies.

Climate change projections not only indicate a rapid increase in ocean temperature in the next century but also lower salinity linked to glacier melting and higher precipitation in some regions, like the northern hemisphere (Luo et al., 2016). Additionally, many marine species use a variety of habitats throughout their life cycle, some spanning freshwater and estuarine environments and thereby experiencing steep salinity clines. A significant body of work supports salinity adaptation in marine organisms (Johannesson et al., 2020), particularly in the Baltic Sea. For instance, whole genome sequencing revealed hundreds of regions across the genome of Atlantic herring (*C. harengus*) that showed significant differentiation between Baltic and Atlantic populations (Han et al., 2020). Equivalent comparisons of Baltic and Atlantic populations have yielded similar results in other species such as Atlantic cod (*G. morhua*) (Berg et al., 2015), sand goby (*Pomatoschistus minutus*) (Leder et al., 2021), and European plaice (*Pleuronectes platessa*) (Le Moan et al., 2021), indicating adaptation to low salinity levels. Within the Baltic, multiple species of mussel have also shown salinity-related adaptation between western and eastern regions (Knöbel et al., 2021). Recently, Stern et al. (2022) showed experimental and genomic evidence of Baltic copepod (*E. affinis*) rapidly adapting to decreasing salinity. Similar to thermal adaptation, species can adapt to salinity changes through either parallel or convergent evolution (Le Moan et al., 2021), involving either few genetic variants of large effect or many loci of small effect (e.g., Berg et al., 2015; Le Moan et al., 2021).

Additionally, it is increasingly clear that the basis of local adaptation in marine taxa extends beyond SNPs to large-scale chromosomal rearrangements, copy number variants (CNVs), and epigenetic variation. For instance, environmental adaptation in American lobster (*Homarus americanus*) was driven almost entirely by CNVs with little to no signal in SNP data (Dorant et al., 2020). In contrast, Layton et al. (2021) reported similar spatial trends in genomic offset calculated from CNV and SNP datasets in Arctic Charr populations from eastern Canada. Additionally, previous work has uncovered differentially methylated regions (DMRs) linked to salinity adaptation in three-spined stickleback (*Gasterosteus aculeatus*) (Heckwolf et al., 2020). Given these findings, Layton and Bradbury (2022) suggest a revised offset approach incorporating normalized read counts and methylation scores alongside allele frequencies which might better reflect overall (genetic + epigenetic) adaptive processes, thereby improving prediction accuracy. Despite a complex landscape of adaptive genomic variation in marine species, only a few studies have leveraged this information for estimating genomic offset in the marine environment.

3 | PREDICTION OF CLIMATE CHANGE IMPACTS USING GENOMIC TOOLS IN MARINE TAXA

As discussed above, local adaptation to ocean climate is widespread (at least at regional scales) across marine species in various taxonomic groups and ecological contexts. However, climate change is expected to disrupt local adaptation in the coming years, resulting in potential maladaptation as the speed of change outpaces natural selection in many species and populations (Razgour et al., 2019). The ability to resolve the genomic basis of adaptation, in conjunction with fine-scale climate projections, presents an opportunity to leverage these datasets to forecast future climate-associated genomic composition and maladaptation. Genomic offset, defined as the difference between current genomic composition and the predicted future composition required to maintain adaptation, was first introduced by Fitzpatrick and Keller (2015) and later by Bay et al. (2018) and has been used to identify populations most vulnerable to future climate change. Additionally, the genomic offset approach can be employed across historical timescales, for instance, by calculating the difference between current genomic composition and past genomic composition hindcasted at the last glacial maximum.

In the past few years, this method has been increasingly employed across various terrestrial systems (e.g., Capblancq et al., 2020), with more recent work focusing on in situ validation of these offset estimates (Fitzpatrick et al., 2021). To derive the offset estimate, allele frequencies of putatively adaptive, climate-associated loci are the response variables to environmental predictor data to model climate-associated genomic variation using any number of modelling approaches. The most common modelling approaches include generalized dissimilarity modelling (GDM) and gradient forest (GF)—both of which accommodate for nonlinear associations of genomic and environmental data. The former uses distance matrices to model climate-associated genomic variation while the latter employs a regression-tree approach that is especially suitable in the context of steep environmental gradients (Fitzpatrick & Keller, 2015). The model is then used alongside environmental data from both current and future time periods and across the species' range to predict current and future adaptive indices, respectively. The difference between these values represents offset, with larger values indicating that a population is more likely to be maladapted to future climate. This method has typically been used in species with strong population structure distributed across well-defined environmental gradients, but its utility and downstream interpretation in marine species has been understudied. However, recent work has begun to address this gap, demonstrating its potential utility in 11 species of fish, invertebrates, and marine plants (Table 1).

