

2 **Higher mortality rates leave heated ecosystem with similar size-**  
3 **structure despite larger, younger, and faster growing fish**

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## Abstract

Ectotherms are often predicted to “shrink” with global warming, in line with general growth models and the temperature-size rule (TSR), both predicting smaller adult sizes with warming. However, they also predict faster juvenile growth rates, leading to larger size-at-age. Hence, the result of warming on the size-structure of a population depends on the interplay between how mortality rate, juvenile- and adult growth rates are affected by warming. In this study, we use time series of biological samples spanning more than two decades from a unique enclosed bay heated by cooling water from a nearby nuclear power plant to become +8C warmer than its reference area. We used growth-increment biochronologies (12658 reconstructed length-at-age estimates) to quantify how the >20 years of warming has affected body growth and size-at-age and catch data to quantify mortality rates and population size-structure of Eurasian perch (*Perca fluviatilis*). In the heated area, growth rates were higher for all sizes, and hence size-at-age was larger for all ages, compared to the reference area. However, mortality rates were also higher, such that the difference in the size-spectrum exponent (describing the proportion of fish by size) was relatively minor and statistically uncertain. As such, our analysis reveals that mortality, in addition to plastic growth and size-responses, is a key factor determining the size structure of populations exposed to warming. Understanding the mechanisms by which warming affects the size-structure of populations is critical for prediction the impacts of climate change on ecological functions, interactions, and dynamics.

## Significance statement

Ecosystem-scale warming experiments provide unique insight into potential impacts of climate change but are very rare. Our work utilizes an experimental set-up consisting of an enclosed bay heated by cooling water from a nuclear power plant for more than two decades, and a reference area. We analyze how changes in growth and mortality have affected the size- and age distribution in a common freshwater fish using time series of catch data and growth-increment biochronologies derived from their gill lids. Despite fish in the heated area being ~10% larger at a given age, elevated mortality rates have caused similar size structures. Accounting for the interplay between mortality and growth is key for predictions of climate impacts on the size-structure of populations.

## Introduction

Ectotherm species, constituting 99% of species globally (Atkinson & Sibly, 1997; Wilson, 1992), are commonly predicted to shrink in a warming world (Cheung et al., 2013; Gardner et al., 2011; Sheridan & Bickford, 2011). Mean body size responses to temperature may however be uninformative, as the size-distribution of many species spans several orders of magnitude. For instance, warming can shift size-distributions without altering mean size if increases in juvenile size-at-age outweigh the decline in size-at-age in adults, which is consistent with the temperature size-rule, TSR (Atkinson, 1994). Resolving how warming induces changes in population size-distributions may thus be more instructive (Fritschie & Olden, 2016), especially for inferring warming effects on species' ecological role, biomass production, or energy fluxes (Yvon-Durocher et al., 2011). This is because key processes such as metabolism, feeding, growth, mortality scale with body size (Andersen, 2020; Blanchard et al., 2017; Brown et al., 2004; Pauly, 1980; Thorson et al., 2017; Ursin, 1967). Hence, as the value of these traits at mean body size is not the same as the mean population trait value (Bernhardt et al., 2018), the size-distribution within a population matters for its dynamics and for how it changes under warming.

The population size distribution can be represented as a size-spectrum, which generally is the frequency distribution of individual body sizes (A. M. Edwards et al., 2017). It is often described in terms of the size-spectrum slope (slope of individuals or biomass of a size class over the mean size of that class on log-log scale (A. M. Edwards et al., 2017; Sheldon et al., 1973; White et al., 2007)) or simply the exponent of the power law individual size-distribution (A. M. Edwards et al., 2017). The size-spectrum thus results from temperature-dependent ecological processes such as body growth, mortality and recruitment (Blanchard et al., 2017; Heneghan et al., 2019). Despite its rich theoretical foundation (Andersen, 2019) and usefulness as an ecological indicator (Blanchard et al., 2005), few studies have evaluated

warming-effects on the species size-spectrum in larger bodied species (but see Blanchard *et al.*(2005)), and none in large scale experimental set-ups. There are numerous paths by which the species size-spectrum could change with warming(Heneghan et al., 2019). For instance, the clearest consequence of TSR for the size-spectrum is a decline in maximum size. However, unless warming also alters the relative abundances of juveniles and adults, the same number of adults will accumulate in a smaller size-range, resulting in a less steep slope of the size-spectrum. Warming can also lead to elevated mortality, which truncates the age-distribution towards younger individuals(Barnett et al., 2017). Increased growth rates can, however, counter the effects of mortality on abundance-at-size, unless only small individuals benefit from warming(Daufresne et al., 2009; Lindmark et al., 2022). Growth rates can increase due to physiological responses to higher temperatures, or reduced density-dependence following warming-induced mortality, or both. Hence, the effect of warming on the size-spectrum depends on several interlinked processes affecting abundance-at-size and size-at-age.

Size-at-age is generally predicted to increase with warming for small individuals, but decrease for large individuals (according to the mentioned TSR(Atkinson, 1994; Ohlberger, 2013)). Several factors likely contribute to this pattern, such as increased allocation to reproduction (Wootton et al., n.d.) and larger individuals in fish populations reaching optimum growth rates at lower temperatures(Lindmark et al., 2022). Empirical support in fishes for this pattern seem to be more consistent for increases in size-at-age of juveniles(Huss et al., 2019; Rindorf et al., 2008; Thresher et al., 2007) than declines in adult size-at-age, for which a larger diversity in responses is observed among species(Barneche et al., 2019; Baudron et al., 2014; Huss et al., 2019). Potentially this is due to most studies being done on commercially exploited species (generally monitored in long time series), for which any size- and growth relationships with temperature may be confounded with plastic and/or genetic responses to size-selective mortality(Audzijonyte et al., 2016). Moreover, the effect of temperature on mortality rates of

wild populations are more studied using among-species analyses. These relationships based on thermal gradients in space may not necessarily be the same as the effects of *warming* on mortality on single populations. Hence, the effects of warming on growth and size-at-age and mortality within natural populations constitute a key knowledge gap for predicting the consequences of climate change on population size-spectra.

Here we used data from a unique, large-scale 23-year-long heating-experiment of a coastal ecosystem to quantify how warming changed fish body growth, mortality, and the size structure in an unexploited population of Eurasian perch (*Perca fluviatilis*, ‘perch’). We compare fish from this enclosed bay exposed to temperatures approximately 8°C above normal (‘heated area’) with fish from a reference area in the adjacent archipelago (Fig. 1). Using hierarchical Bayesian models, we quantify differences in key individual- and population level parameters, such as body growth, asymptotic size, mortality rates, and size-spectra, between the heated and reference coastal area.

