31 Detection of kinship structures in prehistoric burial sites based on odontological traits[1]

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31.1 INTRODUCTION

The reconstruction of kinship structures in burial sites is one of the major challenges in prehistoric research. Epigenetic and odontological traits are possible fundamental elements for such a reconstruction. The basic idea can be summarised as follows: A "family" is regarded as a set of genetically related individuals. Heritable traits can represent these relationships: for each family there exists a set of traits typical of this family, i.e., all members of the family shows several of these traits. In this paper we present a strategy to solve the task of searching for such structures. We use discrete traits of the teeth and jaws.

31.2 METHOD

For any attempt to reconstruct kinship structures the first step is to choose appropriate traits. In anthropology, non–metric traits of the human cranium are used for comparative studies between archaeological populations and for kinship analysis among these (Sjøvold 1973; Rösing 1990). In forensic medicine, they are used for personal and familial identification (Finnegan 1977). These epigenetic variants have long been subject to criticism, because information on important features of the traits (e.g. heredity) is still lacking. For kinship analysis, tooth traits seem to be more suited, as they are easily observable in living populations and as information on the heredity of many traits is already available. In many cases, teeth and jaws are also in a better state of preservation than other skeletal remains. Our aim was therefore to identify odontological traits that are heritable, which are rare and which can be recorded easily. We developed a list of 140 traits, most of them observable on several teeth (Alt, in press). Studies on animal populations, on skull series of individuals with known family relationships and twin data disclosed genetic factors in connection with the manifestation of these traits. Environmental effects on them are minimal as compared with metric traits.

The second step is the recording of the traits for the individuals of a burial site. All the dental traits are bilateraly expressed, though some traits on the jaws occur asymmetrically. Because of the state of preservation of the material, not all traits can be registered on all individuals. In most cases, traits are recorded by three possible alternatives: the trait may be present, it may be absent, or it may be indiscernible, i.e., the corresponding tooth or bone is missing or not in a state that allows one to discern whether the trait is present or absent (e.g. if the occlusal surface of a tooth shows attrition). There are some traits that are not recorded by exclusive alternatives only, for example the fissure patterns of premolars or the number of tooth cusps or roots. In these multivariant traits, the corresponding variant is recorded, in the cases of numerical variants the actual number of cusps or roots is counted. Over all, we record about 800 entries for each individual.

In a third step, it is necessary to build new, multivariate traits representing one genetic information. Most traits are recorded bilateraly, but if they occur on the same tooth both in the right and left side of the jaw, they are evaluated as only one item of genetic information. Additionally, if a bilateral trait is present on one side only, we can regard the genetic information as present. If a trait is absent on one side and the other side is indiscernible, this poses problems, because it could

1 An extended version of this paper written in german is available from the authors on request

have been present onthe other side. For some of the new traitsk, it is necessary to join more than two of the recorded traits, because phenotypical presence on several different teeth represents only one genetic information item. An example is the aplasia of teeth within the group of the wisdom teeth, the second premolars, the second incisors of the maxilla and the first incisors of the lower jaw (Schulze 1987). Hence the data matrix we want to analyse is built mainly by multivariate traits, for which each component is binary, but may additionally show missing values.

If we want to interpret the joint occurrence of traits in several individuals as a hint to familial relationships, the genetic independence of the traits is absolutely necessary. Unfortunately the complexity of the set of odontological traits results in the occurrence of genetically interdependent traits. The problems are caused by the recording of multiple traits on the same tooth which are not genetically independent of each other. Interdependency can be also of functional nature, if the presence of one trait depends on the presence of another. Such pairs or sets of interdependent traits need special treatment in the further analysis.

The fourth and main step is the analysis of the data matrix itself. Let us recall the basic idea: If a group of individuals of a burial site is encountered which exhibits a number of common traits, and each member of the group exhibits several of these traits, and these traits occur more frequently within the group than outside of it, then one may regard this as an indication for familial relationships within the respective group. It is our aim to find such groups.

The classical methods of cluster analysis are unable to solve this task, because they are based on dissimilarity coefficients for pairs of individuals, which cannot reflect similarity based on only a few traits. "Block Clustering" methods (Hartigan 1972) are considered inappropriate, because they assume a global block structure of the matrix. Our aim to detect only a local structural change of the matrix without posing a global structure, and the need to deal with missing values in an appropriate manner also prevents the use of other classical methods like correspondence analysis.