Most of these studies have focused on generating offset estimates in single species across different spatial scales, with variable patterns across taxonomic groups and geographic areas. For instance, in eastern Canada, offset estimates were highest in southern populations of Arctic charr (*S. alpinus*) (Layton et al., 2021), indicative of a scenario of contraction of the southern range limit of this Arctic species. Alternatively, genomic offset values were higher in northern (subarctic) populations of a widely distributed seagrass species (*Z. marina*) across a similar area (Jeffery et al., 2024). Estimates of future offset in *Acropora digitifera* in Western Australia are more spatially complex, but populations living at the upper thermal limits (i.e., at lower latitudes) were predicted to require less of an adaptive shift than mid-latitude reefs (Adam et al., 2022). Similarly, Wood et al. (2021) show a spatially complex pattern of future offsets in a forest-forming seaweed (*Phyllospora comosa*) in Australia, demonstrating that offset estimates do not follow a simple latitudinal cline and rather vary with standing genetic diversity and predicted rates of climate change. Finally, Nielsen et al. (2021) in a comparative study of three marine invertebrates, explore genomic offset values and reveal a strong correlation among temperature and genomic variation in some species but not others, demonstrating that species-specific patterns were better predictors of required adaptive shifts than environmental data alone. These findings suggest that broad generalizations of climate change vulnerability in marine species, even among closely related taxa or within similar geographic regions, might be challenging. However, they clearly indicate that additional investigations of genomic offset in marine organisms are necessary. This is especially true when considering validation, as no studies to date have attempted to validate genomic offset estimates in marine species.

4 | VALIDATING GENOMIC OFFSET IN MARINE SYSTEMS

Predictions of climate change vulnerability via genomic offset are correlative in nature and as such, these models can be prone to misinterpretation or errors when the underlying genomic data, climate projections, or their associations are of low resolution or

TABLE 1 List of current publications employing genomic offset estimates in marine species.

Organisms	Region	Method	Climate variables	Validated	Reference
Macrophytes					
Eelgrass (*Zostera marina*)	Coastal North America	RDA	Seasonal, annual bottom and surface temperature, and salinity	No	Jeffery et al. (2024)
Seaweed (*Phyllospora comosa*)	Southeastern Australia	GDM	Sea surface temperature	No	Wood et al. (2021)
Kelp (*Ecklonia radiata*)	Western Australia	GF	Dissolved oxygen, sea surface salinity, sea surface nitrate, seawater velocity, and attenuation	No	Vranken et al. (2021)
Vertebrates					
Arctic Charr (*Salvelinus alpinus*)	Newfoundland/Labrador	GF	Precipitation and air temperature	No	Layton et al. (2021)
Sockeye salmon (*Oncorhynchus nerka*)	British Columbia and Yukon	GF	Precipitation and air temperature	No	Tigano et al. (2024)
Invertebrates					
Urchin (*Parechinus angulosus*), crab (*Cyclograpsus punctatus*), and limpet (*Scutellastra granularis*)	South Africa	GF	Sea surface temperature, sea surface salinity, and air temperature	No	Nielsen et al. (2021)
Coral (*Acropora digitifera*)	Western Australia	GF and GDM	Sea surface temperature	No	Adam et al. (2022)
Tubeworms (*Galeolaria caespitosa* and *G. gemineoa*)	Southeast Australia	GF	Sea surface temperature	No	Gallegos et al. (2023)

Note: The statistical method used to generate offset estimates, and the environmental predictors used, is also listed (GDM, generalized dissimilarity modelling; GF, gradient forest; RDA, redundancy analysis).