## Results

Analysis of fish (perch) size-at-age using the von Bertalanffy growth equation (VBGE) revealed that fish cohorts (year classes) in the heated area both grew faster initially (larger size-at-age and VBGE  $K$  parameter) and reached larger predicted asymptotic sizes than those in the unheated reference area (Fig. 2). The model with area-specific VBGE parameters ( $L_\infty$ ,  $K$  and  $t_0$ ) had best out of sample predictive accuracy (the largest expected log pointwise predictive density for a new observation; Table S1), and there is a clear difference in both the estimated values for fish asymptotic length ( $L_\infty$ ) and growth rate ( $K$ ) between the heated and reference area (Fig. 2B-E). For instance, the distribution of differences between the heated and reference area of the posterior samples for  $L_\infty$  and  $K$  only had 11% and 2%, respectively, of the density below 0, illustrating that it is unlikely that the parameters are larger in the reference area or

similar in the two areas (Fig. 2C, E). We estimated that the asymptotic length of fish in the heated area was 1.16 times larger than in the reference area ( $L_{\infty heat} = 45.7[36.8, 56.3]$ ,  $L_{\infty ref} = 39.4[35.4, 43.9]$ , where the point estimate is the posterior median and values in brackets correspond to the 95% credible interval). The growth coefficient was 1.27 times larger in the heated area ( $K_{heat} = 0.19[0.15, 0.23]$ ,  $K_{ref} = 0.15[0.12, 0.17]$ ). Also  $t_{0 heat}$  was larger than  $t_{0 ref}$  ( $-0.16[-0.21, -0.11]$  vs  $-0.44[-0.56, -0.33]$ , respectively). These differences in growth parameters lead to fish being approximately 10% larger in the heated area relative to the reference area (Fig. S4).

In addition, we found that growth rates were both slower and declined faster with size compared to the heated area (Fig. 3). The best model for growth ( $G = \alpha L^{\theta}$ ) had area-specific parameters (Table S2). Initial growth was estimated to be 1.18 times faster in the heated than in the reference area ( $\alpha_{heat} = 509.7[460.1, 563.5]$ ,  $\alpha_{ref} = 433.5[413.3, 454.1]$ ), and growth of fish in the heated area decline more slowly with length than in the reference area ( $\theta_{heat} = -1.13[-1.16, -1.11]$ ,  $\theta_{ref} = -1.18[-1.19, -1.16]$ ). The distribution of differences of the posterior samples for  $\alpha$  and  $\theta$  both only had 0.3% of the density below 0 (Fig. 3C, E), indicating high probability that growth rates have differentiated between the heated and reference area.

By analyzing the decline in catch-per-unit-effort over age, we found that the instantaneous mortality rate  $Z$  (rate at which log abundance declines with age) is higher in the heated area (Fig. 4). The overlap with zero is 0.05% for the distribution of differences of posterior samples of  $Z_{heat}$  and  $Z_{ref}$  (Fig. 4C). We estimated  $Z_{heat}$  to be  $0.7[0.67, 0.82]$  and  $Z_{ref}$  to be  $0.63[0.57, 0.68]$ , which corresponds to annual mortality rates of 53% in the heated area and 47% in the reference area.

Lastly, analysis of the size-structure in the two areas revealed that, despite the faster growth rates and larger sizes in the heated area for fish of all sizes, the higher mortality rates in the heated area led to largely similar size-structures. Specifically, while largest fish were found in

the heated area, the size-spectrum exponent was only slightly larger in the heated area (Fig. 5A), and their 95% confidence intervals largely overlap (Fig. 5C).

## Discussion

Our study provides strong evidence for warming-induced differentiation in growth, mortality, and size-structure in a natural population of an unexploited, temperate fish species exposed to an ecosystem-scale experiment with 5-10 °C above normal temperatures for more than two decades. While it is a study on only a single species, these features make it a unique climate change experiment, as experimental studies on fish to date are much shorter and often on scales much smaller than whole ecosystems, and long time series of biological samples exist mainly for commercially exploited fish species (Baudron et al., 2014; Thresher et al., 2007; van Rijn et al., 2017) (in which fisheries exploitation affects size-structure both directly and indirectly by selecting for fast growing individuals). While factors other than temperature could have contributed to the observed elevated growth and mortality, the temperature contrast is unusually large for natural systems (i.e., 5-10 °C, which can be compared to the 1.35 °C change in the Baltic Sea between 1982 and 2006 (Belkin, 2009)). Moreover, heating occurred at the scale of a whole ecosystem, which makes the findings highly relevant in the context of global warming.

Interestingly, our findings contrast with both broader predictions about declining mean or adult body sizes based on the GOLT hypothesis (Cheung et al., 2013; Pauly, 2021), and with intraspecific patterns such as the TSR (temperature-size rule (1994)). The contrasts lie in that both asymptotic size and size-at-age of mature individuals, as well as the proportion of larger individuals were larger and higher in the heated area—despite the elevated mortality rates. This result was unexpected for two reasons: optimum growth temperatures generally decline with body size within species under food satiation in experimental studies (Lindmark et al., 2022),



and fish tend to mature at smaller body size and allocate more energy into reproduction as it gets warmer(Wootton et al., n.d.). Both patterns have been used to explain how growth can increase for small and young fish, while large and old fish typically do not benefit from warming. Our study species is no exception to these rules(Huss et al., 2019; Karås & Thoreson, 1992; Sandström et al., 1995). This suggests that growth dynamics under food satiation may not be directly proportional to those under natural feeding conditions(Railsback, 2022). Moreover, our results suggest that growth changes emerge not only from direct physiological responses to increased temperatures, but also from warming-induced changes in the food web, e.g., prey productivity, diet composition and trophic transfer efficiencies(Gårdmark & Huss, 2020). It also highlights that we need to focus on understanding to what extent the commonly observed increase in size-at-age for juveniles in warm environments can be maintained as they grow older.

Our finding that mortality rates were higher in the heated area was expected—warming leads to faster metabolic rates, which in turn is associated with shorter life span(Brown et al., 2004; McCoy & Gillooly, 2008; Munch & Salinas, 2009) (higher “physiological” mortality). Warming may also increase predation mortality, as predators’ feeding rates increase in order to meet the higher demand of food(Biro et al., 2007; Pauly, 1980; Ursin, 1967). However, most evidence to date of the temperature dependence of mortality rates in natural populations stem from across species studies(Gislason et al., 2010; Pauly, 1980; Thorson et al., 2017) (but see(Berggren et al., 2021; Biro et al., 2007)). Across species relationships are not necessarily determined by the same processes as within species relationships; thus, our finding of warming-induced mortality in a heated vs control environment in two nearby con-specific populations is important.

