



8-1985

A Search for Systematic Variability in Inter-Finger Ridge Count Variation Among European Groups

Kenneth Melvin Binkley
University of Tennessee, Knoxville

Follow this and additional works at: https://trace.tennessee.edu/utk_graddiss



Part of the [Anthropology Commons](#)

Recommended Citation

Binkley, Kenneth Melvin, "A Search for Systematic Variability in Inter-Finger Ridge Count Variation Among European Groups. " PhD diss., University of Tennessee, 1985.
https://trace.tennessee.edu/utk_graddiss/4030

This Dissertation is brought to you for free and open access by the Graduate School at TRACE: Tennessee Research and Creative Exchange. It has been accepted for inclusion in Doctoral Dissertations by an authorized administrator of TRACE: Tennessee Research and Creative Exchange. For more information, please contact trace@utk.edu.

To the Graduate Council:

I am submitting herewith a dissertation written by Kenneth Melvin Binkley entitled "A Search for Systematic Variability in Inter-Finger Ridge Count Variation Among European Groups." I have examined the final electronic copy of this dissertation for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Doctor of Philosophy, with a major in Anthropology.

Richard L. Jantz, Major Professor

We have read this dissertation and recommend its acceptance:

P.S. Willey, William M. Bass, Gary F. McCracken

Accepted for the Council:


Carolyn R. Hodges

Vice Provost and Dean of the Graduate School

(Original signatures are on file with official student records.)

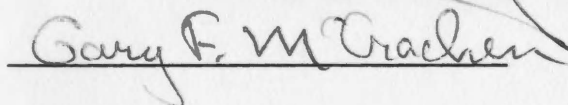
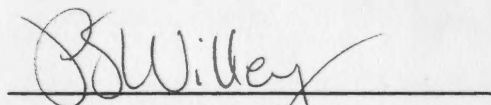
To the Graduate Council:

I am submitting herewith a dissertation written by Kenneth Melvin Binkley entitled "A Search for Systematic Variability in Inter-Finger Ridge Count Variation among European Groups." I have examined the final copy of this dissertation for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Doctor of Philosophy, with a major in Anthropology.

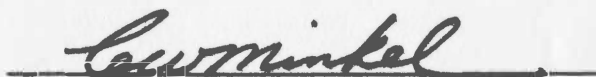


Richard L. Jantz, Major Professor

We have read this dissertation
and recommend its acceptance:



Accepted for the Council:


Vice Provost
and Dean of The Graduate School

A SEARCH FOR SYSTEMATIC VARIABILITY IN INTER-FINGER RIDGE
COUNT VARIATION AMONG EUROPEAN GROUPS

A Dissertation
Presented for the
Doctor of Philosophy
Degree
The University of Tennessee, Knoxville

Kenneth Melvin Binkley

August 1985

ACKNOWLEDGMENTS

This study would not have been completed without the able guidance of Dr. Richard L. Jantz, Professor, Department of Anthropology, The University of Tennessee, Knoxville.

The author also expresses gratitude to Dr. William M. Bass, Professor and Chairman, and Dr. Patrick S. Willey, both of the Department of Anthropology, and Dr. Gary F. McCracken, Department of Zoology, The University of Tennessee, Knoxville for their willingness to serve on the dissertation committee.

Dr. Robert M. Thorne, Co-Director, Center for Archaeological Research, The University of Mississippi, kindly provided office and laboratory space for the completion of this study.

Deborah K. Binkley, my wife, provided financial and moral support, and assisted in the preparation of the manuscript.

Inter-finger ridge count variability has been shown to discriminate among major racial groups. However, little has been accomplished in the way of demonstrating patterned dispersion of inter-finger ridge count variability among groups of a major population. Here, multivariate techniques are used in a series of discovery procedures to search for systematic variability of finger ridge count contrasts among 48 male and 47 female European groups. Among-group biological variability of each sex is defined by principal components analysis, using the finger ridge count means of each group and a pooled within-group, within-sex covariance matrix having 5,474 degrees of freedom. Multiple regression analysis and spatial autocorrelation are used to compare biological group dispersion to geographic and linguistic dispersion. Among-group geographic variability is defined by the variation among group locations on a regression plane, and by specific inter-group direction and distance classes. The discovery of patterned among-group biological variability in a northwest direction is concordant with studies which used serological variables to define among-group biological variability. The findings are interpreted as evidence in support of a Neolithic demic expansion of Near Eastern agriculturalists.

TABLE OF CONTENTS

SECTION	PAGE
1.0 INTRODUCTION.....	1
1.1 Background.....	1
1.2 Scope and Depth of the Study.....	5
2.0 MATERIALS.....	7
2.1 Introduction.....	7
2.2 Individual Finger Ridge Count Means.....	10
2.3 Language and Geographic Coordinates.....	10
2.4 Covariance Matrix.....	14
2.5 Group Principal Component Scores.....	20
3.0 METHODS AND RESULTS.....	24
3.1 Introduction.....	24
3.2 Multiple Regression Analysis.....	25
3.2.1 Definition of the regression plane.....	25
3.2.2 Multiple regression model.....	26
3.2.3 Results of multiple regression analysis.....	27
3.3 Spatial Autocorrelation.....	38
3.3.1 Moran's I statistic.....	38
3.3.2 Connectivity criteria.....	40
3.3.2.1 Direction and distance between group pairs.....	42
3.3.2.2 Gabriel connectivity criterion.....	43
3.3.2.3 Language between group pairs.....	45

TABLE OF CONTENTS
(CONTINUED)

SECTION	PAGE
3.3.3 Results of the geographic spatial autocorrelation analysis.....	47
3.3.3.1 I-correlograms for the 10 principal components.....	61
3.3.3.2 Correlograms for significant I-values on significant principal components.....	63
3.3.3.3 Linear regression of I-values.....	77
3.3.4 Results of the language analysis.....	79
4.0 DISCUSSION.....	88
4.1 Summary of Results.....	88
4.2 Biological Interpretation.....	90
REFERENCES CITED.....	95
APPENDIXES.....	101
APPENDIX A	
COVARIANCE MATRICES, EIGENVALUES, AND EIGENVECTORS OF TWELVE EUROPEAN SAMPLES.....	102
APPENDIX B	
ANALYSIS OF VARIANCE TABLES, REGRESSION STATISTICS, AND RESIDUAL PLOTS.....	115
VITA.....	146

LIST OF TABLES

TABLE	PAGE
2-1 SOURCE OF DERMATOGLYPHIC INFORMATION FOR EUROPEAN GROUPS.....	9
2-2 MALE FINGER RIDGE COUNT MEANS (X 100).....	11
2-3 FEMALE FINGER RIDGE COUNT MEANS (X 100).....	12
2-4 GEOGRAPHIC COORDINATES AND LANGUAGES OF SAMPLES.....	15
2-5 POOLED WITHIN-GROUP WITHIN-SEX COVARIANCE MATRIX (X 100).....	16
2-6 HETEROGENEITY OF COVARIANCE STRUCTURE AMONG TWELVE EUROPEAN COVARIANCE MATRICES.....	17
2-7 EIGENVECTORS (X 1000) OF THE POOLED WITHIN-GROUP WITHIN-SEX COVARIANCE MATRIX.....	19
2-8 MALE GROUPS PRINCIPAL COMPONENT SCORES (X 1000).....	22
2-9 FEMALE GROUPS PRINCIPAL COMPONENT SCORES (X 1000).....	23
3-1 REGRESSION RESULTS OF PRINCIPAL COMPONENTS VS GEOGRAPHY.....	28
3-2 DIRECTION OF MEAN RIDGE COUNT INCREASE ON GEOGRAPHICALLY PATTERNED COMPONENTS.....	30
3-3 GROUP CONNECTIONS IN ACCORDANCE WITH THE DIRECTION/DISTANCE CRITERION.....	44
3-4 GROUPS CONNECTED (CIRCLED) BY THE LANGUAGE CRITERION.....	48
3-5 MONOTONIC SEQUENCES OF I-VALUES FOR MALE GROUPS.....	75
3-6 MONOTONIC SEQUENCES OF I-VALUES FOR FEMALE GROUPS.....	76
3-7 I-VALUES FOR THE LANGUAGE ANALYSIS.....	79

LIST OF TABLES
(CONTINUED)

TABLE	PAGE
3-8 I-VALUES FOR DISTANCES ≤ 700 KM.....	85
3-9 COMMON LANGUAGE GROUPS WITHIN DIRECTION/DISTANCE CLASSES (MALES/FEMALES)	86
A-1 SPN1 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	103
A-2 SPN2 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	104
A-3 ENG1 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	105
A-4 GER1 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	106
A-5 AUS1 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	107
A-6 AUS2 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	108
A-7 SPN1 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	109
A-8 SPN2 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	110
A-9 ENG1 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	111
A-10 GER1 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	112
A-11 AUS1 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	113
A-12 AUS2 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS.....	114
B-1 ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC1 (COL1) AND PC2 (COL2).....	116
B-2 ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC3 (COL3) AND PC4 (COL4).....	117

LIST OF TABLES
(CONTINUED)

TABLE	PAGE
B-3 ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC5 (COL5) AND PC6 (COL6).....	118
B-4 ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC7 (COL7) AND PC8 (COL8).....	119
B-5 ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC9 (COL9) AND PC10 (COL10).....	120
B-6 ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC1 (COL1) AND PC2 (COL2).....	121
B-7 ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC3 (COL3) AND PC4 (COL4).....	122
B-8 ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC5 (COL5) AND PC6 (COL6).....	123
B-9 ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC7 (COL7) AND PC8 (COL8).....	124
B-10 ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC9 (COL9) AND PC10 (COL10).....	125

LIST OF FIGURES

FIGURE	PAGE
2-1 Areal view of study area showing locations of samples.....	8
3-1 Bivariate plot of male groups on PC8 (X-axis) and PC3 (Y-axis).....	32
3-2 Bivariate plot of male groups on PC7 (X-axis) and PC4 (Y-axis).....	33
3-3 Bivariate plot of male groups on components of asymmetry, PC8 (X-axis) and PC7 (Y-axis).....	34
3-4 Bivariate plot of male groups on components of diversity, PC4 (x-axis) and PC3 (Y-axis).....	35
3-5 Bivariate plot of female groups on PC4 (X-axis) and PC3 (Y-axis).....	36
3-6 Male groups connected in accordance with the Gabriel criterion.....	46
3-7 Male Gabriel I-values, means (M), and connections (W).....	49
3-8 Male North I-values, means (M), and connections (W).....	50
3-9 Male Northeast I-values, means (M), and connections (W).....	51
3-10 Male West I-values, means (M), and connections (W).....	52
3-11 Male Northwest I-values, means (M), and connections (W).....	53
3-12 Female Gabriel I-values, means (M), and connections (W).....	54
3-13 Female North I-values, means (M), and connections (W).....	55
3-14 Female Northeast I-values, means (M), and connections (W).....	56

LIST OF FIGURES
(CONTINUED)

FIGURE	PAGE
3-15 Female West I-values, means (M), and connections (W).....	57
3-16 Female Northwest I-values, means (M), and connections (W).....	58
3-17 Idealized I-correlogram for four principal components, two of which exhibit monotonicity.....	60
3-18 I-correlograms for Gabriel connectivity of Males (top) and Females.....	62
3-19 Male North (top) and Northeast I-correlograms.....	64
3-20 Male Northwest (top) and West I-correlograms.....	65
3-21 Female North (top) and Northeast I-correlograms.....	66
3-22 Female Northwest (top) and West I-correlograms.....	67
3-23 I-correlograms of significant principal components for Gabriel connectivity of Males (top) and Females.....	69
3-24 I-correlograms of significant principal components for Male North (top) and Northeast.....	70
3-25 I-correlograms of significant principal components for Male Northwest (top) and West.....	71
3-26 I-correlograms of significant principal components for Female North (top) and Northeast.....	72
3-27 I-correlograms of significant principal components for Female Northwest (top) and West.....	73

LIST OF FIGURES
(CONTINUED)

FIGURE	PAGE
3-28 Regression slopes for I-values (plotted) and I-value means for Gabriel connectivity of Males (top) and Females.....	80
3-29 Regression slopes for I-values (plotted) and I-value means for Male North (top) and Northeast.....	81
3-30 Regression slopes for I-values (plotted) and I-value means for Male Northwest (top) and West.....	82
3-31 Regression slopes for I-values (plotted) and I-value means for Female North (top) and Northeast.....	83
3-32 Regression slopes for I-values (plotted) and I-value means for Female Northwest (top) and West.....	84
B-1 Plot of female PC1 residuals (X-axis) against fitted values.....	126
B-2 Plot of female PC2 residuals (X-axis) against fitted values.....	127
B-3 Plot of female PC3 residuals (X-axis) against fitted values.....	128
B-4 Plot of female PC4 residuals (X-axis) against fitted values.....	129
B-5 Plot of female PC5 residuals (X-axis) against fitted values.....	130
B-6 Plot of female PC6 residuals (X-axis) against fitted values.....	131
B-7 Plot of female PC7 residuals (X-axis) against fitted values.....	132
B-8 Plot of female PC8 residuals (X-axis) against fitted values.....	133

LIST OF FIGURES
(CONTINUED)

FIGURE	PAGE
B-9 Plot of female PC9 residuals (X-axis) against fitted values.....	134
B-10 Plot of female PC10 residuals (X-axis) against fitted values.....	135
B-11 Plot of male PC1 residuals (X-axis) against fitted values.....	136
B-12 Plot of male PC2 residuals (X-axis) against fitted values.....	137
B-13 Plot of male PC3 residuals (X-axis) against fitted values.....	138
B-14 Plot of male PC4 residuals (X-axis) against fitted values.....	139
B-15 Plot of male PC5 residuals (X-axis) against fitted values.....	140
B-16 Plot of male PC6 residuals (X-axis) against fitted values.....	141
B-17 Plot of male PC7 residuals (X-axis) against fitted values.....	142
B-18 Plot of male PC8 residuals (X-axis) against fitted values.....	143
B-19 Plot of male PC9 residuals (X-axis) against fitted values.....	144
B-20 Plot of male PC10 residuals (X-axis) against fitted values.....	145

1.0 INTRODUCTION

1.1 Background

The additive effect of several areas of research provided the impetus for this study of the geographical variation of the European population. A decade ago, Jantz and his associates used multivariate procedures to demonstrate the existence of considerable racial variation with respect to components of finger ridge counts (Jantz, 1974, 1975). Later, using comparable variables, Jantz and Hawkinson (1979) showed that geographical variation among Subsaharan African groups could be detected. Formerly, no such fine-grained discrimination of groups had been accomplished with the use of dermatoglyphic variables. Meanwhile other researchers, working with immunological and archaeological data, were compiling sufficient evidence to offer an alternative to the cultural diffusionist hypothesis of the spread of agriculture into Europe. This alternative, perhaps complementary, concept is simply the idea of Neolithic farmers themselves spreading into Europe from Southwest Asia (Menozzi et al., 1978; Ammerman and Cavalli-Sforza, 1979; Sokal and Mennozi, 1982). The question posed by this research is whether or not present-day phenotypic characters of Europeans support the hypothesis of demic expansion. If they do, the expectation is that such characters would be distributed along the routes of demic diffusion.

Phenotypic characters based on dermatoglyphics would seem to be ideal representatives because of their freedom from direct assortative mating influences (Rife, 1953; Plato, 1970). Finger ridge counts are

also highly heritable traits, although different investigators report somewhat different estimates of heritability (Jantz et al., 1979). Holt (1968) and Jantz et al. (1985) estimate heritability of somewhat over 70 percent for the combined sexes, based upon twin studies. It is important to point out, however, that this study uses multivariate procedures which are based on components of variability derived from the individual finger counts. These components express contrasts of ridge counts from finger to finger on each hand and the contrasts of ridge counts on homologous digits of each hand. These are referred to herein as ridge count "diversity" and "asymmetry," respectively. Little work has been accomplished regarding the heritability of these components, which provide some indication of the relative independence of each digit to express its own ridge count. Holt (1968) claims that family studies indicate no genetic control of asymmetry, but substantial genetic control of ridge count standard deviation, which is a measure of diversity. However, Jantz's (1975) demonstration of population variation with respect to both of these components indicates that the genetic contribution of diversity and asymmetry needs to be rethought. In recent work, Loesch (1983) has demonstrated the possibility of a significant genetic component with respect to finger ridge count asymmetry, both unidirectional and ambidirectional, although the calculated heritability appears to differ somewhat between the sexes.

In addition to the dearth of genetic information with respect to components of diversity and asymmetry, one of several other problems

in using dermatoglyphic characters in population studies is that the variables often fail to register consistently with other sources of variability. The among-group variability in language, immunology, anthropometry, and geography seems to range in agreement with dermatoglyphic variability from excellent (Froelich and Giles, 1981) to nil (Friedlander, 1975), to give but two of several possible examples. These results may have something to do with the definition of the dermatoglyphic variables at the outset of a particular study. Jantz and Chopra (1983) showed that different dermatoglyphic approaches produce somewhat different among-group distances among four groups indigenous to a region of India. Nevertheless, the only quantitative characters which are available for a substantial number of European groups are the mean individual finger ridge counts. These variables fared poorly in providing an indication of among-group biological distance in the Jantz and Chopra (1983) study; however, they appear to be sufficiently discriminating in this study to indicate substantial inter-group biological heterogeneity, as will be shown in the next section.

Another problem with many, if not all, dermatoglyphic variables, is that it is not at all clear what they represent biologically. The generally accepted developmental scenario is that ridge count is dictated by the timing of ridge formation on a finger relative to the size and persistence of its apical pad (Abel, 1938; Cummins and Midlo, 1943; Babler, 1979). Thus, variables defined by elements of ridge count diversity can be interpreted as within-hand among-finger

contrasts of these interactive processes. Along the same line, contrasts of ridge counts on homologous digits would seem to reflect bilateral asymmetry of the same interactive processes. One of the problems with this hypothesis, especially as restated by Mulvihill and Smith (1969), is the difficulty in rejecting it with information short of that collected from in-utero longitudinal growth studies. For example, in another context, Jantz (1975) suggested that within-group homogeneity of ridge counts can be explained as intensive canalization of developmental processes in individuals, or as extensive homozygosity at loci responsible for finger pattern size. Both suggestions fit comfortably in the Mulvihill and Smith (1969) hypothesis, which in turn provides no probabilistic indications of whether one or both or neither processes might be operating. In spite of this shortcoming, without the hypothesis, the observed variability in dermatoglyphic characters makes little sense, so it remains a highly useful heuristic device.

Still another problem area concerns the way ridges are counted, i.e. using the largest count--usually the larger of two counts--for whorl patterns. Roberts and Coope (1975), Jantz and Owsley (1977), and others have demonstrated through factor analysis a relative independence of the radial and ulnar sides of the fingers, at least with respect to ridge counts. Thus, a vector of 10 ridge counts can confound independent biological sources of variability. The impact of this uncontrolled error source is probably not as great on this study as it would be if the sample groups represented widely separated

geographic populations. Mention of the error is made here to reinforce Jantz's (1984) suggestion that individuals are much more accurately represented by a vector of 20 counts instead of the traditional 10.

Finally, a last problem has to do with dermatoglyphic characters in admixed populations and the nature of the demic expansion hypothesis. The spread of farmers into Europe from Southwest Asia is envisioned as a process which proceeded like a blunted ocean wave advancing at the average rate of one kilometer per year, movement taking place at the wave front, absorbing rather than replacing the resident Mesolithic populations (Ammerman and Cavalli-Sforza, 1984). In other research, Jantz (1974) has called attention to the disparity of ridge counts between admixed groups and their parent populations, some groups exhibiting ridge counts in excess of those demonstrated by parent populations. Intuitively, the probability that admixture among Mesolithic groups could have some systematic effect on the patterning of ridge count components, and thereby mimic a wave front, would seem to be quite low.

1.2 Scope and Depth of the Study

It is not the goal of this study to explicate the developmental processes responsible for among-group patterning of ridge counts. Rather, it is to discover and describe the patterns which do exist, and to relate those patterns to the demic expansion hypothesis. Deficiencies in the data are reflected by the depth of the analysis, so the analytical approach is comparatively simple. The results largely are based upon cumulative impressions provided by a number of

relatively unsophisticated statistical techniques rather than rigid statistical testing of a complex model. Such results provide a rough approximation of extant patterning of phenotypic characters in Europe, which would seem to be an appropriate starting point.

The sections which follow are devoted to an exposition of among-group variability of mean finger ridge counts in Europe. The next section defines the study area, describes the data base used in the study, and presents the reference sources. It also shows how the information is manipulated into a form suitable to the multivariate statistical techniques employed. The third section describes the analytical techniques and presents the results of the analysis. The final section interprets the results with respect to the hypothesis of the demic diffusion of Neolithic farmers into Europe. In the interest of preserving space and preventing redundancy, each section is confined to its own topic as much as is possible. Short biological interpretations and brief statements which compare results with expectations are included where clarification is needed. Because of the simplicity in the research design, however, the data base, the analytical techniques, as well as the results, are nearly self-evident.

2.0 MATERIALS

2.1 Introduction

The raw data used in this study are based upon information available for 48 male and 47 female European groups. The dermatoglyphic literature provides most of these data, supplemented by unpublished information kindly made available by cognizant investigators. For each group, the data consist of one, a vector of 10 individual finger ridge count means; two, the group's geographic position; and three, the spoken language. Also, for 12 of the samples--six male and six female--the literature includes finger ridge count covariance and/or correlation matrices. These are used to standardize the covariance structure for all the groups, as is shown later. Specific group affiliations for the covariance matrices are identified later in this section. The term "covariance matrix" is used throughout the text in place of the more precise but cumbersome "variance/covariance matrix." Some inter-observer error in the raw data is probably unavoidable, but hopefully the error is confounded to the extent that no bias exists in the final results of this analysis.

Figure 2-1 presents an areal view of the study area and sample locations. Table 2-1 identifies the national or ethnic origins of the European groups, and shows the sample size and reference source for each group. Group designators such as "EST1" and "DAN" are used throughout the remainder of the text without further reference to Table 2-1.



Figure 2-1. Areal view of study area showing locations of samples.

TABLE 2-1

SOURCE OF DERMATOGLYPHIC INFORMATION FOR EUROPEAN GROUPS

GROUP		MALES	FEMALES	SOURCE
Estonia	(EST1)	1399	1754	Horn, 1974
	(EST2)	200	300	Horn and Mikelsaar, 1974
Byelorussia	(BYL)	94	153	Guseva and Antonyuk, 1969
Bulgaria	(BUL)	1065	1065	Karev, 1984
Poland	(POL)	136	136	Jelisiejew and Marcinkiewicz, 1972
Greece	(GRK1)	145	124	Brehme and Pentzos-Daponte, 1975
	(GRK2)	95	101	Weninger and Rothenbuchner, 1974
	(GRK3)	43	52	Roberts et al., 1965
Lithuania	(LIT)	83	102	Harvey and Suter, 1983a
Czechoslovakia	(CZK1)	200	200	Pospisil, 1963
	(CZK2)	150	136	Pospisil, 1970
Yugoslavia	(YUG1)	52	50	Rudan and Schmutzer, 1976
	(YUG2)	58	65	Rudan and Schmutzer, 1976
Austria	(AUS1)	1000	1000	Aue-Hauser, 1976
	(AUS2)	500	500	Szilvassy, 1978
	(AUS3)	500	-	Weninger, 1975
Hungary	(HUN1)	114	100	Gyenis, 1975
	(HUN2)	121	102	Gyenis, 1975
	(HUN3)	132	140	Gyenis, 1975
	(HUN4)	150	150	Thoma, 1969
	(HUN5)	93	90	Gyenis, 1979
	(HUN6)	200	200	Ostovics et al., 1971
Italy	(IYL)	208	205	Gualdi-Russo et al., 1982
Denmark	(DAN)	8785	9861	Vogelius-Anderson, 1969
Germany	(GER1)	400	400	Brehme et al., 1966
	(GER2)	150	145	Brehme, 1985
Holland	(DUT)	200	200	Geipel, 1961
Belgium	(BEL1)	122	93	Vrydagh-Laoureux, 1971
	(BEL2)	157	130	Bara, 1980
	(BEL3)	202	158	Vrydagh and Leguebe, 1976
	(BEL4)	71	81	Vrydagh-Laoureux, 1983
	(BEL5)	109	134	Vrydagh-Laoureux, 1983
England	(ENG1)	100	100	Holt, 1958
	(ENG2)	1803	2124	Dennis and Sunderland, 1979
Wales	(WAL)	1548	1614	Williams, 1978
Basque	(BAS1)	69	16	Roberts et al., 1976
	(BAS2)	39	56	Roberts et al., 1976
	(BAS3)	97	76	Roberts et al., 1976
	(BAS4)	170	169	Ducros, 1970
Eastern Pyrennes	(ESP)	44	71	Ducros, 1970
Faroe Islands	(FAR)	446	463	Harvey and Suter, 1983b
Spain	(SPN1)	417	416	Martin, 1982
	(SPN2)	339	314	Martin, 1982
Portugal	(POR1)	65	34	Matznetter, 1967
	(POR2)	49	51	Matznetter, 1967
	(POR3)	100	100	da Cunha and Abreu, 1954
Canary Islands	(CAN1)	88	49	Matznetter, 1967
	(CAN2)	100	28	Matznetter, 1967

The remainder of this section considers each category of the raw data and demonstrates how it is manipulated into a form concordant with the analytical methods used in this study.

2.2 Individual Finger Ridge Count Means

Tables 2-2 and 2-3 present the individual finger ridge count means for each European group. One sample of Austrians, AUS3, contains no females. Otherwise the 47 female groups are the complements of the 48 male samples. Abbreviations which appear in the tables without explanation refer to specific digits. The terms "D5" to "D1" indicate the digits from little finger to thumb, while the use of "R" or "L" in place of "D" specifies the particular hand, i.e. right or left.

The ridge count means in Tables 2-2 and 2-3 appear to be about what one expects, with one notable exception: the usual sexual dimorphism is reversed in the YUG2 samples. Rudan and Schmutzer (1976) confirm a sexual reversal of total ridge count, but do not address the phenomenon further. The samples are fairly small, 58 males and 65 females, so an unusual sampling error may be involved here.

2.3 Language and Geographic Coordinates

For the most part, the dermatoglyphic literature contains no explicit information on spoken language or the geographic coordinates associated with a particular sample. In many cases, this presents no difficulty because the sample comes from a major

TABLE 2-2

MALE FINGER RIDGE COUNT MEANS (X 100)

	L5	L4	L3	L2	L1	R5	R4	R3	R2	R1
EST1	1345	1692	1261	1089	1750	1375	1720	1204	1167	2049
EST2	1310	1650	1260	1100	1660	1350	1660	1160	1190	2020
BYL	1456	1642	1300	1139	1664	1410	1667	1333	1280	1801
BUL	1341	1653	1283	1166	1695	1349	1666	1231	1223	1945
POL	1336	1624	1252	1122	1601	1326	1602	1376	1478	1892
GRK1	1282	1567	1202	1086	1733	1348	1546	1160	1168	1926
GRK2	1314	1566	1251	1167	1714	1307	1519	1264	1324	1946
GRK3	1214	1474	1091	1102	1791	1200	1502	1209	1226	1942
LIT	1400	1660	1390	1170	1810	1380	1730	1290	1150	2140
CZK1	1396	1700	1378	1154	1810	1363	1684	1291	1246	2044
CZK2	1387	1659	1310	1098	1677	1290	1654	1248	1161	1872
YUG1	1440	1683	1386	1233	1613	1350	1725	1333	1450	1854
YUG2	1272	1493	1136	1148	1350	1310	1486	1084	1205	1536
AUS1	1330	1610	1234	1077	1648	1304	1594	1193	1144	1875
AUS2	1420	1696	1301	1201	1748	1423	1729	1265	1245	1994
AUS3	1385	1644	1210	1130	1679	1391	1624	1187	1192	1981
HUN1	1394	1668	1269	1140	1621	1340	1675	1174	1261	1790
HUN2	1328	1625	1192	1046	1574	1329	1607	1148	1155	1856
HUN3	1333	1661	1211	1203	1680	1353	1587	1224	1178	1890
HUN4	1289	1527	1049	981	1612	1364	1622	1117	1034	1846
HUN5	1404	1543	1277	1114	1522	1400	1568	1184	1245	1761
HUN6	1316	1640	1201	978	1654	1284	1610	1161	1045	1870
IYL	1364	1568	1218	1100	1785	1372	1530	1224	1196	1970
DAN	1326	1569	1150	982	1533	1304	1576	1121	1053	1846
GER1	1377	1654	1254	1152	1719	1378	1663	1241	1197	1959
GER2	1407	1690	1215	1142	1639	1399	1710	1167	1138	1921
DUT	1280	1480	1080	950	1610	1310	1550	1020	980	1840
BEL1	1351	1588	1228	1107	1628	1368	1566	1169	1051	1955
BEL2	1399	1629	1231	1160	1562	1381	1649	1169	1149	1911
BEL3	1340	1571	1244	1088	1610	1344	1547	1173	1051	1924
BEL4	1372	1483	1134	903	1672	1310	1551	1086	1128	1892
BEL5	1376	1631	1326	1104	1763	1417	1652	1288	1244	2018
ENG1	1361	1566	1239	1164	1623	1399	1598	1214	1170	1916
ENG2	1504	1705	1269	1142	1778	1465	1673	1206	1190	2014
WAL	1458	1659	1217	1110	1698	1435	1639	1182	1175	1929
BAS1	1301	1529	1212	1128	1371	1354	1623	1171	1036	1684
BAS2	1421	1582	1274	1208	1723	1426	1587	1192	1179	2054
BAS3	1444	1605	1163	1055	1499	1488	1638	1137	1195	1864
BAS4	1282	1482	1093	959	1459	1344	1511	1017	1026	1716
ESP	1091	1436	1086	977	1491	1164	1532	966	882	1766
FAR	1150	1370	970	890	1500	1180	1400	960	930	1850
SPN1	1387	1626	1274	1142	1698	1406	1623	1250	1198	1959
SPN2	1366	1580	1234	1076	1651	1379	1595	1224	1251	1940
POR1	1398	1698	1300	1194	1572	1394	1691	1237	1291	1849
POR2	1441	1741	1235	1216	1528	1449	1631	1302	1316	1888
POR3	1373	1573	1180	1118	1670	1352	1591	1147	1098	1945
CAN1	1364	1595	1346	1266	1747	1413	1623	1277	1323	1915
CAN2	1364	1609	1261	1148	1696	1349	1653	1155	1208	1898

TABLE 2-3

FEMALE FINGER RIDGE COUNT MEANS (X 100)

	L5	L4	L3	L2	L1	R5	R4	R3	R2	R1
EST1	1237	1633	1174	1087	1550	1282	1700	1189	1137	1829
EST2	1240	1620	1140	1100	1550	1270	1680	1190	1090	1840
BYL	1350	1506	1284	1194	1468	1386	1550	1302	1332	1588
BUL	1243	1560	1180	1122	1498	1248	1601	1210	1182	1717
POL	1252	1564	1168	1184	1396	1280	1614	1198	1204	1650
GRK1	1258	1513	1148	1171	1578	1202	1502	1138	1162	1711
GRK2	1239	1514	1219	1106	1542	1241	1574	1193	1117	1782
GRK3	1192	1406	1102	1012	1460	1185	1410	1119	1125	1656
LIT	1310	1600	1200	1120	1600	1310	1680	1220	1170	1840
CZK1	1246	1510	1117	1054	1414	1195	1573	1232	1105	1648
CZK2	1258	1644	1181	1063	1538	1180	1521	1105	1152	1693
YUG1	1218	1474	1226	1048	1586	1292	1602	1200	1114	1708
YUG2	1323	1568	1248	1237	1549	1272	1594	1217	1283	1746
AUS1	1179	1477	1107	1031	1491	1175	1493	1110	1098	1688
AUS2	1288	1570	1177	1086	1498	1282	1590	1192	1133	1732
HUN1	1196	1553	1118	1009	1572	1245	1589	1185	1098	1789
HUN2	1218	1554	1055	1033	1449	1249	1544	1147	1057	1655
HUN3	1236	1618	1164	1061	1481	1253	1606	1194	1134	1719
HUN4	1189	1532	1060	1001	1403	1278	1583	1093	1108	1611
HUN5	1277	1516	1259	1121	1463	1327	1599	1221	1145	1594
HUN6	1154	1442	1043	948	1383	1150	1484	1013	1006	1556
IYL	1187	1411	1145	1088	1486	1173	1365	1140	1153	1704
DAN	1188	1453	1023	917	1319	1225	1507	1062	1007	1605
GER1	1241	1568	1139	1038	1484	1222	1600	1160	1008	1686
GER2	1234	1543	1184	1130	1534	1248	1563	1168	1244	1744
DUT	1170	1420	990	980	1410	1180	1490	1080	1040	1630
BEL1	1120	1301	1043	931	1438	1179	1414	1130	1016	1705
BEL2	1199	1447	1035	965	1473	1248	1494	1069	1020	1742
BEL3	1102	1311	985	936	1389	1144	1392	1064	963	1644
BEL4	1242	1460	1145	925	1485	1237	1509	1065	1004	1785
BEL5	1280	1477	1091	1043	1554	1272	1481	1085	1057	1644
ENG1	1215	1515	1099	1039	1385	1245	1559	1126	1189	1661
ENG2	1360	1590	1135	1055	1523	1329	1586	1144	1133	1762
WAL	1334	1540	1096	1038	1495	1334	1576	1133	1131	1693
BAS1	988	1088	931	825	1356	1181	1088	888	956	1544
BAS2	1334	1516	1059	1152	1484	1355	1689	1123	1196	1825
BAS3	1214	1461	1082	943	1425	1217	1514	1179	1066	1658
BAS4	1111	1284	931	869	1372	1169	1409	1001	939	1544
ESP	1054	1282	1010	915	1297	1104	1418	1052	858	1555
FAR	980	1220	850	750	1290	1030	1250	860	790	1590
SPN1	1247	1539	1133	1068	1470	1269	1533	1154	1155	1732
SPN2	1186	1454	1055	1022	1432	1211	1489	1123	1095	1667
POR1	1209	1568	1188	1150	1568	1135	1541	1165	1123	1762
POR2	1370	1745	1231	1243	1521	1422	1708	1263	1308	1758
POR3	1221	1376	1020	1046	1480	1233	1427	1032	1038	1758
CAN1	1375	1665	1261	1345	1620	1431	1667	1280	1422	1759
CAN2	1243	1525	961	864	1371	1161	1571	989	1168	1771

metropolitan area for which geographic coordinates are published, and the spoken language of the area is common knowledge. For example, a sample of Viennese schoolchildren is not problematical with regard to the specification of language and geographic location. Conversely, Byelorussia is a large area and the reported ridge count means by Guseva and Atonyuk (1969) provides no indication of the specific location of the sample. In a case such as Byelorussia, the geographic coordinates assigned to a particular sample area represent an estimate of the sample area's population center. Thus, if a sample area contains a large city which is more or less centrally located, the coordinates of the city appear to be the most reasonable estimate of the sample's geographic position. In all cases, the estimate of sample location is based upon a published geographic landmark to take advantage of published coordinates.

