

GENERATING HYPOTHESES ON PREHISTORIC CULTURAL TRANSFORMATION WITH AGENT-BASED EVOLUTIONARY SIMULATION

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ABSTRACT

We propose an agent-based evolutionary simulation analogous to a genetic algorithm for generating hypotheses on prehistoric cultural transformation. As an application case study, we examine the mechanism of change in the composition of structural remains at the Jomon to Yayoi period sites in Western Japan. The simulations generate hypotheses that the major changes from the middle to the late Jomon periods and from the final Jomon period to the early Yayoi period may have been caused by different mechanisms. The latter could be interpreted as a continuous mechanism, such as inter-settlement exchanges, while the former could be interpreted as a non-continuous mechanism.

1 INTRODUCTION

We propose an agent-based evolutionary simulation analogous to a genetic algorithm for generating hypotheses on prehistoric cultural transformation. To demonstrate our method in applications, we examine the mechanism of change in the composition of structural remains at Western Japanese sites from the Jomon to the Yayoi periods.

The most significant cultural transformation of the Japanese archipelago during the prehistoric period was the transformation from the hunter-gatherer culture of the Jomon period to the agricultural culture of

the Yayoi period. The Yayoi culture was a mixture of the native Jomon culture and agricultural culture, which was introduced along with immigration from mainland China and the Korean Peninsula. The agrarian culture was introduced to Kyushu, the westernmost part of Japan's main islands and the closest to the Chinese mainland and the Korean Peninsula, and spread eastward as the Yayoi culture. The agrarian culture was followed by the spread of rice cultivation to Eastern Japan within a few hundred years.

However, studies aimed for understanding the dynamics of this cultural transformation from a broader perspective have been limited. To examine the mechanism of the transformation to the Yayoi culture, it is necessary to quantitatively evaluate the transition of sites from the Jomon to the Yayoi periods.

In this study, the mechanism of change in the composition of structural remains from the Jomon to the Yayoi periods is investigated via simulations based on the results of statistical analysis of the composition of the structural remains. Results of the simulations generate hypotheses that the major changes in the middle to the late Jomon periods and the final Jomon period to the early Yayoi period (Yamaguchi 2012) may have been due to different mechanisms. The latter could be interpreted as a continuous mechanism, such as inter-settlement exchanges, while the former could be interpreted as a non-continuous mechanism.

2 RELATED WORK

Previously, we conducted a principal component analysis of the changes in the composition of structural remains at Jomon to Yayoi archaeological sites in Western Japan to quantitatively evaluate the evolution of site composition during these periods (Yamaguchi 2012). We used the correspondence of period and phase categories, as shown in Table 1. The results of the principal component analysis are shown in Figure 1. The figure shows the characteristics of the composition of structural remains at each period as the first and second principal components (PC1 and PC2, respectively) on the horizontal and vertical axes, respectively. Without going into details, the first principal component orientation is interpreted as a genus-community orientation in the negative direction and a genus-family orientation in the positive direction. On the other hand, the second principal component is interpreted as a long-term life orientation in the negative direction and a short-term orientation in the positive direction.

The principal component analysis shows major changes from the middle (8th) to late (9th) Jomon periods and from the final Jomon period (15th) to the early Yayoi period (16th). The major change from the middle (8th) to late (9th) Jomon periods is interpreted as a change to a “genus-community orientation” represented by earth mines and ditch-like remains. On the other hand, the major changes from the final Jomon period (15th) to the early Yayoi period (16th) is interpreted as a change toward long-term living represented by moat and storage holes.

This previous study suggests that the major changes in the mid-to-late Jomon period and the final Jomon period to the early Yayoi period indicate that the direction of change is different. Therefore, the question arises of whether the different directions of change in each may mean that their corresponding mechanism of change may also be different.

Therefore, here, we use agent-based simulations to generate hypotheses about the mechanism of each change. Specifically, we determine what parameters are likely to reproduce these two major changes in evolutionary simulations with similar genetic algorithms, and whether there is a difference between them. When considering a simulation model of cultural transformation, it is possible to think of the transformation from one culture to another as evolution. In fact, cultural evolution is often talked about using analogies to biological evolution. Therefore, in this study, we build an agent-based evolutionary simulation and generate hypotheses on cultural transformation in terms of what parameters are more likely to reproduce the solution (i.e., change), rather than searching for the solution itself.