Hence we suggest using a search procedure, which is based on a simple measure defined for an arbitrary set T of traits. A first hint of familial relationships between the traits of T (i.e., the existence of a family for which these traits are typical) results from looking at the number of individuals with two or more of these traits. We define a statistic S, which is a weighted count of these individuals. The weights are the number of traits that are shown by each individual decreased by 1. If there is a family for which T is the set of familial typical traits, then we have several individuals with several of these traits, and the value of S is large. But if we want to compare different sets of traits, we need an appropriate standardisation, because for highly frequent traits the value of S becomes large even if there is no familial relationship between the traits. Therefore we define the measure $P(T)$, which is the probability of observing at least a value of S, assuming independence between the traits, and given the missing patterns of the individuals and the frequency of the traits within each missing pattern. It is important to condition on the missing pattern, because the indiscernability of traits is not independent. Without distinguishing the states "absent" and "indiscernible" the frequency of the joint presence of two traits on the same tooth tends to be larger than expected from the marginal frequencies of the traits, because absence of the tooth implies indiscernability for both traits. The computation of $P(T)$ is considered in the appendix.

Using $P(T)$ we can compare different sets of traits and we can look for sets with a minimal value of $P(T)$, i.e., those that give the strongest hint at a family. However, it is too time–consuming to compute our measure for all sets of traits. To determine the strongest hints we use the following search procedure: We compute our measure for all pairs of traits and select the l pairs with the smallest values. Then we add to each of these pairs each other trait. From all these triples of traits we select again the l ones with smallest values, and so on up to sets with 8 traits. In this way we find those sets of traits that may give the strongest hints of familial relationships. The search procedure is restricted to sets of traits that do not include two interdependent traits.

To evaluate the "significance" of a set of traits T found by our search procedure we compute a further global measure, $G(T)$. This is defined as the probability of finding via our search procedure at least one set of traits of the same size as T which shows a smaller value than $P(T)$, assuming independence between all traits. A high value of this global measure indicates that our hint at familial relationship can be explained purely by random variation in our data, whereas a small value indicates some significance for our hint. In the latter situation the set of individuals with at least two of these traits is regarded as a first suggestion for a family. The search strategy can be further improved by decreasing l with increasing size of T.

I: all individuals (n=208)
T: Set of traits

		freq. within *F*	freq. out of *F*	maximal number	relative freq. (%)
t_1:	lingual marginal ridge 41 31 42 32	3	0	120	2.5
t_2:	accessory ridge 15 25	7	1	44	18.2
t_3:	over developed cusps dist.-ling. 17 27	5	2	106	6.6
t_4:	number of cusps ≥ 5 47 37	6	2	125	6.4
t_5:	shovel-shaped incisors (strong mongolide form) 12 22	7	2	77	11.7
t_6:	accessory cusplets of the mesial marginal ridge 16 26	4	1	66	7.5
t_7:	abnormal size of roots *molars*	2	1	179	1.7

F: Individual with at least two traits of *T*

	t_1	t_2	t_3	t_4	t_5	t_6	t_7	Age anthr.	Sex anthr./arch.	Chronology
30	????	--	--	--	++	++	--	20-30	f/f	I.1-I.2
55	????	+-	--	--	++	--	--	7-14	m/?	I.2
72	-??	??	+?	++	??	??	--	50-60	f?/?	(I.3-II.3)
123	----	??	+?	?+	--	--	--	40-50	f/f	I.3
175	----	??	??	-?	++	--	++	30-40	f?/?	I.2
177	?---	?-	+-	--	++	--	--	30-40	f?/?	I.2
221	----	++	--	?-	--	++	--	15-20	?/f	(II.2)
242	----	++	--	++	--	--	--	15-20	?/m	II.1-II.3
97	--++	??	??	??	++	++	--	7-14	?/f	II.1
101	????	+?	++	??	??	??	++	20-30	f?/f	I.3
167	????	?+	++	++	??	--	--	20-30	f/?	(I.2-I.3)
198	++++	+?	--	+-	++	??	--	15-20	?/f	I.1-I.2
59	--++	+?	--	++	+?	++	--	7-14	?/?	I.2

