# Virtual Neanderthals : a study in agent-based modelling Late Pleistocene hominins in western Europe
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# 11.    ANALYSIS

## 11.1        Introduction

When constructing realistic models, one of the major issues when attempting to describe reality is over-parameterization. Over-parameterized models contain elements that are not constrained by the dataset and where realistic values cannot be determined for all variables. In general, while analysing simulation results one of the implicit aims is to identify those parameters in the model that are significant for the subject being studied (Ligmann-Zielinska *et al.* 2014). This study attempts to construct a realistic but parsimonious Neanderthal model and to find values for the model parameters while exploring hypotheses on Neanderthal behaviour in the landscape. The analysis of the results from all simulations is done in the following sections:

1.  First the validity of the approach is tested in Section 11.2 by analysing correlations (a) between input model parameters and (b) between the `matchedIntervalCoverage` output variable and other output variables. There should be limited correlation between model parameters and maximum correlation between output variables.
2.  The bulk of this chapter is Section 11.3 which contains a sensitivity analysis of the model parameter values from the different scenarios. This includes a variability assessment, identification of correlations in the Standard and Evolved data sets, relative variable importance calculations, and the identification of monotonic trends in parameter value selection.
3.  Section 11.4 presents trends in the simulation output data. This reflects the effect of the genetic algorithm with the evolution of the parameter value set. For each scenario that is explored first the Standard set of simulations is executed. Those model parameter sets that perform best in all scenarios are characterized. This section also presents data on the quality of the archaeological input and a reflection on the different causes of life and death in the simulations.
4.  The modelled environment is analysed in detail in Section 11.5. Key locations in the simulation area were monitored with Climate Monitoring Checkpoints throughout the simulation period. Data from these checkpoints is used in the analysis of the environment reconstruction. An important element of the reconstructed environment is the sea level. The effects of fluctuations in this level are analysed by identifying critical points in time and presenting the resulting topography for those points in time.

A set of R-scripts was developed for the automated mathematical analysis of the simulation results and to produce the relevant data. Instead of manual manipulation of data and creation of output representation such scripting is essential to allow proper replication

of the research and reproduction of the results ([Marwick 2017](#)). These scripts are used to generate the data, tables and figures in this chapter. The scripts and their output are listed in Appendix 2 and included verbatim in the Supplementary Materials.

## 11.2 Correlating input to input and output to output

The HomininSpace system attempts to estimate parameter values by fitting them to measured archaeological data using an optimization technique based on genetic algorithms. To avoid non-identifiability issues where correlations between model parameters make good estimates for individual parameter values difficult it is important to verify that input parameters are not strongly correlated with each other, and thus can be varied independently.

Here I analyse pair-wise (or one dimensional) correlations in the Standard parameter values set. Since the genetic algorithm modifies model parameters slightly between generations introduced correlations can be expected in the Evolved sets, so I focus on the Standard set only. Strong correlations reveal parameter combinations for which good fitting values would be difficult to obtain. The strongest correlated negative and positive input model parameter to input model parameter correlations, from the Standard set are `Years_Before_Group_Maturity` with `Max_ForagingRange`, correlated at -0,0692 (p = 0,01), and `Subsistence_PreFertileCohort` with `GroupSizeFertile_BeforeMerge`, with a correlation of +0,0601 (p = 0,02).

The correlation values show that even the strongest correlations are not very strong (as expected and required). Both the most negative and most positive correlation are significant with a *p* value higher than or equal to 0,01. All other correlations between model parameters are less strong. Note that these correlations are the same for all scenarios since the values for the input parameters in the Standard set are the same in all scenarios and were randomly generated, independent of other model components.

The output variable `matchedIntervalCoverage` is used to assess the validity of the simulations, with a larger value suggesting a better match with the archaeology. But there are several other output variables included in the output data sets, attempting to characterize the match with the archaeology in a slightly different manner. To ensure a relevant and optimal characterization I show here that these do significantly correlate with the selected variable `matchedIntervalCoverage`. Again the pair-wise correlation from the sensitivity analysis is used to describe the relationships between the different

output variables for the simulated scenarios. Figure 68 presents as a representative sample the results for scenario Habitat-A, with all settings to False. All other scenarios have similar results.

Figure 68 presents the pair wise correlations between all output visit counting variables in a Correlation Matrix, showing the Spearman's correlation coefficients between variables. In such a matrix the same variables are used for the rows as well as for the columns (so variable `matchedIntervalCoverage` is used for the data in the first row and the first column). In this specific format, the matrix presents the correlations in the top-right part with significant correlations indicated by three red dots. In the bottom left part of the matrix variables of the intersecting row-column combination are plotted against each other, illustrating the nature of the correlation.

The weakest correlation between `matchedIntervalCoverage` and the other general visit counting output variables has a significant correlation coefficient of 0.89, which is considered very strong. This is with the `totalCSTVisits` variable that keeps track of all visits to the checkpoint inside or outside an interval. The correlation with the variables that keep track of the times that a group during a visit selects the exact same grid cell as the checkpoint as their home range grid cell are slightly weaker (0.73 for those inside an interval and 0.75 for any visits outside intervals). The correlation with the absence visits is weakest with a significant value of 0.61. All correlations are positive. The strengths of these correlations indicate that the value for `matchedIntervalCoverage` can be used to assess the simulation results without need to perform similar analyses for the other variables.

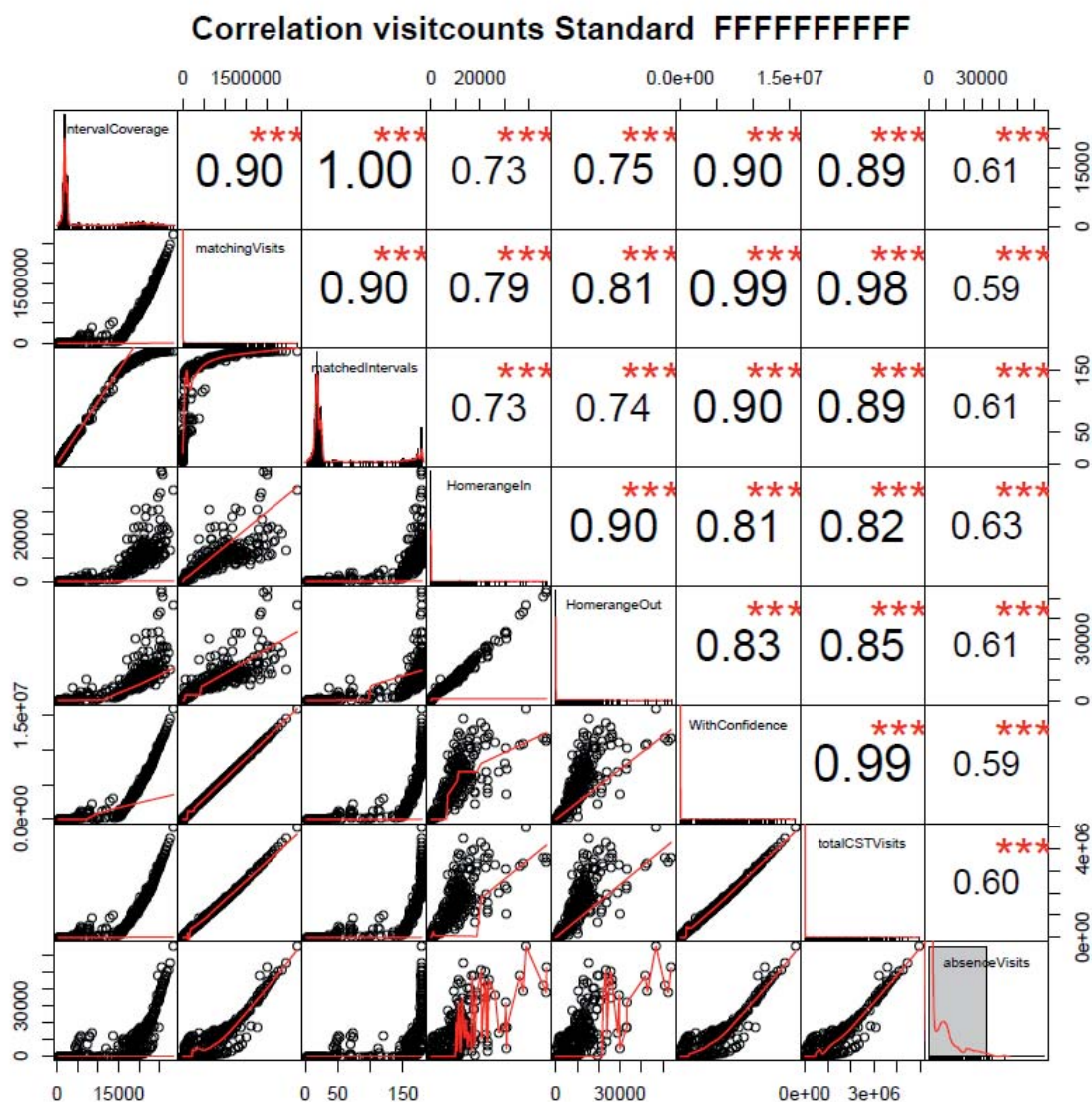**Correlation visitcounts Standard FFFFFFFFFF**



**Figure 68: Correlations between the different visit counting output variables for scenario Habitat-A. Top right part of the matrix contains the correlations. Three red stars indicate a significant correlation. Bottom left part are plotted values.**

## 11.3 Sensitivity analysis in scenario exploration

Sensitivity analysis for simulations is the exploration of the model input parameter values and the associated output results. The aim is to identify those parameters for which small changes cause relevant changes in the output (Ligmann-Zielinska *et al.* 2014). The results can aid in model simplification and improved model accuracy. Here the analysis will contribute to answer specific questions. Note that the use of a genetic algorithm includes a build-in sensitivity analysis when recombining parameter values as the method aims to find those parameters that matter most (Lee *et al.* 2015).

## 11.3.1    Variability in scenarios

Diversity in the simulated models (more specifically, in the model parameter values as optimized by the genetic algorithm) can be graphically explored by displaying the model parameters as visual elements in a larger picture. In HomininSpace there are 16 variables in 18 scenarios with each more than 2000 simulations. Visualizing trends, detecting patterns and identifying outliers in graphs becomes difficult for such large numbers of data items (Guha and Assaf 2018). Graphs for selected variables are easier to interpret, but selection must be guided. Assuming that humans are capable of assimilating data encoded in human faces, complex multivariate data can be presented where the variables each represents the feature of a face (Chernoff 1973). For instance, normalized birthrate values can be used to represent the height of an abstract face (

Figure 69).



Width of the hair: Calories_Per_Kg_Meat

Height of the face: BirthRate

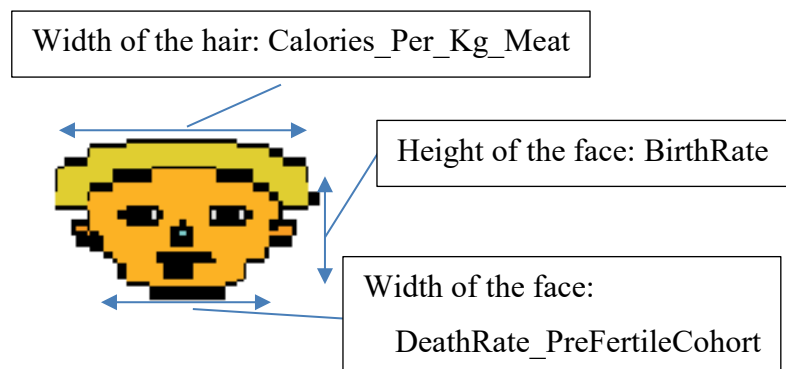Width of the face:
DeathRate_PreFertileCohort

**Figure 69: Explaining three parameter values used to construct Chernoff faces.**

Figure 70 present faces for the top 10 models of all scenarios. The following values are used for the face shape variables:

1-height of face (`BirthRate`);
2-width of face (`DeathRate_PreFertileCohort`);
3-shape of face (`DeathRate_FertileCohort`);
4-height of mouth (`DeathRate_PostFertileCohort`);
5-width of mouth (`Subsistence_PreFertileCohort`);
6-curve of smile (`Subsistence_FertileCohort`);
7-height of eyes (`Subsistence_PostFertileCohort`);
8-width of eyes (`CohortSize_PreFertile`);
9-height of hair (`CohortSize_Fertile`);
10-width of hair (`Calories_Per_Kg_Meat`);
11-styling of hair (`Max_ForagingRange`);
12-height of nose (`Temperature_Tolerance`);
13-width of nose (`Years_Before_Group_Maturity`);

14-width of ears (`GroupSize_BeforeMerge`);
15-height of ears (`GroupSize_BeforeSplit`).

Note that `GroupSizeFertile_BeforeMerge` is not included since that parameter varies little. To add additional discriminative characteristics colors are also coded. For painting elements of a face the colors of are found by averaging of sets of variables: (7,8)-eyes:iris, (1,2,3)-lips, (14,15)-ears, (12,13)-nose, (9,10,11)-hair, (1,2)-face. For the data set a top-10 of best performing models per scenario is selected, ranking based on the `matchedIntervalCoverage` score. An R-script is written to create Figure 70, with the top-10 model parameter values for each scenario ("Analysis draw faces.R", included in the Supplementary Materials, as is the produced output file with the top-10 for each scenario)[42]. Each row contains the data for one scenario, where the first column contains the best performing model parameter value set, the second row the second best performing model, etc. Faces 1 to 10 belong to scenario 1 (Habitat-A); faces 11 – 20 are produced in scenario 2 (Habitat-B), etc.

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[42] This uses the *aplpack* package with the *faces* routine to draw the faces.

**Figure 70: Chernoff faces representing model parameter values for all 18 scenarios, illustrating variability within the top-10 best performing models per scenario (line), with the best scoring model numbered 1 (leftmost).**

While most scenarios have more or less variety in their faces, it immediately becomes clear that scenarios 4 and 6 show hardly any variation at all in their top-10. They have evolved very similar solutions (  , with very low birth rates and high death rates for the pre-fertile cohort). These scenarios implement the absence criterion. Also scenario 5 has limited variation upon  with high birth rates and low death rates, almost the opposite of the scenarios 4 and 6. The two outliers in scenario 2 (wide faces, numbers 15 and 16) are solutions characterized by very high death rates in the pre-fertile cohort, accompanied by high birth rates. In scenario 12 (111-120) all faces sport narrow split eyes with only faces numbered 117, 119, and 120 have round eyes. These last three individuals have very high subsistence needs for the post-fertile cohort. Similarly, in scenario 15 some faces have

wide mouths, indicating high subsistence needs for the pre-fertile cohort (143, 145, 146, and to a lesser extent 141 and 148).

The Chernoff faces representing model parameter values illustrate the variability within each scenario (or the lack thereof), and also suggests that certain types of value combinations perform better in one scenario than in another. A detailed interpretation of this variability is however impossible from the images alone and a deeper exploration of the relation between model parameter values and simulation results follows below.

11.3.2          Correlations between parameter values and simulation results

A correlation analysis aims to see if two measured variable co vary in a linear relationship and quantifies the strength and direction of this relation. Values range from -1.0 for a negative linear relation via 0 with no linear relation to +1.0 for a positive linearity between the two variables. Care must be taken when interpreting correlations, since a third factor can cause the correlation and therefore correlation is not by definition causation (Aldrich 1995). Correlations that are presented here are Spearman's rho rank correlation coefficients. Missing values are deleted, with mid-ranks used in case of ties (Hollander and Wolfe 1973). P-values are approximated by using t of F distributions, and correlations with P-values smaller than 0.01 are removed because they are considered insignificant and are not shown for clarity (for a general discussion about the choice of the 0.01 value for meaning 'very significant' see Nuzzo (2014)).