inaccurate. Moreover, these models largely ignore much of the underlying complexity of real-world evolutionary scenarios including effective population size, rates of mutation, and recombination (Rellstab et al., 2021). The approach assumes that there will be a non-negligible mismatch between current and future optima and that the current genotype–environment association accurately reflects spatial patterns in local adaptation, assumptions that can be impacted by demographic patterns and genetic drift (Láruson et al., 2022; Rellstab et al., 2021). For instance, spatial changes in allele frequencies may reflect neutral drift rather than selection, and this is especially likely when population size varies along environmental gradients. Láruson et al. (2022) employ simulations to demonstrate that although genomic offset is broadly correlated with population mean fitness, it could be confounded by demography, drift, genomic architecture, and the nature of the offset–fitness relationship.

Beyond the recent simulation study, few studies to date have attempted to validate the assumptions inherent to, or the projected vulnerabilities associated with, genomic offset calculations. In theory, validation may come from experimental studies, or comparison of predictions with existing demographic or ecological data. The only examples of experimental validation to date are from terrestrial species, where genomic offset estimates were compared to population performance measured in common garden settings—where distinct populations are grown under the same environmental conditions to identify differences in fitness (e.g., Fitzpatrick et al., 2021; Gain et al., 2023). For instance, Fitzpatrick et al. (2021) reported a negative relationship between genomic offset and common garden performance consistent with significant power of offset estimates to predict population response to climate change, exceeding that of climate differences alone. In contrast, Bay et al. (2018) used genomic offset to identify vulnerable populations of the yellow warbler (*Setophaga petechia*) and compared offset estimates to historical trends in abundance. Although they report a correlation between offset projections and demographic decline, this approach assumes that historical population trends are indicative of future trends, and it can be biased by non-selective or non-demographic influences on the offset prediction (Láruson et al., 2022). Interestingly, no direct attempts to validate genomic offset predictions in marine species have been published to date.

Although very informative and likely the gold standard, the potential for experimental validation of offset estimates through either reciprocal transplant or common garden experiments in marine species are limited by comparison with terrestrial plants or animals. This is largely due to the added complexity of these experiments in the marine environment. For instance, long generation times in many exploited marine species (e.g., 20 years in deepwater redfish, *Sebastes mentella*, COSEWIC, 2010) means that the short timescales with which common garden experiments are typically performed will provide only a snapshot of response. Alternatively, marine species, particularly exploited ones, often have extensive stock assessment and long-term monitoring programs with decades of time series data that can be used for validation in the absence of common garden experiments. Rather than comparing future estimates of climate change impact with past demographic data, time series data allows direct comparison of past demographic trends with predictions of past climate-induced maladaptation (i.e., offset). This approach, although not perfect, offers a means for validation when offset calculations are hindcast to the period over which population monitoring has occurred. Furthermore, sampling programs spanning decades present the opportunity to retrospectively test for temporal changes in allele frequencies in response to climate change. Here, we can pair historical DNA (e.g., from scales or otoliths) with environmental data from the same time to estimate past climate-associated variation (e.g., Atmore et al., 2022). This dataset can then serve as the base model for computing genomic offset, both for contemporary and future scenarios. These approaches to validation, although powerful, are biased toward exploited species whose stocks are already depleted from fishing and thereby teasing apart the relative impacts of climate change and exploitation will be critical in these cases. Nonetheless, we argue that the availability of extensive population data and historical samples for many economically and ecologically relevant marine species creates an unprecedented opportunity for retrospective indirect validation in marine systems.