$P_I(T) = 0.0000009163$ $G_I(T) \approx 0.02$

Table 31.1: Result from analysing all individuals

So far we have tried to reconstruct genetic kinship based on odontological traits only. The incorporation of additional information is important. Information on age, sex, chronology or spatial distribution of the burials can be used in two different ways. First it can be used for the validation of suspected families. A balanced demographic structure and a continuous occupation of the site are indispensable. Further indications can be drawn from the agreement of archaeological and anthropological findings and from the spatial distribution of a suggested family, if it shows hints towards family–oriented burials. Second, it can be used for a preselection of individuals before starting the search procedure, for example we can restrict our search to individuals of one chronological period. This is reasonable, if the likelihood of identifying a family in a given group is greater than in the consideration of all individuals. A preselection of a set *I* of individuals can be incorporated into our strategy by restricting the counting of the statistic *S* to the individuals of *I*. This is better than restricting the whole population, because differences in the frequency of traits within and out of *I* can also indicate familial relationships. The measures $P_I(T)$ and $G_I(T)$ are defined analogously as above. If $G_I(T)$ is small, then we also regard the individuals outside of *I* with at least two of the traits in *T* as potential members of the suggested family.

31.3 EXAMPLE

We used the described approach to analyse kinship structures in the burial site of *Eichstetten/ Kaiserstuhl (Gewann "Wannenberg")*. It is a Merovingian cemetery of the 6th–7th century in South Western Germany. The analysis was based on the skeletal remains of 212 individuals. From the recorded traits we could define 150 traits representing genetic information, which show a relative frequency smaller than 25%.

The first analysis included all individuals. We found a set of 7 traits with an approximate value of 0.02 for $G(T)$. The result is summarised in Table 31.1. In the above part for the seven traits the frequency within and out of the suggested family *F* is shown. We see that here the traits occur almost exclusively within the family. The table further allows judging the distribution of age, sex and chronology within the suggested family. The