Some of the most popular studies using agent-based simulation on archaeological sites are on the examination of the factors of demographic dynamics of ancient Anasazi people from 800 to 1350 in Long House Valley in Arizona, USA (Dean et al. 2000; Axtell et al. 2002). These studies examined factors influencing the population dynamics in Long House Valley by using several parameters including paleoenvironment variables from social unit and empirical data. They reported that research related to the

Anasazi history has reached about 30% of all archaeology studies using ABS (Cegielski and Rogers 2016). This means that the Anasazi history has been one of the mainstream of current research.

On the other hand, the study of Matsumoto and Sasakura (2016) approached the diffusion of the Yayoi culture with a simulation model, which focused on the process of cultural transmission, how people moved, and from whom the culture was transmitted and learned to uncover the diffusion of the Yayoi culture. However, their study did not explain the differences in cultural transformation shown in Yamaguchi (2012) because their main focus was to understand the speed of diffusion of the Yayoi culture.

Table 1: Correspondence of period and phase categories in Yamaguchi (2012). The years are given as a guide for the general reader.

Phase	Period	Years
0th	Incipient Jomon	About 16,000 to 11,500 years ago
1st	Initial Jomon	About 11,500 to 7,000 years ago
2nd		
3rd	Early Jomon	About 7,000 to 5,500 years ago
4th		
5th		
6th	Middle Jomon	About 5,500 to 4,500 years ago
7th		
8th		
9th	Late Jomon	About 4,500 to 3,200 years ago
10th		
11th		
12th	Final Jomon	About 3,200 to 2,800 years ago
13th		
14th		
15th	Final Jomon/Initial Yayoi	About 2,800 to 2,350 years ago
16th	Early Yayoi	

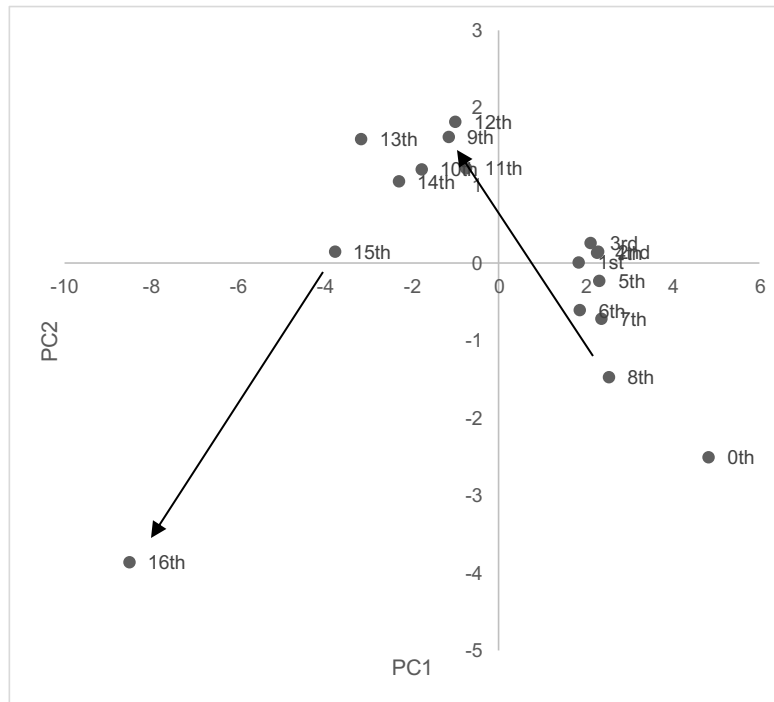


Figure 1: Principal component (PC) analysis for each phase in Yamaguchi (2012). The two arrows indicate the major changes that are the subject of the simulations in this study.

3 SIMULATION MODEL

We construct an agent-based evolutionary simulation model similar to a genetic algorithm. The target of the simulation is the same site as Yamaguchi (2012) and each archaeological site is considered as an agent.

