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UTILIZATION OF MATHEMATICAL METHODS IN THE STUDY OF THE HUMAN EVOLUTION: THE PROBLEM OF THE MORPHOFUNCTIONAL RESEARCH IN PALEOANTHROPOLOGY

ABSTRACT. — *The endeavour to make morphological information objective resulted in introduction of mathematical and statistical methods in morphology. These methods are especially important when fossil material and the evolutionary process is investigated. The description of the biological shape is of utmost importance in the analysis of the fossil material. Parameters, characterizing the form have to be not only optimal, but also adequate to the problem in question. In biomechanical analyses mathematical modelling is of great importance, even if its methods have to be further developed, so that they would be consistent with given types of biological problems or would not simplify the problems too much. To evaluate results statistical methods are especially important, particularly when data are processed. It is necessary to consider thoroughly the suitability of the application of univariate or multivariate methods, both with the respect to the given problem and the potential results. Multivariate methods offer, in spite of their intricacy, results of complex character, which can be very useful especially in evolutionary studies. In the study the analysis of the proximal epiphysis of the femur of primates is used as a concrete example for the utilization of the multivariate methods. Transformations of the input data used show the possibilities of corrections when samples are deficient in various ways. Results of the treatment of groups with different systematical structure stress the necessity of a preliminary biological and evolutionary analysis of the sample before the proper application of the multivariate methods. Neglect of these principles could result in distorted or even erroneous results.*

The only direct evidence about our biological predecessors are fossil remains of their skeletons, or, in some cases traces of their behavior. By this methodology of palaeoanthropology and methods by which its research proceeds are given. The main object of the paleoanthropological research is thus the biological shape and its aim is to obtain the maximum information about the fossil shape and its function as well as to interpret the data obtained under conditions given by the degree of the knowledge concerning the corresponding period.

The oldest and still widely used methods enabling us to analyse the fossil material are the methods of the descriptive morphology. One of the greatest drawbacks of the classical descriptive morphology has been the small communicability as well as a subjectivity of the results obtained (a more detailed discussion of the problems of the descriptive morphology can be found elsewhere — see Vančata and Lukovcová, 1980, Vančata 1980a). For this reason attempts to reach a clean-cut quantification and thus an objectification of the results appeared already at the beginning of the present century (Pearson, Martin, Thompson, Fischer and many others).

Connection of quantitative biological methods with mathematical and physical methods resulted in a whole series of new branches of science (biocybernetics, biomechanics, morphometry and others). Thus also a branch of enormous importance for the contemporary paleoanthropology originated — morphometry, which became a basis of further branches important for paleoanthropology, e.g., of biomechanics. In view of the fact that biological processes and thus also biological features possess a stochastic

character it is essential that corresponding mathematical disciplines, especially mathematical statistics, are used when considering these problems. In this way, with the assistance of statistical and other methods, morphometry becomes a new and separate branch of biology (sometimes denoted as biometrics or morphometrics) and, at the same time, also one of a very important auxiliary biological as well as paleontological disciplines.

It is not the aim of the present contribution to discuss the mathematical aspects of biomathematical methods, but rather the possibilities and strategy of their application. The character of the fossil material (which is fragmentary and not numerous) requires application of specific methods (low frequency resulting sometimes also from a lack of recent comparative material), both in the statistical evaluation and in the description of (the main requirement being precision and fitness of the description) as well as in the study of its function. Together with the development and more elevated utilization of modern mathematical methods discussions between classical morphologists (including anatomists) and groups using morphometric and other mathematical methods have become more frequent; similar discussions take place also among groups utilizing quantitative methods (Howells 1969, Howell et al. 1978, Oxnard 1973, 1975, 1979a, b, Corruccini 1978, Lewis 1977, Lovejoy 1979, Wood 1978, Day 1979, Joufroy and Lessertiseur 1979, Bookstein 1977, 1978, Preuschoft 1979, etc.).

However, the contradictions do not arise from errors or inaccuracies of individual investigators, or from theoretical inadequacies of methods, even though these facts do also affect the results of studies, but first of all from the method of obtaining the data itself, i.e. from the primary description of the biological shape.

In studies of the classically morphological character the information is obtained by human senses (first of all, by sight). Information thus obtained is exact and owing to the analytical ability of the brain the complex character of the data is preserved, however, data of this type cannot be objectively quantified and hence not objectively compared either. On the other hand the classical methods of morphometry made the shape comparable, however, using individual dimensions without stressing their relation to the shape and preferring the good measurability the shape was in the most cases very considerably, sometimes even inadmissibly, simplified. The inadequacy of the "descriptivity" of these dimensions was then compensated by the use of indexes and their comparison. Index thus became something as an expression of the shape of the region in question. The use of indexes, still very abundant, can on the one hand give a vivid information about a relation of two variables, but on the other hand it has only little in common with the character of the original shape. By calculating an index the individuality of the dimensions extracted from the original shape is lost; index is thus unusable for further analyses in this sense that it is no more able to give informations concerning the original shape. For the above

reasons the results of classical morphometrical methods were often irrelevant, sometimes even absurd, and were therefore justly criticized.

