

# **Coping with climate change.**

**Implications of the Yellow-Bellied Marmot's (*Marmota flaviventeris*)  
body mass evolution in the last half-century.**



**uOttawa**

Comprehensive exam proposal

by

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2025-01-22

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A proposal submitted as a partial requirement for a PhD degree  
at the University of Ottawa, Department of Biology

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# **Introduction**

## **Climate change**

The impacts of climate change on natural environments are well-documented and can, obviously, no longer be ignored (Intergovernmental Panel On Climate Change (Ipcc) 2022). Broadly speaking, climate change encompass melting ice caps, rising sea levels. More specifically, main characteristics of this global change, usually documented, includes: **Raising temperature; Changing season lengths; Environmental variability and unpredictability; More frequent and severe droughts; Increasing frequency and severity of extreme weather events** (Intergovernmental Panel On Climate Change (Ipcc) 2022).

Climate change do impact human society, this is, for example, well represented in the city of Ottawa, ON, Canada. Temperature, snowing and raining trends in the Canadian capital over the last century, reveals worrying figures (Walsh and Patterson 2022), and future projections are not much more reassuring (Zhai et al. 2019). A concrete consequences of these changes in Ottawa is the management of the Rideau canal ice skating rink. Indeed, in later years the opening of the world's longest ice staking risk has been more and more uncertain, and its future is unfortunately but, fatally, questionable.

But most of all, climate change seriously impacts the vast majority of Earth's ecosystems, as shown by countless studies (Intergovernmental Panel On Climate Change (Ipcc) 2022). These profound ecological changes are putting a large number of species at risk, and they must act accordingly to avoid extinction, either by dispersing or adapting (Gienapp and Brommer 2014). It is crucial to improve our comprehension of how natural population react to this rapid and unpredictable changes in order to conduct efficient conservation policies.

## **Body mass as a Life-History Traits (LHT)**

Life history traits (LHT) are phenotypic characteristics that impact directly an individual's survival and reproduction representing its selective value, or “**fitness**” (Roff 1992). The concept of life history theory relies on the fact that organisms have limited resources and must allocate them strategically between competing functions such as growth, maintenance, and reproduction (Roff 1992; Stearns 1992).

Various traits can be considered as LHTs, as they represent the outcome of this resource allocation process. Among these, body mass plays a crucial role in many species. Individuals

with greater body mass typically have greater energetic resources, making them more resilient to environmental pressures by giving them a greater capacity to buffer poor years in terms of resources (!!).

Additionally, individuals with greater energy reserves have a better capacity to reproduce and are often more attractive to potential mates, leading to higher reproductive success. In this context, body mass is considered to be an “honest signal” of an individual capacity to accumulate resources and its quality as a reproducer (!!). Therefore body mass can be considered a key LHT influencing directly both survival and reproduction in many species.

However, as said before, energy quantity are limited and cannot be invested only in body mass. Moreover, a too large body mass can become a handicap (Jebb et al. 2021), and even though some handicaps have been theorized to be an asset in sexual selection (Zahavi 1997), beyond a certain threshold, too large individuals will be counter-selected against smaller ones. Hence, as predicted in Life History Theory, trade-off must be made between available energy and individual's performances to find the optimal body mass.

## **Link with hibernation**

The importance of body mass as a LHT is particularly true for a specific group of species: **Hibernating species**. To survive unfavorable season (usually winter) some species disperse to milder environments, others cope with it and find ways to survive through (!!). A way found by some species to survive through is to enter a specific state of torpor, called “hibernation”.

This strategy consists of reducing the metabolism to a minimum survival level. More specifically, “Fat-storing” hibernators (in opposition to “Food-storing hibernators”) will sustain on their energetic resources, stocked in their white adipose tissue, through the winter, then emerge at the start of the favourable season (Spring/Summer) (Carey et al. 2003; Geiser 2013; Nedergaard and Cannon 1990).

A commonly required adaptation for that kind of behaviour is therefore the capacity to stock important quantities of reserve (i.e., large body mass) in order to have sufficient energetic stocks to survive without foraging for a full season.

Furthermore, this energy gathering must be done in a short amount of time, hibernating species are usually active only for a small part of the year, during which they must forage as efficiently as possible to gain enough mass to survive through next hibernating season. Some fat-storing hibernators nearly double their weight during the active season (Armitage 2014; Carey et al. 2003).

Hence, not only a prerequired adaptation is an important body mass, but also a sufficiently efficient metabolism to gain weight quickly, which represent a lot of challenges and specific adaptation. Body mass and metabolism are therefore highly constrained in hibernating species (!!).

Additionally, for some species, reproduction occurs right at the onset of the active season, which means that before entering into hibernation, individuals must reach a threshold body mass sufficient not only to survive, but also to have to reproduce directly after. Body mass is therefore a keystone LHT for hibernating species' biodemography.

Meanwhile, Climate change is expected to have significant impact on such LHT. It has been theorized that change in body size could be a third universal response to climate change, alongside modification in phenology and geographic range (Daufresne et al. 2009; Durant et al. 2007; Gardner et al. 2011; Visser and Both 2005)

### **Expected effect of global warming on body mass**

As reminded earlier, one of the most significant consequences of climate change is an increase in global temperature (which is why climate change is also commonly referred to as *global warming*, although this term is often used in climate sceptics rhetoric during unusually intense episodes of cold<sup>1</sup>).

This average temperature increase is suspected to influence phenotypic traits such as body mass or size. However, the direction of the response remains uncertain. Some authors argue that a shrinking body size should be a universal response to climate change (Daufresne et al. 2009). This hypothesis follows Bergmann's rules, which state that smaller body size should be favoured in warmer environment as it raises the surface to volume ratio, thus facilitating heat dissipation (Bergmann 1847). Therefore, in a warmer environment, due to global warming, an adaptive response could indeed be a shrinking body size.

However, as noted by Gardner et al. (2011), a lack of large-scale comparative studies prevent us to demonstrate that this response is universal. In addition, in 2022, the IPCC's report stated that "Evidence is weak for a consistent reduction in body size across taxonomic groups in terrestrial animals" (Intergovernmental Panel On Climate Change (Ipcc) 2022; Siepielski et al. 2019).

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<sup>1</sup>"[...] Large parts of the Country are suffering from tremendous amounts of snow and near record setting cold. [...] Wouldn't be bad to have a little of that good old fashioned Global Warming right now!" U.S. President, Jan 20, 2019.

Moreover, several studies at higher latitude yield opposite results (i.e., increasing body mass in response to climate change, Guillemain et al. 2010; Ozgul et al. 2010; Sheridan and Bickford 2011; Yom-Tov et al. 2008). At higher latitudes and altitude, climate change is synonym of milder conditions, so individuals have access to a large food supply for a longer time and face less hard conditions during the less favorable season which overall is less energetically demanding. Hence these new, milder, conditions allows individuals to become larger.

