

PREDATOR-PREY INTERACTIONS ACROSS SCALE AND DIMENSIONALITY

by

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DECLARATION

I declare that this thesis has not been submitted as an exercise for a degree at this or any other university and it is, unless otherwise referenced, entirely my own work. I agree to deposit this thesis in the University's open access institutional repository or allow the library to do so on my behalf, subject to Irish Copyright Legislation and Trinity College Library conditions of use and acknowledgement.

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SUMMARY

Predator-prey interactions are an important evolutionary driver and a central component of ecosystem structure. However, the context dependent nature of these interactions, as reflected by the diversity of species involved, means that understanding them at a fundamental level is required for purposeful predictions. In this thesis I explore the role of two fundamental components of predator-prey interactions: habitat dimensionality and body size. I investigate the fundamental role of body size and habitat dimensionality across three chapters that represent stand-alone publications consisting of: the role of body size on the ability of species to perceive the temporal dimension of their environment; the role of habitat dimensionality and other traits relating to predation pressure on life history evolution; and the role of habitat dimensionality on the evolution of venom in snakes. Throughout my thesis I use a comparative approach to show that both habitat dimensionality and body size are key components that determine the mechanics of predator-prey interactions and hence ecological and evolutionary systems as a whole.

PREFACE

Several chapters from my thesis have been published elsewhere:

CHAPTER ONE has been previously published as:

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and

Healy K. 2015. Eusociality but not fossoriality drives longevity in small mammals. *Proc. R. Soc. B*, 282, 20142917 .

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CHAPTER 1

GENERAL INTRODUCTION

The ability to both obtain and avoid becoming food is one of the primary selection pressures driving animal evolution. Predator-prey interactions not only shape the species directly involved but also form the fundamental building blocks of ecosystem structure making them key to our understanding of biological systems as a whole (ref). However while these interactions are ubiquitous across diverse ecosystems each predator-prey interaction plays out within its own specific context. For example, even if hunting the same prey one predator may rely on venom to incapacitate prey while another may rely on a strategy of high performance aerobatics to meet the same ends. However amongst these context dependencies commonalities arise across which provide a clear approach to understand how these interactions emerge and effect the systems in which they are embedded.

While the arms race between predators and their prey plays out across a diversity of forms, all players must abide to the fundamental constraints imposed by physics. For example biomechanical and physiological limitations result in flying species remaining relatively small while the largest species are invariably found in the oceans. Within such physical boundaries the evolution process also selects across the trade off between investing in traits associated with both escape and capture, and the energetic costs associated with developing such traits. Such energetic trade-offs are themselves are also linked to such fundamentally limitations such as body size and environmental dimensionality.

Body size has been known to be a strong determinant of metabolic rate since first demonstrated by Kieber in the 1940s. More recent formulations have attempted to use the fractal structure of physiological systems as a first principle approach to unify many aspect of biology such as physiology, behavior and ecology. Irrespective of the debate surrounding the formulation of this scaling relationship body size has become one of the most useful proxies many elements of interactions from searching ability to interaction strength. Another fundamental determinant affecting predator-prey interaction fractals at its beginnings is habitat dimensionality.

Similar to the formulation of metabolic theory in the mid 90's the role of habitat complexity in biology has its roots in utilizing the fractal structure of biological systems. Morse in the mid 80's utilized the newly developed mathematical system of fractals to describe how vegetation dimensionality can determine arthropod community densities through the available habitat structure created by plants space filling properties. More recently habitat dimensionality has also been shown to be important in determining interaction strength between predators and their prey through differential scaling in search rate with body size between three and two-dimensional habitats.

This thesis draws on how these two fundamental pillars of biological structure affect predator-prey interactions across the range of contexts these interactions take place. By using comparative methods I will focus on three areas; how do species sample and perceive the temporal dimension; the role of habitat dimensionality in prey species life history; and the role of habitat dimensionality in the evolution of predatory traits. By understanding the forces shaping species within the dimensions of their habitats we can gain deeper understanding of the mechanics of predator-prey interactions as a whole.

1.1 RESEARCH OUTLINE

Something about the general structure.

Chapter 2: Body size, metabolic rate and visual temporal perception in vertebrates.

All organisms must perceive the temporal dimension of their environment. This is particularly true of predators and their prey that need to accurately track and predict their adversaries' motion. Here I collate data on a measure of visual temporal perception called critical flicker fusion to test whether species that are predicted to be more maneuverable can perceive events at finer scales. I show that, as expected, small species with high metabolic rates have the fastest perception of time. This has important consequences for the ability of predators to capture their prey and I discuss some examples of adaptations in predator species that potentially mitigate against this general trend.

Chapter 3: Ecology and mode-of-life explain lifespan variation in birds and mammals.

Maximum lifespan varies strongly with body mass yet many species live far longer than expected given their size. This may reflect interspecific variation in extrinsic mortality, as life-history theory predicts investment in long-term survival when extrinsic mortality is reduced. Here, I investigate how ecological and mode-of-life traits that are predicted to reduce extrinsic mortality influence lifespan across mammals and birds. I show that species associated with high dimensional habitats, namely arboreal and volant species, show longer lifespan than expected for their body size. I discuss how habitat dimensionality may affect exposure of prey to predation pressures and the role of other ecological traits including fossoriality, eusociality, and activity patterns.

Chapter 4: Habitat dimensionality and a diet of eggs; the evolution of venom loss in snakes.

Despite the obvious advantages of possessing venom there is little explanation for variation in the volume and toxicity of venom in snakes. This is particularly apparent in species that partially or fully lose the capacity to produce venom such as demonstrated in sea snake species. As venom is primarily used for capturing prey I test whether fundamental factors, including habitat dimensionality and diet, affect the amount of venom produced within a species through their influence of encounter rates and prey toxicity resistance. By collating data on venom toxicity (LD50), diets, body size, environment dimensionality and both maximum and minimum venom volumes comprising of over 75 species, I show that species found in high dimensional environments or that have egg-based diets produce less venom than their counterparts. I also demonstrate the prey-specific nature of venom toxicity using phylogenetic distance between diet species and LD50 model species as a test. I discuss the possible mechanisms and the implications of these results in relation to both evolution of venom and costly predatory traits in general.

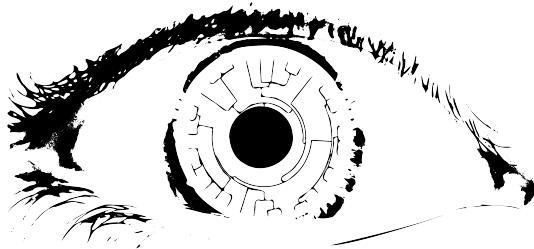
Finally, in ??, I close with a discussion of the limitations of the methods used in the thesis, and suggest some future directions.

1.2 ADDITIONAL WORK

In addition to the chapters enclosed in this thesis, I have also been involved in the following research during my studies:

CHAPTER 2

METABOLIC RATE AND BODY SIZE ARE LINKED WITH PERCEPTION OF TEMPORAL INFORMATION



“Time is an illusion. Lunchtime doubly so.”

Douglas Adams

2.1 SUMMARY

Body size and metabolic rate both fundamentally constrain how species interact with their environment. While many mechanisms leading to these constraints have been explored, their effects on the resolution at which temporal information is perceived have been largely overlooked. The visual system acts as a gateway to the dynamic environment and the relative resolution at which organisms are able to acquire and process visual information is likely to restrict their ability to interact with events around them. As both smaller size and higher metabolic rates should facilitate rapid behavioural responses, we hypothesized that these traits would favour perception of temporal change over finer timescales. Using critical flicker fusion frequency, the lowest frequency of flashing at which a flickering light source is perceived as constant, as a measure of the maximum rate of temporal information processing in the visual system, we carried out a phylogenetic comparative analysis of a wide range of vertebrates that supported this hypothesis. These results have implications for the evolution of signalling systems and predator-prey interactions, and, combined with the strong influence that both body mass and metabolism have on a species’ ecological niche, suggest that time perception may constitute an important and overlooked dimension of niche differentiation.

2.2 INTRODUCTION

All biological systems, from organisms to ecosystems, are shaped by universal constraints. For example, body size and metabolic rate are both known to be important determinants of organism biology, influencing life history, energetics and behaviour (Brown et al., 2004; Woodward et al., 2005; Sibly et al., 2012). More recently the fundamental role of sensory biology in ecological interactions has gained attention, such as in the limitations of identification of targets (Tosh and Ruxton, 2010) and the scaling allometry of sensory organs (Howland et al., 2004; Cronin, 2005; Garamszegi et al., 2002). The limitations such sensory systems are constrained by can heavily determine ecological interactions through, for example, predation and mate selection were the abilities of the parties involved to capture, escape or be seduced is dependent on how they perceive their environment (Fig. 1; Cronin 2005; Clark et al. 2012; Hornstein et al. 2000; Stevens 2007). While the ability and importance of an organism to perceive the spatial dimensions of its environments are relatively well studied (Cronin, 2005; Clark et al., 2012), how they perceive the 4th dimension, time, is less well known.

As the environment is fundamental dynamic in nature the ability to integrate information over a time period is a necessity for any organism interacting within it. Furthermore, the ability to integrate information over shorter timescales, that is, at higher resolutions, is a direct limitation on the degree to which it can interact with the environment itself. From an evolutionary perspective this leads to a trade-off between the demand for information at high temporal resolutions and the costs of its acquisition given the energetic demands associated with increased rates of neural processing in the visual system (Laughlin, 2001). This trade-off is likely to be shaped by various ecological (e.g. mode of predation) and environmental factors (e.g. light levels) as well as intrinsic factors (e.g. morphology) that will ultimately shape an organism's optimal temporal resolution for sensory perception (Autrum, 1958).

This ability to perceive and react to a dynamic environment is also likely to be an important behavioural and ecological trait. Ecologically, interaction strengths can be affected by the ability to identify and track fast-moving objects such as prey or mates (Fig. 1; Land and Collett 1974; Fritsches et al. 2005). The necessity of this ability to perceive one's environs accurately is perhaps best demonstrated in cases where temporal resolution is too coarse to allow the observer to follow the motion of a moving target accurately. A stark demonstration of this can be seen

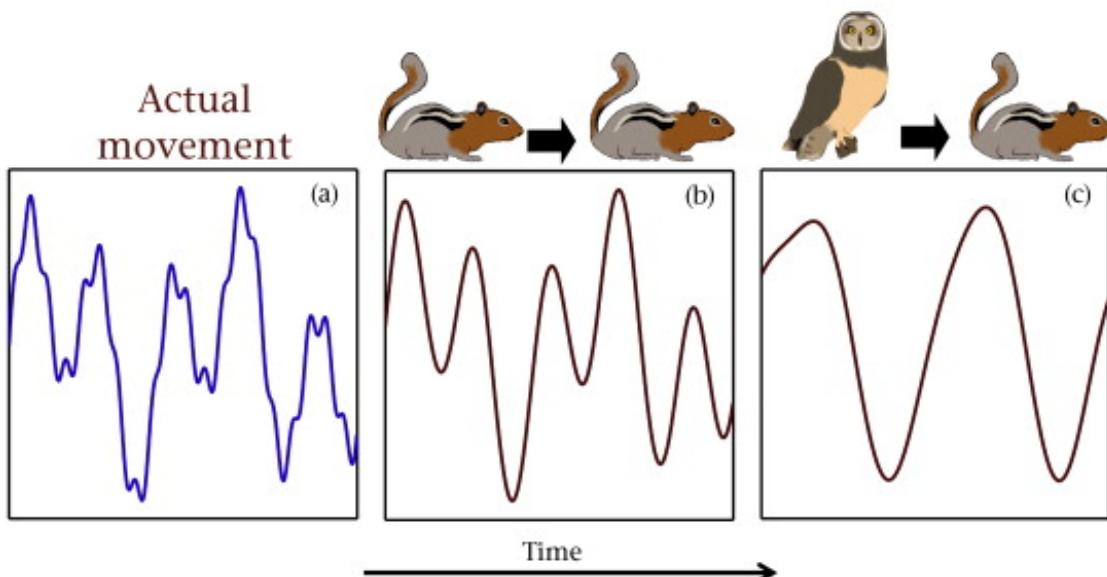


FIGURE 2.1: The ability of an organism to track a moving object depends on the time integral over which the individual can obtain its information. This is determined by its ability to resolve temporal information. In cases where an animal, such as a ground squirrel, displays complex movement (a), conspecifics may perceive the individual as moving according to a first-order integral of its actual movement owing to its high temporal resolution abilities (b). However a species with lower temporal resolution abilities, such as a short-eared owl, may perceive the motion as an even higher order derivative of the actual motion, meaning information of prey motion at finer temporal scales is not available to it (c).

in the tiger beetle, *Cicindela hudsoni*, which, owing to the relatively low temporal resolution of its visual system, must take a stop-start approach in order to recalibrate the position of its prey when hunting (Gilbert, 1997). In humans, the limitations of our temporal perception are apparent when tracking fast-moving objects such as the curving trajectory of a ball in soccer (Dessing and Craig, 2010) and baseball (Bahill and Baldwin, 2004) and is also directly linked to the perception of the passage of time itself (Hagura et al., 2012).

Two intrinsic factors that may shape the costs and benefits of the temporal resolution of the sensory system, in particular with respect to their effects on an individual's ability to interact with the environment on short timescales, are body size and metabolic rate. As larger body sizes decrease manoeuvrability (Heglund and Taylor, 1988; Dudley, 2002; Biewener, 2003; Sato et al., 2007; Vogel, 2008; Hedrick, 2011; Watanabe et al., 2012) and higher metabolic rates increase both manoeuvrability and the physiological ability to process information (Li et al., 2008; Franz and Ronacher, 2002), smaller organisms and those with higher metabolic rates would be predicted to perceive temporal change on finer timescales.

To quantify the temporal perceptual abilities of a range of species I take advantage of the all or nothing nature of neural firing in the visual system. Owing to this binary firing, temporal resolution must be encoded in terms of discrete units, as biological visual systems must discretise the continuous-time and continuous-space information reaching the retina and then integrate this information over some time period. This "integration time" of visual systems can be quantified using the critical flicker fusion frequency (CFF): the lowest frequency of flashing at which a flickering light source is perceived as constant (D'EATH, 1998; Schwartz and Meese, 2010). As light intensity can increase the number of flashes that can be observed per second, the maximum CFF value, as measured in a response curve of CFF against light intensity (Ferry, 1892; Porter, 1902), can be used as a proxy for the temporal resolution of the sensory system.

Here I use maximum CFF to compare the temporal resolution of the visual system in a wide range of vertebrate species including representatives from Mammalia, Reptilia, Aves, Amphibia, Elasmobranchii and Actinopterygii. Using phylogenetic comparative methods and controlling for the light levels each species typically experiences, I test whether the temporal resolution of the sensory system increases with mass-specific metabolic rate and decreases with body mass.