Spearman's rho rank correlation is used because this does not require input parameter values to satisfy of any assumptions about the distribution of the data. Spearman does not require a normal distribution as for instance the Pearson correlation method (Fletcher and Lock 2005). The random created values of the Standard set and the recombined values in the Evolved set both violate the Pearson correlation assumptions of variable value distribution. Spearman's rank order correlation measures the strength and direction of the associations between ranked, monotonic variables. The results are calculated per batch and should be interpreted as an index of sensitivity (Grimm and Railsback 2005). Using a more conservative P-value of 0.001 to avoid spatial auto-correlation does not create a different picture (as suggested in Wiegand et al. (2004)).

Table 46 presents the correlations for the Standard sets of all batches that were explored. The correlations for the Standard sets must be compared with those for the Evolved parameter sets, with parameter values that have been improved by the GA. The nature of

the values for the randomly generated Standard set and the directionally improved Evolved set are different. Correlations for the complete set would of course average the values for Standard and Evolved sets. The Spearman correlation coefficients for the Evolved set are presented in .

**Table 46: For all Standard sets the significant Spearman correlation coefficients for parameters versus matchedIntervalCoverage. Green are positive correlations, red negative. Darker colors indicate stronger correlations.**

| Scenario (Standard) | BirthRate | DeathRate_PreFertileCohort | DeathRate_FertileCohort | DeathRate_PostFertileCohort | Subsistence_PreFertileCohort | Subsistence_FertileCohort | Subsistence_PostFertileCohort | Years_Before_Group_Maturity | GroupSize_BeforeMerge | GroupSizeFertile_BeforeMerge | GroupSize_BeforeSplit | Temperature_Tolerance | CohortSize_PreFertile | CohortSize_Fertile | Calories_Per_Kg_Meat | Max_ForagingRange | ViabilityIndex |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Habitat-A | 0.45 | -0.24 | -0.45 | | | 0.10 | 0.07 | | | -0.17 | 0.21 | -0.14 | -0.08 | | -0.13 | | 0.66 |
| Habitat-B | 0.38 | -0.22 | -0.40 | | | 0.12 | 0.08 | | | -0.20 | 0.25 | -0.12 | -0.09 | | -0.12 | | 0.58 |
| Habitat-C | 0.38 | -0.19 | -0.45 | | | | | | | -0.19 | 0.09 | -0.14 | | | -0.09 | 0.22 | 0.59 |
| Habitat-D | -0.20 | 0.12 | 0.19 | | | | 0.09 | | | -0.25 | -0.09 | | | | | -0.43 | -0.24 |
| Habitat-E | 0.33 | -0.15 | -0.42 | | | | | | | -0.18 | 0.14 | -0.31 | | | | 0.39 | 0.51 |
| Habitat-F | -0.35 | 0.19 | 0.35 | | | -0.07 | -0.08 | | | -0.17 | -0.07 | | | | 0.10 | -0.19 | -0.52 |
| Habitat-G | 0.41 | -0.24 | -0.41 | | | 0.09 | 0.08 | | | -0.10 | 0.17 | -0.13 | | | -0.09 | | 0.61 |
| Habitat-H | 0.46 | -0.27 | -0.36 | -0.18 | | | 0.08 | -0.09 | | 0.16 | 0.19 | -0.15 | | | -0.10 | | 0.71 |
| Habitat-I | 0.26 | -0.13 | -0.33 | | | | | | | -0.12 | | | | | | 0.60 | 0.41 |
| Habitat-J | 0.27 | -0.12 | -0.34 | | | | | | | -0.12 | | | | | | 0.60 | 0.41 |
| Energy-A | 0.45 | -0.25 | -0.48 | | 0.08 | 0.13 | 0.10 | | | -0.17 | 0.17 | -0.13 | -0.08 | | -0.14 | | 0.68 |
| Energy-B | 0.25 | -0.12 | -0.36 | | 0.07 | 0.07 | | | | -0.15 | | -0.11 | | 0.08 | | 0.31 | 0.45 |
| Energy-BR | 0.25 | -0.11 | -0.33 | | | | | | | -0.16 | | -0.21 | | | | 0.54 | 0.38 |
| Energy-C | 0.13 | | -0.17 | | 0.07 | 0.10 | | | | -0.10 | | -0.07 | | | -0.07 | | 0.23 |
| Energy-CR | 0.07 | | -0.14 | | | | | | | -0.10 | | -0.10 | | | | 0.32 | 0.11 |
| Energy-D | 0.26 | -0.12 | -0.36 | | 0.07 | 0.07 | | | | -0.16 | | -0.11 | | 0.08 | | 0.32 | 0.45 |
| Energy-E | 0.19 | -0.07 | -0.30 | | | | | -0.09 | | -0.14 | -0.08 | | | | | 0.71 | 0.33 |
| Energy-ER | 0.19 | -0.09 | -0.31 | | | | | -0.09 | | -0.14 | -0.08 | | | | | 0.72 | 0.34 |

When analysing the correlation results for the Standard sets, the following general patterns stand out:

- Overall there is a strong positive correlation between birth-rate and simulation results, and a corresponding negative correlation with the death rate of the fertile cohort. There is also a noticeable negative correlation overall with the death rate of the pre-fertile cohort;
- There is an overall but not large negative correlation with group size fertile before split, and a similar but smaller correlation with the temperature tolerance. The group size before split is more positive;
- The maximum foraging range is generally strong and positively correlated with the simulation results;
- The viability index (a value calculating the effectiveness of the demographic model alone) has a very strong and positive correlation with the simulation results.

These are general trends where the actual values for the correlations differ per batch. There are two noticeable exceptions, and those are batches Habitat-D and Habitat-G. Values for

correlations for both batches are opposite of the described trends above. Both batches explore a combination of a limited foraging range, the production from core areas and a limiting absence restriction. Since most checkpoints are in the south of the simulation area, where also the core areas are located, most matches with the archaeology can here be obtained from Neanderthals that do not disperse quickly to the north, where the absence check (access to the UK) is implemented. Lower birth rates and higher death rates will actually accomplish that (since new groups will be produced from core areas anyhow), as will smaller foraging ranges (since the foraging range also defines how far a dispersal event can reach per time step). Note that it is the combination that restricts the parameter values, since Habitat-B (absence) and Habitat-C (maximum foraging range) do not exhibit this divergence from the general pattern.

A positive correlation for simulation results with birth rates, and negative correlations with death rates for the pre-fertile and even stronger for the fertile cohort suggests that more Neanderthals is better. This is a general phenomenon that is easily understood: the more groups there are in space and time, the better the overall chances for an improved match with the archaeology. There is one limit to an omni-present Neanderthal, and that is a limiting carrying capacity. There is only so much food in the environment, which also fluctuates with a changing climate and is consumed by present Neanderthals. However, many correlations can be better understood with the tendency to fill the area with Neanderthal groups in mind. The non-correlation with the death rate for post-fertile Neanderthals can be understood in this context: they do no longer contribute to more Neanderthals, and a higher death rate would not influence the number of new Neanderthals.

Also, groups that live longer can help with a better match with the archaeology. For instance a larger foraging range will allow a group to retrieve resources from a larger area and this will keep Neanderthals alive, even when circumstance deteriorate. Those batches that are not correlated with the maximum foraging do not have the setting Maximum Foraging range activated (batches Habitat-A, Habitat-B, Habitat-E, and Habitat-H; note that Energy-C with an activated Maximum range also does not correlate this value to the simulation results). A lower value for the temperature tolerance means better survival chances when average temperatures drop, and this would explain the negative correlation with this parameter. Since only few checkpoints are in areas known to become cold, the correlation is not very strong.

An overall negative correlation with the parameter group size fertile before merge means that smaller values lead to better results. A lower value means that groups will more quickly attempt to merge with other groups if there are fewer individuals in the fertile cohort, increasing survival changes for the group members. A more positive correlation of the GroupSize_BeforeSplit parameter means that it requires a larger group before the group is forced to split into two groups. Smaller groups are more vulnerable, especially in the areas where the climate deteriorates more or faster (generally, the northern sections of the simulation area).

Therefore it is very surprising that there is overall no negative correlation with the subsistence parameters. One expects that lower energy needs would allow for more Neanderthals. For instance this can explain the effect of the (small) negative correlation with the Calories_Per_Kg_Meat. Also surprising is the absence of any correlation with the CohortSize_Fertile, since a larger value for this parameter allows a female Neanderthal to conceive more Neanderthal babies. One would also expect a positive correlation with the DeathRate_PostFertileCohort, since post-fertile Neanderthals only consume resources and are not expected to contribute to survival of the group as such.
Years_Before_Group_Maturity and GroupSize_BeforeMerge are also parameters that are not correlated with the simulations results at all.

**Table 47: The Spearman correlation coefficients of the Evolved sets for parameters versus matchedIntervalCoverage. Green are positive, red are negative correlations.**

| Scenario (Evolved) | BirthRate | DeathRate_PrefertileCohort | DeathRate_FertileCohort | DeathRate_PostfertileCohort | Subsistence_PreFertileCohort | Subsistence_FertileCohort | Subsistence_PostFertileCohort | Years_Before_Group_Maturity | GroupSize_BeforeMerge | GroupSizefertile_BeforeMerge | GroupSize_BeforeSplit | Temperature_Tolerance | CohortSize_Prefertile | CohortSize_Fertile | Calories_Per_Kg_Meat | Max_ForagingRange | ViabilityIndex |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Habitat-A | 0.25 | -0.35 | -0.49 | 0.16 | -0.19 | | | | | -0.35 | -0.67 | -0.12 | -0.19 | 0.41 | | 0.21 | 0.72 |
| Habitat-B | 0.21 | -0.20 | -0.24 | | | | | | | | | | | | | | 0.59 |
| Habitat-C | 0.38 | -0.16 | -0.55 | 0.14 | -0.21 | | 0.23 | | | | -0.41 | -0.22 | -0.31 | 0.12 | | 0.12 | 0.76 |
| Habitat-D | -0.13 | | | | -0.09 | | | | -0.08 | -0.17 | | -0.09 | | 0.11 | | | |
| Habitat-E | 0.70 | -0.67 | -0.56 | 0.20 | -0.10 | 0.21 | -0.11 | | 0.24 | -0.55 | -0.75 | -0.32 | -0.56 | | 0.23 | | 0.87 |
| Habitat-F | -0.24 | | | | -0.10 | -0.14 | | | -0.16 | -0.12 | | | | | 0.10 | | -0.27 |
| Habitat-G | 0.33 | -0.28 | -0.61 | 0.17 | -0.13 | 0.13 | 0.16 | | -0.14 | -0.37 | | -0.24 | -0.36 | | | | 0.74 |
| Habitat-H | 0.33 | -0.22 | -0.62 | 0.17 | | -0.35 | | -0.32 | -0.49 | -0.56 | -0.20 | | -0.21 | 0.22 | | | 0.70 |
| Habitat-I | 0.24 | -0.30 | -0.64 | 0.22 | | -0.40 | 0.34 | | -0.36 | -0.36 | -0.27 | -0.41 | -0.58 | 0.17 | 0.21 | 0.40 | 0.80 |
| Habitat-J | | -0.19 | -0.57 | | | | | | -0.18 | -0.34 | -0.23 | -0.26 | -0.44 | 0.12 | 0.15 | 0.26 | 0.70 |
| Energy-A | 0.20 | -0.56 | -0.62 | | -0.33 | | | | | | -0.34 | -0.30 | -0.40 | 0.16 | -0.21 | 0.21 | 0.83 |
| Energy-B | 0.26 | -0.26 | -0.37 | | -0.22 | -0.15 | -0.11 | 0.13 | -0.10 | -0.46 | -0.54 | -0.20 | -0.32 | 0.09 | 0.18 | -0.17 | 0.65 |
| Energy-BR | 0.29 | -0.20 | -0.37 | | -0.15 | | -0.15 | | | -0.25 | -0.56 | -0.21 | -0.32 | 0.23 | -0.11 | 0.12 | 0.66 |
| Energy-C | 0.25 | -0.13 | -0.26 | 0.23 | | -0.12 | | | | | -0.43 | | -0.12 | | | -0.40 | 0.42 |
| Energy-CR | | | | | | | | | | | | | -0.11 | | | | |
| Energy-D | 0.25 | -0.37 | -0.47 | | -0.15 | | | | | | -0.40 | | -0.27 | | | | 0.72 |
| Energy-E | 0.12 | -0.18 | -0.42 | 0.13 | -0.32 | | | | -0.23 | -0.42 | -0.39 | -0.20 | -0.35 | 0.19 | 0.17 | 0.32 | 0.61 |
| Energy-ER | | -0.26 | -0.42 | 0.16 | | | | 0.11 | -0.32 | -0.49 | -0.38 | -0.35 | -0.16 | | | 0.27 | 0.58 |

When comparing the correlations for the Evolved parameter values with those in the Standard batches one thing is obvious: there are more correlations in the Evolved batches, and most correlations are larger. That means that the values for the parameters as generated by the genetic algorithm are more strongly associated with the simulation results than the randomly generated values from the Standard set. This is to be expected since the aim of the genetic algorithm is to positively influence the simulation results by changing the parameter values, so more correlations will be found, also for parameters that are not correlated at all in the Standard set. Since the genetic algorithm changes mostly a few parameter values, others might seem correlated simply due to the fact that they remain untouched for several generations. Very surprizing is the generally positive correlation of GroupSize_BeforeSplit in the Standard set is overall changed to a very negative correlation in the Evolved sets. Also remarkable is the evolved negative correlation with CohortSize_Prefertile.

### 11.3.3    Relative Variable Importance (RVI) - what makes a Neanderthal tick?

The relative importance of variables attempts to rank parameters by building a predictive model from the simulation results, suggesting which subset of parameters is most

important for creating a good match with the archaeology ([Johnson 2000](#)). This can be done by creating a linear regression model and calculating the relative contribution (importance) of individual variables. The method thus assumes that a linear model exists to explain the output. This study uses the *remaimpo* package in R for calculating such a *lm* model. After this the parameters are ranked according to importance scaled to 100 using the *calc.relimp* method. The dependant variable is `matchedIntervalCoverage`. For the relative variable importance, all values below 5% are not shown. The RVI is calculated for the Standard set of all scenarios (Table 48) and the Evolved set (Table 49).