The language spoken by individuals in each of the samples is presumed to be the language normally associated with the national, political, or ethnic boundaries of the sample area, unless otherwise noted in the literature. Only one sample, ESP, is problematical in that the French text by Ducros (1970) does not include the ethnic affiliation of the sample. The language is presumed to be Romance, i.e. either Spanish or French, but Basque remains a possibility.

The geographic coordinates and languages associated with the male groups, which are inclusive of the female groups, are

presented in Table 2-4, along with the geographic features used as the sample locations. The Ural-Altaic and Basque languages are presented in their highest degree of generality in Table 2-4. All other languages shown represent branches of the Indo-European family.

2.4 Covariance Matrix

Although ridge count means are readily available for a number of European groups, only a few correlation or covariance matrices can be found in the literature. Authors of the works dealing with the ENG1 (Holt, 1958), AUS1 (Aue-Hauser, 1976), AUS2 (Szilvassy, 1978), and GER1 (Brehme et al., 1966) samples have included correlation matrices, along with sample sizes and individual finger ridge count variance. Covariance matrices can be calculated from these data. Martin (1982) has made available the covariance matrices for the SPN1 and SPN2 samples. Pooling of these six male and six female covariance matrices, within-group and within-sex, results in a covariance matrix having 5,474 degrees of freedom, shown in Table 2-5.

There is biological justification for pooling the various covariance matrices, because each matrix is representative of a group which is considered at the outset to be a member of a single major geographic population. Even so, it is interesting to compare the covariance structure of the component groups on a statistical basis. One test of the heterogeneity of covariance matrices, described by Uytterschaut and Wilmink (1983), is to compare the

TABLE 2-4

GEOGRAPHIC COORDINATES AND LANGUAGES OF SAMPLES

GROUP	LAT	LONG	BASIS OF COORDINATES	LANGUAGE
EST1	58-49N	25-29E	Turi (town)	Ural-Altaic
EST2	58-03N	26-31E	Otepaa (town)	Ural-Altaic
BYL	53-54N	27-35E	Minsk (city)	Slavic
BUL	42-47N	25-23E	Kazanluk (town)	Slavic
POL	53-08N	23-12E	Bialystok (city)	Slavic
GRK1	40-38N	22-59E	Thessaloniki (city)	Greek
GRK2	38-00N	23-38E	Athens (city)	Greek
GRK3	37-45N	25-12E	Tinos (island)	Greek
LIT	54-52N	23-54E	Kaunas (town)	Baltic
CZK1	48-35N	19-10E	Zvolen (town)	Slavic
CZK2	50-05N	14-25E	Prague (city)	Slavic
YUG1	43-10N	16-35E	(given)	Slavic
YUG2	43-08N	16-55E	(given)	Slavic
AUS1	48-13N	16-22E	Vienna (city)	W. Germanic
AUS2	48-02N	16-29E	Gramatneusiedl (town)	W. Germanic
AUS3	48-06N	16-17E	Modling (town)	W. Germanic
HUN1	47-12N	19-01E	Kiskunlachaza (town)	Ural-Altaic
HUN2	47-12N	19-01E	Kiskunlachaza (town)	Ural-Altaic
HUN3	47-06N	19-00E	Domsod (town)	Ural-Altaic
HUN4	46-15N	20-12E	Szeged (city)	Ural-Altaic
HUN5	46-02N	19-13E	Katymar (town)	Ural-Altaic
HUN6	47-30N	19-05E	Budapest (city)	Ural-Altaic
IYL	44-30N	11-18E	Bologna (city)	Romance
DAN	55-43N	12-27E	Copenhagen (city)	N. Germanic
GER1	52-16N	10-32E	Braunschweig (town)	W. Germanic
GER2	47-59N	7-50E	Frieburg	W. Germanic
DUT	52-40N	5-35E	Urk (island)	W. Germanic
BEL1	50-51N	4-21E	Brussels (city)	Romance
BEL2	50-25N	4-35E	Charleroi (town)	Romance
BEL3	50-51N	4-21E	Brussels (city)	Romance
BEL4	51-14N	2-55E	Oostende (town)	W. Germanic
BEL5	50-27N	3-49E	St. Ghislain (town)	Romance
ENG1	51-30N	7E	London (city)	W. Germanic
ENG2	54-22N	2-07W	Stainmore Pass (pass)	W. Germanic
WAL	52-30N	3-30W	(author's map)	Insular Celtic
BAS1	43-09N	2-04W	Tolosa (town)	Basque
BAS2	43-09N	2-04W	Tolosa (town)	Basque
BAS3	43-15N	2-56W	Bilbao (town)	Basque
BAS4	43-28N	1-30W	Bayonne (town)	Basque
ESP	42-37N	2-33E	Prades (town)	Romance
FAR	62-00N	6-55W	Torshavn (town)	N. Germanic
SPN1	42-10N	4-50W	Tierra de Campos (region)	Romance
SPN2	40-30N	2-45W	La Alcarria (region)	Romance
POR1	37-01N	7-57W	Faro (town)	Romance
POR2	37-08N	8-43W	Lagos (town)	Romance
POR3	39-28N	8-13W	Abrantes (town)	Romance
CAN1	27-37N	18-29W	Hierro (island)	Romance
CAN2	28-00N	18-01W	Gomera (island)	Romance

TABLE 2-5

POOLED WITHIN-GROUP WITHIN-SEX
COVARIANCE MATRIX (X 100)

	L5	L4	L3	L2	L1	R5	R4	R3	R2	R1
L5	2857	2415	2030	2098	1545	2362	2287	1850	2162	1462
L4	2415	4220	2914	2694	1770	2419	3378	2621	2747	1705
L3	2030	2914	4103	3002	1950	2013	2679	3025	2998	1802
L2	2098	2694	3002	4861	2063	2109	2546	2792	3677	1882
L1	1545	1770	1950	2063	3907	1520	1625	1811	2031	2856
R5	2362	2419	2013	2109	1520	2937	2314	1884	2154	1482
R4	2287	3378	2679	2546	1625	2314	4006	2480	2616	1627
R3	1850	2621	3025	2792	1811	1884	2480	3687	2866	1695
R2	2162	2747	2998	3677	2031	2154	2616	2866	5026	1923
R1	1462	1705	1802	1882	2856	1482	1627	1695	1923	3604

log-determinant of a pooled covariance matrix to the log-determinant of each covariance matrix which contributes to the pool. The resultant statistic is transformed to a Chi-square value before testing the null hypothesis. Table 2-6 shows the results of among-group within-sex and within-group among-sex tests of covariance heterogeneity.

The within-sex among-group tests necessarily incorporate the largest sample sizes, and these tests produce the highest Chi-square values. It could be that the differences in covariance structure, while small, achieve statistical significance because of large sample sizes. The within-group between-sex tests produce considerably lower Chi-square values. However, both the male and female German groups demonstrate a relatively low Chi-square value in spite of comparatively large sample sizes, indicating that the between-sex differences may simply be less than the among-group

differences. One way to explore the biological significance of these possible differences in covariance structure is by way of a

TABLE 2-6

HETEROGENEITY OF COVARIANCE STRUCTURE AMONG
TWELVE EUROPEAN COVARIANCE MATRICES

AMONG-GROUP	DF	N	CHI-SQUARE	SIGNIFICANCE
Males	110	2756	185.24	< .01
Females	110	2730	249.78	< .01
*BETWEEN-SEX				
Austrian	55	3000	175.24	< .01
Spanish	55	1487	75.62	.01 < p < .025
German	55	800	54.61	> .20
English	55	200	70.42	.10 < p < .20

*AUS1 & AUS2, SPN1 & SPN2 are pooled within-group

principal components analysis of each of the 12 covariance matrices. Tables A-1 through A-12 in Appendix A present the eigenvectors and eigenvalues calculated for each matrix, as well as the covariance matrices themselves. In each matrix, well over half the variance lies in principal component one (PC1), which can be readily interpreted as a size component. The first component is invariably followed by a contrast of the thumb ridge count with the ridge count of the remaining digits. The third component, PC3, can be interpreted as a contrast of digit two with digits four and five, and PC4 demonstrates a contrast of digit three with digits two and five. The succeeding components become progressively more

difficult to interpret, however the overall pattern is similar in each matrix. The fifth component, PC5, is usually a contrast of digit four with digits five and three, and all succeeding components can be interpreted as evidence of asymmetry, i.e. bilateral contrasts of one or more digits. The only patent difference among the eigenvector matrices is that asymmetry sometimes makes its appearance on PC5 rather than PC6.

From the results of the heterogeneity tests and the principal component analyses, the covariance structure appears to be fairly consistent among the 12 groups used here, at least from a biological viewpoint. No group departs radically from any other with respect to the biological interpretation of the eigenvectors. Large samples are required to demonstrate statistical heterogeneity. It is evident that the pooled within-group within-sex covariance matrix can be used as a basic measurement tool without introducing a high degree of artificiality into the results. Table 2-7 shows the eigenvectors of the pooled within-group within-sex covariance matrix and the percent of total variation on each component. The matrix exhibits considerable dimensionality, the eigenvalues ranging from 247.2 on PC1 to 5.3 on PC10.

An interpretation of the eigenvectors can be made by reference to the loadings on each component. The first component appears to be a size vector, as evidenced by the high loadings and constant positive signs on the coefficients in the eigenvector matrix. It is

TABLE 2-7

EIGENVECTORS (X 1000) OF THE POOLED
WITHIN-GROUP WITHIN-SEX
COVARIANCE MATRIX

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
L5	268	083	-301	388	391	-053	053	-039	016	-720
L4	349	237	-350	-132	-362	080	197	-073	-706	034
L3	346	104	112	-523	324	-012	284	-588	223	048
L2	363	067	500	249	-031	736	-091	015	-020	-011
L1	262	-668	-073	-039	-014	060	578	363	088	043
R5	270	089	-314	405	420	-047	-082	015	031	686
R4	332	242	-359	-090	-485	065	-136	156	642	-020
R3	321	088	143	-470	326	-156	-377	591	-148	-058
R2	371	087	508	319	-267	-642	101	-039	-001	020
R1	248	-627	-116	-017	-138	-057	-600	-375	-093	-038
%	63.0	10.1	7.7	4.8	3.4	3.2	2.3	2.2	1.8	1.4

?: percent of total variability

approximately equivalent to total ridge count (TRC). The next four components, PC2 through PC5, can be interpreted as contrasts of diversity among the digits of each hand. Major loadings appear to favor the following interpretation:

PC2: D1 vs D2 to D5 PC3: D2 vs D4 and D5
PC4: D3 vs D2 and D5 PC5: D4 vs D3 and D5

The remaining components, PC6 through PC10, are evidently bilateral contrasts, primarily of a single digit for each component. Using only the highest loadings, the following interpretation appears appropriate:

PC6: R2 vs L2 PC7: R1 vs L1
PC8: R3 vs L3 PC9: R4 vs L4
PC10: R5 vs L5

Although other interpretations can be made, the one proffered here

seems to be the most concordant with the signs and loadings of the eigenvector coefficients.

2.5 Group Principal Component Scores

Albrecht (1980) has pointed out that some multivariate analysis techniques are useful not only for their inferential aspects but also for their efficient descriptive features. It is this latter feature which renders principal components analysis of use in describing the biological variability among the various European groups. The descriptive group scores, sometimes called synthetic, artificial, or derived variables, are nothing more than the group principal component scores on each of the 10 axes of variability. To effect an expression of among-group variability in units commensurate with the pooled within-group within-sex covariance matrix, the 10 finger ridge count means for each group are first centered on zero by

$$[C_{ijk}] = [X_{ijk}] - M_k$$

where $[X]$ is the j th ridge count mean for the i th group of the k th sex, and M is a scalar representing the grand mean of ridge count means for the k th sex which is used against each element of the $[X]$ argument. After centering, a principal component score Y can be provided for each i th group, k th sex, on each component by

$$[Y_{ijk}] = [C_{ijk}] * [EV] * [L_j]^{-1/2}$$

where $[EV]$ is the matrix of eigenvectors extracted from the

covariance matrix, and $[L]$ is the diagonal matrix of eigenvalues for the j eigenvectors.

Each of the resultant matrices, one for the male groups and one for the females, can be visualized as 10 mutually-orthogonal vectors of equal length, with each of the 47 female or 48 male groups projected on each vector. The difference between the scores of two groups on a particular component can be thought of as a between-group distance; the squared difference between two group scores, summed on all 10 components, is a typical Mahalanobis distance measure. Tables 2-8 and 2-9 present the group principal component scores for males and females, respectively.

The principal component scores comprise the transformed data base which is used throughout the remainder of this study. The group scores are considered as an expression of the biological among-group variability for the major population of Europe. Discovering the way in which the biological variability of the population is aligned with the variability defined by geography and language is the object of this analysis. The next section demonstrates how these comparisons are carried out, and presents the results of the analysis.

TABLE 2-8

MALE GROUPS PRINCIPAL COMPONENT SCORES (X 1000)

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
EST1	090	-180	-192	-128	-231	005	-066	-060	029	086
EST2	036	-105	-055	-077	-219	-017	-123	-241	-006	120
BYL	112	184	048	-028	208	-170	162	292	059	-153
BUL	081	-035	047	095	-117	043	023	-008	015	025
POL	105	124	374	-046	-092	-591	-149	235	-182	-054
GRK1	-035	-182	054	-012	-019	-012	140	051	-052	215
GRK2	045	-141	331	-026	013	-184	035	077	-154	-018
GRK3	-086	-343	311	-047	-219	-093	055	418	-040	-046
LIT	180	-295	-132	-290	013	142	-165	-174	184	-081
CZK1	177	-195	-023	-233	-032	-045	101	-074	-011	-087
CZK2	041	044	-031	-238	-007	015	171	031	004	-285
YUG1	201	260	283	-045	-069	-272	082	-009	111	-270
YUG2	-204	546	357	251	083	061	194	039	-014	126
AUS1	-030	-001	001	-120	-026	008	088	023	-054	-075
AUS2	170	-064	-059	-010	-067	061	-008	043	059	-003
AUS3	047	-088	-060	087	-048	016	-083	-037	-106	001
HUN1	045	206	044	042	-125	-043	286	-001	050	-138
HUN2	-059	096	-055	-010	-104	-062	011	-050	-085	001
HUN3	034	-007	085	001	-043	200	056	140	-241	058
HUN4	-155	-018	-212	091	-087	030	-101	287	132	192
HUN5	-021	259	139	129	266	-142	103	-105	112	-015
HUN6	-086	-023	-206	-219	-091	013	131	048	-096	-088
IYL	022	-256	047	020	147	-078	108	135	-107	023
DAN	-144	081	-144	-039	-015	-017	-085	-051	-039	-086
GER1	084	-074	-034	-041	-045	050	-003	080	-015	-008
GER2	051	061	-188	071	-126	171	-040	-021	003	-041
DUT	-225	-083	-194	073	-031	090	064	011	160	087
BEL1	-039	-080	-095	-049	138	210	-141	-136	-083	028
BEL2	017	109	-052	082	-001	154	-166	-149	004	-083
BEL3	-060	-048	-056	-104	173	168	-096	-149	-069	-005
BEL4	-141	-153	-144	092	044	-314	130	012	174	-189
BEL5	125	-167	-025	-133	088	-171	-017	003	055	116
ENG1	016	004	059	049	137	094	-132	-013	048	087
ENG2	145	-144	-233	137	092	041	088	-037	-076	-126
WAL	060	-033	-170	158	081	008	074	027	-066	-081
BAS1	-138	451	034	-049	161	287	-194	-017	200	120
BAS2	086	-217	015	124	176	161	-145	-196	009	-010
BAS3	-018	210	-172	328	116	-160	-202	-107	021	091
BAS4	-257	201	-092	158	087	010	060	-075	070	184
ESP	-354	031	-015	-206	-275	372	000	-129	225	234
FAR	-405	-151	-007	036	-121	051	-187	-077	-026	072
SPN1	076	-069	-010	-026	106	001	-038	017	-028	042
SPN2	024	-045	049	032	052	-232	-072	-001	-001	023
POR1	105	248	075	032	-073	-030	017	-070	-034	-015
POR2	127	267	076	162	041	-084	-239	040	-404	-018
POR3	-032	-114	-070	074	030	168	-058	-012	005	-084
CAN1	147	-045	271	013	121	028	156	045	120	159
CAN2	037	-026	027	031	-089	059	174	-053	144	-030

TABLE 2-9

FEMALE GROUPS PRINCIPAL COMPONENT SCORES (X 1000)

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
EST1	154	-064	-176	-130	-273	055	-122	-031	038	083
EST2	131	-099	-190	-118	-245	160	-192	024	-010	024
BYL	197	260	272	104	434	-190	172	105	109	063
BUL	110	048	062	-081	-070	015	-007	037	002	-033
POL	107	241	126	043	-058	100	-088	003	008	026
GRK1	070	-105	166	047	-012	174	226	022	-078	-191
GRK2	096	-100	024	-163	042	089	-028	-099	093	-040
GRK3	-075	-044	174	-006	135	-117	089	-017	-057	-057
LIT	197	-117	-133	-051	-086	030	-068	014	100	-059
CZK1	016	143	026	-140	015	-007	-129	193	-002	-231
CZK2	063	-003	-018	-086	-167	015	370	-165	-334	-225
YUG1	082	-077	-029	-181	126	-017	162	078	318	192
YUG2	208	017	204	056	015	055	104	-082	022	-189
AUS1	-038	-055	068	-075	-070	009	096	-016	-040	-042
AUS2	101	029	-068	-044	037	024	-013	-021	-039	-071
HUN1	056	-154	-123	-155	-137	-049	-036	117	-041	099
HUN2	-016	078	-103	-007	-057	081	-015	166	-177	037
HUN3	088	069	-083	-133	-124	-006	-004	006	-145	008
HUN4	-033	174	-094	070	-144	-051	038	069	013	227
HUN5	104	215	042	-090	259	060	176	029	216	114
HUN6	-170	122	-033	-027	-094	048	190	-034	044	-034
IYL	-036	-115	305	-029	181	-029	070	-115	-170	-073
DAN	-148	169	-137	023	-001	-066	-119	-030	001	048
GER1	019	045	-177	-179	-043	186	031	056	-018	-107
GER2	115	-036	146	010	-103	-070	087	-068	-016	015
DUT	-132	028	-001	050	-072	008	-060	151	020	-032
BEL1	-162	-150	090	-112	176	-114	-214	081	153	102
BEL2	-081	-123	-133	055	006	002	-106	-029	-005	088
BEL3	-229	-075	074	-048	088	030	-156	075	061	058
BEL4	-050	-153	-208	-089	099	-057	-040	-300	084	-059
BEL5	-019	-066	-071	127	172	107	300	091	-016	-050
ENG1	005	153	054	071	-122	-153	-071	-051	-014	040
ENG2	108	-022	-203	139	064	-032	020	-056	-100	-148
WAL	060	041	-163	191	090	-061	051	063	-003	-057
BAS1	-452	-197	317	208	482	-191	141	-179	004	567
BAS2	133	-028	-106	358	-160	053	-340	000	251	-036
BAS3	-059	049	-061	-115	088	-161	-091	142	-004	-059
BAS4	-290	016	-026	071	088	-031	021	179	202	118
ESP	-301	084	041	-218	113	189	-174	039	224	081
FAR	-500	-132	-028	-045	-030	029	-098	-149	-057	107
SPN1	052	007	008	030	-002	-049	-046	-065	-121	017
SPN2	-061	016	055	020	-014	-027	-062	073	-046	019
POR1	077	-122	121	-203	-176	214	130	-067	-141	-244
POR2	317	168	-059	154	-090	027	-035	-006	-211	104
POR3	-094	-195	026	212	099	123	-119	-106	020	-027
CAN1	368	065	209	279	010	-016	158	094	-052	134
CAN2	-088	-005	-191	208	-470	-421	-200	-219	-088	-306

3.0 METHODS AND RESULTS

3.1 Introduction

For each European group, the data input to the analysis consist of a vector of 10 principal component scores, latitude and longitude, and the language of each group. (This study considers the sexes separately and two analyses are conducted in parallel; the term "group" should be understood as a dichotomous referent). Differences in the group scores can be thought of as defining inter-group distances on 10 different biological axes. In the analysis, these axes are compared, one by one, to axes of geographic and lingual inter-group separation. Geographic inter-group separation, including both direction and distance components, is established on the basis of latitude and longitude. Inter-group distances with respect to language here are defined binarily.

The comparison of biological with geographic axes involves the use of two analytical tools, multiple regression analysis and spatial autocorrelation. Only the latter is employed in the language analysis. Although the techniques are similar, they differ in the specificity of the results they produce, multiple regression analysis operating at a higher level of generality than spatial autocorrelation. The discussion of these two analytical techniques in this section relies heavily upon Jantz's (1974) discussion of multivariate analysis in dermatoglyphic problems, Albrecht's (1980) demonstration of principal components, and an explication of spatial autocorrelation by Sokal and Oden (1978).

3.2 Multiple Regression Analysis

Multiple regression analysis provides a general view of how inter-group distances on biological axes compare to group separation in space. The technique operates on generalized geographic separation of groups; a two-dimensional plane where direction and distance among groups are confounded. Theoretically, the technique requires that the group principal component scores employed in this study be normally-distributed, however, with biological data, this requirement is almost never met, and is often disregarded with impunity. In this study, regression analysis is complemented by spatial autocorrelation, which uses the distance and direction components of spatial separation, and is not reliant upon an assumption of normally-distributed group principal component scores. Thus, the two techniques together provide a hierarchy of spatial analysis, and also direct attention to any aberrations which might result from violation of the normality assumption.

3.2.1 Definition of the regression plane. The definition of the regression plane is not as easily established as might be thought. Because of the earth's shape, there is a functional relationship between latitude and longitude coordinates. The east-west distance between two meridians of longitude decreases as latitude increases. The use of raw longitude coordinates to define one dimension of the regression plane is somewhat misleading, unless the systematic scale change on the regression surface is inherently recognized. The

problem largely can be alleviated by transforming the longitude of each group to a number which is the product of the raw longitude and the cosine of the latitude for the particular group. The transformed longitude values thus decrease as group latitude increases; and the transformation effectively rescales one dimension of the regression plane. The rescaled dimension more closely reflects the actual east-west distances among groups. The plane arbitrarily is defined such that an increase in latitude and longitude values represent an increase in distance to the north and west.

A second problem arises because the locations of population centers, thus sample areas, tend to be somewhat correlated ($r=.35$). The impact of this phenomenon on regression analysis is that it makes no sense to regard the two dimensions of the regression surface as separable independent geographic components. Statistically, the impact is that no unique among-group sum of squares can be assigned to the effect of either latitude or longitude alone; however, the magnitude and direction of the regression slopes remain meaningful predictive values with respect to both dimensions of the regression plane. This correlation of dimensions, or multicollinearity, and its stricture on the choice of analytical technique is intuitively obvious, and is why multiple regression is used in the first place.

3.2.2 Multiple regression model. The equation for the multiple regression model is the linear regression equation

$$Y_{ijk} = b_{0jk} + b_{1jk}(X_{1i}) + b_{2jk}(X_{2i}) + e_{ijk}$$

where the fitted principal component score Y of the i th group and k th sex on the j th component is calculated by the estimated regression coefficients b_0 , b_1 , and b_2 of the k th sex on the j th component, the latitude X_1 and transformed longitude X_2 of the i th group, and the residual error e . The intercept term b_0 has no meaning in the model. The model uses the least squares method to estimate the regression coefficients. It is employed in a series of discovery comparisons. Each vector of among-group biological variability, defined by the group principal component scores, is regressed on the geographic plane defined by the latitude and transformed longitude of each group.

3.2.3 Results of multiple regression analysis. Results of the multiple regression analysis indicates that the total among-group biological variability for both sexes explained by the geographic model is 19.2 percent. Table 3-1 below shows how this explainable variability is apportioned among the components and between the sexes. It might be expected that total ridge count variability, i.e. the first principal component, would be the most meaningfully patterned vector of biological among-group variability with respect to geography. Such is not the case, as is indicated in Table 3-1. The table also shows the signs of the regression slopes for components which exhibit significant association with geography in both dimensions of the regression plane below the .10 error level, and the signs for slopes which are significant at .05 or below.

In general it is notable that the geographic regression model tends to explain somewhat more variability among male groups than it does among the females. The sexes exhibit geographic patterning on

TABLE 3-1
REGRESSION RESULTS OF
PRINCIPAL COMPONENTS VS GEOGRAPHY

	MALES				FEMALES			
	F	p>F	RSQ	Slope lat lon	F	p>F	RSQ	Slope lat lon
PC1	.67	.52	.03		2.53	.09	.10	- -
PC2	.75	.48	.03		.53	.59	.02	
PC3	11.62	.0001	.34	- -	4.07	.02	.16	-
PC4	3.54	.04	.14	+	7.56	.002	.26	+
PC5	2.60	.09	.10		.13	.88	.00	
PC6	1.48	.24	.06		1.55	.22	.07	
PC7	4.33	.02	.16	- -	2.38	.10	.10	- -
PC8	5.98	.005	.21	- -	.89	.42	.04	
PC9	.38	.68	.02		.39	.68	.02	
PC10	.87	.42	.04		.37	.69	.02	

about the same components. PC1 in females is significant only at the .10 level, but in both dimensions of the regression plane. The male groups show no patterning on this component. PC8 in males is significant but not so in females. The directions of the regression slopes are the same for both sexes. The actual value of each slope is not particularly relevant in this analysis, however these are presented in Appendix B, Tables B-1 through B-10 along with complete analysis of variance tables. The residual plots for all principal components are shown in Figures B-1 through B-20.

The regression results must mean that the contrasts of diversity and asymmetry, as reflected by group means, are patterned with respect to geography. By referring to one, the sign of the regression slopes in Table 3-1; two, the definition of the regression plane; three, the Table 2-7 signs of the coefficients in the eigenvector matrix; and four, to the biological interpretation of the significantly-patterned principal components, the contrasts of diversity and asymmetry can be interpreted with regard to what is happening, spatially, to mean finger ridge counts.

To illustrate, the geographic plane is defined such that values of latitude and longitude increase to the north and west, and the male PC3 regression slopes are negative. This indicates a decrease in the contrast of digit two with digit four/digit five to the north and west. Since in the eigenvector matrix the values are negative on the coefficients for digits four and five and positive on digit two, there must be a relative decrease in ridge counts on digit two and a comparative increase on digits four and five to the north and west.

Table 3-2 shows the directions of relative ridge count increase for the significant principal components, and presents the quadrant of highest contrast. The table can be interpreted by first noting the quadrant of highest contrast, and then following the direction of relative ridge count increase for the digits on each component.

For example, the average finger pattern size in females is weakly associated with geography, with total ridge count generally

increasing to the south and east. Male groups are significantly geographically patterned on PC3, and exhibit a relative increase in ridge count means to the north and west on digits four and five and

TABLE 3-2

DIRECTION OF MEAN RIDGE COUNT
INCREASE ON GEOGRAPHICALLY
PATTERNED COMPONENTS

	L5	L4	L3	L2	L1	R5	R4	R3	R2	R1	HIGH
*PC1	SE	SE	SE	SE	SE	SE	SE	SE	SE	SE	SE
PC3	NW	NW		SE		NW	NW		SE		SE
PC4	W		E	W		W		E	W		W
PC7					SE					NW	SE
**PC8			NW					SE			SE

*females only

**males only

corresponding decrease on digit two. The most significantly patterned component in females, PC4, indicates that mean ridge counts tend to increase to the west on digits four and five relative to a decrease on digit three. The highly significant PC8 in males shows an increase of mean ridge count on digit three of the left hand to the north and west and a concomitant decrease on the right. Thus, the expectation is that male groups in the south and east would be marked by a low mean ridge count on the left middle finger and a correspondingly high mean count on the right, while north and

west groups would have about the same number of counts on the middle fingers of each hand.

Following the same procedure, the remainder of the geographically-patterned components can be interpreted with respect to the change in relative numbers of ridges on the digits.

