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Why big brains? A comparison of models for both primate and carnivore brain size evolution --Manuscript Draft--

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Full Title:	Why big brains? A comparison of models for both primate and carnivore brain size evolution
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Keywords:	Brain size; primates; carnivores; sociality; diet; encephalisation
Abstract:	<p>Despite decades of research, much uncertainty remains regarding the selection pressures responsible for brain size variation. Whilst the influential social brain hypothesis once garnered extensive support, more recent studies have failed to find support for a link between brain size and sociality. Instead, it appears there is now substantial evidence suggesting ecology better predicts brain size in both primates and carnivores. Here, different models of brain evolution were tested, and the relative importance of social, ecological, and life-history traits were assessed on both overall encephalisation and specific brain regions. In primates, evidence is found for consistent associations between brain size and ecological factors, particularly diet; however, evidence was also found advocating sociality as a selection pressure driving brain size. In carnivores, evidence suggests ecological variables, most notably home range size, are influencing brain size; whereas, no support is found for the social brain hypothesis, perhaps reflecting the fact sociality appears to be limited to a select few taxa. Life-history associations reveal complex selection mechanisms to be counterbalancing the costs associated with expensive brain tissue through extended developmental periods, reduced fertility, and extended maximum lifespan. Future studies should give careful consideration of the methods chosen for measuring brain size, investigate both whole brain and specific brain regions where possible, and look to integrate multiple variables, thus fully capturing all of the potential factors influencing brain size.</p>
Order of Authors:	Helen Rebecca Chambers Sandra Andrea Heldstab Sean J O'Hara
Response to Reviewers:	<p>Reviewer #1</p> <p>1) I am not sure why this manuscript deals with just primates and carnivores. Why these two orders of mammals? Why not other orders such as rodents, lagomorphs, shrews, and bats? In fact, there are plenty of extensive datasets for these (and other) orders. For example, see Mace et al (1981) J. Zool. 193:333-354, which presents brain size data for 261 species of terrestrial small mammals, and Hutcheon et al. (2002) Brain Behavior Evolution 60:165-180 for 63 species of bats. I would have thought that a comparative approach across the entire class Mammalia would have been more fruitful than simply presenting data on primates and (incongruously) carnivores. The authors make no attempt to justify their selection of mammalian orders.</p> <p>Whilst we understand that brain data are available for more species than which were included within the manuscript, we wanted to run analyses on a complete dataset with all covariates available for all species, as this enabled more robust analyses, especially when conducting model comparisons. We could access all the required covariates for primates and carnivores, which governed our choice. In addition, in efforts to address the current confusion within the field regarding the proposed selection pressures responsible for increased brain size, we chose to use both primate and carnivore data as these two groups have received considerable attention, and thus by drawing clarity</p>

within these two groups, further groups can be studied using more appropriate methods/procedures. We have added wording to emphasise our reasoning for this choice.

2) The literature cited is not representative of the field. A good deal of previous work has been omitted from this ms, including the two papers mentioned in (1) above, as well as Harvey et al. (1980) PNAS 77:4387-4389 (this paper explicitly deals with primate brain sizes). And there are many more papers that deal with ecological correlates of brain sizes that have not been mentioned.

Additional citations have been added.

3) Although the manuscript is generally well written, there are some sections that are difficult to interpret and/or to follow. This is particularly true for the Methods section, which is often ambiguous or at least incomplete. See below for where more detail is needed.

Wording has been rephrased for added clarity.

4) There is no definition of what is meant by the different brain volumes that are presented in the ms. For example, how was "endocranial brain volume" measured? And was it measured in the same way in the different papers where this information was extracted and collated? If not, then how can we be sure that we are comparing like with like?

5) The same comment applies to "neocortex" and "cerebellum" volumes.

Definitions have been added for endocranial and regional brain volumes. When sourcing all whole and regional brain volumes these measurement methods were considered to ensure the data was comparable. In terms of the ECV data, sources were checked for comparability and common measurement techniques were found between studies. We further tried to minimise the risk of this problem by sourcing data from whole datasets e.g., DeCasien et al., 2019 where the information has been weighted to account for multiple methods. However, this was more difficult with the carnivore data where regional brain volume data was tricky to source.

6) Again, how was social cohesion measured? I can see that it was scored on a point system of 1 to 4, but what does it mean for a species to have a social cohesion of 1? or 2? etc.

Definition revised for greater clarity.

7) I found the ecological data simplistic and not at all credible. The authors will need to justify exactly what they mean by each of the ecological variables. And then, they will need to convince the reader that the ecological data are actually meaningful. I am happy to include "diet" (although "frugivore" or "omnivore" are diet categories rather than strictly speaking diet itself (and the authors actually refer to diet categories, but they don't explicitly make the distinction). But what do they mean by diet breadth? According to their definition it is: "dietary breadth was also used, estimated using the total number of food sources used by a species". But what are these "food sources"? Are they the number of species of plants/animals taken? If so, an insectivorous species will by definition have a wider breadth than a carnivorous one (because there are more species of insects than vertebrates). If "sources" refers to something else, then what is it? And then, once the definition has been clearly stated, how can we be sure that the different studies have scored "number of food sources" in the same way?

Definitions of dietary categories and dietary breadth revised for greater clarity. All dietary breadth data was taken from one source: Wilman et al., (2014) and is referred to in the manuscript.

8) I have even more issue with the number of habitats used by a species. Wider ranging species will use a greater number of habitats, so why didn't the authors correct for this? Or simply use distributional range size instead of number of habitats?

Whilst we understand and appreciate this point, it does not always follow that wider ranging species will always use a greater number of habitats. One species may have a large home range size but may only move within the same habitat type. What we instead aim to look at here is whether the type of habitat matters, thus, do species which navigate and confront multiple habitat types, have larger brains than those which only move within one or two habitat types? Or vice versa? We also use home range size to proxy habitat use.

9) The authors do not mention where they get their home range sizes from in the ms (although these are clearly mentioned in the supplementary material). I find it hard to believe that the various range sizes compiled by numerous authors will be directly comparable due to differences in techniques used to estimate home range. Furthermore, there is enormous amount of variation in home range size, which is partly (and only partly) attributable to sex and age. Using a single metric is hardly informative or convincing.

We did not want to mention the citations specifically within the manuscript due to the high number of citations. We agree with this point about transferability of the methods used to measure home range size. We did our best to reduce the number of sources due to this problem, however, due to limited data availability, the only way to retrieve home range size for all species was to use data from multiple studies. To minimise the issue highlighted, we chose to use hectares to measure home range size as this was the most prevalent method found. We converted all home range data collected to this metric. We agree a single metric is not always useful, which is why we used both habitat variability and home range size to proxy habitat use.

10) Statistical analysis. This entire section (lines 218 to 239) needs to be reworked and more detail provided. And unambiguous statements rephrased. I will make just a few examples (but these are not the only problems).

Wording has been rephrased for clarity.

11) Lines 219-220 "using residuals from a regression line". Regression of what on what? And exactly using what regression? Simple linear regression e.g. $lm()$? On log transformed or untransformed data?

Phrase removed as this aspect has been moved to supplementary methods. This regression analysis is discussed in full within that document... "Phylogenetic generalised least-squares regression analysis (PGLS) was used to regress log brain volume against log body mass".

12) What is the encephalisation quotient and how was it calculated? In fact, the equation is presented a bit further down, so perhaps the authors just need to refer to this e.g. say something like "see below for equation".

Definition revised for greater clarity. This aspect – as mentioned above – has been moved to the supplementary methods.

13) Line 220. "The former method is often preferred...". But you can't use "former" when there are three methods presented. "Former" and "latter" can only be used when comparing two things.

Thank you for highlighting. Phrase removed.

14) Line 226. "...therefore we considered it prudent to use both methods in the analyses...". Which two methods are being referred to? Because the authors have mentioned three methods (which have even been numbered).

Phrase removed.

15) Please provide a basic description of "Phylogenetic generalised least-squares regression analysis" and how it differs from typical GLMs.

Definition revised to provide greater clarity.

16) VIF was used to check for collinearity (which is good). But what does it mean "almost all scores" were below 5. Which variables were autocorrelated? And were any removed from the analyses, as a result of this?

Almost all VIF scores produced were below 5, however there were a few outliers. For example, body mass and weaning age produced scores of 7.25 and 5.93, when inputted into the primate endocranial model. Whilst moderately high, we chose to retain all variables within the statistical models, as the scores were only found in a few models and were still considerably low. Thus, no variables were removed from the analyses. VIF scores were also checked when rerunning analyses, specifically when using the 'rest of brain' regional volume technique, with no scores produced of concern.

This sentence has been updated to provide greater clarity.

17) Possible limitations. I find this paragraph difficult to accept. The authors are well aware that any models with AICs within 2 points are not "statistically different". Then how can they justify their approach? To me, this is the weakest aspect of the ms, because it affects all of their interpretations. There must be better ways of dealing with this. For example, list all competing models, and then count the number of times a particular variable (e.g. social cohesion) appears in the top models? This may make the results much more difficult to interpret, but this may be because there really is no simple and easy answer to the question that they are asking. Simplifying a complex problem with incorrect statistics is not acceptable.

We appreciate this comment. We agree this was a weak point in the analyses. To address this highlighted shortcoming, rather than just choosing the model with the absolute lowest score, we have now adopted the approach of presenting and discussing the results of all the 'best fit' models, which usually included a subset of models (simply, all the models within 2 points of the absolute lowest model). We have also rerun the analysis using BIC rather than AIC, in acknowledgement of this scoring system being more conservative.

Reviewer #2

•Line 33: See my comment in the Discussion section on the use of "counterbalancing".

Wording rephrased.

•There is a critical part currently missing this section, which is an explicit discussion of how this study is different from the many previous analyses of brain ~ socioecology relationships (e.g., inclusion of more variables, updated phylogeny, higher individual/species sample sizes)?

Thank you for this comment, we agree this was lacking in the manuscript. Introduction has been updated with this discussion.

•Line 75: The importance of pair-bondedness to brain size evolution was also discussed in other papers, which should be cited here (Schillaci 2006, 2008; MacLean et al. 2009).

•Line 83: This reference is only for carnivores – please add a reference for primates.

Citations added.

•Paragraph starting with Line 90:

ol think a discussion of issues with relative brain size measures is important, however, I don't think it warrants using measures that have been previously established as inappropriate (i.e., residuals, EQ).

•Lines 141-144: Again, it is unnecessary to include analyses using EQ or brain size residuals.

•Lines 218-220: Again, it is unnecessary to include analyses using EQ or brain size residuals.

•Paragraph starting with Line 467: As previously mentioned, previous studies have demonstrated that the use of EQ or residuals is inappropriate, so I think this paragraph and the relevant results are unnecessary and make the overall findings harder to

follow.

We appreciate that these methods have previously been suggested to be inappropriate for measuring the relationship between brain size and body mass. We feel it is necessary to further address this problem, however, especially considering we are using updated data, updated statistical analysis, more variables and an updated phylogenetic tree. After considering this point, we decided to move the results produced using the methods of concern (i.e., residuals, EQ) to the supplementary material and these will no longer be discussed in the main manuscript. This moves the focus away from those methods, but still allows the comparison between methods which may be useful to some readers.

oThe findings from the most recent study on brain ~ body size evolution (Smears et al. 2021) should be considered/discussed here.

oFreckleton's (2009) "seven deadly sins of comparative analysis" should be mentioned here, as it includes a discussion on why it is inappropriate to use residuals as outcome variables in regression models.

oLines 105-107 – Papers on lag between primate brain and body size should be mentioned here (e.g., Deaner and Nunn 1999).

Thank you. Citations added.

oLine 108: It is unclear what "over statistically controlled methods" means here.

Wording rephrased.

oLine 109: How and why does van Schaik et al. (2021) specifically demonstrate that EQ is inappropriate? The authors should elaborate a bit here.

Some elaboration has been added, as recommended.

•Paragraph starting with Line 111:

oHow would social and ecological variables specifically relate to neocortical and cerebellar functions?

•Increased brain size is the result of selection on specific abilities and related neural systems. Accordingly, at some point in this Introduction, I would appreciate a brief but explicit discussion of this (e.g., why might frugivory require greater visual information processing? Given that a large proportion of the brain is neocortex, and a large proportion of the neocortex is comprised of visual information processing areas, might this explain the link between something like frugivory and overall brain size?)

These points are now discussed.

oI think it would be appropriate to discuss Powell et al. (2019) here (currently only mentioned in the Discussion).

Powell et al., (2019) has been discussed further in the methods section.

•Line 126: What kind of "models"?

Sentence has been elaborated upon.

•Line 155: Please add sample sizes for the neocortex and cerebellum.

Sample sizes updated.

•Lines 157-161: This is Introduction material and should be removed from the Methods.

•Paragraph starting with Line 163: It might be useful to include some of this in the Introduction, since readers have any background surrounding issues with various "social complexity" measures.

•All descriptions of the links between socioecological variables and selection for cognitive abilities would be more appropriate in the Introduction.

These sections have been moved to the introduction.

•Lines 171-174: What were levels 2 and 3? How were pairbonded species or those that only sleep in pairs categorized? These levels need more explanation, especially since this “social cohesion” proxy was included in many best fit models in the Results.

Agreed. Definition revised for greater clarity.

•Lines 196-197: Diet imposes both temporal and spatial cognitive demands, so I suggest re-wording this.

•Lines 200-203: The authors appear to be suggesting that certain life history variables are drivers of evolutionary changes in brain size. I suggest altering the language here to mimic that in Lines 421-424.

Sentences rephrased for clarity.

•Paragraph starting with Line 200: This section is missing a discussion of ideas that the relationship between brain size and lifespan is driven by maternal investment and between specific brain regions and developmental periods (see e.g., Barton et al. 2011; Powell et al. 2019)

This point has been discussed.

•Lines 238-239: Why was body mass used as the covariate for the neocortex and cerebellum models? Many other papers have used brain size (with the brain region of interest removed) or medulla size as a covariate. This decision should be justified in the text or analyses should be re-run using a brain size measure.

Thank you for this comment, we agree that this method needed to be altered. Neocortex and cerebellum size were recalculated using endocranial volume minus the brain region of interest. Analyses were re-run using this brain size measure. The method (brain transformations) section has been updated to reflect this change.

•Model comparisons section:

oThis section as written is unclear – were the best fit models within Models 1-4 first identified, and then combined to make Model 5?

oIn any case, I do not think this approach is appropriate since it may, in some cases, force the inclusion of low information variables into the “combined” model. It would be more appropriate to create models that include all combinations of all predictor variables, compare these models using information criterion (I suggest using BIC since it is more conservative), and then select the best fit model or subset of models (e.g., all models with $\Delta BIC < 2$) to present detailed results.

Models one to four contained all combinations of the predictor variables, specifically looking at 1) social, 2) ecological, 3) social & ecological and 4) life history. Then usually models 3 and 4 were combined to determine whether incorporating the models together produced a better information criterion score. I say usually because sometimes incorporating social variables did not improve the score, therefore models 2 and 4 were combined instead. This combined model was also compared against a model including all variables together. We chose to use this ‘combined’ model because it would take too much time to try every combination of the 11 variables, therefore we thought by combining best fit models, this would bypass this problem and produce superior models. We appreciate your comment about the inclusion of low information variables, and it is definitely something we considered. After your suggestion, to better address the issue, the analyses have been re-run using BIC instead of AIC, due to the fact it is more conservative and would reduce the likelihood of low information variables being included. We also chose to present the results of the ‘best fit’ models, which was usually a subset of models (presenting all models within $\Delta BIC < 2$ of the absolute lowest model).

•Lines 260-261: The meaning of “presently, and subsequently” is unclear.

Phrase removed for clarity.

•This section is a bit difficult to follow as written. I suggest, within each section, more clearing separating/identifying the different groups of results. I think it would be most

appropriate to first discuss results using the information criterion (i.e., tell the readers which variables are included in the best fit models) and then the frequentist results (i.e., tell the readers which coefficient estimates within the best fit model are “significant” and the direction of the relationship)?

Thank you for this comment, we agree and the results section has been rewritten to allow greater clarity.

•Table 2: The diet category results (DFrug, DOmni) only demonstrate differences between these dietary groups (frugivory and omnivory) and folivory. This needs to be explicitly stated in the relevant areas of the results section. In addition, models should be run with the levels switched so that potential differences between frugivory and omnivory can also be tested.

Thank you for this comment, we agree that this needed highlighting. This has now been explicitly stated in the primate results section. In addition, as suggested, models were run with the levels switched, to identify any potential differences between frugivory and omnivory. This was checked on all ‘best fit’ models where diet was included, thus, on both the primate neocortex and cerebellum combined models. To do this, primate regional volume data was used, with linear regression models implemented, using the same combination of variables seen in the combined models (Neo ~ D + HR + ML + WA, Cere ~ D + HR + ML + WA).

Just included for your information...

Looking at primate neocortex data, when folivory was used as the baseline, negative significant associations were found with both omnivory and frugivory. However, when frugivory was used as the baseline, a positive association was found with folivory, whereas a negative association was found with omnivory. When omnivory was used as the baseline, positive associations were found with both frugivory and folivory. Thus, folivores appear to have larger neocortex volumes when compared to those with frugivorous and omnivorous diets, and this statement holds when the levels are switched (frugivorous and omnivorous species have smaller neocortex volumes when compared to those with a folivorous diet). However, frugivores appear to have larger neocortex volumes when compared to omnivores, and again, this statement holds when the levels are switched (omnivorous species have smaller neocortex sizes when compared to frugivorous species).

Looking at primate cerebellum data, the results are similar; both folivorous and frugivorous species appear to have larger cerebellar volumes when compared to those with an omnivorous diet, with this statement holding when the levels are switched (omnivorous species have smaller cerebellum volumes when compared to those with folivorous and frugivorous diets). However, there appears to be no discernible difference between folivorous and frugivorous species in terms of cerebellum volume.