**Table 48: Relative variable importance assuming a linear model for all Standard sets.**

| Scenario | BirthRate | DeathRate_PreFertileCohort | DeathRate_FertileCohort | DeathRate_PostFertileCohort | Subsistence_PreFertileCohort | Subsistence_FertileCohort | Subsistence_PostFertileCohort | Years_Before_Group_Maturity | GroupSize_BeforeMerge | GroupSizeFertile_BeforeMerge | GroupSize_BeforeSplit | Temperature_Tolerance | CohortSize_PreFertile | CohortSize_Fertile | Calories_Per_Kg_Meat | Max_ForagingRange |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Habitat-A | 0.40 | 0.14 | 0.36 | | | | | | | | | | | | | |
| Habitat-B | 0.32 | 0.09 | 0.26 | | | | | | | 0.14 | | | | | | |
| Habitat-C | 0.34 | 0.11 | 0.39 | | | | | | | | | | | | 0.07 | |
| Habitat-D | 0.17 | 0.08 | 0.17 | | | | | | | 0.27 | | | | | 0.26 | |
| Habitat-E | 0.09 | | 0.21 | | | | | | 0.07 | | 0.13 | | | | 0.44 | |
| Habitat-F | 0.38 | 0.11 | 0.30 | | | | | | | 0.10 | | | | | | |
| Habitat-G | 0.40 | 0.14 | 0.36 | | | | | | | | | | | | | |
| Habitat-H | 0.38 | 0.14 | 0.28 | | | | | | | 0.06 | | | | | | |
| Habitat-I | 0.30 | 0.10 | 0.34 | | | | | | | | | | | | 0.18 | |
| Habitat-J | 0.31 | 0.10 | 0.35 | | | | | | | | | | | | 0.16 | |
| Energy-A | 0.41 | 0.14 | 0.35 | | | | | | | | | | | | | |
| Energy-B | 0.23 | 0.07 | 0.37 | | | | | | | | | | | | 0.22 | |
| Energy-BR | 0.17 | | 0.25 | | | | | | | | | | 0.11 | | 0.32 | |
| Energy-C | 0.21 | | 0.38 | 0.06 | 0.09 | | | | | 0.10 | | | | 0.06 | | |
| Energy-CR | | | 0.11 | | | | | | | 0.05 | 0.06 | | | | 0.67 | |
| Energy-D | 0.23 | 0.07 | 0.37 | | | | | | | | | | | | 0.22 | |
| Energy-E | 0.26 | 0.07 | 0.33 | | | | | | | | | | | | 0.26 | |
| Energy-ER | 0.25 | 0.08 | 0.32 | | | | | | | | | | | | 0.26 | |

**Table 49: Relative Variable Importance for the Evolved sets from all scenarios.**

| Scenario | BirthRate | DeathRate_PreFertileCohort | DeathRate_FertileCohort | DeathRate_PostFertileCohort | Subsistence_PreFertileCohort | Subsistence_FertileCohort | Subsistence_PostFertileCohort | Years_Before_Group_Maturity | GroupSize_BeforeMerge | GroupSizeFertile_BeforeMerge | GroupSize_BeforeSplit | Temperature_Tolerance | CohortSize_PreFertile | CohortSize_Fertile | Calories_Per_Kg_Meat | Max_ForagingRange |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Habitat-A | 0.10 | 0.13 | 0.40 | | | | | | 0.09 | 0.06 | | | 0.05 | 0.06 | | |
| Habitat-B | 0.26 | 0.13 | | 0.12 | | | 0.16 | | 0.12 | | | | | | | |
| Habitat-C | 0.17 | 0.08 | 0.31 | | | | | | | 0.07 | 0.07 | 0.09 | | | | |
| Habitat-D | 0.24 | | 0.24 | | | | | | 0.06 | 0.13 | | | | | 0.08 | 0.07 |
| Habitat-E | 0.15 | 0.16 | 0.14 | | | | | | 0.12 | 0.20 | | 0.10 | | | | |
| Habitat-F | 0.26 | 0.12 | 0.18 | 0.06 | | | 0.07 | | | 0.12 | | | | | | 0.07 |
| Habitat-G | 0.11 | 0.19 | 0.37 | | | | | | | | | 0.09 | | | | |
| Habitat-H | 0.13 | 0.07 | 0.57 | | | | | | 0.09 | | | | | | | |
| Habitat-I | | | 0.32 | | | | | | | 0.08 | | 0.10 | | | | 0.25 |
| Habitat-J | 0.11 | 0.11 | 0.33 | | | | | | 0.07 | | | 0.12 | | | | 0.12 |
| Energy-A | 0.21 | 0.19 | 0.35 | | | | | | | | 0.05 | 0.07 | 0.05 | | | |
| Energy-B | 0.06 | 0.07 | 0.19 | | | | | | 0.15 | 0.19 | | 0.08 | | | | |
| Energy-BR | 0.09 | 0.06 | 0.17 | | | | | | | 0.25 | 0.13 | 0.08 | | | | 0.07 |
| Energy-C | 0.10 | 0.05 | 0.17 | 0.07 | | | | | 0.29 | | | | | | | 0.21 |
| Energy-CR | | | 0.11 | 0.05 | | 0.25 | 0.06 | | | 0.06 | 0.17 | | | | | 0.14 |
| Energy-D | 0.09 | 0.15 | 0.29 | | | | | | | 0.20 | | 0.07 | | | | 0.10 |
| Energy-E | 0.08 | | 0.22 | | | | | | 0.11 | 0.09 | | 0.06 | | | | 0.22 |
| Energy-ER | 0.09 | 0.09 | 0.23 | | | | | | 0.15 | 0.11 | 0.09 | 0.06 | | | | 0.12 |

### 11.3.4 Monotonic trends in parameter values

A variable in a series of observations that consistently increases or decreases through time displays a monotonic upward (or downward) trend. Such a trend does not have to be linear but the presence of these trends suggests a purposeful change. To detect monotonic trends in time series again the Spearman's rho test is useful (D'Abrera and Lehmann 1975; Sneyers 1991). The method does not explain the causes of any trend. Here the test is used to statistically identify changes that the genetic algorithm has induced.

Therefore input parameter values are correlated against the simulation number that ranks the simulations through time in the scenarios. A (strong) correlation indicates that the parameter changes into one direction as the experiment progresses. Such changes could be induced by the genetic algorithm attempting to optimize the simulation results. Table 50 lists for the Evolved series of all scenarios the results for the Spearman's rho correlations of parameters and simulation numbers. Values are only calculated for the Evolved data sets since there should be by definition no direction in the Standard parameter value sets. Note that more simulations in a scenario (Habitat-I) will result in more and stronger patterns (compare to Habitat-A).

**Table 50: Correlations between model input parameters and scenario number, for the Evolved datasets. Positive correlations are green colored and darker colors indicate stronger correlations.**

| Scenario (Evolved) | BirthRate | DeathRate_PreFertileCohort | DeathRate_FertileCohort | DeathRate_PostFertileCohort | Subsistence_PreFertileCohort | Subsistence_FertileCohort | Subsistence_PostFertileCohort | Years_Before_Group_Maturity | GroupSize_BeforeMerge | GroupSizeFertile_BeforeMerge | GroupSize_BeforeSplit | Temperature_Tolerance | CohortSize_PreFertile | CohortSize_Fertile | Calories_Per_Kg_Meat | Max_ForagingRange | ViabilityIndex |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Habitat-A | 0.17 | -0.26 | -0.31 | 0.12 | | | | | -0.23 | -0.52 | -0.13 | -0.13 | 0.34 | | | 0.17 | 0.52 |
| Habitat-B | | -0.15 | | | | | | | -0.13 | | | | 0.12 | | | | 0.15 |
| Habitat-C | 0.25 | | -0.37 | | | 0.23 | | | | -0.31 | -0.16 | -0.19 | | | | | 0.46 |
| Habitat-D | -0.12 | | -0.09 | | | | | 0.09 | -0.15 | -0.27 | -0.19 | -0.09 | -0.11 | | | 0.16 | 0.14 |
| Habitat-E | 0.62 | -0.59 | -0.46 | 0.18 | | 0.21 | -0.09 | | 0.23 | -0.48 | -0.65 | -0.28 | -0.51 | | 0.17 | | 0.76 |
| Habitat-F | -0.15 | -0.11 | -0.17 | | -0.13 | | | | | -0.16 | | | | | 0.13 | | |
| Habitat-G | 0.20 | -0.15 | -0.47 | 0.16 | | 0.13 | | | -0.23 | | -0.18 | -0.26 | | | | | 0.52 |
| Habitat-H | 0.27 | -0.13 | -0.48 | 0.12 | | -0.29 | | -0.27 | -0.39 | -0.45 | -0.15 | | -0.17 | 0.16 | | 0.10 | 0.53 |
| Habitat-I | 0.18 | -0.26 | -0.54 | 0.19 | 0.11 | -0.34 | 0.31 | | -0.33 | -0.29 | -0.22 | -0.37 | -0.50 | 0.13 | 0.18 | 0.30 | 0.67 |
| Habitat-J | | -0.12 | -0.45 | | 0.11 | | | | -0.14 | -0.27 | -0.18 | -0.21 | -0.38 | | 0.16 | 0.23 | 0.51 |
| Energy-A | 0.14 | -0.40 | -0.41 | | -0.29 | | | | | -0.26 | -0.26 | -0.30 | 0.14 | | -0.19 | 0.21 | 0.61 |
| Energy-B | 0.19 | -0.21 | -0.30 | | -0.20 | -0.14 | | 0.13 | -0.39 | -0.48 | -0.18 | -0.27 | | | 0.12 | -0.17 | 0.53 |
| Energy-BR | 0.18 | -0.14 | -0.24 | | -0.18 | | -0.14 | | -0.15 | -0.48 | -0.15 | -0.23 | | 0.19 | | | 0.48 |
| Energy-C | 0.16 | | -0.25 | 0.19 | | -0.17 | | | | -0.31 | | | | | | -0.27 | 0.31 |
| Energy-CR | | | | | | | -0.16 | | | | | | -0.13 | | | | |
| Energy-D | 0.14 | -0.27 | -0.36 | | | | | | | -0.39 | | | -0.22 | | | | 0.48 |
| Energy-E | | -0.14 | -0.39 | 0.13 | -0.27 | | | | -0.18 | -0.34 | -0.29 | -0.18 | -0.28 | 0.13 | 0.12 | 0.18 | 0.49 |
| Energy-ER | | -0.17 | -0.30 | 0.16 | | | | | -0.23 | -0.27 | -0.24 | -0.22 | | | | 0.22 | 0.41 |

### 11.3.5 Creating impossible Neanderthals and other cheats

In the Standard batch of simulations the values for the parameters are randomly selected from a given range. In the Evolved batch, the GA has taken good performing parameter value sets and mutated these or combined them with others in order to create even more successful parameter sets. The mutations are done to one randomly selected parameter value, and involve an increase or decrease of the original value with ten percent. This occasionally produces parameter values that fall outside of the initial range. For most parameters this was allowed because avoidance of user bias is one of the underlying aims of this study. When extreme values are produced it is interesting why the system evolves the given parameter in the chosen direction. Sometimes however evolved values were clearly impossible. The following parameters were occasionally manipulated beyond the initial boundaries:

- **Birth-rate**: birth-rates evolved to values larger than 50%, or below 1%;
- **Death rates** for all cohorts evolved to values smaller than 1%;
- **Subsistence** needs for all cohorts were reduced to 0 or less;
- The value for **years before group maturity** became occasionally less than 1 year;

- The values for **group size before merge**, **group size fertile cohort before merge** and **group size before split** sometimes became less than 1;
- **Cohort sizes** for fertile and pre-fertile cohort were manipulated to less than 1;
- **Maximum foraging ranges** fell to values below 1 or became larger than 20.

These changes are followed by the genetic algorithm to avoid certain imposed limits (where only a certain range is offered, for example the birth and death rates) or to change functionality (for instance the group maturity variable). The evolved directionality can be surprizing. It is important to realize that the algorithm just manipulates values and then runs simulations to see if these changes are successful. The algorithm does not know the *meaning* of parameters. Therefore it is natural for the algorithm to change death rates to zero, since Neanderthals that never die will be very present everywhere and thus match the archaeology very well. Also birth rates above 50, ignoring any physical limits for Neanderthal women, are for the system very successful parameter values, especially combined with low energy needs.

To avoid clearly impossible Neanderthals, the system was subsequently restricted in the allowed mutation directions for certain parameters: birth rates, death rates, and subsistence needs are now not allowed below one (1), and a maximum foraging range cannot impose a limit of less than one (1) or more than 20. Cohort sizes are kept at a minimum size of one (1). The other mutations were not restricted and the resulting evolved values violating pre-conditions are presented in Table 51. Note that the empty columns here remain to illustrate the effects of imposed restrictions. The strongest violations are scenario Energy-B, with 79 out of a total of 2,278 simulations having a value of 0 or lower for GroupSizeFertile_BeforeMerge (effectively disabling this variable and thus allowing all groups to always merge; but many more scenarios violate this criterium), and Habitat-E with 48 simulations with a Birthrate larger than 50% (out of a total of 2,420).

**Table 51: Number of model parameter value sets per scenario with parameter values manipulated beyond the initial limits. Darker colors identify larger table values.**

| Scenario | BirthRate<=0 | BirthRate>50 | DeathRate_FertileCohort<=0 | DeathRate_FertileCohort<=0 | DeathRate_PostFertileCohort<=0 | Subsistence_PreFertileCohort<=0 | Subsistence_FertileCohort<=0 | Subsistence_PostFertileCohort<=0 | Years_Before_Group_Maturity<=0 | GroupSize_BeforeMerge<=0 | GroupSizeFertile_BeforeMerge<=0 | GroupSize_BeforeSplit<=0 | CohortSize_PreFertile<=0 | CohortSize_Fertile<=0 | Max_ForagingRange<=0 | Max_ForagingRange>20 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Habitat-A | | 11 | | | | | | | | 5 | 6 | | | | | |
| Habitat-B | | 3 | | | | | | | 2 | | | | | | | |
| Habitat-C | | 25 | | | | | | | 1 | | 1 | | | | | |
| Habitat-D | | | | | | | | | 1 | 7 | 10 | | | | | |
| Habitat-E | | 48 | | | | | | | 3 | 4 | 16 | | | | | |
| Habitat-F | | 1 | | | | | | | | 9 | 6 | | | | | |
| Habitat-G | | 1 | | | | | | | | 1 | 8 | | | | | |
| Habitat-H | | 8 | | | | | | | 14 | 17 | 36 | | | | | |
| Habitat-I | | 5 | | | | | | | 2 | 3 | 8 | | | | | |
| Habitat-J | | 6 | | | | | | | | 4 | 14 | | | | | |
| Energy-A | | 9 | | | | | | | 2 | 14 | 1 | | | | | |
| Energy-B | | 12 | | | | | | | 5 | 1 | 79 | | | | | |
| Energy-BR | | 11 | | | | | | | 1 | | 2 | | | | | |
| Energy-C | | 10 | | | | | | | 10 | 2 | 20 | | | | | |
| Energy-CR | | 2 | | | | | | | | 10 | 3 | | | | | |
| Energy-D | | | | | | | | | 1 | | 16 | | | | | |
| Energy-E | | | | | | | | | | 6 | 21 | | | | | |
| Energy-ER | | 1 | | | | | | | | 6 | 14 | | | | | |

## 11.4 Trends in the simulation output

A general observation of the simulation results could suggest that the model behaves in a linear fashion, where more Neanderthals mean a better match with the archaeological data. More or less as expected since presence is a success criterion and will only be limited by resources and the presence of other hominins. But correlations from the previous section show that this relation is not straightforward. This section therefore focusses on relevant patterns in the simulation output, in order to understand the simulation process in more detail.

