



# Phylogenetic Applications for Comparing United States Senators



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## Introduction / Research Questions

Reconstructing an evolutionary tree helps define relationships among entities based on similarities and differences in their genetic characteristics. DNA is the basis for understanding how species are related. Comparisons of genetic material focus on the mutations caused by random processes and preserved or eliminated by natural selection. The beliefs and processes that motivated biologists to track genetic mutations can also be applied to other fields. This research applies the methods of phylogenetic tree inference to try to answer three specific questions:

- Is partisan politics truly present within our government (specifically the United States Senate)?
- If partisanship is present, can its severity be seen in those records?
- Is evolution of an individual's voting habits tree-like?

## Methods

Biological models require quantifiable variation among individuals in order to compare a population. The voting habits of Senators provide a visible way to compare individuals, as the outcomes of specific votes can be used to mimic different bases in a DNA sequence.

- To meet the criteria of models designed to compare multiple organism's genetic material, when selecting votes the following criteria were met: any vote used must have an objective and independent result (compared to other votes), and votes cannot be chosen with regard to the Senators being compared. This selection process was repeated for votes during the 101<sup>st</sup> -112<sup>th</sup> Senates.
- For each acceptable vote, a Senator's response was recorded in binary ("Yea"=1, "Nay"=0). If a Senator was absent or decided not to participate in a vote, this lack of information was treated as missing data. I appended a second copy of the data with the states completely reversed to increase the length of each Senator's "DNA" strand.

## Software and Model Choice

- I chose to use MrBayes, a program for Bayesian inference using Markov Chain Monte Carlo methods, to estimate the posterior distribution of model parameters.
- My choice to describe "Yea" and "Nay" votes as 1 and 0 respectively was arbitrary, and I needed to select a model within MrBayes that incorporated this labeling system.
- I used a Standard model analogous to a 2-state JC model. All of the rates of change are equal, and the model will produce results that are the same regardless of the way in which each state was labeled.

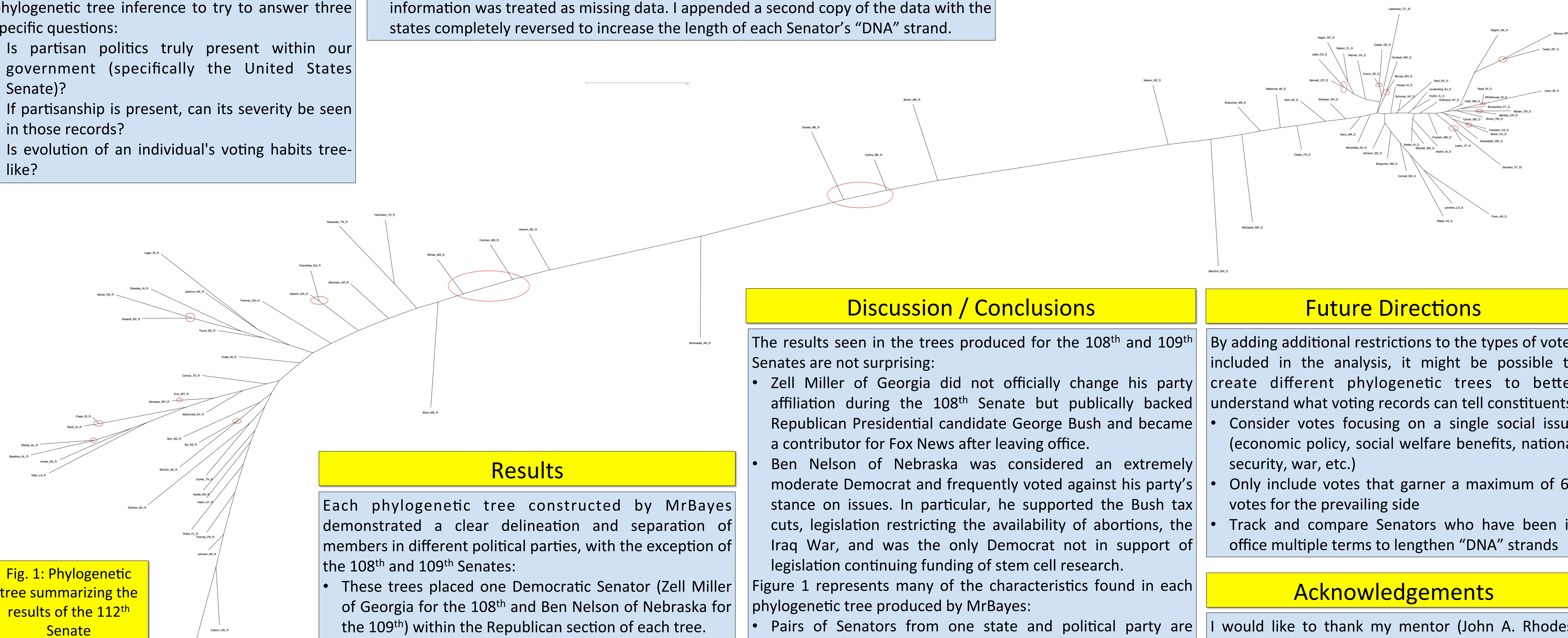
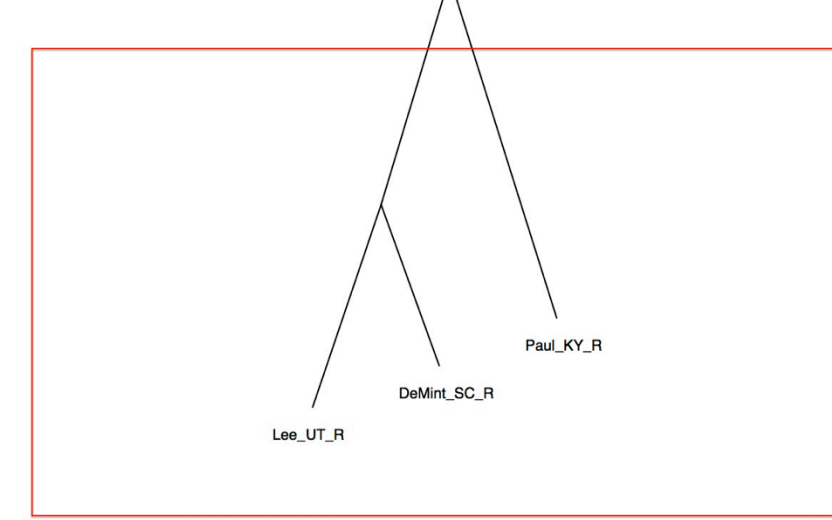