The modern morphometrics starts from the principle that the shape possess a complex character and hence it has to be described in this sense as perfectly as possible (Bookstein 1977, 1978). At present three groups of approaches to the quantitative description of the shape can be used. In the first group maximum number of dimensions characterizing the shape is primarily used, to be usually reduced in further analyses. The second way is to use a small number of morphologically, functionally and from the point of view of the shape most significant data, the third group uses a series of transformed variables, characterizing the shape as a whole (skeletons, biorthogonal grids, Cartesian grids, Fourier analysis, etc.). The first group represents a kind of compromising solution between the second and the third method (see also Corruccini 1978). Its advantage rests in the fact that it does not require an a priori exclusion of some variables before the measuring and primary processing of the data themselves. The disadvantage is sometimes difficult reduction of the number of data and also the fact that the shape is always to some degree simplified. The second group starts from the assumption of a generalized biological model of the structure studied, where dimensions represent basic parameters of its structure. Its relative simplicity of description as well as of analysis is advantageous (mostly it is not necessary to reduce the number of variables); relatively high probability of erroneously or incorrectly chose variables as well as considerable simplification of the shape studied are disadvantageous. The most problematic, of course, is the basis of this approach as such, attributing a functional significance to the parameters chosen, which is mostly questionable and often even incorrect (cf. Vančata 1980a). The third group offers the greatest possibilities as far as the precision of the description of form is concerned. The disadvantage rests in the unsatisfactory technical and to a certain degree also theoretical state of these methods, in the first place when the form is described in space (Bookstein 1978, Corruccini 1978). Very often these complex methods do not bring adequate results (Corruccini 1978), but it cannot be doubted that at least some of them will find extensive possibilities in morphology, especially for the potentiality of the complex description of the shape.

The drawback of all the three methods is that they are unable to describe adequately most features of the type of groove, tuberosity, pit (little hollow), etc. These traits can have, especially in comparative studies, a great importance and in view of the necessary objectivity of the study they must not be neglected. From this it clearly follows that even the most modern morphometrical analyses cannot manage without the classical morphological approach, which inevitably makes the information obtained more precise.

Data resulting from description of fossil material (of form or model) have a multidimensional

character and they are mostly obtained from samples which are not numerous or even from single individuals. In view of these facts it is on one hand necessary to respect strictly the complexity and hence the unique character of individual finds, on the other to take into account the fact that fossil data can never have the complete character as it is the case of the work with recent material. This specific characteristics should be respected not only when processing the data, but first of all when interpreting them.

In the studies of the evolution of man the mathematical methods can be applied on two levels. The first of them, less widely spread, is the mathematical modelling of phylogenically or ontogenically important processes and phenomena, the other one is the statistical processing of data.

MATHEMATICAL MODELLING

Mathematical modelling is more widely used especially in studies of biochemical character and also in studies of ontogenic growth or in reconstructions of the morphological evolution in phylogenic lines.

Mathematical models are used in biomechanical analyses to solve three basic problems, which, however, overlap in practice considerably.

1. Modelling of biomechanical processes and phenomena.

Typical example is formation of the mathematical model of locomotion of primates (Yamazaki et al. 1979), which is used to study analogies in the locomotion of primates and to reconstruct the origin of human bipedality. Another example is formation of the model of changes of the action of tension and compressive forces at the origin of bipedality from the quadrupedal locomotion (Preuschoft 1978). The models produced can be used for further theoretical, but above all for "practical" purposes.

2. Reconstruction of biomechanical relationships in various parts of the skeleton of recent primates and their exploitation for interpretation of fossil material.

Classical studies of this type are studies concerning the problems of biomechanics and evolution of the skull and of the masticatory apparatus (e.g. du Brul 1977, Smith 1978, Pesce Delfino 1978, Pesce Delfino et al. 1980), aiming at the explanation of the existence of the sagittal crest of the australopithecines and the reasons of its disappearance and of gracilization of mandibles.

Another sphere of the use of mathematical methods in problems of anthropogenesis is represented by the reconstruction of pressure and tensile forces in bones and joints of the locomotion apparatus of recent primates (e.g., Preuschoft 1970, 1973a, Kummer 1962, Lovejoy and Burstein 1977, Lovejoy et al. 1977) and the study of biomechanical characteristics of parts of skeletons of fossil primates (e.g., Preuschoft 1971a, b, 1973b, 1975, Preuschoft and Wienmann 1973, Zihlman and Hunter 1972, Zihl-

man 1978, Lovejoy 1975, 1976, 1979, Lovejoy et al. 1973).

Studies of this type are very useful for the reason that they form a suitable basis for evaluation of the function of the locomotion apparatus and its characteristic features and also for interpretation of fossil finds. The use of the mathematical apparatus, even in a simple form, makes an objective description of the problem possible. On the other hand, an uncritical use of mathematical methods can result and often also results to an inadmissible simplification of biological problems, so that these studies resemble more or less a simple exercise from mechanics, rather than a solution of a problem of a biological character.

3. Processing of concrete biomechanical data and their generalization.

To test hypotheses and to produce new ones new data have to be obtained, which can either support or disprove the hypothesis in question. For this reason methods were developed to evaluate these data and to make thus possible their interpretation in the sense of corresponding hypotheses. These methods find a wide application e.g. in studies of the locomotion apparatus (e.g., Plagenhoef 1968, 1979, Preuschof et al. 1979).