### 11.4.1 The simulation score

The `MatchedIntervalCoverage` variable is a crucial element in the HomininSpace simulation system, because simulation results are assessed on this value alone. The implemented optimization method, genetic algorithms, requires a single number to optimize upon, and therefore is it essential to understand how this value is constructed. Each checkpoint reports at the end of a simulation several output variables, including a

local [checkpoint name]_matchedIntervalCoverage number. This value indicates how well the simulated visits to the checkpoint match with the archaeological attested hominin presence (subsection 7.5.1). All local values are all included in the simulation output file and summed together into this `MatchedIntervalCoverage` variable[43]. Here I describe patterns in the simulation score throughout the simulated scenarios.

Figure 71 presents graphs with `MatchedIntervalCoverage` scores, sorted from low to high (here *not* sorted on simulation number). Overall, the score patterns for all scenarios are similar: up to a certain value the simulations do not result in a very high score. Then there is a (small) range presenting a tipping point: suddenly very high values are scored. Then the graphs plateau with a small but noticeable increase at the end of the spectrum. These figures illustrate three important aspects of the score: (1) until the tipping point which lies generally around 1500 the scores are low and most often from the Standard set (cyan coloured dots); (2) after the tipping point the score increases (sometimes steeply) and then levels again until you reach the small tip at the end which is constructed of very high scores with almost exclusively evolved results; (3) for all scenarios the exact score pattern of `MatchedIntervalCoverage` is different and depends on the model parameters values and settings.

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[43] All relevant simulations from all scenarios are copied into the file "AllData.csv" which is included in the Supplementary Materials.
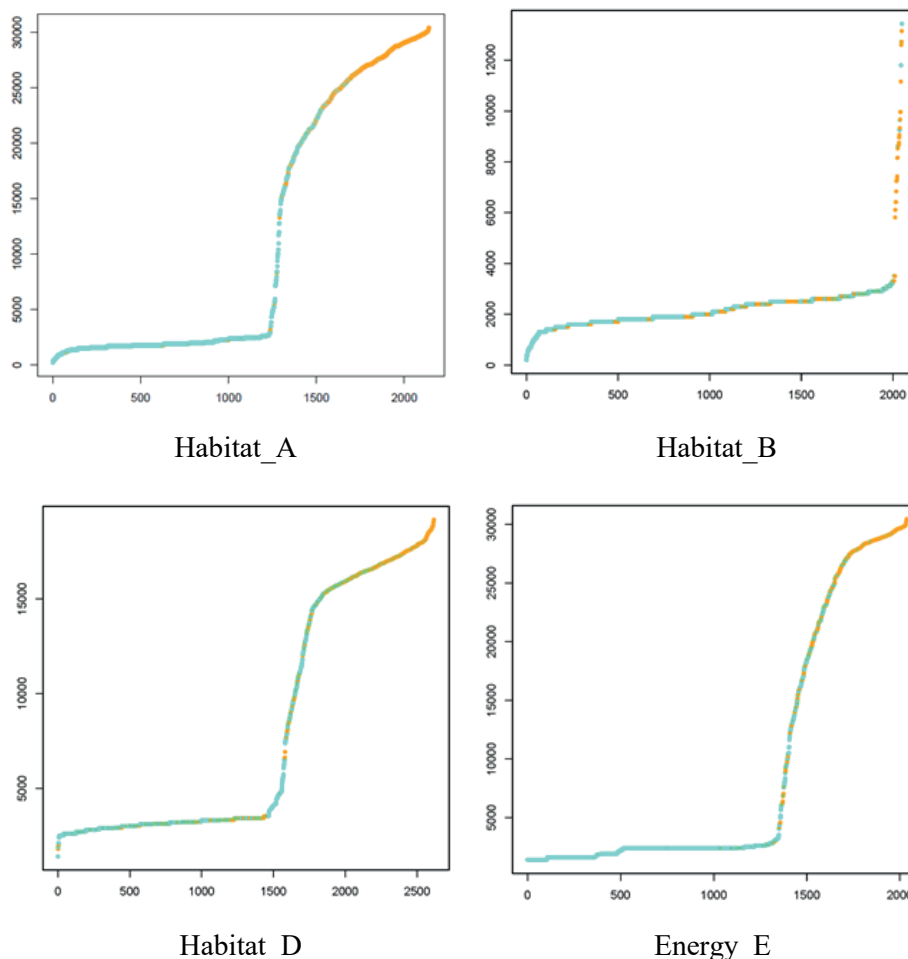
Figure 71: Overview of sorted `MatchedIntervalCoverage` values for different scenarios. Simulations are sorted on score. Scores from the Standard set are colored cyan.

By adding the scores for all simulations for all scenarios together and sorting on resulting sums it is possible to rank the scores for all checkpoints[44]. Values range from 663,545 for Saint-Amand-les-Eaux to a maximum of 29,701,374 for Pech de l-Aze II . This is all scores added together. Note that in individual scenarios the contributions of individual checkpoints differ widely. Excluding the monitoring checkpoints and the checkpoints with absence intervals, the checkpoints that have the lowest `_matchedIntervalCoverage` scores in total are: Saint-Amand-les-Eaux (663,545), Ault (814,400), Savy (814,400), Ormesson (867,377), and Beauvais 1 (1,004,270). These low scoring checkpoints all have one or two short intervals only, all positioned temporarily at or even overlapping with the end of the simulation period (some of these intervals will never be completely matched, since the simulations stop at 50 ka).

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[44] The resulting excel sheet is included in the Supplementary Materials as "Summed data only.xlsx".

The best scoring checkpoints are Grotte de Coudoulous II (10,762,343), Abri Bourgeois-Delaunay (12,030,833), Chez-Pinaud Jonzac (13,464,009), Coudoulous I(14,982,272), and Pech de l-Aze II (29,701,374). The site Pech de l-Aze II has by far the most intervals which helps to explain its very high score (each matched interval counts). Both Coudoulous I and Grotte de Coudoulous II have many very accurate (and thus very short and easily filled) intervals that add bonus to the score when completely matched (and are also positioned in the same grid cell).

## 11.4.2      Characterizing the best models from the Standard set

For the discussion in this subsection I refer to the Top-10 results from the Standard model sets, for all scenarios. These results were retrieved from the simulation output files and are stored for easy reference in the Excel data file named "Results – Top10 Standard sets all scenarios.xlsx", included in the Supplementary Materials. The models in the Standard set have randomly generated parameter values and are executed in each scenario. By chance, some of these models are well suited for simulation in HomininSpace in certain scenarios while unfit for others. See  for good performing models and the associated parameter values.

Roughly there are two successful model groups: those with a very low `ViabilityIndex` value (below 190, with some exceptions) which are very successful in simulations with the absence criterion activated, and those with a viability index of 190 and up, scoring high in most other scenarios. Since there are only four scenarios with absence activated the successful model parameter sets for these scenarios are not represented in .

A low viability index can be due to a low birthrate (e.g. 832, 876, 461, 80, 280), high mortality figures (3, 157, 542, 912) or combinations thereof (3, 83, 533), supplemented by additional measures that can include more positive values for temperature tolerance (178, 857, 1008; sometimes combined with very high values for group size before split (754)), and small foraging ranges (43, 323, 1009). A high viability index is realized with a high birth rate (390, 486, 1355, 1373), low mortality rates (43, 486, 1309), especially for the fertile cohort (120, 1365, 1384), more negative temperature tolerances (39, 1309, 1384), and large foraging ranges (395, 646, 1131).

Models that are successful in multiple scenarios (more than six times) with high values for the viability index are 39, 390, 472, 486, 1131, 1365, 1373, and 1384. 1365 scored by far

the best, but 486 has high places in the top-10 of many scenarios. A high viability index gives a good chance on a high simulation score but is no guarantee. For instance, number 120 has in an index of 62186 (maximum in this list), and finds itself only 4 times in any top 10. Model 1365 (13 times top 10, with 8 x place 1) has an index of 28722, but 1131 (9 times in the top 10) has an index of only 1502. Model 560 has an index of 301 (7 times top 10). Note that almost all small scale foraging societies show the positive growth rates associated with larger viability index figures (Gurven and Kaplan 2007, 347)[45].

**Table 52: Presenting the best performing models from the Standard set. The first column gives the number of times the simulation number appears in the top-10 scores over all scenarios.**

| Times in Top 10 | SimulationNumber | BirthRate | DeathRate_PreFertileCohort | DeathRate_FertileCohort | DeathRate_PostFertileCohort | Subsistence_PreFertileCohort | Subsistence_FertileCohort | Subsistence_PostFertileCohort | Years_Before_Group_Maturity | GroupSize_BeforeMerge | GroupSizeFertile_BeforeMerge | GroupSize_BeforeSplit | Temperature_Tolerance | CohortSize_PreFertile | CohortSize_Fertile | Calories_Per_Kg_Meat | Max_ForagingRange | ViabilityIndex |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 13 | 1365 | 43 | 3 | 1 | 12 | 2000 | 5000 | 3250 | 2 | 4 | 2 | 16 | -17 | 9 | 37 | 2700 | 12 | 28722 |
| 12 | 39 | 47 | 5 | 1 | 11 | 2750 | 3250 | 3750 | 5 | 5 | 2 | 56 | -28 | 12 | 23 | 3000 | 10 | 4053 |
| 9 | 390 | 47 | 6 | 2 | 2 | 3250 | 4750 | 2000 | 1 | 5 | 5 | 56 | -29 | 9 | 38 | 3150 | 13 | 12842 |
| 9 | 1131 | 35 | 8 | 2 | 12 | 3000 | 3750 | 4750 | 4 | 1 | 3 | 46 | -26 | 8 | 40 | 3100 | 15 | 1502 |
| 9 | 1384 | 41 | 11 | 1 | 14 | 4250 | 2750 | 4250 | 10 | 5 | 1 | 46 | -29 | 9 | 28 | 2900 | 11 | 1289 |
| 8 | 486 | 49 | 2 | 2 | 12 | 2750 | 4750 | 4250 | 5 | 2 | 1 | 56 | -23 | 8 | 25 | 2550 | 10 | 41287 |
| 7 | 560 | 27 | 3 | 1 | 15 | 2500 | 4000 | 3500 | 8 | 4 | 2 | 16 | -16 | 14 | 25 | 3100 | 9 | 301 |
| 6 | 472 | 33 | 4 | 2 | 4 | 2500 | 3000 | 4250 | 8 | 1 | 3 | 56 | -17 | 9 | 35 | 3200 | 12 | 1978 |
| 5 | 1339 | 35 | 4 | 2 | 3 | 3750 | 3500 | 3000 | 8 | 1 | 1 | 16 | -23 | 12 | 17 | 2750 | 14 | 280 |

### 11.4.3 Causes of life and death

For each simulation administrative data is stored on the total cumulative number of hominin individuals and groups through time. The variables for these simulation output results are named `created_hominins` and `created_groups`. Within HomininSpace there are two ways in which new hominins can be introduced into a simulation: via the hominin reproduction mechanism and via creation inside core areas (that is, produced by so-called factories if these are activated). Where the size and composition of reproduced groups depend on the parent group (half the size of the parent cohorts), core areas produce new groups (one per time step, and only when conditions are favourable) with a standard group size and structure: 25 individuals of which 8 are in the pre-fertile age, 11 fertile and 6 are post-fertile individuals[46].

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[45] By definition, since prolonged negative growth rate leads to extinction.
[46] These numbers are numeric constants in the source code and can be changed at will. For this research however they were not changed between simulations.

The number of created hominins are stored in the variables `Offspring`[47] for reproduced hominin groups and in the variables `Iberia` and `Italy` for groups created in the two predefined core areas (if these are activated). The number of created groups and hominins help in interpretation of the simulation processes and results. Figure 72 suggests that the number of created hominins is probably very important for obtaining higher simulation scores (later simulations all have high created hominins numbers). For scenario Habitat-A the relation between the simulation score and the number of created hominins is visualized in Figure 73. Also the number of created groups are important, but extreme values are not always necessary for high simulation scores.
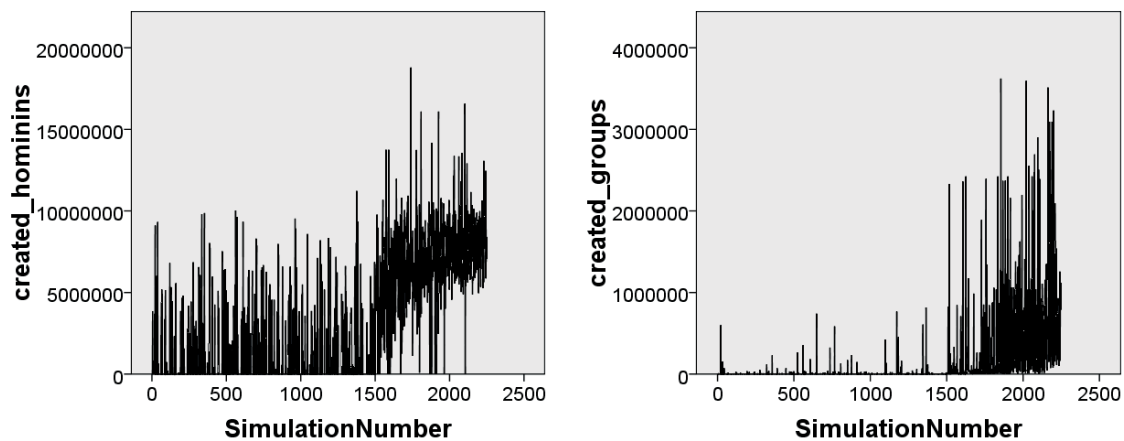


**Figure 72: Overview of created_hominins and created_groups versus SimulationNumber from scenario Habitat-A. The first 1500 simulations are the Standard set.**

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[47] Note that the Offspring variable does not include starting populations and produced groups thereof.
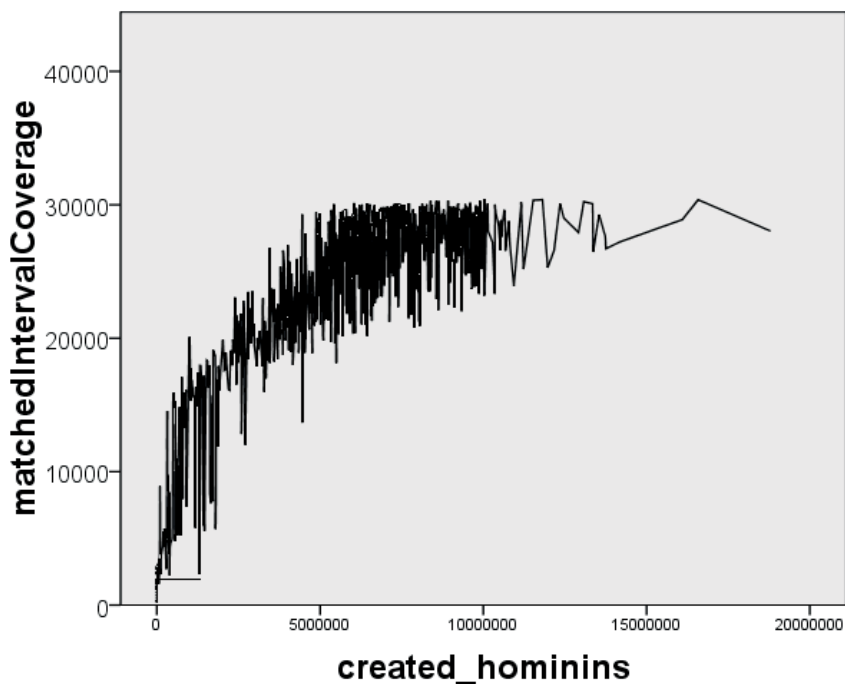
**Figure 73: Relation between the number of created hominins per simulation and the simulation score (scenario Habitat-A).**

Hominins can die in many different ways. In the model underlying the HomininSpace simulation system the mortality rates for all cohorts are applied to all hominin groups every year, reducing the population as a whole. In addition to this natural attrition that varies due to the individual circumstances of each group, a group can succumb as a whole to cold, flooding, hunger (insufficient resources), and to being too small to sustain itself. In all these cases the whole group ceases to exist and disappears. The numbers of hominins that perish in these manners are administrated and totals are reported in the simulation output at the end of each simulation. They also cease to exist in the simulation because they cross the border of the simulation area (if this is possible). Groups that disappear because they merge into other groups are counted separately. Table 53 lists the maxima for all these variables per scenario, to illustrate the differences between scenarios. Note that death by flooding can only happen to static hominins, save very unfortunate exceptions where groups have no choice than to move onto or remain in flooded grid cells.