2.3 METHODS

2.3.1 *Data Collection*

To test our prediction that CFF increases with mass-specific metabolic rate and decreases with body size (when controlling for light levels), data on maximum CFF values in vertebrate species was collated from the literature (Table 4.1). Only values from studies that measured CFF using either behavioural or electroretinogram (ERG) procedures were included. In behavioural studies, CFF is measured through conditional training with the subject trained to respond to a change in its perception of a flashing light (D'EATH, 1998; Rubene et al., 2010). For example, (Lisney et al., 2011) conducted behavioural tests in domestic chickens, *Gallus gallus*, using choice experiments with flickering and non-flickering stimuli windows with choice of the correct stimulus rewarded with food. This is repeated over a range of light intensities and flicker frequencies until individuals can no longer distinguish between the stimuli. In ERG studies, a direct measurement of the electrical response in the retina in reaction to a flashing light source is used as a measure of CFF (D'EATH,

1998; Schwartz and Meese, 2010). As there may be further processing of temporal information after it reaches the retina that may cause behavioural studies to measure lower CFF values (D'EATH, 1998), the experimental procedure used to measure CFF was included as a candidate covariate in our models.

Mean body mass (g) published in the literature and in databases including Fish-Base (Froese and Pauly, 2012) and Animal Diversity Web (Myers et al., 2006) was collected for each species as the measure of body size. For metabolic rates mass-specific resting metabolic rate as measured by oxygen consumption through ventilation was used where the subjects were fasted prior to the measurement. These values were converted to W/g using the conversion of 20 J/ml of oxygen consumption (Makarieva et al., 2008) to allow comparison among species. For ram-ventilation species (which require constant movement to force fluid over the respiratory organs), such as sharks and tuna, the resting metabolic rate was taken as the fitted line of oxygen consumption with swimming speed extrapolated to the intercept (swimming speed = 0 m/s; 4.1). To account for the possible effect of metabolic rate measured at different temperatures in ectothermic species, metabolic rate values were corrected to 20 °C using Q10 values, i.e. the fold change in metabolic rate over a temperature change of 10 °C, for reptiles, amphibians and fish (White et al., 2006). These corrections gave values of temperature-corrected mass-specific resting metabolic rates (qW_g), for each species. Although body mass and mass-specific metabolic rate are expected to be correlated according to an exponent of 0.25 (Brown et al., 2004; Sibly et al., 2012) (Brown et al., 2004 and Sibly et al., 2012), both terms were included as recommended by (Freckleton, 2009) instead of using residuals from a regression of body mass against mass-specific metabolic rate.

As there is a trade-off between sensitivity and movement perception owing to the requirement of longer integration times in low light conditions (Tansley et al., 1965), as is seen in the different light response dynamics of rods and cones (Rubene et al., 2010), light levels was included in the analyses as a categorical variable based on the light conditions experienced by the species during normal activity (i.e. foraging). Species were categorized as inhabiting either high or low light conditions with diurnal terrestrial and nonturbid aquatic species coded as inhabiting high light level environments and nocturnal species coded as inhabiting low light levels. As the light levels of species that inhabit turbid waters are typically orders of magnitude lower than typical daylight levels (40-1000 lx; Ali and Klyne 1985; Palmer and Grant 2010; Kreysing et al. 2012 and the harp seal, *Pagophilus groenlandicus*, regularly

forages at depths greater than 200m (Folkow et al., 2004) where light levels are comparable to nocturnal light levels (Palmer and Grant 2010), these species were categorized as inhabiting low light level environments.

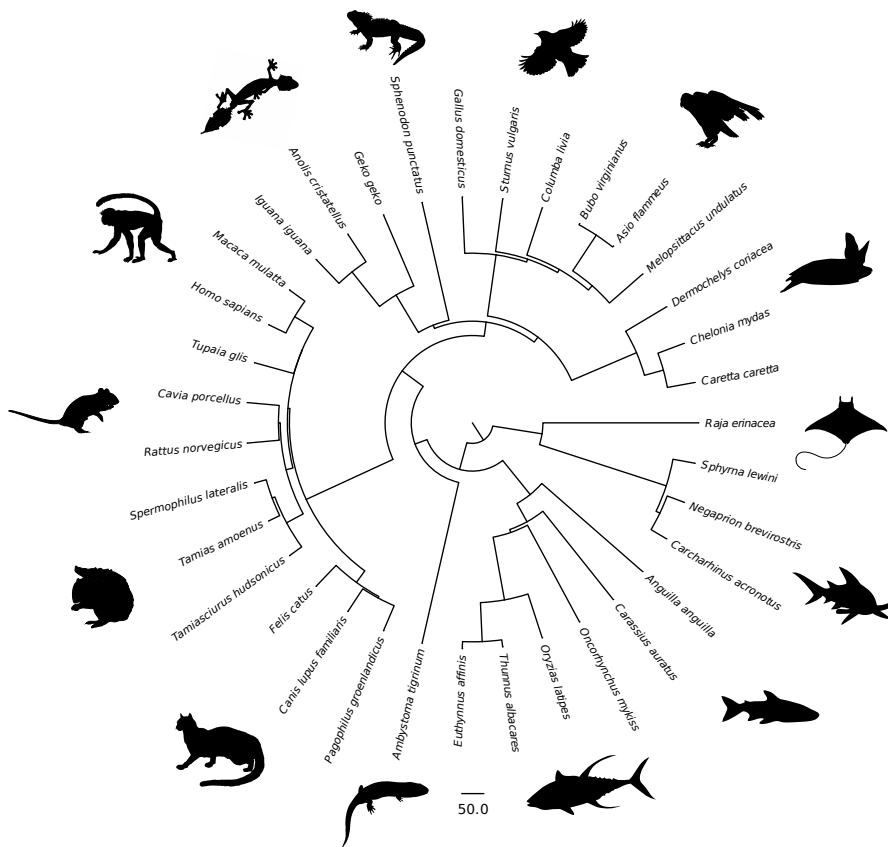


FIGURE 2.2: Composite tree of the study species.

To correct for the phylogenetic nonindependence of species a composite tree of the study species was constructed using published molecular phylogenies and divergence times from various sources (Schoch, 1985; Jánossy, 2011; Mercer and Roth, 2003; Hedges et al., 2006; Wiens et al., 2006; Benton and Donoghue, 2007; Murphy et al., 2007; Brown et al., 2008; Li et al., 2008; Naro-Maciel et al., 2008; Albert et al., 2009; Lim et al., 2010; Little et al., 2010; Perelman et al., 2011) (Schoch, 1985,; see Appendix A and Figure 2.2). In instances in which a divergence time was not available for two species we used the conservatively estimated date of first appearance as the divergence time taken from the Paleobiology Database (Alroy et al., 2008).

As ectotherm metabolic rates vary with temperature, a sensitivity analysis to test the effect of the temperature to which qW_g was corrected was performed by rerunning the main analysis with qW_g corrected to both 5 °C and 35 °C (see Appendix

A). A supplemental analysis on a more restricted data set for species with available brain mass data was also carried out to test for any possible effects of sensory tissue on maximum CFF values (see Appendix A).

In total data on maximum CFF, body mass, qWg and light environments for 34 species across the vertebrate classes Elasmobranchii, Actinopterygii, Aves, Amphiibia, Reptilia and Mammalia was collected with further data on brain mass for 28 of these species (Table 4.1).

2.3.2 *Statistical Analyses*

To test the hypothesis I used a phylogenetic generalized least-squared approach (PGLS) using the caper package (Orme et al., 2011) in R version 2.14.2 (R Core Team, 2014). The PGLS approach is based on standard generalized least-squared models while also accounting for the nonindependence in the data caused by species' phylogenetic relationships by incorporating it through the error term structure (Pagel, 1999; Rohlf, 2001). This error term consists of a matrix of expected trait covariances calculated using the maximum likelihood estimate of lambda (λ), a multiplier of the off-diagonal elements of a phylogenetic variance-covariance matrix that best fits the data. When the data are structured according to a Brownian motion of trait evolution, lambda = 1, whereas when the data have no phylogenetic dependency, then lambda = 0 (Pagel, 1999).

The analysis consists of PGLS models with maximum CFF as the response variable, and all combinations of the following explanatory variables: body mass, qWg, light level (high, low) and experimental procedure (ERG, behavioural) with brain mass included in the sensitivity analysis (see Appendix), with Akaike's information criterion (AIC) used to select the minimum adequate model (Burnham and Anderson, 2002).

2.4 RESULTS

The most parsimonious model (based on AIC) explaining variation in maximum CFF among vertebrates included the terms body mass, temperature-corrected mass-specific resting metabolic rate (qWg) and light level (Table A.3). Body mass had a negative effect on the temporal resolution of the sensory system (Table A.3, Figure 2.3 a). The metabolic rate of organisms, after correcting for mass, was positively associated with CFF while low environmental light levels were associated with an

TABLE 2.1: Data used in analysis

Species	CFF	Mg	qWg	Brain Mass	Light levels
<i>Ambystoma tigrinums</i>	30 ^{e,s,1}	10.78 ²⁸	0.00016 ²⁸	NA	L
<i>Anguilla anguilla</i>	14 ^{b,s,2}	71.1 ²⁸	0.00013 ²⁸	NA	L
<i>Anolis cristatellus</i>	70 ^{e,o,3}	6.0 ²⁹	0.00089 ²⁹	NA	H
<i>Asio flammeus</i>	70 ^{e,o,4}	406.0 ³⁰	0.0032 ²⁸	5.45 ⁶⁹	H
<i>Bubo virginianus</i>	45 ^{e,s,5}	1450.0 ³¹	0.0036 ²⁸	13.7 ⁷⁰	L
<i>Canis lupus familiaris</i>	80 ^{b,s,6}	13900.0 ³²	0.00183 ²⁸	80.0 ⁷¹	H
<i>Carassius auratus</i>	67.2 ^{e,o,7}	10.8 ³³	0.00013 ²⁸	0.01 ⁷¹	H
<i>Carcharhinus acronotus</i>	18 ^{e,o,8}	14491.0 ⁸	0.00114 ^{56*}	NA	L
<i>Caretta caretta</i>	40 ^{e,s,9}	135000.0 ³⁴	0.00008 ⁵⁷	2.7 ⁴⁰	H
<i>Cavia porcellus</i>	50 ^{e,s,10}	629.0 ³⁵	0.00306 ³⁵	3.8 ⁷²	L
<i>Chelonia mydas</i>	40 ^{e,s,9}	128000.0 ³⁶	0.00025 ³⁶	8.6 ⁷¹	H
<i>Columba livia</i>	100 ^{e,s,4}	315.0 ³⁷	0.0045 ²⁸	2.3 ⁷⁰	H
<i>Dermochelys coriacea</i>	15 ^{e,s,11}	354000.0 ³⁸	0.00043 ⁵⁸	30.0 ⁷³	H
<i>Felis catus</i>	55 ^{e,s,12}	3054.4 ³²	0.00394 ⁵⁹	28.4 ⁷¹	L
<i>Gallus gallus domesticus</i>	87 ^{b,o,13}	2710.0 ³⁹	0.0022 ²⁸	3.6 ⁷⁴	H
<i>Gekko gecko</i>	20 ^{e,s,14}	54.8 ⁴⁰	0.00034 ²⁸	0.2 ⁷⁵	L
<i>Homo sapiens</i>	60 ^{b,o,15}	67100.0 ⁴¹	0.00117 ⁶⁰	1300.0 ⁷⁶	H
<i>Iguana iguana</i>	80 ^{e,s,14}	750.0 ⁴²	0.00029 ²⁸	0.61 ⁷⁵	H
<i>Macaca mulatta</i>	95 ^{b,o,16}	7710.0 ⁴³	0.00205 ⁶¹	91.7 ⁷¹	H
<i>Melopsittacus undulatus</i>	74.7 ^{b,s,17}	33.6 ²⁸	0.01204 ²⁸	1.5 ⁷⁰	H
<i>Negaprion brevirostris</i>	37 ^{e,s,18}	92987.0 ⁴⁴	0.00053 ^{62*}	NA	L
<i>Oncorhynchus mykiss</i>	27 ^{b,s,19}	4000.0 ⁴⁵	0.00041 ²⁸	0.5 ⁷¹	L
<i>Oryzias latipes</i>	37.2 ^{e,s,20}	0.21 ²⁰	0.00072 ²⁸	0.01 ⁷⁷	L
<i>Pagophilus groenlandicus</i>	32.7 ^{b,s,12}	119600.0 ⁴⁶	0.00211 ⁶³	228.5 ⁷⁸	L
<i>Raja erinacea</i>	30 ^{e,o,22}	500.0 ⁴⁷	0.00024 ⁴⁷	2.32 ⁷¹	L
<i>Rattus norvegicus</i>	39 ^{e,o,23}	237.0 ⁴⁸	0.00679 ⁴⁸	2.3 ⁷⁹	L
<i>Spermophilus lateralis</i>	120 ^{e,o,10}	215.5 ⁴⁹	0.00335 ⁶⁴	3.6 ⁸⁰	H
<i>Sphenodon punctatus</i>	45.6 ^{b,s,24}	353.75 ⁵⁰	0.00017 ²⁸	NA	L
<i>Sphyrana lewini</i>	27.3 ^{e,o,8}	1893.0 ^{8,51}	0.0010 ^{65*}	60.0 ⁷⁷	L
<i>Sturnus vulgaris</i>	100 ^{e,s,25}	75.0 ²⁸	0.012 ²⁸	1.9 ⁷⁴	H
<i>Tamias amoenus</i>	100 ^{e,o,10}	51.91 ⁵²	0.00937 ⁶⁶	1.98 ⁸⁰	H
<i>Tamiasciurus hudsonicus</i>	60 ^{e,o,10}	215 ³⁵	0.00735 ⁶⁷	4.0 ⁸⁰	H
<i>Thunnus albacares</i>	80 ^{e,s,26}	45349.0 ^{53,54}	0.00158 ^{68*}	6.24 ⁷⁷	H
<i>Tupaia glis</i>	90 ^{b,o,27}	142.0 ⁵⁵	0.00424 ⁵⁵	3.4 ⁷⁹	H

* Indicates species with qWg estimated from swimming speeds extrapolated to zero (see Methods in main text). CFF = Critical flicker fusion (CFF), Mg = body mass (grams), qWg = Temperature corrected (25°C) mass specific resting metabolic rate (W g^{-1}), Light levels: H= High, L= Low. NA = No data available for species. Superscript indicates type of measurement, e = electroretinogram, b = behavioural experiments, o = optimum methodology, s = suboptimum methodology and numbers refer to data references; (1) Crevier & Meister (1998); (2) Adrian & Matthews (1926); (3) Fleishman et al. (1995); (4) Bornshein & Tansley (1961); (5) Ault & House (1987); (6) Coile et al. (1989); (7) Hanyu & Ali (1963); (8) McComb et al. (2010); (9) Levenson et al. (2004); (10) Tansley et al. (1961); (11) Eckert et al. (2006); (12) Loop & Berkeley (1975); (13) Lisney et al. (2011); (14) Meneghim & Hamasaki (1967); (15) Brundrett (1974); (16) Shumake et al. (1968); (17) Ginsburg & Nilsson (1971); (18) Gruber (1969); (19) Carvalho et al. (2004); (20) Carvalho et al. (2002); (21) Bernholz & Matthews (1975); (22) Green & Siegel (1975); (23) Williams et al. (1985); (24) Woo et al. (2009); (25) Greenwood et al. (2004); (26) Southwood et al. (2008); (27) Callahan & Petry (1999); (28) Makarieva et al. (2008); (29) Rogowitz (1996); (30) Gruber (1962); (31) Ganey et al. (1993); (32) Kendall et al. (1982); (33) Hughes et al. (1977); (34) Duermit (2007); (35) Arends & McNab (2001); (36) Jackson & Prange (1979); (37) Terres (1980); (38) Georges & Fossette (2006); (39) Winchester (1940); (40) Hurlburt (1996); (41) Holloway (1980); (42) Howland et al. (2004); (43) Schwartz & Kemnitz (1992); (44) Ally (1947); (45) Ridolfi (2006); (46) Stewart & Lavigne (1984); (47) Hove & Moss (1997); (48) Hart (1971); (49) McKeever (1964); (50) Herrel et al. (2010); (51) Letourneau et al. (1998); (52) Sheppard (1968); (53) Collette & Nauen (1983); (54) Duarte-Neto & Lessa (2004); (55) Bradley & Hudson (2003); (56) Carlson (1999); (57) Lutz et al. (1989); (58) Paladino et al. (1996); (59) Eisenberg (1981); (60) Elgar & Harvey (1987); (61) Bruhn (1934); (62) Bushnell et al. (1989); (63) McNab (1986); (64) Hudson et al. (1972); (65) Lowe (2001); (66) Jones & Wang (1976); (67) Pauls (1981); (68) Dewar & Graham (1994); (69) Garamszegi et al. (2002); (70) Iwanuk & Nelson (2002); (71)

overall reduction in CFF (Table A.3, Figure 2.3 b). Phylogeny was found to have a minimal effect on the resulting models ($\lambda = 0$, Table A.3) and experimental type was not correlated with CFF (Table A.3). Thus, according to our model, small animals

with high mass-specific metabolic rates in high light environments possessed the highest maximum CFF and hence greatest ability to perceive temporally dynamic visual information. Conversely, large animals with low mass-specific metabolic rates in low light environments had the lowest CFF.