•Lines 287-288 and 303-304: Table 2 includes results from best fit models only – it would be appropriate to also mention Table 1.

Table 1 has also been mentioned.

•Lines 288-289: Diet is not included in the best fit model for ECV in Table 1, so I am a bit confused about the claim that diet is positively associated with all brain measures.

What we meant by this sentence was that diet as a whole (dietary categories or dietary breadth) was associated with all brain measures. We agree this should have been better worded. This sentence has been removed, however, following the recommendation to no longer discuss the different brain measures in the main manuscript.

•Paragraph starting in Line 345: The home range results for the neocortex are not mentioned.

Thank you for pointing this out. We have now ensured all results are now appropriately discussed.

	<ul style="list-style-type: none"> •Lines 383-385: The finding that habitat variability is negatively correlated with relative brain size should be discussed in terms of previous work demonstrating a negative impact of seasonality on brain size (e.g., van Woerden et al. 2010). <p>This correlation is no longer found after rerunning statistical analyses so has been removed.</p> <ul style="list-style-type: none"> •Lines 409-410: This is not true. Powell et al. (2019) found correlations between specific brain regions (neocortex) and gestation length. Other regions were correlated with other developmental periods (e.g., cerebellum and juvenile period). <p>Sentence updated to reflect this point.</p> <ul style="list-style-type: none"> •Line 421: What does “counterbalance” mean? It sounds as if animals are actively participating in the evolution of these traits. Can the authors elaborate on how specific selection mechanisms would drive this “counterbalancing”? <p>Sentence updated to reflect this point.</p> <ul style="list-style-type: none"> •Lines 426-427: This sentence makes it seem that diet category is included in the best fit models for carnivores, which is not the case. I suggest removing the sentence. <p>Sentence removed as recommended.</p> <ul style="list-style-type: none"> •Lines 443-446: Sociality is not included in any of the best fit models of relative brain size, so this sentence is misleading as written. <p>Sentence changed following reanalysis of data.</p> <ul style="list-style-type: none"> •Lines 445-457: I would remove this sentence since the cerebellum is showing opposite trends across groups. <p>Sentence removed.</p>
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Additional Information:

Question	Response
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All relevant data are within the manuscript and its Supporting Information files.

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19 **Abstract**

20 Despite decades of research, much uncertainty remains regarding the selection pressures
21 responsible for brain size variation. Whilst the influential social brain hypothesis once
22 garnered extensive support, more recent studies have failed to find support for a link
23 between brain size and sociality. Instead, it appears there is now substantial evidence
24 suggesting ecology better predicts brain size in both primates and carnivores. Here,
25 different models of brain evolution were tested, and the relative importance of social,
26 ecological, and life-history traits were assessed on both overall encephalisation and specific
27 brain regions. In primates, evidence is found for consistent associations between brain size
28 and ecological factors, particularly diet; however, evidence was also found advocating
29 sociality as a selection pressure driving brain size. In carnivores, evidence suggests ecological
30 variables, most notably home range size, are influencing brain size; whereas, no support is
31 found for the social brain hypothesis, perhaps reflecting the fact sociality appears to be
32 limited to a select few taxa. Life-history associations reveal complex selection mechanisms
33 to be counterbalancing the costs associated with expensive brain tissue through extended
34 developmental periods, reduced fertility, and extended maximum lifespan. Future studies
35 should give careful consideration of the methods chosen for measuring brain size,
36 investigate both whole brain and specific brain regions where possible, and look to integrate
37 multiple variables, thus fully capturing all of the potential factors influencing brain size.

38 **Key words:** brain size, primates, carnivores, sociality, diet, encephalisation

39

40

41 **Introduction**

42 Brain size varies considerably amongst mammals; substantial variation is seen among
43 primates, where brain size varies almost a thousand-fold across the order [1]. The adaptive
44 value of such variation has come under extensive scrutiny over the past few decades and
45 yet despite considerable research effort, much uncertainty remains regarding the selection
46 pressures responsible.

47 Frequently proposed to explain variation in brain size are factors related to the physical
48 environment, such as diet and home range size, as well as factors related to the social
49 environment, such as group size and pair-bondedness. Ecological hypotheses mainly involve
50 investigating the cognitive demands associated with foraging [2-7], as foraging is considered
51 mentally demanding due to the pressure of managing, processing and remembering spatial
52 and temporal information about resource availability [8-12]. Additionally, differing home
53 range size is of interest to researchers due to the supposed cognitive demands imposed by
54 larger home ranges, such as processing requirements of navigating spatially-complex
55 information, especially in terms of food availability, location and distribution [9, 13-15]. This
56 has resulted in many studies investigating the cumulative effects of the physical
57 environment on encephalisation, with a specific interest in diet [16-20], home range [13,
58 14], foraging techniques [12, 21-23] and behavioural responses in a fluctuating environment
59 [24].

60 In contrast to ecological hypotheses, the social brain hypothesis (SBH) suggests sociality –
61 specifically the cognitive demands of tracking, negotiating and maintaining social
62 relationships – to be the main driving force behind variation in primate brain sizes [25-27].

63 The study of primates lends credence to this hypothesis, with brain size found to correlate

64 with many social proxies, such as social group size [28], tactical deception [29] and grooming
65 clique size [30]. Evidence has since not been limited to studies of the primate lineage, with
66 corroboration coming from research on spotted hyenas [31, 32] as well as other carnivorans
67 [33-35], ungulates [36, 37], birds [38-40], and some fish species [41-43]. The focal point of
68 much of the early work investigating sociality was social group size, due to the information-
69 processing demands group of increasing sizes are thought to incur [26]. However, the use of
70 this proxy for measuring social complexity has been criticised [44] and instead, focus has
71 shifted to the consequences of varying levels of relationship complexity [45], and toward
72 investigating the influence of pair-bondedness [27, 46-48]. This developed from the
73 proposition that relationship quality [45, 49] connotes cognitive complexity.

74 Despite the hypothesis receiving considerable support in the past, more recent
75 investigations have failed to find statistical support for a link between brain size and
76 sociality [14, 19, 20, 50, 51]. Instead, it appears there is now substantial, strong,
77 phylogenetically-corrected comparative data reinforcing the assertion that diet better
78 predicts brain size in both primates and carnivores [14, 20, 52]. In addition, the obvious
79 exceptions to the SBH, taxa ~~who~~ possess large brains but ~~who~~ are not considered social,
80 suggest factors other than sociality may be influencing brain size [19, 53, 54]. For example, if
81 sociality is to be accepted as the causal agent for increased encephalisation in mammals, it
82 should be widespread across bears and musteloids, ~~who~~ show similar encephalisation
83 increases to Canidae [55].

84 A further problem to have dogged comparative analyses of brain evolution is deciding on
85 the correct brain measure. Whilst most studies tend to focus on whole brain size, even this
86 can become an arduous task since there is little clarity in the literature regarding the most
87 appropriate body size correction factor, making decisions on the correct method of choice

88 challenging. Typically, cognitive abilities are estimated using relative brain size, by taking
89 residuals from a regression curve or calculating encephalisation quotients [56, 57]. This
90 became the method of choice when brain and body size were found to be tightly coupled
91 allometrically across vertebrates; therefore, accounting for this allometric relationship
92 became of great importance [35, 58]. However, the use of relative brain size and
93 encephalisation quotients is not without criticism; for example, using residuals as data
94 points in regression models has been discouraged, as the estimates produced are thought to
95 be biased, which influences subsequent analyses [59, 60]. Encephalisation quotients
96 possibly reflect the result of recent decreases or increases in body size [61], evidence for
97 such was uncovered by Swanson et al. [19]. They found carnivore brain size to lag behind
98 body size over evolutionary time, therefore hinting that the use of brain estimates may be a
99 poor representation of carnivore brain size. However, no evidence for a lag is found for
100 primates [62], suggesting a taxonomic difference for this group. Alongside this, the
101 prevalent use of relative brain size is thought to possibly hide other evolutionary pathways
102 which may be influencing adaptations in body mass [63]. For example, a recent analysis of
103 mammalian brain size found the brain-to-body relationship to uncover more than just
104 selection on brain size, indicating relative brain size measures are not accurately capturing
105 brain size variation [64]. Thus, van Schaik et al., [65] suggest the use of encephalisation
106 quotients should be avoided in future studies, as EQs repeatedly fail to accurately predict
107 brain size, and thus, varying levels of cognitive ability. For example, Deaner et al., [57] found
108 absolute brain size measures, over statistically produced methods i.e., residuals, to be the
109 best predictors of primate cognitive abilities.

110 Alongside the use of total brain size, particular emphasis has been put on specific brain
111 regions in recent years. The social brain hypothesis suggests the neocortex is the brain

112 structure of interest, with primates' large brains thought to be mainly the consequence of a
113 dramatic increase in neocortical volume [66-68]. The neocortex is thought foremost
114 responsible for the processing of more demanding cognitive and social skills [69, 70]
115 associated with intelligent and flexible behaviour [61]. Neocortical enlargement in primates
116 is thought to be partly due to selection on visual mechanisms [71] which is important for
117 frugivorous species, for example when needing to distinguish between fruits of different
118 colours [72-74] or when manipulating small fruit and seeds that require fine motor
119 coordination [75]. Alternatively, these visual mechanisms are thought to be important for
120 processing complex and rapid social interactions, including understanding facial expressions,
121 gaze direction and posture [76], suggesting that neocortical modifications associated with
122 complex social lives primarily involve areas specialised for visual processing of social
123 information [77]. In primates, the neocortex constitutes a substantial portion of the brain
124 [66, 67] and a large proportion of the neocortex is comprised of visual information
125 processing areas [71, 78, 79], which is thought to explain links found between frugivory and
126 brain size (see [20]), as well as social group size and neocortex volume (see [1, 71]).
127 Alongside research into the neocortex, attention is focused on the cerebellum and its
128 importance. The cerebellum was found to co-evolve with the neocortex [61], with a
129 significant correlation found between these two brain regions [80]. Increased cerebellar
130 volume is suggested to allow increased processing capacity, in terms of enhanced motor
131 abilities and manipulative abilities [81, 82]. For example, in primates positive correlations
132 are found between cerebellum volume and extractive foraging techniques [1], as well as the
133 presence of neural activation in the cerebellum during tool use in monkeys [83]. This
134 highlights the influential role played by the cerebellum in technical intelligence [84].
135 Alongside this, the cerebellum is thought to be important in social intelligence [1],

136 particularly in terms of the links between sensory-motor control and social interactions and
137 understanding [85, 86]. Indeed, it is now thought the expansion of the cortico-cerebellar
138 system is the primary driver of brain expansion in anthropoid primates [87], suggesting the
139 increased behavioural complexity in mammals could be partly explained by selection on the
140 cerebellum [88]. So much so, that Fernandes et al., [89] found residual cerebellar size to be
141 the most appropriate proxy when compared to a measure of general intelligence; as
142 cerebellar models produced the most similar model fit results when compared to those
143 produced using a measure of general intelligence.

144 Here, using data aggregated from the literature the relative importance of social, ecological
145 and life history traits are assessed on both overall encephalisation and specific brain regions,
146 and different models of brain size evolution are tested. Considerable attention has been
147 paid to primate brain evolution (e.g., [14, 20, 90, 91]) perhaps since there are substantial
148 data available on this taxonomic group making comparative tests easy to implement.

149 Likewise, carnivorans are also now receiving attention (e.g., [19, 88, 92, 93]) since variation
150 in their brain and body size, and ranging social and physical environments, makes them
151 excellent models for these tests too. Indeed, most of the literature surrounding brain size
152 hypotheses is based on analyses of these two groups.

153 One aim here, therefore, is to provide greater clarity within these two groups. Integrating
154 predictors into a framework which allow the assessment of multiple hypotheses
155 simultaneously has become increasingly important for tests of brain evolution [94, 95].

156 Therefore, phylogenetically-corrected generalised least squares (PGLS) models are used
157 here to account for shared evolutionary history, whilst assessing the potential variables
158 influencing encephalisation. We use a recently updated phylogenetic tree to ensure
159 phylogenetic relationships are contemporary. Further, the inclusion of multiple variables

160 allows the comparison of multiple hypotheses, as well as models of varying complexity.
161 While brain data are available for more taxa than are included in our dataset, we found
162 some limitations on the completeness of the necessary covariate data. We present here our
163 analyses of two orders where complete datasets with all covariates are available for all
164 species, ensuring the most robust model comparisons.

165

166 **Methods**

167 **Data Collection**

168 **Brain data**

169 Endocranial volume (ECV) and body mass data for primates ($n = 83$) and carnivores ($n = 85$)
170 were compiled from multiple sources (see supplementary material). Volumes were matched
171 for species composition and predictor variables, and whilst this resulted in smaller sample
172 sizes when compared to available brain data, in doing so it provided a complete dataset
173 with all covariates available for all species, better enabling robust analyses. ECV data were
174 preferred over brain mass data since it is thought ECV provides a more reliable estimate of
175 brain size, due to the influence of preservation techniques on brain mass [96]. The standard
176 technique for estimation of ECV is through filling the cranium with beads (or similar), which
177 is then measured using a graduated cylinder or by weighing the beads and converting the
178 weight to volume [96]. Neocortex and cerebellum volumes were also collated, where
179 available, for both primates (Neo = 52, Cere = 49) and carnivores (Neo = 44, Cere = 38).
180 Regional brain volumes are commonly measured using one of two different techniques:
181 virtual endocasts (e.g., [19]) or physical sectioning of the individual brain volumes using

182 paraffin and staining substances (e.g., [97]). When sourcing whole and regional brain
183 volumes these measurement methods were considered to ensure the data were
184 comparable; for example, all ECV data sources used common measurement techniques (as
185 described above) making the whole brain data comparable across multiple studies.

186 **Social data**

187 Both social group size and social cohesion data were collected for primates and carnivores.
188 Group size – based on the simple principle that as group size increases the information-
189 processing demands [26] and corresponding internal structures [98, 99] should also increase
190 – became perhaps the most commonly used proxy for social complexity. Despite this, the
191 use of this proxy has been criticised as it is often considered crude, weak, and not always
192 relevant [44]. Greater attention is now paid to differing levels of relationship complexity [45]
193 often indicated through the presence of pair-bonds [27, 34, 100]. Therefore, to ensure the
194 influence of sociality was fully captured, alongside group size, a social cohesion proxy was
195 used: a categorisation system ranging from 1) being primarily solitary living aside from
196 breeding seasons, 2) pair-living, 3) fission-fusion societies, to 4) being obligatorily social
197 (e.g., [91, 101]). This index aims to better encapsulate sociality, rather than relying solely on
198 group size numbers.

199 **Ecological data**

200 Four ecological variables were chosen for analysis: dietary categories, dietary breadth,
201 habitat variability and home range size. Dietary categories were assigned following previous
202 designations in the published literature (see supplementary material for sources) and
203 included six different categories: carnivorous, herbivorous, piscivorous, folivorous,
204 frugivorous and omnivorous. Alongside this traditional classification system, dietary breadth

205 was also used, estimated using the total number of food sources used by a species, with
206 data taken from [102]. This included a total of 10 different food types: invertebrates,
207 mammals and birds, reptiles, fish, unknown vertebrates, scavenge, fruit, nectar, seed or
208 other plant material, marked either as absent (0) or present (1). For this dataset, this
209 resulted in a dietary breadth scale of one to six. Habitat variability, another ecological
210 measure, was formed using data from the IUCN Red List [103], based on the total number of
211 habitat-types used by a species, following the same habitat classification system used in the
212 IUCN Red List. Additionally, home range size data were collected. By including variables
213 related both to diet and habitat, it allowed greater incorporation of possible variables within
214 the physical environment affecting brain size.

215 **Life-history data**

216 Life-history variables have been found to be critical in counterbalancing the costs of
217 increased brain size and facilitating the growth of large brains [104]. In fact, they appear to
218 be influencing the potential adaptive pathways available to a species [94], for example in
219 terms of balancing shifting developmental and maturation periods. Developmental costs are
220 also thought to influence correlations between specific primate brain structures and life
221 history variables, with the neocortex most strongly correlated with gestation length, and the
222 cerebellum with juvenile period length, suggesting that these brain regions exhibit distinct
223 life-history correlates which concur with their unique developmental trajectories [105].
224 Hence, it was necessary to include certain life history variables in the analysis to further
225 understand how life-history characteristics potentially act as a filter [104, 106] for the
226 production of large brains. Gestation length was chosen as it has received considerable
227 attention and is thought to be of great importance in bypassing the constraints of

228 precociality in mammals and facilitating brain growth [107]. Maximum lifespan was included
229 as there is substantial support that encephalisation is correlated with extended longevity
230 [104], especially in primates [108, 109]. The relationship found between brain size and
231 lifespan is thought to be driven primarily by maternal investment, with subsequent
232 correlations found between specific brain regions and developmental periods, reflecting this
233 brain size-lifespan association (see [105, 110]). Ultimately encephalisation has been found to
234 correlate with expansion of most developmental life history stages, including an extended
235 reproductive lifespan [111]. Therefore, data on age at first reproduction, weaning and
236 fertility (measured as number of offspring per year) were added to our dataset (see
237 supplementary material for sources).

