**Running title:**

**Title**

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# Introduction

we define data-poor fishery as a fishery where available data are insufficient for

conducting a conventional stock assessment and/or bioeconomic analysis, which includes fisheries

with few or limited data, as well as poor data quality. For simplicity, we do not intend to explicitly

distinguish between the terms of “data-poor” and “data-limited” and may use both terms

interchangeably.

Just as the cost of acquiring accurate economic and biological information for data poor fisheries is

prohibitive, some management arrangements (such as ITQs) are too costly to implement.

Consequently, a different approach is required. For smaller fisheries, a more generic set of

information is required that can assist fisheries managers to integrate economic objectives in a

practical and cost-effective manner and be useful for monitoring the economic health of these

fisheries.

To ensure sustainable exploitation of these data-poor stocks, research is needed to develop suitable

quantitative reference points or proxies consistent with the intent of the Commonwealth Harvest

Strategy Policy. In addition to biological sustainability, Harvest Strategy Policy requires that the

maximum economic yield be achieved for the fishing fleet. Hence, it will be important that any

target reference points adopted for fisheries also incorporate economic considerations, so that the

MEY objective of maximising the long term economic returns to the fishing industry from the

management of the fishery is actively pursued.

Unfortunately, it is challenging, if not impossible, to estimate

directly such reference points for many stocks due to limited, or absence of, economic data as well

as biological data. In most cases, this is due to the relatively small size of the fishery or the relatively

low economic importance of the species concerned, making the routine collection of appropriate

data too costly.

# Material and methods

The model is an extension of the model developed in Vincenzi (2014). Further details on the model and parameter values are in Supplementary Information. The choice of parameter values for the present work was informed by the results of Vincenzi (2014).

## Overview of the model

I consider a population of monoecious individuals living in a habitat whose population ceiling is *K* (Mangel and Tier 1993). The population is geographically isolated, with neither immigration nor emigration. A single quantitative trait *a* corresponding to its breeding value for a phenotypic trait *z* characterized the individuals. The population has discrete overlapping generations with *N*(*t*) total individuals, where *t* is time in years. The environment is described by an optimum phenotype *Θ* (*t)* that changes over time as a result from variations in a climate driver (e.g., rainfall, temperature), selecting for the phenotypic trait *z.* The distance between the optimum phenotype *Θt)* and the trait *z*iof the individual *i* defines the maladaptation of the individual *i* with respect to the optimum phenotype. Point extreme events such as floods or fires cause non-selective (i.e., every phenotype has the same chances of surviving the event) high mortality in the population.

## Temporal change of optimum phenotype

The expected optimum phenotype*Θ**t*) moves at a constant speed over time (i.e. trend), fluctuating randomly around its expected value  (Fig.1). The optimum phenotype *Θt)* is randomly drawn at each time step *t* from a normal distribution ***Θ****t*)*~* (*Θ**t*),*Θ*(*t*)). It is equivalent to consider *Θt)* as both the optimum phenotype and the value of a continuous climate variable such as temperature, and I will use the two terms interchangeably throughout this work.

Mean and variance of the climate variable at time *t* are thus:

 (1)

where *t*ch is the time at which there is a change (*ch*) in the climate, is and indicator function equal to 1 when is trueand 0 otherwise. The model formulation indicates that the directional climate trend steadily increases through time after *t*ch years and that the increase in variability starts after *t*ch years, but stops after *t*ch+*t*inc years. The goal of this model formulation is to avoid variability building up to unrealistic values through time.

Point extreme events *E* leading to trait-independent high mortalities occur with annual probability p(*E*b) when *t*<*t*ch (i.e. b - before climate change) and p(*E*a) when *t*>*t*ch.

## Quantitative trait and survival

I model the phenotype *z* of an individual *i*, *z*i, as the sum of its genotypic value *a*i and a statistically‑independent random environmental effect *e*­i drawn from **(**E, ):

*z*i = *a*i + *e*i (2)

The narrow sense heritability *h*2 = / is the proportion of the phenotypic variance present in the population that is explained by the additive genetic variance  (i.e. the variance of ***a*** in the population).

For an individual, the genetic value *a*i is determined by *n*l freely recombining diploid loci, with additive allelic effects within- and among-loci, that is , where  is the sum of the allelic values at locus *j*. For computational reasons I chose *n*l = 10. For simplicity, I did not model either dominance or epistatic variation or other complicating factors such as genotype‑environment interaction and linkages. However, converging insights from model and non-model organisms suggest that a largely additive model explains most quantitative trait variation wherein very large numbers of contributors have small individual effects (Hill et al. 2008, Bloom et al. 2013).