**Table 53: Maxima for the numbers of created hominins and groups, and maxima for the number of different possible deaths in any simulation. Color coding is per column and darker colors indicate higher scores within the column.**

| Scenario | Max CreatedHominins | Max CreatedGroups | Max CreatedOffspring | Max Iberia | Max Italy | Max DeathsCold | Max DeathsFlooding | Max DeathsHunger | Max DeathsMerging | Max DeathsTooSmall |
|---|---|---|---|---|---|---|---|---|---|---|
| Habitat-A | 18795432 | 3622260 | 3621991 | | | 165967 | | 8857 | 3620674 | 251099 |
| Habitat-B | 1138269 | 93108 | 93087 | | | 834 | | 10 | 92964 | 104 |
| Habitat-C | 13721186 | 8090115 | 8089607 | | | 233517 | | 10448 | 7977343 | 269545 |
| Habitat-D | 8904608 | 1972062 | 1830538 | 151187 | 194166 | 377484 | | 5963 | 1511144 | 1379726 |
| Habitat-E | 19827306 | 5470156 | 5469788 | 158762 | 185920 | 254238 | 1 | 55062 | 5384471 | 1405852 |
| Habitat-F | 8899456 | 1588281 | 1514281 | 158762 | 185920 | 254238 | | 6429 | 1395871 | 1405852 |
| Habitat-G | 13539102 | 2946697 | 2946546 | | | 78030 | | 11097 | 2918412 | 119754 |
| Habitat-H | 14481376 | 4604894 | 4522427 | 150057 | 184333 | 359509 | 17 | 7556 | 4590155 | 1497503 |
| Habitat-I | 15777251 | 6095733 | 6095362 | | | 52375 | 18 | 5748 | 5984937 | 148395 |
| Habitat-J | 20138638 | 3286710 | 3286511 | | | 69212 | 311 | 5256 | 3278679 | 207564 |
| Energy-A | 5801491 | 2314134 | 2313957 | | | 53017 | | 6523 | 2312831 | 60427 |
| Energy-B | 12826469 | 6211677 | 6211276 | | | 163483 | 1 | 33627 | 6163162 | 656422 |
| Energy-BR | 6960929 | 3954676 | 3954421 | | | 48730 | 65 | 11059 | 3931901 | 88748 |
| Energy-C | 1364805 | 9245 | 9232 | | | 24 | | 22 | 9197 | 732 |
| Energy-CR | 2791 | 404 | 242 | | | 28 | | 14 | 186 | 56 |
| Energy-D | 7612793 | 1718926 | 1718811 | | | 137895 | | 7010 | 1712553 | 93514 |
| Energy-E | 10221491 | 1746704 | 1746589 | | | 25829 | 91 | 3381 | 1739833 | 83280 |
| Energy-ER | 9091567 | 2163739 | 2163621 | | | 54276 | 90 | 6098 | 2106022 | 105571 |

The output variables detailing mortality are named: `deathsCrossing`, `deathsCrossingIberia`, `deathsCold`, `deathsFlooding`, `deathsHunger`, `deathsMerging`, and `deathsTooSmall`. These numbers are included in the simulation results to aide in interpreting the simulation process and results. The geographical distribution of the deaths as they occurred in the simulated environment can be visualized in maps (subsection 8.7.2). They are also used to illustrate the batch simulation process and the effect of the evolution implemented in the Genetic Algorithm. An example of this is presented in Figure 74, which illustrates that in scenario Habitat-E the Evolved hominins perish in colder circumstances than the Standard hominins. In this scenario there is a relatively strong negative correlation between `Temperature_Tolerance` and simulation number, resulting in hominins that can sustain much colder temperatures.
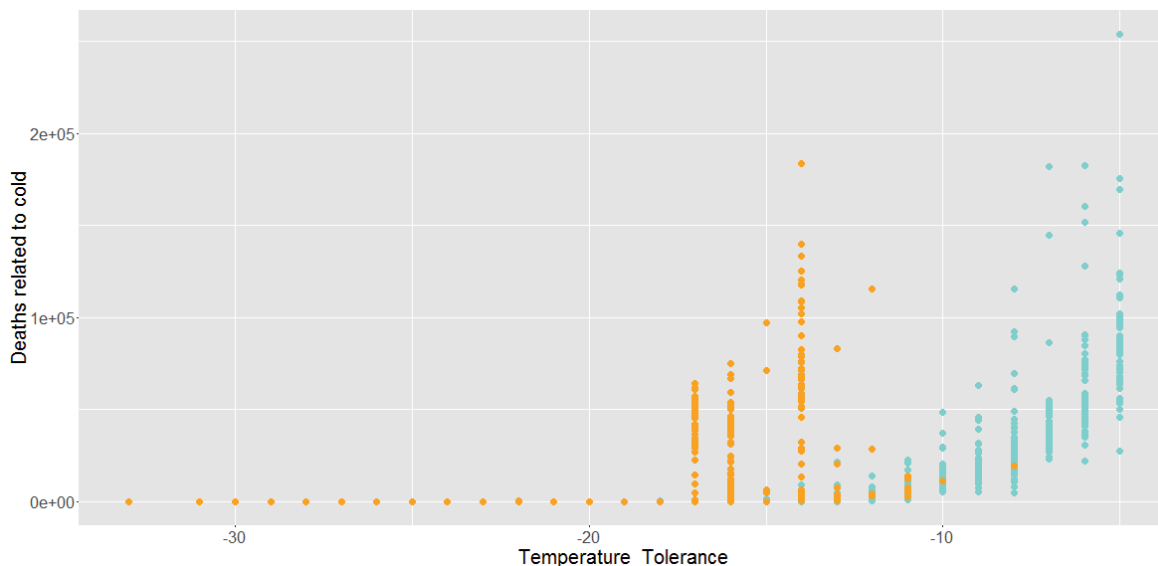
**Figure 74: Depicted the numbers of groups that perished due to cold temperatures versus temperature tolerance. In orange evolved hominins, in cyan results from the Standard set (scenario Habitat-E).**

The lives of individual hominins are not tracked in the HomininSpace system, but groups can survive for many years, outlasting the individual hominins they are composed of. The lifetime or age of the hominin groups is variable and depends on group composition, model parameters and local circumstances. Sometimes groups can survive up to 50,000 years or more. The average group age per simulation is depicted for scenario Energy_E to illustrate the possible variation within the resulting models in Figure 75. Note that for some very successful simulations the average age is not necessarily very high.
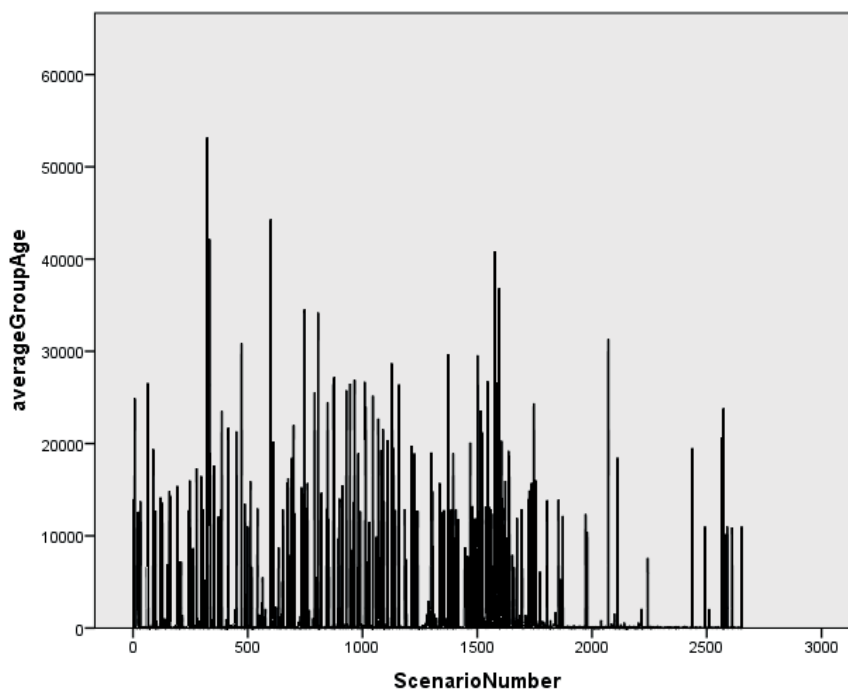


**Figure 75: Average group age for scenario Energy_B.**

11.4.4          Influence of data quality on the simulation score

Each interval has been assigned a quality indication. This quality value can be used in
assessing the total simulation score with all checkpoint intervals versus the score excluding
the bad quality intervals. To facilitate this comparison two results `matchingVisits` and
`matchingVisitsWithConfidence` are included in the simulation results file. The
variable `matchingVisits` counts the number of years that has visits inside an interval.
The `matchingVisitsWithConfidence` stores the interval visit results with the
confidence level as a factor included in the count (see subsection 6.3.1). To force a strong
influence of the confidence level, a visit of confidence level one (1) is counted once, for
level two (2) a visit adds four to the count and for level three (3) nine points are added to
the score. Thus `matchingVisitsWithConfidence` always scores at least the same
as `matchingVisits`, but depending on the confidence levels of the visited intervals can
score much higher. In total there are 29 intervals that were classified as unreliable with
level one, 206 with level two and 236 with level three (n=471).
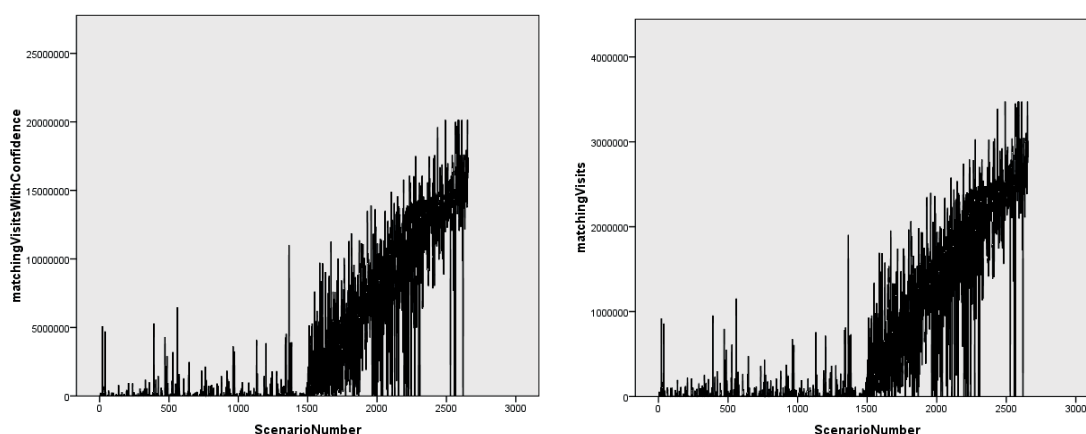


**Figure 76: Output of the simulation variables `matchingVisitsWithConfidence`
(left) and `matchingVisits` (both from Scenario Energy-B).**

Both graphs have an almost identical shape, with the absolute values being different and
the values for `matchingVisitsWithConfidence` consistently almost a factor 5
higher. This illustrates clearly that the influence of the unreliable dates is constant
throughout the simulations. This suggests that the presence of these few unreliable dates
has a minimum influence on the resulting output.

The correlation between `matchingVisits` and
`matchingVisitsWithConfidence` is for all scenarios nearly perfect, with a
significant correlation value of +1.00, the maximum score possible. Correlations between
the simulation score (`MatchedIntervalCoverage`) and both variables are also

similar, both significant and with a value around +0.96, indicating a near perfect correlation (understandable since the simulation score is constructed using primarily the matching visits results). Since the simulation score is based on matching visits it includes matches for intervals that are classed as unreliable, but overall this inclusion should therefore not influence the results.

Intervals are constructed using the one standard deviation value for lower and upper bounds. This presents a 68% confidence interval around the mean. Thus a less reliable date has a larger standard deviation which results in a larger interval. To ensure that a larger interval does not produce a higher score, the reported score per interval is divided by the length of the interval, resulting in a coverage percentage, not an absolute number. All percentages added together and multiplied by 100 to avoid rounding form the `MatchedIntervalCoverage` score.

## 11.5        Analysing the modelled environment

The environment in HomininSpace uses the reconstructed topography and the reconstructed climate parameters temperature and precipitation. A fluctuating sea level defines available landmasses where the climate determines how much energy there is available in the landscape. The energy level per grid cell is calculated directly by extrapolation or via habitat reconstruction. The reconstruction is analysed here visually with the user interface of the application and by using the data from the climate recording checkpoints. Identified are larger patterns and local deviations.

Table 2 identifies local and global climatic maxima and minima in the data supplied by Bintanja and van de Wal (2008). Those points in time that are part of the simulation period are used to illustrate the topography and energy reconstructions. All dates are in ka, with temperature offsets between brackets in degrees Celsius. The minima are at: 112 (-9.70°), 88 (-12.07°), 78 (-11.85°), and 61 (-13.31°), and maxima can be found around 124 (2.19°), 120 (0.57°), 97 (-6.53°) and 83 (-6.51°). With the starting point at 131 ka (-5.6°) and simulation termination at 50 ka (-12.0°) this encompasses in total ten points in time to capture the reconstructions. These moments are listed in Table 54 ordered by time step, with the given temperature given as offset to the current global mean temperature.

**Table 54: Relevant points in time (climate extremes) for screen capturing.**

| Description | Time step | Date (years ago) | Temperature (Celsius) |
|---|---|---|---|
| *Start of the simulation period* | 1 | 131,000 | -5.6 |
| An absolute maximum around 124 ka | 6,200 | 124,800 | 2.19 |
| A local maximum around 120 ka | 9,600 | 121,400 | 0.57 |
| A local minimum around 112 ka | 18,200 | 112,800 | -9.70 |
| A local maximum around 97 ka | 33,800 | 97,200 | -6.53 |
| A local minimum around 88 ka | 42,300 | 88,700 | -12.07 |
| A local maximum around 83 ka | 47,200 | 83,800 | -6.51 |
| A local minimum around 78 ka | 52,900 | 78,100 | -11.85 |
| A local minimum around 61 ka | 69,500 | 61,500 | -13.31 |
| *End of the simulation period* | 81,000 | 50,000 | -12.0 |

To assess changes in energy level values in the simulation the climate recording checkpoints are used. To interpret the observed dynamics it is important to realize that both energy computational methods use values for precipitation and temperature that are calculated by interpolation between and extrapolation from current day and reconstructed LGM values. Table 55 presents the recording checkpoints with their LGM and current day values. Note that for climate monitor 1 the LGM and current day values for precipitation are the same, so there is minimal variance throughout the simulation period.