238 **Statistical Analyses**

239 **Brain transformations**

240 Whole brain volumes were incorporated in analyses by simple incorporation of **log ECV**
241 volume with log body mass included as a covariate. This method is often preferred over the
242 use of residuals as variables in ecological datasets often covary thereby producing biased
243 parameter estimates when calculating residuals [59]. Including body mass as a covariate in
244 the model avoids this problem, controls for its effect on brain volume, as well as potentially
245 controlling for any effects body mass may have on other variables included. Regional brain
246 volumes were incorporated in analyses by simple incorporation of log ROB (rest of brain)
247 volume. To calculate ROB volume for both the neocortex and cerebellum, a calculation was
248 performed: whole brain volume minus the region volume of interest. This method has been
249 previously implemented and proved useful in measuring relative regional brain volumes
250 (e.g., [91]). Further analyses were also conducted in order to test how uniform results were

251 when using different brain size measures. The results of these analyses are displayed and
252 discussed in the supplementary material.

253 **PGLS analysis**

254 All statistical analyses were performed using R 4.0.1, using the 'caper', 'ape' and 'geiger'
255 packages. Phylogenetic generalised least-squares (PGLS) regression analysis was used to
256 identify those variables influencing whole and regional brain evolution, whilst avoiding the
257 problem of phylogenetic non-independence. This technique differs from standard
258 generalised least squares analysis, as it uses knowledge of phylogenetic relationships or
259 relatedness to produce estimates of the expected covariance across species [112]. Pagel's λ
260 was estimated by maximum likelihood. The tree used for all phylogenetic analyses was that
261 of Upham et al's [113]. All continuous variables, brain volumes and body mass were log
262 transformed prior to analysis to satisfy the assumption of normality. Variance Inflation
263 Factor (VIF) scores were used to check for the presence of multicollinearity, with almost all
264 scores found to be below 5, and no scores above 7. There were no scores produced which
265 highlighted concern, and thus, all socioecological and life-history variables were retained for
266 analysis (see supplementary material).

267 **Model comparisons**

268 A series of PGLS models were implemented which varied in complexity, including 1) social,
269 2) ecological, 3) social and ecological, 4) life history and 5) variables of interest. Models one
270 to four included all possible combinations of the selected variables; for example, the social
271 model included i) group size, ii) social cohesion, iii) group size and social cohesion. BIC
272 (Bayesian Information Criterion) values of each model were then compared [114]. As lower
273 BIC values indicate the presence of better fitting, more parsimonious models, the model

274 with the lowest BIC value was deemed to best explain the data, therefore considered
275 preferable and retained. BIC values were preferred over Akaike Information Criterion
276 values because BIC resolves the problem of overfitting, by using a more conservative
277 penalty for additional variables. Model number five was constructed using all variables
278 previously highlighted of interest within the social, ecological, and life history models. This
279 allowed us to compare the importance of social versus ecological models, as well as
280 construct models including those variables that best explained the data. Once computed,
281 model five was compared alongside the previous models, and those found to have the
282 lowest BIC value were then considered the '*best fit*' models, which in some cases represents
283 a subset of models (simply, any model within $\Delta\text{BIC} < 2$ of the lowest model). This is because
284 BIC values with a difference of between 2 and 6 indicate moderate evidence that the model
285 with the lower BIC provides a relatively better model fit, whilst greater than 6 indicates
286 strong evidence for improved fit.

287 **Results**

288 **Primates**

289 The results from PGLS analysis on the primate data are shown in Table 1. Almost all models
290 were highly significant. For most models λ was close to one, indicative of a Brownian motion
291 model of trait evolution; however, certain neocortex models stand in contrast to this, with λ
292 equal to zero, implying the data have no phylogenetic structure [84]. Combined models
293 were preferred when investigating both whole and regional brain volumes, with significantly
294 improved (equal or greater than two BIC units lower than another) BIC scores when
295 combining variables indicated to be of importance in previous model iterations. When

296 comparing the influence of ecology versus sociality, ecological models were found to be
 297 preferable to social models, evidenced by the presence of significantly improved BIC scores.
 298

299 Table 1. Phylogenetic generalised least-squares (PGLS) regression analyses examining the effects of social,
 300 ecological and life-history variables* on primate whole and regional brain volumes.

Brain input	Overall model	Preferred model	BIC score	P
Endocranial volume	Social	ECV ~ Mass + SC	-184.199	<0.001
	Ecological	ECV ~ Mass + DB	-190.8458	<0.001
	Social & Ecological	ECV ~ Mass + SC + DB	-192.0528	<0.001
	Life History	ECV ~ Mass + GL + ML + WA	-201.2257	<0.001
	Combined	ECV ~ Mass + GS + DB + GL + ML + WA	-208.5244	<0.001
	All	ECV ~ Mass + GS + SC + D + DB + HV + HR + GL + ML + F + FR + WA	-183.9911	<0.001
Neocortex	Social	Neo ~ SC	36.43372	<0.05
	Ecological	Neo ~ D + HR	20.04	<0.001
	Social & Ecological	Neo ~ SC + D + HR	23.04369	<0.001
	Life History	Neo ~ ML + WA	-9.507772	<0.001
	Combined	Neo ~ D + HR + ML + WA	-17.54041	<0.001
	All	Neo ~ GS + SC + D + DB + HV + HR + GL + ML + F + FR + WA	9.397628	<0.001
Cerebellum	Social	Cere ~ SC	26.55957	<0.05
	Ecological	Cere ~ D + HR	0.2775847	<0.001
	Social & Ecological	Cere ~ SC + D + HR	3.144599	<0.001
	Life History	Cere ~ ML + WA	-17.40863	<0.001
	Combined	Cere ~ D + HR + ML + WA	-25.9437	<0.001
	All	Cere ~ GS + SC + D + DB + HV + HR + GL + ML + F + FR + WA	-10.45452	<0.001

301 *GS = Group size, SC = Social cohesion, D = Diet, DB = Dietary breadth, HV = Habitat variability, HR = Home
 302 range, GL = Gestation length, ML = Maximum longevity, F = Fertility, FR = Age at first reproduction, WA =
 303 Weaning age.

304 Overall encephalisation

305 The results of PGLS analysis on endocranial volume data are presented in Table 1, with the
 306 'best fit' models presented in Table 2. The variables which were indicated to be of

307 importance and included in the ‘*best fit*’ endocranial volume models were: group size,
 308 dietary breadth, gestation length, maximum lifespan and weaning age. Also present in the
 309 subset of ‘*best fit*’ models were: social cohesion and home range. After accounting for
 310 phylogeny, both group size and social cohesion were found to be positively associated with
 311 ECV (P <0.05). Although, social cohesion failed to reach significance in certain model
 312 iterations (P = 0.06). In terms of the ecological variables, dietary breadth was consistently
 313 associated with ECV (P <0.001); however, home range size failed to reach significance (P =
 314 0.11). Three of the life-history variables were significantly associated with ECV: gestation
 315 length, maximum lifespan and weaning age (P <0.01).

316

317 Table 2. Phylogenetic generalised least-squares (PGLS) regression analyses examining the effects of social,
 318 ecological and life-history variables* on primate whole and regional brain volumes.

Brain input	Preferred models	BIC score	Predictor	T	P
Endocranial volume	ECV ~ Mass + GS + DB + GL + ML + WA	-208.5244	Intercept	-6.6214	<0.001***
			LogMass	18.9909	<0.001***
			GS	2.1248	<0.05*
			DB	3.2392	<0.01**
			LogGL	2.8949	<0.01**
			LogML	3.0356	<0.01**
			LogWA	3.3570	<0.01**
	ECV ~ Mass + SC + DB + GL + ML + WA	<2	Intercept	-6.5280	<0.001***
			LogMass	18.8287	<0.001***
			SC	2.0765	<0.05*
			DB	3.5498	<0.001***
			LogGL	2.8406	<0.01**
			LogML	2.7985	<0.01**
			LogWA	3.2441	<0.01**
	Mass + SC + DB + HR + GL + ML + WA	<2	Intercept	-6.6062	<0.001***
			LogMass	17.6895	<0.001***
			SC	1.9298	0.06
			DB	3.6480	<0.001***
LogHR			1.6222	0.11	
LogGL			3.0146	<0.01**	

			LogML	2.7384	<0.01**
			LogWA	3.0851	<0.01**
Neocortex	Neo ~ D + HR + ML + WA	-17.54041	Intercept	6.0124	<0.001***
			DFrug	-2.1200	<0.05*
			DOmni	-3.9187	<0.001***
			LogHR	3.2303	<0.01**
			LogML	4.4548	<0.001***
			LogWA	6.4547	<0.001***
Cerebellum	Cere ~ D + HR + ML + WA	-25.9437	Intercept	7.4158	<0.001***
			DFrug	-1.5536	0.13
			DOmni	-3.0869	<0.01**
			LogHR	4.2338	<0.001***
			LogML	3.0810	<0.01**
			LogWA	5.8047	<0.001***
	Cere ~ D + HR + GL + ML + WA	<2	Intercept	1.2227	0.23
			DFrug	-1.0319	0.31
			DOmni	-2.7180	<0.01**
			LogHR	4.4768	<0.001***
			LogGL	1.8597	0.07
			LogML	2.4562	<0.05*
			LogWA	3.6953	<0.001***

319 *GS = Group size, SC = Social cohesion, D = Diet, DB = Dietary breadth, HV = Habitat variability, HR = Home
320 range, GL = Gestation length, ML = Maximum longevity, F = Fertility, FR = Age at first reproduction, WA =
321 Weaning age.

322 Regional brain volumes

323 The results of PGLS analysis on the neocortex and cerebellum data are presented in Table 1,
324 with the '*best fit*' models presented in Table 2. The variables which were indicated to be of
325 importance and included within the '*best fit*' neocortex model were: diet, home range size,
326 maximum lifespan and weaning age. After accounting for phylogeny, diet, specifically
327 frugivory and omnivory were found to be negatively associated with neocortex volume (P
328 <0.05, P <0.001). This is the result produced when a folivorous diet is used as the baseline
329 category, therefore the dietary category results produced here only demonstrates
330 differences between these dietary groups (frugivory and omnivory) and folivory. Alongside
331 these associations, home range size was positively correlated with neocortex volume (P

332 <0.01). Similar to whole brain models, both maximum lifespan and weaning age were
333 significantly associated with neocortex volume ($P < 0.001$).

334 The variables which were indicated to be of importance and included in the '*best fit*'
335 cerebellum models were: diet, home range size, maximum lifespan and weaning age. Also
336 present within the subset of '*best fit*' models was: gestation length. After accounting for
337 phylogeny, diet, specifically omnivory was found to be negatively associated with
338 cerebellum volume ($P < 0.01$). Frugivory failed to be significant ($P = 0.13$, $P = 0.31$). As above,
339 this results when folivorous diet is used as the baseline category. Home range size was
340 positively associated with cerebellum volume ($P < 0.001$). Similar to previous life-history
341 results, maximum lifespan and weaning age were significantly associated with cerebellum
342 volume ($P < 0.01$, $P < 0.001$). Gestation length was close to being significantly correlated with
343 cerebellum volume ($P = 0.07$).

344

345 **Carnivores**

346 The results of PGLS analysis on the carnivore data are presented Table 3. Almost all models
347 were highly significant. Lambda was not consistent between the models, ranging from one
348 to zero across the dataset. In terms of the '*best fit*' models, those producing the lowest BIC
349 score (or any score within $\text{dBIC} < 2$ of the lowest model), there was no significant difference
350 between life history and combined models, and thus the results of all these models are
351 discussed below. When comparing the influence of ecology versus sociality, ecological
352 models were found to be preferable to social models when investigating regional brain
353 volumes, evidenced by the presence of significantly improved BIC scores. However, this was

354 not the case in whole brain models, where there was no significant difference between the
 355 preferred social and ecological models.

356

357 Table 3. Phylogenetic generalised least-squares (PGLS) regression analyses examining the effects of social,
 358 ecological and life-history variables* on carnivoran whole and regional brain volumes.

Brain input	Overall model	Preferred model	BIC score	P
Endocranial volume	Social	ECV ~ Mass + GS	-137.3671	<0.001
	Ecological	ECV ~ Mass + HV	-138.8228	<0.001
	Social & Ecological	ECV ~ Mass + GS + HV	-135.0748	<0.001
	Life History	ECV ~ Mass + F	-140.9778	<0.001
	Combined	ECV ~ Mass + DB + F	-140.4778	<0.001
	All	ECV ~ Mass + GS + SC + D + DB + HV + HR + GL + ML + F + FR + WA	-106.9128	<0.001
Neocortex	Social	Neo ~ GS	71.58854	0.06425
	Ecological	Neo ~ HR	68.10774	<0.01
	Social & Ecological	Neo ~ GS + HR	70.20444	<0.01
	Life History	Neo ~ FR	58.64386	<0.001
	Combined	Neo ~ HR + FR	59.78632	<0.001
	All	Neo ~ GS + SC + D + DB + HV + HR + GL + ML + F + FR + WA	87.42208	<0.001
Cerebellum	Social	Cere ~ GS	35.60386	0.07056
	Ecological	Cere ~ HR	20.3267	<0.001
	Social & Ecological	Cere ~ GS + HR	22.22221	<0.001
	Life History	Cere ~ GL + ML + FR	4.668459	<0.001
	Combined	Cere ~ HR + GL + ML + FR	3.803654	<0.001
	All	Cere ~ GS + SC + D + DB + HV + HR + GL + ML + F + FR + WA	28.10051	<0.001

359 *GS = Group size, SC = Social cohesion, D = Diet, DB = Dietary breadth, HV = Habitat variability, HR = Home
 360 range, GL = Gestation length, ML = Maximum longevity, F = Fertility, FR = Age at first reproduction, WA =
 361 Weaning age.

362 Overall encephalisation

363 The results of PGLS analysis on endocranial volume data are presented in Table 3, with the
 364 'best fit' models shown in Table 4. The variables which were indicated to be of importance

365 and included within the *'best fit'* endocranial volume models were: fertility, dietary breadth,
 366 maximum longevity and age at first reproduction. After accounting for phylogeny, fertility
 367 was found to be negatively associated with ECV ($P < 0.05$), with this being the only variable
 368 significantly associated with endocranial volume. For example, dietary breadth was close to
 369 being negatively associated with ECV, but fell short of significance ($P = 0.05$). In addition,
 370 both maximum lifespan and age at first reproduction, failed to reach significance ($P = 0.08$, P
 371 $= 0.10$).

372

373 Table 4. Phylogenetic generalised least-squares (PGLS) regression analyses examining the effects of social,
 374 ecological and life-history variables* on carnivoran whole and regional brain volumes.

Brain input	Preferred models	BIC score	Predictor	T	P
Endocranial volume	ECV ~ Mass + F	-140.9778	Intercept	-5.3678	<0.001***
			LogMass	25.7757	<0.001***
			LogF	-2.0993	<0.05*
	ECV ~ Mass + DB + F	<2	Intercept	-4.4263	<0.001***
			LogMass	25.6777	<0.001***
			DB	-1.9622	0.05
			LogF	-2.4784	<0.05*
	ECV ~ Mass + ML	<2	Intercept	-7.0336	<0.001***
			LogMass	24.0699	<0.001***
			LogML	1.7925	0.08
	ECV ~ Mass + FR	<2	Intercept	-6.0877	<0.001***
			LogMass	21.5774	<0.001***
LogFR			1.6682	0.1	
Neocortex	Neo ~ FR	58.64386	Intercept	35.4993	<0.001***
			LogFR	5.6022	<0.001***
	Neo ~ ML + FR	<2	Intercept	3.3575	<0.01**
			LogML	1.3334	0.19
			LogFR	2.6229	<0.05*
	Neo ~ HR + FR	<2	Intercept	17.222	<0.01**
LogHR			1.856	0.07	
LogFR			3.786	<0.001***	
Cerebellum	Cere ~ HR + GL + ML + FR	3.803654	Intercept	1.8971	0.066599
			LogHR	2.0374	<0.05*

		LogGL	2.0974	<0.05*
		LogML	2.7665	<0.01**
		LogFR	2.1567	<0.05*
Cere ~ GL + ML + FR	<2	Intercept	2.0734	<0.05*
		LogGL	1.8730	0.07
		LogML	2.8402	<0.01**
		LogFR	3.8113	<0.001***
Cere ~ ML + FR	<2	Intercept	5.9931	<0.001***
		LogML	3.1178	<0.01**
		LogFR	4.9662	<0.001***
Cere ~ HR + ML + FR	<2	Intercept	5.9347	<0.001***
		LogHR	1.8137	0.08
		LogML	3.0414	<0.01**
		LogFR	3.1242	<0.01**
Cere ~ ML + FR + WA	<2	Intercept	4.7991	<0.001***
		LogML	2.7130	<0.05*
		LogFR	4.4666	<0.001***
		LogWA	1.6954	0.1

375 *GS = Group size, SC = Social cohesion, D = Diet, DB = Dietary breadth, HV = Habitat variability, HR = Home
376 range, GL = Gestation length, ML = Maximum longevity, F = Fertility, FR = Age at first reproduction, WA =
377 Weaning age.

378

379 **Regional brain volumes**

380 The results of PGLS analysis on the neocortex and cerebellum data are presented in Table 3,
381 with the '*best fit*' models shown in Table 4. The variables which were indicated to be of
382 importance and included in the '*best fit*' neocortex models were: age at first reproduction,
383 maximum lifespan and home range size. After accounting for phylogeny, age at first
384 reproduction was found to be positively associated with neocortex ($P < 0.001$), with this
385 being the only variable significantly associated with neocortex volume. For example, home
386 range size was close to being positively associated with neocortex volume, but fell short of
387 significance ($P = 0.07$). In addition, maximum lifespan failed to reach significance ($P = 0.19$).

388 The variables which were indicated to be of importance and included within the '*best fit*'
389 cerebellum models were: home range size, gestation length, maximum lifespan and age at
390 first reproduction. Also present within the subset of '*best fit*' models were: different
391 iterations of the previously mentioned variables and weaning age. After accounting for
392 phylogeny, home range size was found to be significantly associated with cerebellum
393 volume ($P < 0.05$). Three of the life-history variables were significantly associated with
394 cerebellum volume: gestation length, maximum lifespan and age at first reproduction (P
395 < 0.05 , $P < 0.01$, $P < 0.001$). Although, home range size and gestation length failed to reach
396 significance in certain model iterations ($P = 0.08$, $P = 0.07$). Weaning age also failed to reach
397 significance ($P = 0.10$).

