No-analogue ecological communities since the Last Glacial Maximum inferred from fossil pollen records for North America

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Abstract: Anthropogenic climate change may require adaptation strategies that include predicting and managing no-analogue ecological communities. This study contributes an analysis of 51,427 palaeoecological pollen records from 1,384 North American locations, with the objective to (1) discover no-analogue communities of the past, (2) infer the cause of their emergence, and (3) test if they can retrospectively be predicted. The analysis revealed three pollen communities that have no modern equivalent. The most widespread no-analogue community was a birch parkland ecosystem, which also occupied distinct no-analogue climate space. The analysis also revealed a spruce woodland with a high diversity of broadleaf species and a montane steppe ecosystem in the Rocky Mountains with no modern equivalents. While species distribution models could accurately hindcast species frequencies in most palaeoecological communities, they failed to predict the unique characteristics of each no-analogue community, highlighting the limitations of predictive modeling to support climate change adaptation.

(Selected Figures and Tables provided below, for more information, contact the author)

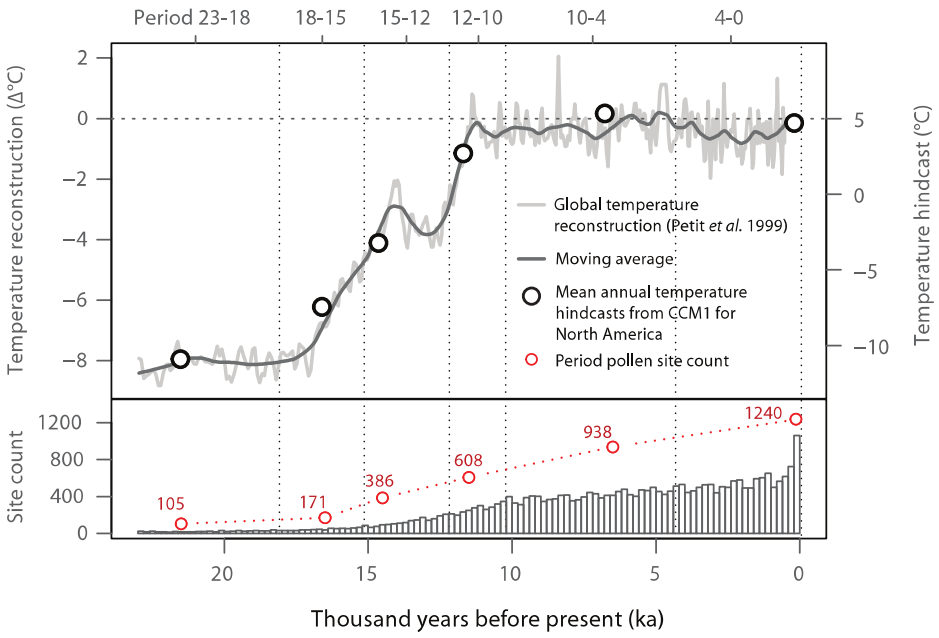

Fig. 1. Reconstructed temperature and available pollen sites for six periods from the Last Glacial Maximum to present. Global temperature reconstruction from ice cores proxy (*25*) were used to delineate periods that approximately represent CCM1 climate model hindcasts for 21, 16, 11, and 6 thousand years before present. Red circles represent the cumulative number of available pollen sites for each of the six periods, and the number of pollen sites for 200-year intervals are shown as a histogram.