## **Phenotypic plasticity vs microevolution**

Evolution by natural selection was defined by Darwin (1859) as so: individuals that are best adapted to their environment will have better survival and reproductive success. This process result in a population composed mainly of individuals adapted to their environment. So, observed phenotype in natural populations is expected to be the best fit for a specific environment.

However, when this environment changes, as expected with climate change, individuals have two solution to avoid disappearance: **disperse** to a more favorable environment, or **adapt** to their new conditions through phenotypic changes (Gienapp and Brommer 2014).

To adapt, there are two further possibilities: **phenotypic plasticity**, defined as a change in phenotype expressed by a given genotype, which allows for a rapid response within an individual lifetime, is highly flexible and does not involve any changes at the genetic level (!!!); and **microevolution**, defined as a change in alleles frequencies in a population over time (!!!). When an individual with a better-fitted phenotype for its new environment appears, it would have a better survival and more reproductive success. If this advantage relies on a heritable genetic difference (i.e., transmitted to its descendants, Lynch and Walsh (1998)) the new genotype is going to rapidly increase in proportion in the population, ultimately replacing the old one.

Hence, adaptation through microevolution can be slow but is a long-term solution, better fitted for a persistent ecological change. However if the change is transient, plasticity might be better suited. As noted by DeWitt et al. (1998) and Gardner et al. (2011), phenotypic plasticity solely is unlikely to be the most optimal long-term response to climate change as it is usually a transient answer to a temporary change, presenting costs and limits (DeWitt et al. 1998). Furthermore, if the optimal response to the new environment is a canalized phenotype (i.e., very low phenotypic variance), plasticity can even be maladaptive (Nussey

et al. 2007). Therefore, the expected optimal answer to a long-term environmental change, as those expected with climate change, is evolution through natural selection.

Phenotypic plasticity and microevolution are not expected to be mutually exclusive. This is particularly evident in highly plastic traits such as body mass which can vary significantly up and down throughout an individual's life in response to among- and within-year changes in environmental conditions but can also change via microevolution at the population level over the same time period.

Nevertheless, as the consequences of these mechanisms can be highly different on the long term (evolution being more permanent than plasticity), quantifying the extent to which each of these mechanisms contributes to the observed change over a long study period remains a challenging but fundamental task to understand the adaption and evolution of species.

## Quantitative Genetics and Animal Models

As we have discussed, climate change is expected to cause long-term environmental changes. Thus, natural populations will need to adapt to these new conditions in order to persist (!!). As mentioned earlier these adaptations can involve shifts in geographical ranges, phenology, or phenotype (Dufresne et al. 2009; Durant et al. 2007; Gardner et al. 2011; Visser and Both 2005). As climate change implies deep and long-term environmental modification, we expect natural populations to **evolve**, allowing them to be better suited to new environments (Darwin 1859; Sih et al. 2011).

However, estimating evolutionary signals in natural conditions can be complicated, and an observed phenotypic change is not necessarily due to evolution (i.e., phenotypic plasticity). Fortunately, quantitative genetics provides us a robust and well-established method to address this by decomposing the total phenotypic variance ( $V_P$ ) into its genetic ( $V_A$ ) and environmental ( $V_{PE}$ ) components:  $V_P = V_A + V_{PE}$  (Lynch and Walsh 1998; Wilson et al. 2010).

A well-known statistical method to estimate these variance components from observed phenotypic data is the **Animal Models** (Kruuk 2004). This method allows a robust estimation of the genetic variance in a trait affected by a large number of genes, each with small effects (Kruuk et al. 2014; i.e., a "quantitative trait," Lynch and Walsh 1998). An Animal model is a specific kind of mixed model using individual identity as a non-independant random effect, linked to a relatedness matrix between each individual, extracted from the population pedigree (i.e., parental links between each individuals in the population population, Lynch and Walsh (1998)).

This method has the advantage of being relatively simple to employ, enabling genetic parameters estimation directly from phenotypic data. Only parental links between individuals need to be known, making this method applicable to wild populations (Kruuk 2004; Lynch and Walsh 1998).

As emphasized by Kruuk et al. (2014), there is a pressing need for quantitative genetics studies on long-term wildlife populations, as the most common problem in such studies is the lack of statistical power, which can be resolved thanks to the quantity of data brought by long-term studies. Such studies would improve our understanding of the relationship between animals and their environment, as well as the genotype-phenotype-environment relationship, especially in a context of global change.

### **Traits coevolution**

A well-recognised challenge when studying evolution in natural context, is to consider the genetic correlation between several traits, causing **traits coevolution** (Gould and Lewontin 1979; Roff 1992). Indeed a trait cannot evolve independently without impacting other traits. This constraint narrows the range of possibility and reachable outcomes in the adaptive landscape (Arnold et al. 2001; Gould and Lewontin 1979; Teplitsky et al. 2014).

When studying the evolution of a specific trait (especially ones having important phenotypic consequences), failing to account for its link with other traits is an oversimplification. This misconception can bias not only our understanding of the causes and consequences of phenotypic change, but also the estimations of its evolutionary potential [Teplitsky et al. (2014); !!!]. To effectively study traits' evolution, it is essential to consider that selection generally acts on multiple traits simultaneously, as phenotype is the result of a combination of various traits (Phillips and Arnold 1989).

A continuation of this reasoning is the extended **Pace Of Life Syndrome** (POLS) suggesting that life-history strategy, physiological and behavioral traits coevolve in response to the environment (Dammhahn et al. 2018; Réale et al. 2010).

So, if climate change induces LHT modifications, it is to expect that other key physiological or behavioural trait will coevolve with it. For example, it has been observed that certain behavioural types will be consistently associated with certain Life-History strategies (Biro and Stamps 2008; e.g., individual with faster life-cycle will tend to be bolder Stamps 2007; Wolf et al. 2007).

As such, changes in LHTs are expected to have even greater impacts on the global phenotype. A robust method to study such changes are **Multivariate Animal models** (i.e., an Animal model with multiple phenotypic traits as dependant variables) which allows us to estimate the genetic covariance between each trait [!!!].

However such models are heavily data-consuming, and the main reason that significant results with such methods are quite rare today is that only a few studies have enough data to support the statistical power required for these complex models. Again, using long-term datasets brings a lot of expectation to address such limitations (Teplitsky et al. 2014).

*TRANSITION TRANSITION TRANSITION TRANSITION TRANSITION*

## **Individual variation in their plasticity**

As explained above, evolution and plasticity are not mutually exclusive, but even more so, plasticity itself can evolve (!!).