TABLE 2.2: Coefficients of the model with all factors included. Mg = body mass (grams), qWg = Temperature corrected mass-specific resting metabolic rate Wg-1, Light.l (low) = effect of low light levels on CFF in comparison to high light levels, exp = effect of experimental type (ERG = electroretinogram) in comparison to behavior based CFF measures.

<i>Variable</i>	<i>Estimate</i>	<i>S.E</i>	<i>t-value</i>	<i>P-value</i>
Intercept	141.48	15.15	9.34	4^{-10}
Mg	-4.40	2.01	-2.18	0.038
qWg	16.89	4.31	3.92	5^{-4}
Light levels (low)	-37.74	5.94	-6.36	7^{-7}
Measurement type (exp)	-3.66	6.24	-0.59	0.56
Data quality (high)	-3.86	6.14	-0.63	0.53
		Mode	Lower 95% C.I	Upper 95% C.I
Lambda (Low)	0	0	0.34	
				$R^2 = 0.69$

These results were robust to the sensitivity analysis on both the temperature used to correct ectotherms qWg (taken as 20 °C in the main models above; see Methods) with the best models (based on AIC) including the same terms and trends as found in the main analysis (Appendix). Including brain mass in a restricted data set of 28 species for which brain mass was available did not change the effect of the explanatory variables light levels, qWg and body mass on maximum CFF (Tables A4 and A8 in the Appendix (I still need to fix these tables in the appendix up a bit).

2.5 DISCUSSION

Many of the interspecific and intraspecific interactions that shape species' behaviour and ecology rely on the ability of organisms to process high temporal resolution sensory information. These results show that, while there is considerable variability in the ability to resolve temporally dynamic visual information across vertebrates, body mass and metabolic rate act as important general constraints on this ability. This is the first study to indicate a general trend in the ability of vertebrates to resolve temporal information; previous studies have generally focused on specific cases of sensory adaptations (Fritsches et al., 2005) and particular environments (Frank,

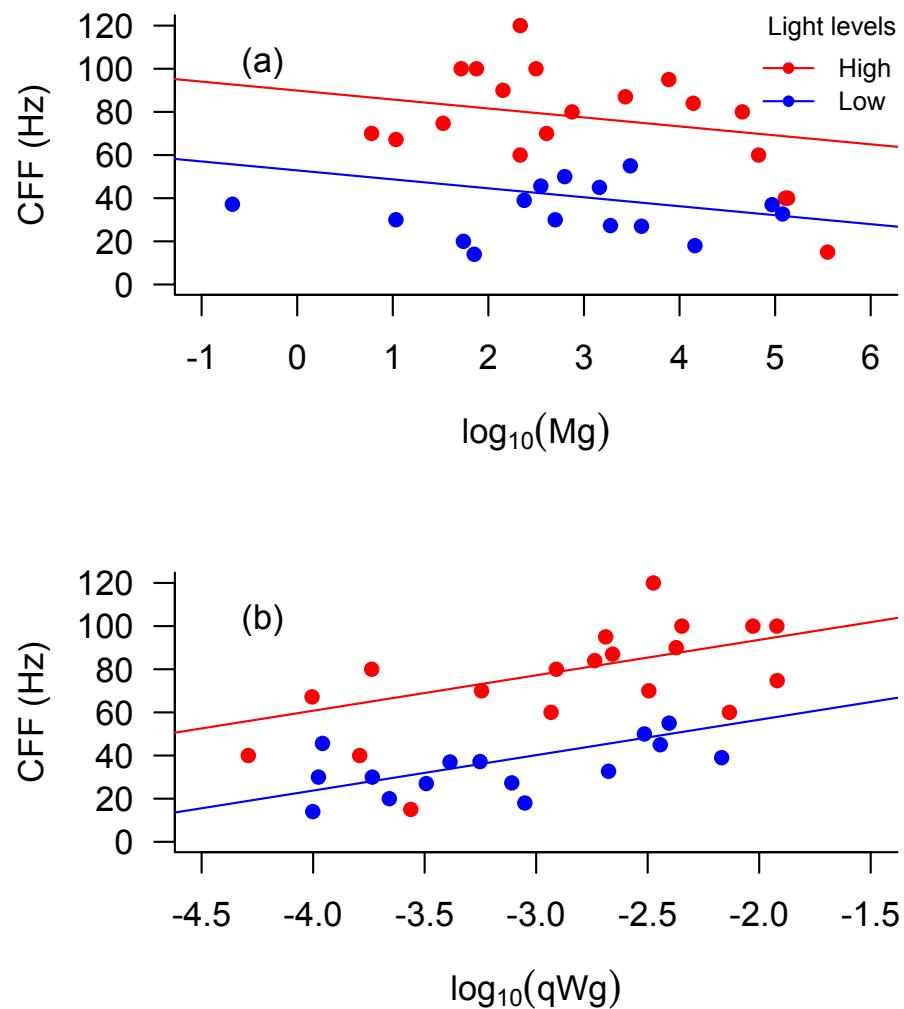


FIGURE 2.3: The effect of log body mass, light levels and log temperature corrected mass-specific resting metabolic rate (qWg) on critical flicker fusion frequency (CFF). The minimal adequate model (Results) indicates CFF increases with $\log qWg$ but decreases with body mass. Low light levels (blue) are associated with low CFF values in comparison to high light levels (red).

1999; Frank et al., 2012), hence focusing on the particular ecological context of each adaptation or environment. These findings illustrate the relationship between both physiology and the effects of body mass on the ability to resolve temporal features of the environment on fine timescales, hence linking sensory adaptations to fundamental constraints and trade-offs imposed on all organisms.

The finding that metabolic rate strongly influences temporal perception extends the known influence metabolism has on organism biology. The rate at which sensory tissue can function is dependent on both the energy available and the tissues

temperature. Furthermore, the rate at which neurons can transmit information is dependent on the rate at which proton pumps can re-establish a gradient potential after firing, which in turn is dependent on both metabolic rate (Laughlin, 2001) and the number of proton pumps available. It is unsurprising hence that species which have high metabolisms also benefit from an increased in the rate of sensory system functioning. In contrast species which cannot benefit from the increased rates of sensory firing are likely to reduce investment into such sensory systems, such as seems to be the case in the visual system of the deep sea escolar (Landgren et al., 2014). This is likely to partially explain the separate negative affect of body size on temporal perception as larger species in general have decreased manouverability (Heglund and Taylor, 1988; Dudley, 2002; Biewener, 2003; Sato et al., 2007; Vogel, 2008; Hedrick, 2011; Watanabe et al., 2012) and hence less ability to react to the environment. This idea is also supported by research showing that faster and more manoeuvrable fly species have higher temporal resolutions (Laughlin and Weckström, 1993) and that less manoeuvrable scavenger crabs display slower response dynamics than deeper living predatory species which are likely to have more active lifestyles (Frank et al., 2012).

While these findings establish a fundamental scaling between temporal perception, metabolism and body size many species demonstrate physiological adaptations which allow for increase sensory perception despite their size and metabolic rate. For example despite their large predatory swordfish (Fritsches et al., 2005) are capable of a ten-fold increase in their CFF, to levels expected of a small endotherm in this model. This is achieved through specialised heating tissues that increase the temperature, and hence the metabolic rate, in their visual systems allowing them to up-regulating their CFF when hunting (Fritsches et al., 2005). Similar adaptations are also seen in other species of large, fast-swimming predatory fish (Carey, 1982; Block and Carey, 1985) and species of blowfly (Tatler et al., 2000). Physiological adaptations for high-resolution motion detection are also found within specific areas of the retina in some flies, commonly referred to as the "love spot", which allow them to identify female flight patterns accurately and thus detect mates (Land and Collett, 1974). However these species are likely to define the exception over the rule, as most species in our analysis fit well to the predict scaling.

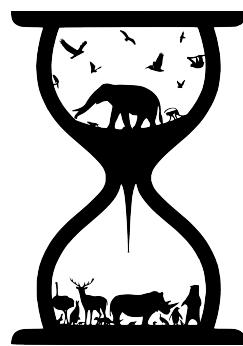
The effects of body size and metabolic rate on temporal resolution and the presence of sensory adaptations also point towards an interesting dimension of niche space. Disparity in size and metabolic rate among species within an ecological

setting may select for particular sets of adaptations creating a diverse set of sensory systems and interactions. In such a system, species might occupy the same spatial and temporal niche, but could be separated owing to differential responsiveness to environmental signals and cues as a result of having evolved divergent signalling systems along a dimension represented by temporal resolution. For example, it seems at least theoretically possible to encode information in high-frequency signals that can be detected by intended receivers such as conspecifics but that are not susceptible to "eavesdropping" by (generally larger) predators. In fact this idea has already been utilized to develop fishing lures which signal towards specify catch species yet are well camouflaged to unwanted by-catch such as marine turtles (Jordan et al., 2013; Crognale et al., 2008). Ecological systems in which this may be apparent include deep-sea systems where visual signalling is an important determinant of the ability of organisms to interact, and where bioluminescence flashing over wide frequency ranges is ubiquitous (Haddock et al., 2005; Widder, 2010). Similarly urban lighting may also create such variation in perceptual space for species with possible negative affects on species with high temporal perceptions as the flickering rate of street light may both reduce the advantages such species have over their prey or cause increased stress such as observed in birds species kept in captivity (Inger et al., 2014).

Overall these results show that not only are body size and metabolic rate good proxies for the rate of biological interactions they are good proxies for the ability to perceive such interactions. While interaction rates are strongly coupled with the spatial dimensionality of the environment and searching rates associated with them (Pawar et al., 2012) the temporal dimension in which an individual resides will also strongly influence its ability to interact with that environment. The generality of these findings suggest that temporal resolution may play a much more important role in sensory ecology than previously indicated, in particular because of its universal effects relating to body size. Further investigations into both the underlying mechanisms of these findings and their importance to ecological functioning are needed.

CHAPTER 3

ECOLOGY AND MODE-OF-LIFE EXPLAIN LIFESPAN VARIATION IN BIRDS AND MAMMALS



“Achieving life is not the equivalent of avoiding death.”

Ayn Rand

3.1 SUMMARY

Many species live far longer than expected given their body mass. This may reflect interspecific variation in extrinsic mortality, with species capable of reducing mortality expected to exhibit longer lifespans. One such factor that may strongly influence such extrinsic mortality is habitat dimensionality. As higher dimensional habitats create multiple escape routes from predation, species associated with such environments would be expected to have higher maximum lifespans. Here, I investigate how such traits associated with habitat dimensionality inducing volancy, arboreality and fossoriality, along with other potential traits, including activity patterns and eusociality, influence lifespan across birds and mammals. Using phylogenetic comparative analyses with over 1300 species I show that, over and above the effect of body mass, species associated with high dimensional habitats, through arboreality and the ability to fly, live the longest. Within volant species, lifespan depended upon when (activity patterns), but not where (foraging habitats), species are active. However, the opposite was true for non-volant species, where lifespan correlated positively

with both arboreality and whether they were eusocial. These results indicate that dimensionality can affect the ability of prey to escape predation with the resulting affects on species life-history evolution.

3.2 INTRODUCTION

Lifespan, or longevity, is a fundamental life-history trait that exhibits considerable variation both within and among species. Maximum lifespan in vertebrates, for example, ranges from up to 211 years in the bowhead whale (*Balaena mysticetus*;(De Magalhaes and Costa, 2009)), down to just eight weeks in the pygmy goby (*Eviota sigillata*; (Depczynski and Bellwood, 2005)). Like most other life-history traits, lifespan varies strongly with body size such that large species tend to live longer than smaller species (Lindstedt and Calder III, 1981; Promislow, 1993; De Magalhães et al., 2007; Ricklefs, 2010b). However, many species have far longer, or indeed shorter, lives than expected given their body mass (Figure 3.1)). Understanding the mechanisms underlying these deviations from predicted lifespan may reveal the secrets to treating and combating human ageing (Ricklefs, 2010a; Zhang et al., 2013).

One explanation for species living longer than expected, given their body size, is that low extrinsic mortality (i.e. low risk of death due to external causes such as disease, predation, food shortages or accidents) will, on average, select for longer lifespans than when extrinsic mortality is high (Stearns, 1992; Williams, 1957). This is because when untimely death is more likely, investment in early and frequent reproduction is favoured rather than investment in long-term maintenance and survival. Therefore, species with adaptations that reduce the risks of extrinsic mortality should live longer than expected, given their body mass (Partridge and Barton, 1993). These ideas have led to myriad, taxon-specific hypotheses about traits that may reduce extrinsic mortality and result in increased lifespan (Ricklefs, 2010a). However, there is little consensus about the general drivers of increased lifespan across clades.