The site agent has as a gene for the presence or absence of each structural remains. Following Yamaguchi (2012), we consider the following 14 structural remains: moats, sinkholes, buildings, ditch-like remains, accumulation remains, dwellings, paddy field remains, pillar holes, storage holes, earthenware burial, earthenware pools, earth mines, tombs, and furnaces. At the start of the simulation, the presence or absence of each structural remains at each site is reflected in the genes.

In this study, we examine whether the influence of either imitation or mutation parameters is stronger to reach the principal component score more quickly in the next phase, i.e., the 9th or 16th, starting with each of the 8th- or 15th-period site agents. In other words, with each next phase as a goal, we generate hypotheses based on the parameters that are more likely to reproduce the changes leading up to it and the factors that explain each change.

The details of the formulation model are described below, which follows the Overview, Design concepts, and Details (ODD) protocols (Grimm et al. 2006; 2010). The ODD protocol is in response to earlier criticisms that agent-based models lack reproducibility. The protocol also aims to improve the standardization and completeness of the explanation. Our simulation model is implemented and run on the agent-based simulator, artisoc 4.2 (KOZO KEIKAKU ENGINEERING Inc. 2018).

3.1 Agent and State Value

We consider an archaeological site as an agent, which possesses the following attribute variables.

3.1.1 ID and Spatial Position

An agent has information about positional coordinates (“X” and “Y”) corresponding to the latitude and longitude of the actual site, respectively. For convenience, we assume that each offspring of the site agent group generated during the simulation has the same positional coordinates as its parent positions. As will be discussed below, the distance between each offspring (site agent) affects the selection of another offspring to imitate the structural remains gene. All offspring from the same period are used as evaluation units (offspring group) for simulations.

3.1.2 Structural Remains Gene

We consider the following structural remains genes: moats, sinkholes, buildings, ditch-like remains, accumulation remains, dwellings, paddy field remains, pillar holes, storage holes, earthenware burial, earthenware pools, earth mines, tombs, and furnaces. Each is set to 1 if it is present and 0, otherwise.

3.2 Process Overview and Scheduling

Similarly to the general genetic algorithm, one generation is one step, and within one step, 1) 20 copies of an offspring group are generated from the parent group, 2) imitation and mutation operations are applied within each offspring, and 3) each offspring group is evaluated such that the highest-valued site offspring group is left as the next generation parent group and the rest is deleted. The agents are randomly selected for the operation.

3.3 Design Concept

Of the 11 design concepts of the ODD protocol, we use seven concepts, as shown in Table 2. Because the model in this study is simple, the description of the model in this paper and the ODD design concepts are used to ensure the reproducibility of the model.

Table 2: Design concepts.

No.	Design concepts	Elements
1	Basic Principles	Similarly to a genetic algorithm, offspring are generated based on a parent. Within each offspring group, selected offspring apply the imitation and mutation operations of the structural remain genes. The offspring group closest to the composition of the structural remains gene of the next generation for the real site group is left as the next parent group and the others are deleted.
2	Emergence	Imitation and mutation change the structural remains genes of each offspring.
3	Adaption	The goal is to approach the composition of the structural remains genes of the next phase site group in reality.
4	Objective	The difference in the first and second principal component scores of the structural remains composition of the next phase site group.
5	Interaction	According to the imitation rate, an offspring imitates a structural remains gene from another offspring in the same group.
6	Stochasticity	Choosing another offspring to imitate a remains gene. Location of the imitating and the mutating structural remains gene. Execution order of the agent.
7	Observation	The first and second principal component scores for each offspring group.

		The number of steps when the difference in the first and second principal component scores of the structural remains composition of the next phase site group are $\pm 5\%$, respectively.
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3.4 Submodels

The simulation model comprises the following three rules: generating offspring, imitation and mutation, and evaluation and selection. The rules are run sequentially similarly to conventional genetic algorithms (Figure 2).

3.4.1 Rules of Generating Offspring Agent Sites

For each offspring, we inherit the parent's location coordinates and structural remains genes to create 20 copies of the offspring group. The 20 copies of the offspring group are called as the assemblage of the offspring group. In accordance with conventional genetic algorithm parameter settings, we set the number of copies to 20. Note that the structural remains genes of the parent are the same as those of the real site only at the start of the simulation.