Since a key question for understanding the implications of warming on ectotherm populations is if larger individuals in a population become rarer or smaller(Ohlberger, 2013;

Ohlberger et al., 2018), within-species mortality responses to warming need further study. Importantly, this requires accounting also for effects of warming on growth, and how responses in growth and mortality depend on each other. For instance, higher mortality (predation or natural, physiological mortality) can release intra-specific competition and thus increase growth. Conversely, altered growth and body sizes can lead to changes in size-specific mortality, such as predation or starvation. In conclusion, individual-level patterns such as the TSR may be of limited use for predicting changes on the population-level size structure. This is because while warming increases growth for small fish, the effect on large fish is less consistent, and the TSR also does not account for changes in mortality or density dependence. Mortality may, however, be an important driver of the observed shrinking of ectotherms (Peralta-Maraver & Rezende, 2021). Understanding the mechanisms by which the size- and age-distribution change with warming is critical for predicting how warming changes species functions and ecological roles (Audzijonyte et al., 2020; Fritschie & Olden, 2016; Gårdmark & Huss, 2020). Our findings demonstrate that a key to do this is to acknowledge temperature effects on both growth and mortality and how they interact.

## Materials and Methods

### *Data*

We use size-at-age data from perch sampled annually from an artificially heated enclosed bay ('the Biotest basin') in the western Baltic Sea and its reference area (Fig. 1) with natural temperatures in the years after the onset of warming. Heating started in 1980, the first analyzed cohort is 1981, and first and last catch year is 1987 and 2003, respectively, to omit transient dynamics and acute responses, and to ensure we use cohorts that only experienced one of the thermal environments during its life. A grid at the outlet of the heated area (Fig. 1) prevented fish larger than 10 cm from migrating between the areas (Adill et al., 2013; Huss et al., 2019),

and genetic studies confirm the reproductive isolation between the two populations during this time-period(Björklund et al., 2015). However, since the grid removal in 2004, fish growing up in the heated Biotest basin can easily swim out, meaning we cannot be sure fish in the reference area did not recently arrive from the Biotest basin. Hence, we use data only up until 2003. This resulted in 12658 length-at-age measurements from 2426 individuals in net deployments.

We use data from fishing events using survey-gillnets that took place in October in the heated Biotest basin and in August in the reference area when temperatures are most comparable between the two areas(Huss et al., 2019), because temperature affect catchability in static gears. The catch was recorded by 2.5 cm length classes during 1987-2000, and into 1 cm length groups 2001-2003. To express lengths in a common length standard, 1 cm intervals were converted into 2.5 cm intervals. The unit of catch data is hence the number of fish caught per 2.5 cm size class per net per night (i.e., a catch-per-unit-effort [CPUE] variable). All data from fishing events with disturbance affecting the catch (e.g., seal damage, strong algal growth on the gears, clogging by drifting algae) were removed (years 1996 and 1999 from the heated area in the catch data).

Length-at-age throughout life was reconstructed for a semi-random length-stratified subset of caught individuals each year. This was done using growth-increment biochronologies derived from annuli rings on the operculum bones (with control counts done on otoliths). Such analyses have become increasingly used to analyze changes in growth and size-at-age of fishes(Essington et al., 2022; Morrongiello & Thresher, 2015). Specifically, we used an established power-law relationship between the distance of annual rings and fish length:  $L = \kappa R^s$ , where  $L$  is the length of the fish,  $R$  the operculum radius,  $\kappa$  the intercept, and  $s$  the slope of the line for the regression of log-fish length on log-operculum radius from a large reference data set for perch(Thoresson, 1996). Back-calculated length-at-age were obtained from the relationship  $L_a = L_s(\frac{r_a}{R})^s$ , where  $L_a$  is the back-calculated body length at age  $a$ ,  $L_s$  is the final

body length (body length at catch),  $r_a$  is the distance from the center to the annual ring corresponding to age  $a$  and  $s = 0.861$  for perch(Thoresson, 1996). Since perch exhibits sexual size-dimorphism, and age-determination together with back calculation of growth was not done for males in all years, we only used females for our analyses.

## *Statistical Analysis*

The differences in size-at-age, growth, mortality, and size structure between perch in the heated and the reference area were quantified using hierarchical linear and non-linear regression models fitted in a Bayesian framework. First, we describe each statistical model and then provide details of model fitting, model diagnostics and comparison.

We fit the von Bertalanffy growth equation (VBGE)(Beverton & Holt, 1957; von Bertalanffy, 1938) on a log scale, describing length as a function of age to evaluate differences in size-at-age and asymptotic size:  $\log(L_t) = \log(L_\infty(1 - e^{(-K(t-t_0))}))$ , where  $L_t$  is the length at age ( $t$ , years),  $L_\infty$  is the asymptotic size,  $K$  is the Brody coefficient ( $yr^{-1}$ ) and  $t_0$  is the age when the average length was zero. We used only age- and size-at-catch as the response variables (i.e., not back-calculated length-at-age). This was to have a simpler model and not have to account for parameters varying within individuals as well as cohorts, as mean sample size per individual was only  $\sim 5$ . We let parameters vary among cohorts rather than year of catch, because individuals within cohorts share similar environmental conditions and density dependence(Morrongiello & Thresher, 2015). Eight models in total were fitted (with area being dummy-coded), with different combinations of shared and area-specific parameters. We evaluated if models with area-specific parameters led to better fit and quantified the differences in area-specific parameters. The model with all area-specific parameter can be written as:

$$L_i \sim \text{Student-}t(\nu, \mu_i, \sigma) \quad (1)$$

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$$\log(\mu_i) = A_R \log \left[ L_{\infty Rj[i]} \left( 1 - e^{(-K_{Rj[i]}(t-t_{0Rj[i]}))} \right) \right] + A_H \log \left[ L_{\infty Hj[i]} \left( 1 - e^{(-K_{Hj[i]}(t-t_{0Hj[i]}))} \right) \right] \quad (2)$$

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$$\begin{bmatrix} L_{\infty Rj} \\ L_{\infty Hj} \\ K_{Rj} \\ K_{Hj} \end{bmatrix} \sim \text{MVNormal} \left( \begin{bmatrix} \mu_{L_{\infty R}} \\ \mu_{L_{\infty H}} \\ \mu_{K_R} \\ \mu_{K_H} \end{bmatrix}, \begin{bmatrix} \sigma_{L_{\infty R}} & 0 & 0 & 0 \\ 0 & \sigma_{L_{\infty H}} & 0 & 0 \\ 0 & 0 & \sigma_{K_R} & 0 \\ 0 & 0 & 0 & \sigma_{K_H} \end{bmatrix} \right) \quad (3)$$