5 | IMPLEMENTING GENOMIC OFFSET IN MARINE MANAGEMENT

Validating offset estimates in the marine environment will continue to be an important avenue for future work, but the integration of these estimates in marine management is even more vital. This is because existing management approaches typically rely on SDMs, which although informative, are best used to compliment methods that explicitly consider adaptation. To first generate and integrate genomic offset estimates into marine management decisions, the following steps should be taken (Figure 1). First, comprehensive sampling across the range of the species of interest is needed (i.e., covering all known populations, latitudes, conservation areas, spawning areas, temperature regimes, etc.). Next, suitable genomic sampling is required to inform population structure and to produce accurate and robust allele frequencies (i.e., minimum 30 individuals per sampling location, and genomic variants through high-resolution whole genome sequencing, including pool-sequencing, or methylation sequencing at depths >2–10X). Then, high-resolution long-term climate data are needed for the study region, covering biologically relevant environmental variables, and preferably validated with in situ measurements accounting for depth and seasonal variation. To complement this, future climate change scenario models of the same resolution as contemporary climate data are required, which often show a trade-off of model resolution and geographic scale. Selection of future emissions scenarios should be justified, aligning with relevant management priorities in a region (e.g., RCP 4.5 vs. 8.5). The resulting offset estimates offer valuable insights, particularly for identifying populations or areas expected to be hotspots of future maladaptation, thereby serving as focal points for proactive management. In such cases, we recommend