3.4.2 Rules of Imitation and Mutation

Within each offspring group, we apply the imitation operation from other offspring and then the mutation operation. The unit of imitation and mutation is a single gene. As mentioned above, a single gene represents the kind of structural remains, and its value is binary (either 0 or 1). We imitate the structural remains genes of other offspring according to a parameter representing the probability of occurrence of imitation (the imitation rate). The structural remains gene to imitate is a single gene selected at random according to the unit of mutation described below. In other words, we adopt a behavior that imitates one gene of another individual in a single gene unit rather than a crossover. We select the sites to be imitated according to the probability based on the distance between the sites. The selection probability (P) is described as follows:

$$P_{i,j} = \frac{\exp^{(D_{max}-D_{i,j})}}{\sum_{k,m=1}^n \exp^{(D_{max}-D_{k,m})}},$$

where $P_{i,j}$ is the probability that offspring i will choose offspring j , D_{max} is the maximum distance between offspring (site) across all offspring, and D_{ij} is the distance between offspring i and offspring j .

Because it is unclear what kind of network was built between the sites, assuming a specific network would be problematic (Brughmans 2010). Hence, the candidates for imitation are all offspring within their offspring group. However, because this study is a logit model, we assume that the further the distance of a site is, the lower the chance of it being selected.

According to a parameter indicating the probability of the mutation occurring (the mutation rate), a structural remains gene is selected at random, and then its value is changed to 1 (has) if it is 0 (does not have) or 0 if it is 1.

3.4.3 Rules of Evaluation and Selection

The first and second principal component scores of each offspring group are calculated. Then, the offspring group closest to the principal component score of the target phase (i.e., if the 8th phase begins, the 9th phase is the target; if the 15th period begins, the 16th period is the target) is left as the parent group for the next step. If the offspring is not the closest, then it is deleted. The proximity of the scores of the first and second principal components is defined as the proximity of the Euclidean distance of the map on those principal component axes. This Euclidean proximity corresponds to cultural proximity based on the composition of the structural remains.

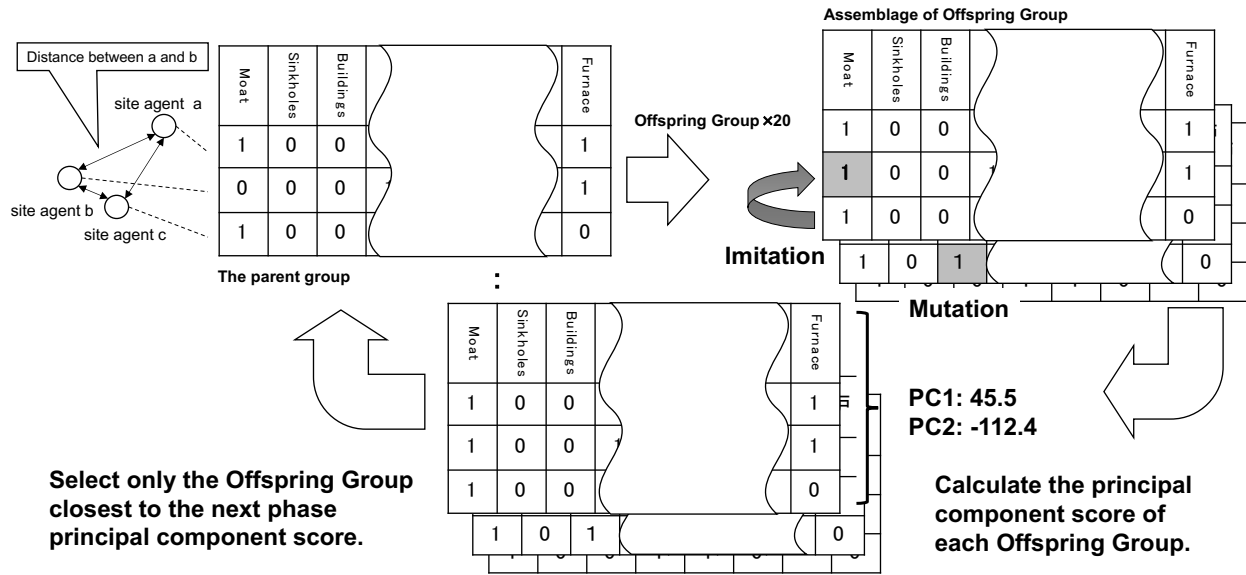


Figure 2: Overview of the simulation model.