Plasticity is usually studied using **Reaction Norm framework** (!!), i.e., studying the value of a phenotypic trait (e.g., body mass) in response to an environmental proxy (e.g., temperature, precipitation). A plastic response correspond to a different phenotypic value associated to a different environment. In this reasoning, a trait is plastic if the slope of the reaction norm is different from 0 (Nussey et al. 2007).

A reaction norm has two parameters: **Elevation**, which is the expected phenotypic value in the average environment; and the **Slope** corresponding to the linear regression of the phenotype over the environmental gradient. In statistical terms, these parameters correspond respectively to the “Intercept” and the “Slope” of the linear regression of the phenotype over the environment.

This is how phenotypic plasticity is usually studied. However, as emphasized by Nussey et al. (2007), a lot of information is lost when plasticity is only studied at the population level (i.e., fixed linear model of the phenotype over the environment). First using a linear mixed model is crucial to estimate different elevations for each individual, this allows the model to account for the individual variability in their phenotype in the average environment. However, that kind of model doesn't allow to estimate individual-level difference in their plastic response to the environment, which can be biologically significant and must be accounted for.

Nussey et al. (2007) proposed a framework to estimate that individual variance in plasticity, which is now fairly accepted and used: **Random Regression**. Let's go back to the Linear

Mixed Models (LMMs), the most classical type of mixed models is to add a random individual term on the intercept to estimate the “individual variance” by allowing the model to fit one intercept per individual, however in this compilation, the slope is the same for each individuals; now, if we add a random term also on the slope, not only the model estimate one intercept per individual, but also one slope (so, one reaction norm) per individual, estimating thus the individual variance in the phenotype expected in the average environment (*elevation*) but also the individual variation in phenotypic variation (*slope*) which is commonly called **I \* E**.

Once we’ve estimated this between-individual variance in plasticity, we can use quantitative genetic methods using Random Regression Animal Model: “RRAM” (Nussey et al. 2007) to decompose this variance into it’s genetic and environmental parts in order to get the between-individual genetic variation in plasticity, commonly referred to as **G \* E**. From that we can estimate the heritable variation in reaction norm’s slope and have an idea of the evolutionary potential of a trait’s phenotypic plasticity itself.

From a theoretical point of view, this method allows for proper estimations of a trait’s  $I * E$  and  $G * E$ . However, as underlined by Ramakers et al. (2023), an important limitation is the environmental proxy used for the reaction norm. Indeed, if this latter isn’t good enough (i.e., too far from the real predictor of the trait’s plastic response), an important part of the actual individual variation in their plasticity is missed, this is what Ramakers et al. (2023) called the “hidden  $I * E$ ”.

Furthermore, it is often impossible to identify the real driver of plasticity in natural conditions, as natural environments are exceptionally complex systems, and individuals generally have to react to a combination of environmental variables rather than one. Therefore, the real driver of plasticity is often unknown, unmeasurable and a combination of a lot of different variables. In response to that, Ramakers et al. (2023) proposed a new method, using Environment Specific Mean phenotype (ESM). Although they have shown that this method is indeed efficient, they emphasized that we still need a really good knowledge of the study system, and specific conditions to be more efficient than classic the random regression method. Hence, although it’s a progress, more work is needed to deal with this  $I * E$  detection problem in natural environments.

The good news is that a promising, fairly new, statistical method could bring new interesting insights to that matter: the “Double Hierarchical Generalized Linear Model” (DHGLM). DHGLM is a kind of mixed model estimating the distribution for both the mean and the residual variance (Lee and Nelder 2006). In other words, DHGLM estimates the *variance*

in the residual variance hereafter referred to as  $V_{V_e}$ . This correspond to the variance in the proportion of the residual variance attributable to each individual.

We are confident that DHGLM can be applied to developp a more powerfull method to detect individual variation in plasticity ( $I * E$ ) in natural systems. Indeed, a  $V_{V_e}$  significantly greater than 0 indicate some disparities in the individual contributions to the residual variance. To put it differently, it shows that the range of phenotypic values expressed by each individuals is different, which can be interpreted as an individual variance in their plastic response, so  $I * E$ .

Although a non-zero variance isn't necessarily due to the presence of  $I * E$  in the system, it would justify further investigations by testing different environmental proxies. In contrast, except in very specific conditons, almost impossible in natural conditions (i.e., **perfect** contrary effect, Figure 6), a  $V_{V_e}$  equal to 0 indicate that the relative contribution to the residual variance in phenotype isn't significantly different between each individual, and so that there's no individual variation in plasticity in the studied system.

An important feature of this method is that it should be free from the problems of bad environmental proxies as it detects  $I * E$  from the structure of the residual variance in phenotype. And obviously, as for the random regreession with the RRAM, we can use quantitative genetics to also detect  $G * E$  if  $I * E$  is detected by combining a DHGLM with an Animal model, giving a “Double Hierarchical Animal Model” (DHAM).

This is a very promising method, however, as most new statistical methods, it is often poorly understood/used. Hence, a general framework, including clear applications showing how DHGLM should be used to detect  $I * E$  would be really helpful for the community, especially with the rising need to study efficiently phenotypic plasticity and it's evolution, in natural condition in a context of climate change.

## Bet-hedging

Bet-hedging strategy can be summerized as betting on the best fitness for the long term, even though it means lower a bit your immediate fitness, in order to cope with an unpredictable environment (Starrfelt and Kokko 2012). With climate change, environment are less predictable than ever, therefore, bet-hedging is expected to be a relevant adaptive strategy in such context. Let's take body mass increase as an example again.

increase you body size to “buffer” is not a crazy strategy, but can be risky in the future => potential phenological mismatch (i.e., [...], Stenseth and Mysterud (2002); Visser and

Both (2005)), bet-hedging is a bet, so you're not sure to win in the end, and it can end in maladaption...

But, by definition, a “bet” comports risks, and in such variable conditions due to an extremely fast climate change, betting on the future can end in evolutionary traps (Robertson et al. 2013; Schlaepfer et al. 2002).

## Species and study

Since 1962, a wild population of Yellow-Bellied Marmots (*Marmota flaviventris*, “YBM”) is followed yearly, first supervised by Kenneth Armitage, and today by Julien Martin and Daniel Blumstein, at the Rocky Mountain Biological Laboratory (RMBL) in Gothic, Colorado, USA ( $38^{\circ}56'34'' - 38^{\circ}59'13''$  N /  $106^{\circ}58'60'' - 107^{\circ}0'45''$  W), this is the second longest-term study of a natural mammal population in the world. YBM is a ground-dwelling sciurid (rodentia, sciuridae) inhabiting alpine habitats in western North America with a life cycle divided between an “active season” representing approximately a third of the year (from May to September) where individuals must forage to reach a threshold body mass in order to survive hibernation for the remainder of the time (Armitage 2014). Individuals experience high seasonal fluctuation in body mass, with a critical threshold to be reached before the onset of hibernation in order to 1) survive through the next active season and 2) have sufficient energy left for hibernation (which occurs in the first weeks of the active season, Armitage 1965, 2014). Consequently, body mass is considered being a critical LHT for the marmots. YBM lives in colonies composed usually by one or more matriline with one adult male, multiple adult females and their offspring (Armitage 2014). Our population is composed of seven main colonies divided between an “up” and a “down valley” with an elevation difference around 300m (“up” = 3,000m; “down” = 2,700m) implying some difference in weather (Armitage 2014; e.g., delayed snowmelt and vegetation growth onset, temperature difference up to  $2^{\circ}\text{C}$ , Blumstein et al. 2004) and so delayed emergence up to two weeks in the up-valley (Blumstein 2009; Monclús et al. 2014). This two different conditions offers an amazing opportunity to test the impact on environment on several factors while working in natural conditions.

