

Results

06-10-2021

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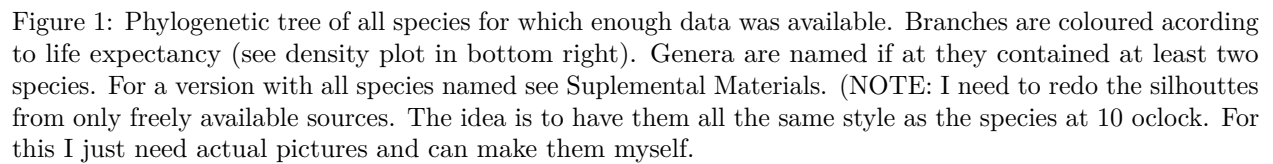
This markdown compiles all the results for the paper.

Some steps cannot be reproduced because data cannot be shared. All other steps can be reproduced. Some intermediate results are too large to fit on GitHub. If steps are sourced in the right order, these intermediate results will be stored locally.

You can also skip the intermediate steps and directly reproduce the figures. Figures are saved in ANALYSIS/RESULTS/figures.

Phylogenetic tree

This step creates the phylogenetic tree with branches coloured by life expectancy. The icons were later added in Inkscape, so this step will reproduce a barebones version of the final figure.



Slopes

This chunk plots the slopes for the beta parameters in model 2.

```
## pdf
## 2
```