3.5 Initialization and Number of Simulation Cases

The parameters of the simulation are the imitation and mutation rates, as described earlier. The sum of the imitation and mutation rates should be less than 100% in order to comply with general genetic algorithm parameter settings and leave the offspring unchanged. Eight simulation cases are created by combining them (Table 3). Twenty trials are conducted in each case. The random number seeds for the 20 trials are the same across cases. 20 trials are chosen because it is the minimum number of trials required to produce the distribution of the simulation results, after taking into account the computational cost.

Table 3: Simulation cases.

Case No.	Start phase to Target phase	Imitation rate	Mutation rate
1	8th to 9th	95.0%	0.5%
2	8th to 9th	80.0%	1.0%
3	8th to 9th	70.0%	2.0%
4	8th to 9th	60.0%	4.0%
5	15th to 16th	95.0%	0.5%
6	15th to 16th	80.0%	1.0%
7	15th to 16th	70.0%	2.0%
8	15th to 16th	60.0%	4.0%

3.6 Evaluation Index

The number of steps required to complete the simulation is used as an evaluation measure. The exit condition should start from the group of site agents in the 8th or 15th phase until it approximates ($\pm 5\%$ error) the 9th or 16th phase, which is the next phase on the first and second principal components scores. We set the imitation and mutation rates as parameters and examine the set of parameters that ended with fewer steps. In other words, we interpret a small number of steps as a parameter that is more likely to reproduce change and more convincing for change than a large number of steps.

4 RESULTS AND DISCUSSION

The simulation results show that changes from the 8th to the 9th periods have fewer steps with higher mutation rates, while changes from the 15th to the 16th periods have fewer steps with higher imitation rates (Figure 3). For example, in the former, fewer steps are needed to reach case 4 than those to reach case 1, and in the latter, fewer steps are needed to reach case 5 than those to reach case 8. We find that there is no statistically significant difference between case 1, case 2, and case 3, but there is a statistically significant difference between case 3 and case 4. The p-value calculated based on a t-test is $1.097e-10$ between these cases. Similarly, there is no statistically significant difference between case 5, case 6, and case 7, but there is a statistically significant difference between case 7 and case 8. The p-value calculated based on a t-test is 0.0002727 between these cases.

It is more explanatory to think that the change from the 15th to the 16th periods is due to high imitation rates, that is, frequent inter-settlement exchanges. This change can be interpreted as a continuous mechanism from the 15th period onwards. However, we can better explain the change from the 8th to the 9th periods if we consider it to be due to factors other than inter-settlement exchanges (something mutational). This change can be interpreted as a non-continuous mechanism from the 8th period.

In this study, we verify the possibility that the different directions of change in the composition of the remains from the Jomon to the Yayoi periods may be due to different mechanisms of change. Furthermore, for these different mechanisms, we generate hypotheses about major changes in the mid-to-late Jomon period and the final Jomon period to the early Yayoi period (Yamaguchi 2012), with the latter being a continuous mechanism, such as inter-settlement exchanges, and the former a non-continuous mechanism.

Because the simulation results are only computer-generated numbers, it is necessary to interpret and verify the archaeological implications of the computer-generated hypotheses. In the case of this study, we need to interpret what is meant by a “non-continuous mechanism”.

Based on discussion with archaeological researchers, the non-continuous mechanism of this study may indicate a possible migration of the population from Eastern Japan. A study on the number of dwellings in the site (Yano 2004) suggested that a certain degree of population migration from Eastern Japan is possible. In this simulation, the data do not include the structural remains of Eastern Japan, so there is a possibility that the propagation of culture from Eastern Japan may appear as a non-continuous mechanism. It is generally believed that the spread of agrarian culture in the Japanese archipelago proceeded from west to east, but there is a possibility that the spread was in the opposite direction at some point. To further test this hypothesis, we plan to re-simulate the change from the 8th to the 9th phases with data from Eastern Japan in the future. If the imitation rate is lower in the number of steps reached at the end of the simulation than in the height of the mutation rate than from the 15th to 16th phases, then it is plausible that the change is due to inter-settlement exchanges. In other words, it is material that theoretically reinforces the possibility of cultural transmission from east to west that accompanies population movement from east to west.