398

399 **Discussion**

400 Applying robust statistical analyses, a recently updated phylogenetic tree, a comprehensive
401 dataset and models of varying complexity, the correlates of brain size in primates and
402 carnivores were reconsidered. Consistent associations were found between brain size and
403 ecological variables in primates, thus highlighting the influence of ecology on
404 encephalisation. However, support was also found for the prominent social brain
405 hypothesis, specifically revealing evidence for a link between whole brain volumes and two
406 measures of sociality. In carnivores, data suggest ecological variables shape brain size,
407 suggesting alternative evolutionary patterns influencing carnivoran encephalisation. In both
408 groups, life history variables appear crucial in counterbalancing the costs of producing and
409 maintaining increased brain size, through extended developmental periods, reduced fertility
410 and increased maximum lifespan.

411 **Primates**

412 Here, consistent with current literature, robust correlations were found between brain size
413 and ecological variables. The most prominent of these were diet related, with dietary
414 categories or dietary breadth appearing in all '*best fit*' models, for both whole brain and
415 regional brain data. These findings are similar to those of DeCasien et al., [20] and Powell et
416 al. [14], who found stronger and more consistent associations with ecological variables than
417 those related to the social environment. Akin to the result of DeCasien et al. [20], support
418 was found for omnivory, as well as frugivory, as correlates of brain size. However, in
419 contrast to the literature, here the correlations between regional brain volumes and dietary
420 categories, were negatively correlated. This perhaps reflects both the need to sustain the
421 energetic cost of brain tissue (highlighted by [115]; [116]), as well as meeting the cognitive
422 foraging challenges imposed by omnivorous and frugivorous diets [3]. In addition to the
423 dietary categories, dietary breadth was significantly (positively) correlated with whole brain
424 volumes, further reinforcing the proposition that diet influences brain size, whilst
425 highlighting how useful this proxy can be in understanding how availability and variety of
426 food sources can be important in setting the cognitive challenge. For example, MacLean et
427 al. [50] also suggested dietary breadth to be an important ecological correlate, with greater
428 cognitive flexibility allowing individuals to explore and exploit new food sources, as well as
429 deploy extractive foraging techniques. Evidence for associations between regional brain
430 volumes and home range size were also found, supporting the view of Powell et al. [14] in
431 that certain dietary categories, such as frugivory, may covary with home range. Similar
432 results were also found by Graber et al. [117].

433 In the past considerable support indicated that sociality was the major driver of
434 encephalisation in primates. More recent works, however, contest this long-held viewpoint,
435 failing to find support for a link between brain size and sociality measures [14, 19, 20, 50,
436 51]. Our findings, however, confirm support for the social brain hypothesis. Here, our
437 models revealed evidence of a link between brain size and sociality in primates. This
438 association was present only in the whole brain '*best fit*' models, with both variables
439 reaching significance, indicating both increasing social group size and varying levels of social
440 cohesion are influencing brain size in primates. Interestingly, use of the social cohesion
441 proxy was often preferred when comparing models, thereby suggesting the use of this proxy
442 is superior when testing multiple ecological and social variables simultaneously. The
443 inference too is that there may be greater importance in relationship quality, over quantity,
444 as suggested by past research into primate sociality and pair-bonds [34, 45, 49, 95, 118]. It is
445 important to note however, that whilst there was support for this hypothesis, ecological
446 models were preferable over social ones and ecological variables appear to be more robust
447 correlates of brain size when compared to measures of sociality (see [117]).

448 Consistent with the literature, support was found for correlations between life-history
449 variables and brain size. As suggested within the developmental cost [110] and maternal
450 energy [119] hypotheses, relationships found possibly reflect the developmental costs
451 associated with growing large brains, which appear to be bypassed through extended
452 developmental periods and increased maternal investment [120, 121]. Similarly, Powell et
453 al. [105] found correlations between neocortex volume and gestation length, as well as
454 cerebellum volume and juvenile period. Whilst the associations found here differ in terms of
455 the specific regions involved, this supports the theory as to why relatively large-brained
456 mammals often exhibit slow maturation times and reduced fertility; thus, by increasing

457 developmental periods and maternal investment, primates possess these slow life histories
458 which ultimately facilitates the production of big brains. This therefore makes the 'extended
459 parenting' association critical to the evolution of cognition [90, 120, 122, 123]. However,
460 one mystery still left to solve is the reasoning behind the association found here between
461 brain size and maximum longevity. One proposition is that selection mechanisms work
462 towards counterbalancing the costs of large brains in mammals with a longer reproductive
463 lifespan [124], and thus, by extending the reproductive lifespan of a species, it counteracts
464 the time and effort spent producing and maintaining large brains and aims to maximise the
465 time species can spend producing young, which in turn have large brains. Whereas others
466 propose the correlation is indirect and that a longer reproductive lifespan is a by-product of
467 shifting developmental and maturation periods [105].

468 **Carnivores**

469 Akin to the primate results, for carnivores, support is found for a link between regional brain
470 volumes and home range size. This relationship reached significance in the cerebellum
471 models, concurring with research suggesting this region is important for spatial memory
472 processing [1, 125, 126]. Simply, larger home range sizes are thought to require the use of
473 complex information about food location and distribution [9], which for example in
474 carnivores, may represent the challenges of locating travelling herds of herbivores.
475 Alongside this association, indicating spatial demands influence brain size in carnivores,
476 dietary breadth was another ecological variable included in the '*best fit*' endocranial volume
477 models. However, in contrast to the results of MacLean et al. [50] and Swanson et al. [19],
478 the relationship between dietary breadth and brain size is negatively directed, suggesting
479 greater dietary breadth is actually associated with smaller brain size in carnivores. This

480 result could perhaps be a consequence of those species who are classified as obligate meat
481 eaters, whose dietary breath is limited to one or two categories, thereby producing this
482 negative correlation. Despite this, obligate meat-eating carnivores consume the highest
483 caloric diet, which is thought to provide greater energy for producing large brains. This
484 highlights how carnivores cannot simply be compared and likened to other mammalian
485 orders, such as Primates, and suggests different evolutionary mechanisms at work in
486 carnivoran lineages. It is important to note, however, that this association, whilst close to,
487 failed to reach significance ($P = 0.05$), suggesting this relationship is not a strong influence
488 on brain size in carnivores.

489 Whilst previous work has suggested sociality plays a role in the evolution of brain size in
490 carnivoran lineages [31, 33-35], here, we find no support for a link between measures of
491 sociality and brain size in carnivores. Similarly, MacLean et al. [50], Benson-Amram et al.
492 [127], and Swanson et al. [19], found no support for the social brain hypothesis in mammals.
493 The contrasting results present in the literature could be due to the fact that sociality
494 appears to be limited to a select few carnivore taxa, specifically social species from the
495 families Hyaenidae, Procyonidae and Felidae [128]. This is suggested in the findings of
496 Finarelli & Flynn [55], who identified that support for the SBH in Carnivora was dependent
497 on data from Canidae, without which, no association is found. Thus, whilst sociality
498 evidently plays an important role in primates, leading to complex, multi-faceted societies,
499 this is less common in carnivore species, and therefore does not hold the same importance.
500 Consistent with the previously discussed primate results, associations were found between
501 life-history variables and brain size in carnivores. Age at first reproduction, gestation length
502 and maximum lifespan were all found to positively correlate with regional brain volumes,

503 suggesting both an increase in developmental periods as well as an extension in
504 reproductive lifespans. Additionally, findings are consistent with the expensive brain
505 hypothesis [121], which proposes either an increase in energy turnover or a reduction in
506 energy allocation is needed in order to meet the costs of increased brain size. This is seen
507 here with a negative correlation between fertility and endocranial volume, suggesting a
508 reduction in reproductive output. This, when paired with an increase in maternal
509 investment and developmental periods, as suggested by the aforementioned results,
510 bypasses the developmental constraints of producing a large brain through reduced fertility
511 and slow maturation times.

512 **Whole versus regional brain volumes**

513 Our study highlights the benefit of investigating both whole brain and regional brain
514 volumes. Whole brain volumes are often more readily available for species and thus by
515 choosing to use this brain measure it increases sample sizes and commensurate statistical
516 power. In addition, it has been argued the neocortex comprises a large proportion of whole
517 brain volume, making the two brain volumes closely related [34, 95]. However, it is possible
518 the inclusion of specific brain regions may uncover further associations that were not
519 significant or present before. This was the case here, where for primates, the home range
520 association only became significant in the neocortex and cerebellum models, having not
521 reached significance in endocranial volume models. Additionally, in carnivores, many of the
522 life-history associations, for example age at first reproduction, only reached significance in
523 the regional brain volume models. Therefore, without investigating specific brain regions,
524 the influence of these associations would have been missed. In addition to this, the use of
525 whole brain size does not necessarily allow the study of the ways in which different selective

526 pressures act on different neural systems, as proposed by theories of mosaic evolution [5,
527 61]. This often makes it difficult to relate whole brain size to individual selection pressures
528 [129]. By investigating specific brain regions, where brain data and the corresponding
529 covariates are available, it allows the further analysis of how multiple functional systems can
530 evolve in a mosaic fashion in response to different selection pressures.

531 **Conclusion**

532 To conclude, the evidence presented here supports the proposition that ecological variables
533 hold greater influence in determining brain size in primate lineages. However, critical
534 support is also found for the SBH in primates, confirming sociality does hold significance in
535 encephalisation. Ecological variables, most notably home range size, appear to shape
536 carnivoran brain size. Yet no support is found there for measures of sociality, indicating that
537 sociality may not hold the same importance within that order. Life-history traits reveal
538 evidence for the transition to slow life histories, which work toward facilitating the
539 production of big brains and bypassing the cost of expensive brain tissue. Whilst data
540 availability limits the application of comparative studies of brain evolution in many species,
541 future studies should strive to integrate multiple variables, fully encompassing all the
542 potential variables influencing brain size. In addition, where possible, researchers should
543 investigate both whole brain and specific brain regions, as the inclusion of such may reveal
544 further associations, capturing how different brain regions can evolve independently
545 through varying selection pressures.

546

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555

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558

559 **Author Contributions:** conceptualisation and methodology, HRC and SOH; investigation and
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565

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850 **Supporting information**

851 **S1 File. Supplementary analyses.** This document includes information about the extra
852 analyses conducted using different measures of brain size.

853 **S2 File. Supplementary results tables.** This document includes all the supplementary results
854 tables associated with the supplementary analyses.

855 **S3 File. Supplementary BIC scores.** This excel file includes all the BIC scores used to conduct
856 model comparisons during the main analyses.

857 **S4 File. Additional BIC scores.** This excel file includes all the BIC scores used to conduct
858 model comparisons during the extra analyses.

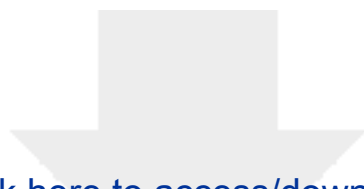
859 **S5 File. Supporting data.** This excel file includes all the data used within the statistical
860 analyses.

861 **S6 File. VIF results.** This document includes all the VIF score results.

862 **S7 File. Data collection sources.** This document includes all the data collection sources.

863 **S8 File. R code.** This text file contains the R script used to conduct the statistical analyses.

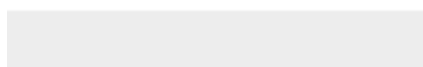
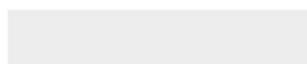
864 **S9 File. Phylogenetic tree.** This file is the phylogenetic tree used during statistical analyses.

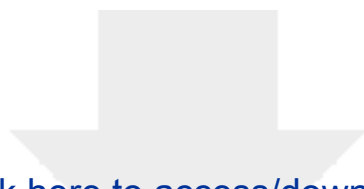


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S1 File_Supplementary analyses.docx

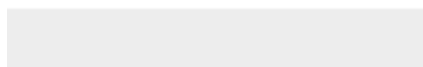
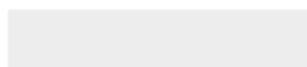


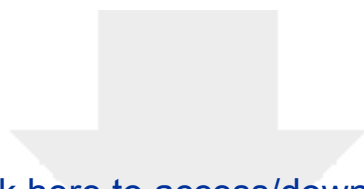


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S2 File_Supplementary results tables.docx

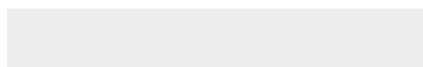
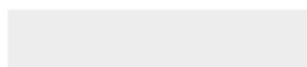


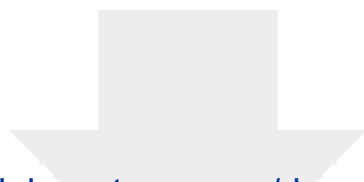


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[S3 File_Supplementary BIC scores.xlsx](#)

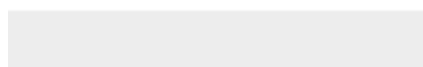
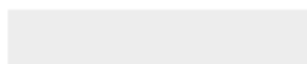


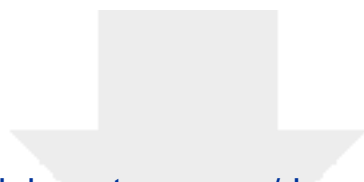


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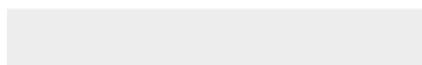
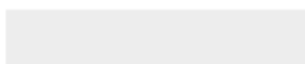
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S4 File_Additional BIC scores.xlsx





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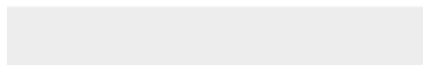
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S7 File_Data collection sources.docx





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S8 File_R code.txt



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S9 File_Phylogenetic tree

1 **Title:** Why big brains? A comparison of models for both primate and carnivore
2 brain size evolution

3 **Running title:** Why big brains?

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20 Abstract

21 Despite decades of research, much uncertainty remains regarding the selection pressures
22 responsible for brain size variation. Whilst the influential social brain hypothesis once
23 garnered extensive support, more recent studies have failed to find support for a link
24 between brain size and sociality-acting as an evolutionary driver. Instead, it appears there is
25 now substantial evidence suggesting ecology better predicts brain size in both primates and
26 carnivores. Here, different models of brain evolution were tested, and the relative
27 importance of social, ecological, and life-history traits were assessed on both overall
28 encephalisation and specific brain regions. In primates, evidence is found for consistent
29 associations between brain size and ecological factors, particularly diet; however, evidence
30 was also found advocating sociality as a selection pressure driving brain size. In carnivores,
31 evidence suggests ecological variables, most notably home range size, are influencing brain
32 size; whereas, no support is found for the social brain hypothesis, perhaps reflecting the fact
33 sociality appears to be limited to a select few taxa. In carnivores, evidence suggests multiple
34 selection pressures, both ecological and social, are influencing brain size within the
35 Carnivora order. Life-history associations reveal complex selection mechanisms to be large-
36 brained primates and carnivores are counterbalancing the costs associated with expensive
37 brain tissue through extended developmental periods, reduced fertility, and extended
38 maximum lifespan. Critically, the use of different body size correction factors, such as
39 relative brain size or encephalisation quotient, yielded disparate results. This hinders
40 modern research, as without clarity regarding what is the most suitable correction measure,
41 there is little certainty concerning the 'true' correlates of brain size. Future studies should
42 give careful consideration of the body size correction factors, methods chosen for measuring

43 ~~brain size as outlined herein, investigate both whole brain and specific brain regions where~~
44 ~~possible,~~ and look to integrate multiple variables, thus fully capturing all of the potential
45 factors influencing brain size.

46 **Key words:** brain size, primates, carnivores, sociality, diet, encephalisation

47

48

49 **Introduction**

50 Brain size varies considerably amongst mammals; substantial variation is seen amongst
51 primates, where brain size varies almost a thousand-fold across the order (1) ~~(Barton, 2012).~~
52 The adaptive value of such variation has come under extensive scrutiny over the past few
53 decades and yet despite considerable research effort, much uncertainty remains regarding
54 the selection pressures responsible.

55 Frequently proposed to explain variation in brain size are factors related to the physical
56 environment, such as diet and home range size, as well as factors related to the social
57 environment, such as group size and pair-bondedness. Ecological hypotheses mainly involve
58 investigating the cognitive demands associated with foraging (2-7) ~~(Parker & Gibson, 1977;~~
59 ~~Milton, 1981; Barton, Purvis & Harvey, 1995),~~ as foraging is considered mentally demanding
60 due to the pressure of managing, processing and remembering spatial and temporal
61 information about resource availability (8-12) ~~(Clutton-Brock & Harvey, 1980; Barton, 2000;~~
62 ~~Heldstab et al., 2016).~~ Additionally, differing home range size is have been of interest to
63 researchers for many years; due to the supposed cognitive demands imposed by larger
64 home ranges, such as processing requirements of navigating spatially-complex information,

65 especially in terms of food availability, location and distribution (9, 13-15). This has resulted
66 in many studies investigating the cumulative effects of the physical environment on
67 encephalisation, with a specific interest in diet (16-20)(Walker et al., 2006; (17)van Woerden
68 et al., 2010;(18) Swanson et al., 2012; DeCasien et al., 2017), home range (13, 14)(Parker,
69 2015; Powell et al., 2017), foraging techniques (12, 21-23)(Gibson, 1986;[Reader, 2011
70 #220] Reader et al., 2011; Plante et al., 2013; Heldstab et al., 2016) and behavioural
71 responses in a fluctuating environment (24)(Sol et al., 2005).