This hibernation (life) cycle is highly environmentally dependant, with the onset and end of the active season believed to be mediated mostly by weather variable such as temperature and snow cover of the region (Armitage 2014). Thus, body mass is expected to be a keystone phenotypic trait for the marmots. It is therefore crucial to understand how this trait and this species responds to global warming, both for conservation purposes and to elucidate links between phenotype and environment.

## **Long-term study data**

The monitored population is distributed over 7 main and 31 smaller colonies, divided between an “up” and a “down” valleys (Figure 1). Each Spring-Summer (May - September) since 1962, marmots are regularly trapped (between 1 and 20 times per individual, with an average of 4.5) using baited Towahawk live traps ( $81 * 25 * 30\text{cm}$ ) situated near burrow entrances. If the individual is captured for the first time, it is identified by placing a unique numbered ear tag on both ears, and with a nontoxic black Nyzanol dye fur mark for distant identification during behavioral observations. Over 95% of individuals are captured between the first two years of their lives and thus have know year of birth and age, from that each we define four age classes, the **juveniles** between 0 and 1 year old, **yearlings** between 1 and 2 years old, **subadults** between 2 and 3 years old, and **adult** over 3 years old.

At each capture, individuals are sexed, weighted (initially with a spring scale ( $\pm 50\text{g}$ ) and now with a digital balance ( $\pm 10\text{g}$ )) measured and DNA samples are taken. Behavioral observations and experiments (running speed and Flight Initiation Distance (FID) (!!!)) are conducted all along the season. More descriptions can be found in Armitage (2014).

**Population pedigree** Population pedigree for most of the individuals (4,652 individuals to this date)

**Body mass:** “Body mass is a highly plastic trait, particularly for a hibernating species that experiences considerable fluctuations in body mass throughout the active season. It is, for obvious reasons, impossible to record all individual body mass at the same time. Therefore, it is necessary to estimate the body mass of each individual at the same time of the year. Using repeated measures for each individual throughout each year’s active season, ranging from 1 to 20 with an average of 4.5, a linear mixed model was fitted to predict each individual’s body mass on August 15 each year (for details see Ozgul et al. (2010) and Jebb et al. 2021).”

**Weather data** (Prather et al. 2023)

Data are stored in the R package “ybamaRmot” (Martin 2024), analysis will be performed on R (R Core Team 2024), Animal models will be performed using R package “MCMCglmm” (Hadfield 2010), DHGLM and other bayesian analysis (excluding MCMCglmm) will be done with “brms” (Bürkner 2021), figures will be made with “ggplot2” (Wickham 2016).

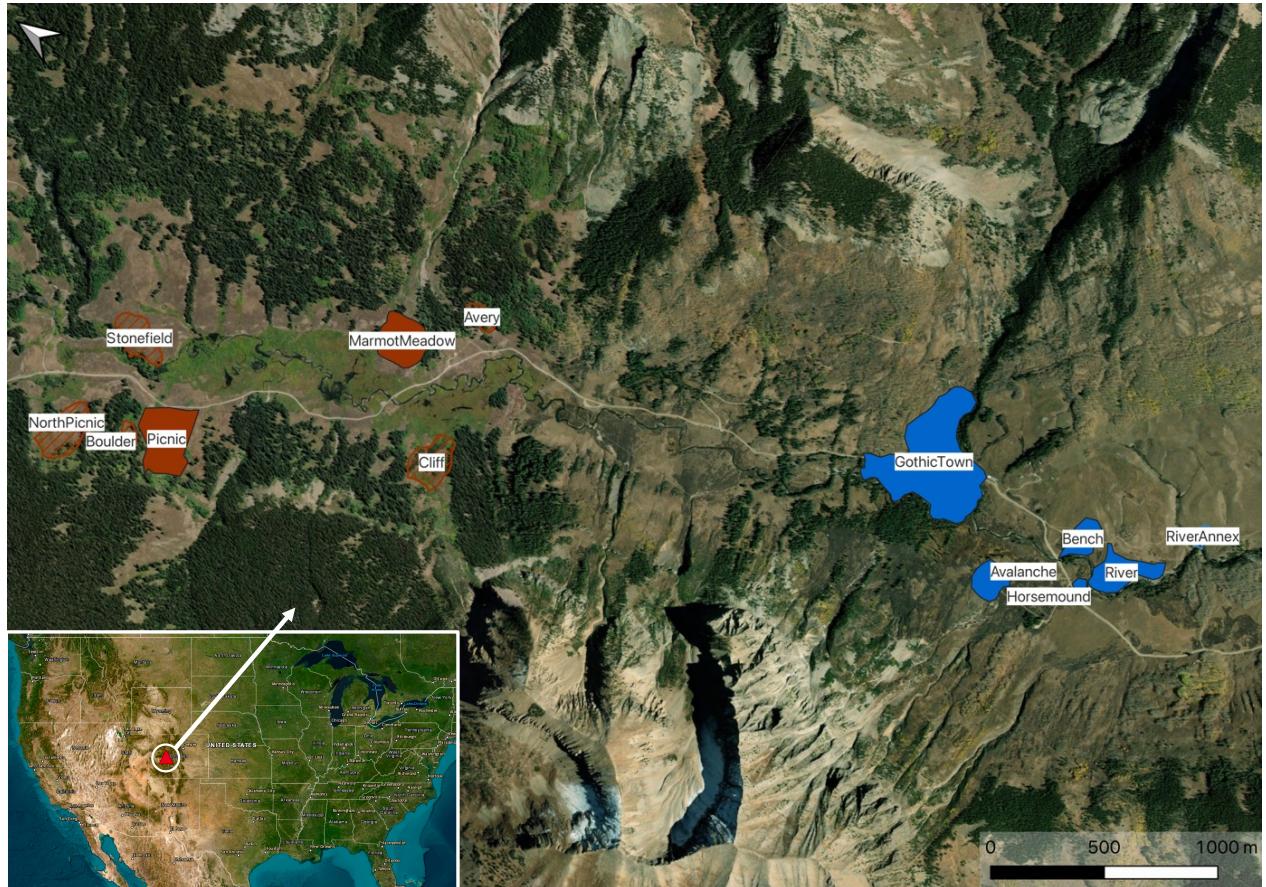


Figure 1: Red colonies represent the “**up**” valley, blue represent the “**down**” valleys. Plain background polygons represent the seven main colonies. Map created with QGIS software (QGIS Development Team 2024), base map from ESRI (“GIS Mapping Software, Location Intelligence & Spatial Analytics | Esri” n.d.).