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where lengths are *Student - t* distributed to account for extreme observations,  $v$ ,  $\mu$  and  $\phi$  represent the degrees of freedom, mean and the scale parameter, respectively. Henceforth, subscripts  $H$  and  $R$  are used for the heated and reference area, respectively (except in figures and main text where subscripts are spelled out for clarity).  $A_R$  and  $A_H$  are dummy variables such that  $A_R = 1$  and  $A_H = 0$  if it is the reference area, and vice versa for the heated area. The multivariate normal distribution in Eq. 3 is the prior for the cohort-varying parameters  $L_{\infty Rj}$ ,  $L_{\infty Hj}$ ,  $K_{Rj}$  and  $K_{Hj}$  (for cohorts  $j = 1981, \dots, 1997$ ) (note that cohorts extend further back in time than the catch data), with hyper-parameters  $\mu_{L_{\infty R}}$ ,  $\mu_{L_{\infty H}}$ ,  $\mu_{K_R}$ ,  $\mu_{K_H}$  describing the non-varying population means and a covariance matrix with the between-cohort variation along the diagonal (note we did not model a correlation between the parameters, hence off-diagonals are 0). The other seven models include some or all parameters as parameters common for the two areas, e.g., substituting  $L_{\infty Rj}$  and  $L_{\infty Hj}$  with  $L_{\infty j}$ . To aid convergence of this non-linear model, we used informative priors chosen after visualizing draws from prior predictive distributions (Wesner & Pomeranz, 2021) using probable parameter values (*Supporting Information*, Fig. S1, S7). We used the same prior distribution for each parameter class for both areas to not introduce any other sources of differences in parameter estimates between areas. We used the following priors for the VBGE model:  $\mu_{L_{\infty R,H}} \sim N(45, 20)$ ,  $\mu_{K_{R,H}} \sim N(0.2, 0.1)$ ,  $t_{0R,H} \sim N(-0.5, 1)$  and  $v \sim \text{gamma}(2, 0.1)$ .  $\sigma$ ,  $\mu_{L_{\infty R}}$ ,  $\mu_{L_{\infty H}}$ ,  $\mu_{K_R}$ ,  $\mu_{K_H}$  were given a *Student - t*(3, 0, 2.5) prior.

We also compared how body growth scales with body size (in contrast to length vs age) in the two areas, by fitting allometric growth models describing how specific growth rate scales with length:  $G = \alpha L^\theta$ , where  $G$ , the annual specific growth between year  $t$  and  $t + 1$ , is defined as:  $G = 100 \times (\log(L_{t+1}) - \log(L_t))$  and  $L$  is the geometric mean length:  $L = (L_{t+1} \times L_t)^{0.5}$ . Here we also used back-calculated length-at-age, resulting in multiple observations for each individual. As with the VBGE model, we dummy coded area to compare models with different combinations of common and shared parameters. We assumed growth rates were *Student – t* distributed, and the full model can be written as:

$$L_i \sim \text{Student} - t(v, \mu_i, \sigma) \quad (4)$$

$$\mu_i = A_R(\alpha_{Rj[i],k[i]} L^{\theta_R}) + A_H(\alpha_{Hj[i],k[i]} L^{\theta_H}) \quad (5)$$

$$\alpha_{R,Hj} \sim N(\mu_{\alpha_{R,Hj}}, \sigma_{\alpha_{R,Hj}}) \quad (6)$$

$$\alpha_{R,Hj} \sim N(\mu_{\alpha_{R,Hj}}, \sigma_{\alpha_{R,Hj}}) \quad (7)$$

$$\theta_{R,Hj} \sim N(\mu_{\theta_{R,Hj}}, \sigma_{\theta_{R,Hj}}) \quad (8)$$

$$\theta_{R,Hj} \sim N(\mu_{\theta_{R,Hj}}, \sigma_{\theta_{R,Hj}}) \quad (9)$$

We assumed only  $\alpha$  varied across individuals  $j$  within cohorts  $k$  and compared two models: one with  $\theta$  common for the heated and reference area, and one with an area-specific  $\theta$ . We used the following priors, after visual exploration of the prior predictive distribution (*Supporting Information*, Fig. S8, S10):  $\alpha_{R,H} \sim N(500, 100)$ ,  $\theta_{R,H} \sim N(-1.2, 0.3)$  and  $v \sim \text{gamma}(2, 0.1)$ .  $\sigma$ ,  $\sigma_{id:cohort}$  and  $\sigma_{cohort}$  were all given a *Student – t*(3, 0, 13.3) prior.

We estimated total mortality by fitting linear models to the natural log of catch (CPUE) as a function of age (catch curve regression), under the assumption that in a closed population, the exponential decline can be described as  $N_t = N_0 e^{-Zt}$ , where  $N_t$  is the population at time  $t$ ,  $N_0$  is the initial population size and  $Z$  is the instantaneous mortality rate. This equation can be rewritten as a linear equation:  $\log(C_t) = \log(vN_0) - Zt$ , where  $C_t$  is catch at age  $t$ , if catch is assumed proportional to the number of fish (i.e.,  $C_t = vN_t$ ). Hence, the negative of the slope of the regression is the mortality rate,  $Z$ . To get catch-at-age data, we constructed area-specific

age-length keys using the sub-sample of the total (female) catch that was age-determined. Age length-keys describe the age-proportions of each length-category (i.e., a matrix with length category as rows, ages as columns). Age composition is then estimated for the total catch based on the “probability” of fish in each length-category being a certain age. With fit this model with and without an *age-area*-interaction, and the former can be written as:

$$\log(CPUE_i) \sim \text{Student-}t(v, \mu_i, \sigma) \quad (10)$$

$$\mu_i = \beta_{0j[i]}(area_R) + \beta_{1j[i]}(area_H) + \beta_{2j[i]}age + \beta_{3j[i]}(age \times area_H) \quad (11)$$

$$\begin{bmatrix} \beta_{0j} \\ \beta_{1j} \\ \beta_{2j} \\ \beta_{3j} \end{bmatrix} \sim \text{MVNormal} \left( \begin{bmatrix} \mu_{\beta_0} \\ \mu_{\beta_1} \\ \mu_{\beta_2} \\ \mu_{\beta_3} \end{bmatrix}, \begin{bmatrix} \sigma_{\beta_0} & 0 & 0 & 0 \\ 0 & \sigma_{\beta_1} & 0 & 0 \\ 0 & 0 & \sigma_{\beta_2} & 0 \\ 0 & 0 & 0 & \sigma_{\beta_3} \end{bmatrix} \right) \quad (12)$$