As predation is one of the main sources of extrinsic mortality, species which possess the ability to reduce it, for example through the use of toxin defences, show increased lifespans (Hossie et al., 2013). One fundamental ecological aspect that would be expected to affect such predation pressures is the dimensionality of the habitat a species lives within. The dimensionality of trophic interactions is a key

element in predation pressures where consumption rates scale higher with body mass in high dimensional interactions (Pawar et al., 2012). While this increased scaling of potential predation pressures may be expected to decrease prey species longevity in such environments the converse may also be expected through the increase ability of prey species to escape due to the increased availability of escape routes in terms of directionality and cover (Møller, 2010). Two common ways a species may access such escape paths are arboreality and the ability to fly.

The ability to fly, and thus more easily escape predation and unfavourable conditions, is perhaps the most effective way a terrestrial species can evolve to reduce its extrinsic mortality and increase its lifespan (Partridge and Barton, 1993; Holmes and Austad, 1994; Pomeroy, 1990). This is supported strongly by striking differences in the lifespan of volant (flying) and non-volant (non-flying) vertebrates; on average, bats live 3.5 times longer than similarly-sized non-volant placental mammals (Wilkinson and South, 2002; Austad and Fischer, 1991), while birds live up to four times longer than similarly sized mammals (Lindstedt and Calder III, 1981; Holmes and Ottinger, 2003). Similarly arboreality has also been cited as extending longevity in species mainly through decreasing predations risks (Shattuck and Williams, 2010). However, these may not be the only route to reducing extrinsic mortality and thereby increase lifespan. Ecological factors may also be important. Previous studies have investigated the relationship between lifespan and various ecological variables, but most only investigated select groups of species and few considered multiple traits simultaneously (e.g. Shattuck and Williams (2010)).

Here I investigate how multiple ecological and mode-of-life traits simultaneously influence maximum lifespan across birds and mammals. I test several hypothesis regarding the relationships among lifespan and ecological and mode-of-life traits known to influence extrinsic mortality risk; including flight capability (volant or non-volant), activity period (diurnal, crepuscular [i.e. active at dawn and dusk], nocturnal or cathemeral [i.e. active both day and night]), foraging environment (terrestrial, semi-arboreal, arboreal, aerial or aquatic), and fossoriality (i.e. living in burrows; fossorial, semi-fossorial, non-fossorial). I approach these questions by using the largest number of species to date in such an analysis ($N = 589$ birds and 779 mammals) and by using the most up to date phylogenetic comparative approach that includes using a distribution of 500 combined bird and mammal phylogenies to control for the phylogenetic autocorrelation introduced by shared ancestry (Harvey and Pagel, 1991) and body mass (Lindstedt and Calder III, 1981).

I predict that, after controlling for body mass, (i) species which can access escape routes within high dimensional habitats including volant and arboreal species will either show reduced or enhanced lifespans in comparison to other species; (ii) semi-arbooreal, semi-aquatic and semi-fossorial species which can seek refuge across different environments would be expected to live longer than terrestrial species; species with nocturnal, crepuscular or cathemeral activity patterns will live longer than diurnal species, because species that are active at night or dusk are likely to be harder for predators to detect (Holmes and Austad, 1994; Promislow and Harvey, 1990); and (4) fossorial (i.e. species that live in permanent burrows) will live longer than purely terrestrial species, because they possess means to escape predation and unfavourable conditions through refuge (Buffenstein and Jarvis, 2002).

As ecological factors that influence lifespan are likely to vary among volant and non-volant species because sources of extrinsic mortality will differ in these two groups, these groups were split species into volant (most birds and all bats), and non-volant (some birds and most mammals) subgroups, to discover general, broad-scale correlates of lifespan in endotherms, rather than separate correlates for birds and mammals. I then tested the above hypotheses on volant and non-volant species separately. As predicted, after controlling for body mass and phylogeny, volant and arboreal species live longer than terrestrial species. Surprisingly of the species capable of transitioning across environments only semi-arbooreal species showed increased lifespan while only volant crepuscular species showed any effect of activity period on longevity.

3.3 MATERIALS AND METHODS

3.3.1 *Data*

I used maximum longevity as a measure of lifespan as it is thought to be the best available estimator of a species' ageing rate (De Magalhães et al., 2007) and because of the amount of high quality longevity data available. Data on maximum longevity (years) and adult body mass (g) was obtained from the AnAge database (De Magalhaes and Costa, 2009; Tacutu et al., 2012). In the main analysis species with maximum longevity estimates based on fewer than ten longevity records, or with low or questionable data quality as defined in the AnAge database were excluded (De Magalhães et al., 2007). As maximum values are dependent on sample size a sensitivity analysis excluding species with maximum longevity estimated from fewer

than 100 longevity records we also run. Note that longevity records for non-volant mammals tend to come from captive individuals, whereas data for bats and birds tend to come from wild caught individuals. Although we expect captive individuals to live longer than wild individuals, on average maximum longevity tends to remain unchanged between captive and wild populations Ricklefs and Scheuerlein (2001). Further, given that bats and birds live longer than non-volant mammals, this should make the analyses more conservative.

To test the hypotheses concerning the relationships between lifespan, mode-of-life and ecological traits, data was collected on the flight capability (volant or non-volant), activity period (diurnal, crepuscular, nocturnal or cathemeral), foraging environment (terrestrial, semi-arboreal, arboreal, aerial or aquatic), and fossoriality (fossorial, semi-fossorial or non-fossorial) of each species using Walker's Mammals of the World (Nowak, 1999), the Handbook of Birds of the World series (Hoyo et al., 1992), the Handbook of the Birds of Europe, the Middle East and North Africa series (Cramp, 1977) and some additional sources (Appendix B, (Fry and Fry, 2010; Parr and Juniper, 2010; Williams et al., 1995)). I used the taxonomy of Wilson and Reeder (Wilson and Reeder, 2005) for mammals and Jetz et al. Jetz et al. (2012) for birds and excluded purely aquatic mammals (Cetacea and Sirenia) from the analyses because we expect selection pressures to be very different in these groups. Gliding mammals were also excluded because there were too few species ($N = 9$) to run a separate analysis and because this group could equally fit into either the volant or non-volant subgroups.

Rather than basing the analyses on just a single phylogenetic tree and assuming this tree was known without error, a distribution of trees was used. For birds 500 trees were extracted from the posterior distribution of a recent bird phylogeny generated under a Bayesian inference framework (Jetz et al., 2012), and for mammals the 10,000 mammal trees constructed by Kuhn et al. (2011) was used. Each individual mammal tree comprises one resolution of the polytomies of a previously published supertree (Bininda-Emonds et al., 2007). These were treated as equivalent to a Bayesian posterior distribution of trees because no such tree analysis exists for all mammals. To create a distribution of phylogenies containing both birds and mammals, randomly selected bird tree and mammal trees were selected without replacement and bound to make a combined tree. The trees were bound with a root age of 315 million years, corresponding to the fossil calibration for all amniotes, i.e., *Archerpeton anthracos* (Appendix B; (Reisz and Müller, 2004)). This procedure was

repeated 500 times to generate a distribution of 500 combined bird and mammal trees.

In total the analyses used data from 589 birds (579 volant and 10 non-volant) and 779 mammals (83 volant and 696 non-volant; see Appendix B: Table A1 for more details), which was reduced to 474 birds and 435 mammals in the sensitivity analysis using only species with 100 or more longevity records.

3.3.2 Analyses

To test the hypotheses the following three models were fitted, with Maximum longevity and Body mass incorporated as continuous variables; Flight capability, Foraging environment, Activity period and Fossoriality as factors and with Body mass:Flight capability representing the interaction between Body mass and Flight capability:

1. For all species (N =1368: Maximum longevity = $f(\text{Body mass} + \text{Flight capability} + \text{Body mass: Flight capability})$)
2. For volant species only (N = 662): Maximum longevity = $f(\text{Body mass} + \text{Foraging environment} + \text{Activity period})$
3. For non-volant species only (N =706): Maximum longevity = $f(\text{Body mass} + \text{Foraging environment} + \text{Fossoriality} + \text{Activity period})$

All analyses were carried out in R v3.0.2 (R Core Team, 2014). Maximum longevity and body mass were \log_{10} transformed before being mean centred and expressed in units of standard deviation. The models were fitted using Bayesian phylogenetic mixed models from the MCMCglmm package (Hadfield et al., 2010), to account for non-independence in species traits introduced as a result of common ancestry (Harvey and Pagel, 1991). MCMCglmm uses a Markov chain Monte Carlo estimation approach and accounts for non-independence among closely-related species by including the phylogenetic relationships among species as a random variable. I determined the number of iterations, thinning and the burn-in period for each model run across all trees using diagnostics in the coda package (Plummer et al., 2006) and checked for convergence between model chains using the Gelman-Rubin statistic, the potential scale reduction factor (PSR), with all models required have a PSR below 1.1 (Gelman and Rubin, 1992). Following the recommendations of Hadfield (Hadfield et al., 2010), an uninformative inverse-Wishart distribution (with variance, V, set to 0.5 and belief parameter, nu, set to 0.002) and a parameter

expanded prior, with a half-Cauchy distribution (described by the parameters $V = 0.5$, $\text{nu} = 1$, the prior mean $\text{alpha.mu} = 0$, and $\text{alpha.V} = 102$, which represents the prior standard deviation with a scale of 10), was used for the random factor to improve mixing and decrease autocorrelation among iterations.

As noted above, rather than using one phylogenetic tree and assuming this tree was error free, a distribution of 500 combined bird and mammal trees was used with each of the models fitted to each of these trees. The resulting model outputs were then combined to give model estimates which incorporate the error across the 500 trees. As the posterior outputs of MCMC models are combinable, coefficient distributions were created by amalgamating each coefficient posterior.

To determine whether the conclusions held when species with fewer than 100 longevity records was excluded, models 1-3 were repeated with the reduced dataset of species with 100 or more longevity records. I also repeated Models 2 and 3 for birds and mammals (rather than volant and non-volant species) separately to ensure that differences between the volant and non-volant subgroups were due to differences in flight capability and were not simply representing the difference between mammals and birds. The deviance information criteria (DIC), a hierachal generalization of AIC, was calculated for each paired bird and mammal models and compared to the paired volant and non-volant models of the same phylogeny to compare model "fit" of each approach.

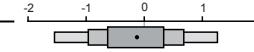
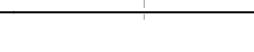
Finally, Since publication of this work (Healy et al., 2014) new analysis performed by Williams and Shattuck (2015) outlined the potential importance of eusociality in small mammals associated with fossoriality. The analysis uses the data described above along with new data on eusociality, defined using reproductive skew (Williams and Shattuck, 2015), to show that eusociality is also a predictor of increased maximum lifespans. To further investigate the role of eusociality using the methods developed here I run a further analysis on this composite dataset to control for both phylogeny and the error within phylogenetic reconstructions.

3.4 RESULTS

The analysis show that volant species live longer than non-volant species of a similar body mass (Table 1, Figure 1). In addition, for a given increase in body mass, the lifespans of volant species (modal slope estimate [after converting from mean-centred values] = 0.25; Table 1) increase significantly more than the lifespans of non-

volant species (modal slope estimate [after converting from mean-centred values] = 0.13; Table 1).

TABLE 3.1: Relationship between maximum longevity (years), body mass (g) and flight capability (volant or non-volant) in 1368 birds and mammals. Estimates are modal estimates from 500 models. Lower CI = Lower 95% confidence interval from 500 models. Upper CI = Upper 95% confidence interval from 500 models. Posterior distribution = distribution of estimates from 500 models. Body mass × Flight capability = interaction between body mass and flight capability.

Fixed Terms	Estimate (β)	Lower CI	Upper CI	Posterior distribution
Intercept	-0.145	-1.544	1.260	
Body Mass	0.554	0.467	0.639	
Flight capability - Volant	0.507	0.033	0.981	
Body Mass: Flight capability	0.456	0.302	0.613	
<hr/>				
Random Terms				
Residual variance	0.107	0.090	0.127	
Phylogenetic variance	1.542	1.264	1.871	

Notes: 24000000 iterations with 4000000 burnin and thinning interval of 10000.

The relationships among our ecological variables and lifespan differed between the volant and non-volant subgroups. Within volant taxa, crepuscular species (i.e. those active at dusk and dawn) had significantly shorter lifespans than both diurnal and nocturnal species (Table 2). In contrast, activity period was not associated with lifespan in non-volant species (Table 3). Foraging environment did not influence lifespan significantly in volant species; bats and birds that forage on the ground do not have shorter lifespans than species that forage in the air or in trees (Table 2). Within non-volant species, however, those foraging arboreally have longer lifespans than those foraging terrestrially, and fossorial (i.e. burrowing) species live longer than non-fossorial ones (Table 3).

In the supplementary analysis with maximum longevity estimates based on 100 or more records, the models showed qualitatively comparable results to the findings in the main analysis (Appendix B: Tables B2-B4). In the repeated Models 2 and 3 for birds and mammals (rather than volant and non-volant species), the results were qualitatively identical apart from a predictable reduction in the phylogenetic residual term and also a lower combined DIC value for Models 2 and 3 (modal volant and non-volant DIC = 1184) in comparison to a taxonomically split model (modal birds and mammals DIC = 1227) (Appendix B: Tables B5-B6). The phylogenetic residual term was high in all of our models (model 1: 1.542; model 2: 1.555; model 3: 1.627;

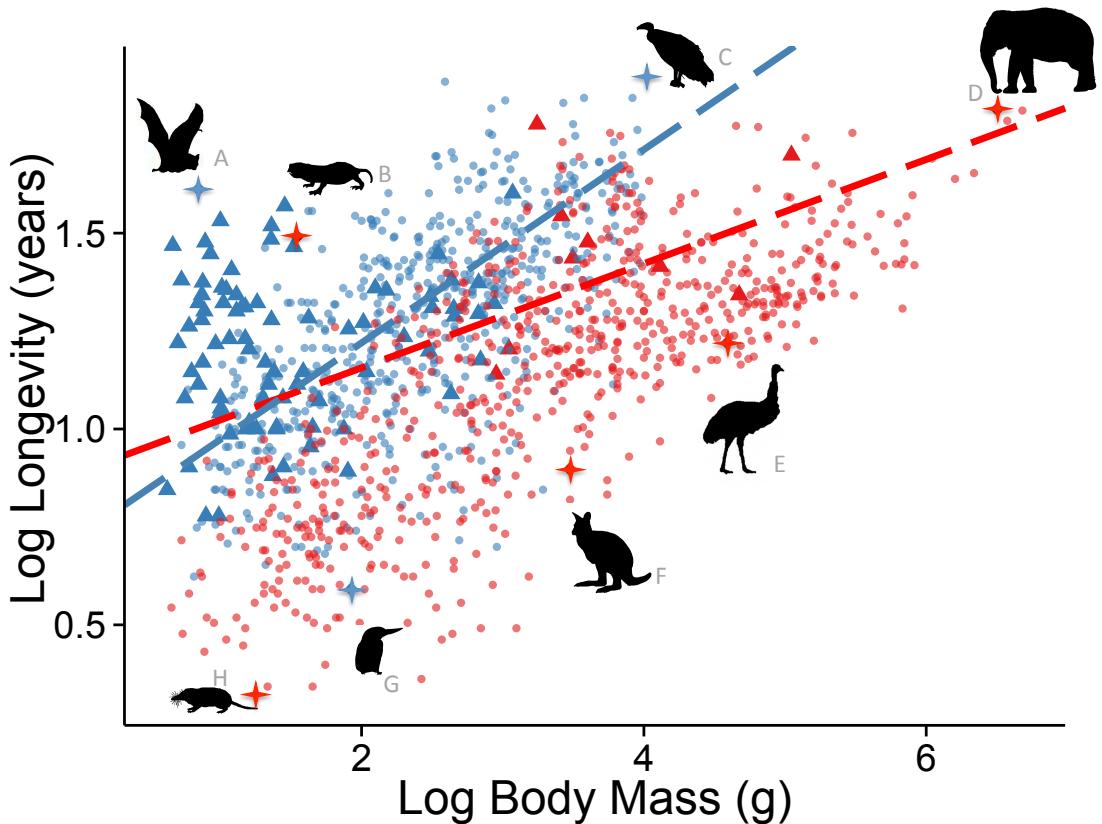
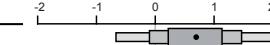
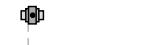
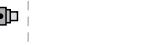


FIGURE 3.1: Relationships between body mass and maximum lifespan in birds and mammals. Silhouettes highlight a selection of species with much longer or shorter lifespans than expected given their body size. These species are (A) *Myotis brandtii*, Brandt's bat; (B) *Heterocephalus glaber*, Naked mole rat; (C) *Vultur gryphus*, Andean condor; (D) *Loxodonta Africana*, African elephant; (E) *Dromaius novaehollandiae*, Emu; (F) *Dorcopsulus macleayi*, Papuan forest-wallaby; (G) *Ceryle rudis*, Pied kingfisher; and (H) *Myosorex varius*, Forest shrew. Blue points and line represent volant birds and mammals ($N = 662$; slope = 0.25, intercept = 0.73). Red points and line represent non-volant birds and mammals ($N = 706$; slope = 0.13, intercept = 0.89). Blue triangles represent bat species and red triangles represent non-volant bird species. Estimates of slopes and intercepts represent back transformed values from mean centred values given in Table 1.