## **Body mass increase in Yellow-Bellied Marmots (YBM)**

An important body mass increase has been observed in this population over the past half-century (estimated around 600 g for the adult females). Precedent studies attributed this major change mostly to phenotypic plasticity (Ozgul et al. 2010). This hypothesis made in fact a lot of sense, with climate change active season is getting longer (milder condition, higher temperature, less snow, shorter winter, etc.), hence marmots have more time to forage, gain weight, and the hibernation period is getting shorter so less time for the individuals to lose mass, at the end of the day, we have heavier individuals, makes sense! However, using animal models to properly assess the genetic attributable part of this change, estimating explicitly the body mass' evolutionary signal for the adult females over the time cohort (i.e., year of birth) during the study period, we found an increase, at the genetic scale, estimated around 400 g, with a heritability of 56% (Birot & Martin, Manuscript in progress, Figure 2). So, in fact, around two third of the body mass increase seems to be due to evolution, not just plasticity. Furthermore, although the lengthening active season is indeed a good potential explanation for the body mass increase through phenotypic plasticity, it doesn't match with the observed evolutionary signal. If the main selective pressure on body mass is survival through hibernation (i.e., heavier individuals having more chance to survive through winter as they have more resources), then the expected evolutionary response (i.e., average body mass increase) is occurring when the pressure is decreasing, which seems counter-intuitive. There is a pressing need to explore which environmental factors may have triggered this shift, the mechanisms behind this increase, and the potential implications for the population's future to better understand how can natural populations cope with climate change.

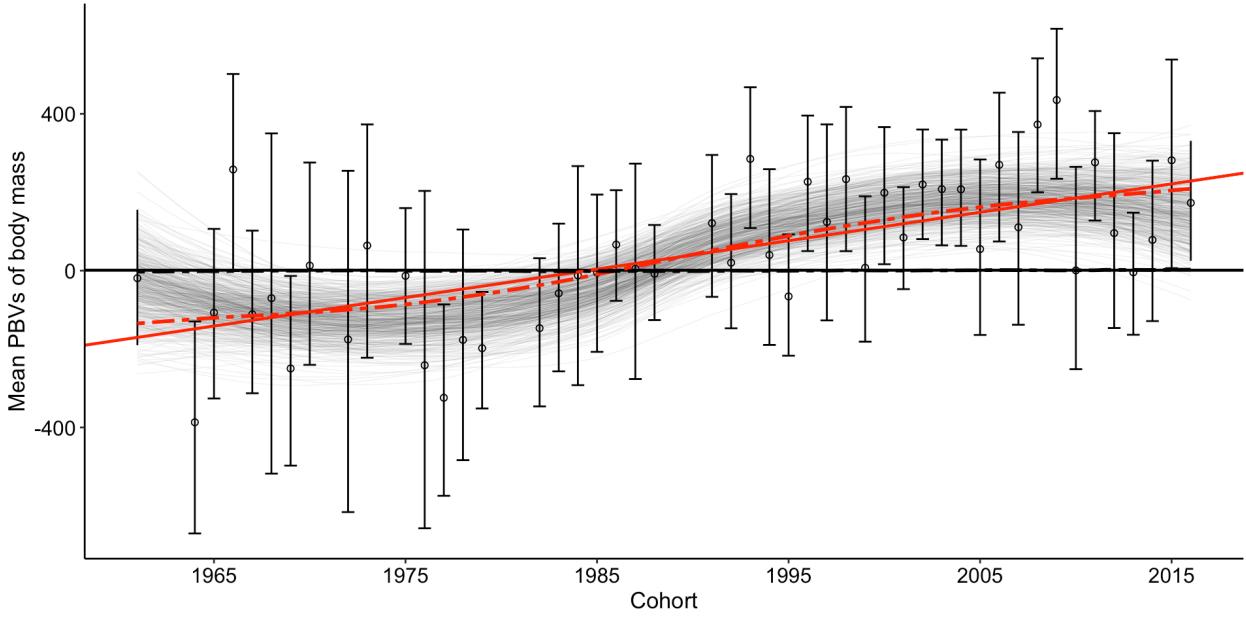


Figure 2: Mean cohort's predicted breeding values trend over 5,000 iterations (gray lines). The median trends of the observations (red line) and under the null scenario (drift alone, black line) are represented, according to linear (solid line) or generalized additive models (two dashed lines). Points and error bars represent the median and 95% credibility interval of the posterior mean PBV for each cohort.

## Research objective

Since this major phenotypic shift for the YBM in the last half-century has been miss considered, knowing that there is in fact a strong evolutionary signal, we need to reconsider the evolutionary scenario behind this body mass increase.

I will explore which environmental factors could have triggered this shift, but also the mechanism behind this increase and finally the potential implication for the population's future.

# Chapter 1 - Mechanisms

*Marmot's Biology: What mechanisms are behind the body mass increase?*

As emphasized in the introduction, we know that the body mass has increased in the last half-century, however we still know very few about it. And for starter, we don't know yet what has changed in the marmots in the last decades: do they have a bigger constitution (i.e., are they born bigger, their Intercept in statistical term), or does their growing capacity has increased through time (in statistical term again, this would correspond to their slope)?

**I \* A and G \* A A: AGE =>** Reaction norm over individual lifetime rather than Environmental gradient

Growth? Baseline? Both?

Double random (Intercept, Slope)

Body mass in juvenile was predicted to stay stable as it favour a higher running speed allowing juvenile to escape predators more efficiently during foraging (Jebb et al. 2021). This was one of the main argument to explain why YBM body mass was (before the 70s) stable in adults, the “invisible fraction” explained by Jebb et al. (2021).

However, we see that even if the body mass at birth is indeed stable (Figure 3 a)), the mass at the end of the individuals first season however, shows a pattern found in Figure 2. Indeed, the body mass at the end of our juveniles' first foraging season has increased by 23% in 23 years (23 cohorts), meaning that between 1977 and 2000, each cohort was 1% heavier than the last one at the end of their first foraging season (Figure 3 b)). This could be a serious clue to explain the sudden body mass increase observed in adults arround the same period. We can hypothesized that a relax on the juvenile body mass constrained has occured. Now we must find which constraint has change during this specific period of time (Section ).