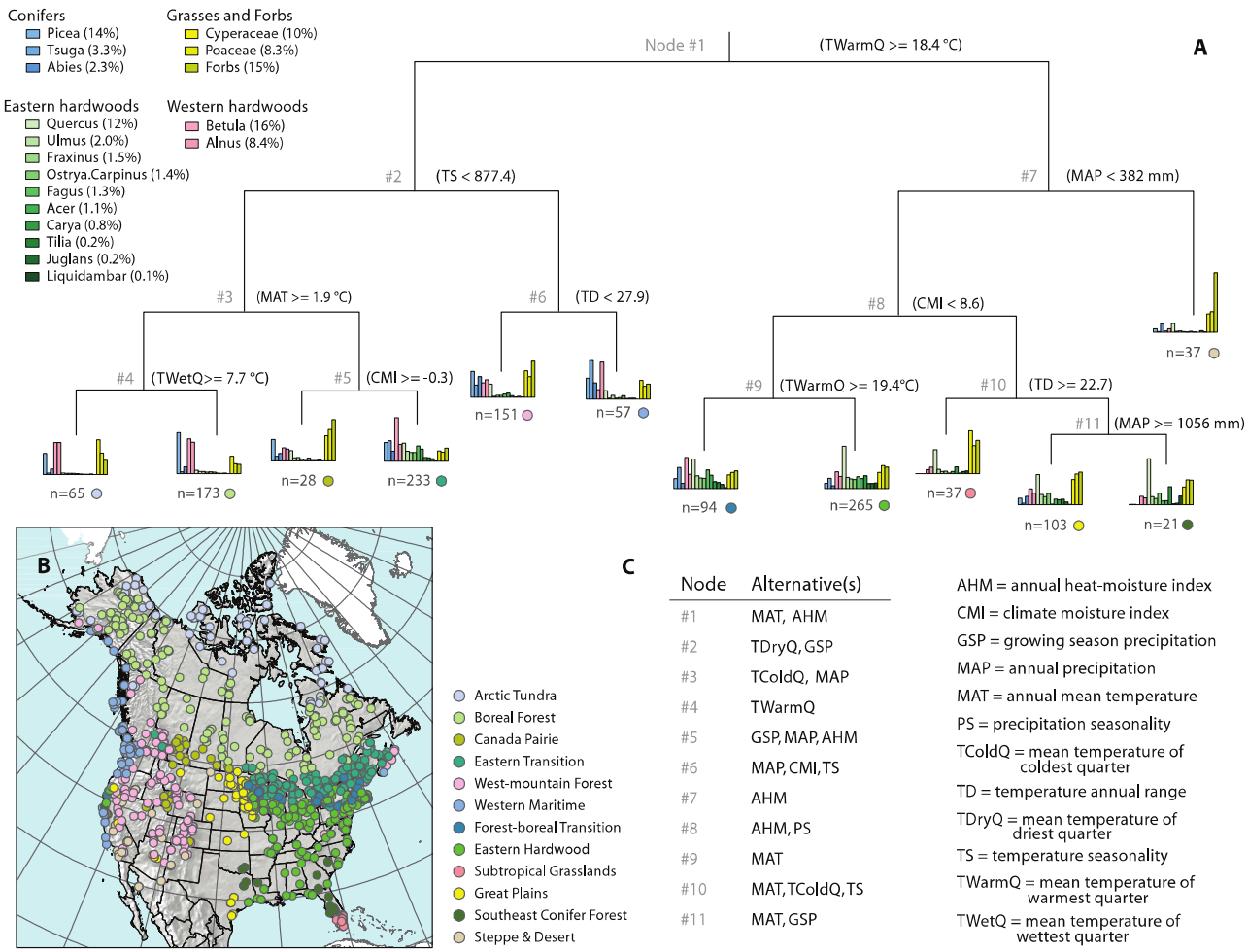

Fig. 2. Clustering modern pollen data with Multivariate Regression Tree (MRT) analysis. The regression tree for modern pollen data **(A)** reports the primary climate variable and its value for each split, the number of pollen communities, and the square root transformed frequency of pollen taxa as a bar chart. The overall frequency of pollen taxa across all sites is reported in parenthesis in the legend. The colors and the order of the legend in the map of pollen sites **(B)** correspond to the groups determined by the MRT above. Auto-correlated climate variables that could have been used as alternative criteria for each split are reported in panel **(C)**.