Bivariate plots of the principal components which are significantly patterned geographically should provide a visual indication of whatever tendency there is for groups to cluster on biological axes, which then can be compared to geographic axes. Figures 3-1 through 3-5 are bivariate plots of those components which indicate significant patterning with respect to geography at or below the .05 probability level. In all the bivariate plots, groups geographically situated in the south and east tend to be located to the top and right of the bivariate space, groups from the north and west tend to be placed to the bottom and left, while centrally-located groups tend to plot between the two extremes.

Figure 3-1 is a plot of the two most significant components in males, PC3 and PC8. It is evident that the plot must be studied to discern the pattern described above. The more obvious pattern is a central dispersion in the bivariate space, plus a number of outlying groups. Three of the Belgian groups do tend to be tightly clustered, and other western groups such as BAS and ESP are fairly close to the Belgians. However, the overwhelming tendency is for a more or less homogeneous dispersion of all groups, the geographic patterning of which is evident only through scrutiny of the plot. Figure 3-2 shows

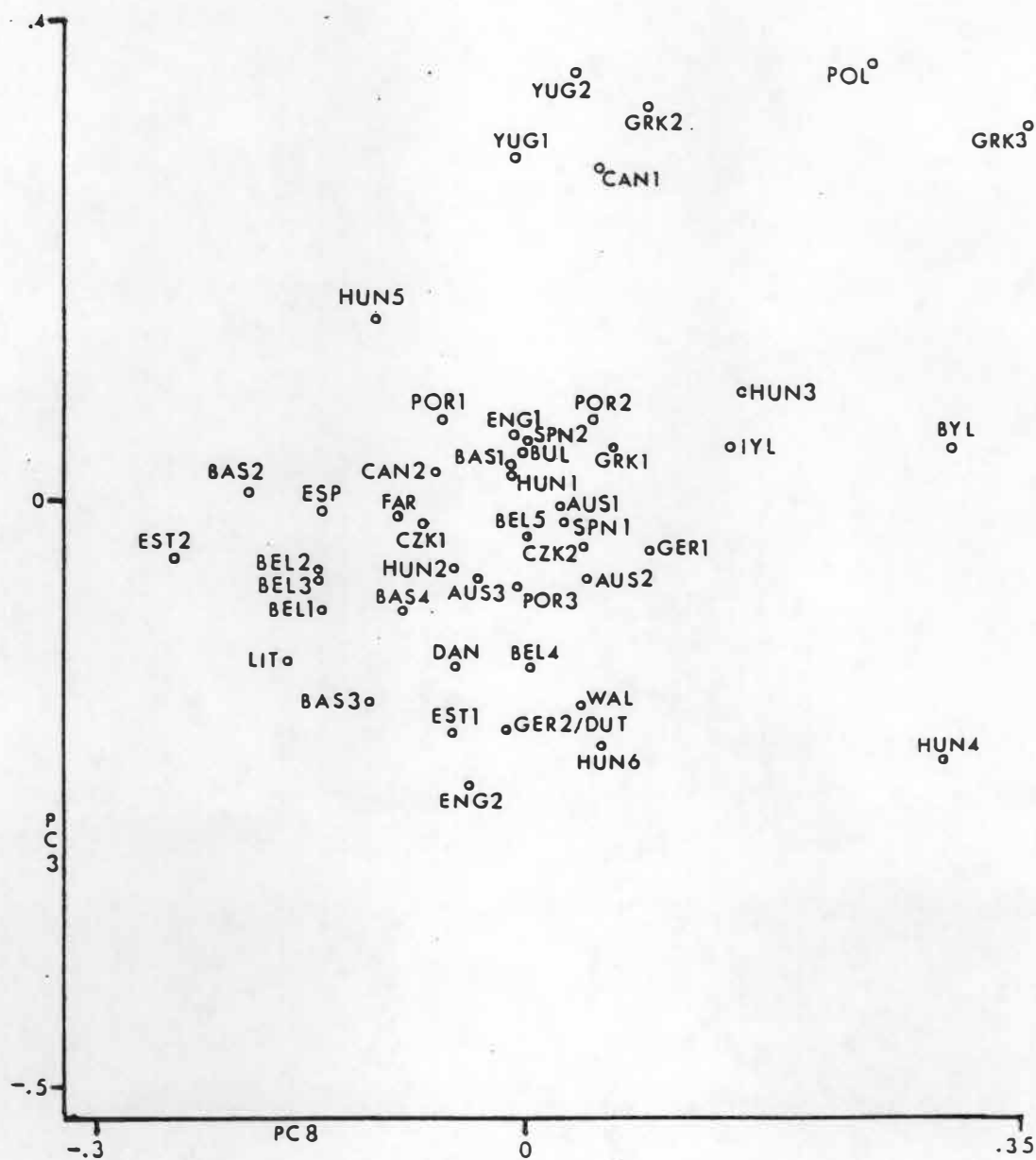


Figure 3-1. Bivariate plot of male groups on PC8 (X-axis) and PC3 (Y-axis).

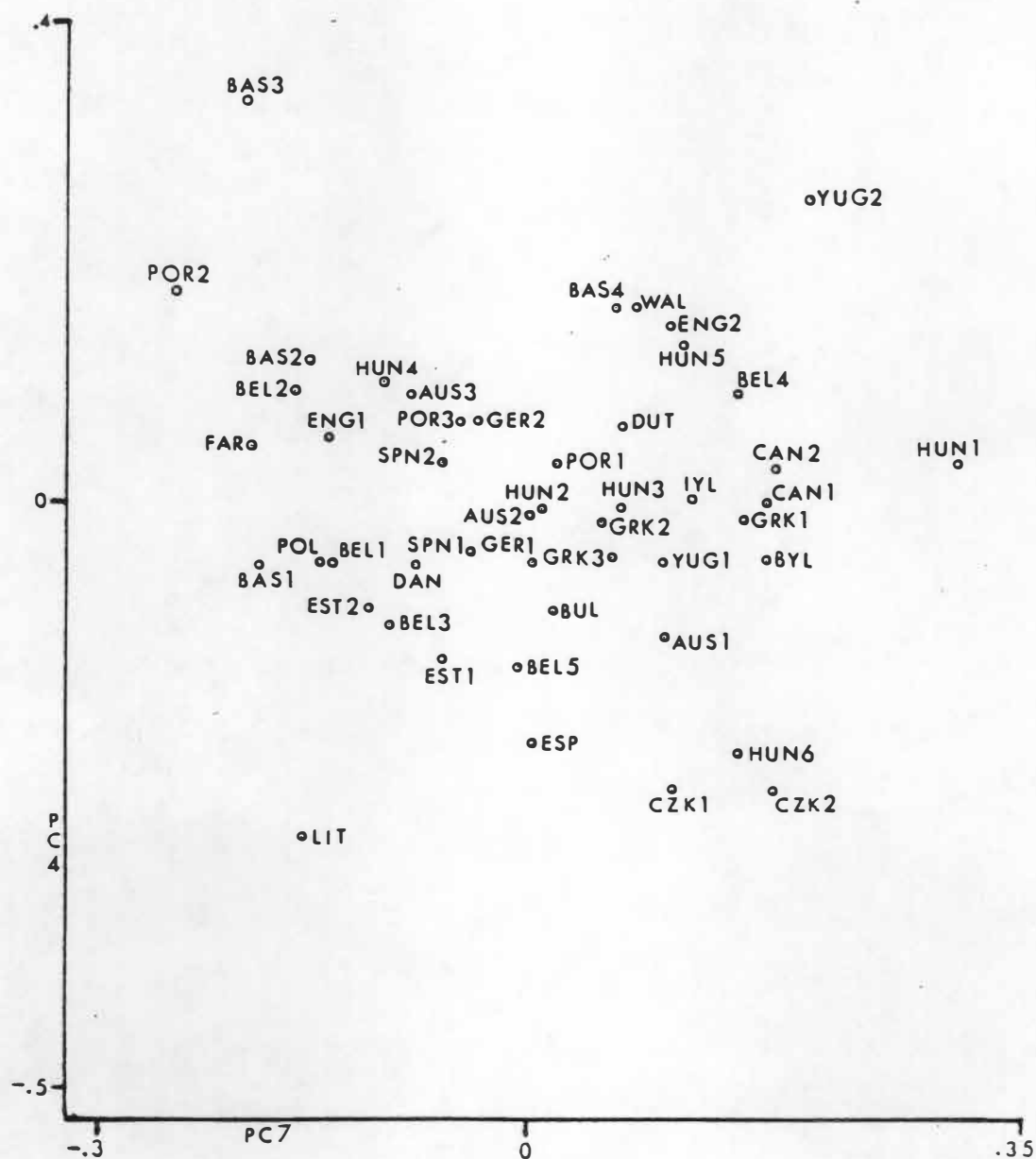


Figure 3-2. Bivariate plot of male groups on PC7 (X-axis) and PC4 (Y-axis).

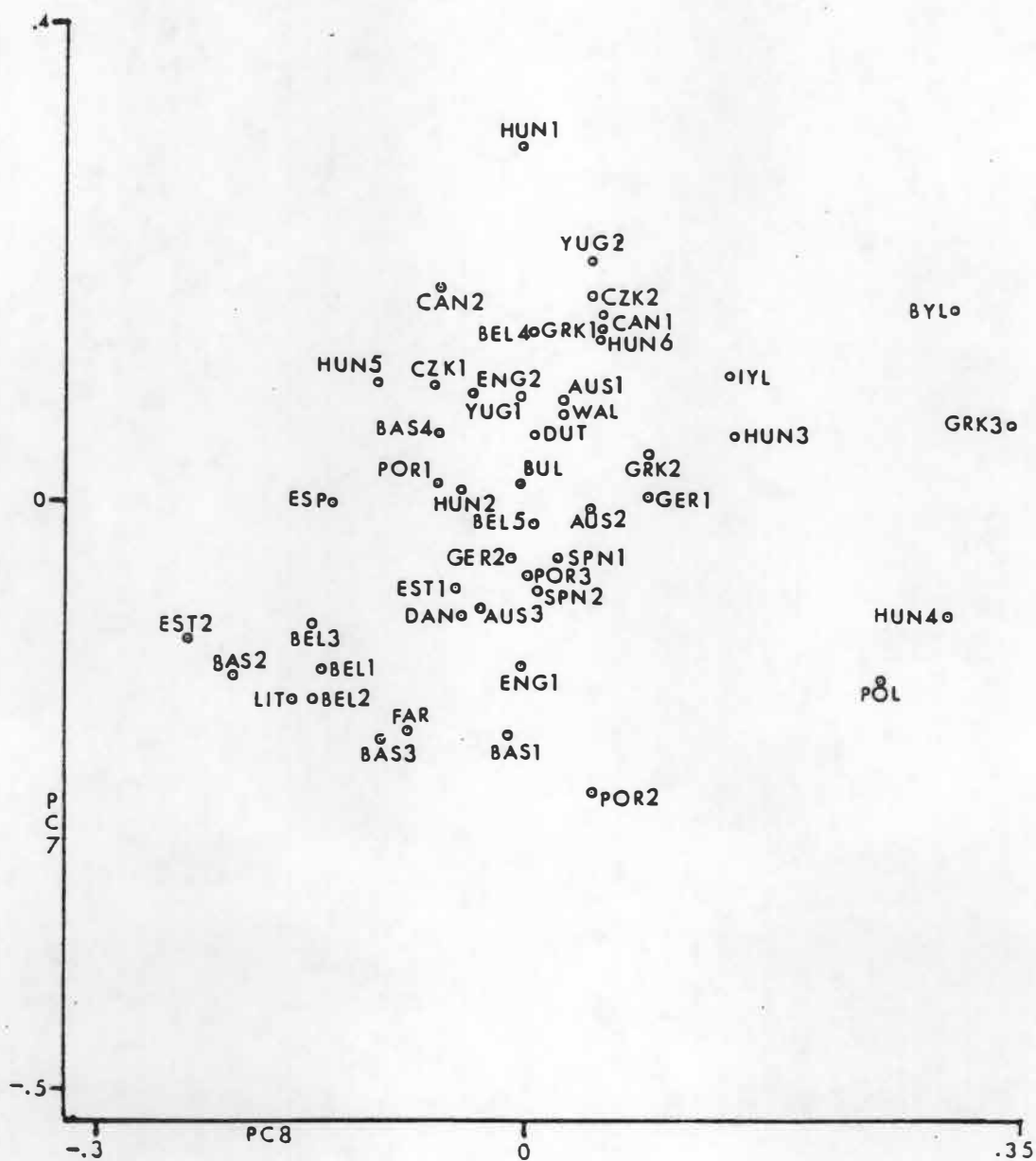


Figure 3-3. Bivariate plot of male groups on components of asymmetry, PC8 (X-axis) and PC7 (Y-axis).

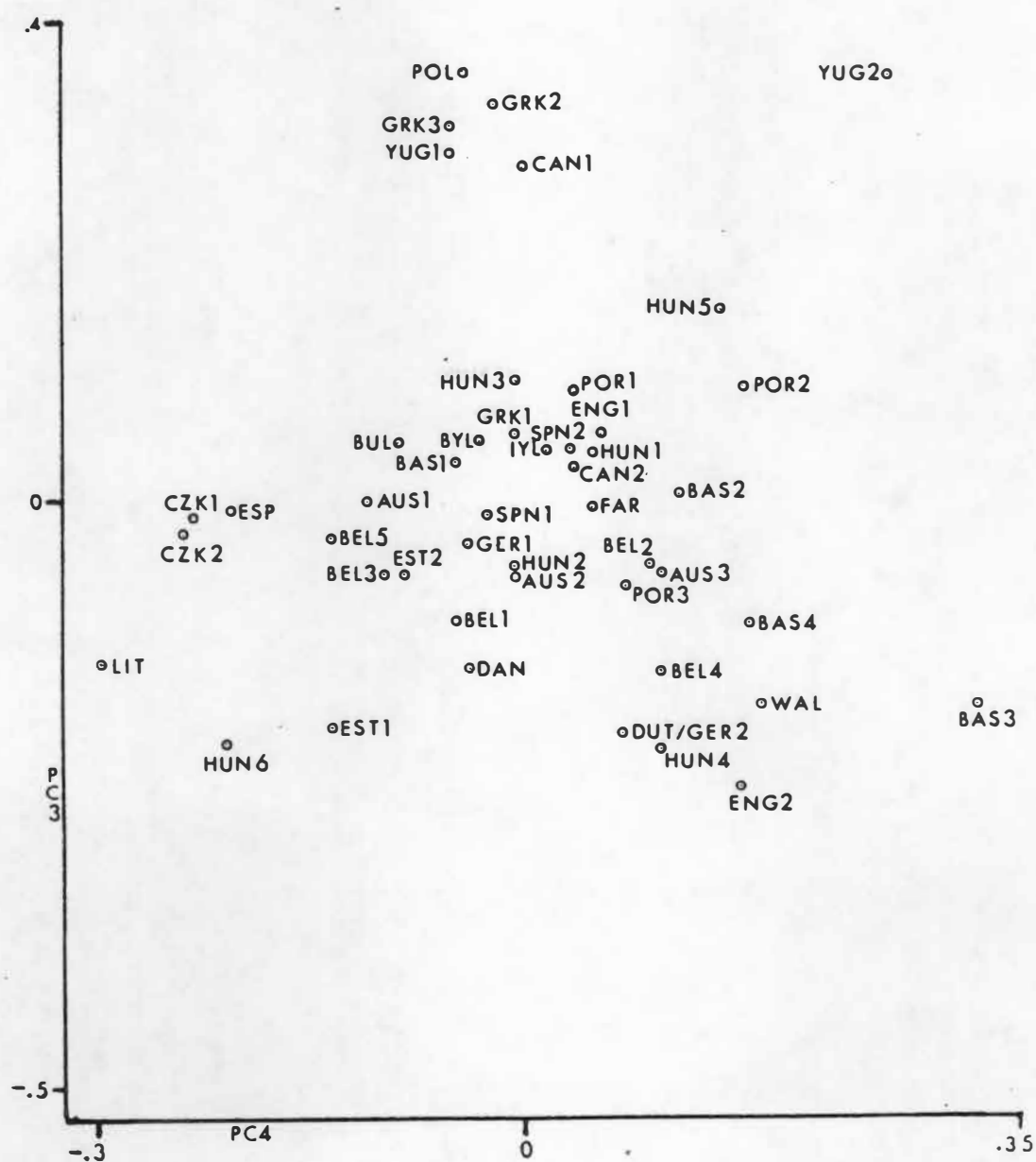


Figure 3-4. Bivariate plot of male groups on components of diversity, PC4 (X-axis) and PC3 (Y-axis).

the other two significantly-patterned components in males. Again, visual indication of group clustering is not obvious, but geographic patterning is discernible.

Figures 3-3 and 3-4 represent an attempt to discover group clustering with respect to components of diversity and asymmetry, respectively. Figure 3-3 is a bivariate plot of PC3 and PC4, and Figure 3-4 that of PC7 and PC8 for males. There is no obvious clustering of groups in either figure. Like the foregoing plots, there is a general tendency for similarly-located groups to score similarly, but there are many exceptional groups.

In looking at the female components PC3 and PC4, shown plotted in Figure 3-5, there seems to be a tendency for female groups to exhibit somewhat more homogeneity around the center of the bivariate space, although this tendency is not marked. As in the males, no group clustering is apparent, but geographic association can be discerned.

The impression gained from examining the various bivariate plots is that both male and female groups tend to be separated concordantly on both biological and geographic axes. The tendency is by no means marked, but neither do only a few groups dominate the conservative association between geography and biology. This trend can be further explored by analytical techniques which are capable of dissecting the geographic plane into distance and direction components and examining the relationship between biological group separation and spatial separation on the components of the geographic plane. Spatial autocorrelation is such a technique.

3.3 Spatial Autocorrelation

Spatial autocorrelation is somewhat akin to regression analysis in that the technique tests whether or not the value of an observation at a particular location is independent of the values at other locations. As in regression analysis, "location" can be defined spatially or temporally or with regard to some other criterion. However, regression analysis is usually employed to discover the general trend of supposedly normally-distributed observations relative to some systematically-changing independent variables. Thus, in this study, a geographic plane surface is defined, and the biological vectors of sample means are fitted to it. In spatial autocorrelation, a surface of biological variability is generated relative to components of geography which are supplied by the investigator. The surface is generated by calculating autocorrelation coefficients. These are values which represent the extent of biological correlation among the groups which are included in the analysis. The presence or absence of a group in the analysis is dictated by what components of geography are defined by the investigator. The difference in the results of regression and autocorrelation is comparable to the difference between a technique which shows the average trend in elevation among a number of points and one which shows the actual topography among them.

3.3.1 Moran's I statistic. One statistic used to express the degree of autocorrelation among a number of points, and the only one used in this study, is Moran's I. The required data base for the

computation of I consists of a number of points with a value for each point, and a criterion for connecting the points. The criterion for connection of the points is supplied by first defining a binary adjacency matrix of order n, which in this study is 48 for males and 47 for females. Based on a particular criterion, two points either are or are not connected. For example, EST1 and HUN1 male sample locations either are or are not within a specified distance from each other. Group pairs which meet the criterion are weighted by one, other group pairs are weighted by zero.

In this study, the principal component score of each group on a particular component serves as the value for each point. Since each point is represented by a vector of 10 principal component scores, 10 I-values can be generated for each criterion supplied by the investigator.

The I statistic for the jth principal component of biological among-group variability is calculated by

$$I_j = n_j (\sum_{l,m} (z_{jl} \times z_{jm})) / W (z_j^2)$$

where n is the number of groups on the jth component, w is the binary score, either one or zero, for the sample pair l and m, z is the principal component score for group l and group m on the jth principal component, W is the number of connections, or sum of ones, of all of the pairs, and z_j^2 is the sum of squares of the deviates, i.e. the sum of the squared principal component scores of the n groups on the jth component. In the absence of

autocorrelation, the expected value of I_j is $-1 / (n_j - 1)$. Calculated and expected I -values are equal when each group is connected with all other groups. In such a case $W = n(n-1)$, the absolute values of the weighted sum of products $\sum w_{lm} (z_{jl} \times z_{jm})$ and the sum of squares $\sum z_j^2$ are equal, and the equation reduces to $I_j = -n_j / (n_j(n_j - 1))$. If none of the groups are connected, $I_j = 0$. The expected I_j value approaches zero with increasing n_j values.

In addition to a more detailed description of the techniques discussed above, Sokal and Oden's (1978) work contains a comprehensive explication of all the computational algorithms required to test the significance of a particular I value, and these are not repeated here. For all practical purposes, the I value can range from -1 to $+1$ for complete negative or positive spatial autocorrelation, respectively.

3.3.2 Connectivity criteria. The connectivity of group pairs is defined by a binary adjacency matrix of order n , the diagonal elements being zero, the off-diagonal elements being either one or zero depending on whether or not a group pair is or is not connected. The adjacency matrix can be directly defined or it can be based upon one or more other matrices. For example, the distance between all group pairs can be defined by a distance matrix of order n . Distance classes can then be defined, and an adjacency matrix can be based upon the distance matrix. All elements which fall within the distance class are weighted by one, elements outside the class are weighted by zero. Thus, a number of adjacency matrices can be

generated from a single distance matrix, depending upon the number of distance classes defined. The investigator can supply a number of criteria matrices such as the distance matrix just mentioned, a direction matrix, an elevation matrix, etc. By multiplying the resultant binary adjacency matrices, a final adjacency matrix is produced which defines all group pairs which fall within the class boundaries defined by all of the criteria.

Since the adjacency matrix either can be defined directly or can be based upon other matrices, the connectivity criterion can be as arbitrary or systematic as the investigator desires. This way of defining connectivity is especially flexible. For example, a summary measure such as inter-group geographic distance can be dissected into a number of factors which reflect the geomorphic components of distance, such as uphill or downhill, interceding rivers, mountains, etc. While Sokal and Oden (1978) rightfully regard such flexibility as an asset to the experienced analyst, it can also pose a major threat to the timely completion of any study which incorporates spatial autocorrelation. For this reason, the connectivity criteria employed in this study are restricted to summary measures which are systematically defined. These are one, direction and distance between group pairs; two, Gabriel connectivity between group pairs; and three, language commonality. Each criterion is further discussed below.

3.3.2.1 Direction and distance between group pairs. To render this study comparable to that conducted by Sokal and Menozzi (1982), who used allele frequencies at the HLA loci of various European groups to define biological vectors of variability, the four direction classes used here are identical to the ones the authors used. These are North, Northeast, West, and Northwest. In this study--but not mentioned in the HLA study--each class is 45 degrees wide, i.e. 22 degrees 30 minutes on either side of the cardinal or intercardinal directions. The result is four mutually-exclusive collectively-exhaustive direction classes. The direction classes are based upon instrumentally-determined rhumbline directions between groups. The rhumbline is used for directional measure because it is easy to define and probably is the most realistic pathway of biological interaction in Europe, especially for groups separated by great distances. A great circle route, besides being continuously variable relative to True North, can involve considerable change in latitude, with consequent climatic implications. It seems probable, however, that the direction class width is sufficient to negate any effective difference between great circle and rhumbline directions except in ease of definition. The four reciprocal direction classes are not included in the adjacency matrices, resulting in the use of asymmetric matrices; however, an autocorrelation statistic calculated for one direction is identical to that calculated for the reciprocal direction. Therefore, a direction class such as North should be understood as North or South or North-South.

To determine the configuration of the biological surface, and to demonstrate monotonicity, i.e. decreasing autocorrelation with respect to distance, it is necessary to define distance classes within the direction classes. These classes are based upon the great circle distance in kilometers (km) between each pair of groups, calculated in accordance with the procedure given by Spuhler (1972). Great circle distances are used because of their easy definition and computation. Like Sokal and Menozzi (1982), distance classes of 700 km increments are used. The 700 km increment results in seven distance classes, the lowest class being <700 km, and succeeding classes being $>700 \leq 1400$ km, $>1400 \leq 2100$ km, etc., to a final distance class of $>4200 \leq 4900$ km. In most cases the higher distance classes connect too few groups for analysis, and the bulk of the analysis regards the first four to six distance classes, as is shown later. Table 3-3 shows the connected groups for each direction/distance class used in the analysis. Distance classes are identified by their upper limits throughout the remainder of this study.

3.3.2.2 Gabriel connectivity criterion. The Gabriel criterion for connectivity is based upon the distance between group pairs. This nearest-neighbor approach represents the most likely interaction pathway among groups not otherwise isolated, hence the most likely pattern of gene flow which is not induced to flow alternatively (Gabriel and Sokal 1969). Defined mathematically with regard to the Gabriel criterion, two groups are connected if the square of the

distance between them is less than the square of the distance between either group and any third group. To illustrate, EST1 and HUN1 males are connected if $(\text{EST1 to HUN1})^2 < (\text{EST1 to X})^2 + (\text{HUN1 to X})^2$, where X is any one of the 46 remaining male groups. Figure 3-6 provides a map view of Gabriel connectivity for all of the 48 male groups. No females are included in the AUS3 sample. Otherwise a map view for the Gabriel connections among females is identical to Figure 3-6.

Extension of Gabriel connectivity so that all groups are connected requires the calculation of the shortest distance between each group pair not already directly connected by one straight line as shown in Figure 3-6. This distance must follow two or more of the connecting legs already established by the Gabriel criterion, and must be the shortest route through the Gabriel network. While this is a systematic definition of distance, it is difficult to program with high-level logic design; in this study, the matrix of among-group Gabriel distances (not shown) is the result of manually tracing the possible pathways through the Gabriel network and discovering the shortest route. As in the direction classes, 700 km is the distance class increment for Gabriel connectivity.

3.3.2.3 Language between group pairs. The spoken language of each group has been identified in Table 2-4. To achieve connectivity, two groups must speak the same language class as shown in the table. The use of "class" should be understood as a categorization peculiar to this study, and not a sanctioned component of language

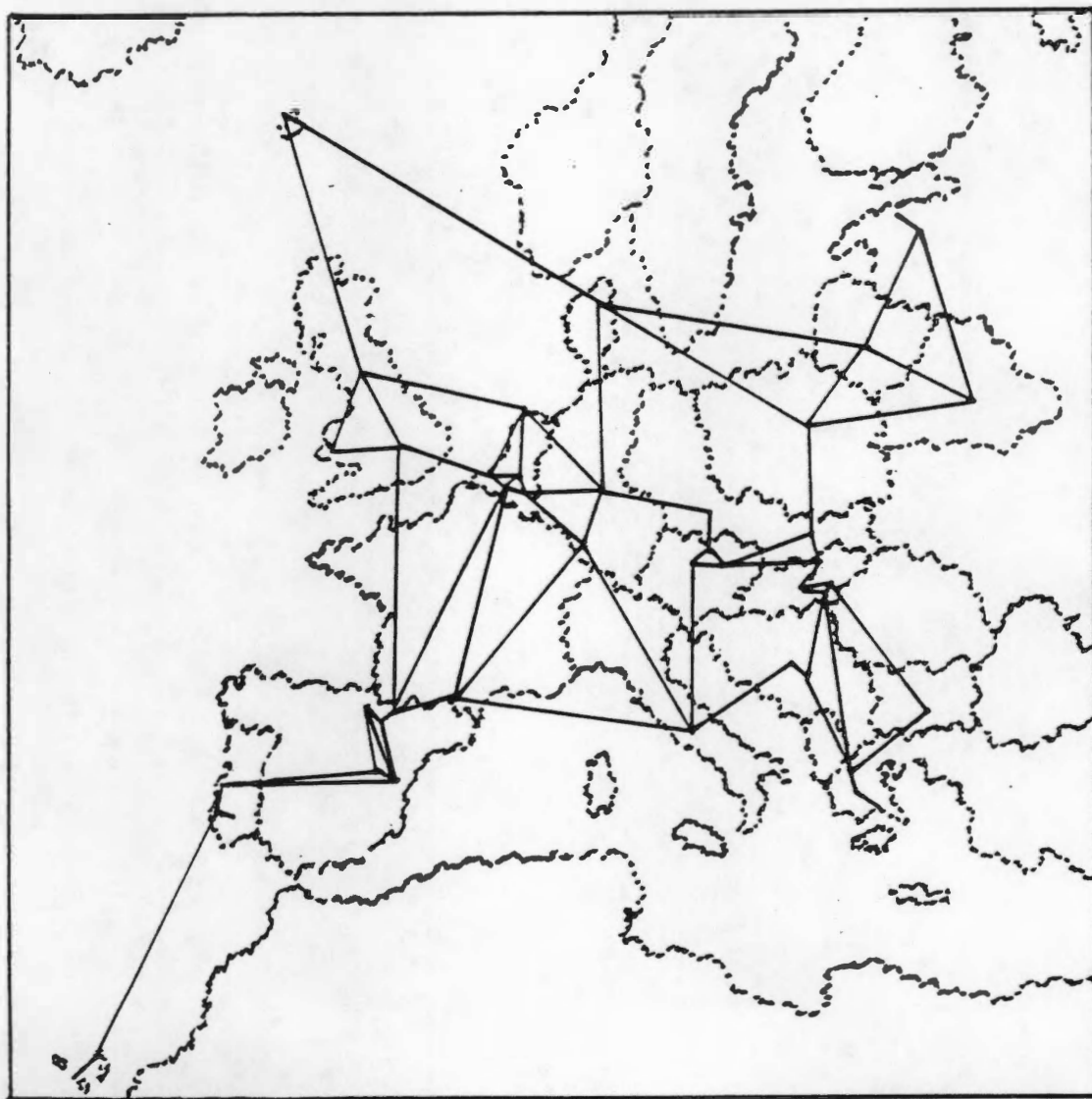


Figure 3-6. Male groups connected in accordance with the Gabriel criterion.

classification. Table 3-4 shows the groups which are connected by the language criterion.

3.3.3 Results of the geographic spatial autocorrelation analysis.

Figures 3-7 through 3-11 present the I-values and their plots for the male groups, including information for Gabriel connectivity and for the four direction classes. The expected I-value, i.e. $-1/n-1$, is constant for each sex. The I-value expected is $-.021$ for male groups and $-.022$ for the females. Figures 3-12 through 3-16 show comparable information for the female groups. It is notable from these figures that the principal components which proved to be significantly aligned with geography in the multiple regression analysis are the same ones which most often yield significant I-values in spatial autocorrelation. For Gabriel connectivity, nine of the 11 significant male I-values are on PC3, PC4, PC7, and PC8; six of the seven significant female I-values are on PC1, PC4, and PC7. In the direction classes for males, 20 of the total 29 significant I-values are on PC3, PC4, PC7, and PC8; for females, nine of 13 are on PC1, PC3, PC4, and PC7.