where  $\beta_{0j}$  and  $\beta_{1j}$  are the intercepts for the reference and heated areas, respectively,  $\beta_{2j}$  is the age slope for the reference area and  $\beta_{3j}$  is the interaction between *age* and *area*. All parameters vary by cohort (for cohort  $j = 1981, \dots, 2000$ ) and their correlation is set to 0 (Eq. 12). We use the following (vague) priors:  $\mu_{\beta_0, \dots, \beta_3} \sim N(0, 10)$  (where  $\mu_{\beta_2}$  is the population-level estimate for  $-Z_R$  and  $\mu_{\beta_2} + \mu_{\beta_3}$  is the population-level estimate for  $-Z_H$ ) and  $v \sim \text{gamma}(2, 0.1)$ .  $\sigma$  and  $\sigma_{\beta_0, \dots, \beta_3}$  were given a *Student - t*(3, 0, 2.5) prior.

Lastly, we quantified differences in the size-distributions between the areas using size-spectrum exponents. We estimate the biomass size-spectrum exponent  $\gamma$  directly, using the likelihood approach for binned data, i.e., the *MLEbin* method in the R package *sizeSpectra* (A. Edwards, 2020; A. M. Edwards et al., 2017, 2020). This method explicitly accounts for uncertainty in body masses *within* size-classes (bins) in the data and has been shown to be less biased than regression-based methods or the likelihood method based on bin-midpoints (A. M. Edwards et al., 2017, 2020). We pooled all years to ensure negative relationships between biomass and size in the size-classes (as the sign of the relationship varied between years).

All analyses were done using R(R Core Team, 2020) version 4.0.2 with R Studio (2021.09.1). The packages within the *tidyverse*(Wickham et al., 2019) collection were used to processes and visualize data. Models where fit using the R package *brms*(Bürkner, 2017). When priors were not chosen based on the prior predictive distributions, we used the default priors from *brms* as written above. We used 3 chains and 4000 iterations in total per chain. Models were compared by evaluating their expected predictive accuracy (expected log pointwise predictive density) using leave-one-out cross-validation (LOO-CV)(Vehtari et al., 2017) while ensuring Pareto  $k$  values  $< 0.7$ , in the R package *loo*(Vehtari et al., 2020). Results of the model comparison can be found in the *Supporting Information*, Table S1-S4. We used *bayesplot*(Gabry et al., 2019) and *tidybayes*(Kay, 2019) to process and visualize model diagnostics and posteriors. Model convergence and fit was assessed by ensuring potential scale reduction factors ( $\hat{R}$ ) were less than 1.1, suggesting all three chains converged to a common distribution)(Gelman et al., 2003), and by visually inspecting trace plots, residuals QQ-plots and with posterior predictive checks (*Supporting Information*, Fig. S2, S9, S11).

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## Code and Data Availability

All data and R code to reproduce the analyses can be downloaded from a GitHub repository ([https://github.com/maxlindmark/warm\\_life\\_history](https://github.com/maxlindmark/warm_life_history)) and will be archived on Zenodo upon publication.

## Author Contributions



ML conceived the idea and designed the study and the statistical analysis. Data-processing, initial statistical analyses, and initial writing was done by MK and ML. AG contributed critically to all mentioned parts of the paper. All authors contributed to the manuscript writing and gave final approval for publication.