I did not model mutation in this work, since previous work (Vincenzi 2014) has shown that mutation does not appear to have any effect short-term on extinction risk and the evolution of traits on contemporary temporal scales.

Stabilizing selection is modeled with a Gaussian function (Bürger and Lynch 1995, Zhang 2012), with fitness *W* (Endler 1986) for an individual with phenotypic trait *z*i equal to:

 (3)

and equivalent in this model to the annual survival probability of individual *i*. The curvature of the fitness function near its optimum increases with decreasing *ω*2; it follows that that the smaller *ω*2, the stronger is selection. Stabilizing selection is usually measured by the standardized quadratic selection gradient **, which is defined as the regression of fitness *W* on the squared deviation of trait value from the mean (Lynch and Walsh 1998). An optimum phenotype in the tails of the distribution is likely to cause a large drop in population size and can be considered an extreme climate event (Fig. 1).

The median ** = -0.1 for stabilizing selection found by Kingsolver et al. (2001) corresponds to a value of , where is the variance of the environmental component of the phenotype defined in Eq. (2), when stabilizing selection is modeled using a Gaussian fitness function.

Eq. 3 can be written:

 (4)

where . With ** = -0.1, = 1, and *h*2 = 0.2, the strength of selection *s* isabout 0.08.

I assumed that both strength of selection *s* and environmental variance  remain constant through time. When a point extreme occurs, the probability of survival of individuals *i* is , where is mortality caused by the point extreme event.

## Simulations

As this study focuses on the more immediate effects of climate change, the simulations last 250 years. Parents mate at time *t*-1, offspring are born at time *t* and become of age 1 at *t*+1. The sequence of operations is mortality of adults, mating and reproduction, mutation, mortality of offspring. At the start of each simulation, for each individual a value of *a* and *e* (Eq. 2) is randomly drawn from their initial distribution.** A population is considered extinct if at any time during the simulation there are fewer than 2 individuals in the population. Parents form mating pairs and produce a number of offspring randomly drawn from a Poisson distribution with intensity . I did not allow for genetic recombination. Offspring receive for the same locus one allele from each parent.

### Choice of parameter values

We needed to limit our simulations to a manageable size because the topic of model set construction and selection applies to a wide range of situations. W

I reduced parameter space by fixing *K =* 500 0, = 1, = 0, =1,  = 0.2, p(*E*I,b) = 0.05, and *tinc* = 25 years. For the other parameter, I chose range of values that are both realistic for natural populations and instrumental for the main goal of the study, e.g. the consequences of extreme events on population dynamics, risk of extinction, and evolution of a quantitative trait.

I performed simulations for combinations of selection strength *s* from 5 (weak selection), to 15 10-2 (strong selection) Kingsolver et al. (2001). For the rate of increase in the mean of the climate variable I used= 1 and 2 10-2 (leading to values of of 1.5 and 3, respectively, at the end of simulation time). The per-generation increase in the mean of the climate variable corresponds to 1% and 2% of the phenotypic standard deviation at time *t*ch. This rate of increase should allow the population in absence of variability to persist indefinitely (Lynch and Lande 1993, Bürger and Lynch 1995), and thus extinctions should not be caused to climate trend alone. I used rate of the increase in the standard deviation of the climate variable from 0.5 to 2 10-2 (leading to standard deviations of the probability distribution for the optimum from 1.125 to 1.5 from year 175 onwards, that is approximately from 12.5 to 50% greater than the phenotypic standard deviation at *t*= 150). According to Bürger and Lynch (1995), when the standard deviation of the distribution of the optimumreaches the same order of magnitude as the width  of the fitness function, the population is at risk of going suddenly extinct, with little role played by genetics. Therefore, I chose values of that substantially increase the probability of climate extremes, but did not inevitably make the population go extinct.

I used frequency of point extreme events p(*E*a) from 5 (no variation before and after climate change, corresponding to a recurrence interval of 20 years) to 12.5 10-2 (i.e., recurrence interval is 8 years) with a step of 2.5 10-2 (Table 1). I used a moderate mortality caused by point extremes (= 0.3) and moderate p(*E*a), since with higher mortality induced by point extremes and higher probability of their occurrence, the system will be largely driven by the point extremes, with no or little role of genetics and demography in determining population dynamics and risk of extinction.