The plotted I-values shown in Figures 3-7 through 3-16 are not sorted with respect to the 10 principal components, as is obvious from the tabular I-values accompanying the plots. Connecting the I-values of each principal component of biological variability across the distance classes results in an I-correlogram for each direction class and for Gabriel connectivity. The I-correlogram is a graphic presentation of each surface generated by the I-values on each

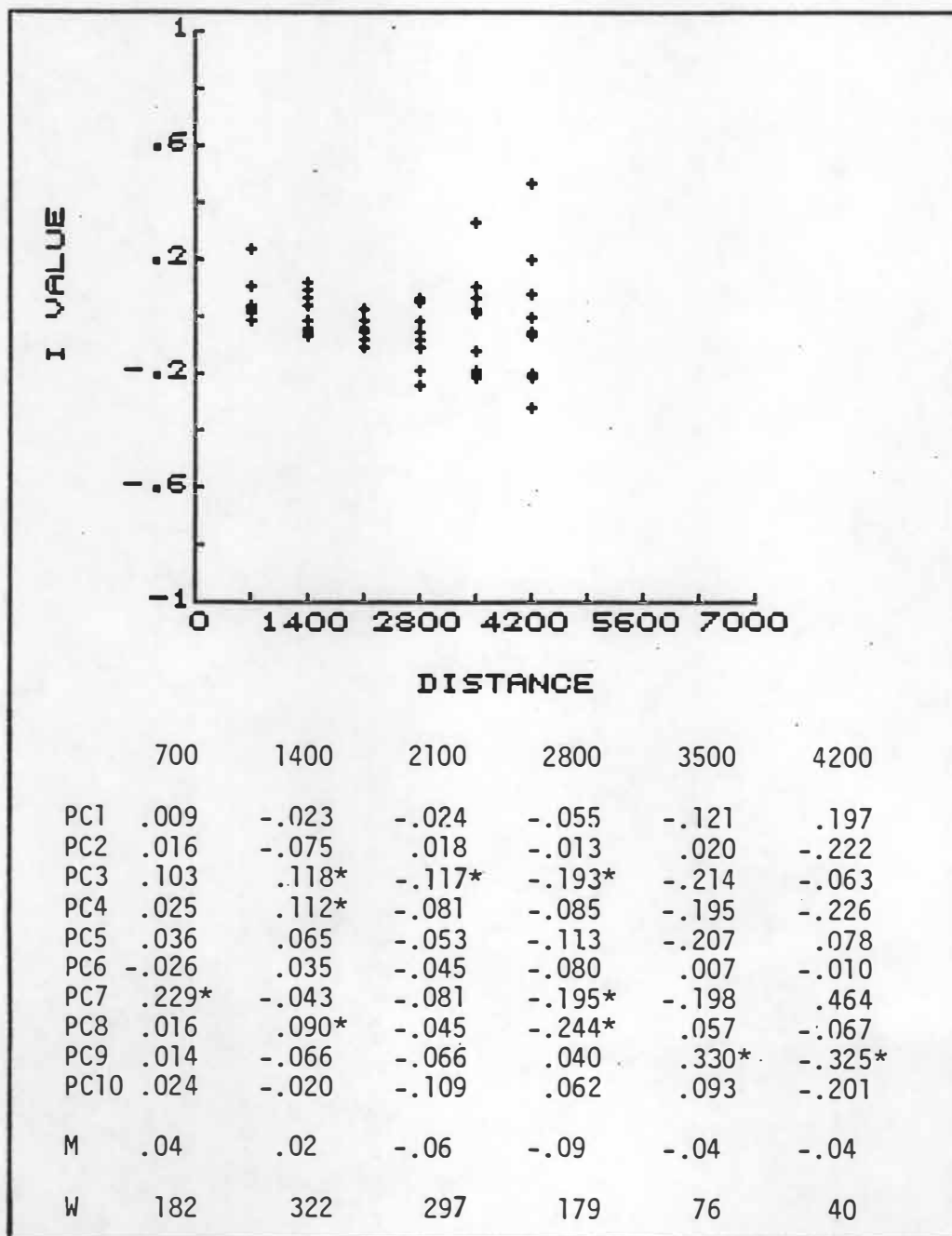


Figure 3-7. Male Gabriel I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

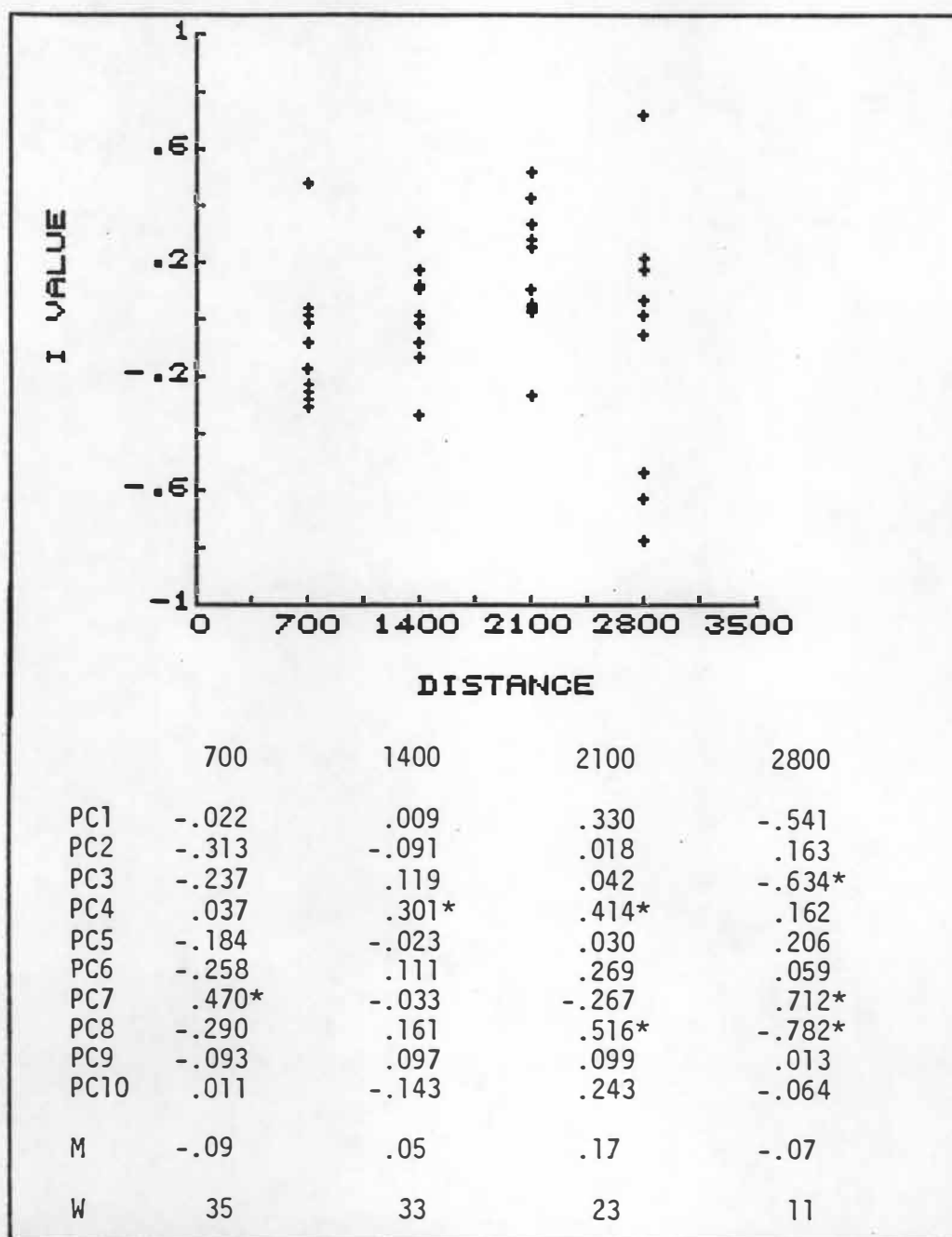


Figure 3-8. Male North I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

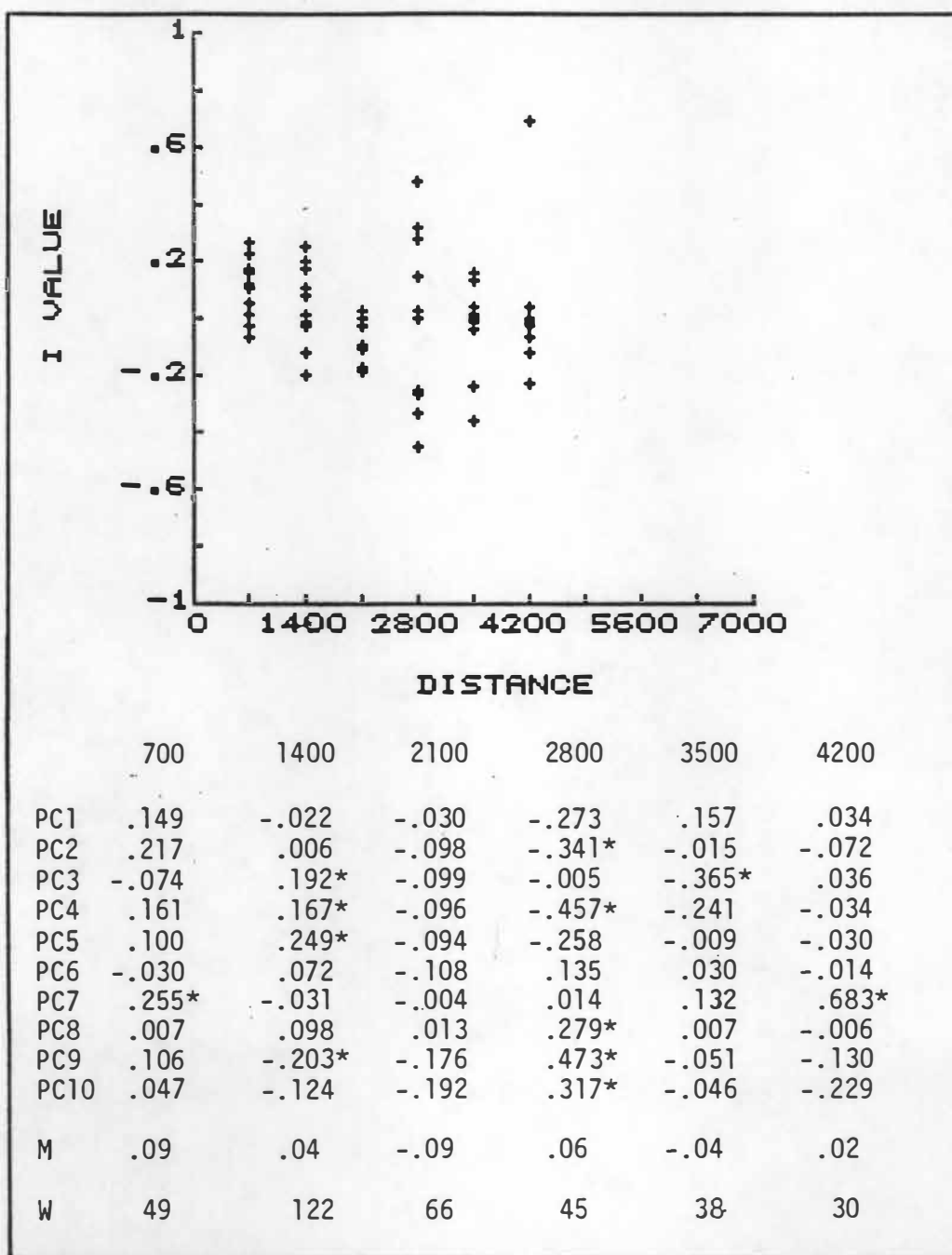


Figure 3-9. Male Northeast I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

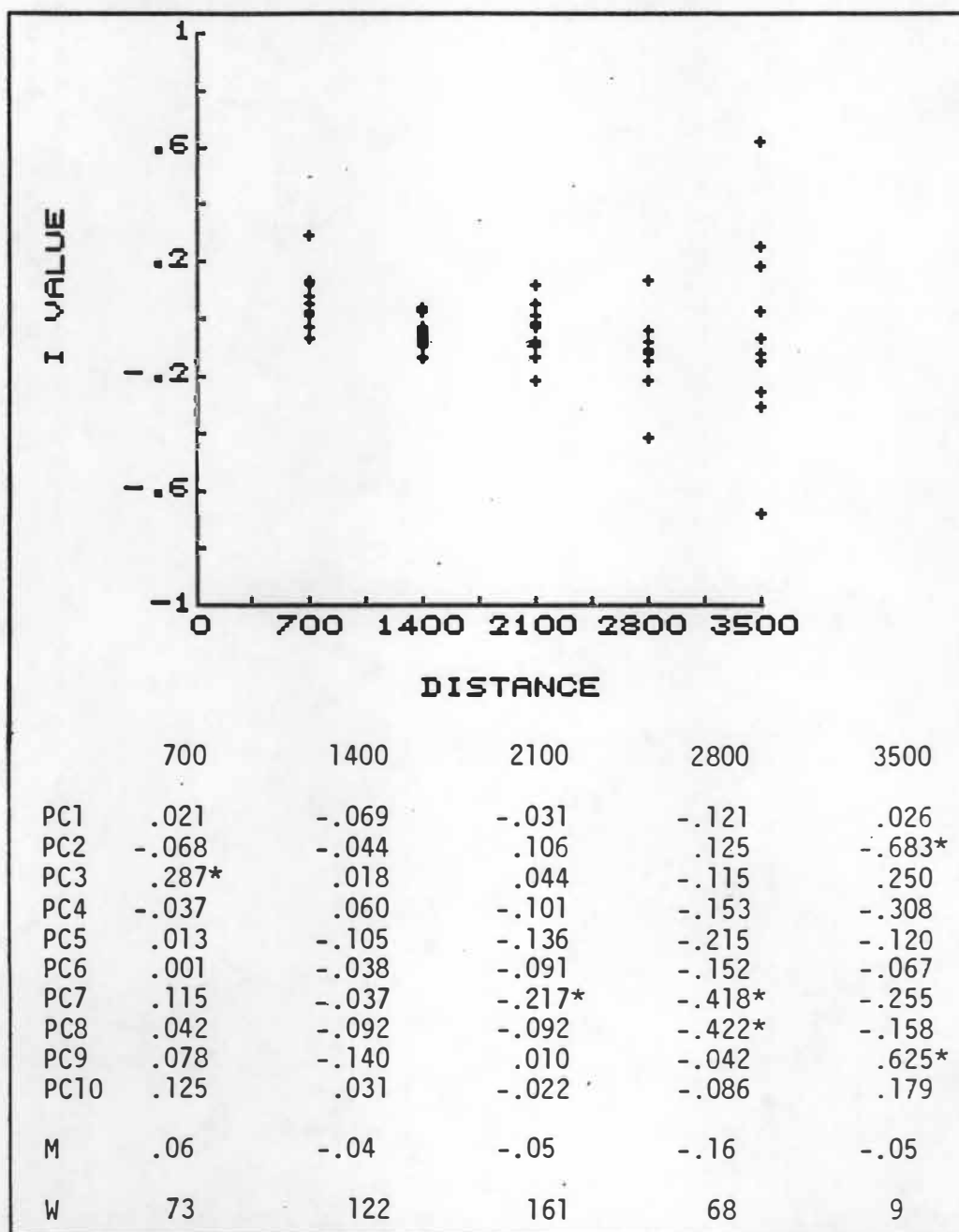


Figure 3-10. Male West I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

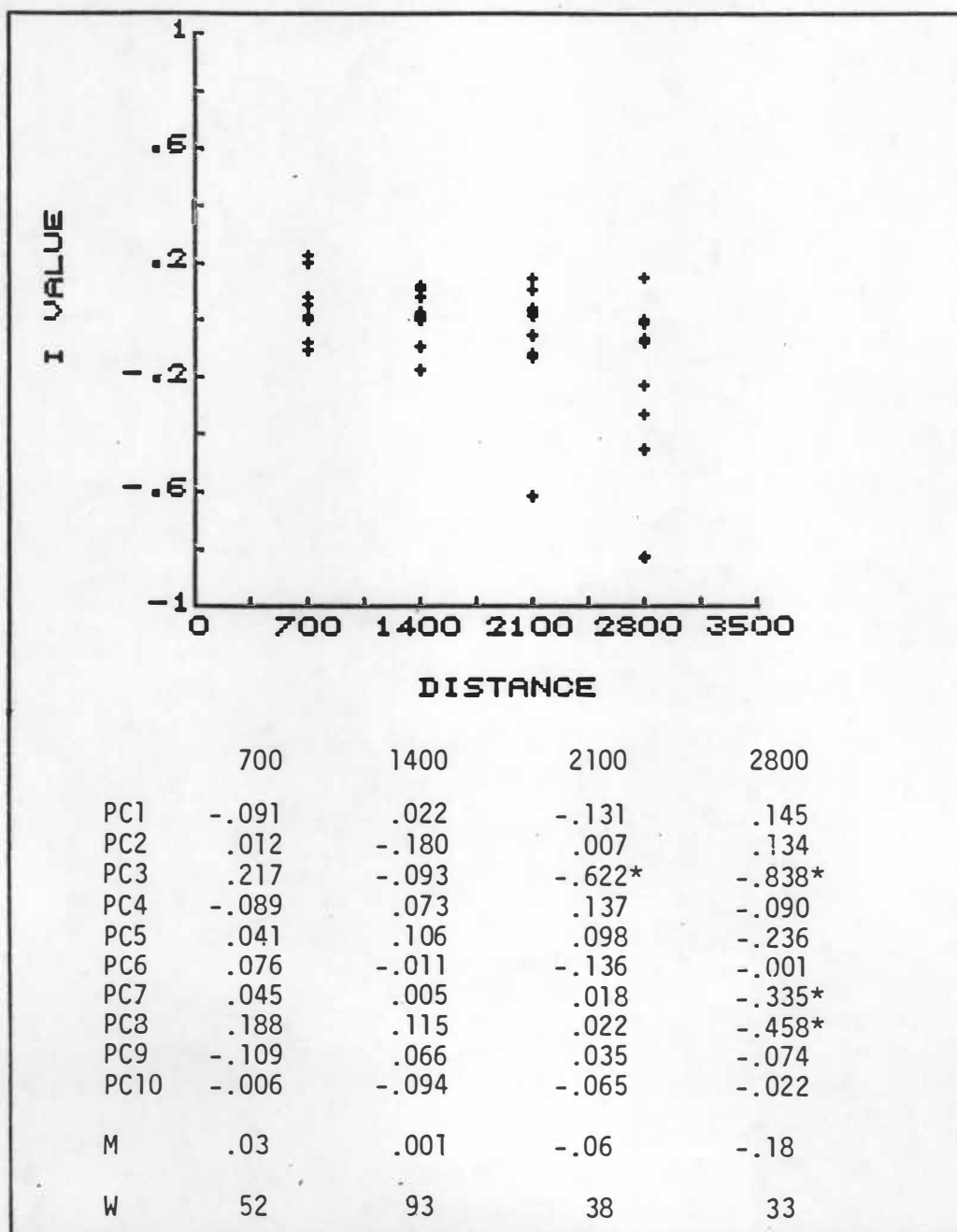


Figure 3-11. Male Northwest I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

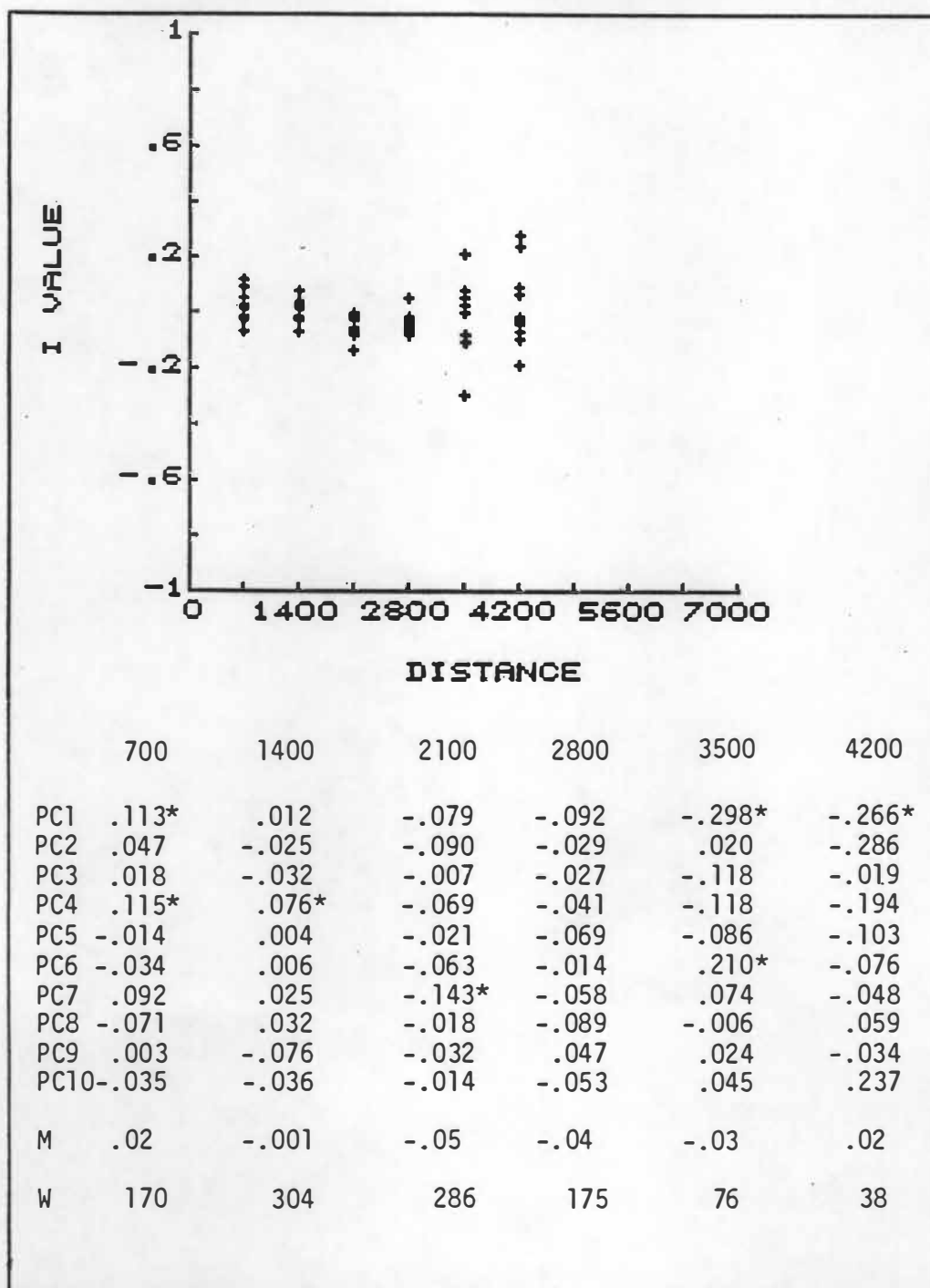


Figure 3-12. Female Gabriel I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

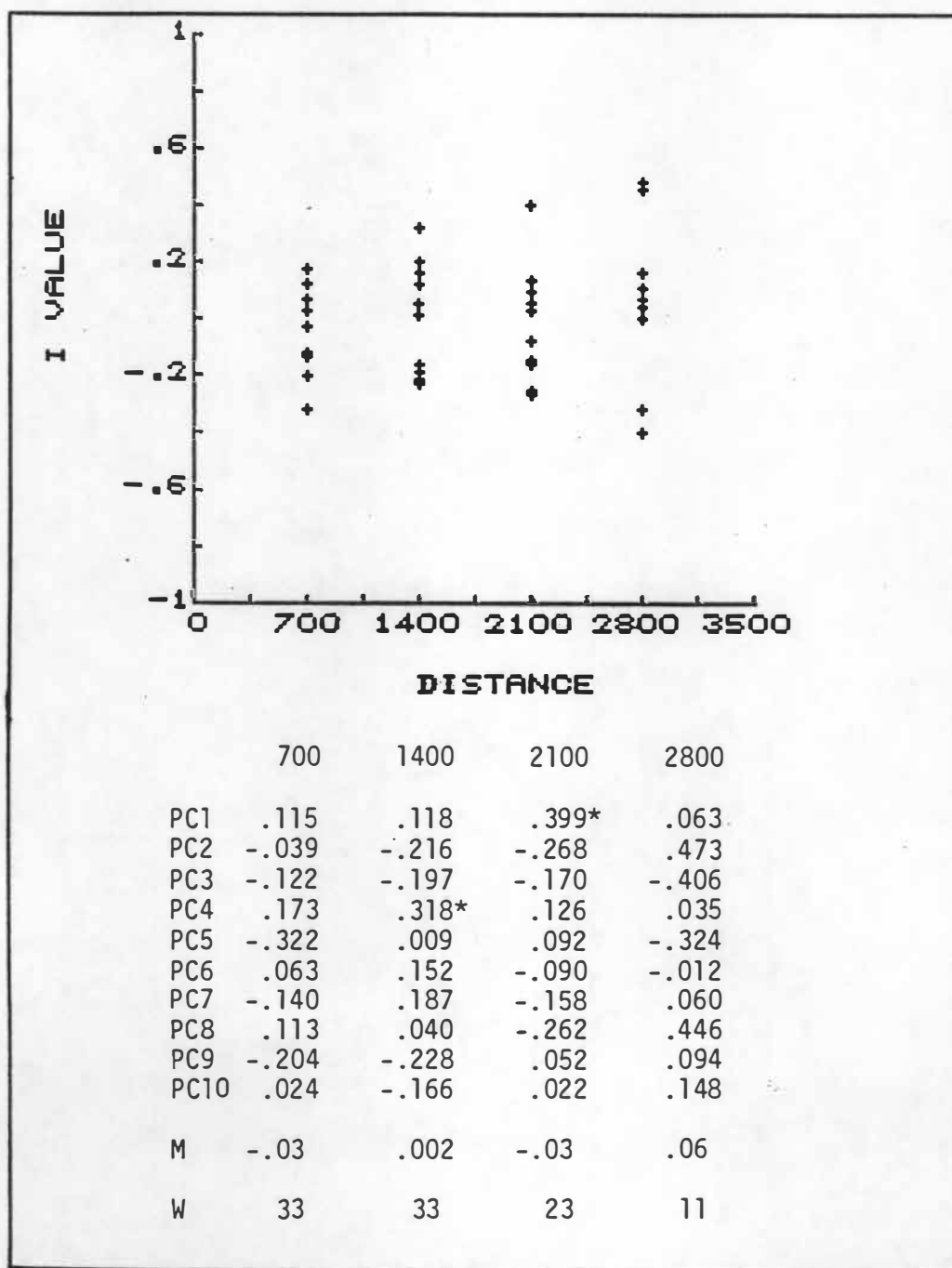


Figure 3-13. Female North I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

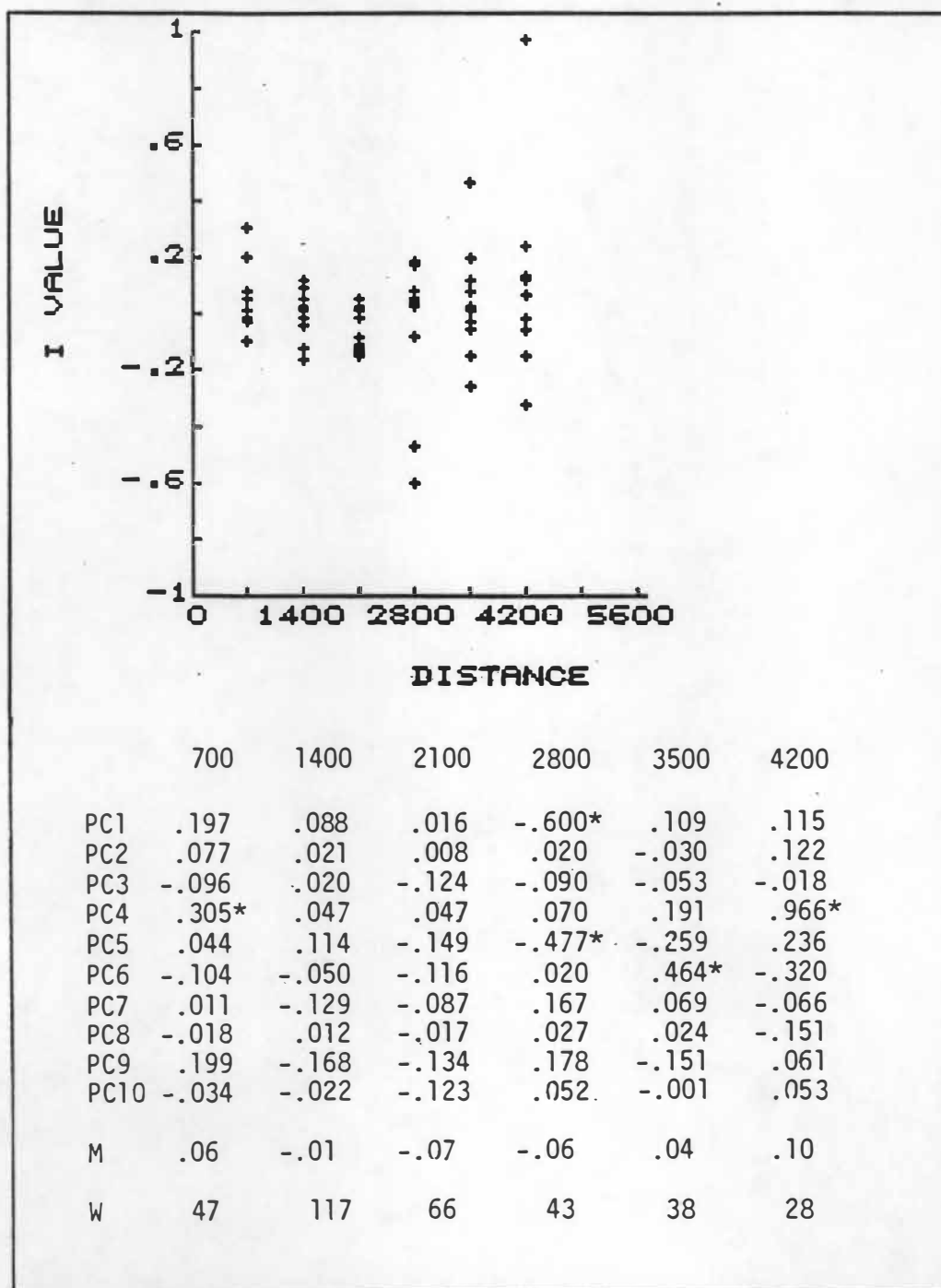


Figure 3-14. Female Northeast I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

