“Brain to Body Mass Ratio Correlation with Rate of Net Diversification Across Mammals.”

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INTRODUCTION

In evolutionary biology, understanding why certain lineages have diversified more than others always remain a crucial topic. Extrinsic factors affecting speciation and/or extinction rates, such as geological changes, climatic cycles, and ecological opportunities, have historically been blamed for variations in the rate at which lineages diversify. Biological traits may help understand why species diversification is so uneven across mammals. (Scholl and Wiens 2016).

The difference in biological traits like brain/body mass ratio can be critical in driving macroevolutionary dynamics. Phenotypic differentiation can lead to reproductive isolation, which can ultimately lead to speciation (Schoenemann 2004). When a trait changes more quickly in certain species than others due to selective pressure, it causes high evolvability. This rapid change can allow for more access to new ecological niches, resulting in a faster speciation rate. Individuals will be able to avoid harsh environmental environments and competitive encounters by the rapid evolution of new phenotypes, lowering extinction rates. The result of these processes can cause an increase in net diversification. The overall effect of these processes on net diversification (net diversification = speciation - extinction) will be determined by which of these rates response more strongly to phenotypic transition (Adams et al. 2009).

Understanding the association between traits and diversification rates is significant because it can explain the causes of widespread heterogeneity in species diversity across clades and geographical areas. The rates at which new species evolve (speciation rate) and existing species become extinct (extinction rate) are referred to as diversification rates. Fossils, records on the species diversity of clades and their ages, and phylogenetic trees can all be used to predict diversification rates.(Scholl and Wiens 2016). In this study, phylogenetic tree was used to calculate the diversification rates with different models, and it is hypothesized that **l**ineages of mammals with larger brains to body mass ratio have higher diversification rates.

MATERIALS AND METHODS

*Data Collection*

Data for brain mass and body mass of 1105 species of mammals divided into 25 clades was used from the work of Heldstab, S. A., K. Isler, and C. P. van Schaik published in 2018 (doi.org/10.5061/dryad.753d06g). They collected their data on brain size and body mass from existing multiple datasets as well as published literature. They used female species (when possible) to minimize the error created by sexual dimorphism. Body mass was obtained from the same specimen as brain size when it was available. In case brain and body mass were not collected from the same specimen, the most extensive sample of wild body mass data available was used (Heldstab et al. 2018). The phylogenic tree was obtained by adding the scientific names of all the species on *vertlife.org*.

*Data Analysis*

Bayesian Analysis of Macroevolutionary Mixtures (BAMM) version 2.5.0 was used to estimate the rates of speciation (λ), extinction (μ), and net diversification (r) across the 1105 species tree. In BAMM, expectedNumberOfShifts parameter was set to 100, numberOfGenerations parameter was set to 107, and acceptanceResetFreq parameter was set to 1000.

The relationship between brain/body mass ratio and macroevolutionary parameters (λ, μ, and r) calculated by BAMM were compared to a null correlation distribution generated using STructured Rate Permutations on Phylogenies (STRAPP). STRAPP is robust to phylogenetic pseudoreplication. The null correlations are created by permuting the evolutionary rates at the phylogenetic tree's tips while keeping the position of rate shift events in the phylogeny constant.

DR (Diversification Rate) is a function of estimating net diversification. When the speciation rate between the species is high, there are shorter branch lengths, resulting in a high level of DR. While the species with longer branches have low diversification and low DR value. DR metric with inverse equal splits was run in R with the data set of all the mammals and the code was written by Pascal Title.

RESULTS

Diagram

Description automatically generated

Figure 01: Phylogenetic tree of all the species in the data set with their brain/body mass ratio. Red color indicates the lowest brain/body mass ratio and dark blue indicates the highest brain/body mass ratio.

The Brain/Body mass ratio Phylogeny tree shows the different value of traits across the 1105 species (Figure 01).

Graphical user interface

Description automatically generated with low confidenceDiagram

Description automatically generated**Diagram

Description automatically generated**Diagram, schematic

Description automatically generated

Net Diversification

Extinction

Speciation

Figure 02: Phylogenetic tree with Speciation, Extinction, and Net Diversification using the BAMM Analysis. Dark blue color indicates the lowest value and bright red color indicates the highest value.

Mean speciation, mean extinction, and mean net diversification was calculated from the BAMM analysis and the phylogeny trees were drawn for each of them (Figure 02). BAMM analysis estimated 8 shifts with the probability of 0.30 and 9 shifts with probability of 0.22.

Chart, scatter chart

Description automatically generated

Figure 03: DR rates calculated by DR analysis plotted against the brain/body mass ratio.

Chart, scatter chart

Description automatically generatedDR rates are most closely related to the diversification. A cor.test was performed on DR rates and Brain/Body mass ratio, using spearman method and rho was estimated as -0.17 (p-value < 0.01) indicating a negative relationship (Figure 03).