72 In contrast to ecological hypotheses, the social brain hypothesis (SBH) suggests sociality –
73 specifically the cognitive demands of tracking, negotiating and maintaining social
74 relationships – to be the main driving force behind variation in primate brain sizes (25-
75 27)(Whiten & Byrne, 1988; Dunbar, 1998; Dunbar, 2009). The study of primates lends
76 credence to this hypothesis, with brain size found to correlate with many social proxies,
77 such as social group size (28)(Dunbar, 1992), tactical deception (29)(Byrne & Corp, 2004)
78 and grooming clique size (30)(Kudo & Dunbar, 2001). Evidence has since not been limited to
79 studies of the primate lineage, with corroboration coming from research on spotted hyenas
80 (31, 32)(Holekamp et al., 2015; Sakai et al., 2011), as well as other carnivorans (33-
81 35)(Dunbar & Bever, 1998; Shultz & Dunbar, 2007; Pérez-Barbería et al., 2007;), ungulates
82 (36, 37),(Pérez-Barbería & Gordon, 2005; Shultz & Dunbar, 2006; Emery et al., 2007) birds
83 (38-40),(Scheiber et al., 2008; Shultz & Dunbar, 2010) and some fish species (41-
84 43)(Gonzalez-Voyer et al., 2008; Bshary, 2011; Triki et al., 2019). The focal point of much of
85 the early work investigating sociality was social group size, due to the information-
86 processing demands group of increasing sizes are thought to incur (26). However, the use of
87 this proxy for measuring social complexity has been criticised (44), and instead, focus has
88 shifted to the consequences of varying levels of relationship complexity (45). Additionally,

89 ~~since being established, the SBH has further developed, moving away from the original focal~~
90 ~~point of group size,~~ and toward investigating the influence of pair-bondedness (27, 46-
91 48)(~~Dunbar, 2009~~). This developed from the proposition that relationship quality (45,
92 49)(~~Silk, 2012; Bergman & Beehner, 2015~~) connotes cognitive complexity.

93 Despite the hypothesis receiving considerable support in the past, more recent
94 investigations have failed to find statistical support for a link between brain size and
95 sociality (~~e.g., (14, 19, 20, 50, 51)Swanson et al., 2012; MacLean et al., 2014; van Schaik et~~
96 ~~al., 2016; Powell et al., 2017; DeCasien et al., 2017~~). Instead, it appears there is now
97 substantial, strong, phylogenetically-corrected comparative data reinforcing the assertion
98 that diet better predicts brain size in both primates and carnivores (14, 20, 52)(~~Holekamp &~~
99 ~~Benson-Amram, 2017~~). In addition, the obvious exceptions to the SBH, taxa who possess
100 large brains but who are not considered social, suggest factors other than sociality may be
101 influencing brain size (19, 53, 54)(~~Holekamp, 2007; Swanson et al., 2012; van Schaik et al.,~~
102 ~~2012~~). For example, if sociality is to be accepted as the causal agent for increased
103 encephalisation in mammals, it should be wide-spread across bears and musteloids, who
104 show similar encephalisation increases to Canidae (55)(~~Finarelli & Flynn, 2009~~).

105 A further problem to have dogged comparative analyses of brain evolution is deciding on
106 the correct brain measure. Whilst most studies tend to focus on whole brain size, even this
107 can become an arduous task since there is little clarity in the literature regarding the most
108 appropriate body size correction factor, making decisions on the correct method of choice
109 challenging. Typically, cognitive abilities are estimated using relative brain size, by taking
110 residuals from a regression curve or calculating encephalisation quotients (56, 57)(~~van~~
111 ~~Schaik, Isler & Burkart, 2012~~). This became the method of choice when brain and body size

112 were found to be tightly coupled allometrically across vertebrates; therefore, accounting for
113 this allometric relationship became of great importance (35, 58)(Shultz & Dunbar, 2010).
114 Thus, relative brain size is now favoured, as absolute brain size has been found to be
115 “invariably strongly correlated with body size” in most taxa (Pérez-Barbería et al., 2007, p.
116 2812). However, the use of relative brain size and encephalisation quotients is not without
117 criticism; for example, using residuals as data points in regression models has been heavily
118 discouraged, as the estimates produced are thought to be biased, which influences any
119 subsequent analyses (59, 60). With encephalisation quotients possibly reflecting the result
120 of recent decreases or increases in body size (61)(Barton, 2000), evidence of which for such
121 was uncovered by (19). They, who found carnivore brain size to lag behind body size over
122 evolutionary time, therefore hinting that the use of brain estimates may be a poor
123 representation of carnivore brain size. H; however, no evidence for this brain size lag
124 hypothesis was found for primates (62)(Deaner & Nunn, 1999), suggesting this may not be
125 the case a taxonomic difference for this group (Deaner & Nunn, 1999). Alongside this, -and
126 the prevalent use of relative brain size is thought to possibly hiding other evolutionary
127 pathways which may be influencing adaptations in body mass (63)(Smaers et al, 2012). F; for
128 example, a recent analysis of mammalian brain size found the brain-to-body relationship to
129 uncover more than just selection on brain size, indicating relative brain size measures are
130 not accurately capturing brain size variation (64). Thus, (65) suggests the use of
131 encephalisation quotients should be avoided in future studies, as EQs have repeatedly failed
132 to accurately predict brain size, and thus, varying levels of cognitive ability. For example,
133 (57) Swanson et al. (2012) for example, found carnivore brain size to lag behind body size
134 over evolutionary time, therefore hinting that the use of brain estimates may be a poor
135 representation of carnivore brain size. Deaner et al. (2007) found absolute brain size

136 measures, over statistically ~~controlled-produced~~ methods i.e., residuals, to be the best
137 predictors of primate cognitive abilities. ~~In fact, van Schaik et al., (2021) suggest the use of~~
138 ~~encephalisation quotients should be avoided in future studies.~~

139 Alongside the use of total brain size, particular emphasis has been put on specific brain
140 regions in recent years. The social brain hypothesis suggests the neocortex is the brain
141 structure of interest, with primates' large brains thought to be mainly the consequence of a
142 dramatic increase in neocortical volume (66-68) ~~(Finlay & Darlington, 1995; Finlay et al.,~~
143 ~~2001; Cantania, 2004)~~. The neocortex is thought foremost responsible for the processing of
144 more demanding cognitive and social skills (69, 70) ~~(Innocenti & Kaas, 1995; Kaas, 1995)~~
145 associated with intelligent and flexible behaviour (61) ~~(Barton & Harvey, 2000)~~. Neocortical
146 enlargement in primates is thought to be partly due to selection on visual mechanisms (71)
147 which is important for frugivorous species, for example ~~who have~~when needing to
148 distinguish between fruits of different colours (72-74) ~~or have to~~when manipulating ~~small~~
149 fruit and seeds ~~that~~which require fine ~~motor~~ coordination (75). Alternatively, these visual
150 mechanisms are thought to be important for processing complex and rapid social
151 interactions, including understanding facial expressions, gaze direction and posture (76),
152 suggesting that neocortical modifications associated with complex social lives primarily
153 involve areas ~~specialized~~ for visual processing of social information (77). In primates, the
154 neocortex constitutes a substantial portion of the brain (66, 67), ~~and a large proportion of~~
155 the neocortex is comprised of visual information processing areas (71, 78, 79), which is
156 thought to explain links found between frugivory and brain size (see -(20)), ~~as well as, social~~
157 group size and neocortex volume (see (1, 71)).

158 Alongside research into the neocortex, attention ~~has been~~ focused on the cerebellum and
159 its importance. The cerebellum was found to co-evolve with the neocortex (61)(~~Barton &~~
160 ~~Harvey, 2000~~), with a significant correlation found between these two brain regions
161 (80)(~~Barton, 2002~~). Increased cerebellar volume is suggested to allow increased processing
162 capacity, in terms of enhanced motor abilities and manipulative abilities (81, 82). F, for
163 example, in primates positive correlations were found between cerebellum volume and
164 extractive foraging techniques (1), as well as the presence of neural activation in the
165 cerebellum during tool use in monkeys (83), ~~suggesting the cerebellum is important.~~ This
166 highlights the influential role played by the cerebellum in technical intelligence (84).
167 Alongside this, the cerebellum is thought to be important in social intelligence (1),
168 particularly in terms of the links between sensory-motor control and social interactions and
169 understanding (85, 86). Indeed, it is now thought the expansion of the cortico-cerebellar
170 system is the primary driver of brain expansion in anthropoid primates (87)(~~Smaers &~~
171 ~~Vanier, 2019~~), suggesting the increased behavioural complexity in mammals could be partly
172 explained by selection on the cerebellum (88)(~~Smaers et al., 2019~~). So much so, that
173 (89)~~Fernandes et al. (2020)~~ found residual cerebellar size to be the most appropriate proxy
174 when compared to a measure of general intelligence models; as cerebellar models produced
175 the most similar model fit results when compared to those produced using a measure of
176 general intelligence.

177 Here, using data ~~collected~~ aggregated from the literature ~~the,~~ the relative importance of
178 social, ecological and life history traits ~~are~~ assessed on both overall encephalisation and
179 specific brain regions, and different models of brain size evolution ~~are~~ tested.

180 Considerable attention has been paid to primate brain evolution, ~~perhaps since there are~~
181 substantial data available on this taxonomic group (e.g., (14, 20, 90, 91)~~Isler & van Schaik,~~

182 ~~2012; Powell et al., 2017; DeCasien et al., 2017; DeCasien & Higham, 2019)~~ perhaps since
183 there are substantial data available on this taxonomic group making comparative tests easy
184 to implement. Likewise, cCarnivorans have are also begun now receiving attention (e.g., (19,
185 88, 92, 93)~~Swanson et al., 2012; Sakai et al., 2016; Smaers et al., 2018; Heldstab et al., 2019)~~
186 with their since variation in their brain and body size, and ranging social and physical
187 environments, making ing them excellent models for these tests too. Indeed, most of the
188 literature surrounding brain size hypotheses is based on analyses of these two groups.
189 One aim here, therefore, is to provide ~~Thus, by drawing greater clarity within these two~~
190 ~~groups, this will hopefully allow for more reliable and robust analyses of other taxonomic~~
191 ~~groups.~~ Integrating predictors into a framework which allow the assessment of multiple
192 hypotheses simultaneously has become increasingly important for tests of brain evolution
193 (94, 95)~~(Dunbar & Shultz, 2007, 2017)~~. Therefore, phylogenetically-corrected generalised
194 least squares (PGLS) models are used here to account for shared evolutionary history,
195 whilst assessing the potential variables influencing encephalisation.
196 We use a recently updated phylogenetic tree to ensure phylogenetic relationships are
197 contemporary. Further, the inclusion of multiple variables allows the comparison of multiple
198 hypotheses, as well as models of varying complexity. While brain data are available for more
199 taxa than are included in our dataset, we found some limitations on the completeness of
200 the necessary covariate data. We present here our analyses of two orders where complete
201 datasets with all covariates are available for all species, ensuring the most robust model
202 comparisons. Ultimately, this study aimed to go beyond previous studies of brain size
203 evolution, which are often restricted by small sample sizes and the method of addressing
204 only one hypothesis at a time, to draw more robust and reliable results on the proposed

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205 correlates of brain size within two well-studied taxonomic groups. To achieve this, we
206 implemented the use of robust statistical analyses which accounted for the influence of
207 relatedness, a recently updated phylogenetic tree to ensure phylogenetic relationships were
208 contemporary, substantial sample sizes which surpassed previous studies and increased
209 statistical power, and importantly, the inclusion of multiple variables which allowed the
210 comparison of multiple hypotheses, as well as, models of varying complexity. Additionally,
211 to further investigate the use and merits of different brain measures in comparative
212 analyses, multiple measures of brain size were used, including the calculation of
213 encephalisation quotients (EQ) and use of residuals as relative brain size (RBS).

214

215 **Methods**

216 **Data Collection**

217 **Brain data**

218 Endocranial volume (ECV) and body mass data for primates (n = 83) and carnivores (n = 85)
219 were compiled from multiple sources (see supplementary material). Volumes were matched
220 for species composition and predictor variables, and whilst this resulted in smaller sample
221 sizes when compared to available brain data, in doing so it provided a complete dataset
222 with all covariates available for all species, better enabling robust analyses. ECV data were
223 preferred over brain mass data since it is thought ECV provides a more reliable estimate of
224 brain size, due to the influence of preservation techniques on brain mass (96) (Isler et al.,
225 2009). ECV is most frequently estimated The standard technique for estimation of ECV is
226 throughby filling the cranium with beads (or similar), which is then measured using a

227 graduated cylinder or by weighing the beads and converting the weight to volume (96).
228 Neocortex and cerebellum volumes were also collated, where available, for both primates
229 (Neo = 52, Cere = 49) and carnivores (Neo = 44, Cere = 38). These two brain measures were
230 selected for use in the analyses since both have received much attention from researchers
231 in recent years. Regional brain volumes are commonly measured using one of two different
232 techniques; virtual endocasts (e.g., (19)) or physical sectioning of the individual brain
233 volumes using paraffin and staining substances (e.g., (97)). When sourcing ~~all~~ whole and
234 regional brain volumes these measurement methods were considered to ensure the data
235 were comparable; for example, all ECV data sources used common measurement
236 techniques (as described above) making the whole brain data comparable across multiple
237 studies. ~~These two brain measures were selected for use in the analyses since both have~~
238 ~~received much attention from researchers in recent years. The neocortical region became~~
239 ~~the focus of many comparative analyses, especially since the SBH was proposed (Dunbar,~~
240 ~~2009). Attention, however, has now shifted to the cerebellum, as it is thought to play more~~
241 ~~of a substantial role in cognition than was previously assumed (Barton, 2012; Barton &~~
242 ~~Venditti, 2014).~~

243 **Social data**

244 Both social group size and social cohesion data were collected for primates and carnivores.
245 Group size – based on the simple principle that as group size increases, the information-
246 processing demands (26) ~~(Dunbar, 1998)~~ and corresponding internal structures (98,
247 99) ~~(Sallet et al., 2011; Powell et al., 2012)~~ should also increase – became perhaps the most
248 commonly used proxy for social complexity. Despite this, the use of this proxy has been
249 criticised as it is often considered crude, weak, and not always relevant (44) ~~(Byrne & Bates,~~

250 ~~2007~~). Greater attention is now paid to differing levels of relationship complexity
251 (45)(~~Bergman & Beehner, 2015~~) often indicated through the presence of pair-bonds (27, 34,
252 100)(~~Shultz & Dunbar, 2007; Dunbar & Shultz, 2007; Dunbar, 2009~~). Therefore, to ensure
253 the influence of sociality was fully captured, alongside group size, a social cohesion proxy
254 was used: a categorisation system ranging from 1 being primarily solitary living aside from
255 breeding seasons, 2 pair-living, 3 fission-fusion societies, to 4 being obligatorily social(~~one~~
256 ~~to four~~) (e.g., (91, 101)~~DeCasien & Higham, 2019; Stankowich et al., 2014~~). This index aims
257 to better encapsulate sociality, rather than relying solely on group size numbers.

258 **Ecological data**

259 Four ecological variables were chosen for analysis: dietary categories, dietary breadth,
260 habitat variability and home range size. Dietary categories were assigned following previous
261 designations in the published literature (see supplementary material for sources) and
262 included six different categories: carnivorous, herbivorous, piscivorous, folivorous,
263 frugivorous and omnivorous. Alongside this traditional classification system, dietary breadth
264 was also used, estimated using the total number of food sources used by a species, with
265 data taken from ~~Wilman et al. (102)(2014)~~. This included a total of 10 different food types:
266 invertebrates, mammals and birds, reptiles, fish, unknown vertebrates, scavenge, fruit,
267 nectar, seed- or other plant material, marked either as absent (0) or present (1). For this
268 dataset, this resulted in a dietary breadth scale of one to six. By incorporating both of these
269 dietary variables into analyses, this allows further investigation into the role diet has in brain
270 evolution. For example, certain diets are thought to be more cognitively demanding, such
271 as, frugivory, which is assumed to require greater spatial memory and food processing
272 techniques, potentially leading to increased encephalisation (Milton, 1981; Parker & Gibson,

273 ~~1997; Barton, 2000~~. Habitat variability, another ecological measure, was formed using data
274 from the IUCN Red List (103)~~(2020)~~, based on the total number of habitat-types used by a
275 species, following the same habitat classification system used in the IUCN Red List.

276 Additionally, home range size data were collected. ~~This variable has been of interest to~~
277 ~~researchers for many years; due to the supposed cognitive demands imposed by larger~~
278 ~~home ranges, such as processing requirements of navigating spatially complex information,~~
279 ~~especially in terms of food availability, location and distribution (Clutton-Brock & Harvey,~~
280 ~~1980; Parker, 2015; Powell et al., 2017)~~. By including variables related both to diet and
281 habitat (~~i.e., imposing both temporal and spatial cognitive demands~~), it alloweds greater
282 incorporation of possible variables within the physical environment affecting brain size.