### Initialization

To reach mutation-selection-drift balance, I first let the population evolve for *t*ch years in an environment in which mean and variance of the distribution of the optimal phenotype ***Θ*** are constant. In preliminary simulations it was found that after *t*ch = 100both phenotypic mean and variance remained basically constant. Then, the mean of ***Θ***** increases for 150 years and variance of ***Θ*********25 years. The variance of ***Θ***was then kept constant up to the end of the simulation.

I started every simulation replicate with 500 individuals. I modeled 5 alleles present in the population for each locus, which value was randomly drawn from a normal distribution *N(0,*  *)*. Since I set  = 1 and  = 0.2, the narrow sense heritability *h*2 was around 0.2 at *t* = 1, close to what commonly observed for life‑history traits (Lynch and Walsh 1998) and consistent with the Gaussian allelic approximation including only quasi-neutral and adaptive mutations, for which (Lande 1995).

### Characterization of simulations

Over simulation time  and *h*2 evolved depending on selection, mutation and population dynamics. At the level of single replicate, to characterize the behavior of the simulated populations I: (a) recorded whether the population was extinct or still persisting at the end of the simulation time (0 for persistence and 1 for extinction), and if extinct I recorded year of extinction; (b) tracked the distribution of the trait *z* in the population as a function of time and, in particular, its mean value at the end of simulation time when the population did not *g*o extinct (to avoid transient effects caused by the stochastic series of optimal phenotypes, I averaged in the last 10 years of the simulation); (c) population size at time *t* after mortality of adults *N(t*;*)* (d) mean fitness of adults at time *t* ; (e) additive genetic variance .

For an ensemble of realizations (50 replicates for a fixed set of parameters) I: (a) computed the frequency of population extinction as the number of replicates in which the population went below two individuals during simulation time, (b) the time to extinction for the populations that went extinct, and (c) the average over the replicates for a fixed set of parameters of mean at the end of simulation time for the replicates in which the populations did not go extinct.

## Statistical analysis

I used simulation results as pseudo-empirical data and proceeded to analyze them with standard statistical techniques. For all models, I centered and scaled the predictors in order to compare their importance (Schielzeth 2010), and I treated strength of selection and probability of point extreme as continuous variables. As I use realistic variable ranges representing the variability that may be observed in nature, the estimated parameters can be compared in terms of effect on a standardized scale.

I estimated parameters of Generalized Additive Models (GAMs, (Wood 2006)) and Generalized Linear Models (or Ordinary Least-Square regression models) using as response variable either (i) extinction(1)/persistence(0), (ii) time to extinction for the populations that went extinct (excluding the few extinctions that occurred before climate change), (iii) mean phenotype at the end of simulation time for the populations that persisted.

Then, I investigated whether a combination of genetic, demographic and environmental factors measured or estimated in a limited time window (“sampling window”) can predict the risk the risk of extinction of the population in the following years (“extinction window”). In particular, I fitted a GLM with population extinction (1) or persistence (0) between (*t*ext - *u)* as response variable, where *t*ext is either (a) the time at extinction for the replicate that went extinct, or (b) a random deviate from a uniform distribution bounded between 175 and 290 (i.e. where > 95% of the extinctions occurred) for the replicates that persisted up to the end of simulation time. *u* is a random deviate from a uniform distribution bounded between 10 and 1 years. This way, I am trying to model extinction or persistence not at a specific time, but in a “extinction window” of 10 years. I used as candidate predictors as measured in the 10 years before the “extinction window” mean population size, mean additive genetic, strength of selection and probability of occurrence of point extreme events. In other words, I wanted to find variables measured over a limited time frame (10 years) that can predict the extinction or persistence of the population in the years following the end of the “sampling window”. In particular, I wanted to know whether the risk of extinction increased with decreasing additive genetic variance. I divided the complete simulation dataset (25 600 replicates) in a calibration data set (80% of the data) and validation data set (20%), keeping the same proportion of replicates that went extinct and that persisted observed in the full dataset both in the calibration and validation dataset. I estimated the optimal cutoff given equal weight to sensitivity (probability that the model predicts extinction when the replicate went extinct) and specificity (probability that the model predicts persistence when the replicate persisted). Then, I tested the model by predicting population extinction and persistence on the validation dataset using the computed optimal cutoff.

As interactions among predictors did not improve model performance, I did not include them in the models in order to improve the interpretability of results. I visually checked residuals for variation to model assumptions.