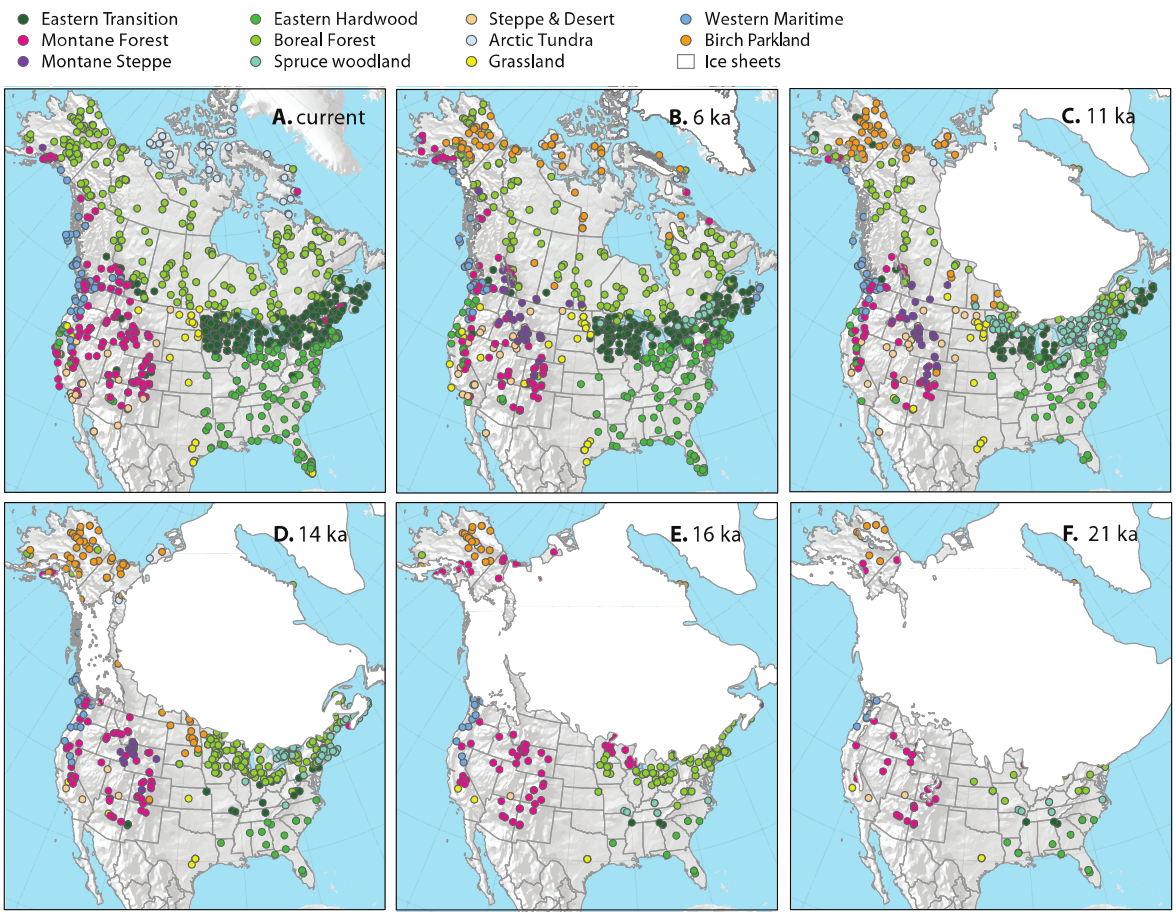

Fig. 3. Geographic distribution of eleven bioclimatic zones for six periods since the Last Glacial Maximum. The eleven pollen groups are based on an initial 22 groups generated by a regression tree analysis across all time periods, which were subsequently summarized into 11 groups in this map for concise reporting, but maintaining all no-analogue communities that were detected (Montane Steppe, Birch Parkland and Spruce Woodland).