The use of mathematical methods in biomechanical studies is without any doubt helpful, since it makes it possible to obtain new views and makes a series of aspects in the evolution of hominids more exact. However, the interpretation, and many analyses as such, is in many cases rather questionable from the point of view of the biological reality. The basic problem rests in the fact that modelling starts with a consistent functionality of biological structures. Thus, e.g., classical biomechanical studies consider the biological shape as a functional one (however, they often forget that the function and characteristics of a dead or even "model" tissue are not identical with properties of a living tissue and still less with characteristics of a living system as a whole). This assumption is not valid in general, since the fact that the shape fulfils some function does not necessarily mean that the shape is functional sensu stricto. Many examples are known in which the shape has to fulfil a function for which it is not well adapted (extremities of some aquatic and semiaquatic mammals, pelvic floor of man) and, on the contrary, cases are known when a suitable shape remains practically unused for a given function (e.g., wings of some birds which do not fly). This, of course, does not mean that biological shape or biological structure in general correspond to some functions better, to others worse and for some functions it is unsuitable at all. Functionality of the shape depends both on operational characteristics of the environment and on the proportionality of the evolution of individual shapes (biological structures), e.g. changes of functionality caused by the allometric growth of the individual structures. From this also follows that methods suitable for analysis of recent organisms and their properties cannot be directly applied in studies of the fossil material. Variable more general

models have to be formed, which can be adapted to the presumed state of the phylogenetically given studied form. Some recent attempts to produce such models (Yamazaki et al. 1979, Preuschoft 1979) gave very interesting and useful results and have shown promissing prospects of this approach.

Studies aiming at modelling of the ontogenetic and phylogenetic processes solve given problems with the assistance of methods of shape transformations, based on Cartesian (Thompson 1961) or biorthogonal transformations (Bookstein 1977, 1978). The most suitable for the description of growth processes appears to be the method of transformations of biorthogonal grids, developed by Bookstein (1977), which consistently starts from the characteristics proper to the given shape is relatively simple but at the same time sufficiently exact and robust and hence also capable to bring about a correct and objective concerning the shape studied. However, the method is still in an initial stage of its development, for the time being it works with planar models and it is not yet quite clear how the spatial modelling will be carried out in practice. It may be that solution of this problem will be made possible by combination of the method of transformations of biorthogonal grids with another method, capable of a description of shape in space (cf. e.g. Oxnard 1973, Jacobshagen 1980 a, b). Be this as it may, as soon as this method will be capable of practical application it can find a wide use in solving problems of the human evolution.

When studying morphological changes in the evolution of higher primates (hominoids) Cartesian transformations were predominantly used (e.g. Kummer 1952, Sneath 1967, Appleby and Jones 1976). The aim of these studies has been rather to illustrate the application of the shape transformations and not to carry out a real analysis of the morphological evolution of hominids. Thus we can say that from an objective viewpoint the shape transformations have not yet found a wide application in evolutionary studies.

The results of modelling biological "problems" and of application of these methods to the fossil material are the data of stochastic character. To process such data statistical methods may be used.

STATISTICAL METHODS

Since fossil data possess a specific character from the statistical point of view (low frequency, samples are not homogeneous, etc.) there are three possible approaches to process fossil data. *Firstly*, not to use statistical processing of the data at all, since statistical methods are either unsuitable or cannot give significant results. *Secondly* the data can be processed using methods modified for the solution of the given problem. *Thirdly* the data can be processed by statistical methods without fundamental adaptations (even if some modifications can be useful). At this point either the input data are transformed or output data are modified according to specific characteristic or the method in question.

The first possibility is, of course, no solution at all, the second method is applicable only in simple univariate or bivariate methods and only the third method is a real and universal one, especially in more complex univariate and multivariate methods.

It has to be noted that the modification of the output data can be on the one hand very elegant, efficient and precise, however, that on the other the risk of a possible desinterpretation of the data is in most cases too high (cf. Oxnard 1973, 1975, 1979 a, b). The most practical for the time being appears to be the transformation of the input data (Vančata and Lukavcová 1980).

Since most modern statistical methods start from the postulate of normal or at least quasinormal distribution of the data in the studied sample (cf. Blackith and Reyment 1971, Oxnard 1973, Maxwell 1977, etc.), it is necessary to carry out transformations which, apart of special requirements, also "normalize" the distribution of parameters in the sample. Such transformations can be e.g., logarithmic transformations and various standartizations and corrections (e.g., concerning the size or allometry) of the input data. In no case be this type of transformations carried out by indexes, which, it is true, remove the effect of size when two shapes are compared (and even remove it absolutely), but which have no "normalizing" effect.

For the processing of the data itself either methods working with individual variables (i.e. univariate and bivariate methods), or methods working with the complex of data (i.e. multivariate methods) can be used.

Univariate methods give a valuable primary information and characteristics of the sample. This information may be of a considerable assistance to obtain orientation in the problems and also decision about the further proceedings (e.g., the use of standardizations and ratio-diagram, correlation and regression).

The usefulness and vividness of the use of the ratio-diagram can be demonstrated on the analysis of the proximal femur of hominoids, characterized by fourteen variables. When a series of standardized variables is compared a single morphological trend in Plio-Pleistocene hominids is clearly apparent, opposite in many aspects to the trend of the oldest sapient forms and obviously to a certain degree also to the trend in Homo erectus *(Fig. 1)*. Perceptible is also the morphological similarity of sapient forms, however, a greater robustness of Neanderthal man is obvious *(Fig. 2)*. It is especially Pan and Pongo, in which similar metric characteristics can be observed, that differ from the recent man in the framework of hominoids. Conclusions derived on the basis of this very simple procedure were later confirmed by further more detailed analyses also on a more general level (Vančata 1980 a, b).