Figure 04: Graph between mean diversification calculated using BAMM analysis and trait.

STRAPP values for relationship between trait and speciation is (estimate = -0.09, p-value = 0.8), for extinction is (estimate = 0.08, p-value = 0.68), and for net diversification is (estimate = -0.30, p-value = 0.28) (Figure 04).

DISCUSSIONS

There was no correlation observed between the brain/body mass ratio and the net diversification. Net diversification is dependent on the speciation rate and the extinction rate. The BAMM analysis indicated a rate of shifts between 8 and 9, indicating diversification happening across the mammals. The results did not give us evidence of our hypothesis for this paper. It was hypothesized that**l**ineages of mammals with larger brains to body mass ratio have higher diversification rates. The STRAPP analysis showed a negative relationship between the trait and the net diversification rate, and a positive relationship with extinction. There is a relationship, but we have a high p-value of 0.8,0.68,0.28 for speciation, extinction, and net diversification, respectively. The higher p-values for all macroevolutionary dynamics suggest that our sample data is insufficient to rule out the possibility of random sample error. Because of that, we cannot conclude any relationship between brain/body mass ratio and net diversification.

DR rates were also calculated, the relationship between DR rates and brain/body mass ratio was calculated using spearman’s method. The rho value observed was estimated as -0.17 (p-value = 1.055 x 10 -8). Note that R gave an error that the exact p-value cannot be calculated, and the best p-value calculated was estimated. This value does not account for the autoregression that is why these numbers can not enough to conclude that there is a correlation between the diversification rate and higher brain/body mass ratio across mammals.

There was no correlation found between the brain/body mass ratio and the diversification rate. There is a study done across birds, where they found no correlation between the brain size of birds and the diversification, but they found a positive correlation between the rate of change in brain size and net diversification rates (Sayol et al. 2019). If further calculations are done on the rate of evolution of brain/body mass ratio and diversification, we may find a relationship.

There are also some potential problems with the data set used in this study. The brain size and the body mass are only taken from one individual from the whole species; one individual cannot represent the average brain and body size across the species. This can create a selection bias in the calculations. This kind of error can be reduced by taking samples of multiple individuals across a single species and taking the average. One other big problem with the data set was the environmental factors involved. Some of the species were under hibernation. It is found that hibernation does constrain brain size in mammals (Heldstab et al. 2018), which effects the value of brain size, effecting the brain/body mass ratio. If we can reduce these errors, we may be able to get a result make a conclusion between the relationship between the brain/body ratio and the diversification.

As the name indicates the DR statistics is mostly represents the diversification rate but Jetz et al. (2012) concluded that DR statistics is a much better representation of speciation and very poorly correlated to net diversification. BAMM is very computational and detects the rate shifts only when having enough calculations. As a result, it would prove to be restrictive in the amount of rate heterogeneity it detects in phylogenies. While DR estimates heterogeneity in tip rates as a function of stochastic variation in branch lengths, even if true rates do not differ among lineages. It was proposed that BAMM is not accurate as the rate shifts estimated are very sensitive to the prior estimation, and parameters are correlated. A recent study by Rabosky et al. (2017) disapproves the claims and reported that BAMM results are accurate and consistent. None of the statistical method is perfect so cautions must be considered when analyzing data to conclude the best results.

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CODE AND DATA AVALIBILTY

R Studio (version 1.4.1103) was used to generate all the graphs and run BAMM, STRAPP, and DR. The code for the statistical analysis and the data used in this paper can be found at [github.com/01raza/Project](https://github.com/01raza/Project).

LITERATURE CITED

Adams, D. C., C. M. Berns, K. H. Kozak, and J. J. Wiens. 2009. Are rates of species diversification correlated with rates of morphological evolution? Proceedings of the Royal Society B: Biological Sciences 276:2729–2738. Royal Society.

Heldstab, S. A., K. Isler, and C. P. van Schaik. 2018. Hibernation constrains brain size evolution in mammals. J. Evol. Biol. 31:1582–1588.

Jetz, W., G. H. Thomas, J. B. Joy, K. Hartmann, and A. O. Mooers. 2012. The global diversity of birds in space and time. Nature 491:444–448.

Rabosky, D. L., J. S. Mitchell, and J. Chang. 2017. Is BAMM Flawed? Theoretical and Practical Concerns in the Analysis of Multi-Rate Diversification Models. Syst Biol 66:477–498.

Sayol, F., O. Lapiedra, S. Ducatez, and D. Sol. 2019. Larger brains spur species diversification in birds. Evolution 73:2085–2093.

Schoenemann, P. T. 2004. Brain Size Scaling and Body Composition in Mammals. Brain Behav Evol 63:47–60.

Scholl, J. P., and J. J. Wiens. 2016. Diversification rates and species richness across the Tree of Life. Proc Biol Sci 283.