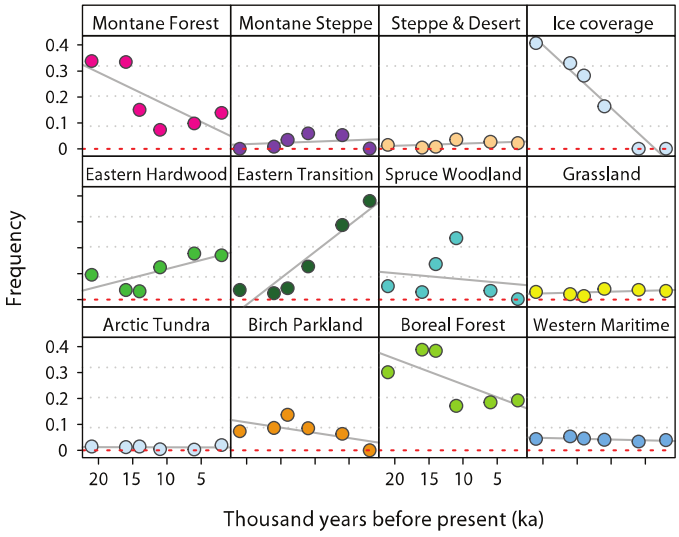

Fig. 4. The relative frequencies of pollen groups from the Last Glacial Maximum to present. Frequencies of eleven pollen communities for six periods are given as percent of all pollen sites available per period. Ice coverage as percentage of total land area is additionally included for reference (top right).