Increasing (estimated from local regressions):

- **Males:** 1976 - 1998 (22 cohorts) => 1,206.18 g ; 1,519.71 g (+313.53 g)
- **Females:** 1979 - 2001 (22 cohorts) => 1,130.64 g ; 1,363.03 g (+232.39 g)

*However we don't find significant interaction between sex and cohort, meaning that the slight difference in patterns between males and females aren't statistically significant*

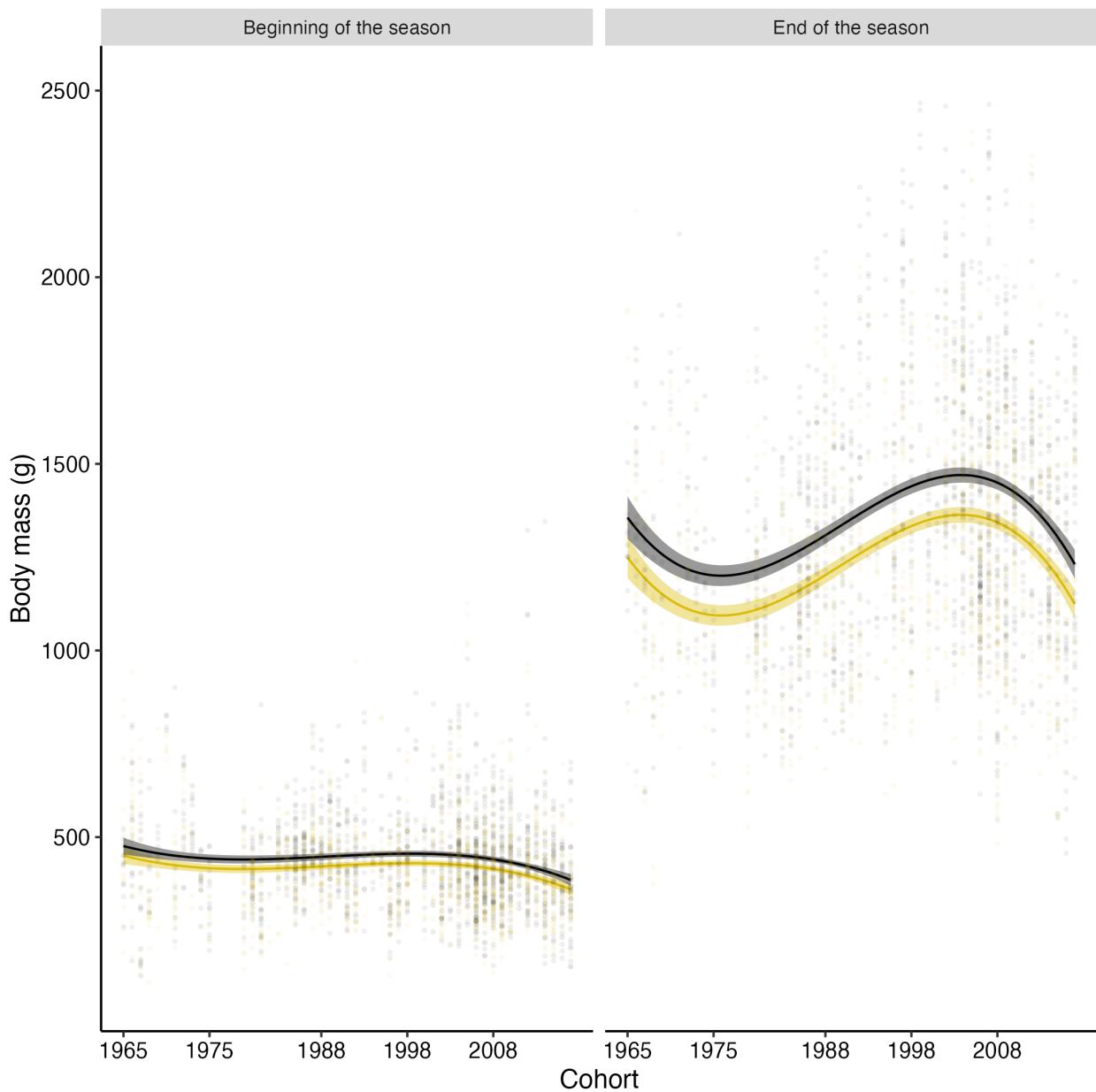


Figure 3: Body mass trend over time cohort for females (gold) and males (black) juveniles compared between the beginning (birth weight) and end of their first active season (mass on August 15th).

As the body mass was previously hypothesized to be stable as an anti-predator strategy, it seems logical to look for a change in predators populations or behaviour between the 1970s and the 2000s at our study site.

## Chapter 2 - Methodology

*Methodology: I\*E detection with Double Hierarchical Generalized Linear Models (DHGLM)*

(Nussey et al. 2007) → double random

So we're doing something different → examining the residuals of the model (if  $I * E$ , still a lot of residual variance ?)

\*\*Look at this one: (Westneat et al. 2015)

DHGLM, brms, Julien's code

Vve (Variance dans la variance résiduel, estime la variance résiduel pour chaque individu et regarde la variance dans cette variance résiduelle, si  $I * E Vve > 0$ )

Attention aux modèle débalancés si pas d'effet fixes corrige pour les variations par effet fixes, puis test pour le  $I * E$ , si y'en a tu pexu chercher la variable environnemental pour lesquels on a de la variation dans la plasitcité ( $I * E$ )