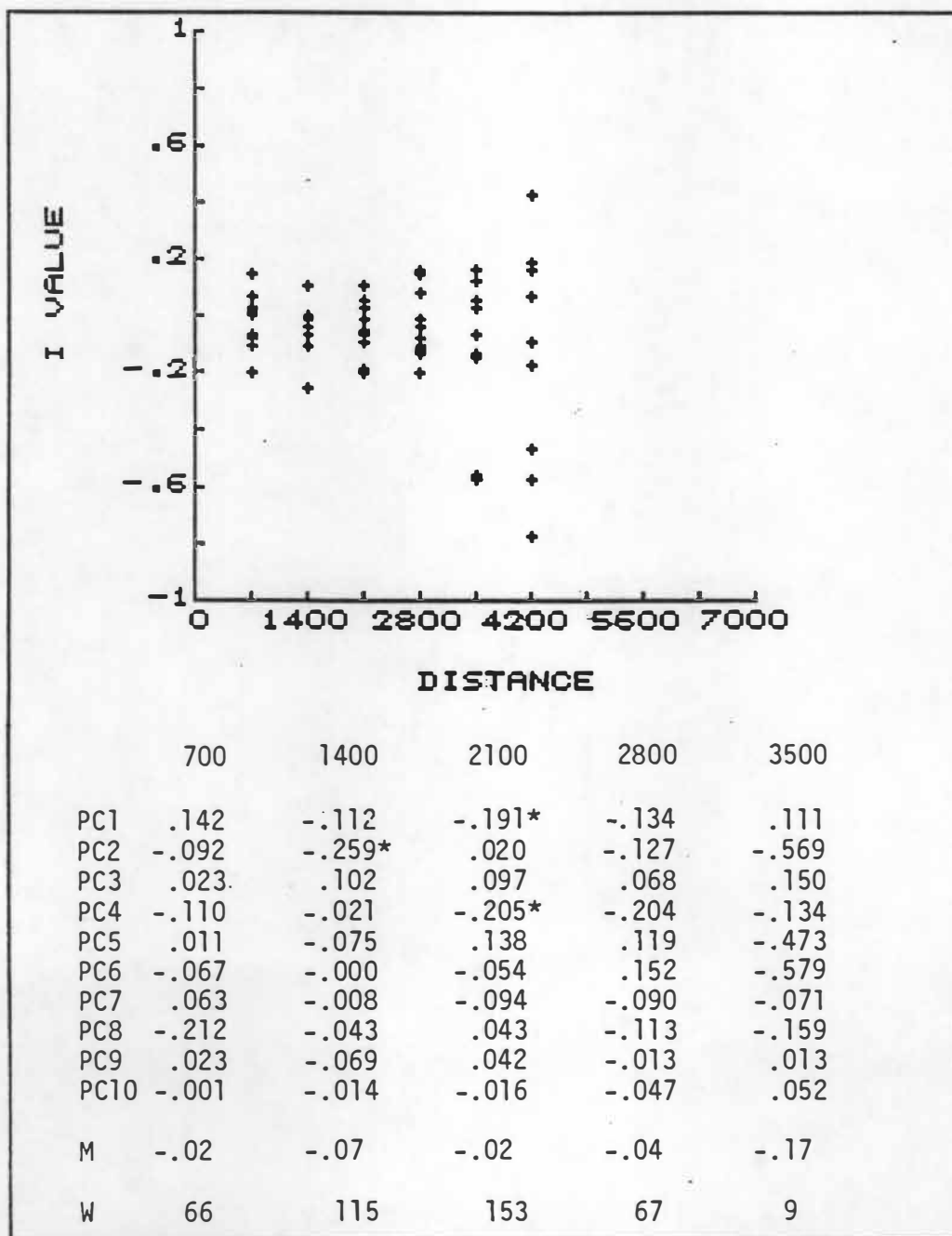


Figure 3-15. Female West I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

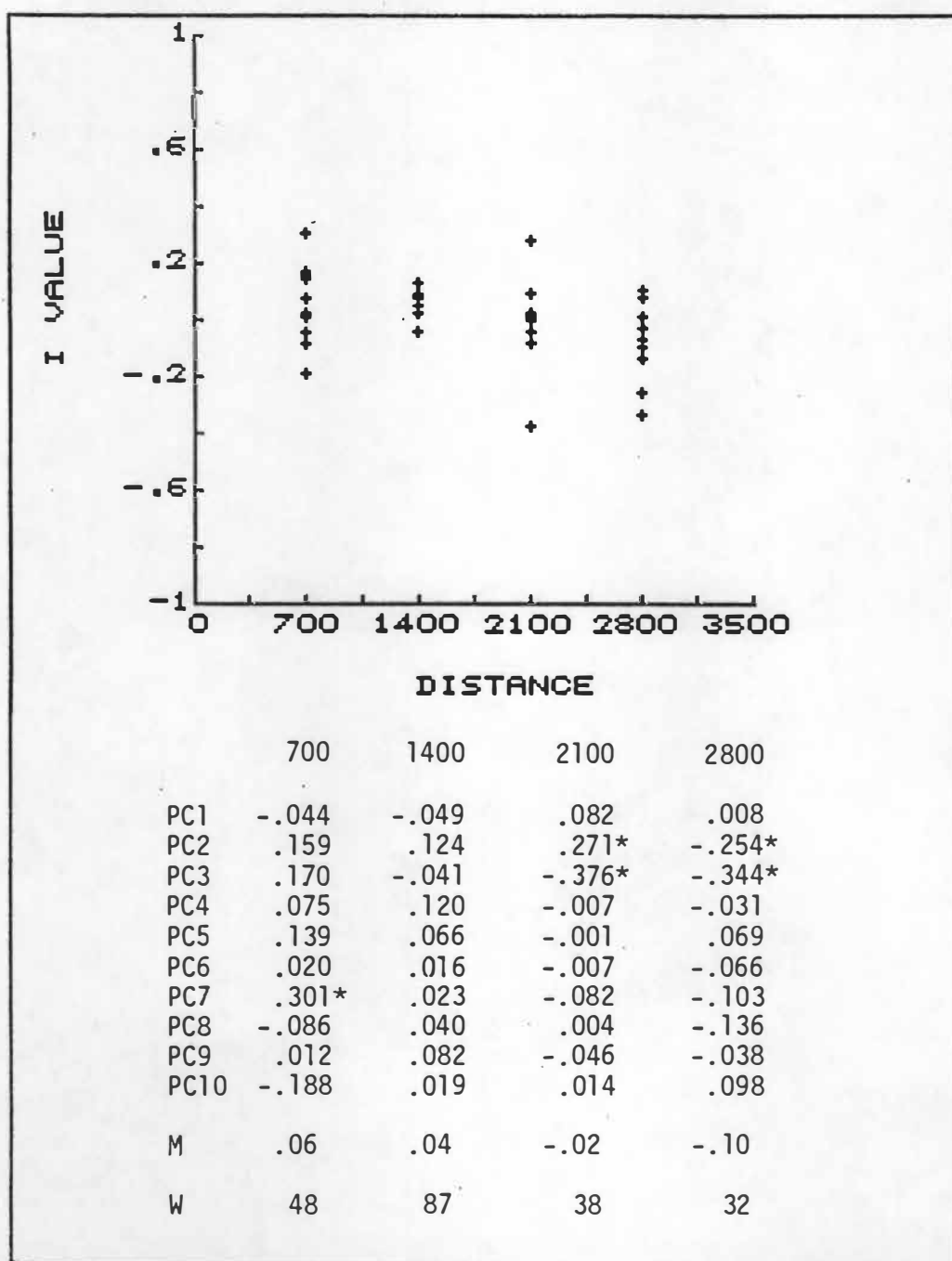


Figure 3-16. Female Northwest I-values, means (M), and connections (W). The * denotes significance at .05, two-tailed.

principal component. Since it is known from the multiple regression analysis which principal components are significantly aligned with geography, the configurations of the correlograms for the direction classes can be anticipated. If the class is one in which some, but not all, biological components of variability are closely associated with the geographic criterion defined by the class, the expected configuration is a number of surfaces which are more or less randomly oriented with respect to each other, and a few surfaces which demonstrate a trend. The randomly-oriented surfaces should be the ones generated by nonsignificant principal components, creating a background noise, while the significant components should generate a definite signal. Figure 3-17 shows an idealized plot of the expected configuration of the surfaces for a hypothetical direction class in which two biological vectors of among-group variability are significantly aligned with the direction class, and two are not aligned. The trend of the surfaces for the significant components is toward a successive decrease in spatial autocorrelation, i.e. they exhibit monotonicity. This must mean that on the significant biological components the groups in geographic proximity are more alike biologically than are groups which are more distant from each other.

It is assumed that in the absence of a factor or factors which cause one or more biological components to demonstrate monotonicity in one direction class or another, Gabriel connectivity will exhibit the most salient evidence of a biological among-group trend. The Gabriel

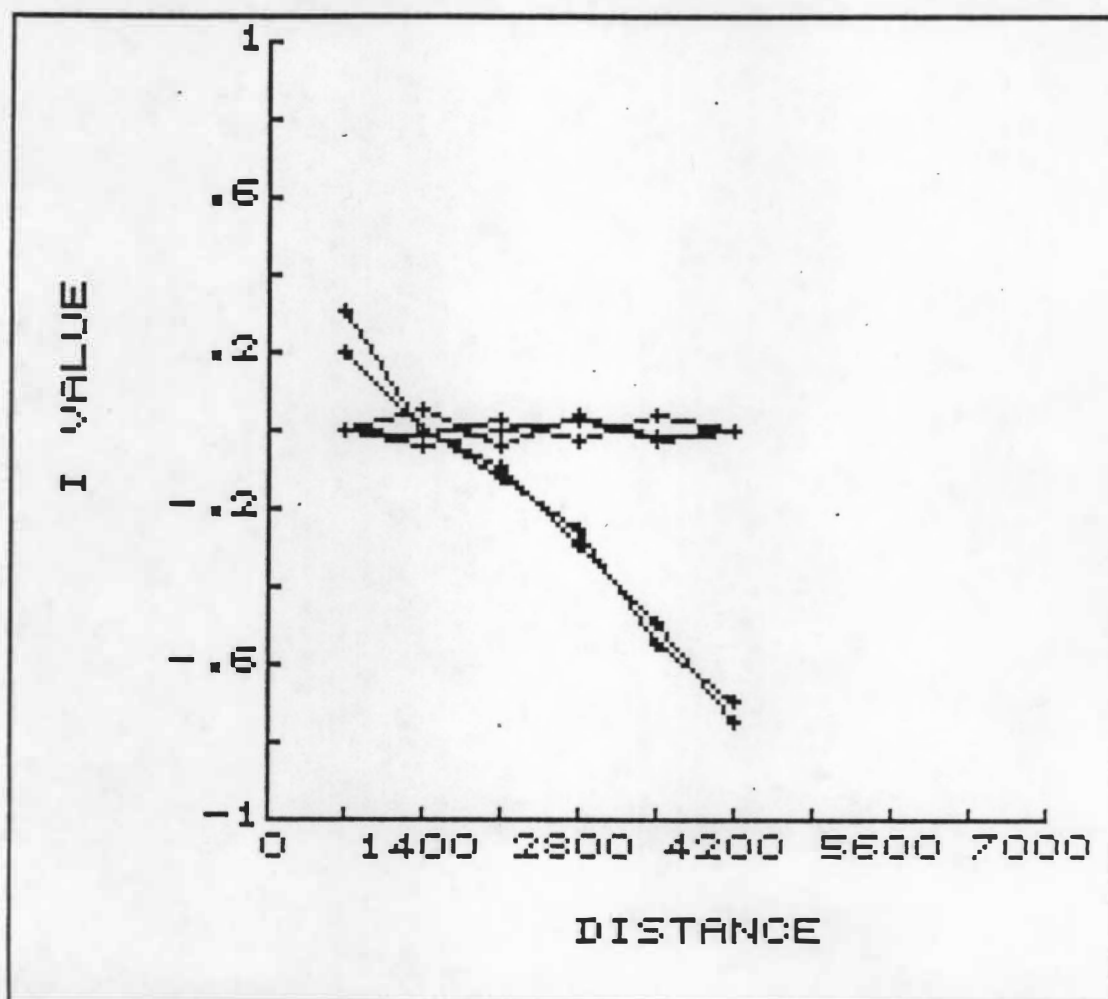


Figure 3-17. Idealized I-correlogram for four principal components, two of which exhibit monotonicity.

criterion connects groups in all directions and, as stated earlier, is the presumed path of gene flow in the absence of other inhibitory or inductive influences. Thus, following the lead set by Sokal and Menozzi (1982) in their HLA allele study, Gabriel connectivity is here considered the prime mover of biological variability against which the direction classes must be compared. The comparison is conducted in three ways. In the first, correlograms of all 10 principal components for each direction class and Gabriel connectivity are compared on an empirical basis. Secondly, Gabriel correlograms are compared to direction class correlograms for principal components which exhibit significant alignment with geography in the multiple regression analysis and also generate significant I-values in one or more distance classes. These same components are imbedded in the previous empirical comparison, but here are emphasized by the deletion of other components. Finally, a linear regression of I-values on the appropriate distance classes is conducted for each direction class and for Gabriel connectivity.

3.3.3.1 I-correlograms for the 10 principal components. Figure 3-18 shows the correlograms for Gabriel connectivity of each sex. There appears to be a high degree of correlation of all surfaces up to 2100 km and of most surfaces up to 2800 km. Thereafter, several components diverge, perhaps because fewer groups become involved in a comparatively higher number of connections within the distance class. No strong signals emerge as separate indicators. This configuration of I-correlograms would be expected in the Gabriel criterion because of

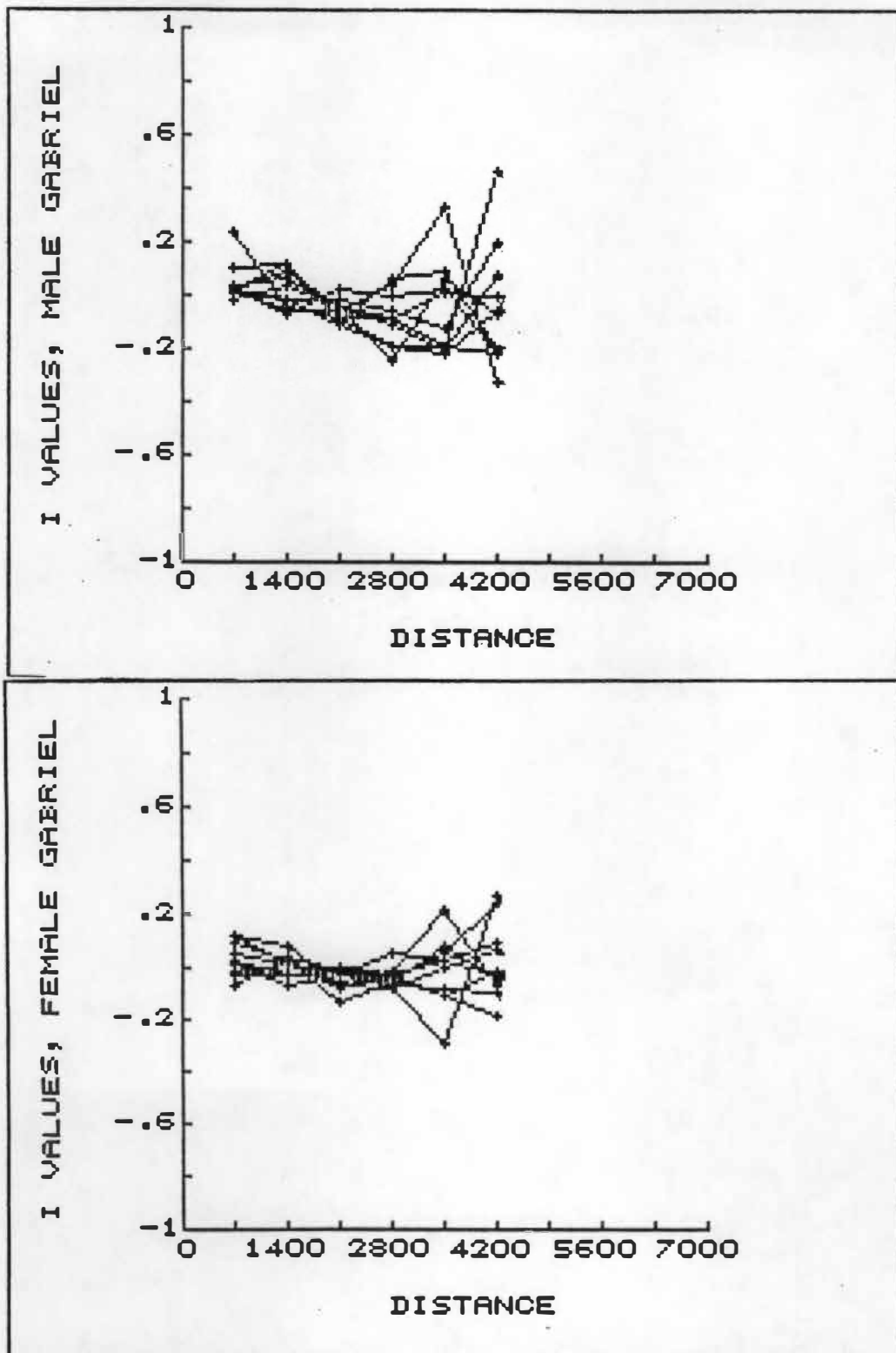


Figure 3-18. I-correlograms for Gabriel connectivity of Males (top) and Females.

its omnidirectional connectivity. It can be interpreted as a tendency for all principal components to be aligned on Gabriel routes.

Figures 3-19 and 3-20 are correlograms for the male groups in North, Northeast, Northwest and West direction classes respectively; Figures 3-21 and 3-22 present the same information for female groups. There can be little doubt that the Northwest and West classes in both sexes exhibit less noise and stronger signals than do the North and Northeast classes. Further, the strongest signals tend toward negative spatial autocorrelation in the greater distance classes. There also appears to be more regularity of the Northwest and West correlograms with respect to all of the principal components. The North direction class exhibits regularity to some degree, but with greater fluctuation of I-values than the West and Northwest classes. The Northeast class seems to demonstrate a random alignment of surfaces with widely fluctuating I-values.

3.3.3.2 Correlograms for significant I-values on significant principal components. Since it is known from the multiple regression analysis which components of biological variability are significantly aligned with geography, direction class and Gabriel connectivity correlograms for these components alone can be presented. To render the presentations more meaningful, only those components which generate a significant I-value in at least one distance class are presented. The assumption is that the force or forces which cause geographical and biological vectors of variability to be aligned in the first place will exert a similar if not identical effect on each

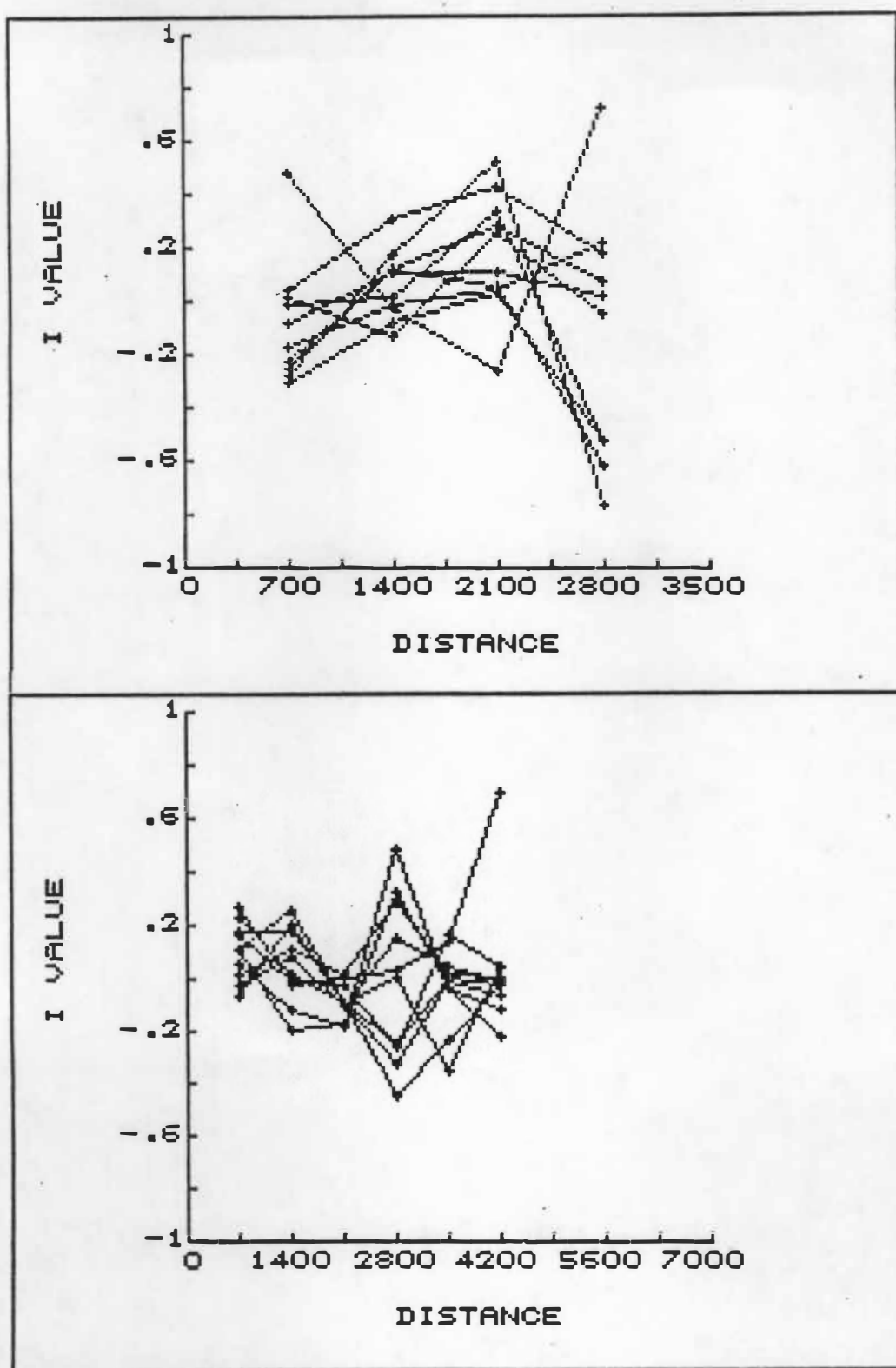


Figure 3-19. Male North (top) and Northeast I-correlograms.

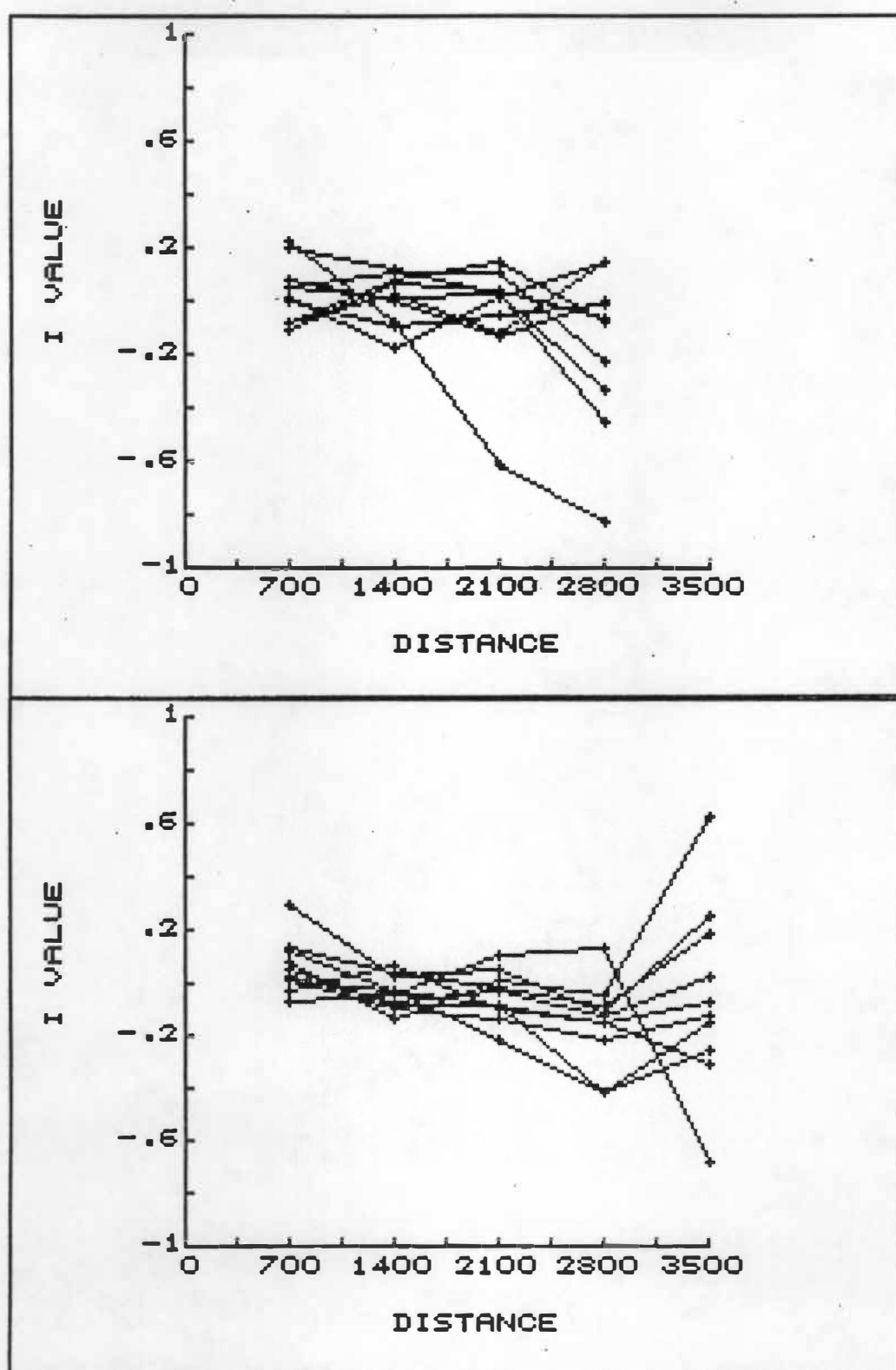


Figure 3-20. Male Northwest (top) and West I-correlograms.

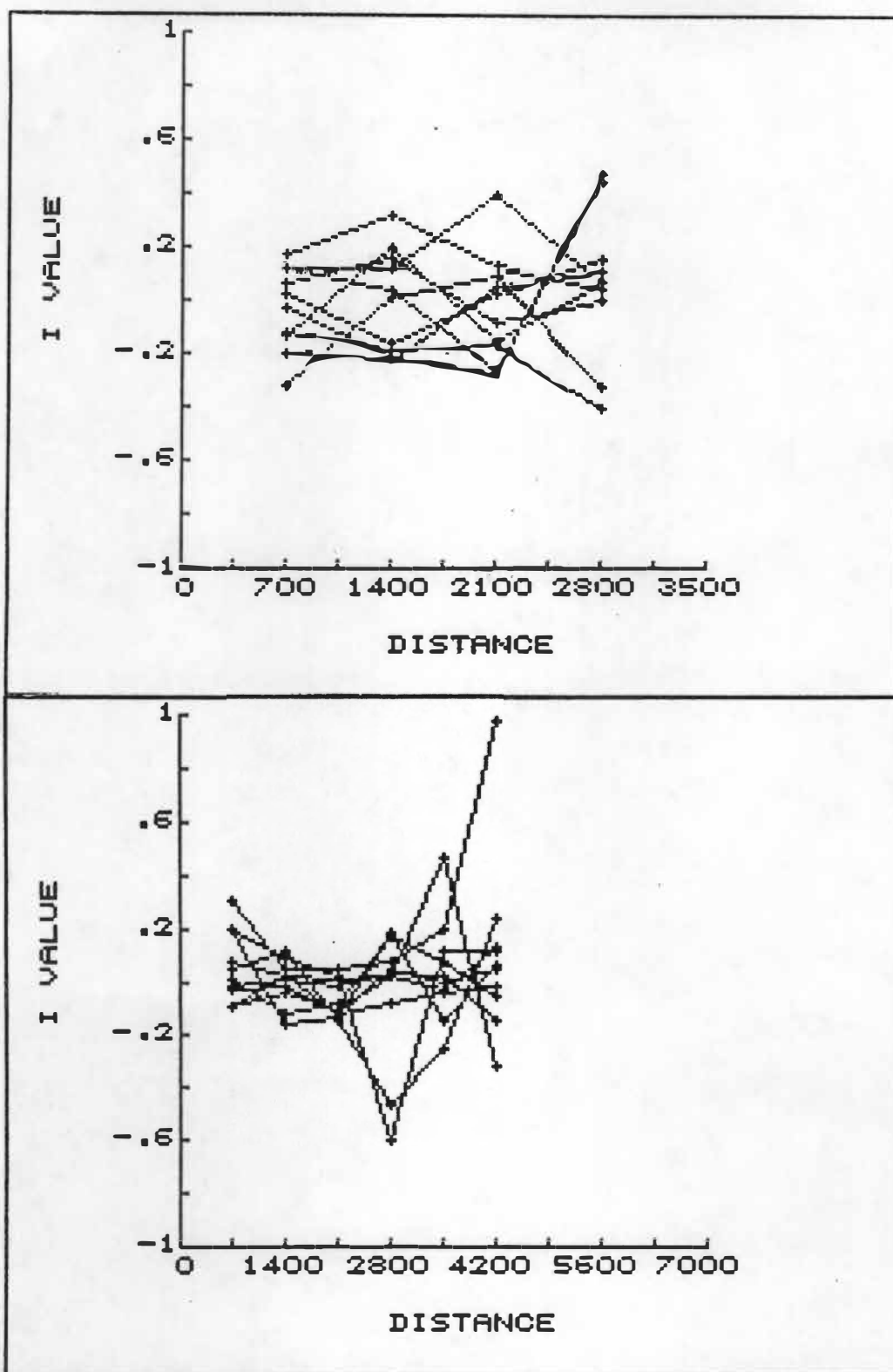


Figure 3-21. Female North (top) and Northeast I-correlograms.

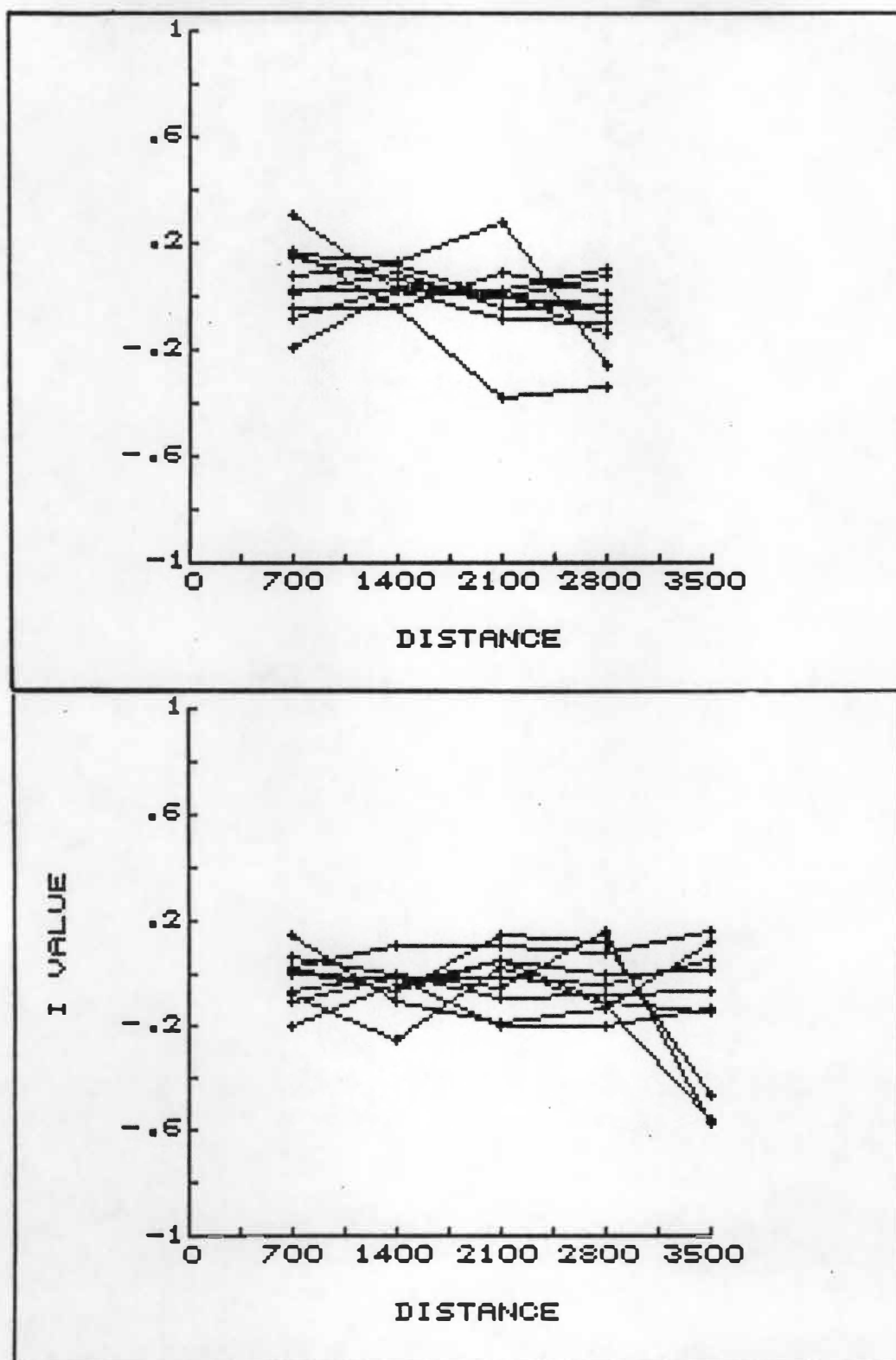


Figure 3-22. Female Northwest (top) and West I-correlograms.

biological surface across all of the groups. Thus, the expectation is that the correlograms of significant components will be superimposed for the direction class which is most indicative of the among-group or geographic track of the causal force. Figures 3-23 through 3-27 show the correlograms for the the significant components. For each sex, there appears to be considerably more contiguity of surfaces in the Northwest and West direction classes than in the other two direction classes, and somewhat more than in Gabriel connectivity, although no class meets the ideal of superimposed correlograms. Only the Northwest direction class produces truly monotonic surfaces. These are generated by PC3 and PC8 in males and PC7 in females. The surface of PC7 in males would be monotonic if it were not for the slight increase of the I-value between the 1400 km and 2100 km distance classes; likewise PC3 in females would generate a monotonic surface except for the increase of I from $-.376$ in the 2100 km distance class to $-.344$ in the 2800 km class.