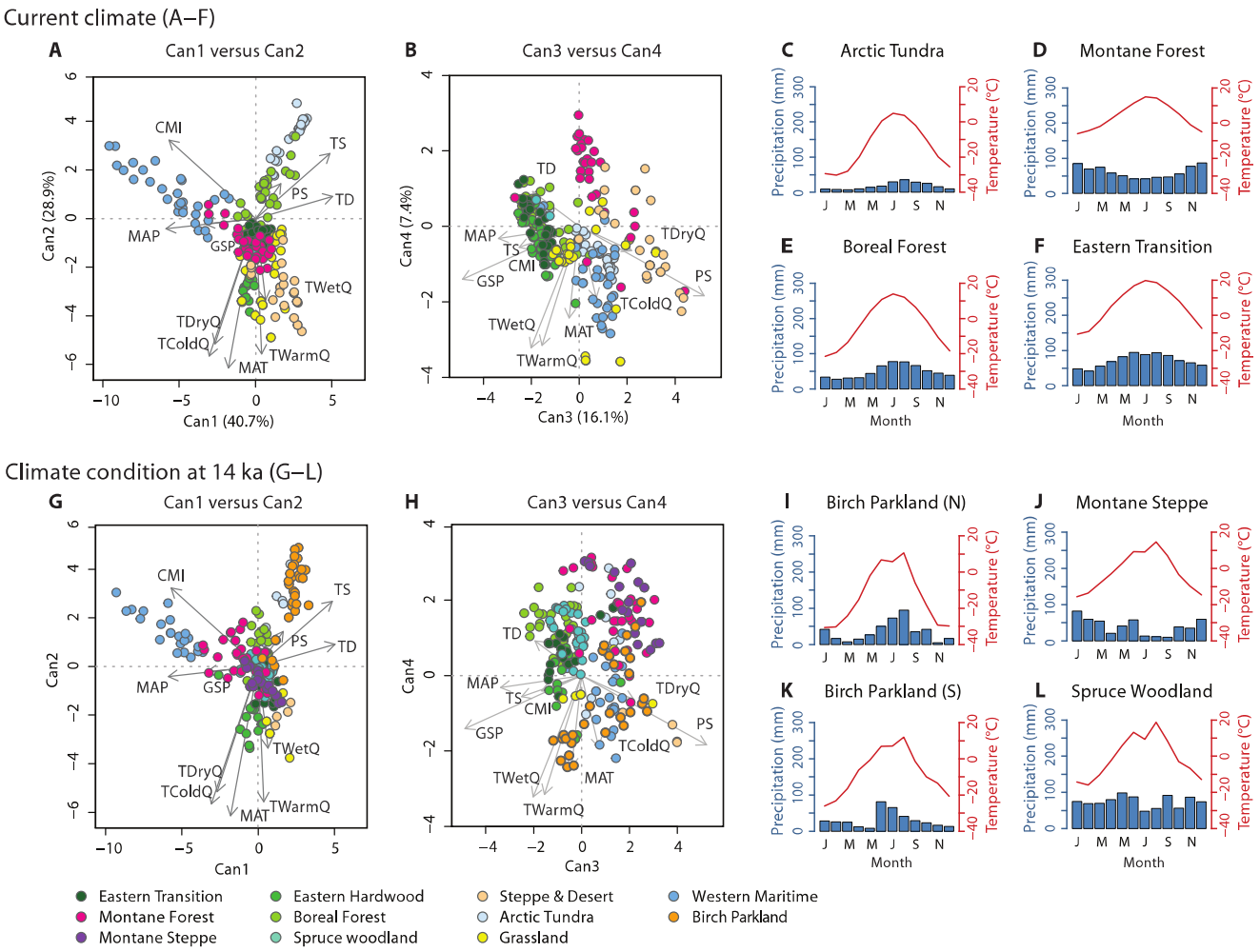

Fig. 5. Multivariate climate conditions for pollen groups and climate diagrams for selected pollen groups. Canonical discriminant analysis of pollen sites in multivariate climate space for current cliamte and climate at 14 ka. Plots for all six climate periods are provided in Fig. S1. The vectors in the canonical discriminant analysis (**A**, **B**, **G**, and **H**) show how pollen comunities are associated with climate variables. Climate variable abbreviations are provided in Fig 2. Selected standard monthly climate diagrams are further provided for four modern pollen communities **(C** to **F)**, and the no-analogue communities **(I** to **L)** where separate diagrams represent Birch Parkland climate conditions in Beringia (**I**) and soutth of the ice sheet (**K**).

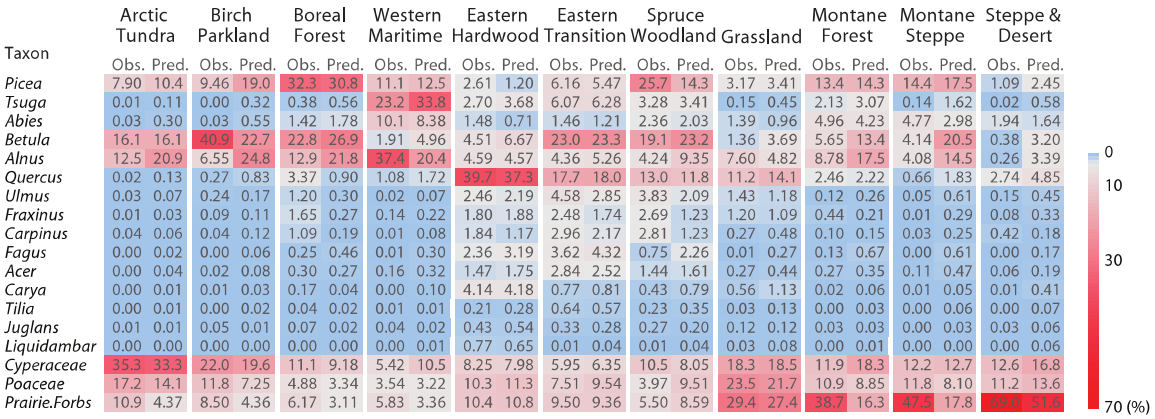

Fig. 6. Average pollen frequencies observed in pollen records and predicted by species distribution models for each taxon. The left column (Obs.) represents the average taxa percentages for eleven pollen groups determined with multivariate regresssion tree analysis. The right column (Pred.), reports the predicted pollen percentages from separate species distribution models for each taxon trained with modern pollen data only. The color legend highlights near absence (blue) and dominant taxa (red).