TABLE 3.2: Relationship between maximum longevity (years), body mass (g), foraging environment and activity period in 662 volant birds and mammals. Estimates are modal estimates from 500 models. Lower CI = Lower 95% confidence interval from 500 models. Upper CI = Upper 95% confidence interval from 500 models. Posterior distribution = distribution of estimates from 500 models.

Fixed Terms	Estimate (β)	Lower CI	Upper CI	Posterior distribution	
Intercept	0.668	-0.664	2.028		
Body Mass	1.035	0.899	1.172		
Foraging environment	- Aerial	0.116	-0.119	0.354	
	- Arboreal	0.068	-0.119	0.258	
	- Semi-arboreal	0.124	-0.056	0.301	
	- Aquatic	-0.166	-0.383	0.049	
Activity period	- Cathemeral	0.085	-0.088	0.261	
	- Crepuscular	-0.479	-0.772	-0.182	
	- Nocturnal	-0.131	-0.385	0.122	
<hr/>					
Random Terms					
Residual variance	0.184	0.151	0.223		
Phylogenetic variance	1.155	0.789	1.693		

Notes: 12000000 iterations with 2000000 burnin and thinning interval of 5000.

Tables 1-3) but was much lower in the taxonomically split bird and mammal models, as expected given their more restricted phylogenetic scope (birds: 0.371; mammals: 0.936; Appendix 3, Table A10). Finally, the additional analysis of Williams and Shattuck (2015) dataset showed that eusociality but not fossoriality (as defined to include both semi-fossorial and fully fossorial species) increased maximum lifespan in small mammals. (Table 4).

3.5 DISCUSSION

As predicted, these analysis found that species capable of exploiting high dimensional environments live longer than species of a similar body mass in environments of lower dimensionality. Volant species, in particular those with nocturnal, cathemeral and diurnal activity patterns, lived longer than non-volant species while the longest-lived non-volant species tended to be arboreal or semi-arboreal. The link between these traits and increased lifespan are in line with previous studies on lifespan evolution in endotherms. Among birds, flightless or weakly-flying species (i.e. game birds) have the shortest lifespans (Ricklefs, 2010b; Williams, 1957; Wilkinson and

TABLE 3.3: Relationship between maximum longevity (years), body mass (g), foraging environment, fossoriality and activity period in 706 non-volant birds and mammals. Estimates are modal estimates from 500 models. Lower CI = Lower 95% confidence interval from 500 models. Upper CI = Upper 95% confidence interval from 500 models. Posterior distribution = distribution of estimates from 500 models.

Fixed Terms	Estimate (β)	Lower CI	Upper CI	Posterior distribution
Intercept	0.013	-1.433	1.467	
Body Mass	0.531	0.449	0.614	
Foraging environment	- Arboreal	0.213	0.358	
	- Semi-arboreal	0.148	0.274	
	- Aquatic	0.064	0.341	
Fossoriality	- Fossorial	0.437	0.785	
	- Semi-fossorial	0.035	0.149	
Activity period	- Cathemeral	0.060	0.173	
	- Crepuscular	-0.050	0.096	
	- Nocturnal	0.038	0.153	
Random Terms				
Residual variance	0.042	0.031	0.059	
Phylogenetic variance	1.627	1.319	1.985	

Notes: 24000000 iterations with 4000000 burnin and thinning interval of 10000.

TABLE 3.4: Relationship between maximum longevity (months), body mass (g), sociality (eusocial or no-eusocial) and fossoriality (fossorial non-fossorial). Estimates are modal estimates from 25 models. Lower CI = Lower 95% confidence interval from 25 models. Upper CI = Upper 95% confidence interval from 25 models. Posterior distribution = distribution of estimates from 25 models.

Fixed Terms	Estimate (β)	Lower CI	Upper CI	Posterior distribution
Intercept	0.552	-0.410	1.546	
Body Mass	0.534	0.383	0.683	
Sociality: Eusocial	0.289	0.070	0.511	
Habitat: Fossorial	0.064	-0.175	0.129	
Random Terms				
Phylogenetic variance	1.002	0.635	1.420	
Residual variance	0.064	0.036	0.103	

Notes: 5100000 iterations with 100000 burnin and thinning interval of 2500.

South, 2002) while among mammals, bats live far longer than similarly sized non-volant mammals (ref). Arboreality is also strongly associated with longer lifespans (Shattuck and Williams, 2010) while gliding species, which mix elements of both

arboreality and volancy, also have greater lifespans than expected given their body mass (Holmes and Austad, 1994). This increased lifespan is likely associated with the decreased predation pressures associated with living within high dimensional environments.

High dimensional environments may reduce predation risks through providing refuge that predators cannot access and through providing more escape routes in terms of directionality. Prey escape strategies often involve retreating to a refuge that cannot be accessed by the predator in pursuit, such as transiting between terrestrial, arbooreal, aquatic or fossorial environments. However the results off this analysis suggest that this is not a major contributor to lifespan evolution in endotherms as semi-aquatic and semi-fossorial species show no difference in longevity in comparison to fully terrestrial species. The increased longevity in higher dimensional environments may hence better reflect the increased options available for escape in such habitats. In fact birds species that escape along vertical flight trajectory's (3D) have been found to have longer lifespans in comparison to those that use horizontal escape routes (Møller, 2010).

Another explanation for these results of increased lifespan in volant and arboreal species is that the environments included within this analysis restrict large predators. Unlike marine environments aerial and arboreal environments severely restrict body size, mainly through biomechanical constraints. This is seen in the largest known aerial predators, *Argentavis*, reaching only 70 kg (Chatterjee et al., 2007) whereas the largest extant terrestrial predators can reach up to 1000 kg (Carwardine, 1995), while the largest extinct theropods species reach over 15 tonnes (Therrien and Henderson, 2007). Similarly arboreal predators are restricted by the weight branches can support with the largest such predators, felids, generally restricted to ticker branches. This exclusion of large body size species may also explain the difference in how lifespan scaled with body mass found in volant and non-volant species. While previous studies generated similar slopes for the relationship between log lifespan and log body mass in birds (slope = 0.20) and mammals (slope = 0.22) (Lindstedt and Calder III, 1981; Hulbert et al., 2007) these analysis show for a given increase in body mass, the lifespans of volant species (modal slope estimate [after converting from mean-centred values] = 0.25) increase significantly more than the lifespans of non-volant species (modal slope estimate [after converting from mean-centred values] = 0.13). This difference in scaling may reflect the relativity predator free existence of large flying species such as found in species of vultures and albatross.

While habitat dimensionality shows an important effect on longevity, activity patterns in both volant and non-volant species seems to show little association with lifespan. Only crepuscularity in volant species showed an effect with these species having shorter maximum lifespans. This may be a result of crepuscular species being exposed to both diurnal and nocturnal predators resulting in higher extrinsic mortality. For example bat species which emerge earliest are susceptible to the highest predation levels (Jones and Rydell, 1994). The scarcity of crepuscular volant species ($N = 16$) in our dataset also suggests that specialisation to be active between nocturnal and diurnal periods is a relatively unsuccessful strategy. Activity period was not related to lifespan in non-volant species, counter to the initial prediction that nocturnal, crepuscular and cathemeral species would be more long-lived, which assumed that diurnal species would be easier for predators to detect. However, there are many additional ways to avoid predation and many alternative reasons for becoming nocturnal, crepuscular or cathemeral. For example, many large mammals are crepuscular or cathemeral in order to avoid the intense heat of the day in tropical areas, while species such as wolves and hyenas may have become nocturnal to access more prey. Consequently, although nocturnality may decrease extrinsic mortality for some species, it may actually increase it for others Prugh and Golden (2014).

Within the main analysis fully fossorial species lived longer than similar sized terrestrial species, as expected based on the inferred protection such a lifestyle may provide against predators. However subsequent analysis here, following Williams and Shattuck (2015), showed that this association is more likely to be driven by the levels of eusociality found in fossorial species. Eusociality is also known to increase longevity through the reduce extrinsic mortality in breeding individuals. For example eusocial insects, perhaps the most extreme example of such systems, show a 100-fold increase in maximum lifespan in the colony queens (Keller and Genoud, 1997). Of the 10 fully fossorial species included in our original analysis the three species which can be best described as eusocial, the naked mole rates *Heterocephalus glaber*; *Cryptomys damarensis*; *Spalax ehrenbergi* have maximum lifespans ranging between 15.5 and 32 years in comparison to the range of 2.5-17 years in the remaining fossorial species. This new analysis suggest that fossoriality itself does not confer additional protection from external mortality. This may be due to fossoriality restricting the means of escape once encountered by a predator within the borrow. Hence this result further supports the idea that dimensionality

is an important aspect of reducing mortality and may offer a partial explanation for the exceptional longevity of naked mole rats (*Heterocephalus glaber*) which live ten times longer than expected, given their body size (Buffenstein and Jarvis, 2002).

These findings highlight the potential importance of habitat complexity in lifespan evolution. The additional options for escape in such habitats may be a defining feature of trophic interactions within birds and mammals. However the biomechanical limitations associated with volancy and arboREALITY, restrict the ability to draw out whether this is the causal factor behind such increased lifespans. Further comparative analysis in marine systems where such body size limitations are less restrictive and where pelagic systems are relatively clear of refuges would provide a further test to the above conclusions. In particular if habitat dimensionality is an important factor in lifespan evolution it would be expected that pelagic species live longer than similar sized benthic species while accounting for phylogeny. Similarly other groups may help further decouple the effects of fossoriality on life history evolution. In particular comparing the diverse ecologies within reptiles would further test the effects of arboreality and fossoriality on lifespan.

Finally, while the ability to escape some of the main sources of mortality is likely to extend species lifespan and the associations between longevity and volancy, arboreality and eusociality is clear the direct causal link is still not clear. Theoretical modelling suggests that how mortality is distributed across a species demography is a key determinant in whether that species increases its lifespan. For example reduced extrinsic mortality, especially due to predation, may increase intraspecific competition resulting in what seems as a counter-intuitive reduction in lifespan (Moorad and Promislow, 2010). To decouple such effects more detailed analysis including mortality rates across species life-histories along with comparative methods which include ecology are needed. By understanding the underpinnings of the evolution of life-history we not only provide an insight into the ecology and evolution of predator-prey interactions but also provide an important basis on which to view and understand our own ageing and the potential paths to circumvent it.

CHAPTER 4

HABITAT DIMENSIONALITY AND A DIET OF EGGS: THE EVOLUTION OF VENOM LOSS IN SNAKES.



“Always keep your smile. That’s how I explain my long life.”

Jeanne Calment

4.1 SUMMARY

The evolution of venom in snakes offers a system of both ecological and medical interest. Despite this many fundamental ecological questions regarding the evolution and current variation of this trait amongst snakes still persist. In particular despite the obvious benefits of possessing venom many species have secondarily either lost or have shown severe reduction in this trait. One of the potential answers to

this paradox the reduction of the costs associated with producing large amounts of venom in species were the benefits of venom are reduced. Here I test several hypothesis on such ecological factors that may be associated with the atrophy of venom in snakes including habitat dimensionality, which is predicted to affect encounter rates, diet and body size. Further to this I test the co-evolutionary relationship between venom toxicity and venom volume along with the levels of prey-specificity in a comparative analysis using over 100 species of venomous snakes. I find that species with associations to high dimensional habitats and a diet of eggs show atrophy of venom through reduced venom volumes and in the case of eggs eating species reduced toxicity. I also show that despite predictions toxicity and venom volume show correlations although snake toxicity does show pre-specific toxicity through increased toxicities in species with similar diet to that of toxicity test species. Overall snake venom provides a remarkable case of predator-prey interactions with rapidly shifting arms race dynamics that are both important to our understanding of predator trait evolution as a whole and the ecology of this important predatory group.

focusing on fundamental aspects of both the environment and the nature of their prey. Using the largest dataset that includes both venom toxicity and volume data I test whether species that are associated with

4.2 INTRODUCTION

The evolution of predatory traits can often be the defining feature of whole clades of animals, from the evolution of the first jawed fish to the use of silk for web construction in arachnids. Perhaps nowhere is this better illustrated than in the evolution of venom in snakes. Through the processes of limb reduction and eventual loss beginning over 160 million years ago (Caldwell et al., 2015) snakes have relied on extreme adaptations in order to capture and kill prey items such as complex cocktails of venoms (Casewell et al., 2013; Fry et al., 2012). This reliance on venom as a primary means to capture prey in many species of snakes makes them an excellent group to study how fundamental aspects of ecology, such as habitat dimensionality, can drive the evolution of predatory traits and predator-prey interactions.