Ned Dochtermann

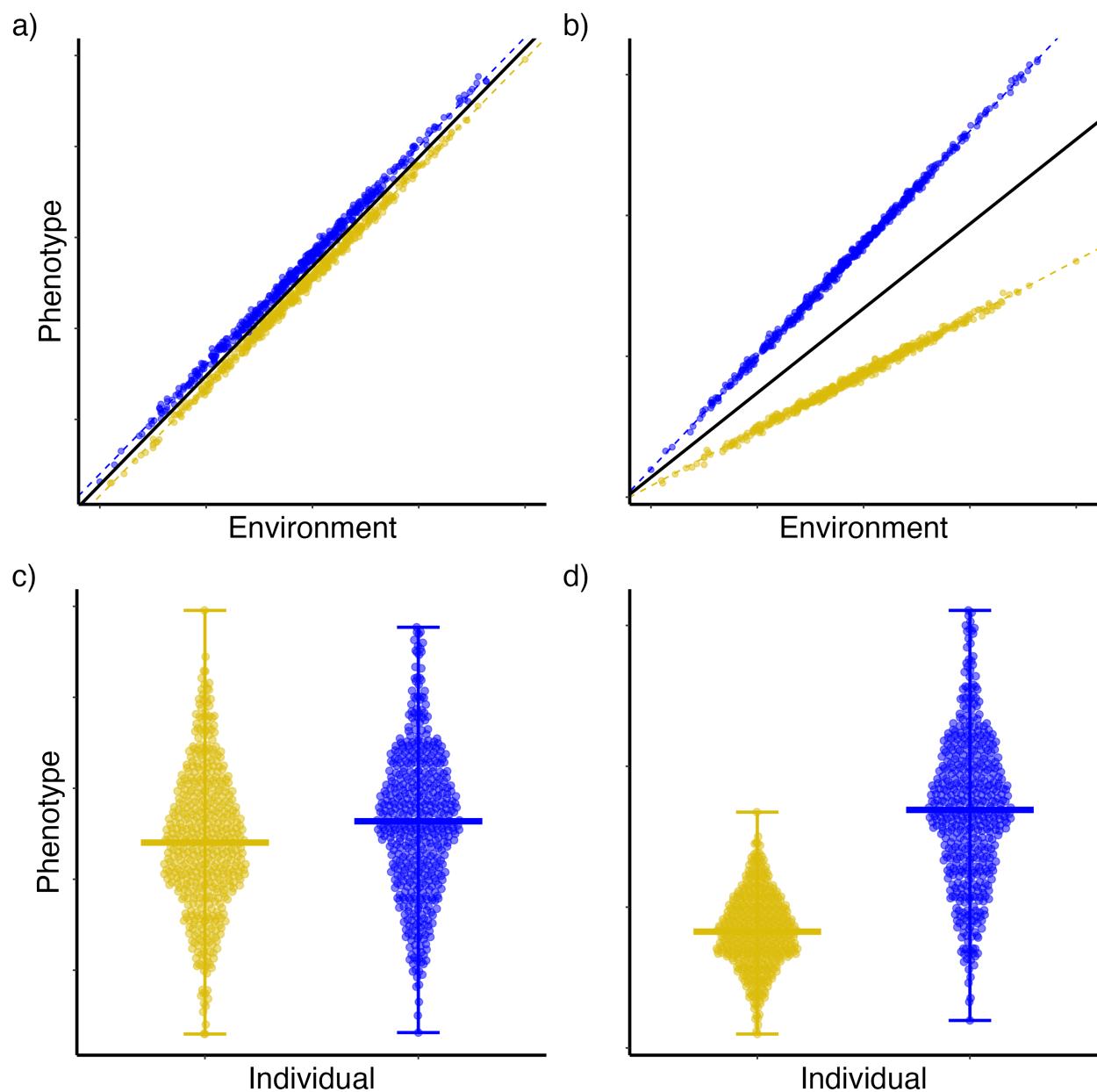


Figure 4: [...]

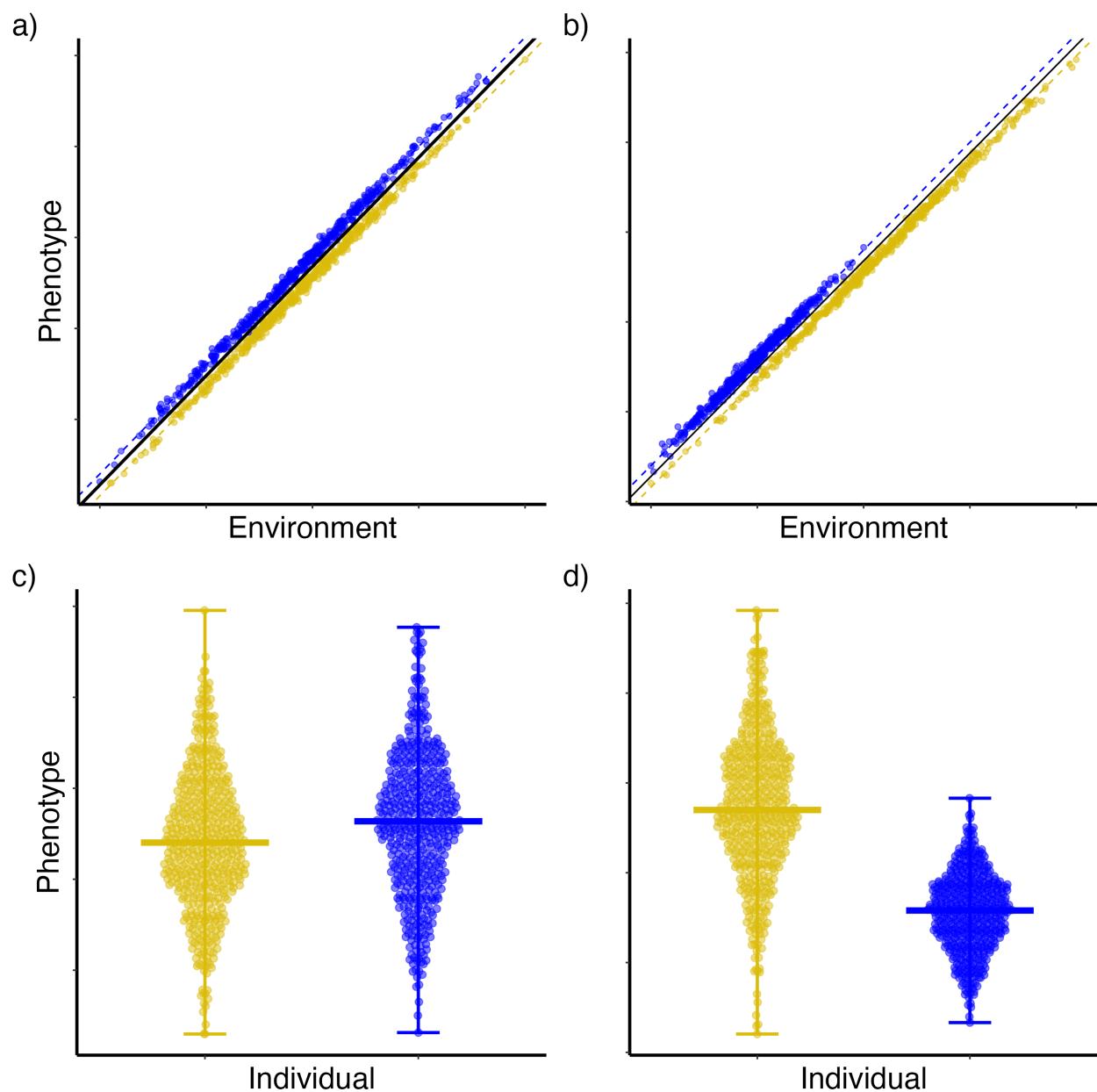


Figure 5: [...]