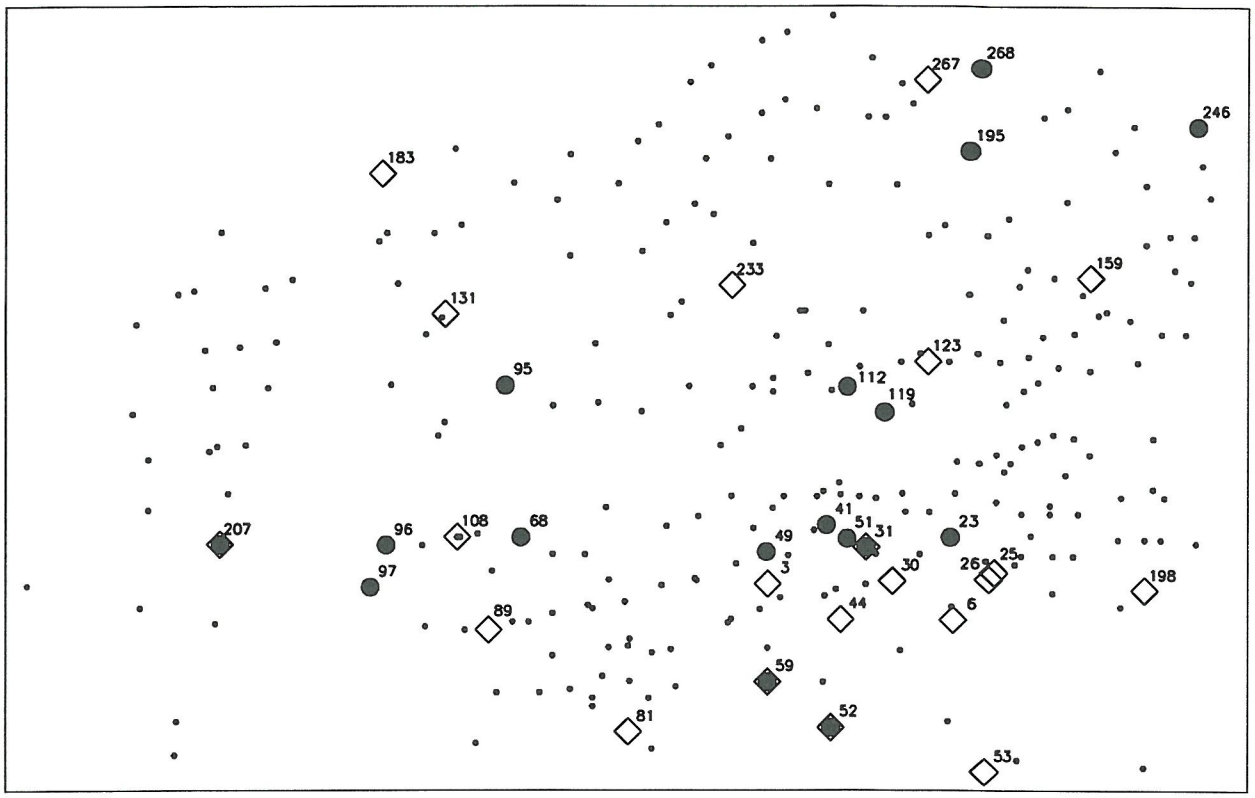

Figure 31.1: Spatial distributions of two of the suggested families in the burial ground. Dots: Family suggested by preselecting male individuals. Diamonds: Family suggested by preselecting female individuals.

imbalance of sex shown here is no momentous contradiction. It can for example be explained by a sex–related rule for changing the social unit at marriage.

In the same manner we analysed further sets of individuals. Three sets of individuals were defined by chronological phases, two by sex and seven by archaeological findings. Three further attempts made use of a preselected set of traits, which occur more frequently in this population than in comparable ones (cf. Alt & Vach, in press). The choice of the individuals of the chronological phase I.1 was, for example, motivated by the question as to whether there are familial relationships among those individuals that probably founded this settlement. We found 6 statistically significant hints of families, which allowed four different suggestions for families. Evaluating the distribution of age, sex and chronology within these groups, no striking contradictions were found. Two of these four groups showed some structure in the spatial distribution of the individuals (Figure 31.1). The family suggested by preselecting all male individuals shows a group of closely buried individuals (31,41,51) and the individuals 23 and 49 are not far away, and additionally we find the pairs 96/97, 112/119 and 195/268. The family suggested by preselecting all female individuals shows a cluster of seven individuals (3,6,25,26,30,31,44) where graves 25 and 26 are overlapping. However it is difficult to judge the significance of these single findings. Tests on spatial clustering may provide objective tools (cf. Alt & Vach, 1991), but it is necessary to adapt them for the occurrence of missing values, because otherwise they may be sensitive to clusters in the spatial distribution of the state of preservation.

A comparison with archaeological findings showed no striking agreement. Here the restrictions due to the state of preservation of the skeletal remains are most distressing. Even an archaeologically rich grave is unable to show any relation to our results, if there are no or only few skeletal remains in it.

The results of our example can be summarised as follows: We found some interesting hints as to families based on odontological traits. A rate of 6 successes within 16 attempts is higher than we can explain by random variation. The validation of the findings by external information showed no contradictions, but on the other hand we found only few hints that support the suggested families.

31.4 DISCUSSION

The reconstruction of social relationships is an important task in prehistoric research. Genetic kinship is one key to discover such relationships, but we must be aware that "families" in prehistoric populations were also formed by other mechanisms. Yet, genetic kinship is one of the mechanisms for which we have a real chance of reconstruction based on information available today. Heritable traits can serve as a basis, but imply the limitation to restrict the analysis to individuals with a good state of preservation of the skeletal remains. This limitation resembles the restriction to graves with archaeological findings, if the latter are used to demonstrate relationships between graves. Furthermore, we have to emphasise, that the suggested families can — under the best circumstances — only be regarded as the core of a group of genetically related individuals. The boundaries of a family defined by genetic relationships is fuzzy by definition.

The presented approach focused on one type of information about familial relationships conveyed by discrete traits: the joint occurrence of traits within a group of individuals. Additional hints from these traits can be given by an increased frequency relative to comparable populations (Alt & Vach 1991), or by the occurrence of rare traits, especially if it is accompanied by a cluster in the spatial distribution. Statistical methods are helpful to detect and evaluate the significance of hints using certain types of information, but joining the results of analyses based on different sources in archaeology and anthropology remains the tasks of interdisciplinary work. A first approach to integrate external information has been presented here, but the development of further concepts is necessary.