Venoms, which can be broadly defined as "a secretion produced in a specialised gland in one animal and delivered to a target animal through the infliction of a wound, which contains molecules that disrupt normal physiological or biochemical

process so as to facilitate feeding or defence by the producing animal" (Casewell et al., 2013), in snakes consist of complex cocktails of proteins and other compounds creating neurotoxic and hemotoxic compounds (Greene, 1997; Casewell et al., 2013). While the biological properties these mixtures possess has lead to a wide body of biomedical research there is surprising little understanding of the ecological pressures associated with the evolution of the diverse venoms found in snakes (Greene, 1997; Casewell et al., 2013). Functionally venoms are used for both foraging and anti-predator defence. However anti-predatory defence is likely to be secondary functionality of venoms, as reflected by the lack of correlation between lifespan and the possession of venom in snakes (Hossie et al., 2013), with aiding in prey acquisition a more likely primary function (ref). However despite the clear functionality and benefits associated with possessing venom many species of snakes have paradoxically lost this ability secondarily. Such atrophy of venom toxicity, production and of the apparatus required to deliver venom is seen at the most extreme vestigial state in the sea snake *Aipysurus eydouxii* (Li et al., 2005), but is also seen as various levels of atrophy of toxicities or venom volumes produced in other species (Fry et al., 2012). One possible solution to this paradox is the investment cost associated with the production of venoms.

Venom synthesis carries an appreciable cost both with regards to energy requirements and through possible lost opportunities. After venom extraction pitvipers have been shown to greatly increase their metabolic rates over a 72 hour periods McCue (2006), and while other species indicate less severe costs (Pintor et al., 2010), species that heavily dependent on their venom to capture prey would undergo lost opportunities over the replenishment period. This cost is reflected in the behaviours of some rattlesnake species that meter the amount of venom they inject into their prey species (HAYES, 1995) and also through the occurrence of dry bites associated with defensive behaviour (Morgenstern and King, 2013). This cost of venom explains the loss or reduction of venom in many species, for example a switch to a diet of eggs in *Aipysurus eydouxii* is likely to be the driver of venom loss in this species due to the removal of the need to incapacitate their prey. However many species of similar size and diet still show considerable variation in the toxicity and volume of venom they produce pointing towards other ecological or evolutionary drivers of venom evolution.

One key component in the evolution of venom is the identity of the target prey species. The venoms of several species of snake show a strong prey-specific ele-

ment with regards to the toxicity. For example Barlow et al. (2009) showed that within *Echis* viper populations that feed on different prey groups, individuals show higher toxicities for their preferred prey items. Similarly Malaysian pit vipers show variation in their venoms that correlate with diet (Daltry et al., 1996). However such prey-specificity in venom does not seem to be present in all snakes species making the ubiquity of this interaction unclear (Williams et al., 1988). One possible explanation for this is the arms race between the evolution of venom potency in snakes and the corresponding evolution of resistance in species under heavy predation, such as ground squirrels showing resistance to their rattlesnake predators (Poran et al., 1987). In fact there is some evidence that such resistance to pitviper venoms in Opossums has led to a switch in predator-prey roles with Opossums now the predators of pitvipers (Voss, 2013). This arms race has resulted in the rapid evolution of genes associated with venom as demonstrated in the king cobra genome (Vonk et al., 2013), however a simpler evolutionary response to such resistance may be to increase the amount of venom a species produces.

The evolution of snake toxicity depends on rapid genomic evolution, such as through gene duplication events, in order to stay apace with prey resistance (Vonk et al., 2013). Such evolutionary events are likely to be relatively rare which may result in species relying on increased venom doses in order to keep pace with short term prey resistance responses. Species which show low toxicities would hence be expected to compensate by producing larger reservoirs of venom with which to increase dosages to prey while species with high toxicities would be expected to reduce venom production in order to offset unnecessary costs (McCue, 2006). Such variation in prey resistance may also lead to "overkill" type behaviours where individuals inoculate doses far in excess of that required to incapacitate prey items (ref). This overkill behaviour is also likely to in part be an artefact to the common use of mice to determine venom toxicities instead of a snakes natural prey. A more realistic interpretation of the data requires including the physiological distance such test species may have in comparison to snakes diet. Overall a correlation between venom toxicity and volume would be expected if snakes use compensatory behaviour while species with a diet close to that of the test model would be expected to show higher toxicities indicative of adaptive prey specific venoms. While the evolution of venom is likely to be strongly influenced by the arms race between predator and prey, the ability to simply find a prey item may also be an important determinant in the volume and toxicity of a snakes venom.

While incapacitating prey is primary function of venom, venom evolution might also be expected to be influenced by the probability of encountering such a prey item. One such aspect which may influence these probabilities is habitat dimensionality (Pawar et al., 2012) as encounter rates show higher scaling with body mass in higher dimensional environments. This may decrease the investment in venom production due to the higher probability of encountering prey reducing lost opportunities of missed strikes or though the faster replenishment rates in order to fully exploit such encounters, which may be associated with the faster digestion rates seen in arboreal species (Lillywhite et al., 2002). Conversely high habitat dimensionality may also increase the venom volume produced through the increased capacity of prey species to escape in multiple directions or selection to higher toxicities (Healy et al., 2014; Møller, 2010).

Here I use a comparative approach in order to test multiple hypothesis on venom evolution in snakes. Using data on venom toxicity, volume produced, size, diet and environment I test using a multiple response model the relationship between venom toxicity using median lethal dose as a measure and both maximum and mean venom volumes found in snakes. I also test whether species that have diets phylogenetically similar to the test animal used to determine toxicity show increased toxicities and whether species that include eggs within their diet show atrophy of both venom toxicity and volume. Finally I test whether species that inhabit high dimensional environments, namely arboreal and aquatic species, show differences in the venom volume and toxicity. Overall I find that species in high dimensional habitats or that consume eggs show a reduction in both maximum and mean venom volumes produced and also that snakes show higher toxicities to species that are physiologically closer to that found within their diet.

4.3 MATERIALS AND METHODS

4.3.1 *Data*

As a measure of venom toxicity I used median lethal dose (LD_{50}), the individual dose required to kill 50% of a population of test animals, were lower values of LD_{50} indicate a higher venom toxicity. As the route of inoculation can affect LD_{50} (ref) only values estimated from either intravenous, subcutaneous, intrapulmonary or intramuscular inoculation routes were used, with a fixed term included to account for the variation between these routes. While most studies determine LD_{50} values

using murine test animals I also included studies that used alternative models as snake venom potency is likely to be linked to diet (Barlow et al., 2009). I used both reported maximum and mean dry weight (mg) as a measure of venom volume as the dry weight represents the active proteinaceous component of venom and as it was the most available reported measure. In the case of multiple studies reported venom volumes the mean values across the studies were taken as the value for that species with the maximum across all studies used as the overall maximum value.

Diet data was collated from the literature using studies with quantitative estimates of prey proportions, mainly from studies of stomach contents (See appendix for data). As prey items were rarely identified to lower taxonomic levels diet was categorized as in (Allen et al., 2013) into six prey categories; invertebrates, fish, amphibians, lizards, birds and mammals. A separate term indicating the inclusion of eggs within a species diet was also included.

To test whether snakes with prey phylogenetically close to the LD₅₀ test had higher toxicities I calculated a score relating to the phylogenetic distance between the test species used to calculate the LD₅₀ value and the groups present in the snakes diet. This was calculated as the sum of the phylogenetic distance, using average estimates from TimeTree (Hedges et al., 2006), between each prey group and the LD₅₀ model by the proportion of each prey group reported in each snake species diet. For example a species with a diet of 20% mammals, 50% fish and 30% reptiles with a LD₅₀ measured using mice would have a score of 0.2(0) + 0.5(400.1) + 0.3(296) = 288.85.

Species habitat was categorised as either terrestrial, fossorial, aquatic or arboreal based on literature accounts. In order to directly test any effect of the dimensionality of habitat environment each environment was scored, as in (Pawar et al., 2012), with terrestrial and fossorial environments scored as two-dimensional and arboreal and aquatic scored as three-dimensional. As venom volume is known to increase with body size (Mirtschin et al., 2002), it was included in the analysis using total length values from the literature, primarily from the compilation of (Boback and Guyer, 2003) and from field guides and other works on regional snake faunas. To allow direct comparison with other allometric scaling studies body length was converted into mass using the conversion in (Boback and Guyer, 2003).

Mass, LD₅₀, venom volume and phylogenetic distance between diet and model were log10 transformed, mean centred and expressed in units of standard deviation prior to analysis. Significance was determined for the fixed effects when 95% of the

data is greater or less than 0. To correct for phylogeny I used the tree from (Pyron and Burbrink (2014), Figure 1).

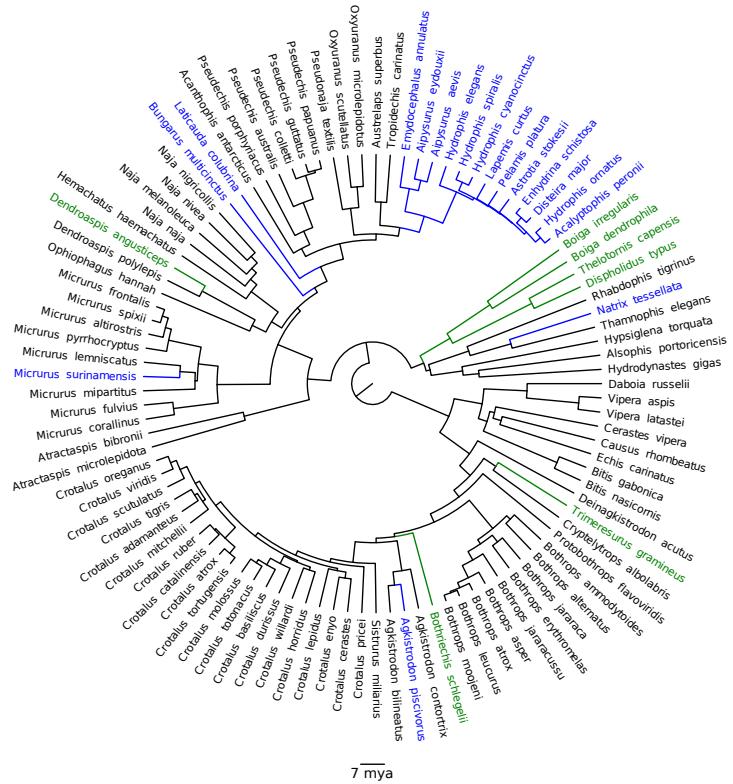


FIGURE 4.1: Phylogeny

Overall data was collated for 101 species (76 species with maximum venom volume estimates, 99 species with average venom volume estimates).

4.3.2 Analyses

To test these hypotheses I fit multiple response phylogenetic mixed models using the MCMCglmm package (Hadfield et al., 2010) in R 2.14.2 (R Core Team, 2014). As venom volume and LD₅₀ are likely to have co-evolved both were included as response variables with mass, LD₅₀ inoculation method, habitat dimensionality, the presence of eggs in diet and phylogenetic distance from LD₅₀ model included as explanatory variables. I fit two separate models; one using maximum venom volume and one with average venom volume. Phylogeny was controlled by including it using the animal term in the MCMCglmm model (Hadfield et al., 2010). Variation due to multiple measures on individual species, mostly to allow the inclusion of separate values for sub-species, was included using a separate random term at the species level. All models were fitted with uninformative priors by using inverse-Wishart parameter expanded priors (Hadfield et al., 2010) with burn-in, thinning and

number of iterations determined to ensure effective sample sizes exceeded 1000 for all parameter estimates and convergence tested using the Gelman-Rubin statistic (Gelman and Rubin, 1992).

4.4 RESULTS

After controlling phylogeny these analysis showed that smaller species that inhabit high dimensional environments have both lower mean and maximum volumes of venom (Figures 1 and 2, Tables 2 and 5). Toxicity was affected by the route of inoculation, with intravenous and intrapulmonary inoculation routes showing lower LD₅₀ in comparison to subcutaneous measures, and the phylogenetic distance between the LD₅₀ model and species diet, with diets closer to the LD₅₀ model showing higher toxicities (Tables 3 and 6). Species with egg based diets showed a reduction in toxicity and maximum venom volume but not average venom volume (Tables 2,3,5,6).

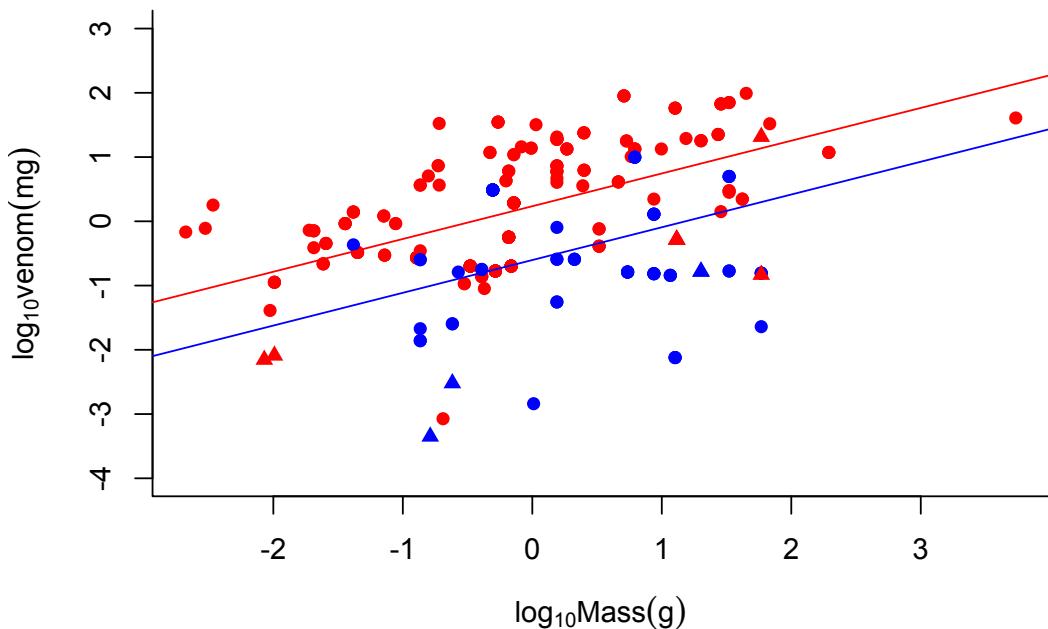


FIGURE 4.2: Mean

There was no correlation between LD₅₀ and either maximum or mean venom volumes (Tables 1 and 4). Both LD₅₀ and venom volume show high phylogenetic

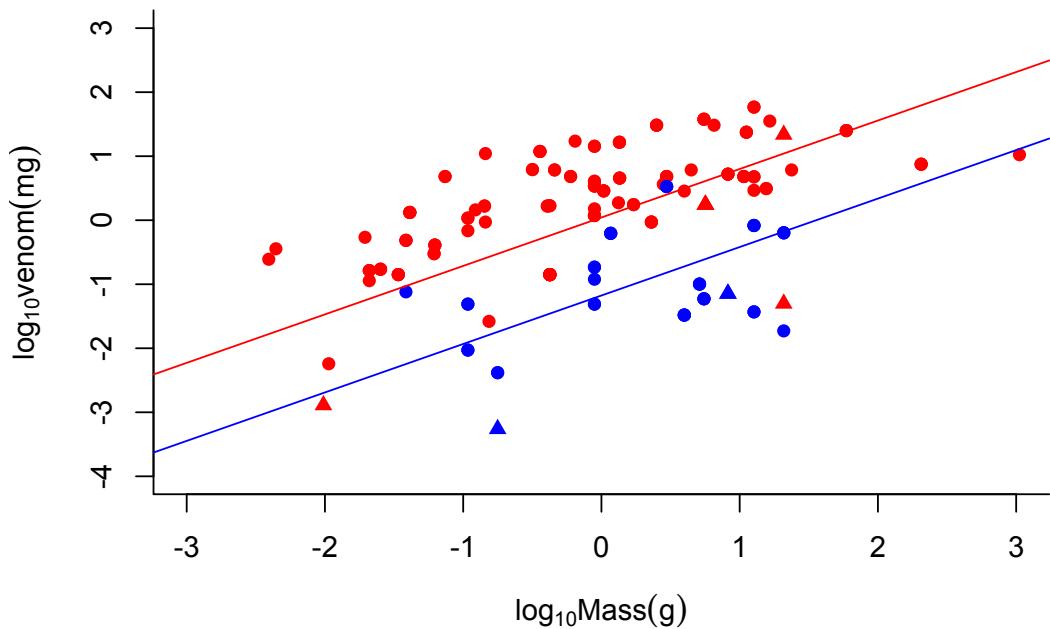


FIGURE 4.3: Max

variance with phylogeny showing a higher association in LD_{50} in comparison to venom volume in both models (Tables 1 and 4).