Fig. 1: Phylogenetic tree summarizing the results of the 112<sup>th</sup> Senate



## Results

Each phylogenetic tree constructed by MrBayes demonstrated a clear delineation and separation of members in different political parties, with the exception of the 108<sup>th</sup> and 109<sup>th</sup> Senates:

- These trees placed one Democratic Senator (Zell Miller of Georgia for the 108<sup>th</sup> and Ben Nelson of Nebraska for the 109<sup>th</sup>) within the Republican section of each tree.

All of the trees not only summarized political connections between Senators but also geographical relationships:

- Senators representing the same state (and members of the same political party) were often grouped together.
- Groups of Senators from the same geographical region of the United States were often grouped together.

## Discussion / Conclusions

The results seen in the trees produced for the 108<sup>th</sup> and 109<sup>th</sup> Senates are not surprising:

- Zell Miller of Georgia did not officially change his party affiliation during the 108<sup>th</sup> Senate but publically backed Republican Presidential candidate George Bush and became a contributor for Fox News after leaving office.
- Ben Nelson of Nebraska was considered an extremely moderate Democrat and frequently voted against his party's stance on issues. In particular, he supported the Bush tax cuts, legislation restricting the availability of abortions, the Iraq War, and was the only Democrat not in support of legislation continuing funding of stem cell research.

Figure 1 represents many of the characteristics found in each phylogenetic tree produced by MrBayes:

- Pairs of Senators from one state and political party are denoted with a red circle (w/ 16 of 25 possible pairs present).
- The tree separates all factions within the Senate: Democrats are on the right, Republicans on the left, and the Tea Party Caucus is contained in the red square.

With these results, it is reasonable to conclude that partisan politics is present within our governmental structure and its severity is visible within a US Senator's voting records.

## Future Directions

By adding additional restrictions to the types of votes included in the analysis, it might be possible to create different phylogenetic trees to better understand what voting records can tell constituents:

- Consider votes focusing on a single social issue (economic policy, social welfare benefits, national security, war, etc.)
- Only include votes that garner a maximum of 60 votes for the prevailing side
- Track and compare Senators who have been in office multiple terms to lengthen "DNA" strands

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