MULTIVARIATE METHODS

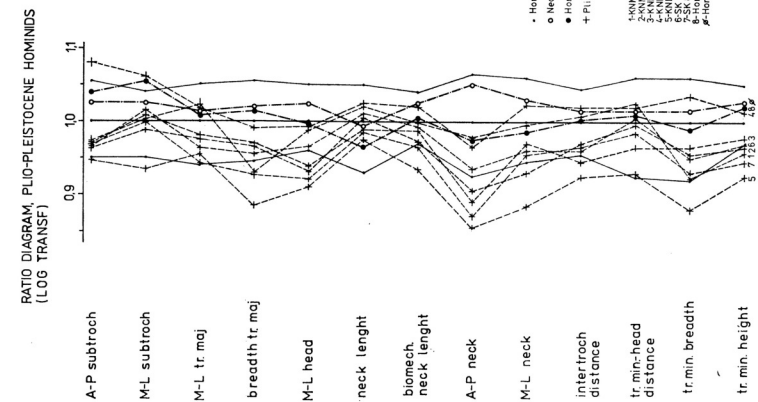When the shape is studied as a whole the application of univariate methods is necessarily limited,

RATIO DIAGRAMM, PLEISTOCENE HOMINIDS
(LOG TRANSF)

FIGURE 2. *Ratio diagramm for genus Homo group (data are logarithmically transformed).*
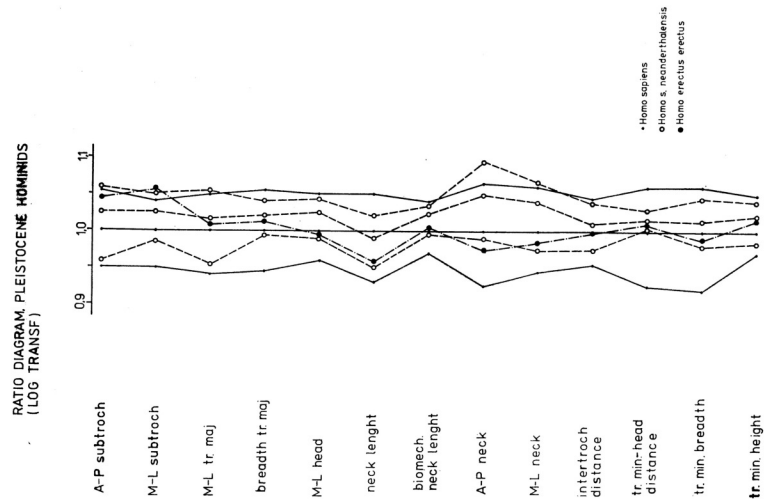

RATIO DIAGRAMM, PLIO-PLEISTOCENE HOMINIDS
(LOG TRANSF)

FIGURE 1. *Ratio diagramm for hominid group (data are logarithmically transformed).*

since they start from individual variables. Multivariate methods are more complicated, however, they take into account all variables, Let us therefore turn our attention directly to these methods.

Multivariate methods represent according to their approach to the processing of data three groups (more exact and complete information can be found elsewhere — Vančata 1980a, Vančata and Lukavcová 1980). 1. Methods studying relations between individual groups (discriminant analyses, D^2, T^2 generalized distances analyses and analyses of canonical variates), 2. methods studying all individuals as parts of a single sample, aiming at generation of new uncorrelated variables and, if need be, also of other characteristise of the sample (principal components analysis, principal coordinates analysis, factor analysis and, with certain reservations, the analysis of variation MANOVA, and a multiple regression analysis) and 3. clustering methods, which on the basis of mathematical similarity cluster individuals into groups (hierarchic and non-hierarchic types of cluster analyses).

It is understandable that the picture given above is very simplified, however, it shows sufficiently clearly on which main principles are these methods based. With all analyses of the discrimination type it is necessary to have the criteria for each group studied determined already before the proper analysis. In some types of the discriminant analyses, however, it is not necessary to eliminate the disturbing influence of some variables (BMDP7M stepwise discriminant analysis — Dixon 1975, Van Vark 1976). Second group of analyses does not require an à priori knowledge of the characteristics of the sample with the exception of the basic data, however, it requires either homogeneity of the sample (when R-modus starting from correlations between variables is used classically) or the knowledge of the specific composition of the sample and eventual elimination of the disturbing influence of some variables. If the sample is too non-homogenous it is better to use the Q-modus, i.e. to start from correlations among individuals rather than among variables. Cluster methods require neither knowledge of the characteristics of the sample, nor a special adjustment of the data. They work on the basis of comparison of coefficients of similarity of the individuals, hence they create groups (clusters) on the basis of the input data. Even if the method itself is independent of the inserted data, its results are very sensitive to the influence of the character of these data. For this reason the cluster analysis can serve to the forming of groups, but biologically real groups can be obtained only when biologically significant data are used.