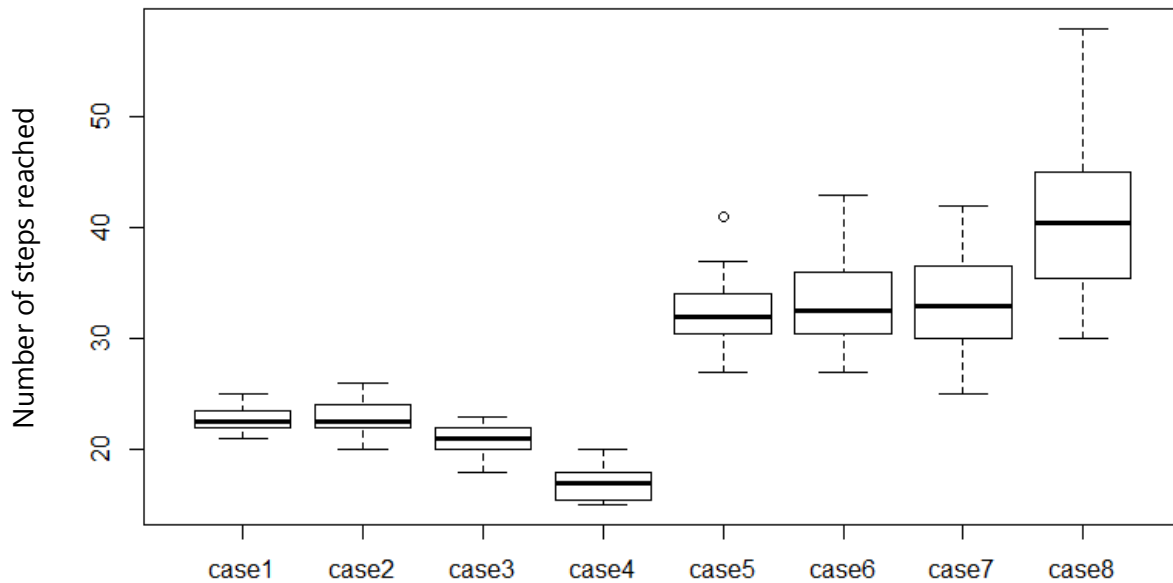


Figure 3: Box plots of the number of steps reached by the simulations. The thick horizontal line near the center of the box represents the median value. The top and bottom lines of the box represent the third and first quartiles, respectively. The short horizontal lines above and below the box represent the maximum and minimum values. The points outside the short horizontal lines above and below the box represent outliers.

5 CONCLUSION

In this study, we simulated the mechanism of change in the composition of the remains from the Jomon period to the Yayoi period. We generated hypotheses that the major changes from the middle to the late Jomon periods and from the final Jomon period to the early Yayoi period were caused by different mechanisms. That is, the latter corresponds to a non-continuous mechanism, e.g., mutations. Furthermore, the possibility of cultural transmission from Eastern Japan was considered as an interpretation of the non-continuous mechanism. In the future, we will verify this in a re-simulation that includes data from Eastern Japan's archaeological sites.

It is important to note that there may be a bias in the archaeological data, to begin with. In other words, only a small portion of the information that originally existed was excavated and kept in the records. Additionally, there are strong assumptions in the simulation models and evaluation indicators. However, these biases and assumptions are not only found in simulation studies but also in conventional studies.

Moreover, we are still in the process of developing a database of archaeological sites. Therefore, it should be noted that the future development of the database may change the results of the principal component analysis, which may change the results of the simulations.

The value of the simulation lies in developing different hypotheses or hypotheses from different perspectives via computational tools, which can be tested experimentally or empirically.