The West direction class exhibits no monotonicity, however PC7 and PC8 in males and PC4 in females generate surfaces which decrease to negative autocorrelation values which remain negative across all of the subsequent distance classes.

Neither North and Northeast direction classes nor Gabriel connectivity are marked by the monotonicity of any surface generated by the significant principal components. Although not monotonic, the surfaces in the Gabriel class for both sexes are reasonably well-approximated, as would be expected.

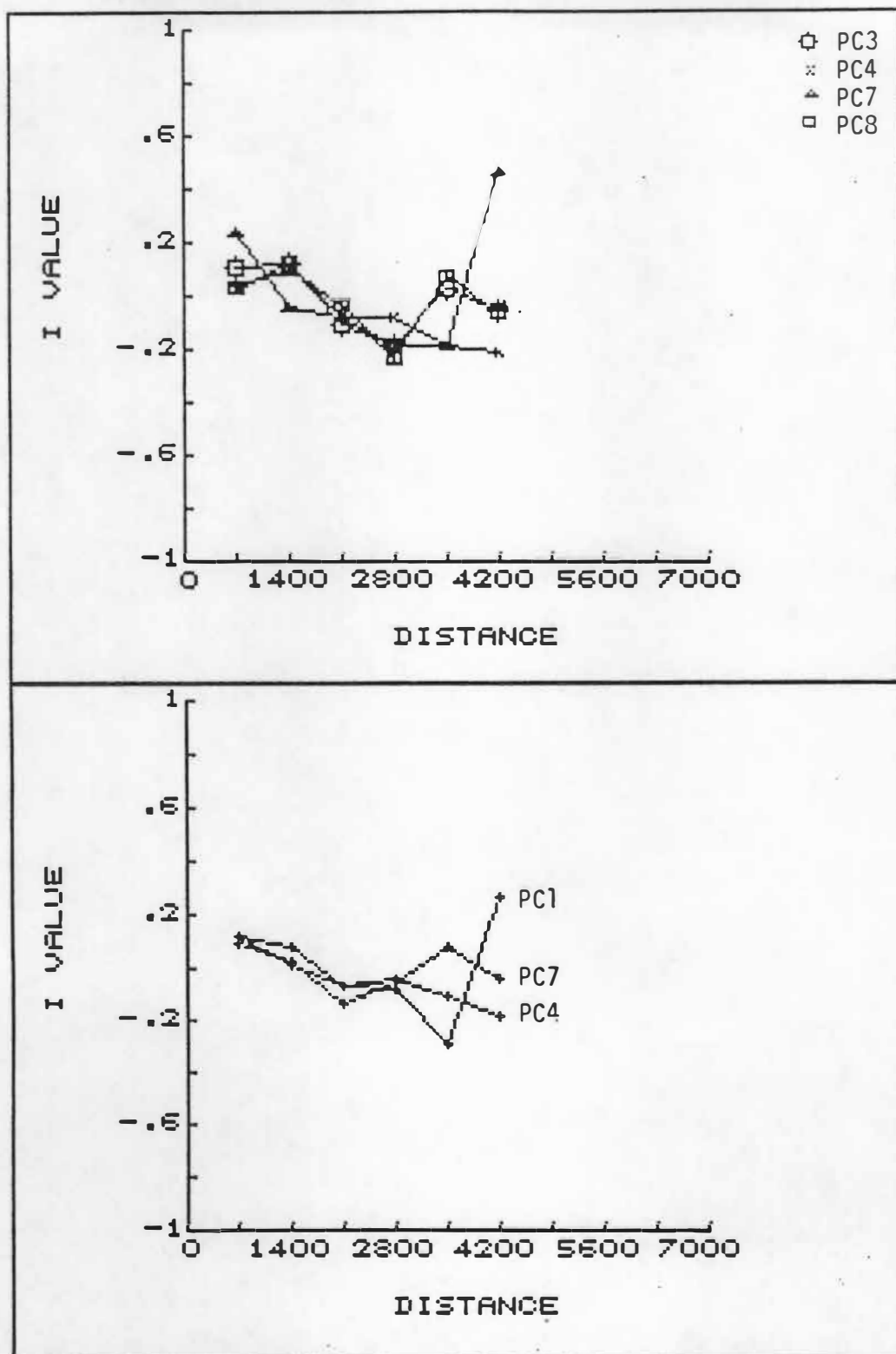


Figure 3-23. I-correlograms of significant principal components for Gabriel connectivity of Males (top) and Females.

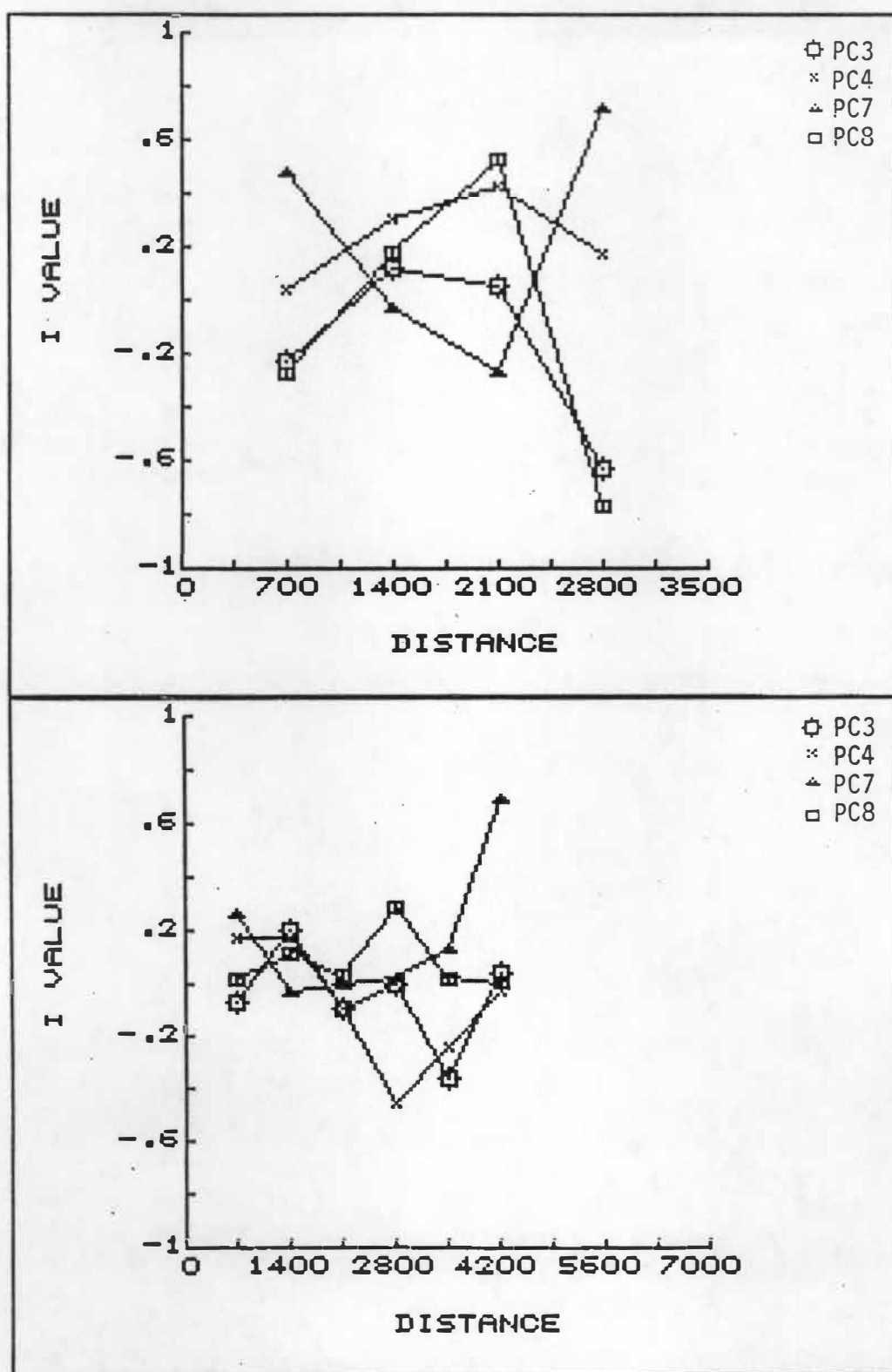


Figure 3-24. I-correlograms of significant principal components for Male North (top) and Northeast.

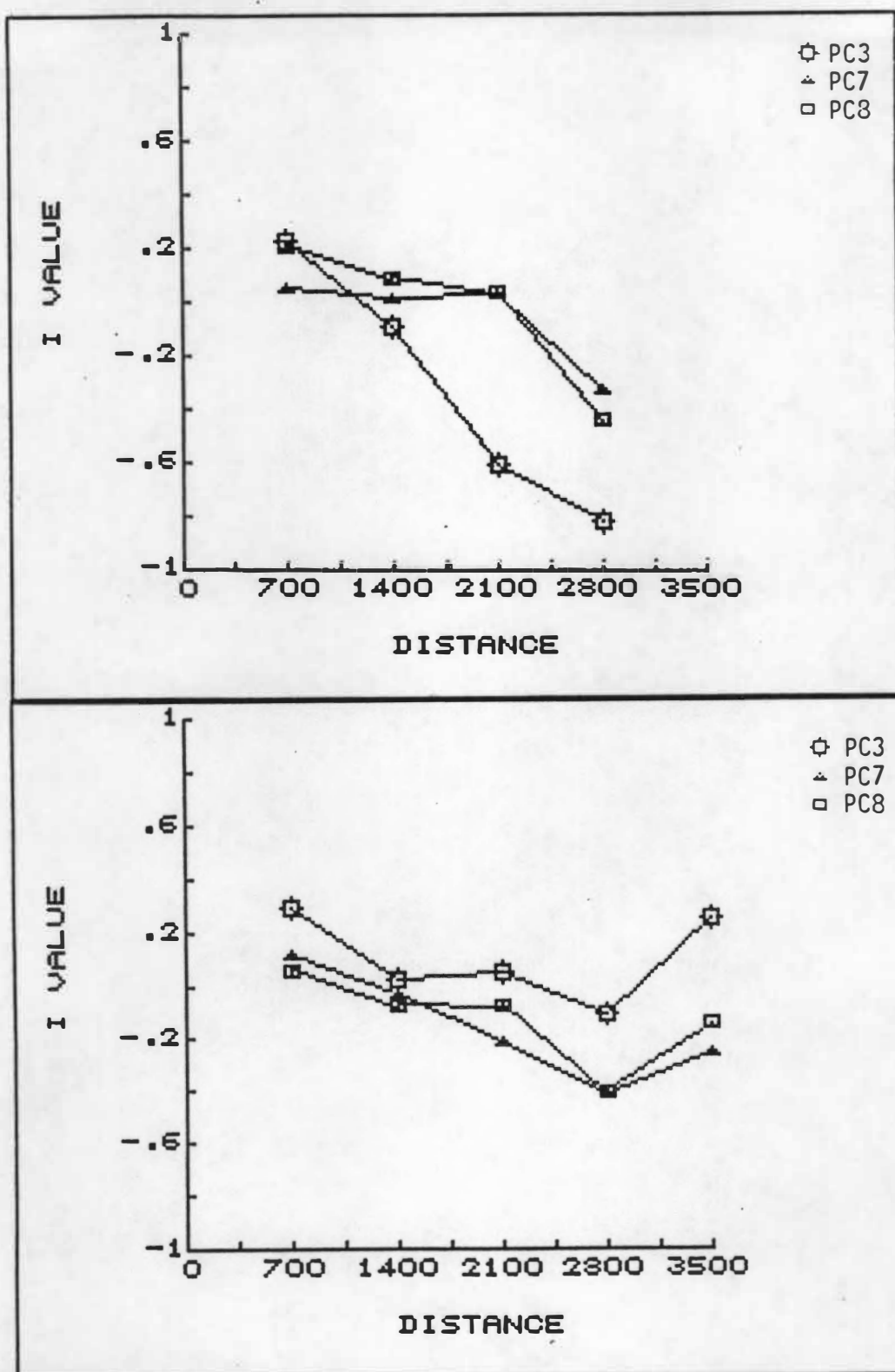


Figure 3-25. I-correlograms of significant principal components for Male Northwest (top) and West.

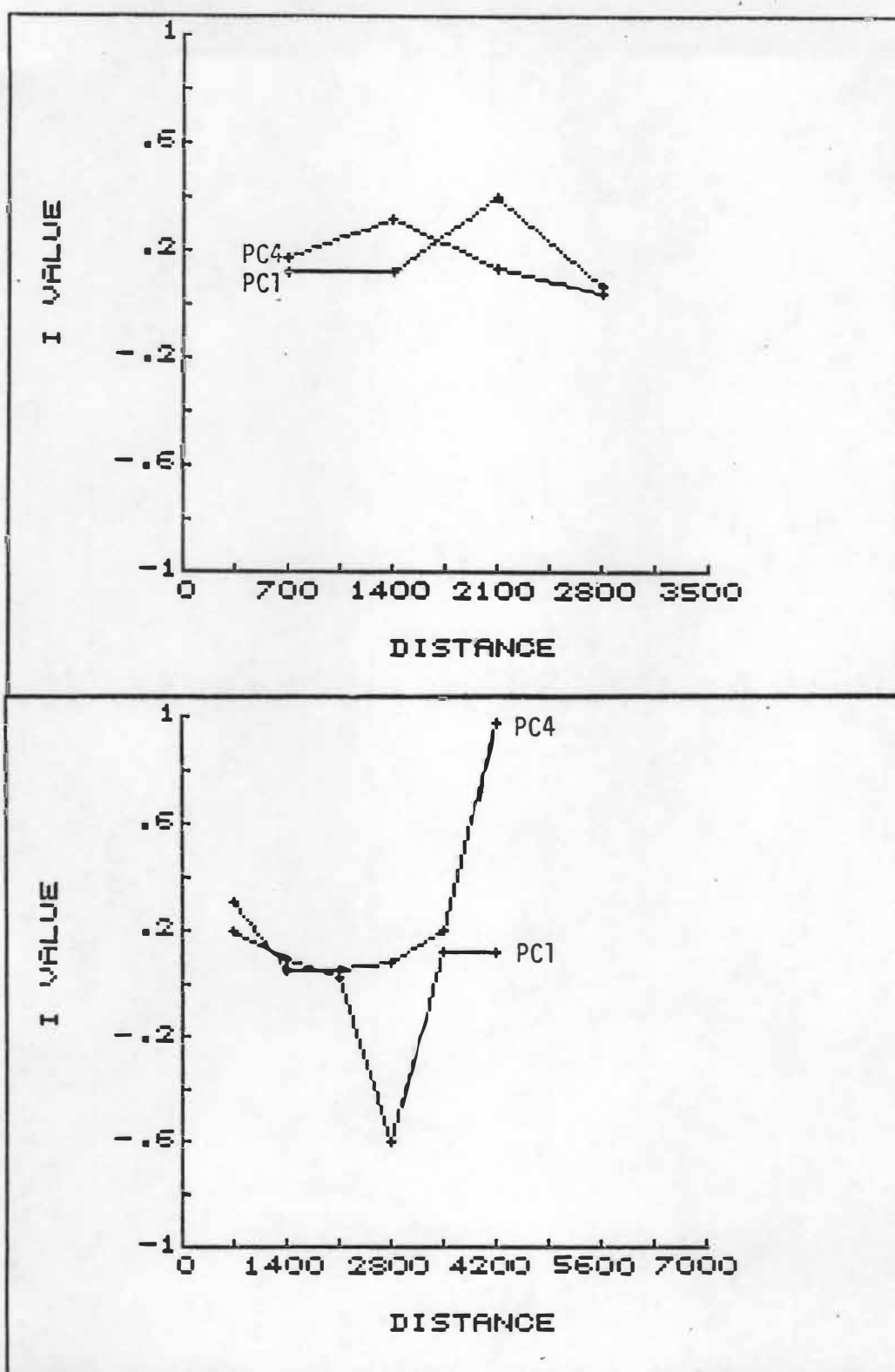


Figure 3-26. I-correlograms of significant principal components for Female North (top) and Northeast.

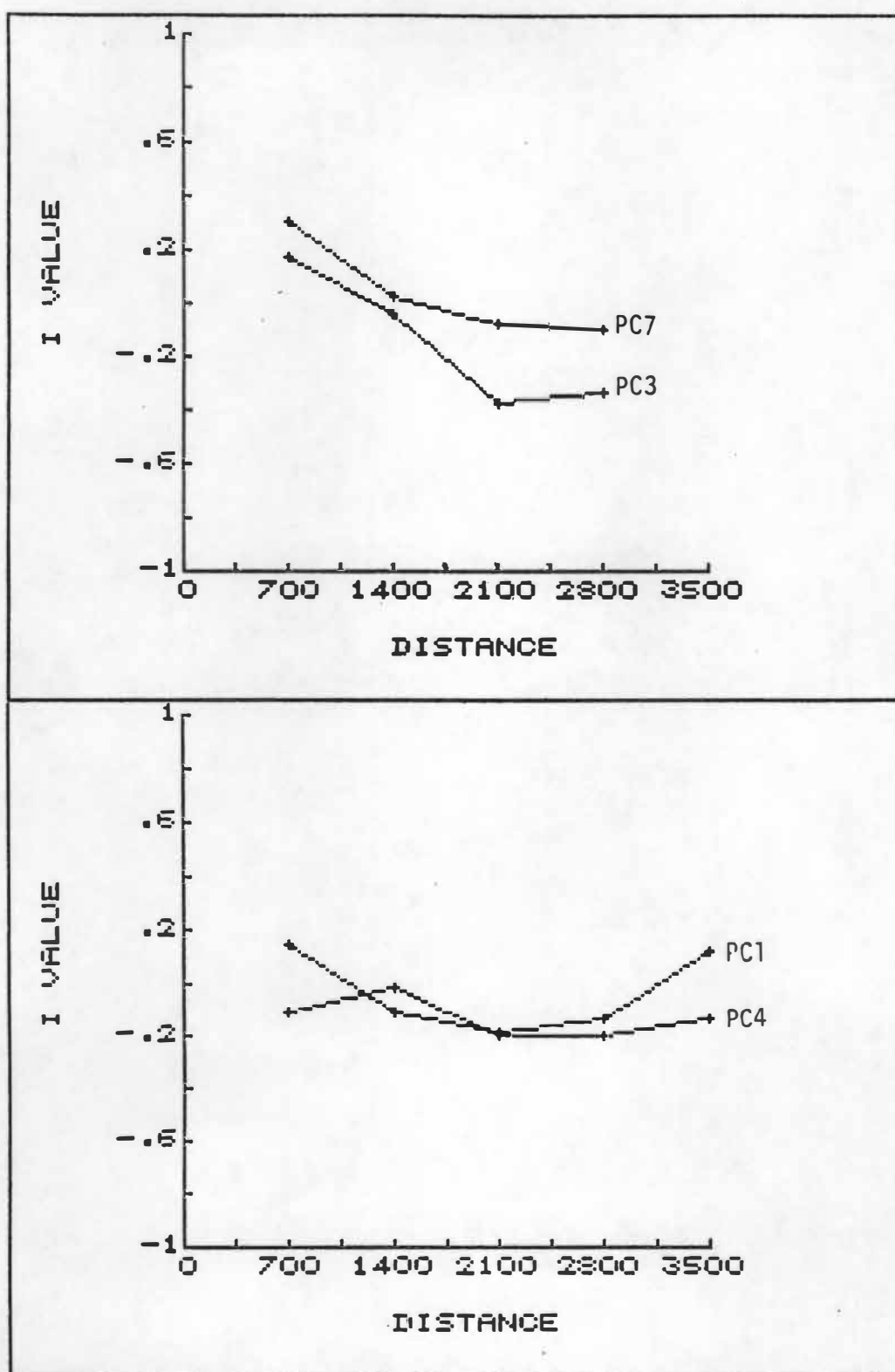


Figure 3-27. I-correlograms of significant principal components for Female Northwest (top) and West.

One of the difficulties in evaluating I-correlograms is the rather rigid definition of monotonicity. To illustrate, PC3 in the Female Northwest direction class, the I-value rises from $-.376$ to $-.344$ between the 2100 km and 2800 km distance classes. Even though the I-value is significantly negative in both classes, the PC3 surface is not monotonic under the strictest definition of monotonicity, i.e. decreasing spatial autocorrelation across a successive distance class. The tabulated I-values previously presented with the I-value plots demonstrate that some surfaces in each direction class, as well as on Gabriel routes, exhibit decreasing spatial autocorrelation, but not across all distance classes. Thus, it is possible that undue emphasis is being placed upon a few distance classes which effectively destroy monotonicity on some components. Tables 3-5 and 3-6 show I-values for all surfaces which run monotonically (decreasing spatial autocorrelation), regardless of the number of distance classes they cross. The only criterion is that at least one I-value in each monotonic sequence must be significant at the .05 level. This criterion eliminates all the components which do not produce a significant I-value.

One way to evaluate these surfaces is to compare, within each direction class, and within the Gabriel connectivity, the total number of observed monotonic connections among the consecutive distance classes to the total number possible. For example, for Gabriel connectivity of male groups in Table 3-5, each component has the potential to produce I-values on six distance classes. Since there are

TABLE 3-5

MONOTONIC SEQUENCES OF I-VALUES FOR MALE GROUPS

	700	1400	2100	2800	3500	4200
GAB						
PC3	X	.118*	-.117*	-.193*	-.214	X
PC4	X	.112*	-.081	-.085	-.195	-.226
PC7	.229*	-.043	-.081	-.195*	-.198	X
PC8	X	.090*	-.045	-.244*	X	X
PC9	X	X	X	X	.330*	-.325*
N						
PC3	X	.119	.042	-.634*	X	X
PC4	X	X	.414*	.162	X	X
PC7	.470*	-.033	-.267	X	X	X
PC8	X	X	.516*	-.782*	X	X
NE						
PC2	.217	.006	-.098	-.341*	X	X
PC3	X	.192*	-.099	-.005	-.365*	X
PC4	X	.167*	-.096	-.457*	X	X
PC5	X	.249*	-.094	-.258	X	X
PC7	.255*	-.031	X	X	X	X
PC8	X	X	X	.279*	.007	-.006
PC9	X	X	X	.473*	-.051	-.130
PC10	X	X	X	.317*	-.046	-.229
W						
PC2	X	X	.125	-.683*	X	X
PC3	.287*	.018	X	X	X	X
PC7	.115	-.037	-.217*	-.418*	X	X
PC8	.042	-.092	-.092	-.422*	X	X
NW						
PC3	.217	-.093	-.622*	-.838*	X	X
PC7	.045	.005	.018	-.335*	X	X
PC8	.188	.115	.022	-.458*	X	X

* significant at .05, two-tailed

TABLE 3-6
MONOTONIC SEQUENCES OF I-VALUES FOR FEMALE GROUPS

	700	1400	2100	2800	3500	4200
GAB						
PC1	.113*	.012	-.079	-.092	-.298*	X
PC4	.115*	.076*	-.069	X	X	X
PC6	X	X	X	X	.210*	-.076
PC7	.092	.025	-.143*	X	X	X
N						
PC1	X	X	.399*	.063	X	X
PC4		.318*	.126	.035		
NE						
PC1	.197	.088	.016	-.600*	X	X
PC4	.305*	.047	.047	X	X	X
PC5	X	.144	-.149	-.477*	X	X
PC6	X	X	X	X	.464*	-.320
W						
PC1	.142	-.112	-.191*	X	X	X
PC2	-.092	-.259*	X	X	X	X
PC4	X	-.021	-.205*	X	X	X
NW						
PC2	X	X	.271*	-.254*	X	X
PC3	.170	-.041	-.376*	-.344*	X	X
PC7	.301*	.023	-.082	-.103	X	X

* significant at .05, two-tailed

five possible connections among the distance classes and five principal components which generate significant I-values, the total possible exhibitions of monotonicity are 25. The observed number calculable from Table 3-5 is 14, or 47 percent of the total possible. The following percentages can be calculated for all of the direction and Gabriel classes:

	Gabriel	North	Northeast	West	Northwest
M	47	50	42	50	89
F	45	50	40	33	78

It should be noted that these results are based upon two arbitrary assumptions; one, that identical I-values in consecutive distance classes are monotonic; and two, same-signed significant I-values in consecutive distance classes are monotonic regardless of their absolute values. These assumptions are relevant only with respect to PC8 in the Male West class, PC7 in the Female Northwest class, and PC4 in the Female Northeast class.

The Northwest direction class for both males and females still appears to exhibit the most intensive patterning. Except for the West class, the percentage of potential monotonicity is remarkably similar for both the sexes.

3.3.3.3 Linear regression of I-values. The final phase of the geographical variation analysis is the regression of I-values on the distance classes. The procedure would seem to offer the only way that differences among the direction classes and the Gabriel class could be stated with objective probability. However, the results of the

regressions must be approached with caution for several reasons. For one, the precision of a direction class boundary is a continuous variable, as is any direction measurement, because the angle included in the class boundaries includes progressively more area as the distance from the origin of the measurement increases. Therefore, the connection of two groups a considerable distance from each other may or may not have taken place had the groups been closer together. Another reason for caution is the relationship between distance and the number of groups involved in connectivity. As distance between groups increases, fewer groups comprise a higher fraction of the total number of connections within a distance class. Thus, what is generating the surface changes somewhat from one distance class to another. The third and probably most important reason is the magnitude of the I-values themselves. The standard errors increase with increase in distance classes because fewer groups are involved in the computation of I-values. Therefore, greater absolute values of I are required to achieve significance in the upper distance classes. Means of I-values are included as a separate regression to provide some indication of the relative placement of the regression line and the within-distance class I-value means. Still, neither I-values nor I-value means can be properly equated across all distance classes. For example, it is possible for a linear regression of I-values to produce a highly significant negative slope, and the data set not contain a single statistically-significant negative I-value.

In spite of the various pitfalls, a linear regression of I-values

and I-value means on distance classes would seem to be of some value in comparing the various direction classes with each other and with the Gabriel class. Figures 3-28 through 3-32 show the regressions of Gabriel connectivity and each direction class. Not surprisingly, the Northwest class demonstrates significant slopes in both sexes, and these are both negative.

3.3.4 Results of the language analysis. If the causal factor for the alignment of geographic and biological vectors of variability has a strong genetic component, the expectation is that groups which speak the same language would be highly positively autocorrelated. Altogether there are 173 connections among the male groups for the language criterion; 165 female groups are connected identically, except the AUS3 row and column. Table 3-7 presents the I-values for the connected groups.

TABLE 3-7
I-VALUES FOR THE LANGUAGE ANALYSIS

	MALES	FEMALES
PC1	-.012	.037
PC2	.053	.056
PC3	.201*	.118*
PC4	.006	.030
PC5	.057	-.018
PC6	.026	-.085
PC7	.045	-.025
PC8	.046	-.049
PC9	-.079	-.057
PC10	.075	.025

* significant at .05, two tailed

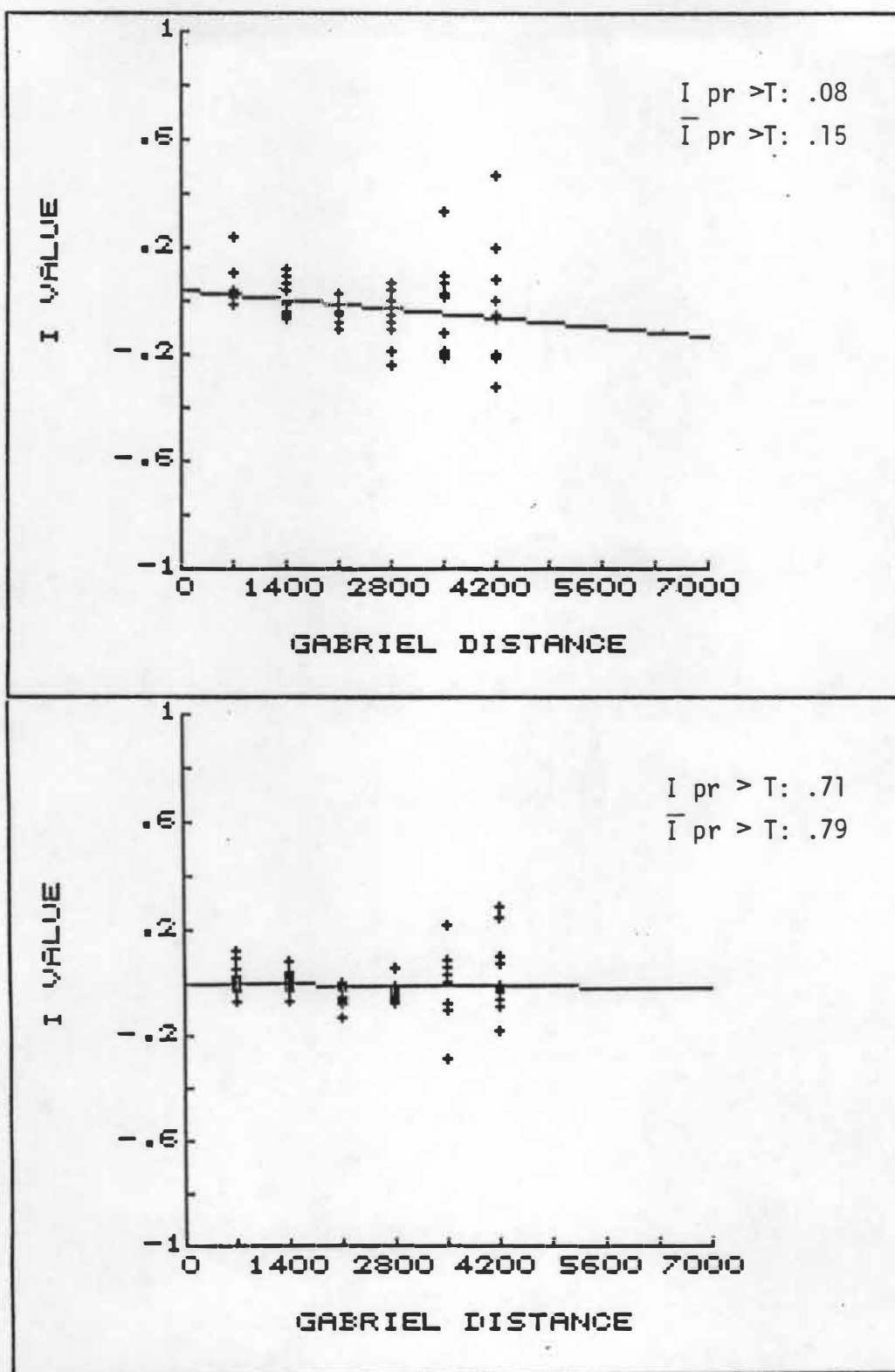


Figure 3-28. Regression slopes for I-values (plotted) and I-value means for Gabriel connectivity of Males (top) and Females.