Until now very many studies were dedicated to analyses and critical reviews of the general mathematical and statistical correctness of certain statistical methods (e.g. Kowalski 1972, Corruccini 1975, 1978, Oxnard 1973, 1975, Van Vark 1976). It has to be said that only very few studies considered the biological basis of the composition of samples and to a considerable degree the same applies to the biological character of the variables. However, mathematics is only an auxiliary method, which should assist the solution of biological problems. Thus the starting point for solution of the problem is determination of biological parameters of the sample and of requirements on the mathematical apparatus in view of solving a concrete biological problem, after which a choice of concrete mathematical methods should follow. For this reason let us terminate the present study by a practical example.

Using multivariate analyses from programs BMDP (Dixon 1975) two samples were studied: Hominidae (man, Neanderthal man, Plio-Pleistocene hominids; 88 femurs) and Hominoidea (Hominidae, gorilla, chimpanzee and orang-utan; 117 femurs). Three types of analysis were used: cluster analysis BMDP2M, factor analysis BMDP4M and stepwise discriminant analysis BMDP7M. Apart of the "raw" data also four types of transformation of the input data were used: logarithmical transformation ($x = \log x$), standardization ($x = x/\overline{x}$), logarithmic transformation after standardization ($x = \log x/\overline{x}$) and logarithmic standardization ($x = \log x/\log \overline{x}$), which had at the same time increased the "normality" of the distribution of the data in the sample.

CLUSTER ANALYSIS

Results of the cluster analysis in the sample Hominidae confirm the close morphological affinity of the individual groups of hominids (and to a considerable degree also of hominoids). Plio-Pleistocene hominids display characteristics, suggesting their mutual affinity; the femur ER 1481 approaches that of the recent man most closely. Results of the cluster analyses show that the results can change markedly already when the input data change little, e.g. when logarithmic transformation and standardization are used.

FACTOR ANALYSIS

Factor analysis results in three factors explaining in average 76 % of the total variation (I. 39 %, II. 21 %, III. 16 %). The first factor has character of size, the second and third are connected with dimensions of the diaphysis, of the greater trochanter, and with dimensions of the neck (sequence and composition of individual factors is different analyses). The group of the Plio-Pleistocene hominids is, with the exception of KNM ER 1481 different from the representants of Homo sapiens (Figs. 3—5) and also from apes (Figs. 6—9). From apes gorilla is the closest to man; their mutual relations are difficult to define unambiguously.

If we compare the results of factor analyses between the groups of hominids (Figs. 3—5) and of hominoids (Figs. 6—9), then the results of factor scores (i.e. relations between individuals) are basically similar, however, the factor loading patterns are different. In the second and third factor the percentual variances, explained by these factors, differs considerably in the group of hominids.
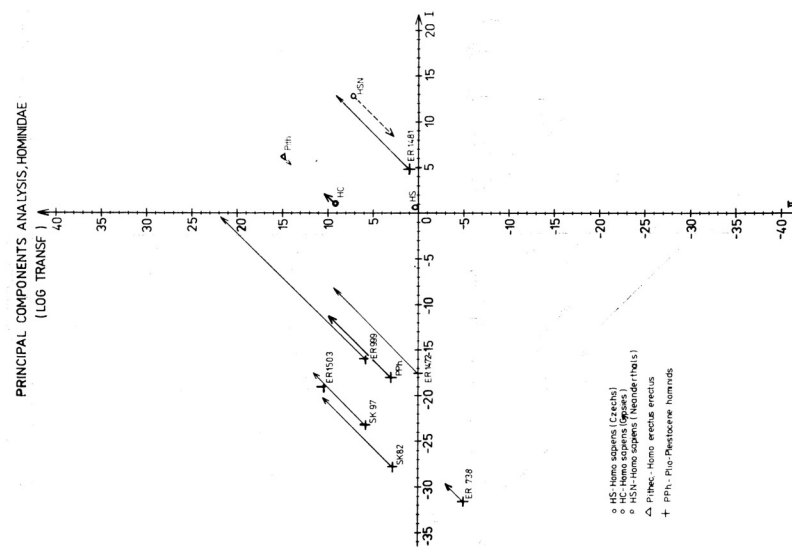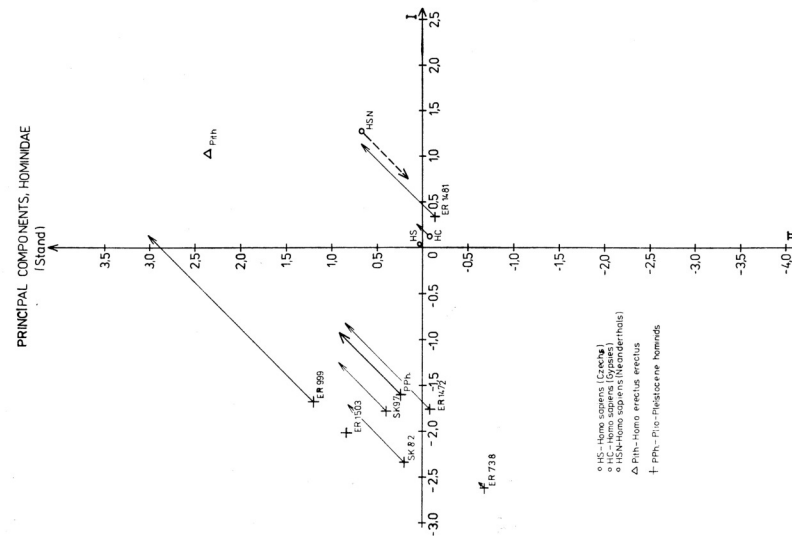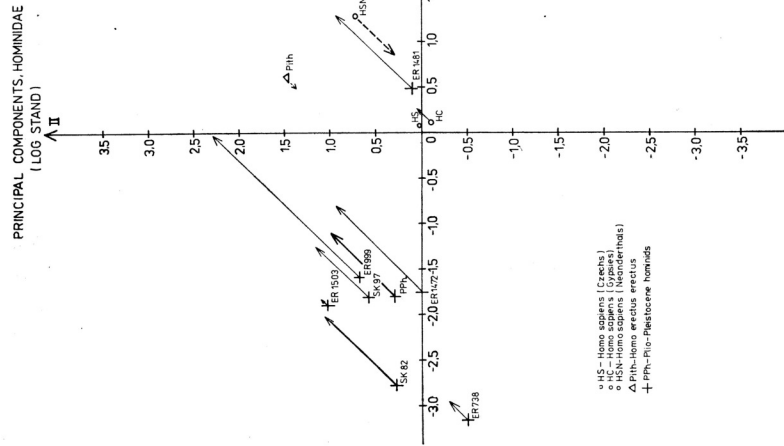
FIGURE 4. *Principal components analysis for hominid group (input data are standartized).*
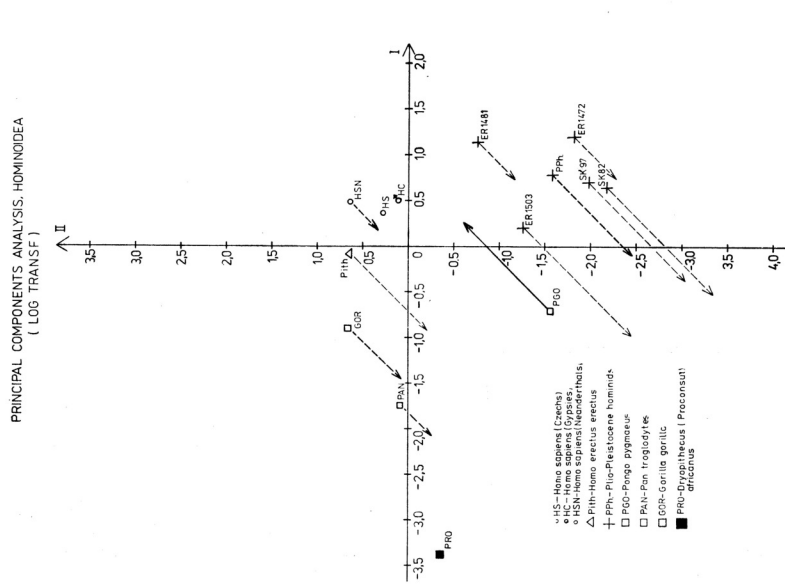