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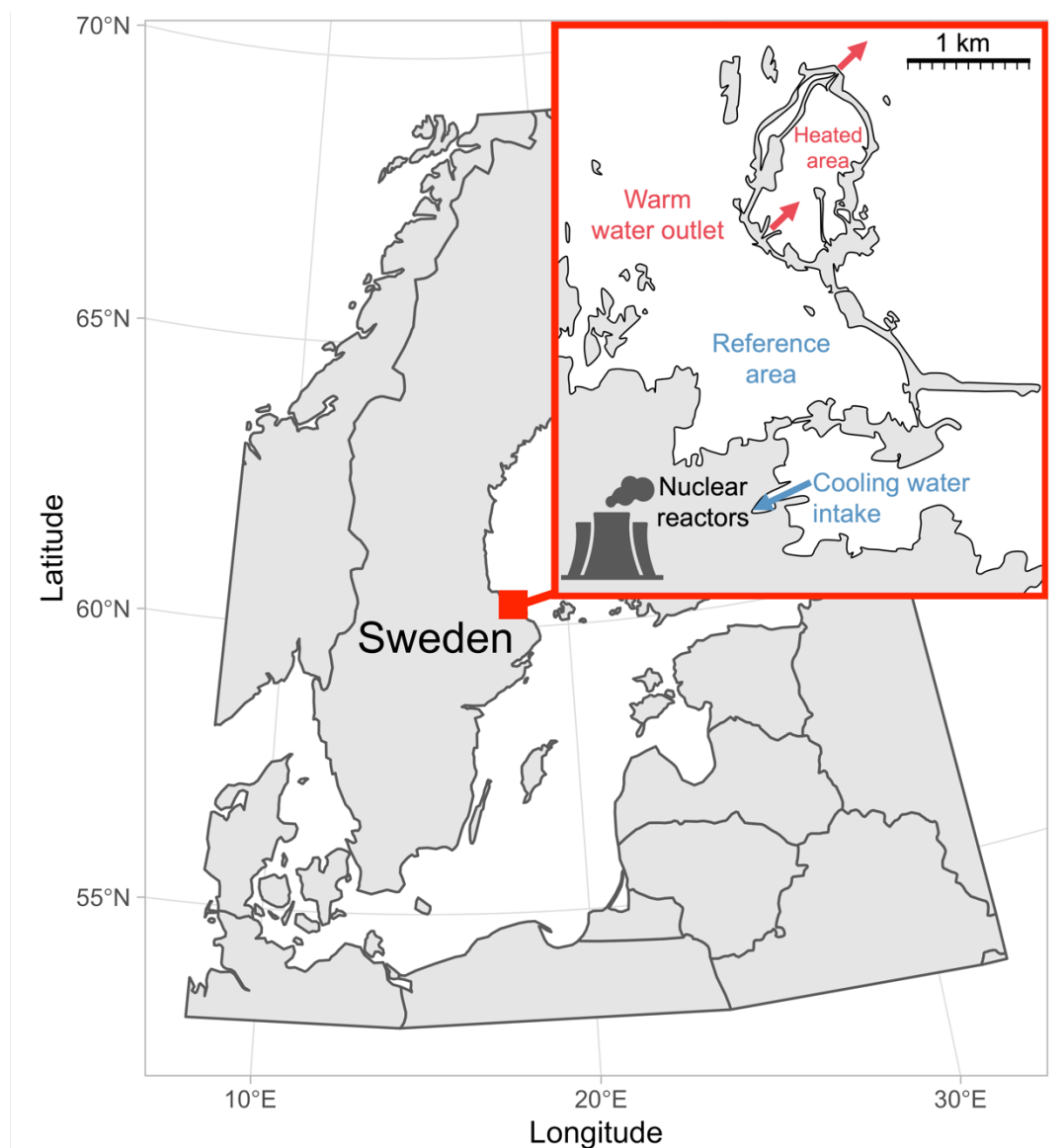
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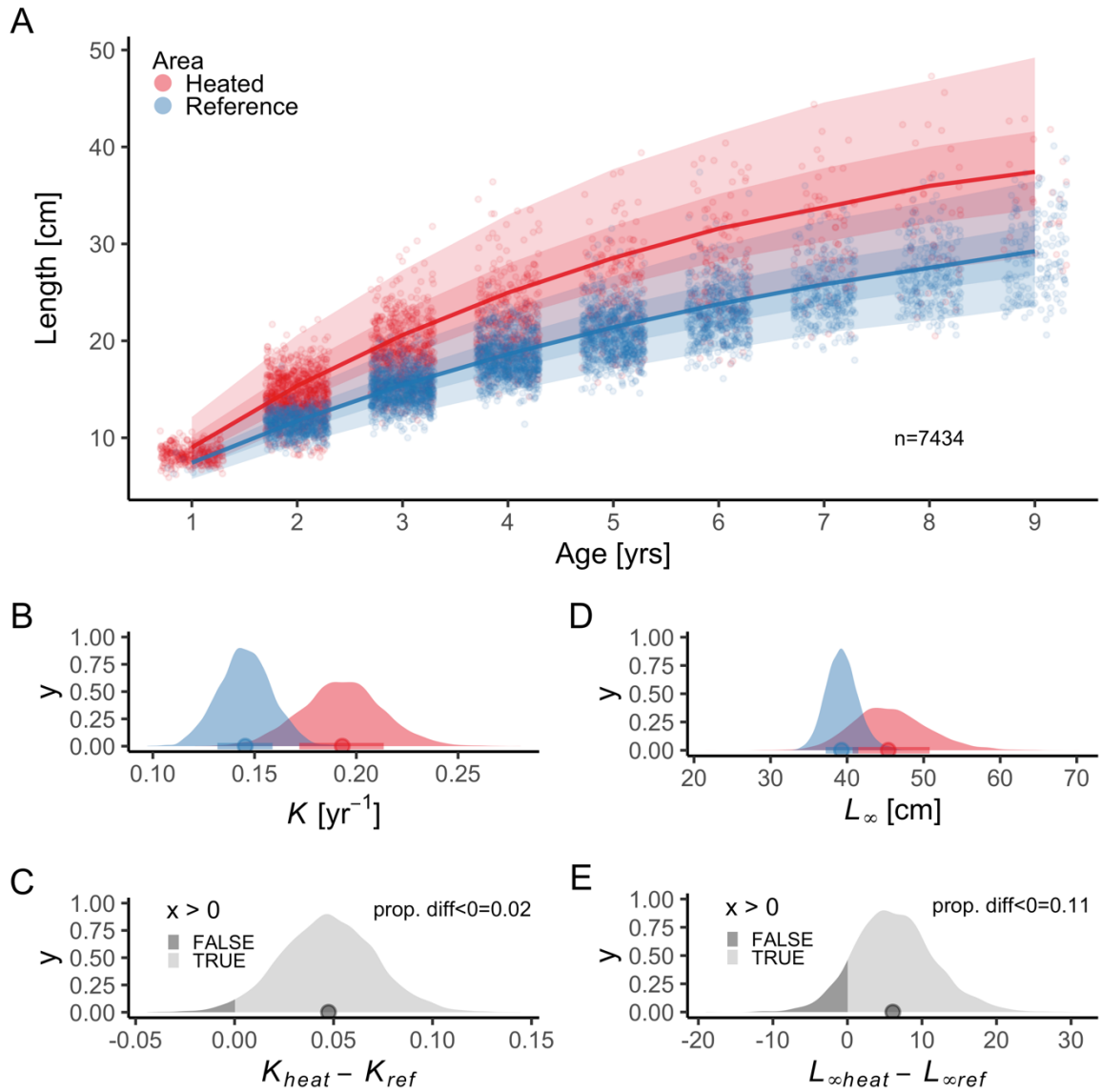
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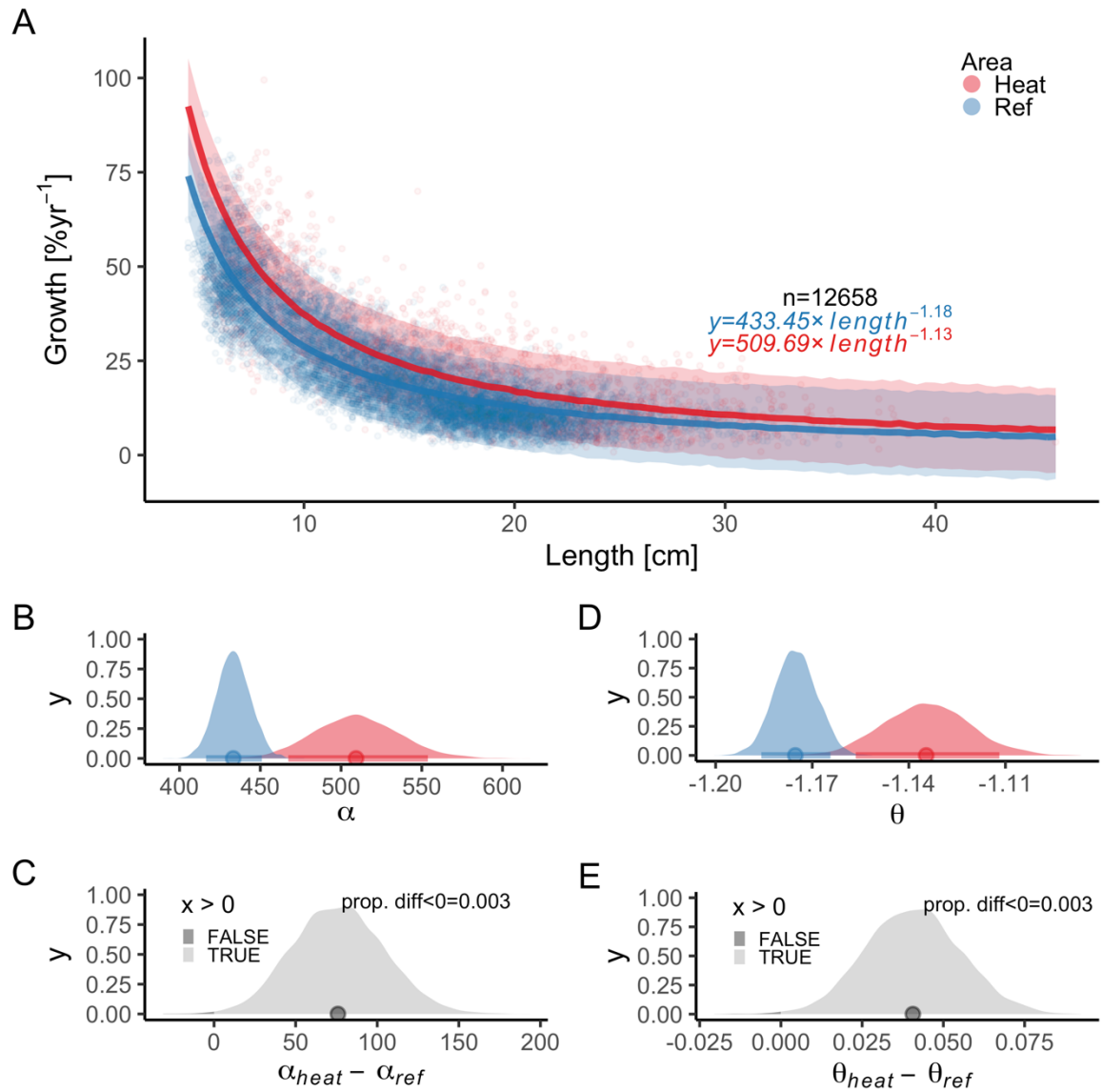
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**Fig. 1.** Map of the area with the unique whole-ecosystem warming experiment from which perch in this study was sampled. Inset shows the 1 km<sup>2</sup> enclosed coastal bay that has been artificially heated for 23 years, the adjacent reference area with natural temperatures, and locations of the cooling water intake and where the heated water outlet from nuclear power plants enters the heated coastal basin.

