

Table 1: Parameters used in random forest models to disentangle the effects of climate and humans on the extinction dynamics of woolly mammoths.

Parameter	Description
X_RangeArea	<i>Range area</i> Range area scaled by population size at the start of the analysis period Defined as the number of 1° x 1° cells with mammoth population > 0 divided by mammoth total population abundance.
ClimX_MagCh_Cont[#]	<i>Climate suitability magnitude</i> Percentage change in climatically suitable cells (cells with climate-driven upper abundance > 0; see Supplementary Material). Defined as $((t_1 - t_{\min})/t_1) * 100$; where t_1 is the number of climatically suitable cells at the first time step of the window and t_{\min} is the minimum number of climatically suitable cells in the analysis window.
ClimX_Pace_S[†]	<i>Climate suitability pace</i> Pace of change in climatically suitable cells. Defined as the mean of the slopes of linear models of climatically suitable cells across time.
ClimX_Cent_Pace_S[†]	<i>Climate centroid pace</i> Pace of change in climate centroid (a weighted measure based on the geographic distribution of climate-driven upper abundance). Defined as the mean of the slopes of linear models of centroid northness across time.
ClimX_Frag[#]	<i>Climate fragmentation magnitude</i> Magnitude of fragmentation of climatically suitable cells. Defined as the $T_{\max} - T_1$, where T_{\max} is the maximum fragmentation during the analysis window, and T_1 is the fragmentation at the start of the window. Calculated using GISFrag metric. See https://gist.github.com/scbrown86/7789d5e49349d37312eadb6a3e6e1742 for R code.
ClimX_Frag_Pace_S[†]	<i>Climate fragmentation pace</i> Pace of fragmentation. Defined as the mean of the slopes of linear models between the amount of habitat fragmentation and time
HumX_MagCh_Exp[#]	<i>Human expansion magnitude</i> Percentage change in human occupied cells (cells with human abundance > 0). Defined as $((t_{\max} - t_1)/t_1) * 100$; where t_{\max} is the maximum number of occupied cells in the analysis window and t_1 is the number of occupied cells at the start of the window.
HumX_Pace_S[†]	<i>Human expansion pace</i> Pace of human occupation (i.e., change in range area). Defined as the mean of the slopes of linear models of number of human occupied cells across time.
HumX_Cent_Pace_S[†]	<i>Human centroid pace</i> Pace of change in human centroid (a weighted measure based on the geographic distribution of human abundance). Defined as the mean of the slopes of linear models of centroid northness across time.
HumX_PopCh_Final[#]	<i>Human population change magnitude</i> Magnitude of total population change. Defined as $T_{\text{final}} - T_1$; where T_{final} is the human abundance at the end of the analysis window and T_1 is human abundance at the start of the analysis window.

[#] = a 3-generation (75 year) smoother was applied to the data before calculating min/max values.

[†] = Values were calculated over a 3-generation moving window (i.e. a 75 year moving average).

X in the parameter names above indicates several different analysis periods in Appendix 3 (Fig. 3-5): 2I = 21 ka BP to 15 ka BP; 15 = 15 ka BP to 11 ka BP; 11 = 11 ka BP to 5 ka BP; OD = Oldest Dryas (17.5 ka BP to 15 ka BP); BA = Bølling–Allerød (12.9 ka BP to 11.7 ka BP).