283 **Life-history data**

284 Life-history variables have been found to be critical in counterbalancing the costs of
285 increased brain size and facilitating exert considerable influence on cognitive evolution and
286 the growth of large brains (104)~~(van Schaik and Deaner, 2003)~~. In fact, they appear ~~crucial to~~
287 be influencing in determining the potential adaptive pathways available to a species
288 (94)~~(Dunbar & Shultz, 2007)~~, for example in terms of balancing shifting developmental and
289 maturation periods. Developmental costs are also thought to influence correlations
290 between specific primate brain structures and life history variables, with the neocortex most
291 strongly correlated with gestation length, and the cerebellum with juvenile period length,
292 suggesting that these brain regions exhibit distinct life-history correlates which concur with
293 their unique developmental trajectories (105). Hence, it ~~seemed was~~ necessary to include
294 certain life history variables in the analysis to further understand how life-history
295 characteristics potentially act as a filter (104, 106)~~(Isler & van Schaik, 2014; van Schaik and~~

296 ~~Deaner, 2003~~) for the production of large brains. Gestation length was chosen as it has
297 received considerable attention and is thought to be of great importance in bypassing the
298 constraints of precociality in mammals and facilitating brain growth (107) ~~(Weisbecker &~~
299 ~~Goswami, 2010)~~. Maximum lifespan was included as there is substantial support that
300 encephalisation is correlated with extended longevity (104) ~~(van Schaik and Deaner, 2003)~~,
301 especially in primates (108, 109) ~~(DeCasien et al., 2018; Street et al., 2017)~~. The relationship
302 found between brain size and lifespan is thought to be driven primarily by maternal
303 investment, with subsequent correlations found between specific brain regions and
304 developmental periods, reflecting this brain size-lifespan association (see (105, 110).
305 Ultimately encephalisation has been found to correlate with expansion of most
306 developmental life history stages, including an extended reproductive lifespan
307 (111) ~~(Barrickman et al., 2008)~~. ~~Therefore,~~ data on age at first reproduction, weaning and
308 fertility (measured as number of offspring per year) were added to our dataset (see
309 supplementary material for sources).

310 **Statistical Analyses**

311 **Brain transformations**

312 ~~Whole b~~Brain volumes were incorporated in analyses ~~by using three different methods: (1)~~
313 simple incorporation of log ~~ECV~~brain volume with log body mass included as a covariate. ~~(2)~~
314 ~~(2) using residuals from a regression line, and (3) calculation of encephalisation quotients.~~
315 ~~This former~~ method is often preferred over the use of residuals as variables in ecological
316 datasets often covary thereby producing biased parameter estimates when calculating
317 residuals (59) ~~(Freckleton, 2002)~~. Including body mass as a covariate in the model avoids this
318 problem, controls for its effect on brain volume, as well as potentially controlling for any

319 effects body mass may have on other variables included. ~~Despite criticism, the use of~~
320 ~~residuals is still present, therefore we considered it prudent to use both methods in the~~
321 ~~analyses for comparative purposes. Phylogenetic generalised least-squares regression~~
322 ~~analysis (PGLS) was used to regress log brain volume against log body mass, which produced~~
323 ~~residual estimates of relative brain size after accounting for body mass. This was repeated~~
324 ~~for neocortex and cerebellum volumes. Encephalisation quotients were also calculated as a~~
325 ~~further measure of relative brain size. EQs were derived from our dataset, using the~~
326 ~~allometric formula $E = kP^\alpha$, where E = brain mass, P = body mass, k = y intercept~~
327 ~~(proportionality constant) and α = allometric exponent. For the primate data this made the~~
328 ~~final equation: $\text{brain volume} / (0.073 \times \text{body mass}^{0.89})$. For the carnivore data this made the~~
329 ~~final equation: $\text{brain volume} / (0.145 \times \text{body mass}^{0.65})$. Regional brain volumes were~~
330 ~~incorporated in analyses by simple incorporation of log ROB (rest of brain) volume. To~~
331 ~~calculate ROB volume for both the neocortex and cerebellum, a simple calculation was~~
332 ~~performed: whole brain volume minus the region volume of interest. This method has been~~
333 ~~previously implemented and proved useful in measuring relative regional brain volumes~~
334 ~~(e.g., [see](#) (91)). Further analyses were also conducted in order to test how uniform results~~
335 ~~were when using different brain size measures. The results of these analyses are displayed~~
336 ~~and discussed in the supplementary material.~~
337 ~~This allowed for seven different brain calculation inputs, (1) log ECV with log body mass, (2)~~
338 ~~relative brain size, (3) encephalisation quotients, (4) relative neocortex volume, (5) relative~~
339 ~~cerebellum volume, (6) log neocortex volume with log body mass, (7) log cerebellum volume~~
340 ~~with log body mass.~~

341 PGLS analysis

342 All statistical analyses were performed using R 4.0.1, using the 'caper', 'ape' and 'geiger'
343 packages. Phylogenetic generalised least-squares (PGLS) regression analysis (PGLS) analysis
344 was used to identify those variables influencing whole and regional brain evolution, whilst
345 avoiding the problem of phylogenetic non-independence. This technique differs from
346 standard generalised least squares analysis, as it uses knowledge of phylogenetic
347 relationships or relatedness to produce estimates of the expected covariance across species
348 (112). Pagel's λ was estimated by maximum likelihood. The tree used for all phylogenetic
349 analyses was that of Upham et al's (113)(2019). All continuous variables, brain volumes and
350 body mass were log transformed prior to analysis to satisfy the assumption of normality.
351 Variance Inflation Factor (VIF) scores were used to check for the presence of
352 multicollinearity, with almost all scores found to be below 5, and no scores above 7. There
353 were no scores produced which highlighted concern, and thus, all socioecological and life-
354 history variables were retained for analysis 8 (see supplementary material).

355 **Model comparisons**

356 A series of PGLS models were implemented which varied in complexity, including 1) social,
357 2) ecological, 3) social and ecological, 4) life history and 5) variables of interest. Models one
358 to four included all possible combinations of the selected variables; for example, the social
359 model included i) group size, ii) social cohesion, iii) group size and social cohesion. BIC
360 (Bayesian Information Criterion) values of each model were then compared (114). As lower
361 BIC values indicate the presence of better fitting, more parsimonious models, the model
362 with the lowest BIC value was deemed to best explain the data, therefore considered
363 preferable and retained. BIC values were preferred over Akaike Information Criterion
364 values because BIC resolves the problem of overfitting, by using a more conservative

365 penalty for additional variables. AIC (Akaike Information Criterion) values of each model
366 were then compared (Akaike, 1974). As lower AIC values indicate the presence of better
367 fitting, more parsimonious models, the model with the lowest AIC value was deemed to
368 best explain the data, therefore considered preferable and retained. Thus, M₅ model
369 number five was constructed using all variables previously highlighted of interest within the
370 social, ecological, and life history models. This allowed us to compare the importance of
371 social versus ecological models, as well as construct models including those variables that
372 best explained the data. Once completed, model five was compared alongside the previous
373 models, and those found to have the lowest BIC value were then considered the 'best fit'
374 models, which in some cases represents a subset of models (simply, any model within
375 ΔBIC < 2 of the lowest model). This is because BIC values with a difference of between 2 and
376 6 indicate moderate evidence that the model with the lower BIC provides a relatively better
377 model fit, whilst greater than 6 indicates strong evidence for improved fit. ~~presently, and~~
378 subsequently, brain size.

379 **Possible Limitations**

380 The *a priori* protocol followed here, that resulted in the model with the absolute lowest AIC
381 score being considered preferable and retained, does draw certain limitations. For
382 example, there may be another model within two AIC units of the 'preferred' model,
383 meaning there is no statistical difference between the two. Therefore, when compared, the
384 'preferred' model and the correlations found therein, are not considered superior or more
385 reliable. However, this *a priori* protocol was chosen to ensure systematic uniformity in
386 procedure and to allow the construction of models using variables of interest.

387 **Results**

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388 **Primates**

389 The results from PGLS analysis on the primate data is shown in Table 1. Almost all models
390 were highly significant. For most models λ was close to one, indicative of a Brownian motion
391 model of trait evolution; however, ~~certain neocortex models both cerebellum models~~
392 ~~(relative cerebellum size and log cerebellum volume)~~ stand in contrast to this, with λ equal
393 to zero, implying the data have no phylogenetic structure (84) ~~(Barton & Venditti, 2014)~~.
394 Combined models were preferred ~~when investigating both whole and regional brain~~
395 ~~volumes when using all but one (EQ) brain inputs~~, with significantly improved (equal or
396 greater than two AIC-BIC units lower than another) AIC-BIC scores when combining variables
397 indicated to be of importance in previous model iterations. When comparing the influence
398 of ecology versus sociality, ~~in contrast to this, within the EQ models, there was no significant~~
399 ~~difference between the ecological, social & ecological, and combined models. Despite this,~~
400 ~~when using all brain transformation methods, e~~ecological models were found to be
401 preferable to social models, evidenced by the presence of significantly improved AIC-BIC
402 scores.

403

404 Table 1 about here

405

406 **Overall encephalisation**

407 The results of PGLS analysis on endocranial volume, ~~data relative brain size and~~
408 ~~encephalisation quotient~~ are presented in Table 1, with the 'best fit' models presented in
409 Table 2. The variables which were indicated to be of importance and included ~~with~~in the

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410 *'best fit'* endocranial volume models were: group size, dietary breadth, gestation length,
411 maximum lifespan and weaning age. Also present *with*in the subset of *'best fit'* models
412 were: social cohesion and home range. After accounting for phylogeny, both group size and
413 social cohesion were found to be positively associated with ECV ($P < 0.05$). Although, social
414 cohesion ~~did~~failed to ~~reach~~find significance in certain model iterations ($P = 0.06$). In terms of
415 the ecological variables, dietary breadth was consistently associated with ECV ($P < 0.001$);
416 however, home range size failed to ~~reach~~find significance ($P = 0.11$). Three of the life-history
417 variables were significantly associated with ECV: gestation length, maximum lifespan and
418 weaning age ($P < 0.01$). After accounting for phylogeny, diet was found to be positively
419 associated with all whole brain measures. Dietary breadth was positively associated with
420 ECV ($P < 0.001$), RBS ($P < 0.001$) and EQ ($P < 0.01$). In addition, omnivory was positively
421 associated with RBS and EQ ($P < 0.01$). As well as the dietary variables, habitat variability was
422 negatively associated with EQ ($P < 0.05$). Three of the life-history variables were significantly
423 associated with ECV: gestation length, maximum lifespan and weaning age ($P < 0.01$),
424 however only gestation length was found to be associated with RBS ($P < 0.05$). Social
425 cohesion was close to being associated with ECV; however, this association fell short of
426 significance ($P = 0.06$). Frugivory, habitat variability and weaning age were also close to
427 being associated with RBS ($P = 0.07$, $P = 0.09$, $P = 0.06$ respectively). In addition, frugivory
428 was close to being significantly correlated with EQ ($P = 0.07$).

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429

430 Table 2 about here

431

432 **Regional brain volumes**

433 The results of PGLS analysis on the neocortex and cerebellum ~~models data~~ are also
434 presented in Table 1, with the *'best fit'* models presented in Table 2. The variables which
435 were indicated to be of importance and included within the *'best fit'* neocortex model were:
436 diet, home range size, maximum lifespan and weaning age. After accounting for phylogeny,
437 diet, specifically frugivory and omnivory were found to be negatively associated with
438 neocortex volume ($P < 0.05$, $P < 0.001$). This is the result produced when a folivorous diet is
439 used as the baseline category, therefore the dietary category results produced here only
440 demonstrates differences between these dietary groups (frugivory and omnivory) and
441 folivory. Alongside these associations, home range size was positively correlated with
442 neocortex volume ($P < 0.01$). Similar to whole brain models, both maximum lifespan and
443 weaning age were significantly associated with neocortex volume ($P < 0.001$).

444 The variables which were indicated to be of importance and included ~~with~~ within the *'best fit'*
445 cerebellum models were: diet, home range size, maximum lifespan and weaning age. Also
446 present within the subset of *'best fit'* models was: gestation length. After accounting for
447 phylogeny, diet, specifically omnivory was found to be negatively associated with
448 cerebellum volume ($P < 0.01$). Frugivory failed to be significant ($P = 0.13$, $P = 0.31$). As above,
449 ~~this is the results produced~~ when a folivorous diet is used as the baseline category. Home
450 range size was positively associated with cerebellum volume ($P < 0.001$). Similar to previous
451 life-history results, maximum lifespan and weaning age were significantly associated with
452 cerebellum volume ($P < 0.01$, $P < 0.001$). Gestation length was close to being significantly
453 correlated with cerebellum volume ($P = 0.07$). After taking phylogeny into account, diet was
454 found to be positively associated with both brain regions. Frugivory and omnivory were
455 positively associated with RNS ($P < 0.001$, $P < 0.001$), neocortex volume ($P < 0.01$, $P < 0.001$),
456 as well as RCS ($P < 0.01$, $P < 0.001$) and cerebellum volume ($P < 0.001$, $P < 0.001$). Social

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457 cohesion was found to be significantly correlated with cerebellum volume ($P < 0.05$).
458 Similarly, to whole brain measures, gestation length was associated with neocortex volume
459 ($P < 0.05$) and weaning age was correlated with cerebellum volume ($P < 0.05$). Additionally,
460 fertility was found to be negatively associated with relative cerebellum volume ($P < 0.05$).
461 Gestation length was close to being associated with relative neocortex size; however, this
462 association fell short of significance ($P = 0.06$). Additionally, social cohesion and dietary
463 breadth were close to being significantly correlated with neocortex volume ($P = 0.06$).
464

465 Carnivores

466 The results of PGLS analysis on the carnivore datas are presented Table 3. Almost all models
467 were highly significant. Lambda was not consistent between the models, ranging from one
468 to zero across the dataset. In terms of the 'best fit' models, those producing the lowest BIC
469 score (or any score within $\Delta BIC < 2$ of the lowest model), there was no significant difference
470 between life history and combined models, and thus the results of all these models are
471 discussed below. When comparing the influence of ecology versus sociality, ecological
472 models were found to be preferable to social models when investigating regional brain
473 volumes, evidenced by the presence of significantly improved BIC scores. However, this was
474 not the case in whole brain models, where there was no significant difference between the
475 preferred social and ecological models. All models including body mass were highly
476 significant; however, only seven models were found to be significant when using different
477 body size transformation methods. Lambda was not consistent between the models,
478 ranging from one to zero across the dataset. Whilst the combined models had the lowest
479 AIC scores for most of the carnivore models, these scores were not significantly improved

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480 upon, as the differences were not equal or greater than two AIC units lower than another.
481 Similarly, within the EQ models, the life history model had the lowest AIC score, however
482 this was not significantly different to the combined model (with a difference of 0.06).
483 Interestingly, in both cerebellum inputs, the social models had the lowest AIC scores;
484 however similarly to the other carnivore results, the scores were within two AIC units of
485 another model. In contrast to the primate data, generally there is no significant difference
486 between the ecological and social models, excluding the cerebellum models where social
487 models have significantly improved AIC scores.

488

489

490 Table 3 about here

491

492 Overall encephalisation

493 The results of PGLS analysis on endocranial volume data are presented in Table 3, with the
494 'best fit' models presented shown in Table 4. The variables which were indicated to be of
495 importance and included within the 'best fit' endocranial volume models were: fertility,
496 dietary breadth, maximum longevity and age at first reproduction. After accounting for
497 phylogeny, fertility was found to be negatively associated with ECV (P <0.05), with this being
498 the only variable significantly associated with endocranial volume. For example, dietary
499 breadth was close to being negatively associated with ECV, but this fell short of significance
500 (P = 0.05). In addition, both maximum lifespan and age at first reproduction, failed to
501 find reach significance (P = 0.08, P = 0.10), relative brain size and encephalisation quotient

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502 are shown in Table 4. After taking phylogeny into account, dietary breadth was found to be
503 negatively associated with endocranial volume ($P < 0.05$). Two life-history variables were
504 also significantly correlated with whole brain measures; fertility was negatively correlated
505 with ECV ($P < 0.05$), RBS ($P < 0.01$) and EQ ($P < 0.05$), as well as weaning age which was
506 negatively correlated with EQ ($P < 0.05$). Dietary breadth was close to being significantly
507 correlated with RBS; however, this association fell short of significance ($P = 0.07$).

508

509

510 Table 4 about here

511

512 Regional brain volumes

513 The results of PGLS analysis on the neocortex and cerebellum data are presented in Table 3,
514 with the 'best fit' models presented shown in Table 4. The variables which were indicated to
515 be of importance and included within the 'best fit' neocortex models were: age at first
516 reproduction, maximum lifespan and home range size. After accounting for phylogeny, age
517 at first reproduction was found to be positively associated with neocortex ($P < 0.001$), with
518 this being the only variable significantly associated with neocortex volume. For example,
519 home range size was close to being positively associated with neocortex volume, but this
520 fell short of significance ($P = 0.07$). In addition, maximum lifespan failed to reach
521 significance ($P = 0.19$). The results of PGLS analysis on the neocortex and cerebellum models
522 are also presented in Table 4. After taking phylogeny into account, social cohesion was
523 found to be negatively correlated with both relative cerebellum and cerebellum volume (P

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524 <0.05). Similar to whole brain measures, fertility and weaning age were found to be
525 negatively associated with relative neocortex and neocortex volume ($P < 0.001$, $P < 0.05$
526 respectively), as well as age of first reproduction, which was also negatively correlated with
527 RNS ($P < 0.05$).

528
529 The variables which were indicated to be of importance and included within the 'best fit'
530 cerebellum models were: home range size, gestation length, maximum lifespan and age at
531 first reproduction. Also present within the subset of 'best fit' models were: different
532 iterations of the previously mentioned variables and weaning age. After accounting for
533 phylogeny, home range size was found to be significantly associated with cerebellum
534 volume ($P < 0.05$). Three of the life-history variables were significantly associated with
535 cerebellum volume: gestation length, maximum lifespan and age at first reproduction (P
536 < 0.05 , $P < 0.01$, $P < 0.001$). Although, home range size and gestation length ~~did~~ failed to
537 find reach significance in certain model iterations ($P = 0.08$, $P = 0.07$). Weaning age also
538 failed to find reach significance ($P = 0.10$).