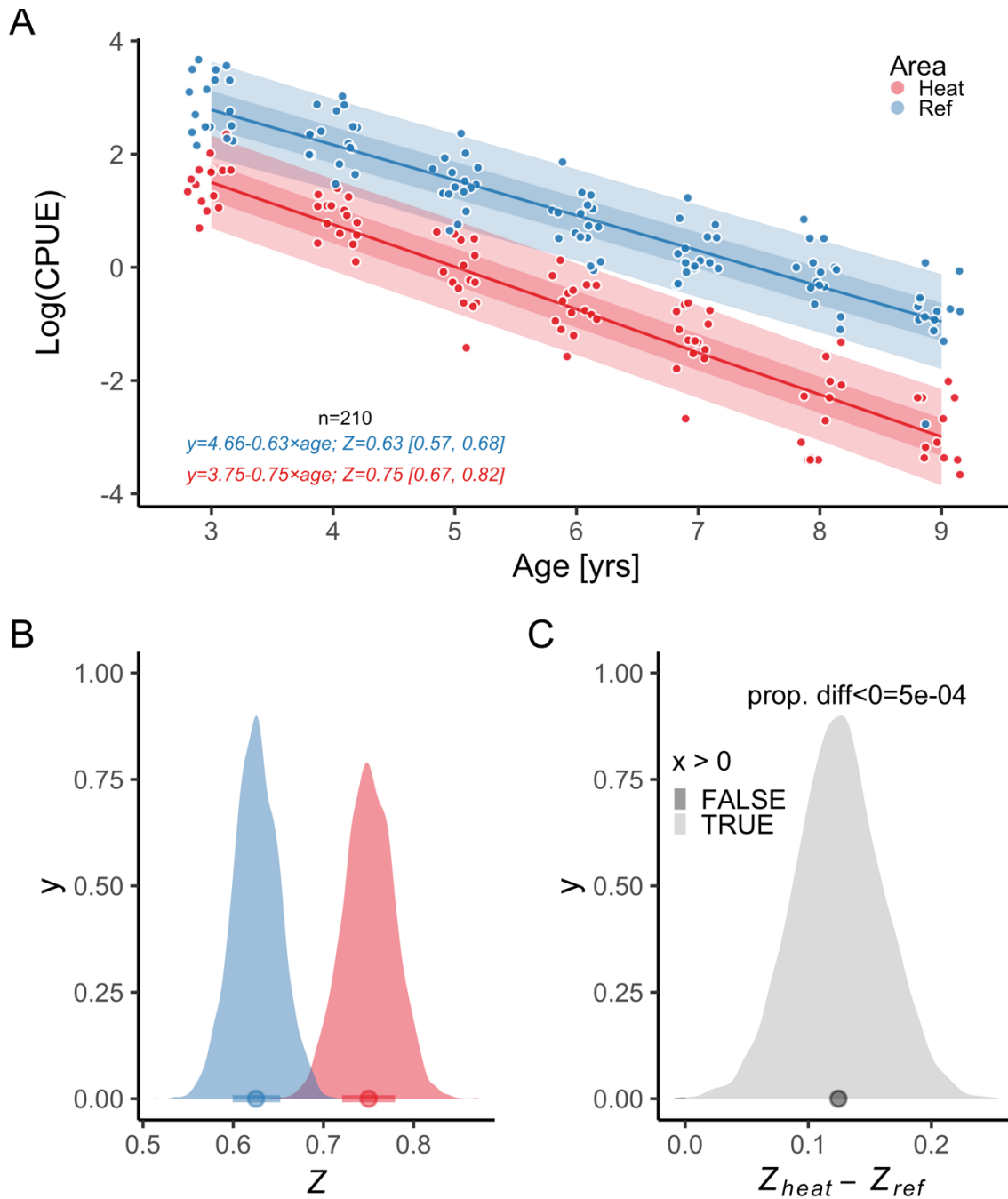


**Fig. 2.** Fish grow faster and reach larger sizes in the heated (red) enclosed bay compared to the reference (blue) area. Points in panel (A) depict individual-level length-at-age and lines show the global posterior prediction (both exponentiated) without group-level effects (i.e., cohort) from the von Bertalanffy growth model with area-specific coefficients. The shaded areas correspond to 50% and 90% credible intervals. Panel (B) shows the posterior distributions for growth coefficient (parameters  $K_{\text{heat}}$  (red) and  $K_{\text{ref}}$  (blue)) and (C) the distribution of their difference. Panel (D) shows the posterior distributions for asymptotic length (parameters  $L_{\infty\text{heat}}$  and  $L_{\infty\text{ref}}$ ), and (E) the distribution of their difference.