31.5 APPENDIX: DETAILS OF STATISTICAL COMPUTING

Let T be a set of traits and I a set of individuals, which is a subset of a given population. For each trait $t \in T$ we denote by M_t the set of all missing patterns of t, i.e. M_t is of the size $2^{|t|}$, where $|t|$ denotes the number of components of t. For $m \in M_t$ we denote by N_m^t the number of individuals in the population with missing pattern m in trait t, and n_m^t denote the size of the subset of these individuals where the trait is expressed, i.e., for which t shows the state "presence" in at least one component. M denotes the set of all joint missing patterns of the traits T, and for $m \in M$ we denote by N_m the number of all individuals with joint missing pattern m for the traits T and by I_m the number of individuals in I with missing pattern m. For each individual i we denote by U_i the number of traits in T, which are expressed at individual i. Then the statistic S is defined by

$$S := \sum_{i \in I, U_i > 1} (U_i - 1)$$

and observing a value s for the statistic S, the measure $P_I(T)$ is defined as

$$P_I(T) := P\left(S \geq s \middle| (N_m)_{m \in M}, (n_m^t)_{t \in T, m \in M_t}, (I_m)_{m \in M} \right)$$

assuming independence between the traits. By combinatorial arguments the following explicit formula is available:

$$\frac{\sum_{(r_m^U, s_m^U)_{m \in M, U \in \rho(T)} \in V_s} \prod_{m \in M} \binom{I_m}{r_m^\varnothing, \ldots, r_m^T} \binom{N_m - I_m}{s_m^\varnothing, \ldots, s_m^T}}{\prod_{t \in T} \prod_{m \in M} \binom{N_m^t}{n_n^t}}$$

where V_s is defined by the restrictions

$$\sum_{m \in M} \sum_{U \in \rho(T) \setminus \varnothing} r_m^U (|U| - 1) \geq s,$$

$$\sum_{U \in \rho(T)} r_m^U = I_m, \quad \sum_{U \in \rho(T)} s_m^U = N_m - I_m, \text{ for all } m \in M, \text{ and}$$

$$\sum_{\substack{m' \in M \\ m'|_t = m}} \sum_{U \ni t} r_{m'}^U + s_{m'}^U = n_m^t \text{ for all } t \in T \text{ and for all } m \in M_t$$

where $\rho(T)$ denotes the set of all subsets of T. If I is the set of all individuals, then the formula simplifies, because $N_m = I_m$ for all m. If furthermore T includes only two traits t_1 and t_2, if both traits have only one component and if no missing values occur, then S follows a hyper geometric law and $P_I(T)$ is the p–value of a one–sided version of the Fisher's exact test in the fourfold table defined by the traits t_1 and t_2.

The use of the above formula is limited by the fact, that V_s becomes very large, if T includes more than two traits. To keep the computations feasible, we use an approximation, where sampling without replacement is substituted by sampling with replacement. Then the contributions

$$S_i := \begin{cases} 0 & \text{if } U_i \le 1 \\ U_i - 1 & \text{if } U_i > 1 \end{cases}$$

of the single individuals to the statistic S are independent, hence the distribution of S is the convolution of the distributions of $(S_i)_{i \in I}$. U_i is the sum of independent random variables

$$U_i^t := \begin{cases} 1 & \text{if trait } t \text{ is expressed at individual } i \\ 0 & \text{otherwise} \end{cases}$$

and $P(U_i^t = 1) = n^t_{m(i,t)} / N^t_{m(i,t)}$, where $m(i,t)$ is the missing pattern of trait t at individual i. Hence the distributions of the single S_i can be easily computed. Since it suffices to know the distribution of S within the range between 0 and s–1 the computation of the convolution of the S_i remains feasible.

If a trait t possesses several components, most missing patterns may occur only once, and the above measures become meaningless. Then it is necessary to build classes of equivalent missing patterns, e.g. to distinguish missing patterns only by the number of missing components. In the above formulas M is then the set of all classes of equivalent missing patterns. The pattern with all components missing should always build one class.

The computation of the global measure $G_I(T)$ is done by simulation. In each repetition for each trait the occurrence is randomly permuted within individuals with the same or equivalent missing pattern. Regarding interdependent traits as independent traits here can be justified by the fact that this probably implies only an overestimation of $G_I(T)$.

In spite of using the approximation for the computation of $P_I(T)$, the search procedure is computationally rather expensive. In the presented example we use a value of 75 for l, but we start with the 225 most suspicious pairs of traits. Analysing all individuals in one run of the search procedure considering sets of traits with a size between 2 and 8 needs about 8 hours on a SUN 4/75 (SPARC station 2). Hence we were only able to carry out 100 repetitions for the computation of $G_I(T)$.

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