539

540 Discussion

541 ~~Using~~ Applying robust statistical analyses, a recently updated phylogenetic tree, ~~substantial~~
542 ~~sample sizes~~ a comprehensive dataset, and models of varying complexity, the correlates of
543 brain size in primates and carnivores were reconsidered. Consistent associations were found
544 between brain size and ecological variables in primates, thus highlighting the influence of
545 ecology on encephalisation. However, support was also found for the prominent social brain

546 hypothesis, ~~with the cerebellum appearing to be of importance for social intelligence,~~
547 specifically revealing evidence for a link between whole brain volumes and two measures of
548 sociality. In carnivores, data suggest ~~both~~ ecological ~~and social~~ variables shape brain size,
549 suggesting alternative evolutionary patterns influencing carnivoran encephalisation. In both
550 groups, life history variables appear crucial in counterbalancing the costs of producing and
551 maintaining increased brain size, through extended developmental periods, reduced fertility
552 and increased maximum lifespan.

553 **Primates**

554 Here, consistent with current literature, robust correlations were found between brain size
555 and ecological variables. The most prominent of these were diet related; with dietary
556 categories or dietary breadth appearing in all- 'best fit' models, for both whole brain and
557 regional brain data. ~~The most prominent of these were diet related; diet being the most~~
558 ~~consistent ecological correlate, with the relationship holding across multiple models, even~~
559 ~~when using different brain size calculations.~~ These findings are similar to those of DeCasien
560 et al., (20)(2017) and Powell et al., (14)(2017) who ~~both~~ found stronger and more consistent
561 associations with ecological variables than those related to the social environment. Akin to
562 the result of DeCasien et al. (20)(2017), ~~strong~~ support was found for- ~~omnivory~~ ~~frugivory~~, as
563 well as ~~omnivory~~ ~~frugivory~~, as ~~key~~ correlates of brain size. However, in contrast with to the
564 literature, here the correlations between regional brain volumes and dietary categories,
565 were negatively correlated. This perhaps reflects both the need to sustain the energetic cost
566 of brain tissue (highlighted by ~~Aiello & Wheeler, 1995~~-(115); (116)~~Fish & Lockwood, 2003~~),
567 as well as meeting the cognitive foraging challenges imposed by ~~frugivorous and~~
568 omnivorous and frugivorous diets (3)(~~Milton, 1981~~) ~~which ultimately leads to increased~~

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569 ~~encephalisation.~~ In addition to the diet categories, dietary breadth was significantly
570 (positively) correlated with ~~all whole brain measures~~whole brain volumes, further
571 reinforcing the suggestion-proposition that diet influences brain size, whilst highlighting how
572 useful this proxy can be in understanding how availability and variety of food sources can be
573 important in setting the cognitive challenge. For example, MacLean et al. (50)~~(2014)~~ also
574 suggested dietary breadth to be an important ecological correlate, with greater cognitive
575 flexibility allowing individuals to explore and exploit new food sources, as well as use-deploy
576 extractive foraging techniques. Evidence for associations between regional brain size
577 volumes and home range size were also found ~~(see supplementary material)~~, supporting the
578 view of Powell et al. ~~(2017)~~(14) in that certain dietary categories, such as frugivory, may
579 covary with home range. Similar results were also found by Graber et al., (117)~~(2017)~~.
580 ~~Interestingly, alongside the home range size associations found here, habitat variability was~~
581 ~~negatively correlated with brain size, possibly suggesting there is also importance in the~~
582 ~~habitat type used by a species.~~

583 In the past considerable support indicated that sociality was the major driver of
584 encephalisation in primates. More recent works, however, conflict-with-contest this long-
585 held viewpoint, failing to find support for a link between brain size and sociality measures
586 (14, 19, 20, 50, 51)~~(Swanson et al., 2012; MacLean et al., 2014; van Schaik et al., 2016;~~
587 ~~Powell et al., 2017; DeCasien et al., 2017)~~. Our findings, however, contrast with current
588 research, confirming support for the social brain hypothesis. Here, our models revealed
589 evidence of a link between brain size and sociality in primates. This association was present
590 only in the whole brain 'best fit' models, with both variables reaching significance, indicating
591 both increasing social group size and varying levels of social cohesion are influencing brain
592 size in primates. ~~The most robust associations were those found in the cerebellum models,~~

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593 ~~which is consistent with research that highlights the importance of the cerebellum in social~~
594 ~~intelligence (Barton, 2012); however, further associations were also found (see~~
595 ~~supplementary material).~~ Interestingly, use of the social cohesion proxy was mostly often
596 preferred when comparing models, thereby suggesting the use of this proxy is superior
597 when testing multiple ecological and social variables simultaneously. The inference too is
598 that there may be greater importance in relationship quality, over quantity, as suggested by
599 past research into primate sociality and pair-bonds (34, 45, 49, 95, 118) (~~Shultz & Dunbar,~~
600 ~~2007, 2017; Layton & O'Hara, 2010; Silk, 2012; Bergman & Beehner, 2015~~). It is important ~~to~~
601 to note however, that whilst there was support for this hypothesis, ecological models were
602 preferable over social ones, and, ecological variables appear to be more robust correlates
603 of brain size when compared to measures of sociality (see (117)).

604 Consistent with the literature, support was found for correlations between life-history
605 variables and brain size. As suggested within the developmental cost (110) (~~Barton &~~
606 ~~Capellini, 2011~~) and maternal energy (119) (~~Martin, 1996~~) hypotheses, relationships found
607 possibly reflect the developmental costs associated with growing large brains, which appear
608 to be bypassed through extended developmental periods and increased maternal
609 investment (120, 121) (~~Heldstab et al., 2019; Isler & van Schaik, 2009~~). Similarly, Powell et al.
610 (105) (~~2019~~) found correlations between neocortex volume brain volumes and gestation
611 length, as well as cerebellum volume and juvenile period. Whilst the associations found here
612 differ in terms of the specific regions involved, ~~Additionally, findings are consistent with the~~
613 ~~expensive brain hypothesis (Isler & van Schaik, 2009), which proposes either an increase in~~
614 ~~energy turnover or a reduction in energy allocation is needed in order to meet the costs of~~
615 ~~increased brain size. This is seen here by the negative fertility correlation, suggesting a~~
616 ~~reduction in reproductive output.~~ ~~†~~ This supports the theory as to why relatively large-

617 brained mammals often exhibit slow maturation times and reduced fertility; thus, by
618 increasing developmental periods and maternal investment, primates possess these slow
619 life histories which ultimately facilitates the production of big brains. This therefore makes
620 the 'extended parenting' association critical to the evolution of cognition (90, 120, 122,
621 123)(Isler & van Schaik, 2012; Heldstab et al., 2019, 2020; Uomini et al., 2020). However,
622 one mystery still left to solve is the reasoning behind the association found here between
623 brain size and maximum longevity. One proposition ~~suggests is that selection mechanisms~~
624 ~~work towards counterbalancing mammals counterbalance~~the costs of large brains ~~in~~
625 ~~mammals~~ with a longer reproductive lifespan (124)(González-Lagos et al., 2010), ~~and thus,~~
626 ~~by extending the reproductive lifespan of a species, it counteracts the time and effort spent~~
627 ~~producing and maintaining large brains, and aims to maximise the time species can spend~~
628 ~~producing young, which in turn have large brains. Whereas others propose whilst others~~
629 ~~propose~~the correlation is indirect and that a longer reproductive lifespan is a by-product of
630 shifting developmental and maturation periods (105)(Powell et al., 2019).

631 **Carnivores**

632 ~~Akin to the primate results, herefor carnivores,~~ support is found for a link between regional
633 ~~brain volumes and home range size in carnivores.~~ This relationship reached significance in
634 ~~the cerebellum models, concurring with research suggesting this region is important for~~
635 ~~spatial memory processing (1, 125, 126). Simply, larger home range sizes are thought to~~
636 ~~require the use of complex information about food location and distribution (9), which for~~
637 ~~example in carnivores, may represent the challenges of locating travelling herds of~~
638 ~~herbivores. Alongside this association, indicating spatial demands influence brain size in~~
639 ~~carnivores, dietary breadth was another ecological variable included within the 'best fit'~~

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640 endocranial volume models. However, in contrast to the results of MacLean et al., (50) and
641 Swanson et al., (19), the relationship between dietary breadth and brain size is negatively
642 directed; suggesting greater dietary breadth is actually associated with smaller brain size in
643 carnivores. Affirming the contemporary viewpoint, here, support is found for a link between
644 brain size and diet in carnivores. However, in contrast to the results of MacLean et al.,
645 (2014) and Swanson et al., (2012), the relationship between brain size and dietary breadth is
646 negatively correlated; contradicting the assertion that dietary generalists possess larger
647 brains and superior skillsets than those more specialised or with more limited food variety.
648 For example, dietary generalists in birds have been found to show more technical
649 innovations and possess larger brains when compared to dietary specialists (Ducatez, Clavel
650 & Lefebvre, 2014; Shultz et al., 2005). Yet, our findings indicate greater dietary breadth is
651 actually associated with smaller brain size in carnivores. This result could perhaps be a
652 consequence of those species who are classified as obligate meat eaters, whose dietary
653 breath is limited to one or two categories, thereby producing this negative correlation.
654 Despite this, obligate meat-eating carnivores consume the highest caloric diet, which is
655 thought to provide greater energy for producing large brains. This highlights how carnivores
656 cannot simply be compared and likened to other mammalian orders, such as Primates, and
657 suggests different evolutionary mechanisms at work in carnivoran lineages. It is important
658 to note, however, that this association, whilst close to, failed to find reach significance (P =
659 0.05), suggesting this relationship is not a strong influence on brain size in carnivores.
660 Additional ecological associations were found specifically related to habitat variables (see
661 supplementary material), with those associations suggesting spatial demands also influence
662 carnivoran brain size.

663 Whilst previous work has suggested sociality plays a role in the evolution of brain size in
664 carnivoran lineages (31, 33-35)(~~Holekamp et al., 2015; Shultz & Dunbar, 2007; Pérez-~~
665 ~~Barbería et al., 2007; Dunbar & Bever, 1998~~), here, we find the relationship between brain
666 size and sociality is negatively correlated~~no support for a link between measures of sociality~~
667 and brain size in carnivores. Similarly, MacLean et al., (50)(~~2014~~), Benson-Amram et al.,
668 (127)(~~2016~~), and Swanson et al., (~~2012~~)(19) found no support for the social brain hypothesis
669 in mammals. The contrasting results present in the literature could be due to the fact that
670 sociality appears to be limited to a select few carnivore taxa, specifically social species from
671 the families Hyaenidae, Procyonidae and Felidae (128)(~~Sakai & Arsznov, 2020~~). This is
672 suggested in the findings of Finarelli & Flynn (55)(~~2009~~), who identified that support for the
673 SBH in Carnivora was dependent on data from Canidae, without which, no association is
674 found. Thus, whilst sociality evidently plays an important role in primates, leading to
675 complex, multi-faceted societies, this is less common in carnivore species, and therefore
676 does not hold the same importance. ~~Interestingly, just as was found in the primate models,~~
677 ~~the influence of sociality was restricted to the cerebellum, further suggesting it is this brain~~
678 ~~region that is predominately underpinning the management of social interactions.~~
679 Consistent with the previously discussed primate results, associations were found between
680 life-history variables and brain size in carnivores. Age at first reproduction, gestation
681 length and maximum lifespan were all found to positively correlate with regional brain
682 volumes, suggesting both an increase in developmental periods as well as an extension in
683 reproductive lifespans. Additionally, findings are consistent with the expensive brain
684 hypothesis (121), which proposes either an increase in energy turnover or a reduction in
685 energy allocation is needed in order to meet the costs of increased brain size. This is seen
686 here by with a negative fertility correlation with between fertility and- endocranial volume,

687 ~~suggesting a reduction in reproductive output. most specifically the expensive brain~~
688 ~~hypothesis (Isler & van Schaik, 2009), fertility, age at first reproduction and weaning age~~
689 ~~were found to be negatively associated with brain size. This result reinforces support for the~~
690 ~~aforementioned hypothesis, confirming the proposition that in order to develop and sustain~~
691 ~~a large brain, there must be a trade-off with another expensive function, which in this case~~
692 ~~is reproduction.~~ This, when paired with an increase in maternal investment and
693 developmental periods, as suggested by ~~the aforementioned results~~ the primate results,
694 bypasses the developmental constraints of producing a large brain through reduced fertility
695 and slow maturation times.

696 Whole versus regional brain volumes ~~Brain size confusion~~

697
698 ~~Choosing the suitable body size correction factor for use in studies of brain evolution has~~
699 ~~been highlighted as a complex problem (van Schaik et al., 2021; Swanson et al., 2012). The~~
700 ~~disparity in results of comparative analyses of brain evolution could be in part the result of~~
701 ~~the use of different correction measures. For example, earlier studies used residuals from~~
702 ~~regression of brain size on body mass, whereas more recent studies are often scaled using~~
703 ~~residuals from regression of brain size on another brain structure or are taken from ratios~~
704 ~~(Deaner et al., 2000). The body size correction methods here produced similar outputs.~~
705 ~~However, some differences were present; for example, in primates, the association between~~
706 ~~habitat variability and EQ, which failed to remain present when using other methods. This~~
707 ~~highlights numerous concerns. First, without the inclusion of this method, the association~~
708 ~~would have been missed. Second, it raises questions regarding the validity of the~~
709 ~~association. Without clarity regarding the most suitable correction measure, it is difficult to~~

710 ascertain which associations are 'true' correlates and which do not actually invoke
711 influential change in brain evolution but are rather the consequence of inaccurate
712 correction methods. This confusion regarding correction measures needs addressing, with
713 the aim of determining the superior method, allowing greater clarity on past and current
714 research whilst guiding future comparative analyses. For example, the fact that most
715 carnivore models using residuals or other statistical calculations failed to be significant is
716 noteworthy. Residuals appear to fail to appropriately account for body size in carnivores, or
717 rather, as previously mentioned, brain estimates appear to be a poor representation of
718 carnivoran brains due to the fact that carnivore brain size shows a lag relative to body size
719 over evolutionary time (Swanson et al., 2012). Thus, inputting body size into a model as a
720 covariate, rather than using any other brain estimate, appears most appropriate when
721 designing comparative analyses of carnivoran brain evolution.

722 Our study highlights the benefit of investigating both whole brain and regional brain
723 volumes. Whole brain volumes are often more readily available for species and thus by
724 choosing to use this brain measure it increases sample sizes and commensurate statistical
725 power. In addition, it has been argued the neocortex comprises a large proportion of whole
726 brain volume, making the two brain volumes closely related (34, 95) (Shultz & Dunbar, 2007;
727 Dunbar & Shultz, 2017). However, it is possible the inclusion of specific brain regions may
728 uncover further associations that were not significant or present before. This was the case
729 here, where for primates, the home range association only became significant in the
730 neocortex and cerebellum models, and failed to have not reached significance in
731 endocranial volume models. Additionally, in carnivores, many of the life-history
732 associations, for example age at first reproduction, were only reached significance in the
733 regional brain volume models. Therefore, without investigating specific brain regions, the

734 ~~influence of these associations would have been missed. This is the case here, where for~~
735 ~~primates, social cohesion was close to significance in whole brain volume models but only~~
736 ~~reached significance in the cerebellum models. Without including this brain region, the~~
737 ~~influence of this association would have been missed.~~ In addition to this, the use of whole
738 brain size does not necessarily allow the study of the ways in which different selective
739 pressures act on different neural systems, as proposed by theories of mosaic evolution (5,
740 61)(~~Barton & Harvey, 1995; Barton & Harvey, 2000~~). This often makes it difficult to relate
741 whole brain size to individual selection pressures (129)(~~Healy & Rowe, 2007~~). ~~Therefore, by~~
742 investigating specific brain regions, where [brain](#) data [and the corresponding covariates](#) are
743 available, it allows the further analysis of how multiple functional systems can evolve in a
744 mosaic fashion in response to different selection pressures.

745 **Conclusion**

746 To conclude, the evidence presented here supports the proposition that ecological variables
747 hold greater influence in determining brain size in primate lineages. However, critical
748 support is also found for the SBH in primates, confirming sociality does hold significance in
749 encephalisation. ~~Ecological variables, most notably home range size, appear to shapeing~~
750 ~~carnivoran brain size in carnivores. Yet no support is found there for measures of sociality,~~
751 ~~indicating that sociality may not hold the same importance within thatis order. Multiple~~
752 ~~variables appear to be shaping brain size in carnivores, including both ecological and social~~
753 ~~variables, which requires greater investigation to unpick.~~ Life-history traits reveal evidence
754 for the transition to slow life histories, which work toward facilitating the production of big
755 brains and bypassing the cost of expensive brain tissue. ~~The use of different body size~~
756 ~~correction methods is found to produce disparate results, which potentially hampers the~~

757 ~~validity of correlates of brain size, as without any indication of the most appropriate~~
758 ~~measure, there is little clarity as to which associations reflect 'true' evolutionary influence.~~

759 Whilst data availability limits the application of comparative studies of brain evolution in
760 many species, future studies should strive to integrate multiple variables, fully
761 encompassing all the potential variables influencing brain size. In addition, where possible,
762 researchers should investigate both whole brain and specific brain regions, as the inclusion
763 of such may reveal further associations, capturing how different brain regions can evolve
764 independently through varying selection pressures.

765

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774

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777

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784

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Reviewer #1

1) I am not sure why this manuscript deals with just primates and carnivores. Why these two orders of mammals? Why not other orders such as rodents, lagomorphs, shrews, and bats? In fact, there are plenty of extensive datasets for these (and other) orders. For example, see Mace et al (1981) *J. Zool.* 193:333-354, which presents brain size data for 261 species of terrestrial small mammals, and Hutcheon et al. (2002) *Brain Behavior Evolution* 60:165-180 for 63 species of bats. I would have thought that a comparative approach across the entire class Mammalia would have been more fruitful than simply presenting data on primates and (incongruously) carnivores. The authors make no attempt to justify their selection of mammalian orders.