TABLE 4.1: Correlation structure on random terms.

Terms	Estimate	Lower CI	Higher CI
Phylogeny			
Variance: Mean volume	0.456	0.145	0.847
Covariance: Mean volume and LD_{50}	-0.003	-0.290	0.301
Variance: LD_{50}	0.909	0.479	1.452
Residuals			
Variance: Mean volume	0.009	0.007	0.011
Covariance: Mean volume and LD_{50}	0.003	-0.004	0.011
Variance: LD_{50}	0.268	0.215	0.328
Species			
Variance: Mean volume	0.308	0.156	0.462
Covariance: Mean volume and LD_{50}	0.030	-0.040	0.118
Variance: LD_{50}	0.055	0.001	0.170

TABLE 4.2: Volume in average volume.

<i>Fixed Terms</i>	<i>Estimate</i>	<i>Lower CI</i>	<i>Higher CI</i>
Intercept	0.200	-0.161	0.567
Body Mass	0.510	0.442	0.564
Inoculation Route			
Intravenous (IV)	-0.011	-0.052	0.030
Intrapulmonary (IP)	-0.010	-0.052	0.030
Intramuscular (IM)	-0.009	-0.056	0.042
Dimension 3D	-0.829	-1.286	-0.396
Eggs in diet	-0.741	-1.325	-0.206
Phylogenetic disparity of diet to model	-0.003	-0.029	0.019

TABLE 4.3: Id50 in average volume model

<i>Fixed Terms</i>	<i>Estimate</i>	<i>Lower CI</i>	<i>Higher CI</i>
Intercept	0.200	-0.161	0.567
Body Mass	0.134	0.016	0.262
Inoculation Route			
Intravenous (IV)	-0.624	-0.842	-0.435
Intrapulmonary (IP)	-0.537	-0.746	-0.309
Intramuscular (IM)	-0.228	-0.455	0.049
Dimension 3D	-0.202	-0.670	0.243
Eggs in diet	0.457	-0.187	1.065
Phylogenetic disparity of diet to model	0.360	0.248	0.463

TABLE 4.4: Correlation structure on random terms in maximum venom

<i>Terms</i>	<i>Estimate</i>	<i>Lower CI</i>	<i>Higher CI</i>
Phylogeny			
Variance: Maximum volume	0.500	0.156	0.960
Covariance: Maximum volume and LD ₅₀	0.156	-0.181	0.496
Variance: LD ₅₀	0.901	0.349	1.477
Residuals			
Variance: Maximum volume	0.003	0.002	0.004
Covariance: Maximum volume and LD ₅₀	0.006	0.001	0.012
Variance: LD ₅₀	0.275	0.001	0.361
Species			
Variance: Maximum volume	0.230	0.103	0.373
Covariance: Maximum volume and LD ₅₀	-0.036	-0.141	0.052
Variance: LD ₅₀	0.061	0.001	0.188

TABLE 4.5: Volume in Maximum volume.

<i>Fixed Terms</i>	<i>Estimate</i>	<i>Lower CI</i>	<i>Higher CI</i>
Intercept	0.043	-0.339	0.379
Body Mass	0.757	0.708	0.797
Inoculation Route			
Intravenous (IV)	-0.006	-0.031	0.019
Intrapulmonary (IP)	0.008	-0.019	0.037
Intramuscular (IM)	0.003	-0.037	0.047
Dimension 3D	-1.212	-1.638	-0.763
Eggs in diet	-0.564	-1.219	0.063
Phylogenetic disparity of diet to model	-0.001	-0.032	0.033

TABLE 4.6: ld50 in maximum volume model

<i>Fixed Terms</i>	<i>Estimate</i>	<i>Lower CI</i>	<i>Higher CI</i>
Intercept	0.043	-0.339	0.379
Body Mass	0.145	-0.018	0.305
Inoculation Route			
Intravenous (IV)	-0.656	-0.892	-0.440
Intrapulmonary (IP)	-0.561	-0.804	-0.326
Intramuscular (IM)	-0.191	-0.531	0.152
Dimension 3D	0.240	-0.300	0.836
Eggs in diet	0.705	0.076	1.510
Phylogenetic disparity of diet to model	0.251	0.080	0.436

4.5 DISCUSSION

These results show that, after controlling for body size and phylogeny, the evolution of venom in snakes is linked to their habitat, prey and the costs associated with producing large amounts of venom. In particular the atrophy of venom seen across venomous snakes is shown to be linked with arboreal and aquatic lifestyles, through a reduction of venom volumes, and, in the case of maximum venom volume, transitions to a diet of eggs. This is likely due to the costs of producing venom (Pintor et al., 2010) outweighing the benefits of producing and maintaining large amount of venom in species in higher dimensions.

One of the drivers behind such as reduced benefit of venom production for species in three dimensional environments may be the expected increased probability of encountering prey items in such environments (Pawar et al., 2012). This would result in species being under less selection pressures to maintain the larger reservoirs of venom required to respond to the rarer event of encountering a prey

item in low dimensional environment. The biomechanical limitations of arboreal lifestyles is also suggested to leading to faster digestion rates in these species (Lillywhite et al., 2002), which in turn may lead to smaller venom volumes which would facilitate faster venom replenishment rates. The limitations affecting predators in these environments would also restricts prey body size in arboreal species. Likewise marine snakes are also known to feed disproportionately on smaller fish than expected (Voris and Moffett, 1981). Since some species are known to meter venom depending on prey size (HAYES, 1995), it may be the size distribution of prey available in these habitats that influences the evolution of venom volume. Hence although the patterns of venom volumes are clearly related to a snakes habitat a snakes prey may be still be the main driver of these differences.

While the pattern of associating within these habitats is clear another explanation to this association between small venom volumes and high dimensionality is that prey items in such environments are smaller. Arboreal environment are extremely selective with regards to size meaning such snakes species are likely to encounter smaller prey items more often than expected than in terrestrial environments. Aquatic snakes are also known for selecting smaller prey items. Data on prey size is hence likely to further the understanding of venom evolution along with the insights of the importance of prey identity.

The nature of a snakes diet was also found to affect venom toxicity and to a lesser extent venom volume. Species with even small proportions of eggs in their diets show both reduced maximum venom volumes and lower venom toxicities. This is unsurprising as the benefits of venom to an oviparous diet are likely to be low (Li et al., 2005). This atrophy in oviparous snakes also reaffirms the primary foraging function of venom with any digestive (Rodríguez-Robles and Thomas, 1992) or defensive functions (Jansa and Voss, 2011) being secondary benefits. However these results should be interpreted with caution due to the low number oviparous species within the analysis (eight with only four having greater than 20% in their diet) with further data required to fully gauge the evolutionary role of egg eating in snakes. Apart from the reduction of the venom apparatus in species which show a shift from carnivory to oviparity (Li et al., 2005), these results also show that snake venom toxicity is prey-specific. While prey specificity has been shown within particular groups of snakes (Barlow et al., 2009,?; Richards et al., 2012) this is the first study to show venom prey specificity across all venomous snakes. This result of increased toxicity with reduced phylogenetic distance between diet LD₅₀ model

suggests that while there are several cases of prey species developing resistance to venom (Lillywhite et al., 2002), snakes in general are "ahead" in the arms race between prey venom resistance and predator venom toxicity.

While these results further demonstrate the arms race venom evolution is locked within they also surprisingly show no evidence of co-evolution between venom volume and venom toxicity evolution. It would be expected that species with low toxicities may evolve compensatory mechanisms such as increased venom volumes to allow them to overcome prey resistance. While the historical lack of appropriate model species for calculating LD₅₀ may account for the underestimation of toxicity levels in some species, even after accounting for such species mismatching here there is no evidence of a correlation between these two aspects of venom functionality. This lack of compensatory evolution may instead be explained by changes in behaviour with species with low toxicities combining the use of venom along with prey holding or constriction in order to incapacitate prey Shine and Schwaner (1985).

While volume and LD₅₀ show no co-variance both traits do show strong phylogenetic effects suggesting evolutionary constraints also partially explain the variation in venom lethality and volume across snakes. As expected, LD₅₀ evolution shows a higher constraint in comparison to venom volume evolution. This is likely to be a reflection of the requirement for major genetic changes, such as gene duplication events, in order to increase venom toxicity (Vonk et al., 2013). While venom volume shows less phylogenetic autocorrelation the physiological requirements necessary to house large volumes of venom is likely to be the main limitation in many rear fanged groups. However many rear fanged snakes such as species of mamba can contain venom volumes similar to that of many front fanged species.

Overall this study shows that across venomous snakes ecological factors associated with predator-prey interactions drive the evolution of venom. While further studies are required to understand the complex nature of predatory trait evolution these results show that fundamental aspects of predator-prey interactions including size, habitat dimensionality and evolutionary constraints can help understand one of the most medically important and iconic predatory traits, venom.

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CHAPTER 5

DISCUSSION

5.1 CONSIDERING DIMENSIONS

One of the central goals in ecology and evolution is to understand the complexity of the biological world. There has been several approaches towards simplifying this complexity including the top down approaches of the metabolic theory of ecology (Brown et al., 2004), the bottom up approach of dynamic energy budget theory (Kooijman, 2009) and the entropy based approach of MaxEnt (Harte et al., 2008). However whatever the approach the physics of our world must be included in order for such models to accurately reflect the reality of nature.

Here I have attempted here to make the case for the further inclusion of perhaps one of the most fundamental elements of physical reality, its dimensions. While all life is embedded within the three spatial and one temporal dimension of the universe, how species exploit or interact within these dimensions can determine the nature of many biological interactions. This is reflected in the results of the above analysis which demonstrate the important influence of the ability of a species to exploit these dimensions which can in turn define these interactions.

While this thesis focuses on how traits associated with predator-prey interactions (spotting, escaping or capturing) are affected by environment dimensionality, these effects are likely to hold important consequences for larger ecological systems in particular through the the strong influence of predator-prey interacts. For example trophic interaction strengths have important influences on ecosystem stability hence systems large bony size ranges are (read up on this a bit more).

While these factors are likely to be important across biological systems many of the questions outlined within this thesis were restricted by limitations in data availability. While large data sources of data related to MET are now available other data relating to fundamental aspects of ecology are still in the early stages accumulation. For example data on species behaviour, diets, sensory capabilities and other morphologocal traits are still often defined in relatively reductionist ways.

Even considering this restriction phylogenetic comparative methods are only likley to . These limitations highlight the large body of reserch to be done in this area of ecology pointing towards a field with good future prospects.

5.2 FUTURE DIRECTIONS

This thesis focused mainly detecting patterns of variation realted to differences in habitat structure. Taking these findings further will require the use of more refined data or other thecnuiques.

One particular useful approach to understand sensory perception is the use of neural netwrk models, perhaps robots etc.

Future direction in the life-history work would likley incude understanding the role of fossorial and the abilty t escape in multiple directions. Here neural network models coupled with agent based approaches may be useful in particular to understand the important of spatial dimensioanlity to the abilty to escape. Further comparitive analyiss would also help in other groups including fossoirailaty in reptiles and other ectoderms. Other data that incudes moreof the complexity of life history may also resolve some of the difficulties in longevity. Such data as the Compdra may help in this in partiuclr in coupling thertical models of aging with different distrubutions of mortality acorss species life-histories.

The analysis presented on the evolution of venom in snakes represents an initail atempt of understanign the ecology of venom evoution on a large scale. Despite the realltive pacuity of data there are clear results. ANother apporach is to use larger evolution binary model or something.

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APPENDIX A

SUPPLEMENTARY INFORMATION TO CHAPTER 2

A.1 PHYLOGENY RECONSTRUCTION

Divergence times and phylogenies from the literature were used to produce a composite phylogeny of the vertebrate species used in our analyses (Figure 2.2). For species with no available divergence dates based on molecular data or available published trees, conservatively estimated first appearance dates from the Paleobiology database (PBDB) were used as an estimate of divergence time (Alroy et al., 2008). Divergence dates for the major groups Batoidea, Actinopterygii and Amphibia were taken from the TimeTree database (Hedges et al., 2006). For divergence dates of Carcharhinus and Sphyna Lim et al. (2010) was used, while the divergence time between *Negaprion brevirostris* and *Carcharchinus acronotus* was estimated based on the first appearance in the fossil record of *Negaprion brevirostris*, the younger of the two species (*Negaprion* spp - 40.3mya, *Carcharchinus* - 46.2). Li et al. (2008) were used to infer phylogenetic relationships and divergence times in Actinopterygii, and Little et al. (2010) was used for perciform divergence times. For divergence time between anapsids (turtles and birds) and suarapids (Squamata and Sphenodon) the estimation from Benton and Donoghue (2007) was used while Perelman et al. (2011) was used for the divergence and phylogenetic relationships among Squamata, Sphenodon, turtles and Aves. For divergence times within the Squamata Wiens et al. (2006) was used, while for turtle species I used Naro-Maciel et al. (2008). I used Brown et al. (2008) for the Aves phylogeny with divergence times between *Asio flammeus* and *Bubo virginianus* estimated using an estimate of the first appearance (Jánossy, 2011). (Murphy et al., 2007) was used for divergence dates of mammalian orders, while for primates I used Perelman et al. (2011). Rodent divergence times were taken from Murphy et al. (2007).

A.2 SENSITIVITY ANALYSES

A series of sensitivity analyses was performed to test if the results of the main analysis were affected by (1) the temperature that ectoderm species metabolic rates were corrected to, (2) the inclusion of brain mass as a control for information processing abilities and (3) the quality of the data used in the analysis.