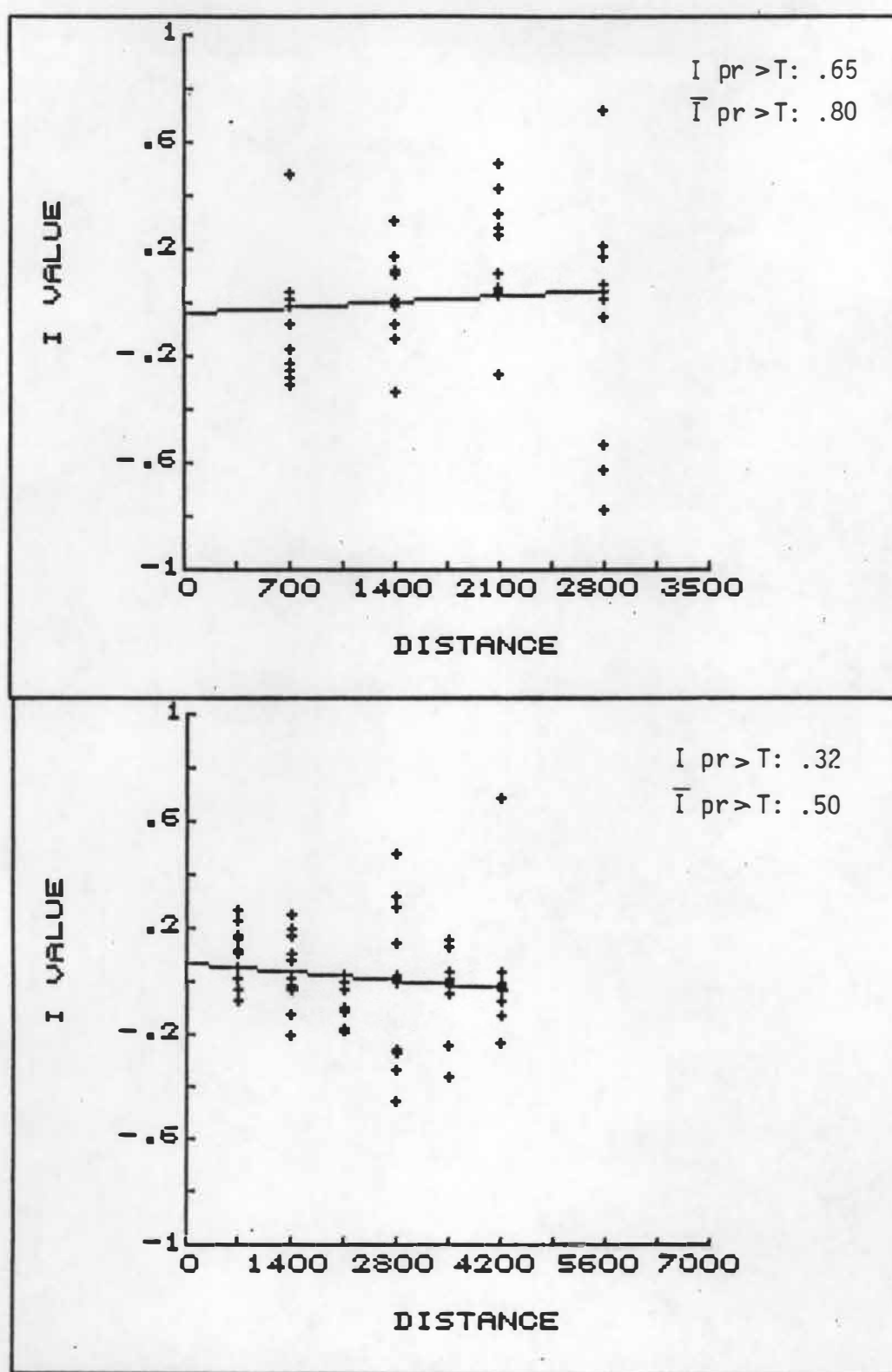


Figure 3-29. Regression slopes for I-values (plotted) and I-value means for Male North (top) and Northeast.

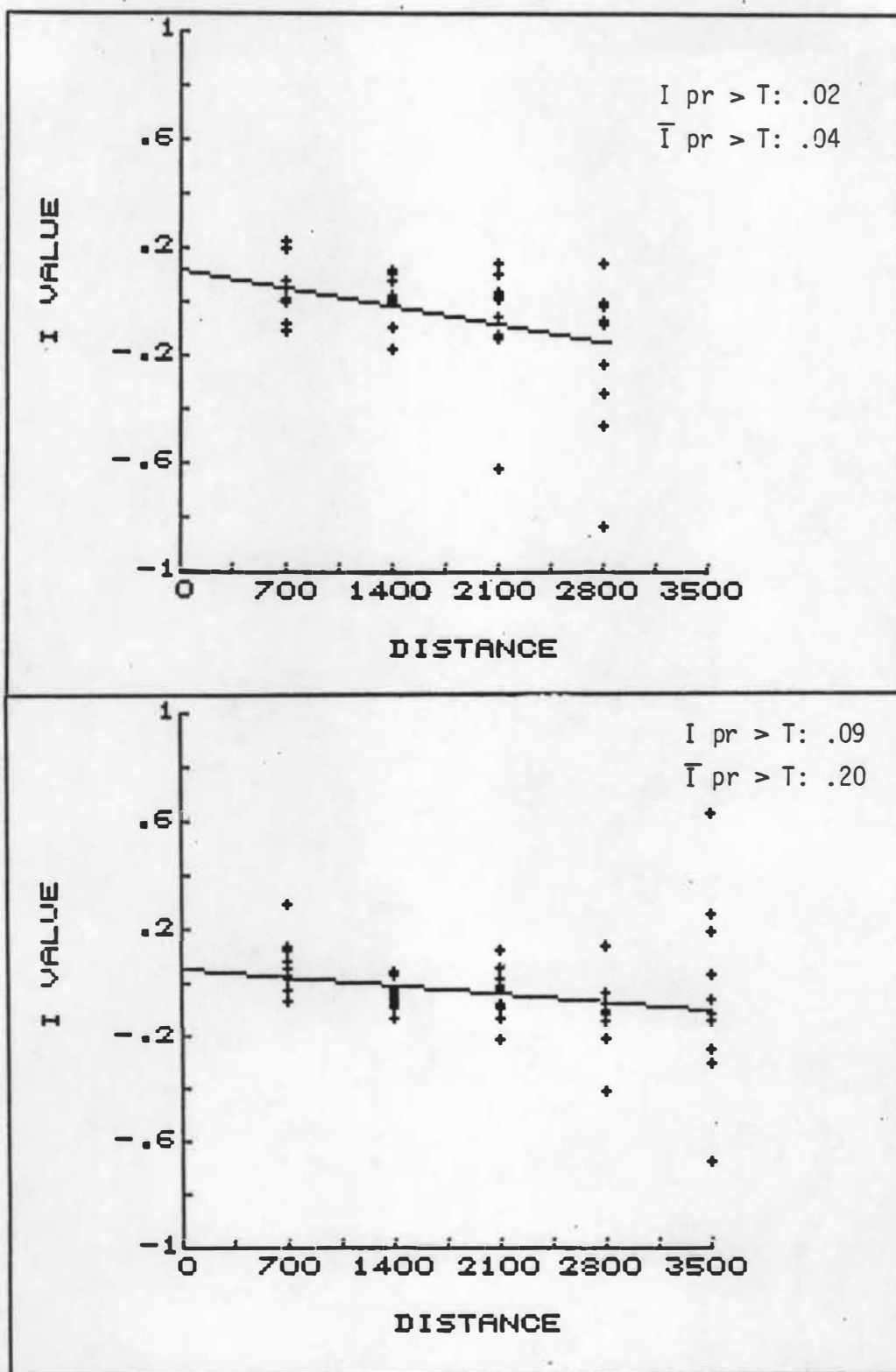


Figure 3-30. Regression slopes for I-values (plotted) and I-value means for Male Northwest (top) and West.

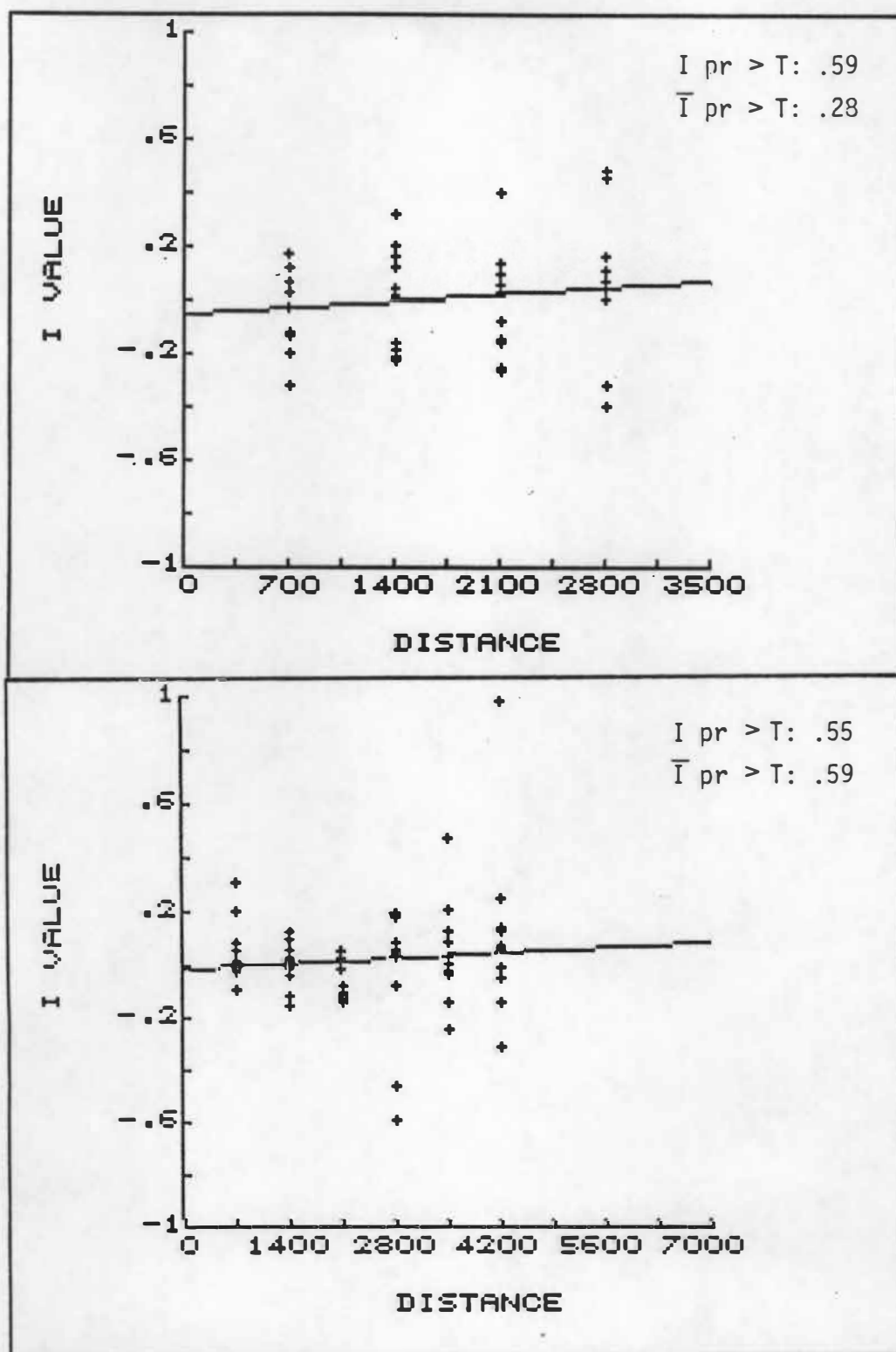


Figure 3-31. Regression slopes for I-values (plotted) and I-value means for Female North (top) and Northeast.

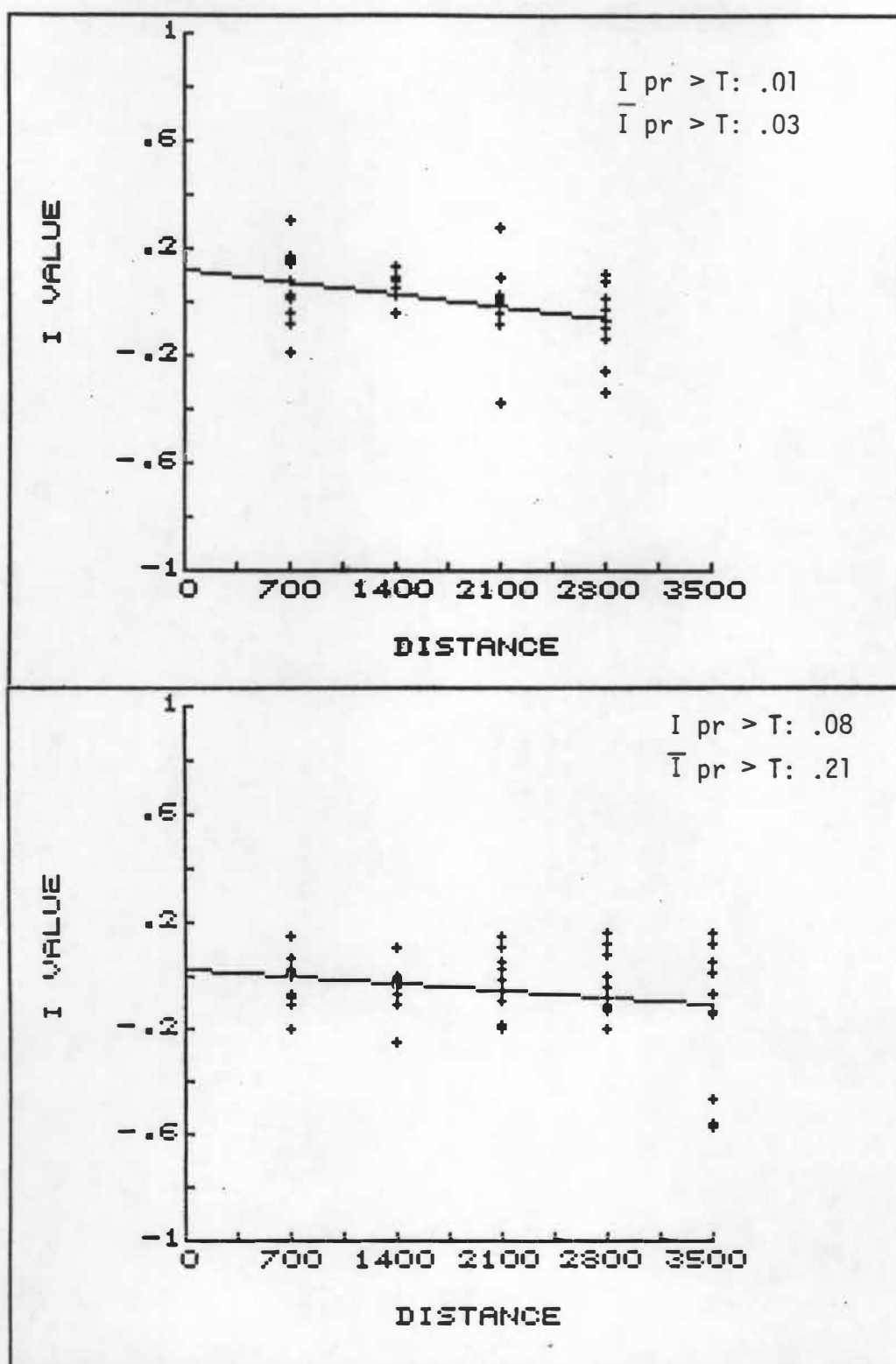


Figure 3-32. Regression slopes for I-values (plotted) and I-value means for Female Northwest (top) and West.

The I-value for PC3 achieves significance in both sexes and the I-value for no other component approaches the significance of PC3. This outcome is not concordant with expectations, since females are patterned on PC1, PC3, PC4, and PC7 in the geographic analysis, and males on PC3, PC4, PC7, and PC8. Further, the surfaces generated by PC7 and PC8 in males tend to parallel the surface of PC3, as does the surface generated by PC7 in females to a lesser degree. It seems unlikely that totally different factors are responsible for the among-group variability on PC3 than are at work with respect to the other components of biological variability. A partial explanation might be that the language criterion connects only groups in close proximity. Male groups in the first distance class tend to have especially high positive I-values on PC3. However, Table 3-8 presents I-values for a ≤ 700 km class which is not slaved to direction classes nor to the Gabriel connectivity criterion.

TABLE 3-8

I-VALUES FOR DISTANCES ≤ 700 KM

	MALES	FEMALES
PC1	.012	.099*
PC2	-.032	.021
PC3	.097*	.002
PC4	.008	.107*
PC5	.029	-.016
PC6	-.015	-.039
PC7	.201*	.070
PC8	.022	-.066
PC9	.010	.031
PC10	.054	-.053

* significant at .05, two-tailed

The pattern of significant I-values follows expectation more closely than do the I-values generated by language connectivity.

The most plausible explanation appears to be that the language criterion connects groups in a predominantly northeasterly direction, especially groups in large distance classes, where biological components are not patterned. In the smaller distance classes, language tends to connect groups in the West and Northwest direction classes. Table 3-9 shows the number of groups within each direction and distance class which are connected by the language criterion.

TABLE 3-9
COMMON LANGUAGE GROUPS WITHIN
DIRECTION/DISTANCE CLASSES
(MALES/FEMALES)

	700	1400	2100	2800	3500
NORTH	13/13	8/8			
NORTHEAST	17/16	25/25	24/24	2/2	10/10
WEST	22/20	16/14	6/5		
NORTHWEST	18/17	9/8			

Of the total 70 language connections in distance class one for males, 40 are West and Northwest connections; for females, 37 of 66. Above distance class one, North and Northeast direction classes contain 69 of the 103 male groups connected by the language criterion, and 69 of the 101 female groups. In the first distance class for male groups, the I-values generated by PC3 are highly positive in the West and

Northwest direction classes, while the values on PC7 are high in the North and Northeast direction classes, where the language criterion connects fewer groups. The I-values for PC4 in females are much higher in the first distance class for North and Northeast than for West and Northwest. It seems possible then that sample locations relative to each other happen to augment spatial autocorrelation coefficients on PC3 and to dampen them on other components. This explanation is not wholly satisfactory, of course, but it seems to be the only one that can be proffered at the present time.

4.0 DISCUSSION

4.1 Summary of Results

There can be little doubt that the multiple regression analysis and the spatial autocorrelation produce results which are concordant with each other and which demonstrate patterned among-group variability in finger ridge count contrasts. The former analytical procedure indicates that several contrasts are patterned with respect to latitude and longitude. These same contrasts tend to produce progressively decreasing autocorrelation coefficients in the Northwest direction class. As made explicit in the introductory chapter, however, these findings cannot be considered as a rigorous test of the demic expansion hypothesis. Nevertheless, the results appear to be quite encouraging.

Ammerman and Cavalli-Sforza (1984) have recently completed a monograph which summarizes a decade of their work with 39 independent gene frequencies among some 58 European localities. The authors found that their first principal component, containing about 27 percent of the total among-group variability in gene frequency, is oriented in a northwesterly direction across the European continent. By interpolating among the principal component scores of 58 European groups, the authors hypothesized scores at selected locations, and produced a biological contour map by connecting equal scores. The result is a series of contours which represent decreasing biological intensity. The decrease is oriented in a northwesterly direction.

In an allied study, Sokal and Menozzi (1982) looked at the

among-group dispersion of 21 allele frequencies of human HLA loci for indications of a northwesterly cline. Results of that study do not support an hypothesis of demic expansion in a northwesterly direction if the direction and distance classes are defined systematically with respect to geography. However, by using a criterion based on the arrival time of agriculture at a particular locality, the authors established five time classes of 1000 year increments each, and connected locality pairs which fall within the same time class. By partitioning this connectivity network into distance classes of 700 km increments, they were able to show some support of the demic expansion concept along these hypothesized routes. The larger distance classes along these routes are oriented primarily in a northwesterly direction. The I-value means for the first five distance classes proved to be .316, .078, -.030, -.014, and -.131, respectively, which values are comparable to the authors' I-value means for group connectivity by the Gabriel criterion, i.e. .213, .036, -.070, -.131, -.258 for the same distance classes. It seems reasonable to assume that the rather complicated migration route network hypothesized by the authors may be more realistic paths of gene flow than is that represented by a generalized direction class. The authors interpret their results with respect to the effects of demic expansion and subsequent migrations.

This study of phenotypic variability is merely corroborative of the pioneer studies described above. To review the comparable findings, the I-value means for the male groups in the Northwest

direction class are .030, .001, -.060, and -.180 for the first four distance classes, respectively, and .060, .040, -.020, and -.100 for the female groups. The extent of monotonicity in these values supercedes the Gabriel class and all other direction classes. However, because phenotypic variability in general is highly sensitive to both genetic or environmental processes, a question posed by the results of this study is which process offers the better interpretative framework to account for the observed systematic among-group variability. The interpretation below reviews the ideas on what mechanisms may be involved in the variability of ridge count contrasts themselves before attempting to account for systematic among-group variability.

4.2 Biological Interpretation

In early studies, Holt (1968) considered the individual fingers to be somewhat free to express their own ridge count as long as they maintained a relationship with the ridge counts on the other fingers sufficient to insure a predictable total ridge count, which she considered to be under tight genetic control. Roberts and Coope (1975) and Jantz and Owsley (1977) interpreted this observation with respect to developmental field theory to account for both the high correlation of ridge counts on adjacent and homologous digits, and the degree of independence in ridge count observed on each digit. Under the provisions of this theory, the ridge count on a particular finger depends upon a general pattern size factor and the location of the finger within the developmental field. Thus, a comparatively few genes controlling both pattern size and field variability could account for

differences in ridge counts among the fingers and the high correlations between adjacent and homologous digits.

Variability among groups thus can be interpreted as differences in developmental fields. Jantz (1975) has suggested two biological scenarios which could account for such differences. One, given that individual ridge counts are dictated by a polygenic system which controls the developmental fields, the population represented by more individuals who are heterozygous at more loci will be marked by the highest ridge count contrasts of diversity and asymmetry. His second suggestion has to do with the extent of developmental stability, or the degree of canalization. The magnitude of developmental stability is presumably a genetic response to long-term environmental stress. Thus, group differences in ridge count contrasts can be interpreted as differences in developmental stability, itself under genetic control.

Looking at the results of this study from the standpoint of developmental stability, one explanation for the observed among-group patterning of phenotypic characters with respect to geography might be a clinal selective force affecting an in-place population. A selective force operating on a gradient could produce an among-group adaptive cline (Sokal and Oden 1978). It is difficult to see how such a mechanism could operate without affecting each contrast in a comparable manner. Among the groups studied here, it is clear that if a pattern size factor can be equated with PC1, its variability is not very well aligned with geography although it explains the most unaligned variability among the various groups of both sexes. In

addition, the European samples are located in areas which are highly diverse environmentally, and no geomorphic component of geography appears to be oriented in any particular systematic among-group direction. Above all, the selective force would be required to affect each independent allele frequency to the same extent in order to produce the clinal variability shown in the studies by Ammerman and Cavalli-Sforza (1984) and Sokal and Menozzi (1982).

Comparable geographic patterning of immunological and ridge count variables favor a genetic basis for the observed among-group variability. However, a genetic basis alone does not imply a demic expansion scenario. One alternative concept briefly referred to in the introductory section, is the idea of geographic patterning produced by the admixing of Mesolithic groups themselves. In this scenario, formerly isolated Mesolithic groups might have increased their numbers more or less concurrently with the advent of agriculture, or as a direct result of its incorporation into the survival strategy. Subsequent group admixture could have proceeded along a wave of purely cultural diffusion, as agricultural practice advanced across the European continent. However, the results of the biological interpretation of the multiple regression analysis previously presented considerably weakens the possibility of this scenario. Among-group variability in ridge count means was shown to be higher for groups located in southeast Europe and lower for groups in the northwest, except for female groups located on the PC4 axis. This finding in itself tends to support an hypothesis of demic expansion,

because it is difficult to see how increased admixture of Mesolithic groups, in response to cultural diffusion alone, could somehow enhance among-group differences in ridge count contrasts.

Another line of evidence which tends to support a migration of people rather than ideas is the relatively broad expanse of patch size, i.e. the extent of homogeneity in ridge count contrasts or the first distance class exhibiting zero or negative spatial autocorrelation. Based on I-value means, the patch sizes are 2100 km for both male and female groups in the Northwest direction class. Only the Female West and Male Gabriel and Male Northeast equal this size.

The two main difficulties with the demic expansion explanation for phenotypic variability is one, the untestable assumption that the migrating population itself was marked by a high degree of ridge count contrast, and two, in accounting for the significant association of PC4 with longitude. This component, interpreted as a contrast between digit three and digits two and five, increases in magnitude from east to west. This apparent discrepancy could have something to do with the northwest orientation of the putative wave of demic expansion relative to the sample locations. Among-group increments of longitude are fewer than comparable distance increments in a northwest direction because of the geometry involved. Thus, a relatively moderate and perhaps insignificant increase in contrast in a northwest direction could appear greater per unit of longitude. It may be enlightening to note that PC4 appears to have practically no systematic association with latitude in the multiple regression analysis, and it is not

significantly negatively autocorrelated in the Northwest direction class for either sex. The surface generated by its I-values parallels the surface of PC1 in the West class for females only, where it increases in autocorrelation in the final distance class. It is also possible, of course, that the dispersion of variability on this component represents another migratory event.

The results of this study, on the whole, support an hypothesis of demic expansion. The biological components of variability herein defined are patterned the most convincingly on a northwest vector. These components are few in number and represent highly composite measures of biological variability. It seems probable that the use of additional biological variables will provide a much more resolute picture of the relationship with geography, which is no doubt more variegated than shown here. Certainly one thing which needs to be done is to classify group-pairs according to their geographical locations and then compare patch sizes with the biological contour maps prepared by Ammerman and Cavalli-Sforza (1984) which reflect differing intensities of variability on the principal components of the 39 alleles. Until a sufficient number of such variables are collected and more studies are conducted, these results can serve as a general indicator.

REFERENCES CITED

REFERENCES CITED

- Abel, W (1938) Kritische Studien über die Entwicklung der Papillarmuster auf den Fingerbeeren. Zeitschr f. menschl. Vererbungs- u. Konstitutionslehre. 21:497-529.
- Albrecht GH (1980) Multivariate analysis and the study of form, with special reference to canonical variate analysis. Amer. Zool. 20:679-693.
- Ammerman AJ, and Cavalli-Sforza, LL (1979) The wave of advance model for the spread of early farming. In C Renfrew and KL Cooke (eds): Transformations: Mathematical Approaches to Culture Change. New York. Academic Press, pp. 275-285.
- Ammerman AJ, and Cavalli-Sforza, LL (1984) The Neolithic Transition and the Genetics of Populations in Europe. Princeton. Princeton University Press.
- Aue-Hauser, G (1976) Fingerbeerenmuster und quantitative Werte von 1000 males und 1000 females Wiener. Sonderabdruck aus: Mitteilungen der Anthropologischen Gesellschaft in Wien, 106:126-141.
- Babler, WJ (1979) Quantitative differences in morphogenesis of human epidermal ridges. Birth Defects 15:199-208.
- Bara, L (1980) Dermatoglyphes digito-palmaires des habitants de Viroinval. Bull. Soc. Roy. Belge Anthropol. Prehist. 91:5-20.
- Brehme, H (1985) Personal communication.
- Brehme, H, and Pentzos-Daponte, uA (1975) Über Finger- und Handleeistenmuster von Personen aus dem Raum Thessaloniki/Griechenland. Sonderabdruck aus: Mitteilungen der Anthropologischen Gesellschaft in Wien, 105:98-110.
- Brehme, H, Riedel, V, and Baitsch, H (1966) Über Korrelationen zwischen den quantitativen Werten aller Finger- und Zehenbeerenmuster. Anthropol. Anz. Jg. 28(4):285-293.
- Cummins, H, and Midlo, C (1943) Finger Prints, Palms and Soles. New York. Dover Publications, Inc.
- da Cunha, AX, and Abreu, MDA (1954) Impressões digitais de Portugueses. Instituto da Antropologia Contribuições para o estudo da Antropologia portuguesa. 5:315-347.

- Dennis, RLH, and Sunderland, E (1979) Dermatoglyphic variation in the human populations of the North Penine Dales, North England. *Am. J. Phys. Anthrop.* 50:309-324.
- Ducros, J (1970) Interet anthropologique du nombre de cretes des dessins digitaux: application a des Basques francais. *L'Anthrop.* Paris 74:57-70.
- Friedlander, JS (1975) Patterns of Human Variation. The Demography, Genetics, and Phenetics of Bougainville Islanders. Cambridge. Harvard University Press.
- Froelich, JW, and Giles, E (1981) A multivariate approach to fingerprint variation in Papua, New Guinea: Perspectives on the evolutionary stability of dermatoglyphic markers. *Am. J. Phys. Anthrop.* 54:93-106.
- Gabriel, KR, and Sokal, RR (1969) A new statistical approach to geographic variation analysis. *Sys. Zool.* 18:259-270.
- Geipel, G (1961) Das Tastleistensystem der Hande bei Vorderindern. *Z. Morph. Anthrop.* 52:181-207.
- Gualdi-Russo, EM, Zannotti, M, and Cenni, S (1982) Digital dermatoglyphics in Italians. *Hum. Bio.* 54:373-386.
- Guseva, IS, and Antonyuk, SA (1969) Simmetriya v stroyenni kozhnovo relyefa konechnykh falang paltsev ruki cheloveka i yeyo geneticheskaya osnova. *Voprosi Antrop.* 31:33-41.
- Gyenis, G (1975) Dermatoglyphics of three Hungarian populations. *Am. J. Phys. Anthrop.* 42:229-232.
- Gyenis, G (1979) Digital dermatoglyphics of a southern Slav (Bunjevaca) population in Hungary. In W Wertelecki and C Plato (eds): *Dermatoglyphics--50 Years Later. Birth Defects: Original Article Series Vol. 15, No. 6.* New York. Alan R Liss, pp. 417-420.
- Harvey, RG, and Suter, D (1983a) Dermatoglyphic affinities of the Lithuanians. *Hum. Bio.* 55:165-181.
- Harvey, RG, and Suter, D (1983b) Digital dermatoglyphics of the Faroe Islanders. *Am. J. Phys. Anthrop.* 61:337-345.
- Holt, SB (1958) Genetics of dermal ridges: the relation between total ridge count and the variability in counts from finger to finger. *Ann. Hum. Genet., Lond.* 22:323-339.

Holt, SB (1968) *The Genetics of Dermal Ridges*. Springfield. Chas. C. Thomas.

Horn, A (1974) Finger ridge-count for Estonians. *Anthrop. Anz.* 34:112-123.

Horn, AV, and Mikelsaar, RV-A (1974) Dermal patterns in normal Estonians. *Hum. Hered.* 24:488-495.