Whilst we understand that brain data are available for more species than which were included within the manuscript, we wanted to run analyses on a complete dataset with all covariates available for all species, as this enabled more robust analyses, especially when conducting model comparisons. We could access all the required covariates for primates and carnivores, which governed our choice. In addition, in efforts to address the current confusion within the field regarding the proposed selection pressures responsible for increased brain size, we chose to use both primate and carnivore data as these two groups have received considerable attention, and thus by drawing clarity within these two groups, further groups can be studied using more appropriate methods/procedures. **We have added wording to emphasise our reasoning for this choice.**

2) The literature cited is not representative of the field. A good deal of previous work has been omitted from this ms, including the two papers mentioned in (1) above, as well as Harvey et al. (1980) *PNAS* 77:4387-4389 (this paper explicitly deals with primate brain sizes). And there are many more papers that deal with ecological correlates of brain sizes that have not been mentioned.

Additional citations have been added.

3) Although the manuscript is generally well written, there are some sections that are difficult to interpret and/or to follow. This is particularly true for the Methods section, which is often ambiguous or at least incomplete. See below for where more detail is needed.

Wording has been rephrased for added clarity.

4) There is no definition of what is meant by the different brain volumes that are presented in the ms. For example, how was "endocranial brain volume" measured? And was it measured in the same way in the different papers where this information was extracted and collated? If not, then how can we be sure that we are comparing like with like?

5) The same comment applies to "neocortex" and "cerebellum" volumes.

Definitions have been added for endocranial and regional brain volumes. When sourcing all whole and regional brain volumes these measurement methods were considered to ensure the data was comparable. In terms of the ECV data, sources were checked for comparability and common measurement techniques were found between studies. We further tried to minimise the risk of this problem by sourcing data from whole datasets e.g., DeCasien et al., 2019 where the information has been weighted to account for multiple methods. However, this was more difficult with the carnivore data where regional brain volume data was tricky to source.

6) Again, how was social cohesion measured? I can see that it was scored on a point system of 1 to 4, but what does it mean for a species to have a social cohesion of 1? or 2? etc.

Definition revised for greater clarity.

7) I found the ecological data simplistic and not at all credible. The authors will need to justify exactly what they mean by each of the ecological variables. And then, they will need to convince the reader that the ecological data are actually meaningful. I am happy to include "diet" (although "frugivore" or "omnivore" are diet categories rather than strictly speaking diet itself (and the authors actually refer to diet categories, but they don't explicitly make the distinction). But what do they mean by diet breadth? According to their definition it is: "dietary breadth was also used, estimated using the total number of food sources used by a species". But what are these "food sources"? Are they the number of species of plants/animals taken? If so, an insectivorous species will by definition have a wider breadth than a carnivorous one (because there are more species of insects than vertebrates). If "sources" refers to something else, then what is it? And then, once the definition has been clearly stated, how can we be sure that the different studies have scored "number of food sources" in the same way?

Definitions of dietary categories and dietary breadth revised for greater clarity. All dietary breadth data was taken from one source: Wilman et al., (2014) and is referred to in the manuscript.

8) I have even more issue with the number of habitats used by a species. Wider ranging species will use a greater number of habitats, so why didn't the authors correct for this? Or simply use distributional range size instead of number of habitats?

Whilst we understand and appreciate this point, it does not always follow that wider ranging species will always use a greater number of habitats. One species may have a large home range size but may only move within the same habitat type. What we instead aim to look at here is whether the type of habitat matters, thus, do species which navigate and confront multiple habitat types, have larger brains than those which only move within one or two habitat types? Or vice versa? We also use home range size to proxy habitat use.

9) The authors do not mention where they get their home range sizes from in the ms (although these are clearly mentioned in the supplementary material). I find it hard to believe that the various range sizes compiled by numerous authors will be directly comparable due to differences in techniques used to estimate home range. Furthermore, there is enormous amount of variation in home range size, which is partly (and only partly) attributable to sex and age. Using a single metric is hardly informative or convincing.

We did not want to mention the citations specifically within the manuscript due to the high number of citations. We agree with this point about transferability of the methods used to measure home range size. We did our best to reduce the number of sources due to this problem, however, due to limited data availability, the only way to retrieve home range size for all species was to use data from multiple studies. To minimise the issue highlighted, we chose to use hectares to measure home range size as this was the most prevalent method found. We converted all home range data collected to this metric. We agree a single metric is not always useful, which is why we used both habitat variability and home range size to proxy habitat use.

10) Statistical analysis. This entire section (lines 218 to 239) needs to be reworked and more detail provided. And unambiguous statements rephrased. I will make just a few examples (but these are not the only problems).

Wording has been rephrased for clarity.

11) Lines 219-220 "using residuals from a regression line". Regression of what on what? And exactly using what regression? Simple linear regression e.g. $\ln()$? On log transformed or untransformed data?

Phrase removed as this aspect has been moved to supplementary methods. This regression analysis is discussed in full within that document... "*Phylogenetic generalised least-squares regression analysis (PGLS) was used to regress log brain volume against log body mass*".

12) What is the encephalisation quotient and how was it calculated? In fact, the equation is presented a bit further down, so perhaps the authors just need to refer to this e.g. say something like "see below for equation".

Definition revised for greater clarity. This aspect – as mentioned above – has been moved to the supplementary methods.

13) Line 220. "The former method is often preferred...". But you can't use "former" when there are three methods presented. "Former" and "latter" can only be used when comparing two things.

Thank you for highlighting. Phrase removed.

14) Line 226. "...therefore we considered it prudent to use both methods in the analyses...". Which two methods are being referred to? Because the authors have mentioned three methods (which have even been numbered).

Phrase removed.

15) Please provide a basic description of "Phylogenetic generalised least-squares regression analysis" and how it differs from typical GLMs.

Definition revised to provide greater clarity.

16) VIF was used to check for collinearity (which is good). But what does it mean "almost all scores" were below 5. Which variables were autocorrelated? And were any removed from the analyses, as a result of this?

Almost all VIF scores produced were below 5, however there were a few outliers. For example, body mass and weaning age produced scores of 7.25 and 5.93, when inputted into the primate endocranial model. Whilst moderately high, we chose to retain all variables within the statistical models, as the scores were only found in a few models and were still considerably low. Thus, no variables were removed from the analyses. VIF scores were also checked when rerunning analyses, specifically when using the 'rest of brain' regional volume technique, with no scores produced of concern.

This sentence has been updated to provide greater clarity.

17) Possible limitations. I find this paragraph difficult to accept. The authors are well aware that any models with AICs within 2 points are not "statistically different". Then how can they justify their approach? To me, this is the weakest aspect of the ms, because it affects all of their interpretations. There must be better ways of dealing with this. For example, list all competing models, and then count the number of times a particular variable (e.g. social cohesion) appears in the top models? This may make the results much more difficult to interpret, but this may be because there really is no simple and easy answer to the question that they are asking. Simplifying a complex problem with incorrect statistics is not acceptable.

We appreciate this comment. We agree this was a weak point in the analyses. To address this highlighted shortcoming, rather than just choosing the model with the absolute lowest score, we have now adopted the approach of presenting and discussing the results of all the 'best fit' models, which usually included a subset of models (simply, all the models within 2 points of the absolute lowest model). We have also rerun the analysis using BIC rather than AIC, in acknowledgement of this scoring system being more conservative.

Reviewer #2

- Line 33: See my comment in the Discussion section on the use of "counterbalancing".

Wording rephrased.

- There is a critical part currently missing this section, which is an explicit discussion of how this study is different from the many previous analyses of brain ~ socioecology relationships (e.g., inclusion of more variables, updated phylogeny, higher individual/species sample sizes)?

Thank you for this comment, we agree this was lacking in the manuscript. **Introduction has been updated with this discussion.**

- Line 75: The importance of pair-bondedness to brain size evolution was also discussed in other papers, which should be cited here (Schillaci 2006, 2008; MacLean et al. 2009).
- Line 83: This reference is only for carnivores – please add a reference for primates.

Citations added.

- Paragraph starting with Line 90:
 - I think a discussion of issues with relative brain size measures is important, however, I don't think it warrants using measures that have been previously established as inappropriate (i.e., residuals, EQ).
- Lines 141-144: Again, it is unnecessary to include analyses using EQ or brain size residuals.
- Lines 218-220: Again, it is unnecessary to include analyses using EQ or brain size residuals.
- Paragraph starting with Line 467: As previously mentioned, previous studies have demonstrated that the use of EQ or residuals is inappropriate, so I think this paragraph and the relevant results are unnecessary and make the overall findings harder to follow.

We appreciate that these methods have previously been suggested to be inappropriate for measuring the relationship between brain size and body mass. We feel it is necessary to further address this problem, however, especially considering we are using updated data, updated statistical analysis, more variables and an updated phylogenetic tree. **After considering this point, we decided to move the results produced using the methods of concern (i.e., residuals, EQ) to the supplementary material and these will no longer be discussed in the main manuscript.** This moves the focus away from those methods, but still allows the comparison between methods which may be useful to some readers.

- The findings from the most recent study on brain ~ body size evolution (Smears et al. 2021) should be considered/discussed here.
- Freckleton's (2009) "seven deadly sins of comparative analysis" should be mentioned here, as it includes a discussion on why it is inappropriate to use residuals as outcome variables in regression models.
- Lines 105-107 – Papers on lag between primate brain and body size should be mentioned here (e.g., Deaner and Nunn 1999).

Thank you. Citations added.

- Line 108: It is unclear what "over statistically controlled methods" means here.

Wording rephrased.

- Line 109: How and why does van Schaik et al. (2021) specifically demonstrate that EQ is inappropriate? The authors should elaborate a bit here.

Some elaboration has been added, as recommended.

- Paragraph starting with Line 111:
 - How would social and ecological variables specifically relate to neocortical and cerebellar functions?
- Increased brain size is the result of selection on specific abilities and related neural systems. Accordingly, at some point in this Introduction, I would appreciate a brief but explicit discussion of this (e.g., why might frugivory require greater visual information processing? Given that a large proportion of the brain is neocortex, and a large proportion of the neocortex is comprised of visual information processing areas, might this explain the link between something like frugivory and overall brain size?)

These points are now discussed.

- I think it would be appropriate to discuss Powell et al. (2019) here (currently only mentioned in the Discussion).

Powell et al., (2019) has been discussed further in the methods section.

- Line 126: What kind of “models”?

Sentence has been elaborated upon.

- Line 155: Please add sample sizes for the neocortex and cerebellum.

Sample sizes updated.

- Lines 157-161: This is Introduction material and should be removed from the Methods.
- Paragraph starting with Line 163: It might be useful to include some of this in the Introduction, since readers have any background surrounding issues with various “social complexity” measures.
- All descriptions of the links between socioecological variables and selection for cognitive abilities would be more appropriate in the Introduction.

These sections have been moved to the introduction.

- Lines 171-174: What were levels 2 and 3? How were pairbonded species or those that only sleep in pairs categorized? These levels need more explanation, especially since this “social cohesion” proxy was included in many best fit models in the Results.

Agreed. Definition revised for greater clarity.

- Lines 196-197: Diet imposes both temporal and spatial cognitive demands, so I suggest rewording this.
- Lines 200-203: The authors appear to be suggesting that certain life history variables are drivers of evolutionary changes in brain size. I suggest altering the language here to mimic that in Lines 421-424.

Sentences rephrased for clarity.

- Paragraph starting with Line 200: This section is missing a discussion of ideas that the relationship between brain size and lifespan is driven by maternal investment and between specific brain regions and developmental periods (see e.g., Barton et al. 2011; Powell et al. 2019)

This point has been discussed.

- Lines 238-239: Why was body mass used as the covariate for the neocortex and cerebellum models? Many other papers have used brain size (with the brain region of interest removed) or medulla size as a covariate. This decision should be justified in the text or analyses should be re-run using a brain size measure.

Thank you for this comment, we agree that this method needed to be altered. **Neocortex and cerebellum size were recalculated using endocranial volume minus the brain region of interest. Analyses were re-run using this brain size measure.** The method (brain transformations) section has been updated to reflect this change.

- Model comparisons section:
 - This section as written is unclear – were the best fit models within Models 1-4 first identified, and then combined to make Model 5?
 - In any case, I do not think this approach is appropriate since it may, in some cases, force the inclusion of low information variables into the “combined” model. It would be more appropriate to create models that include all combinations of all predictor variables, compare these models using information criterion (I suggest using BIC since it is more conservative), and then select the best fit model or subset of models (e.g., all models with $\text{dBIC} < 2$) to present detailed results.

Models one to four contained all combinations of the predictor variables, specifically looking at 1) social, 2) ecological, 3) social & ecological and 4) life history. Then usually models 3 and 4 were combined to determine whether incorporating the models together produced a better information criterion score. I say usually because sometimes incorporating social variables did not improve the score, therefore models 2 and 4 were combined instead. This combined model was also compared against a model including all variables together. We chose to use this ‘combined’ model because it would take too much time to try every combination of the 11 variables, therefore we thought by combining best fit models, this would bypass this problem and produce superior models. We appreciate your comment about the inclusion of low information variables, and it is definitely something we considered. **After your suggestion, to better address the issue, the analyses have been re-run using BIC instead of AIC, due to the fact it is more conservative and would reduce the likelihood of low information variables being included. We also chose to present the results of the ‘best fit’ models, which was usually a subset of models (presenting all models within $\text{dBIC} < 2$ of the absolute lowest model).**

- Lines 260-261: The meaning of “presently, and subsequently” is unclear.

Phrase removed for clarity.

- This section is a bit difficult to follow as written. I suggest, within each section, more clearly separating/identifying the different groups of results. I think it would be most appropriate to first discuss results using the information criterion (i.e., tell the readers which variables are

included in the best fit models) and then the frequentist results (i.e., tell the readers which coefficient estimates within the best fit model are “significant” and the direction of the relationship)?

Thank you for this comment, we agree and the results section has been rewritten to allow greater clarity.

- Table 2: The diet category results (DFrug, DOmni) only demonstrate differences between these dietary groups (frugivory and omnivory) and folivory. This needs to be explicitly stated in the relevant areas of the results section. In addition, models should be run with the levels switched so that potential differences between frugivory and omnivory can also be tested.

Thank you for this comment, we agree that this needed highlighting. This has now been explicitly stated in the primate results section. In addition, as suggested, models were run with the levels switched, to identify any potential differences between frugivory and omnivory. This was checked on all ‘best fit’ models where diet was included, thus, on both the primate neocortex and cerebellum combined models. To do this, primate regional volume data was used, with linear regression models implemented, using the same combination of variables seen in the combined models (Neo ~ D + HR + ML + WA, Cere ~ D + HR + ML + WA).

Just included for your information...

Looking at primate neocortex data, when folivory was used as the baseline, negative significant associations were found with both omnivory and frugivory. However, when frugivory was used as the baseline, a positive association was found with folivory, whereas a negative association was found with omnivory. When omnivory was used as the baseline, positive associations were found with both frugivory and folivory. Thus, folivores appear to have larger neocortex volumes when compared to those with frugivorous and omnivorous diets, and this statement holds when the levels are switched (frugivorous and omnivorous species have smaller neocortex volumes when compared to those with a folivorous diet). However, frugivores appear to have larger neocortex volumes when compared to omnivores, and again, this statement holds when the levels are switched (omnivorous species have smaller neocortex sizes when compared to frugivorous species).

Looking at primate cerebellum data, the results are similar; both folivorous and frugivorous species appear to have larger cerebellar volumes when compared to those with an omnivorous diet, with this statement holding when the levels are switched (omnivorous species have smaller cerebellum volumes when compared to those with folivorous and frugivorous diets). However, there appears to be no discernible difference between folivorous and frugivorous species in terms of cerebellum volume.

- Lines 287-288 and 303-304: Table 2 includes results from *best fit models only* – it would be appropriate to also mention Table 1.

Table 1 has also been mentioned.

- Lines 288-289: Diet is not included in the best fit model for ECV in Table 1, so I am a bit confused about the claim that diet is positively associated with all brain measures.

What we meant by this sentence was that diet as a whole (dietary categories or dietary breadth) was associated with all brain measures. We agree this should have been better worded. This sentence has been removed, however, following the recommendation to no longer discuss the different brain measures in the main manuscript.

- Paragraph starting in Line 345: The home range results for the neocortex are not mentioned.

Thank you for pointing this out. We have now ensured all results are now appropriately discussed.

- Lines 383-385: The finding that habitat variability is negatively correlated with relative brain size should be discussed in terms of previous work demonstrating a negative impact of seasonality on brain size (e.g., van Woerden et al. 2010).

This correlation is no longer found after rerunning statistical analyses so has been removed.

- Lines 409-410: This is not true. Powell et al. (2019) found correlations between specific brain regions (neocortex) and gestation length. Other regions were correlated with other developmental periods (e.g., cerebellum and juvenile period).

Sentence updated to reflect this point.

- Line 421: What does “counterbalance” mean? It sounds as if animals are actively participating in the evolution of these traits. Can the authors elaborate on how specific selection mechanisms would drive this “counterbalancing”?

Sentence updated to reflect this point.

- Lines 426-427: This sentence makes it seem that diet category is included in the best fit models for carnivores, which is not the case. I suggest removing the sentence.

Sentence removed as recommended.

- Lines 443-446: Sociality is not included in any of the best fit models of relative brain size, so this sentence is misleading as written.

Sentence changed following reanalysis of data.

- Lines 445-457: I would remove this sentence since the cerebellum is showing opposite trends across groups.

Sentence removed.