**Table 55: The locations of the climate recording checkpoints and their modelled LGM and current day precipitation (P) and temperature (T) values.**
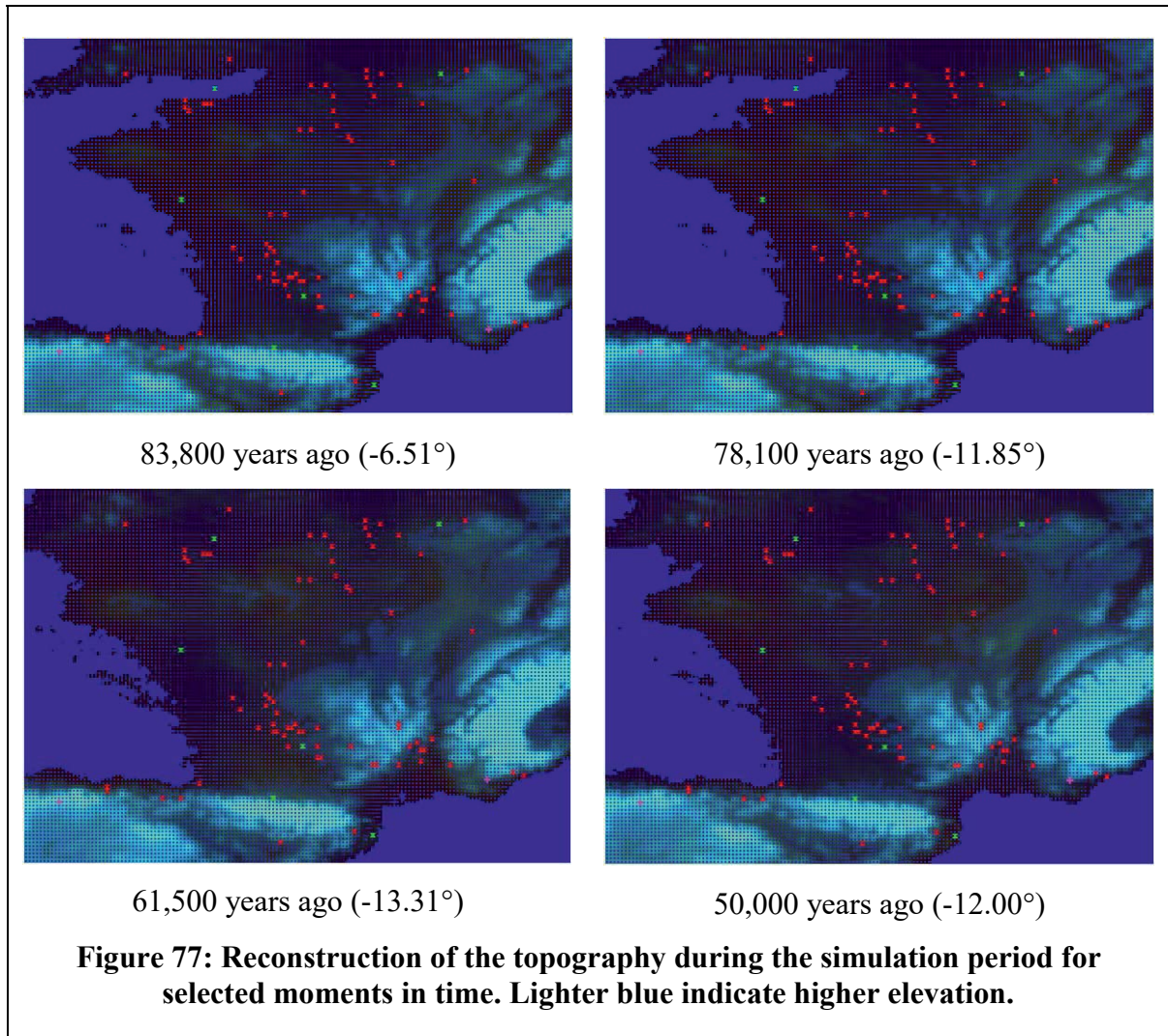
| # | Name | Lat | Long | LGM T | LGM P | Cur T | Cur P |
|---|---|---|---|---|---|---|---|
| 1 | Climate Monitor 1 Atlantic | 47.0 | -2.0 | 4.4 | 828.5 | 11.9 | 828.5 |
| 2 | Climate Monitor 2 Occitanie | 44.4 | 1.3 | 7.1 | 934.5 | 12.2 | 814.6 |
| 3 | Climate Monitor 3 Mediterranean | 42.0 | 3.2 | 11.8 | 655.0 | 15.9 | 583.6 |
| 4 | Climate Monitor 4 Pyrenees | 43.0 | 0.5 | 5.8 | 1143.9 | 10.4 | 892.2 |
| 5 | Climate Monitor 5 Scladina | 50.5 | 5.0 | -5.1 | 870.0 | 9.4 | 865.6 |
| 6 | Climate Monitor 6 Channel | 50.0 | -1.1 | -4.0 | 823.8 | 11.4 | 800.5 |

### 11.5.1 Topography

The only factor in HomininSpace influencing the topography is the changing sea level. Large areas of land currently under water in the Channel between the European mainland and the British Islands, and at the Atlantic coastal side of France become dry land when the sea level drops due to colder temperatures. The effects are less pronounced for the Iberian Peninsula and minimal in the Mediterranean areas. Screenshots for the indicated moments in time are given in Figure 77, with date and temperature offset. These figures illustrate that the available land mass varies considerably through time, with large areas becoming

submerged when water level rises due to warmer global climates and melting of glaciers, and subsequently becoming dry land when the temperatures and sea level drop. Coloring of grid cells is according to the relative height to sea level.



131,000 years ago (-5.6°)

124,800 years ago (2.19°)

121,400 years ago (0.57°)

112,800 years ago (-9.7°)

97,200 years ago (-6.53°)

88,700 years ago (-12.07°)

**Figure 77: Reconstruction of the topography during the simulation period for selected moments in time. Lighter blue indicate higher elevation.**
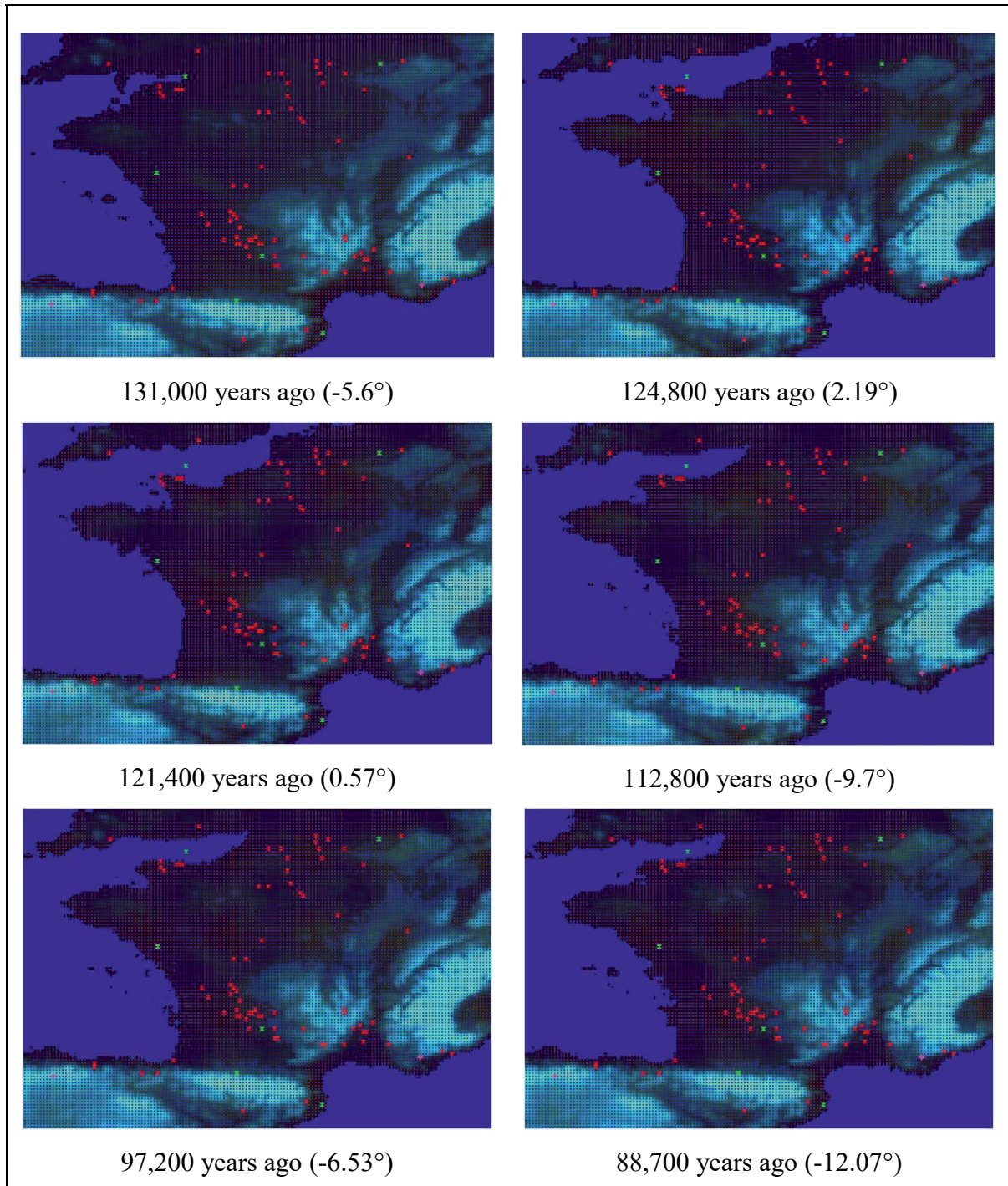
Climate recording checkpoints monitor, among other environmental data, the topography of the grid cell they are located in. One checkpoint in particular is positioned to monitor the changing sea level, and that is "Climate Monitor 6 Channel", located at 50.0 latitude and -1.1 longitude (Figure 78). Climate recording checkpoints are depicted as small green crosses in Figure 77, and checkpoint 6 is the top left green cross. Today it would be located right in the middle of the Channel but at the start of the simulation period it finds itself on land very close to shore where at the end of the simulation it lies deep inland. Right after the start of the simulation the grid cell where this checkpoint is located becomes submerged, resurfacing around 110,500 years ago. Then drowning again shortly after that (106,101 years ago), only to become dry land around 74,700 years ago until the end of the simulation. The recorded topography type is visualized in Figure 78. Note that whenever the grid cell is dry land located directly next to a sea grid cell it becomes a beach type grid cell (topography type 2 in Figure 78).
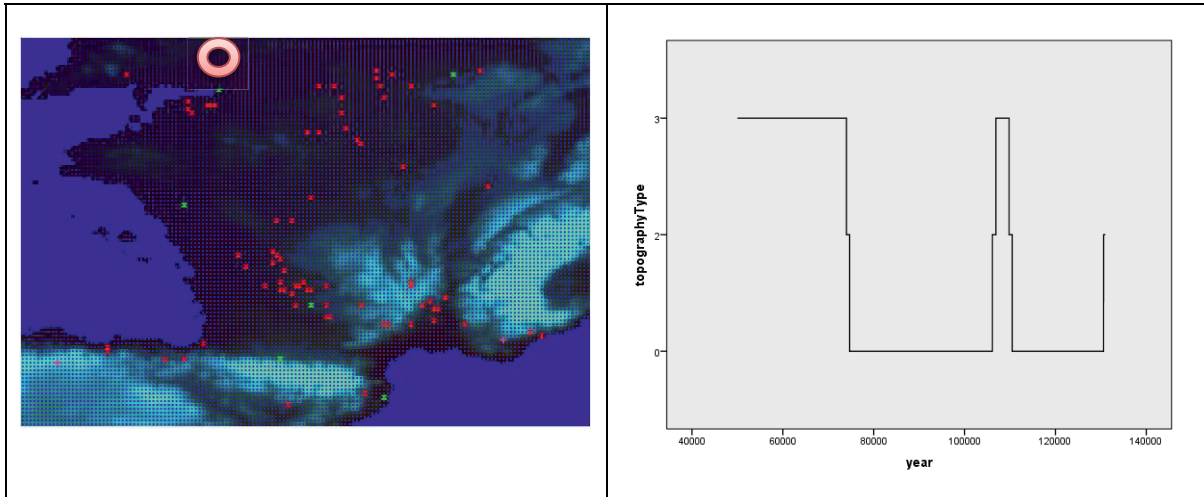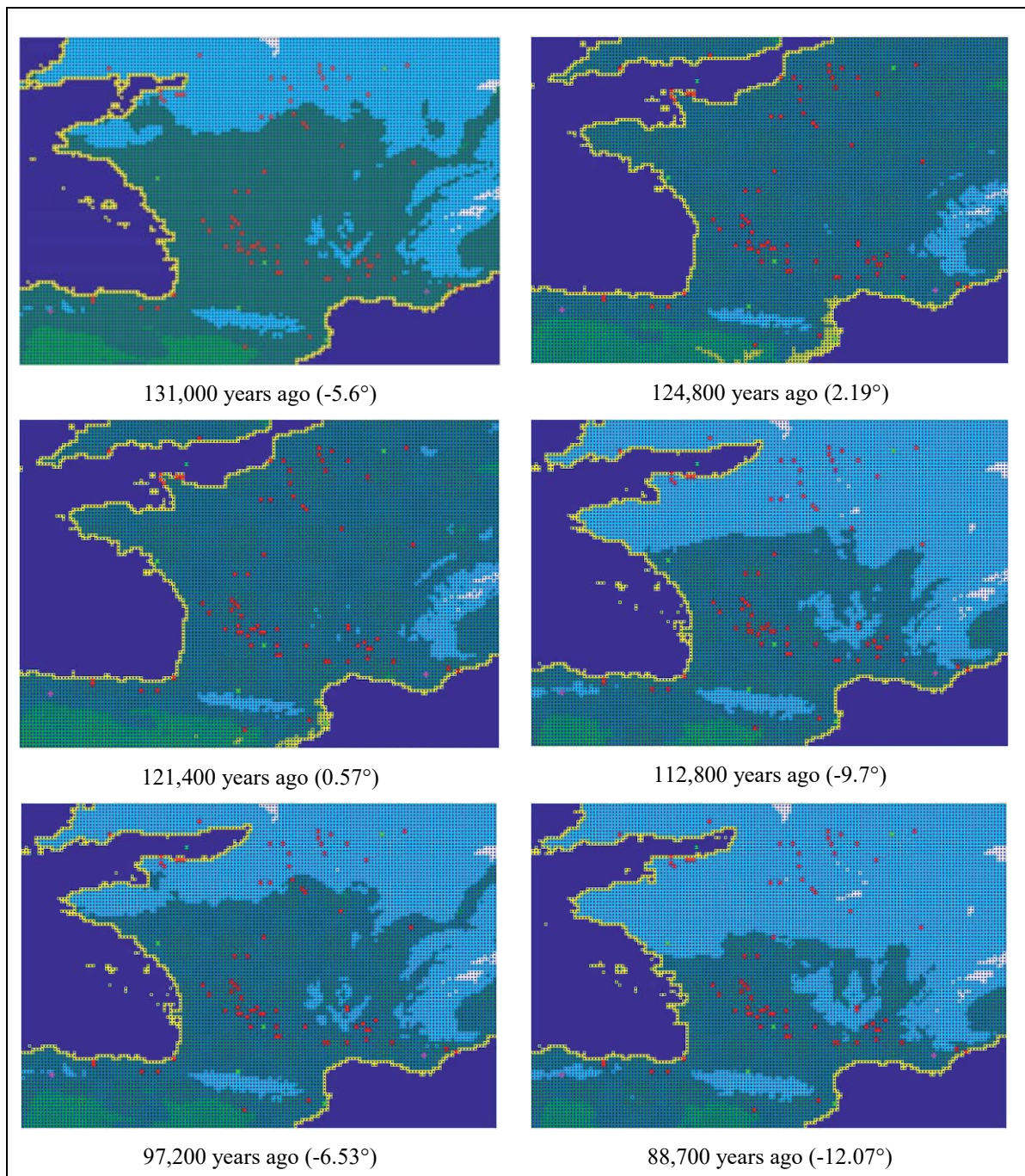
**Figure 78: Location of Climate Monitor 6 Channel (left) and the topographical output for the simulation period. Topography type 0 in the graph is water, 2 is beach and 3 is plain.**
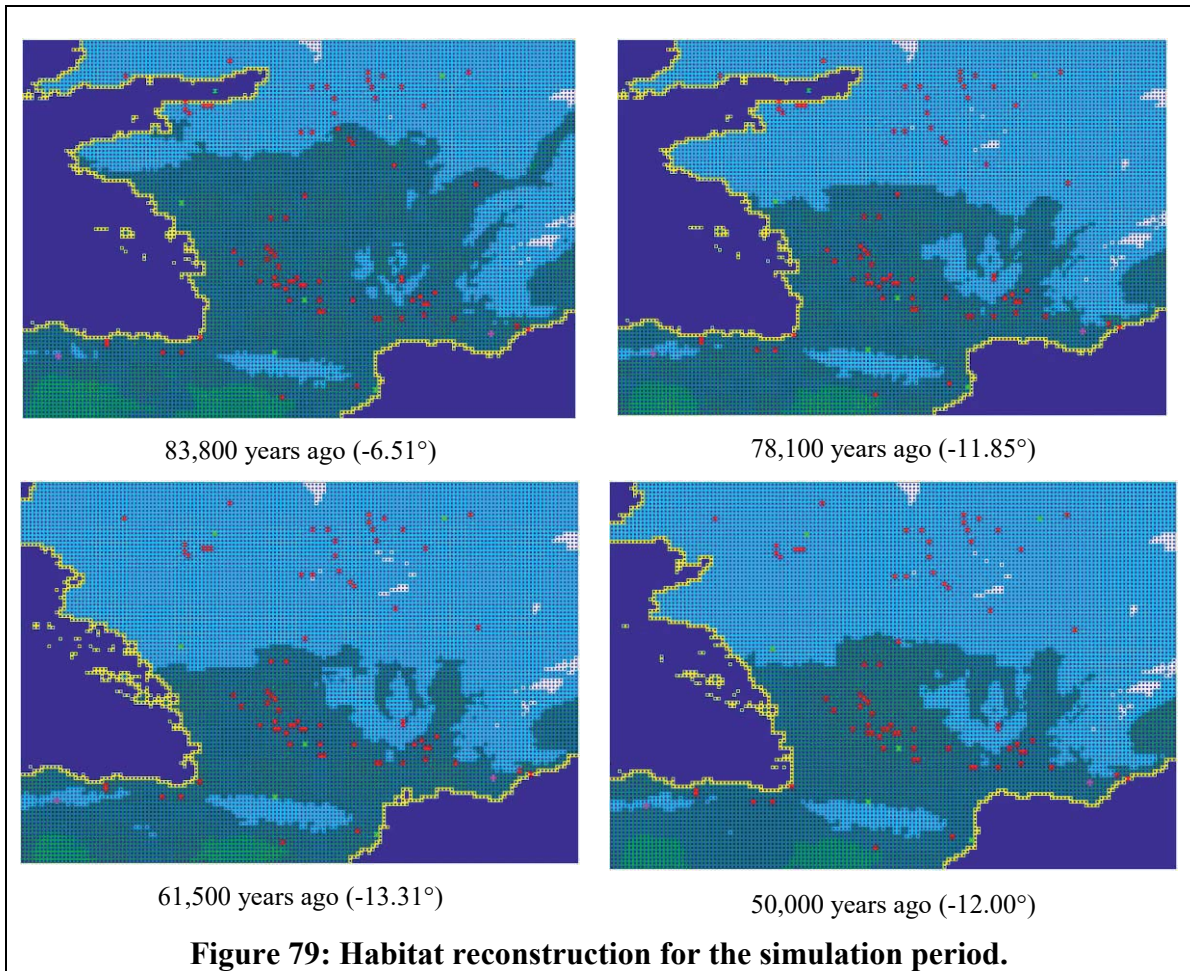
The results show that a land bridge exists to the UK at the location of this checkpoint for a limited period of time during the simulation. At other locations (to the north) access to the British Islands would have been longer possible. The British Islands were only really separated from the European main land during a relatively short period in the simulations. This period of island status in HomininSpace starts around time step 4,220 and ends at 15,815 (that is between 126.8 ka and 115 ka), spanning roughly 11,000 years. These results are similar to for instance the reconstruction by Ashton and Lewis (2002), Figure 3. These authors identify a similar time frame with direct access to Britain, but prevent hominins to cross the dry Channel area in most of MIS 3 with climatic factors. When they include a progressive subsidence of the North Sea Basin floor, access from the main land was limited to a very small window in time around 125 ka (Ashton *et al.* 2011).