**Fig. 3.** The faster growth rates in the heated area (red) compared to the reference (blue) are maintained as fish grow. The points illustrate specific growth estimated from back-calculated length-at-age (within individuals) as a function of length (expressed as the geometric mean of the length at the start and end of the time interval). Lines show the global posterior prediction without group-level effects (i.e., individual within cohort) from the allometric growth model with area-specific coefficients. The shaded areas correspond to the 90% credible interval. The equation uses mean parameter estimates. Panel (B) shows the posterior distributions for initial growth ( $\alpha_{heat}$  (red) and  $\alpha_{ref}$  (blue)), and (C) the distribution of their difference. Panel (D) shows the posterior distributions for the allometric decline in growth with length ( $\theta_{heat}$  and  $\theta_{ref}$ ), and (E) the distribution of their difference.

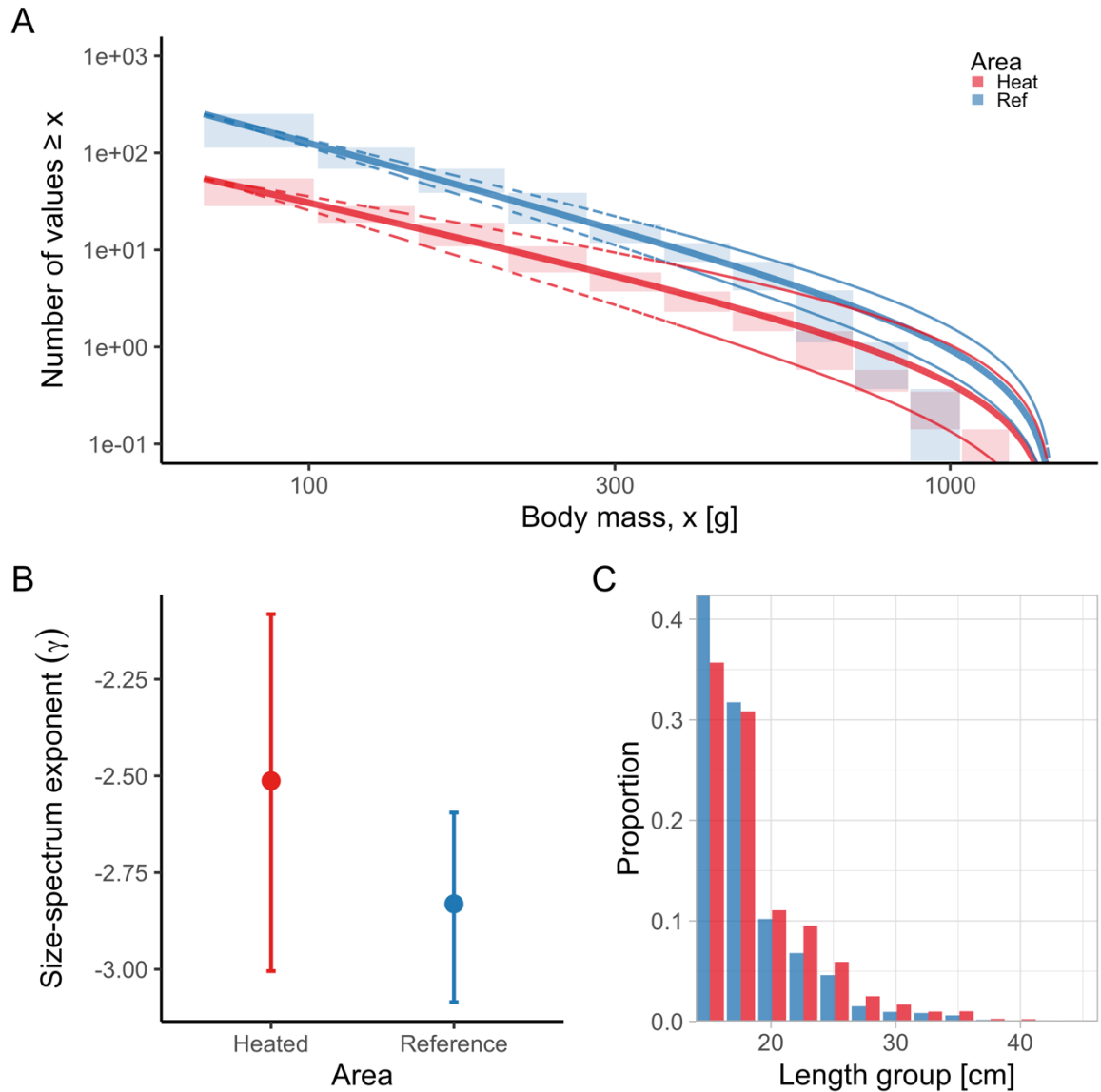




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634 **Fig. 4.** The instantaneous mortality rate ( $Z$ ) is higher in the heated area (red) than in the  
 635 reference (blue). Panel (A) shows the  $\log(\text{CPUE})$  as a function of  $\text{age}$ , where the slope  
 636 corresponds to the global  $-Z$ . Lines show the posterior prediction without group-level effects  
 637 (i.e., cohort) and the shaded areas correspond to the 50% and 90% credible intervals. The  
 638 equation uses mean parameter estimates. Panel (B) shows the posterior distributions for  
 639 mortality rate ( $Z_{\text{heat}}$  and  $Z_{\text{ref}}$ ), and (C) the distribution of their difference.

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**Fig. 5.** The heated area (red) has a larger proportion of large fish than the reference area (blue), illustrated both in terms of the biomass size-spectrum (A), and histograms of proportions (C), but the difference in the slope of the size-spectra between the areas is not statistically clear (B). Panel (A) shows the size distribution and MLEbins fit (red and blue solid curve for the heated and reference area, respectively) with 95% confidence intervals indicated by dashed lines. The vertical span of rectangles illustrates the possible range of the number of individuals with body mass  $\geq$  the body mass of individuals in that bin. Panel (B) shows the estimate of the size-spectrum exponent,  $\gamma$ , and vertical lines depict the 95% confidence interval. Panel (C) illustrates histograms of length groups in the heated and reference area as proportions (for all years pooled).