FIGURE 3. *Principal components analysis for hominid group (input data are logarithmically transformed).*

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PRINCIPAL COMPONENTS ANALYSIS, HOMINOIDEA

o HS—Homo sapiens (Czechs)
o HC—Homo sapiens (Gypsies)
o HSN—Homo sapiens (Neanderthals)
△ Pith—Homo erectus erectus
+ PPh—Plio-Pleistocene hominids
□ PGO—Pongo pygmaeus
□ PAN—Pan troglodytes
□ GOR—Gorilla gorilla
■ PRO—Dryopithecus (Proconsul) africanus

FIGURE 6. *Principal components analysis for hominoid group.*

PRINCIPAL COMPONENTS ANALYSIS, HOMINOIDEA (STAND)

o HS—Homo sapiens (Czechs)
o HC—Homo sapiens (Gypsies)
o HSN—Homo sapiens (Neanderthals)
△ Pith—Homo erectus erectus
+ PPh—Plio-Pleistocene hominids
□ PGO—Pongo pygmaeus
□ PAN—Pan troglodytes
□ GOR—Gorilla gorilla
■ PRO—Dryopithecus (Proconsul) africanus

FIGURE 8. *Principal components analysis for hominoid group (input data are standartized).*

PRINCIPAL COMPONENTS, HOMINIDAE (LOG STAND)

o HS—Homo sapiens (Czechs)
o HC—Homo sapiens (Gypsies)
o HSN—Homo sapiens (Neanderthals)
△ Pith—Homo erectus erectus
+ PPh—Plio-Pleistocene hominids

FIGURE 5. *Principal components analysis for hominid group (input data are logarithmically standartized).*

PRINCIPAL COMPONENTS ANALYSIS, HOMINOIDEA (LOG TRANSF)