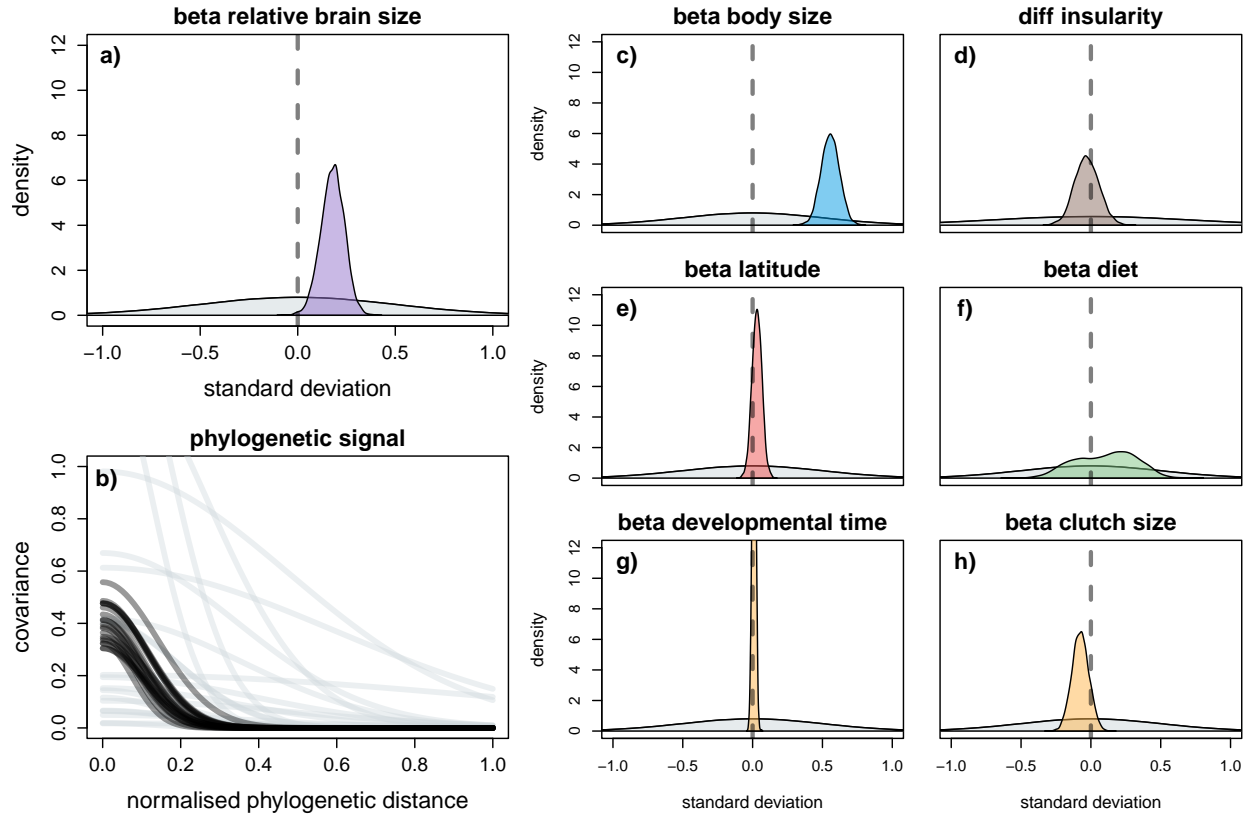


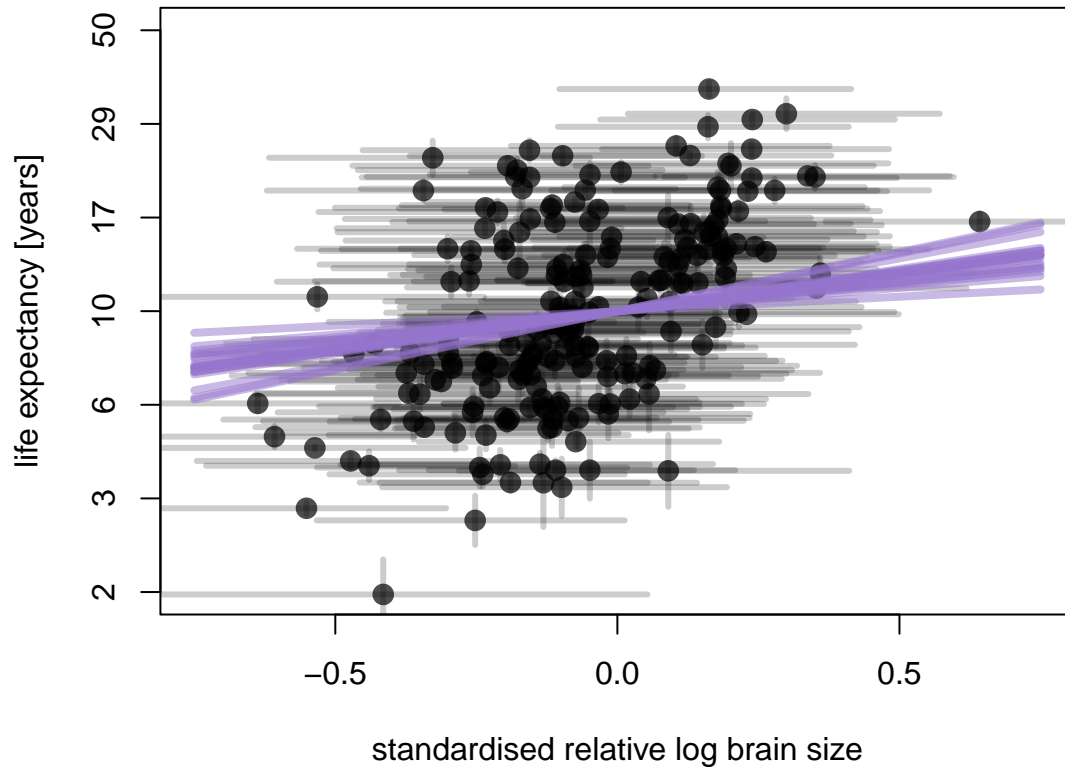
Figure 2: Slope estimates for predictor variables and phylogenetic signal in model 2. For insularity the difference between islandic and continental species is shown. Grey density plots and lines are the regularising priors. Coloured areas are the posterior densities for the parameters. Black lines are 20 samples of the posterior for the phylogenetic covariance.

Scatterplot

This chunk plots the relative brain size vs life expectancy plot to pdf.

```
## pdf
## 2
```

```
\begin{figure}
```



```
{
```

```
}
```

```
\caption{Standardised relative log brain size vs life expectancy for model 2. Pink points represent species where life expectancy was available, pink vertical lines represent the SE for life expectancy. Grey points represent imputed values for life expectancy, grey vertical lines represent the 89% PI for life expectancy. Horizontal lines (pink and grey) represent the 89% PI for standardised relative log brain size. Purple lines represent 20 samples from the posterior for the slope (beta) of the effect of standardised relative log brain size on life expectancy. Standardised relative log brain size is defined in equation X.}
```