With the proliferation of agent-based simulation research in archaeology, there is a concern about the lack of arrangements and feedback between archaeologists and modelers (Romanowska 2015). This is attributed to the lack of comprehensive textbooks and introductory books for archaeologists on simulation

techniques. Conversely, a guide for building simulation models for archaeologists has been developed (Romanowska 2015). However, the complexity of the software is a barrier for archaeologists wanting to adopt agent-based simulations. Therefore, a software system that does not require advanced programming knowledge is needed (Cegielski and Rogers 2016).

However, archaeologists' mastery of model building and programming does not link simulation and field research. Rather than aligning researchers, we must align research findings (Sakahira 2019).

Finally, we emphasize that the hypotheses generated based on the numerical results of the simulations must be tested by examining them archaeologically. Then, the verification result must be fed back to the input data of the simulation and the simulation is performed again to improve the verification result's reliability. It is this cycle that allows for feedback between archaeologists and modelers and demonstrates the potential of simulation studies to contribute to archaeological research.

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A APPENDICES

The python-like pseudo-code of our simulation model is shown below.

```
Procedure step():
  for steps:
    for i = 0 to Parent_Group.length - 1:
      Parent = Parent_Group[i]
      for j = 0 to 19
        d = Random value between 0.0 and 1.0
        if d < Imitation_Rate:
          Imitation(Parent, j)
        elif d < (Imitation_Rate + Mutation_Rate):
          Make a copy with a different gene of Parent and add it to
          Assemblage_of_Offspring_Group[j]
        else:
          Make a copy of Parent and add it to Assemblage_of_Offspring_Group[j]

    for j = 0 to 19:
      Offspring_Group = Assemblage_of_Offspring_Group[j]
      for i = 0 to Offspring_Group.length - 1:
        Offspring = Offspring_Group[i]
        for k = 0 to 13:
          Offspring.PC1 += Offspring.Gene[k] * Coefficient_of_PC1[k]
          Offspring.PC2 += Offspring.Gene[k] * Coefficient_of_PC2[k]
          Total_PC1[j] += Offspring.PC1
          Total_PC2[j] += Offspring.PC2
        C_Euclidean[j] = Euclidean distance between Target and
        Assemblage_of_Offspring_Group[j] on PC1 and PC2

    for j = 0 to 19:
      if Min_Euclidean > C_Euclidean[j]:
        Min_Euclidean = C_Euclidean[j]
        Min_ID = j
```

```
for i = 0 to Parent_Group.length - 1:
  Parent = Parent_Group[i]
  for k = 0 to 13:
    Parent.PC1 += Parent.Gene[k] * Coefficient_of_PC1[k]
    Parent.PC2 += Parent.Gene[k] * Coefficient_of_PC2[k]
    P_total_PC1 += Parent.PC1
    P_total_PC2 += Parent.PC2
  P_Euclidean = Euclidean distance between Target and Parent_Group on PC1 and
PC2

if C_Euclidean_dist[Min_ID] < P_Euclidean_dist:
  Parent_Group = Assemblage_of_Offspring_Group[Min_ID]
  P_total_PC1 = Total_PC1[Min_ID]
  P_total_PC2 = Total_PC2[Min_ID]

if Parent_Group approximates the target on PCA1 and PCA2(±5% error):
  Exit the simulation

def Imitation(Parent, j):
  for i = 0 to Parent_Group.length - 1:
    Total_exp += Napier's constant ^ (MaxDist - Dist[Parent, i])
  d = Random value between 0.0 and 1.0
  for i = 0 to Parent_Group.length - 1:
    if Parent is not Parent_Group[i]:
      Exp += Napier's constant ^ (MaxDist - Dist[Parent, i])
      if d < (Exp / Total_exp):
        Other_Parent_ID = i
        Break
  for k = 0 to 13:
    Offspring.Gene[k] = Parent.Gene[k]
    Offspring.X = Parent.X
    Offspring.Y = Parent.Y
  Other_Parent = Parent_Group[Other_Parent_ID]
  Imitation_point = Integer of (Random value between 0.0 and 1.0) * 14
  Offspring.Gene[Imitation_point] = Parent.Gene[Imitation_point]
  Add Offspring to Assemblage_of_Offspring_Group[j]
```

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