o HS—Homo sapiens (Czechs)
o HC—Homo sapiens (Gypsies)
o HSN—Homo sapiensi (Neanderthals)
△ Pith—Homo erectus erectus
+ PPh—Plio-Pleistocene hominids
□ PGO—Pongo pygmaeus
□ PAN—Pan troglodytes
□ GOR—Gorilla gorilla
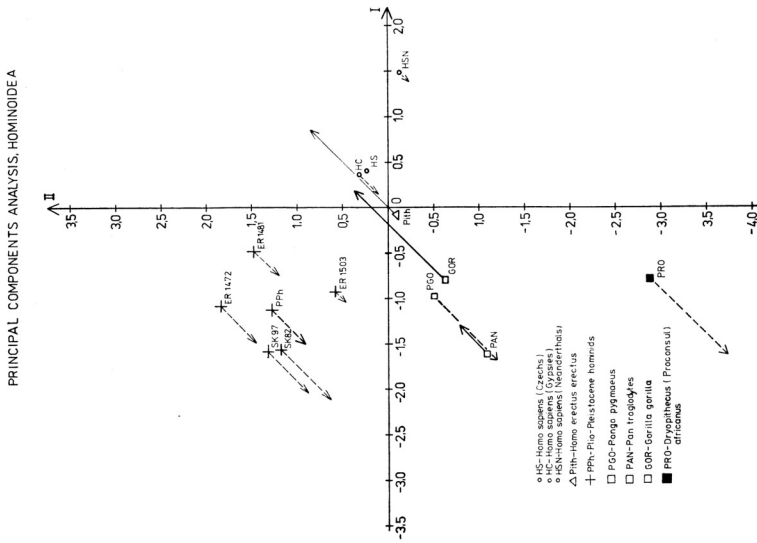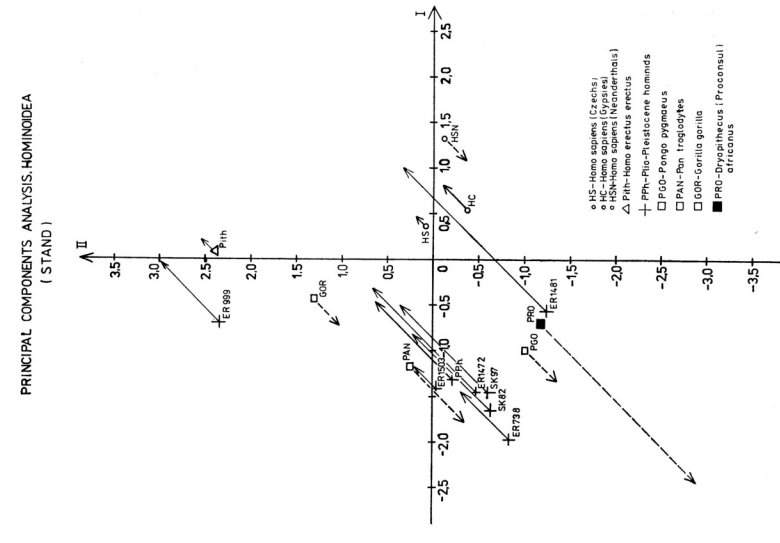■ PRO—Dryopithecus (Proconsul) africanus

FIGURE 7. *Principal components analysis for hominoid group (input data are logarithmically transformed).*
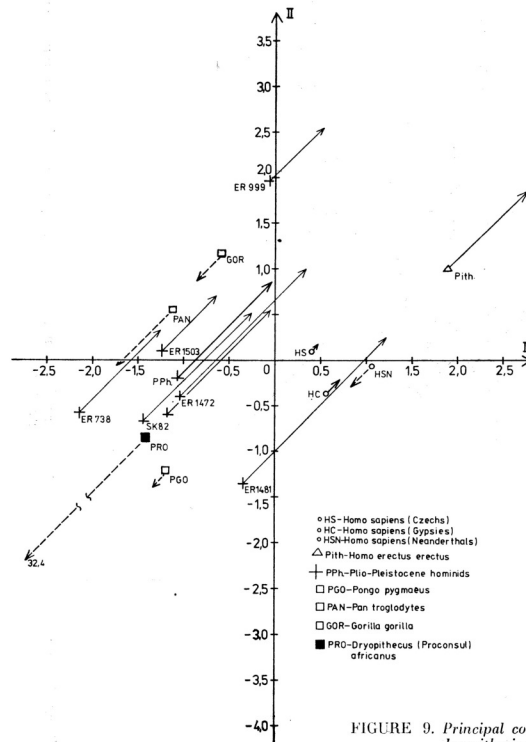
FIGURE 9. *Principal components analysis for hominoid group (input data are logarithmically standartized).*

DISCRIMINATION ANALYSIS

There are many analogies between the results of the discriminant analyses and those of factor analyses. The group of apes differs from that of hominids, gorilla being most closely related to man and certain relations between chimpanzee and orangutan can be found as well *(Figs. 12—14)*. The group of Plio-Pleistocene hominids is homogeneous, only ER 1481 is classified with the probability 0.35 into the group of Homo sapiens *(Figs. 10—11)*. Neanderthal man differs from the contemporary man and also, very markedly, from Plio-Pleistocene hominids (by which the preliminary results of standartization *[Figs. 1—2]* are confirmed). In the individual discriminant functions occur most often: the width of the neck, head diameter, the biomechanical neck length and the distance from the lesser trochanter to the head. The average correctness of the classification into groups is 92.6 %.

Results of all analyses of canonical variates are analogous *(Figs. 10—14)*, however, appreciable differences can be found between the discriminant functions for hominids and hominoids.

If we compare the results of the cluster, factor and discriminant analyses in hominids and hominoids, for which there are two reasons. The first are easily and well interpretable from the biological point of view, since they express directly the morphological differences. Considerably more complicated is the interpretation of the analyses of hominoids, then the results of the analyses of hominoids reason is the considerable heterogeneity of characteristic patterns (i.e., morphological heterogeneity) for individual analyses (i.e., of factor loading patterns and discriminant functions), the second reason is the lower consistency of the sample, both morphological and phylogenetical. E.g., presence of some parallelly originating features (e.g., features resulting from the great body weight during the evolution of the skeletons of man and gorilla) can complicate the interpretation of the results considerably.