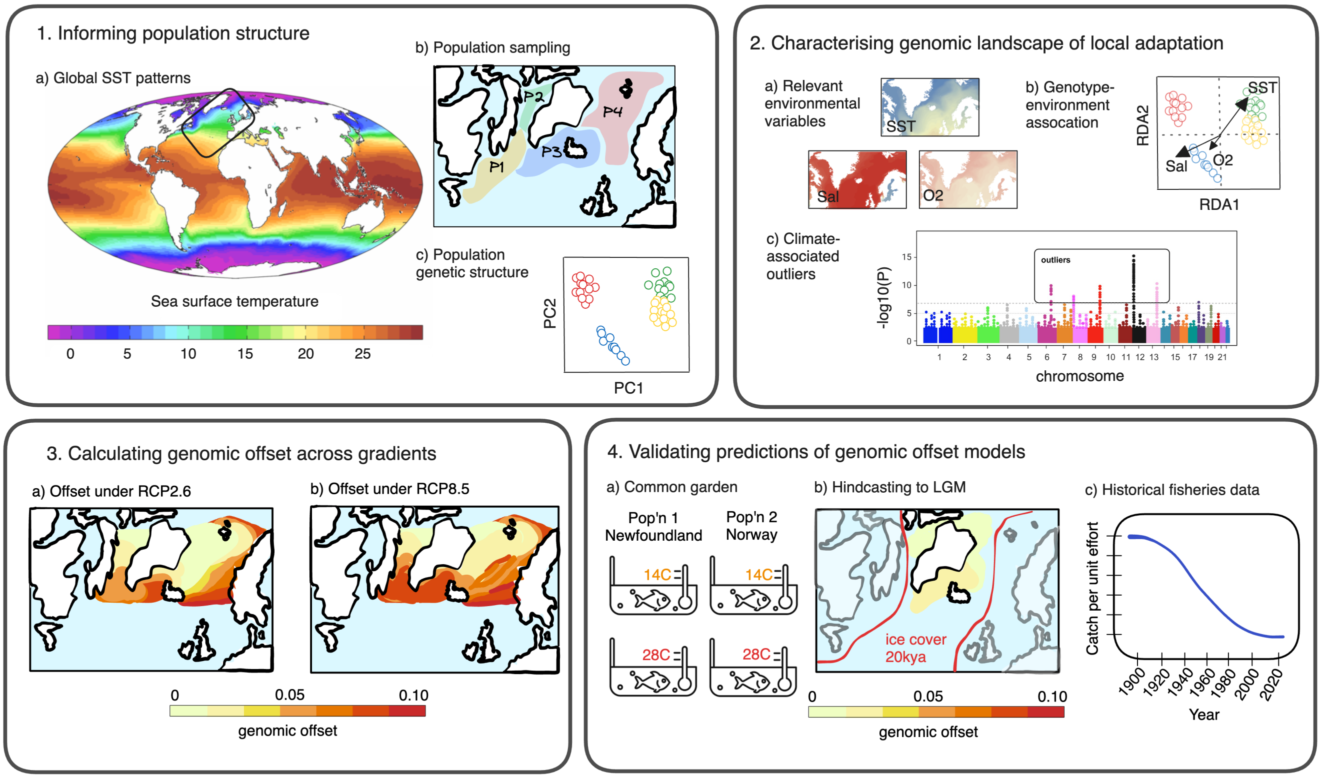

FIGURE 1 The first step in calculating genomic offset estimates in the marine environment is to sample populations from across the range, ideally from steep environmental gradients, to inform population structure in the species of interest (1a–c). Next, allele frequencies/read counts/methylation scores (response) and environmental (predictor) data are used for genotype–environment association (GEA) analyses to identify climate-associated outlier variants (see Bernatchez et al. (2023) for a detailed overview of GEA approaches) (2a–c). Allele frequencies/read counts/methylation scores from outlier variants are used alongside current and projected future environmental data in a modelling framework to generate genomic offset estimates (3a,b). Lastly, multiple methods can be employed to validate these model-based offset estimates, including assessing the fitness of constituent populations in common garden experiments (4a), generating historical offset estimates using publicly available climate data (e.g., Bio-Oracle) (4b), and comparing historical offset estimates with recent/historical demographic patterns uncovered through long-term fisheries data (4c). O_2, dissolved oxygen; Sal, salinity; SST, sea surface temperature. Figure 1 was generated in Excalidraw (retrieved from https://excalidraw.com/) and specific attributions include: (1a) Image derives from Plumbago on Wikimedia. (2b) Data from Bio-ORACLE v2.0 (Assis et al., 2017) was extracted and plotted using the *sdmpredictors* (Bosch & Fernandez, 2023) and *raster* (Hijmans, 2023) packages in R. (2c) Manhattan plot was adapted from "Manhattan Plot for Genome-Wide Association Studies (GWAS)" by BioRender.com (2024) (retrieved from https://app.biorender.com/biorender-templates).

applying genomic offset estimates in the real-world through "assisted evolution" or restoration through transplantation, enhancing resilience to a changing climate (e.g., Wood et al., 2021). Although straightforward in theory, this proposed workflow can be challenging to implement in practice given constraints on budget and time. For instance, generating dense genomic datasets for many individuals and populations can be expensive; and thus, targeting a smaller subset of climate-associated loci might be a feasible alternative. Additionally, sampling from all known populations across a species range can be logistically challenging and thus selecting a subset of populations that best represent variation (both genomic and environmental) in the system could be an alternative approach.

As genomic offset models are refined and applied to other taxa of conservation interest, there will be a need to integrate predictions into management and decision-making. While validating genomic offset models, through experiments or observations over time, should foster trust in the method, there are consequences to inaction as well (Salafsky & Redford, 2013). The standards of proof for a model or prediction can vary depending on the potential consequences of action versus inaction, and whether management or mitigation strategies are reversible. When inaction might result in long-term ecological consequences and when there is some certainty regarding a positive outcome for a population or species, a relatively low standard of proof may suffice (Salafsky & Redford, 2013). In a management context, a plain-language report that states the results of the study, the caveats of the genomic offset estimates, and potential consequences of action versus inaction is vital for informing decision-making processes.

6 | CONCLUSIONS

Climate change is restructuring marine ecosystems, diminishing biodiversity, and compromising ecosystem function. The global reliance on marine resources means that these changes will undoubtedly have clear repercussions on food security, economic stability, and human health (Payne et al., 2021). Our ability to mitigate these changes and "future-proof" management decisions and conservation actions through placing them in the larger context of climate change impacts could be a powerful tool. However, achieving this will depend on a thorough understanding of the basis of biological adaptation to climate and accurate predictions of the impacts of climate change on marine species.

Here, we reveal a growing wealth of examples of climate-associated adaptation in marine taxa, whose demonstration is only now possible with high-depth genomic sequencing and high-resolution marine climate data. Yet, there remains a general lack of application and validation of genomic offset estimates, heightening the uncertainty of these predictions. Here, we argue that future work should focus on leveraging the wealth of long-term population data available for many economically and ecologically vital marine species to validate offset estimates when more traditional approaches are logistically challenging. A particularly exciting avenue for future work is the potential for generating models of past climate-associated variation with historical samples. Beyond validation, there is even greater uncertainty on how to apply offset estimates in real-world fisheries management and marine conservation scenarios. To this end, we provide a "standard operating procedure" for marine managers, outlining how to generate offset estimates and modify workflows in the face of budgetary and time constraints. Genomic offset has the potential to transform marine management and is highly complementary to other genetic and non-genetic approaches to conserving vital marine resources.

AUTHOR CONTRIBUTIONS

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