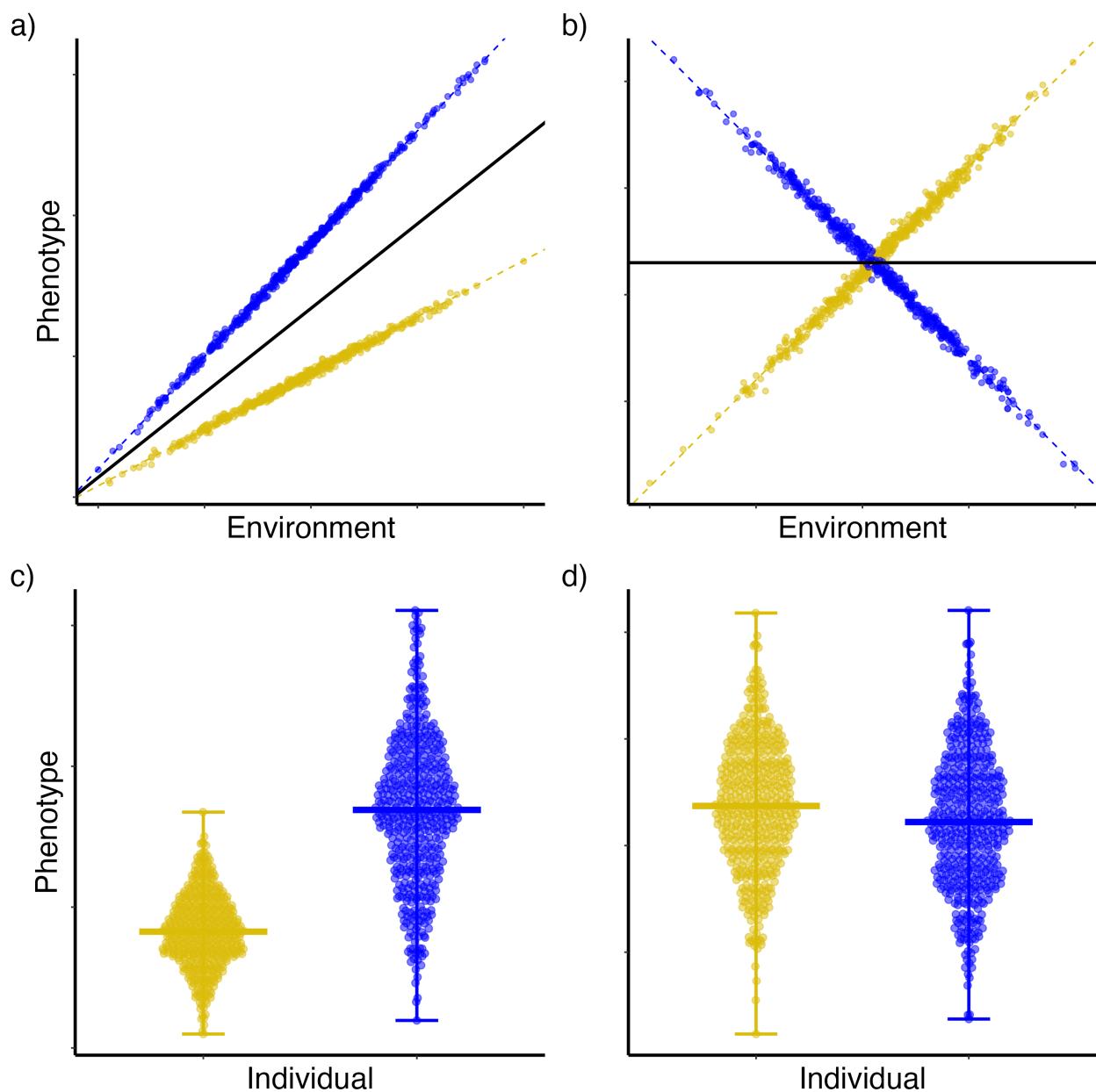


Figure 6: [...]

## **Chapter 3 - Triggers**

*Marmot's Biology: Which environmental factors have triggered the phenotypic shift?*

Extensive and detailed weather data at site from 1975 to 2022 (Prather et al. 2023)

E1 - E10 ( $T^\circ$ , Precipitation, ...), Seasonal Gradient

Predators, Diet?

## **Chapter 4 - Implications**

*Marmot's Biology: What could be the implications of that for the population's future?*

**POLS**

Manuscript models Body Mass/active season with survival => Phenological mismatch??  
(e.g., thermal stress)

## **Significance and impacts**

# Timeline

RE-DO RE-DO

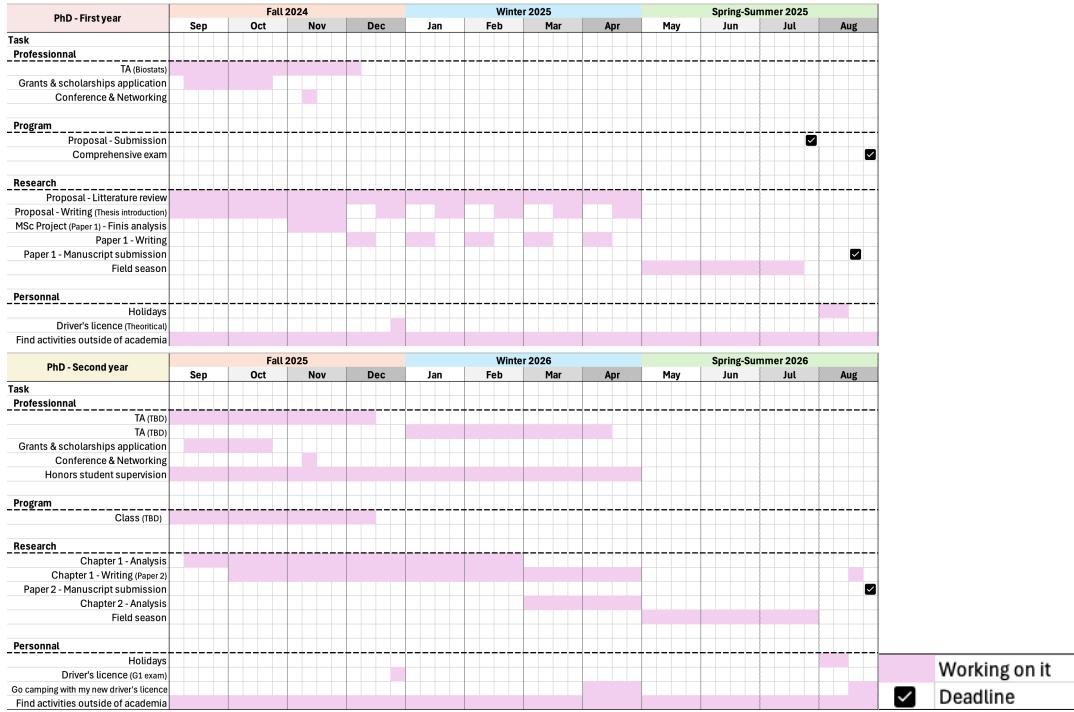


Figure 7

RE-DO RE-DO

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