Note that height in the topography does not have an explicit effect on movement of hominins. In other words, topography does not prevent nor promote hominin groups to certain areas in the landscape. However, the reconstructed climate parameters for especially elevated grid cells result in limited availability of resources in for instance the wider Alpine and Pyrenean regions (see the next subsections). Thus these areas are less attractive for hominins which results in lower presence densities during simulations. Mountainous areas specifically do not prevent access by modelled Neanderthal hominins as Neanderthal presence is attested in occasional archaeological finds from higher altitudes (Domingo *et al.* 2017).

11.5.2    Energy via habitat reconstruction

To visualize changes in the reconstructed habitat Figure 79 presents screenshots from identified global and local climate minima and maxima within the simulation period. Each habitat type is defined by precipitation and temperature parameter values, and has associated energy levels (subsection 4.4.3). In the following figures white coloured grid cells are tundra, light blue is boreal forest, dark green is evergreen forest and lighter green is grassland (see Table 22). The yellowish coloured patches in the Mediterranean area in warmer periods are very productive woodlands. The reconstructed habitats are independent of the chosen scenario settings and cannot be manipulated by the foraging hominins.



131,000 years ago (-5.6°)        124,800 years ago (2.19°)

121,400 years ago (0.57°)        112,800 years ago (-9.7°)

97,200 years ago (-6.53°)        88,700 years ago (-12.07°)

83,800 years ago (-6.51°)

78,100 years ago (-11.85°)

61,500 years ago (-13.31°)

50,000 years ago (-12.00°)

**Figure 79: Habitat reconstruction for the simulation period.**

Six climate recording checkpoints are installed when a simulation is started. Two of them were positioned specifically to monitor changing habitats: "Climate Monitor 1 Atlantic" and "Climate Monitor 3 Mediterranean". See Figure 80 for the resulting changes through time. Near the Atlantic coast the habitat oscillates between what is referred to as cool forest and boreal forest. Near the Mediterranean Sea there is a period of (very productive) grass land, where during the warmer middle of MIS 5e there even exist a habitat that is referred to as warm grassland, or a habitat comparable to the current day African Savannah (yellowish grid cells in Figure 79).
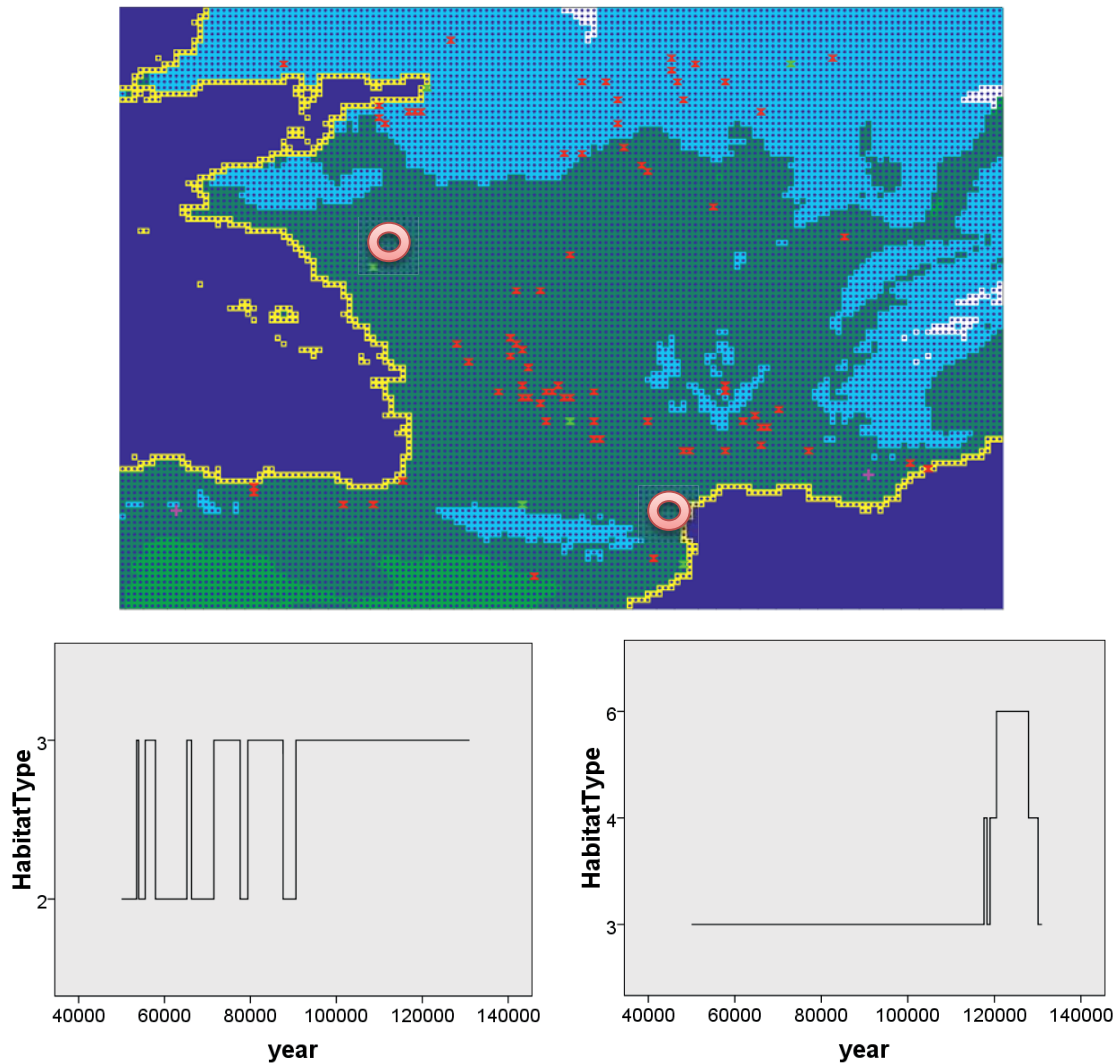
**Figure 80: Geographical positions and Habitat types for the checkpoints Climate Monitor 1 Atlantic (bottom left) and Climate Monitor 3 Mediterranean (right). Habitat type 2 is boreal forest, 3 is cool forest, 4 is cool grass, and 6 is warm grass.**

Climate Monitor 5 is positioned at the Scladina archaeological site, to monitor changes in this specific area. It is a site for which extensive climate reconstruction efforts have been made (López-García *et al.* 2017), some of which can be compared against the reconstructions in HomininSpace for the simulation period. Figure 81 plots the resulting habitat reconstruction in HomininSpace together with the reconstruction from survey C4 (López-García *et al.* 2017, 629). In HomininSpace throughout the simulation period a forested environment is reconstructed, characterizes for most of the time as boreal forest, and only during a short period before 120 ka this was replaced by cool forest. The reconstructed C4 survey also contains mostly woodland, with a varying percentage of open environment, never surpassing 50% of the non-water landscape. In HomininSpace the Scladina area the climatic parameters never throughout the simulation period allow reconstruction of extensive grass lands.
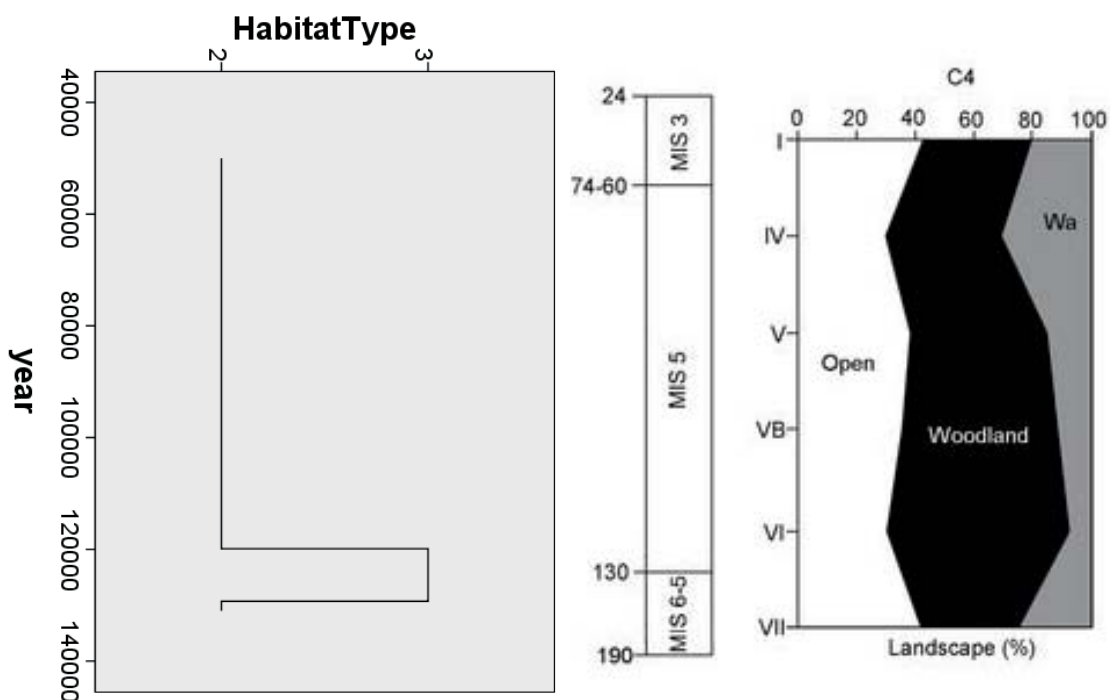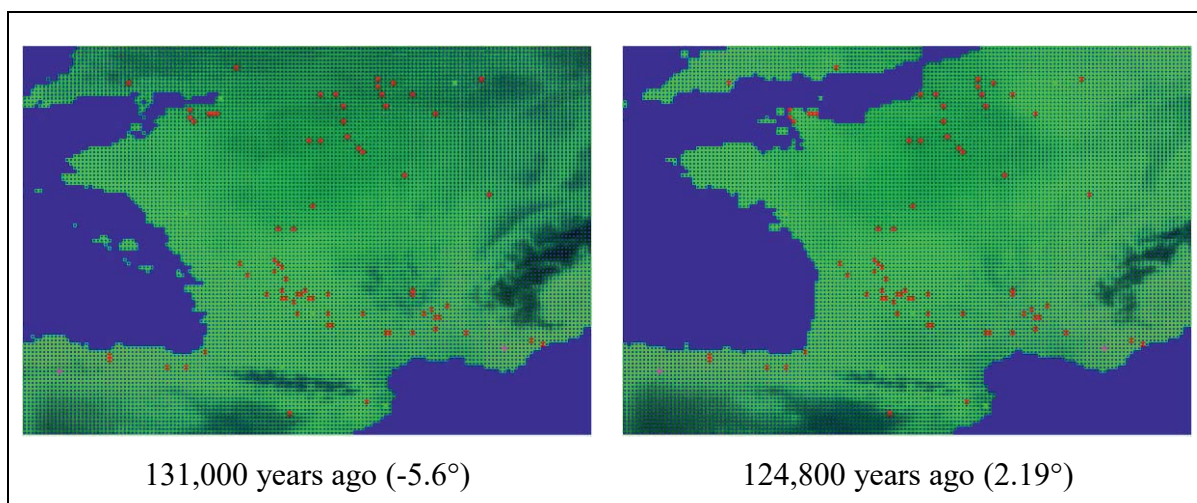
**Figure 81: Reconstructing habitat types for the Scladina area. Results from HomininSpace (left, with HabitatType 2 = booreal forest, and 3 = cool forest) and López-García *et al.* (2017).**