A.2.1 *Ectotherm temperature sensitivity*

I used Q10 values, the fold change in metabolic rate over a temperature change of 10°C, as defined for each of the major groups (i.e. reptilian, amphibian etc; See Methods in main text) to correct ectotherm mass specific metabolism (qWg) over a temperature range of 5°C to 35°C. This analysis was performed by re-running the main analysis with qWg corrected to 5°C and then corrected to 35°C. The resulting set of models and the terms which they included are given in Tables S2 and S3. In both analyses the model with the lowest AIC includes the same terms as found in the main analysis, i.e., body mass (Mg), temperature corrected mass-specific resting metabolic rate (qWg) and light levels, with qualitatively the same significant affects (Tables S6 and S7).

TABLE A.1: Coefficients of the model with all factors included. Mg = body mass (grams), qWg = Temperature corrected mass-specific resting metabolic rate $Wg-1$, Light.l (low) = effect of low light levels on CFF in comparison to high light levels, exp = effect of experimental type (ERG = electroretinogram) in comparison to behavior based CFF measures.

Variable	Estimate	S.E	t-value	P-value
Intercept	141.48	15.15	9.34	4^{-10}
Mg	-4.40	2.01	-2.18	0.038
qWg	16.89	4.31	3.92	5^{-4}
Light levels (low)	-37.74	5.94	-6.36	7^{-7}
Measurement type (exp)	-3.66	6.24	-0.59	0.56
Data quality (high)	-3.86	6.14	-0.63	0.53
Lambda (Low)	Mode 0	Lower 95% C.I 0	Upper 95% C.I 0.34	$R^2 = 0.69$

A.2.2 *Brain Mass analysis*

As the amount of sensory tissue available to an organism may aid in its ability to perceive and process information, brain mass values, measured as wet weight

TABLE A.2: Coefficients of the model with all factors included. Mg = body mass (grams), qWg = Temperature corrected mass-specific resting metabolic rate Wg-1, Light.l (low) = effect of low light levels on CFF in comparison to high light levels, exp = effect of experimental type (ERG = electroretinogram) in comparison to behavior based CFF measures.

<i>Variable</i>	<i>Estimate</i>	<i>S.E</i>	<i>t-value</i>	<i>P-value</i>
Intercept	141.48	15.15	9.34	4^{-10}
Mg	-4.40	2.01	-2.18	0.038
qWg	16.89	4.31	3.92	5^{-4}
Light levels (low)	-37.74	5.94	-6.36	7^{-7}
Measurement type (exp)	-3.66	6.24	-0.59	0.56
Data quality (high)	-3.86	6.14	-0.63	0.53
Lambda (Low)	Mode 0	Lower 95% C.I. 0	Upper 95% C.I. 0.34	$R^2 = 0.69$

(g), were taken from the literature (Table 1, Methods). As data on brain mass was available for only a subset of twenty-eight species, the term brain mass was included along with the terms used in the main analysis (light levels, qWg, experimental design and body mass) in a series of models performed on the restricted data set (Table S4). While a similar trend to the first analysis was found, a positive effect of mass specific resting metabolic rate () and negative effects of low light levels () and body mass (), brain mass was found to have no significant effect on CFF levels ().

TABLE A.3: Coefficients of the model with all factors included. Mg = body mass (grams), qWg = Temperature corrected mass-specific resting metabolic rate Wg-1, Light.l (low) = effect of low light levels on CFF in comparison to high light levels, exp = effect of experimental type (ERG = electroretinogram) in comparison to behavior based CFF measures.

<i>Variable</i>	<i>Estimate</i>	<i>S.E</i>	<i>t-value</i>	<i>P-value</i>
Intercept	141.48	15.15	9.34	4^{-10}
Mg	-4.40	2.01	-2.18	0.038
qWg	16.89	4.31	3.92	5^{-4}
Light levels (low)	-37.74	5.94	-6.36	7^{-7}
Measurement type (exp)	-3.66	6.24	-0.59	0.56
Data quality (high)	-3.86	6.14	-0.63	0.53
Lambda (Low)	Mode 0	Lower 95% C.I. 0	Upper 95% C.I. 0.34	$R^2 = 0.69$

APPENDIX B

SUPPLEMENTARY INFORMATION TO CHAPTER 3

B.1 ADDITIONAL DETAILS OF DATA COLLECTION AND SOURCES

B.1.1 *Flight capability*

Species were categorised as either volant, non-volant or gliders. Most birds, apart from ratites, penguins and some flightless rails, are volant. All mammals apart from bats are non-volant. We classed mammals as gliders if they regularly use gliding as a means of locomotion and have adaptations that aid their descent e.g., skin flaps.

B.1.2 *Activity period*

Most animals will be active to some extent at both day and night. Therefore activity period was define using the times when a species is feeding/foraging as this is when they are most likely to be exposed to predation. For example, many bats often fly around their roosts during the day but only leave their roosts to feed at night; therefore such species are classed as nocturnal. We defined species as diurnal, nocturnal, crepuscular or cathemeral by looking for the following key phrases in the literature:

- **Diurnal:** diurnal, active in the day, mainly/predominantly/mostly/generally diurnal or active in the day, crepuscular and diurnal or active in the day, diurnal or active in the day and sometimes/occasionally/infrequently/rarely diurnal or active in the day.
- **Nocturnal:** nocturnal, active at night, mainly/predominantly/mostly/generally nocturnal or active at night, crepuscular and nocturnal or active at night, nocturnal or active at night and sometimes/occasionally/infrequently/rarely diurnal or active in the day.
- **Crepuscular:** crepuscular, active at dusk and dawn, active early morning and evening (not afternoon). Note that crepuscular and diurnal animals are classed as diurnal; crepuscular and nocturnal animals are classed as nocturnal

- **Cathemeral:** cathemeral, diurnal and nocturnal, active any time of the day or night, nocturnal and often/frequently diurnal or active in the day, diurnal and often/frequently nocturnal or active at night.

In cases where none of the above keywords were present activity pattern was also defined if all other alternatives could be ruled out, for example species with roosting behaviour described as beginning before sunset and ending only after sunrise can be described as diurnal as it excludes nocturnal, cathemeral and crepuscular daily activity feeding patterns.

B.1.3 *Foraging environment*

Foraging environments were defined as terrestrial, semi-arboreal, arboreal, aerial or aquatic, by looking for the following key phrases in the literature:

- **Terrestrial:** terrestrial, feeds at ground-level (including rocky areas), mainly/predominantly feeds at ground-level, feeds at ground-level and sometimes/occasionally/infrequently/rarely feeds above ground-level.
- **Arboreal:** arboreal, feeds at above ground-level (including trees), mainly/predominantly/feeds at ground-level, feeds at ground-level and sometimes/occasionally/infrequently/rarely feeds above ground-level.
- **Semi-arboreal:** semi-arboreal, semi-terrestrial, feeds at above ground-level and at ground-level, feeds at ground-level and often/frequently feeds at above ground-level, feeds at above ground-level and often/frequently feeds at ground-level.
- **Aerial:** volant, feeds while flying, mainly/predominantly/mostly/generally aerial forager, aerial forager and sometimes/occasionally/infrequently/rarely feeds at ground-level or above ground-level. Includes insectivorous bats and birds.
- **Aquatic:** aquatic, feeds in water, mainly/predominantly/mostly/generally feeds in water, feeds in water and sometimes/occasionally/infrequently/rarely feeds at ground-level or above ground-level. Includes marine birds, ducks, seals and otters. If feeds in both terrestrial and aquatic environments counted as terrestrial.

B.1.4 *Fossoriality*

Species were defined as either fossorial, non-fossorial or semi-fossorial by looking for the following key phrases in the literature:

- **Fossorial:** fossorial, lives in burrows and rarely leaves them, mainly/predominantly/mostly/generally fossorial, fossorial and sometimes/occasionally/infrequently active above ground.
- **Non-fossorial:** non-fossorial, terrestrial, mainly/predominantly/mostly/generally terrestrial or non-fossorial, terrestrial or non-fossorial and sometimes/occasionally/infrequently burrows, may excavate shallow scrapes but nothing useful for predator defense, incapable of excavating burrows.
- **Semi-fossorial:** semi-fossorial, lives in burrows and leaves them frequently, fossorial and often/frequently active above ground, non-fossorial and often/frequently uses burrows, capable of excavating burrows.

B.1.5 *Chronogram calibration diagnosis*

Following the recommendations of Parham et al. (2011), our chronogram calibration used the following fossil:

Taxa: *Archerpeton anthracos*

Holotype: RM 12056

Author: Carroll 1964

Phylogeny: (Reisz and Müller, 2004)

Epoch: Westphalian A (Canada Nova Scotia)

Age: 318.1 - 314.6 Myr

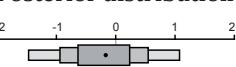
Dating: International Commission on Stratigraphy 2009

B.2 SUPPLEMENTARY TABLES

TABLE B.1: Breakdown of numbers of species in each category included in the analyses. Values under the Sample column represent the number of species with 100 or more available longevity studies. Values under the BMR column represent the number of species with available basal metabolic rate (BMR) data.

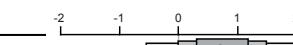
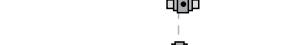
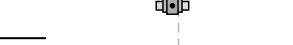
Category*		Volant			Non-volant			Total		
		Full	Sample	BMR	Full	Sample	BMR	Full	Sample	BMR
Foraging environment	-Terrestrial	235	199	58	494	257	223	729	456	281
	-Arboreal	120	83	12	115	61	35	235	144	47
	-Semi-Arboreal	96	72	23	76	44	36	172	116	59
	-Aerial	111	92	35	NA	NA	0	111	92	35
	-Aquatic	105	90	19	16	11	6	121	101	25
Activity pattern	-Diurnal	451	361	84	206	139	62	657	500	146
	-Nocturnal	117	95	44	335	133	163	452	228	207
	-Cathemeral	78	65	15	115	70	58	193	135	73
Fossoriality	-Fossorial	0	0	0	10	5	7	10	5	7
	-Semi-fossorial	10	9	3	209	77	131	219	86	134
	-Non-fossorial	652	527	144	487	291	162	1139	818	306
Total		662	536	147	706	373	300	1368	909	447

TABLE B.2: Table B2: Relationship between maximum longevity (years), body mass (g) and flight capability (volant or non-volant) in 909 species of birds and mammals with over 100 maximum lifespan records.

Fixed Terms	Estimate (β)	Lower CI	Upper CI	Posterior distribution
Intercept	-0.194	-1.466	1.079	
Body Mass	0.551	0.444	0.658	
Flight capability - Volant	0.855	0.316	1.401	
Body Mass: Flight capability	0.477	0.305	0.652	
<hr/>				
Random Terms				
Residual variance	0.130	0.107	0.156	
Phylogenetic variance	1.222	0.934	1.598	

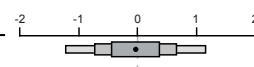
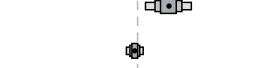
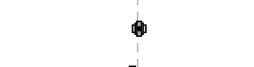
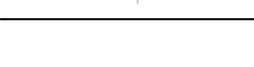
Notes: 18000000 iterations with 3000000 burnin and thinning interval of 75000.

TABLE B.3: Table B3: Relationship between maximum longevity (years), body mass (g), foraging environment and activity period, in 536 species of volant birds and mammals with over 100 samples of longevity.

Fixed Terms		Estimate (β)	Lower CI	Upper CI	Posterior distribution
Intercept		0.749	-0.549	2.040	
Body Mass		1.039	0.891	1.187	
Foraging environment	- Aerial	0.073	-0.197	0.242	
	- Arboreal	0.017	-0.203	0.234	
	- Semi-arboreal	0.125	-0.087	0.329	
	- Aquatic	-0.188	-0.422	0.037	
Activity period	- Cathemeral	0.152	-0.043	0.346	
	- Crepuscular	-0.502	-0.811	-0.194	
	- Nocturnal	-0.100	-0.380	0.172	
Random Terms					
Residual variance		0.202	0.163	0.249	
Phylogenetic variance		1.046	0.677	1.612	

Notes: 12000000 iterations with 2000000 burnin and thinning interval of 5000.

TABLE B.4: Table B4: Relationship between maximum longevity (years), body mass (g), foraging environment, fossoriality and activity period, in 373 species of nonvolant birds and mammals with over 100 samples of longevity.

Fixed Terms		Estimate (β)	Lower CI	Upper CI	Posterior distribution
Intercept		-0.045	-1.222	1.158	
Body Mass		0.542	0.455	0.629	
Foraging environment	- Arboreal	0.293	0.117	0.468	
	- Semi-arboreal	0.125	-0.015	0.265	
	- Aquatic	0.081	-0.209	0.376	
Fossoriality	- Fossorial	-0.522	0.134	0.915	
	- Semi-fossorial	-0.048	-0.190	0.095	
Activity period	- Cathemeral	0.028	-0.086	0.141	
	- Crepuscular	-0.087	-0.231	0.057	
	- Nocturnal	0.116	-0.004	0.237	
<hr/>					
Random Terms					
Residual variance		0.036	0.025	0.051	
Phylogenetic variance		1.040	0.792	1.366	

Notes: 18000000 iterations with 3000000 burnin and thinning interval of 7500.

TABLE B.5: Relationship between maximum longevity (years), body mass (g), foraging environment and activity period in 589 birds.

Fixed Terms	Estimate (β)	Lower CI	Upper CI	Posterior distribution
Intercept	0.192	-0.353	0.676	
Body Mass	1.025	0.889	1.164	
Foraging environment	- Aerial	0.017	-0.258	
	- Arboreal	0.040	-0.151	
	- Semi-arboreal	0.100	-0.075	
	- Aquatic	-0.110	-0.329	
Activity period	- Cathemeral	0.100	-0.714	
	- Crepuscular	-0.444	-0.749	
	- Nocturnal	-0.077	-0.330	
<hr/>				
Random Terms				
Residual variance	0.181	0.147	0.222	
Phylogenetic variance	0.371	0.245	0.579	

Notes: 18000000 iterations with 3000000 burnin and thinning interval of 7500.

TABLE B.6: Relationship between maximum longevity (years), body mass (g), foraging environment, fossoriality, and activity period 779 mammals..

Fixed Terms		Estimate (β)	Lower CI	Upper CI	Posterior distribution
Intercept		-0.248	-1.166	0.666	
Body Mass		0.540	0.458	0.623	
Foraging environment	- Aerial	0.411	0.085	0.740	
	- Arboreal	0.233	0.084	0.381	
	- Semi arboreal	0.151	0.019	0.285	
	- Aquatic	-0.067	-0.347	0.209	
Fossoriality	- Fossorial	0.423	0.054	0.789	
	- Semi-fossorial	0.022	-0.099	0.144	
Activity period	- Cathemeral	0.051	-0.071	0.175	
	- Crepuscular	-0.063	-0.217	0.090	
	- Nocturnal	0.029	-0.092	0.151	
Random Terms					
Residual variance		0.051	0.038	0.071	
Phylogenetic variance		0.936	0.753	1.146	

Notes: 18000000 iterations with 3000000 burnin and thinning interval of 7500.