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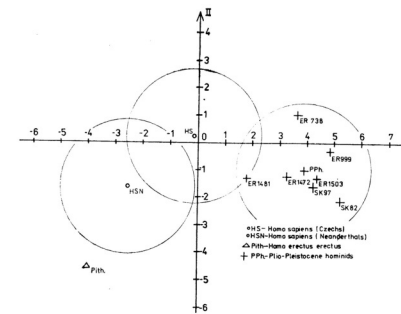
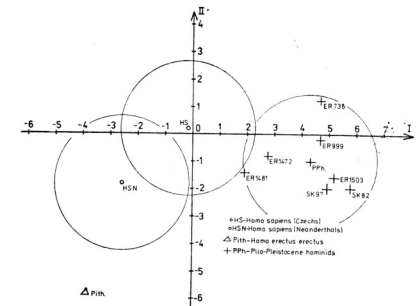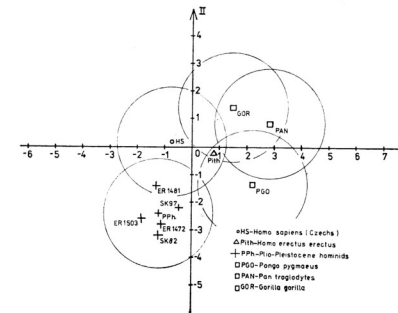FIGURE 10. *Stepwise discriminant analysis for hominid group (first two canonical variables).*
FIGURE 11. *Stepwise discriminant analysis for hominid group (first two canonical variables, input data are logarithmically transformed).*
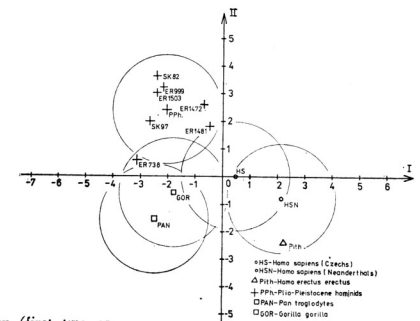

FIGURE 12. *Stepwise discriminant analysis for hominoid group (first two canonical variables).*
FIGURE 13. *Stepwise discriminant analysis for hominoid group (first two canonical variables, input data are standartized, Pongo group is not included in this analysis).*
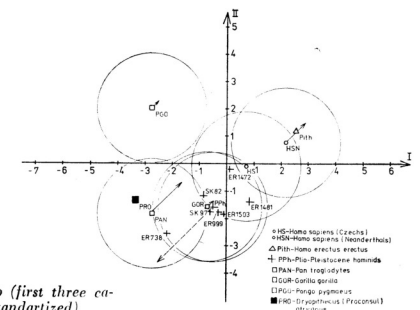

FIGURE 14. *Stepwise discriminant analysis for hominoid group (first three canonical variables, input data are logarithmically standartized).*

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THE INFLUENCE OF THE SAMPLE STRUCTURE ON THE RESULTS OF MULTIVARIATE ANALYSES

Let us close the above practical demonstration by the following consideration. If we carry out morphofunctional studies it is necessary to discriminate consistently, also as far as the hierarchy of the signification is concerned, between two types of the studied groups of individuals, differing in their basic structure. The first type of groups should contain phylogenetically related samples, which should be studied in order to observe the evolution of individual features as well as of the whole morphology. In the second type of groups then should be studied broader relationships, above all it is necessary to search for analogies and parallellisms, which make it possible to interpret consistently problems in phylogenetically related groups. The establishment of the hierarchy is purely practical rather than theoretical, it results from the characteristic properties of multivariate methods. On the basis of results of these analyses groups of in general morphologically similar individuals are formed (or, of individuals with similar parameters) and the differences and similarities between such individuals can be in many cases interpreted only with great difficulties without the knowledge of the morphofunctional differences in the corresponding phylogenetical groups. Multivariate methods search for groups of variables, satisfying optimal criteria for the given method (e.g., that of the highest correlation or discrimination), regardless whether the groups of features or even individual features possess as results of the analysis itself, a biological meaning from the point of view of a problem to be solved. In other words, the objective result of the multivariate analysis need not have in this case any explanatory value from the morphofunctional point of view, rather it points only to similarities or differences between individual groups, which, however, can be exploited in further analyses, e.g., after the reduction of "noise" variables. I believe that neglect of these facts and interpretations "at any cost" are the main reasons for contradictory opinions on the analyses of virtually identical fossil samples.

CONCLUSION

In the present study I attempted to show the extent and possibilities of mathematical studies in research concerning the human evolution. Nowadays we can hardly imagine the investigation of the human evolution without mathematical methods; their great significance is indisputable. The main problem rests, as it has been perhaps obvious from the above pages, in understanding and correct application of these methods. Mostly, however, the possibilities of mathematical methods as a unique source of quantitative information about the fossil material are not sufficiently used. It is often said that for a certain type of problems a definite type of analysis or modelling approach is suitable. This may be true to a certain extent but in no case does it mean that methods of different type cannot give important information, even if of a minute character. This fact becomes the more important, the more we realize how exceedingly significant is any information about the fossil material. For this reason whole complexes of programs examining the problem from the most diverse viewpoints should be used in future, providing valuable information of complex character. In this way the possibilities of investigation of fossil material would be considerably increased.

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