### 11.5.3 Energy via direct extrapolation

Energy in the landscape can also be recreated by using temperature and precipitation values to extrapolate from known environmental data. Figure 82 illustrates the continuous energy landscape reconstruction in HomininSpace (subsection 4.4.2), for selected moments in time. Per grid cell the resulting energy levels are calculated. In this figure darker colours indicate less energy in the landscape.
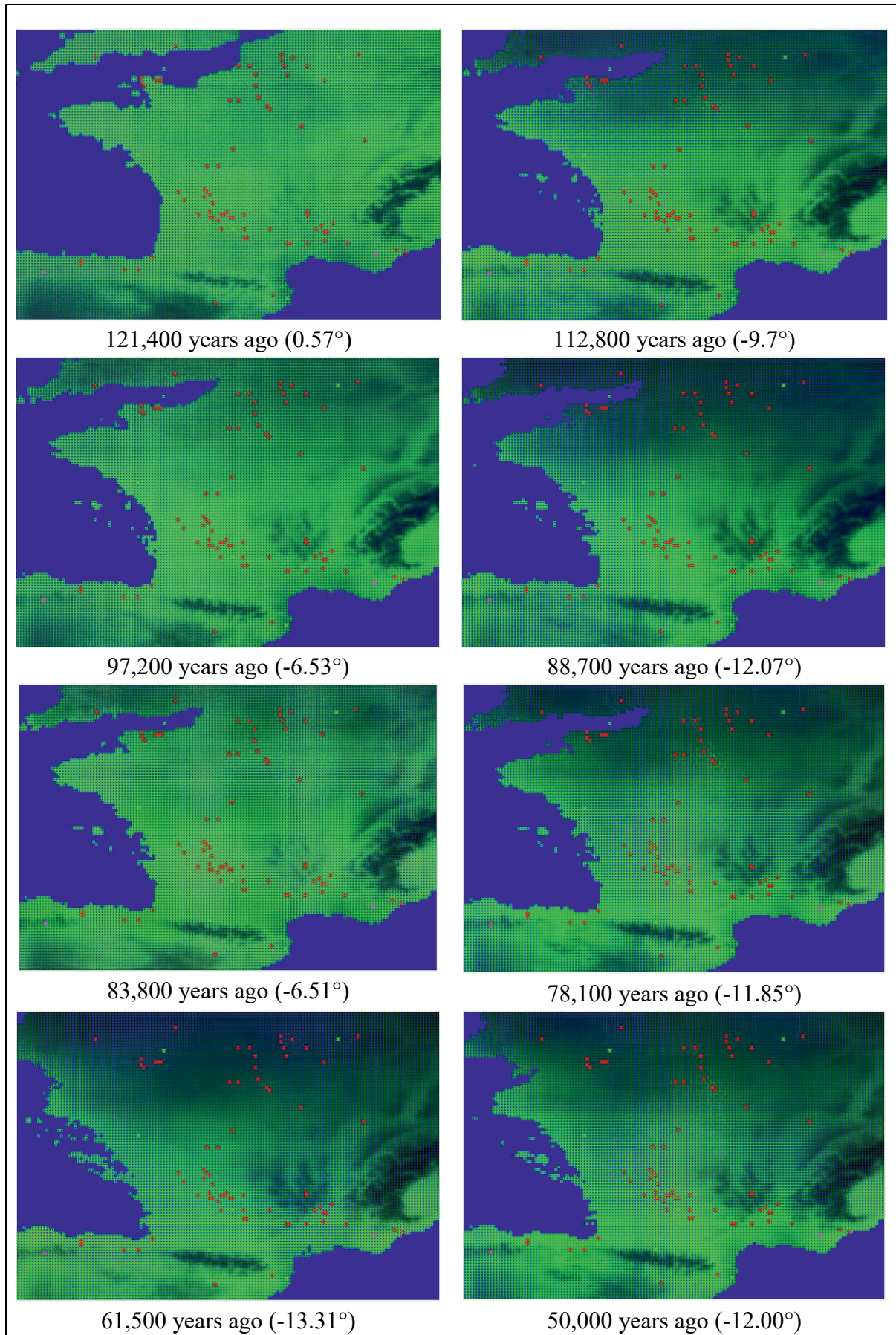


131,000 years ago (-5.6°)          124,800 years ago (2.19°)

121,400 years ago (0.57°)

112,800 years ago (-9.7°)

97,200 years ago (-6.53°)

88,700 years ago (-12.07°)

83,800 years ago (-6.51°)

78,100 years ago (-11.85°)

61,500 years ago (-13.31°)

50,000 years ago (-12.00°)

**Figure 82: Reconstruction of the energy levels in the landscape for the complete simulation period. Darker colors indicate less energy.**

To further quantify the energy levels in the landscape, Figure 83 presents the energy levels for all climate recording checkpoints. Note that recording checkpoint 6 (located in the Channel and colored red in the figure) is submerged during longer periods and has energy levels of zero during those time frames. For beach type grid cells the energy levels are effectively doubled which explains the non-continuities for that same checkpoint which after and before submergence becomes beach and then turns into regular land area when the water retreats further or becomes flooded when the sea level rises further.
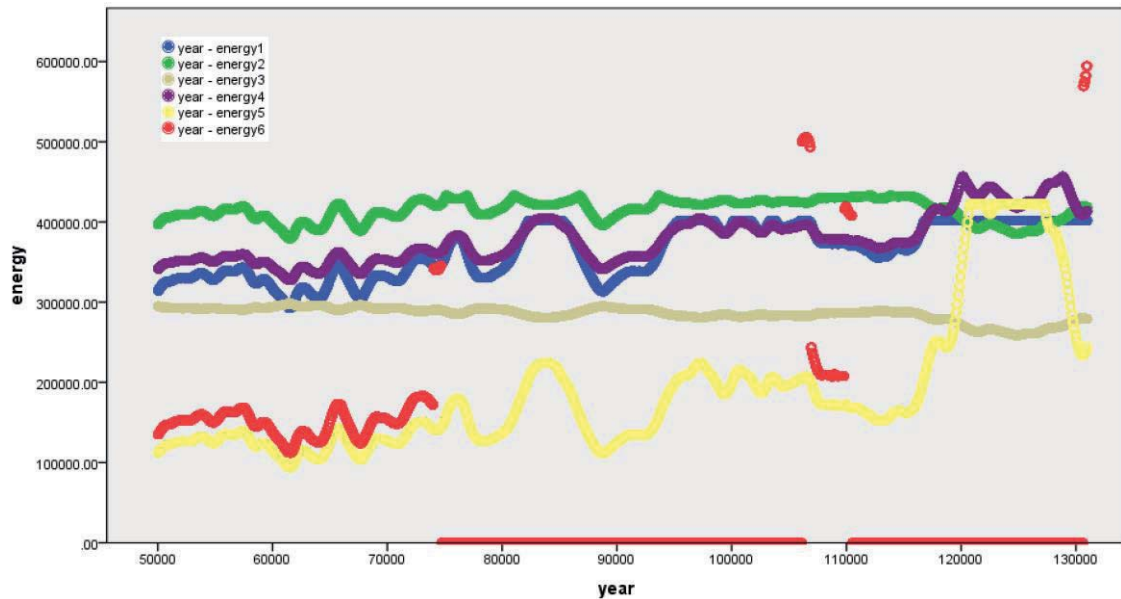


**Figure 83: Energy levels per year recorded by the Climate Recording Checkpoints for the whole simulation period. Blue line is for Checkpoint 1, Red for 6.**

Both checkpoints 5 (Scladina) and 6 (Channel) are located in the top (or northern) area of the map. This area suffers most from deteriorating of the environment due to colder climates. Both of them offer substantially less energy than the others that are further south. The very noticeable peak (can be inferred from the beach production in 6) in the beginning of the simulation is due to the significant improvement during MIS 5e. The effects are very pronounces for northern sites due to the large temperature differences between LGM and current day conditions. Furthermore it is quite interesting to find that the conditions in the Mediterranean area hardly change at all, but does not produce the most energy. Best conditions can be found in Occitanie (2) and near the Pyrenees (4), where the latter is most benign and outperforming 2 during MIS 5e conditions. Note that the production for Occitanie is also very constant through time.

These patterns are as can be expected. Energy levels are directly derived from reconstructed precipitation and temperature values (see Figure 84 and Figure 85). Interesting is the effect for the Pyrenees area (purple colored in the figures), where a

relatively high precipitation level results in an unexpected high energy production throughout the simulation period making this a very attractive place for hominin groups.
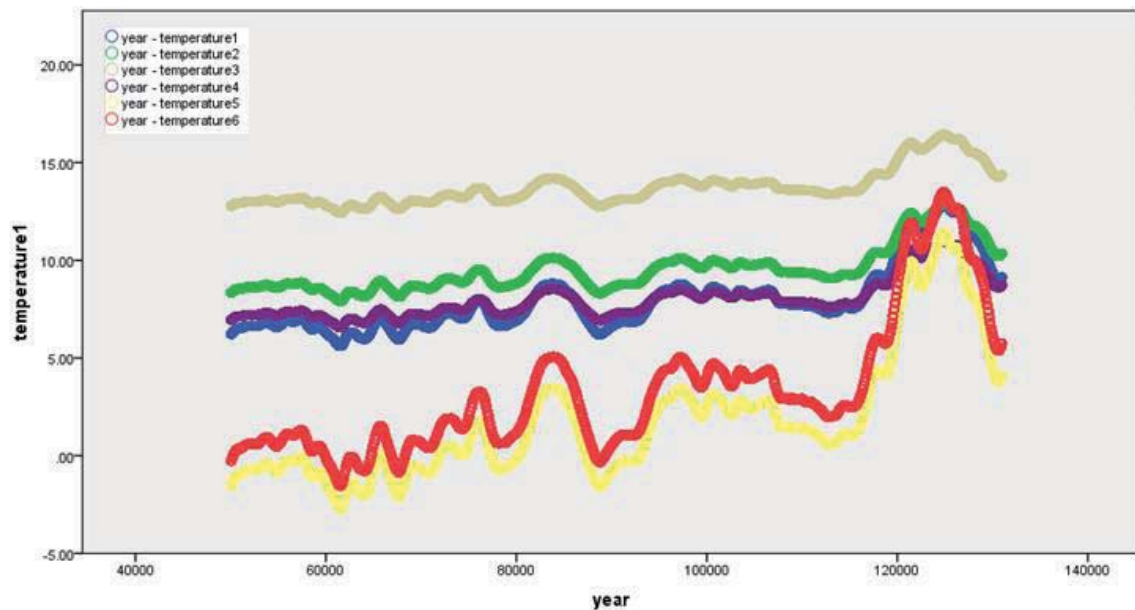


**Figure 84: Recorded values for reconstructed temperatures per Climate Recording Checkpoint.**
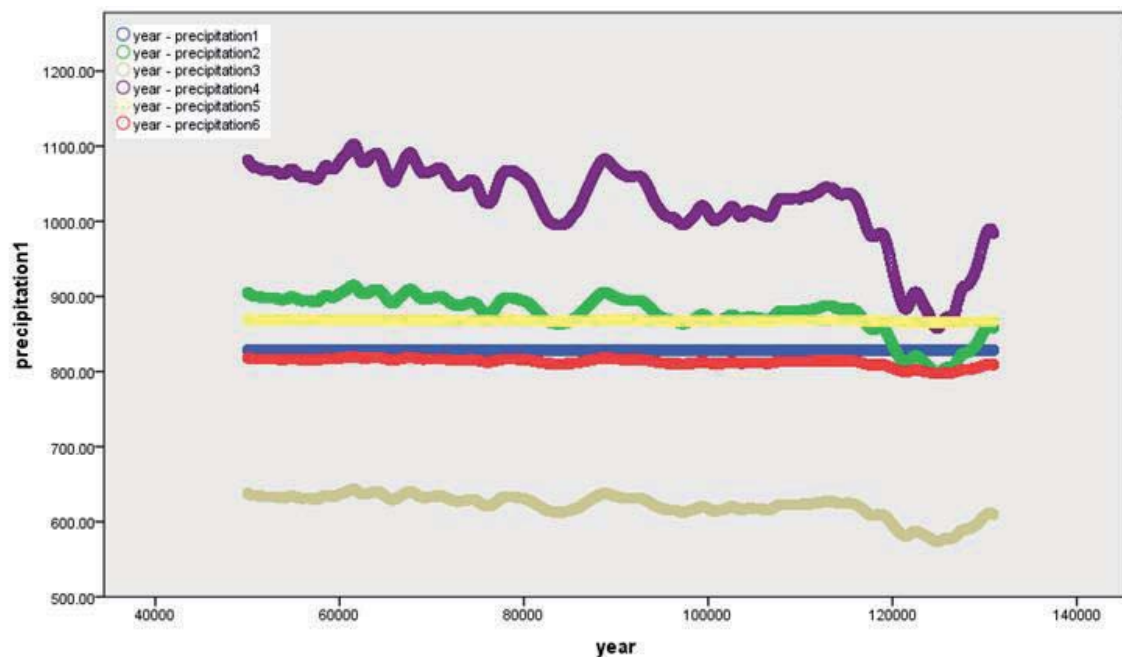


**Figure 85: Recorded values for reconstructed precipitation values per Climate Recording Checkpoint.**

Note that the modelled environment is the same in all simulations for all scenarios. The simulated hominins have no influence on the reconstructed sea level, temperature, precipitation, or primary production values. They can however consume some or all of the calculated secondary biomass, which influences availability of such biomass for the next year.