Jantz, RL (1974) Multivariate analysis of dermatoglyphic variation in man. *Yearbook Phys. Anthrop.* 18:121-139.

Jantz, RL (1975) Population variation in asymmetry and diversity from finger to finger for digital ridge counts. *Am. J. Phys. Anthropol.* 42:215-224.

Jantz, RL (1984) How should finger ridges be counted and analyzed? *Am. Derm. Assoc. Nwsltr.* 3:19-20.

Jantz, RL, Brehme, H, and Bender, K (1985) Genetic and environmental variation of ridge-counts on fingers, palms, soles, and toes: A twin study. *Acta Genet. Med. Gemello.* (in press).

Jantz, RL, and Chopra, VP (1983) A comparison of dermatoglyphic methodologies in population studies. *Am. J. Phys. Anthropol.* 60:61-67.

Jantz, RL, Fohl, FK, and Zahler, JW (1979) Finger ridge-counts and handedness. *Hum. Bio.* 51:91-99. Jantz, RL, and Hawkinson, CH (1979) Finger ridge-count variability in Sub-Saharan Africa. *Ann. Hum. Bio.* 6:41-53.

Jantz, RL, and Owsley, DW (1977) Factor analysis of finger ridge-counts in Blacks and Whites. *Ann. Hum. Bio.* 4:357-366.

Jelisiejew, T, and Marcinkiewicz, S (1972) Numbers of cutaneous ridges on the fingers and their heredity in the Polish population. *Folia Morph.* 31:219-225.

Karev, G (1984) Personal communication.

Loesch, DZ (1983) *Quantitative Dermatoglyphics: Classification, Genetics, and Pathology*. Oxford Monographs on Medical Genetics No. 10. Oxford. Oxford University Press, p. 173.

Martin, J (1982) Personal communication.

- Matznetter, T (1967) Hautleistenuntersuchung an Sudportugiesen und Kanarischen Spaniern. *Z. Morph. Anthropol.* 58:286-307.
- Menozzi, P, Piazza, A, and Cavalli-Sforza, L (1978) Synthetic maps of human gene frequencies in Europeans. *Science* 201:786-792.
- Mulvihill, JJ, and Smith, DW (1969) The genesis of dermatoglyphics. *J. Pediatrics* 75:579-589.
- Ostovics, M, Czeizel, E, Revesz, P, and Tusnady, G (1971) Dermatoglyphic data in a sample of the population of Budapest. *Acta Paediatrica Academiae Scientiarum Hungaricae* 12:183-198.
- Plato, CC (1970) Dermatoglyphics and flexion creases of the Cypriots. *Am. J. Phys. Anthropol.* 33:421-427.
- Pospisil, MF (1970) Die dermatoglyfik der Slowakei. *Acta F.R.N. Univ. Comen., Anthropologia* 15:153-179.
- Pospisil, MF (1963) Dermatoglyfika prstu ruky a dlani obyvatelstva Horehroni. *Acta F.R.N. Univ. Comen., Anthropologia* 8:445-459.
- Rife, DC (1953) Dermatoglyphics of Egyptians. *Hum. Biol.* 25:154-158.
- Roberts, DF, and Coope, E (1975) Components of variation in a multifactorial character: A dermatoglyphic analysis. *Hum. Biol.* 47:169-188.
- Roberts, DF, Coope, E, and Kerr, B (1976) Dermatoglyphic variation among the Spanish Basques. *Man* 11:492-504.
- Roberts, DF, Luttrell, V, and Slater, CP (1965) Finger prints in a Greek sample. *Man* 5,6:21-22.
- Rudan, P, and Schmutzer, L (1976) Dermatoglyphs of the inhabitants of the Island of Hvar, Yugoslavia. *Hum. Hered.* 26:425-434.
- Sokal, RR, and Menozzi, P (1982) Spatial autocorrelations of HLA frequencies in Europe support demic diffusion of early farmers. *Am. Naturalist* 119:1-17.

- Sokal, RR, and Oden, NL (1978) Spatial autocorrelation in biology: 1. Methodology. *Bio. J. Linnean Soc.* 10:199-228.
- Spuhler, JN (1972) Genetic, linguistic, and geographical distances in native North America. In JS Weiner and J Huizinga (eds) *The Assessment of Population Affinities in Man*. Oxford. Clarendon Press, pp. 72-95.
- Szilvassy, VJ (1978) Quantitative Hautleistenwerte der Finger- und Zehenbeeren von 500 Männern und 500 Frauen aus Ostosterreich (Wien, Niederosterreich und Burgenland). *Ann. Naturhistor. Mus. Wien* 81:637-642.
- Thoma, A (1969) Total finger ridge-count in a Hungarian population. *Hum. Bio.* 41:213-217.
- Uytterschaut, HT, and Wilink, FW (1983) On the assumption of equality of variance-covariance matrices in the sex and racial diagnosis of human skulls. *Am. J. Phys. Anthropol.* 60:347-357
- Vogelius-Anderson, CH (1969) *The Finger Prints of Danish Males and Females. A Qualitative and Quantitative Analysis.* NYT Nordisk Forlag. Kobenhavn. Arnold Busck.
- Vrydagh-Laoureux, S (1983) Dermatoglyphes des Belges: Ostende (Flandre occidentale) et Saint-Ghislain (Hainaut). *Bull. Soc. Roy. Belge Anthropol. Prehist.* 94:91-106.
- Vrydagh-Laoureux, S (1971) Dermatoglyphes digitaux et palmaires d'un echantillon de bruxellois. *Bull. Soc. Roy. Belge Anthropol. Prehist.* 82:213-239.
- Vrydagh, St, and Leguebe, A (1976) Variabilite du nombre de cretes par doigt chez des sujets belges. *Bull. Mem. Soc. Anthropol. Paris* 3:91-104.
- Weninger, M (1975) Fingerbeerenmuster von 500 Mittelschulern aus Modling bei Wien. Sonderabdruck aus: *Mitteilungen der Anthropologischen Gesellschaft in Wien*, CV:111-117.
- Weninger, M, and Rothenbuchner, G (1974) Finger- und Handabdrucke von Griechen. In *Bevolkerungsbiologie*. W Bernhard und A Kandler (eds). Stuttgart. Fischer-Verlag.
- Williams, WR (1978) A study of dermatoglyphic variability in the populations of central Wales and Shropshire. Unpublished PhD dissertation, Univ. of Durham.

APPENDIXES

APPENDIX A

COVARIANCE MATRICES, EIGENVALUES, AND EIGENVECTORS OF TWELVE EUROPEAN SAMPLES

TABLE A-1

SPN1 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

SPNF1	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	31.33	27.67	23.01	24.13	16.98	26.17	26.14	19.52	21.53	15.31
ROW2	27.67	48.94	32.22	31.92	19.57	27.35	38.47	26.74	27.59	18.58
ROW3	23.01	32.22	41.75	32.27	20.81	22.68	30.34	31.82	29.34	18.73
ROW4	24.13	31.92	32.27	51.63	22.58	22.8	29.79	28.65	36.53	19.89
ROW5	16.98	19.57	20.81	22.58	42.89	15.69	18.83	18.52	21.95	28.79
ROW6	26.17	27.35	22.68	22.8	15.69	29.99	26.59	18.66	21.3	13.79
ROW7	26.14	38.47	30.34	29.79	18.83	26.59	44.13	25.9	25.44	18.22
ROW8	19.52	26.74	31.82	28.65	18.52	18.66	25.9	36.8	27.7	17.2
ROW9	21.53	27.59	29.34	36.53	21.95	21.3	25.44	27.7	45.61	19.23
ROW10	15.31	18.58	18.73	19.89	28.79	13.79	18.22	17.2	19.23	32.99

LAMBDA	COL 1
ROW1	263.184
ROW2	40.5041
ROW3	29.8086
ROW4	19.0423
ROW5	14.2415
ROW6	11.4171
ROW7	8.66693
ROW8	8.19943
ROW9	6.72582
ROW10	4.26593

EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.279	0.141199	0.275989	-0.387759	-0.392982	-0.203798	0.0822744	0.187482	0.0711102	0.657838
ROW2	0.369661	0.305584	0.272174	0.159547	0.379477	0.264509	-0.252087	0.558754	-0.282397	-0.0310648
ROW3	0.345951	0.0843279	-0.14568	0.44551	-0.276524	-0.304078	-0.040289	-0.323424	-0.611881	0.0628601
ROW4	0.369114	-0.00259138	-0.493902	-0.341151	0.467	-0.518013	0.0381583	0.0748121	0.0751227	-0.0655857
ROW5	0.264398	-0.692801	0.235321	-0.00476558	0.017771	-0.0594048	-0.604854	-0.107052	0.114572	0.0210175
ROW6	0.271346	0.18192	0.278373	-0.367591	-0.377576	-0.0847884	0.00339034	-0.0480189	0.00781226	-0.727001
ROW7	0.347403	0.27061	0.307807	0.0876412	0.35647	0.165945	0.134164	-0.643175	0.323418	0.113021
ROW8	0.309304	0.0462057	-0.22309	0.53493	-0.299985	-0.0450775	0.0514702	0.283454	0.620415	-0.0796484
ROW9	0.337251	-0.0862121	-0.509426	-0.272886	-0.191728	0.694795	-0.0213579	-0.101836	-0.0945748	0.0711819
ROW10	0.23654	-0.532633	0.217217	0.0766858	0.101527	0.0683559	0.734601	0.155844	-0.15332	-0.0698138

TABLE A-2

SPN2 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

SPNF 2	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	31.45	29	20.09	24.95	17.72	26.33	27.66	19.42	22.65	17.58
ROW2	29	50.77	33.77	33.42	21.66	29.09	42.12	32.14	32.21	23.36
ROW3	20.09	33.77	46.04	34.78	21.39	21.99	31.09	34.54	32.53	22.03
ROW4	24.95	33.42	34.78	54.76	23.71	25.07	31.59	32.2	42.32	24.58
ROW5	17.72	21.66	21.39	23.71	41.72	19.28	20.53	21.28	23.02	32.97
ROW6	26.33	29.09	21.99	25.07	19.28	32.3	28.66	21.53	24.86	18.5
ROW7	27.66	42.12	31.09	31.59	20.53	28.66	48.49	30.17	31.31	22.03
ROW8	19.42	32.14	34.54	32.2	21.28	21.53	30.17	38.58	29.32	21.65
ROW9	22.65	32.21	32.53	42.32	23.02	24.86	31.31	29.32	54.04	24.31
ROW10	17.58	23.36	22.03	24.58	32.97	18.5	22.03	21.65	24.31	42.45

LAMBDA		COL 1
ROW1	288.955	
ROW2	41.3208	
ROW3	33.4379	
ROW4	23.2059	
ROW5	13.8599	
ROW6	11.328	
ROW7	8.77607	
ROW8	7.56969	
ROW9	7.10467	
ROW10	5.04172	

EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.258292	0.0974889	-0.3343	0.360368	-0.392026	0.0844913	-0.205962	0.1111	-0.00766067	0.683018
ROW2	0.364372	0.264705	-0.323726	-0.131383	0.269548	-0.22439	-0.0192432	0.61401	0.375464	-0.1837
ROW3	0.332364	0.114594	0.230843	-0.562442	-0.22216	0.310638	-0.222852	0.257483	-0.454768	-0.0128787
ROW4	0.366023	0.0647221	0.484567	0.259425	-0.343166	-0.637587	0.0878754	-0.00363164	-0.090303	-0.139909
ROW5	0.259782	-0.64733	-0.121535	-0.0257226	-0.100044	0.124731	0.649386	0.213705	-0.0618602	0.0357563
ROW6	0.270193	0.0766935	-0.301721	0.305925	-0.341015	0.368092	-0.0867084	-0.222442	0.0352439	-0.653042
ROW7	0.348676	0.270329	-0.345545	-0.0516732	0.401329	-0.190278	0.260566	-0.44787	-0.458041	0.0878686
ROW8	0.311648	0.0705416	0.118631	-0.451638	-0.170166	0.0731661	0.11285	-0.468537	0.617479	0.178878
ROW9	0.35394	0.0469208	0.494844	0.406741	0.488355	0.44876	-0.00584635	0.0378539	0.099204	0.10503
ROW10	0.267612	-0.630819	-0.105827	-0.0537998	0.227439	-0.213313	-0.624451	-0.166292	0.00512959	-0.0388395

TABLE A-3

ENG1 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

ENG1	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	34.49	32.32	28.59	26.99	16.3	30.16	28.02	24.61	28.2	15.88
ROW2	32.32	52.45	37.7	31.7	16.75	31.94	36.95	32.62	32.76	17.44
ROW3	28.59	37.7	45.73	34.53	22.28	28.19	26.88	32.15	32.94	17.61
ROW4	26.99	31.7	34.53	53.21	20.66	29.09	27.07	29.2	37.57	15.06
ROW5	16.3	16.75	22.28	20.66	33.42	15.02	12.26	16.27	18.91	20.17
ROW6	30.16	31.94	28.19	29.09	15.02	36.51	29.86	24.57	29.01	14.55
ROW7	28.02	36.95	26.88	27.07	12.26	29.86	43.9	28.18	29.97	13.68
ROW8	24.61	32.62	32.15	29.2	16.27	24.57	28.18	39.12	30.03	13.22
ROW9	28.2	32.76	32.94	37.57	18.91	29.01	29.97	30.03	48.38	14.37
ROW10	15.88	17.44	17.61	15.06	20.17	14.55	13.68	13.22	14.37	24.16

	LAMBDA	CGL 1
ROW1	277.246	
ROW2	34.6606	
ROW3	26.7438	
ROW4	18.055	
ROW5	13.7226	
ROW6	11.8462	
ROW7	10.5253	
ROW8	7.25535	
ROW9	6.4353	
ROW10	4.87554	

EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.307872	0.0878665	-0.183969	-0.283816	-0.216414	-0.377356	-0.21103	0.148168	-0.184822	-0.702296
ROW2	0.379635	0.290671	-0.302381	0.302475	-0.239631	0.133663	0.537213	0.14124	-0.429129	0.143092
ROW3	0.357221	-0.144838	-0.00636495	0.517254	-0.260618	-0.285822	0.0377523	-0.34829	0.554222	-0.0656836
ROW4	0.357831	-0.202311	0.641692	-0.133826	-0.395808	0.476232	-0.0369646	0.0977201	-0.0367232	-0.0749879
ROW5	0.20877	-0.688655	-0.248491	-0.0627076	0.195956	0.0916708	-0.0182774	-0.45443	-0.403537	0.00197114
ROW6	0.313231	0.154183	-0.0896028	-0.41119	-0.260381	-0.280495	-0.329937	-0.118743	-0.020288	0.65663
ROW7	0.325063	0.42196	-0.204384	-0.258475	0.33799	0.489796	-0.016604	-0.366595	0.302261	-0.165938
ROW8	0.315734	0.0778828	0.0448673	0.490741	0.381589	0.0788185	-0.608973	0.301038	-0.181318	0.0723601
ROW9	0.35471	-0.0185865	0.424419	-0.171691	0.550521	-0.415065	0.417595	0.102792	0.0193964	0.0557339
ROW10	0.180475	-0.40423	-0.411361	-0.179922	0.0399765	0.160543	0.0968261	0.609142	0.430478	0.0965614

TABLE A-4

GER1 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

GEKF	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
KU#1	34.03	29.36	23.74	22.46	19.91	27.98	28	21.49	24.36	19.29
KU#2	29.36	49.12	33.66	30.06	22.05	27.12	39.74	29.59	31.34	21.02
KU#3	23.74	33.66	48.04	34.47	21.9	24.03	31.05	34.72	33.81	20.92
KU#4	22.46	30.06	34.47	53.96	24.06	24.51	28.16	32.17	41.04	21.85
KU#5	19.91	22.05	21.9	24.06	42.08	21.33	19.18	20.53	22.96	32.36
KU#6	27.98	27.12	24.03	24.51	21.33	35.24	26.35	21.98	26.08	21.04
KU#7	28	39.74	31.05	28.16	19.18	26.35	48.41	29.14	30.36	19.95
KU#8	21.49	29.59	34.72	32.17	20.53	21.98	29.14	43.12	31.5	20.1
KU#9	24.36	31.34	33.81	41.04	22.96	26.08	30.36	31.5	52.38	21.88
KU#10	19.29	21.02	20.92	21.89	32.36	21.04	19.95	20.1	21.88	39.36
			LAMBDA		COL 1					
			ROW1		285.911					
			ROW2		41.7243					
			ROW3		35.3394					
			ROW4		21.0866					
			ROW5		15.7252					
			ROW6		12.0067					
			ROW7		11.2104					
			ROW8		8.92952					
			ROW9		7.64345					
			ROW10		6.16305					
EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
KU#1	0.275824	-0.0512851	0.350687	-0.316308	-0.372846	-0.0842926	0.0158122	0.115528	-0.011608	-0.733762
KU#2	0.351201	0.18281	0.392744	0.0922984	0.347037	-0.226757	-0.241208	0.465007	-0.444268	0.191911
KU#3	0.344874	0.201181	-0.132449	0.480276	-0.332352	-0.173276	-0.574031	-0.325498	0.124265	-0.0315601
KU#4	0.353013	0.14161	-0.531047	-0.269356	0.180031	-0.601969	0.296067	-0.117905	-0.0453896	-0.0486812
KU#5	0.265519	-0.640864	-0.0803235	0.120605	0.144384	-0.106235	-0.101662	0.389705	0.549147	0.0435405
KU#6	0.280878	-0.112591	0.237166	-0.399414	-0.506346	-0.0337212	0.0830611	-0.119746	0.0312189	0.642585
KU#7	0.33699	0.227856	0.434638	0.0613853	0.433843	0.154562	0.268248	-0.424647	0.421017	-0.0139276
KU#8	0.319021	0.166663	-0.163029	0.476218	-0.304515	0.28949	0.573754	0.324491	-0.0770672	0.0112157
KU#9	0.356153	0.164778	-0.380132	-0.404727	0.151323	0.633129	-0.318394	0.109501	0.00133574	-0.0241114
KU#10	0.255828	-0.610895	-0.0229745	0.140642	0.128847	0.16768	0.068124	-0.432148	-0.547043	-0.0753949

TABLE A-5

AUST FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

AUSF1	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	28.2	23.65	19.25	20.08	13.36	22.98	21.42	16.98	21.53	12.92
ROW2	23.65	42.64	27.95	26.54	15.64	27.14	33.2	24.48	28.27	15.52
ROW3	19.25	27.95	38.81	27.38	16.6	18.06	25.17	27.19	28.6	16.02
ROW4	20.08	26.54	27.38	45.43	16.26	19.4	24.58	26.59	34.59	16.25
ROW5	13.36	15.64	16.6	16.26	32.83	12.58	13.76	15.12	15.85	24.7
ROW6	22.98	27.14	18.06	19.4	12.58	27.98	20.76	16.3	19.63	13.21
ROW7	21.42	33.2	25.17	24.58	13.76	20.76	37.7	22.95	25.72	14.77
ROW8	16.98	24.48	27.19	26.59	15.12	16.3	22.95	33.06	27.57	14.36
ROW9	21.53	28.27	28.6	34.59	15.85	19.63	25.72	27.57	49.65	16.37
ROW10	12.92	15.52	16.02	16.25	24.7	13.21	14.77	14.36	16.37	32.55
				LAMBDA	COL 1					
				ROW1	230.87					
				ROW2	37.4286					
				ROW3	29.8588					
				ROW4	17.944					
				ROW5	13.0179					
				ROW6	12.6166					
				ROW7	8.47923					
				ROW8	8.15295					
				ROW9	7.74699					
				ROW10	3.1345					
EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.274927	0.0402881	0.310427	-0.378746	0.213423	-0.372482	0.105819	0.26004	-0.449466	-0.466743
ROW2	0.371405	0.18059	0.406307	0.127358	-0.161035	0.204569	-0.108822	-0.400078	0.416747	-0.484537
ROW3	0.343298	0.0583709	-0.133982	0.544955	0.209861	-0.410692	-0.562369	-0.0386152	-0.153699	0.0986384
ROW4	0.363061	0.125561	-0.431325	-0.273855	0.541749	0.531337	-0.107801	-0.0424418	-0.03253	-0.0330248
ROW5	0.230333	-0.663684	-0.0159289	0.0214105	0.0184903	-0.0282916	0.257836	-0.590442	-0.286352	0.0867022
ROW6	0.27187	0.0488825	0.417231	-0.356277	0.215138	-0.20721	-0.0186858	-0.0335267	0.337921	0.646373
ROW7	0.336486	0.164039	0.304306	0.264405	-0.306794	0.461591	0.120626	0.242856	-0.471053	0.30781
ROW8	0.314343	0.0672627	-0.21349	0.374703	0.157174	-0.192577	0.705741	0.234276	0.307719	-0.0353305
ROW9	0.380111	0.189442	-0.471209	-0.35932	-0.633865	-0.235239	-0.0336286	-0.0808269	0.00309006	0.0606867
ROW10	0.230914	-0.660609	0.00175809	-0.0392896	-0.154101	0.138552	-0.261726	0.546701	0.294688	-0.107521

TABLE A-6

AUS2 FEMALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

AUSF2	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	34.36	28.05	23.78	24.45	16.25	26.73	27.03	21.16	25.07	15.34
ROW2	28.05	44	30.27	26.99	18.1	25.03	35.22	25.7	27.4	18.06
ROW3	23.78	30.27	40	29.66	19.62	20.86	27.92	28.33	28.69	17.69
ROW4	24.45	26.99	29.66	48.9	21.16	23.43	25.31	25.58	35.25	18.59
ROW5	16.25	18.1	19.62	21.16	39.47	15.51	17.59	17.84	22.07	26.79
ROW6	26.73	25.03	20.86	23.43	15.51	33.25	25.68	20.08	24.03	15.42
ROW7	27.03	35.22	27.92	25.31	17.59	25.68	42.24	24.43	26.33	17.18
ROW8	21.16	25.7	28.33	25.58	17.84	20.08	24.43	34.79	26.77	16.36
ROW9	25.07	27.4	28.69	35.25	22.07	24.03	26.33	26.77	48.43	20.65
ROW10	15.34	18.06	17.69	18.59	26.79	15.42	17.18	16.36	20.65	34.7

LAMBDA	COL1
ROW1	254.194
ROW2	38.2978
ROW3	28.1646
ROW4	19.5131
ROW5	13.7225
ROW6	13.3115
ROW7	10.0433
ROW8	8.93933
ROW9	7.62549
ROW10	6.32853

EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.303692	-0.208164	0.164533	-0.39642	0.0692825	-0.296857	0.0957116	0.396205	-0.146904	-0.632119
ROW2	0.352612	0.289702	0.298381	0.195593	-0.207979	0.339532	-0.0230916	0.226799	-0.595752	0.314677
ROW3	0.336767	0.0857801	-0.0950963	0.528787	0.00985658	-0.255071	0.00283411	0.506406	0.4941	0.157551
ROW4	0.353976	-0.0534849	-0.596506	-0.12181	-0.662707	-0.100638	-0.131144	-0.163071	-0.0688158	-0.0578722
ROW5	0.254267	-0.650706	0.233432	0.0243908	-0.119226	-0.111525	0.643751	-0.057161	-0.0683635	0.0725791
ROW6	0.287226	0.169951	0.155208	-0.544448	0.136328	-0.349918	-0.0790773	-0.154622	0.169343	0.606826
ROW7	0.339486	0.29422	0.340908	0.0658223	-0.147231	0.361682	0.108043	-0.471085	0.469555	-0.266581
ROW8	0.302498	0.0490234	-0.0974783	0.411431	0.420708	-0.401536	-0.109066	-0.493185	-0.340717	-0.133691
ROW9	0.360005	-0.0969732	-0.481153	-0.19407	0.529385	0.528554	0.137749	0.10759	0.028559	0.028951
ROW10	0.24217	-0.558433	0.28849	-0.0430274	0.0307862	0.122925	-0.714064	0.0681274	0.0623861	-0.0997499

TABLE A-7

SPN1 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

SPNMI	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	22.41	19.44	16.78	17.52	14.69	18.85	17.96	15.19	18.15	13.46
ROW2	19.44	38.5	26.21	25.66	18.52	20.53	27.95	22.82	24.81	18.06
ROW3	16.78	26.21	38.2	28.71	20.96	18.3	22.87	28.1	30.64	17.99
ROW4	17.52	25.66	28.71	47.17	21.95	19.23	23.33	26.1	37.45	19.91
ROW5	14.69	18.52	20.96	21.95	41	14.67	16.9	19.89	21.66	28.97
ROW6	18.85	20.53	18.3	19.23	14.67	25.51	20.02	17.25	20.05	14.66
ROW7	17.96	27.95	22.87	23.33	16.9	20.02	32.92	20.78	22.51	16
ROW8	15.19	22.82	28.1	26.1	19.89	17.25	20.78	32.85	28.22	17.83
ROW9	18.15	24.81	30.64	37.45	21.66	20.05	22.51	28.22	52.12	20.37
ROW10	13.46	18.06	17.99	19.91	28.97	14.66	16	17.83	20.37	38.65

LAMBDA	COL 1
ROW1	232.046
ROW2	36.9334
ROW3	29.6062
ROW4	16.3395
ROW5	13.4245
ROW6	11.4498
ROW7	9.98537
ROW8	7.91457
ROW9	6.82687
ROW10	4.80391

EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.234047	0.0282316	0.301062	0.316336	0.348831	0.265606	0.0498708	0.250642	0.0449325	-0.702966
ROW2	0.33247	0.138239	0.441138	-0.0947493	-0.365036	-0.304277	-0.250456	0.444673	0.403469	0.132997
ROW3	0.34635	0.148209	-0.0532775	-0.58958	0.124555	0.0761689	0.126202	0.365753	-0.579601	0.0260358
ROW4	0.375577	0.208649	-0.370099	0.312271	-0.588206	0.363253	0.319324	0.0311091	0.00442016	-0.00516115
ROW5	0.296915	-0.637241	-0.0935039	-0.109142	-0.0290632	0.460322	-0.507586	-0.0340364	0.0608061	0.0993499
ROW6	0.25448	0.0610853	0.317276	0.339103	0.413281	0.207626	0.234892	-0.0187808	-0.0210214	0.667812
ROW7	0.301821	0.130343	0.423752	0.0318995	-0.225966	-0.118296	-0.193959	-0.663704	-0.38874	-0.130518
ROW8	0.31725	0.083023	-0.0714236	-0.48711	0.20934	0.0574065	0.315949	-0.400723	0.57688	-0.0988481
ROW9	0.390008	0.265156	-0.528243	0.244596	0.340219	-0.381353	-0.419924	-0.0307439	0.0131801	0.00916182
ROW10	0.277311	-0.640778	-0.0428118	0.144268	-0.0358609	-0.530461	0.436225	0.034111	-0.104949	-0.0686413

TABLE A-8

SPN2 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

SPNM2	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	27.55	22.74	20.37	18.24	16.99	20.95	22.66	18.49	20.18	16.1
ROW2	22.74	39.55	28.26	22.86	16.87	20.81	33.77	26.91	25.96	16.56
ROW3	20.37	28.26	38.37	28.2	19.77	17.81	28.69	29.07	29.51	17.21
ROW4	18.24	22.86	28.2	47	18.59	16.43	23.86	25.29	36.43	17.44
ROW5	16.99	16.87	19.77	18.59	43.01	14.58	16.12	17.15	21.54	32.25
ROW6	20.95	20.81	17.81	16.43	14.58	25.79	21.2	17.74	18.13	14.68
ROW7	22.66	33.77	28.69	23.86	16.12	21.2	41.51	26.46	29.51	16.65
ROW8	18.49	26.91	29.07	25.29	17.19	17.74	26.46	35.38	27.28	17.59
ROW9	20.18	25.96	29.51	36.43	21.54	18.13	28.51	27.28	45.91	21.65
ROW10	16.1	16.56	17.21	17.44	32.25	14.68	16.65	17.55	21.65	41.18
LAMBDA				COL 1						
ROW1				239.849						
ROW2				46.0543						
ROW3				31.7073						
ROW4				16.5139						
ROW5				12.8103						
ROW6				10.6776						
ROW7				8.9531						
ROW8				7.15209						
ROW9				6.32981						
ROW10				5.20262						
EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.266862	0.0167435	-0.282787	0.499642	-0.241379	0.0260557	-0.132266	0.17397	0.313258	-0.627742
ROW2	0.339992	0.231941	-0.34757	-0.153395	0.219966	0.18791	0.340174	-0.308767	0.578019	0.239621
ROW3	0.345674	0.153716	0.0405574	-0.390975	-0.418765	0.167499	-0.187301	0.624764	0.0999992	0.252077
ROW4	0.344051	0.127053	0.646069	0.279279	-0.0912626	0.148896	0.569903	0.0179925	-0.11032	-0.0479781
ROW5	0.279409	-0.647033	-0.0335718	-0.107393	-0.172118	0.556907	-0.129169	-0.329078	-0.159199	-0.0229609
ROW6	0.244716	0.0341866	-0.257472	0.542374	-0.240384	-0.208397	-0.0714507	-0.104493	-0.293425	0.594096
ROW7	0.34796	0.263202	-0.304319	-0.0963093	0.496887	0.177836	0.018043	0.175921	-0.591744	-0.218646
ROW8	0.323261	0.14156	-0.00748121	-0.40803	-0.377849	-0.514615	0.0120498	-0.442154	-0.179592	-0.270963
ROW9	0.371378	0.0677777	0.440968	0.102115	0.389816	-0.119372	-0.644956	-0.152169	0.201479	0.0817325
ROW10	0.271806	-0.626437	-0.058661	-0.0638349	0.283946	-0.499507	0.262082	0.339011	0.105559	0.0354496

TABLE A-9

ENGL MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

ENGL	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	27.65	26.23	22.84	23.06	20.82	23.18	24.87	20.35	22.36	21.2
ROW2	26.23	43.08	33.77	31.87	23.82	26.46	37.6	31.71	36.18	24.3
ROW3	22.84	33.77	44.67	38.21	27.78	24.43	34.28	34.42	38.42	27.39
ROW4	23.06	31.87	38.21	61.34	30.49	24	34.96	35.85	46.88	30.55
ROW5	20.82	23.82	27.78	30.49	43.53	10.44	26.81	25.17	32.22	37.95
ROW6	23.18	26.46	24.43	24	18.44	28.9	29.01	22.22	22.44	20.61
ROW7	24.87	37.6	34.28	34.96	26.81	29.01	44.38	32.19	36.73	27.75
ROW8	20.39	31.71	34.42	35.85	25.17	22.22	32.19	40.42	36.56	23.96
ROW9	22.36	36.18	38.42	46.88	32.22	22.44	36.73	36.56	62.03	31.24
ROW10	21.2	24.3	27.39	30.55	37.95	20.61	27.75	23.96	31.24	43.71
			LAMBDA		COL1					
			ROW1		310.593					
			ROW2		35.0894					
			ROW3		32.3515					
			ROW4		16.3197					
			ROW5		13.3416					
			ROW6		8.85047					
			ROW7		7.94349					
			ROW8		6.91264					
			ROW9		5.337					
			ROW10		2.97074					
EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.233306	0.0395658	0.377741	-0.20434	-0.280482	-0.58887	-0.219868	-0.0900022	0.0574888	0.523808
ROW2	0.322774	0.308311	0.269709	0.246482	-0.0940471	0.0451002	-0.0291989	-0.672536	-0.266475	-0.363621
ROW3	0.336976	0.140534	-0.0303264	0.00899445	0.563551	-0.344988	0.649866	0.0389573	0.0498091	0.052601
ROW4	0.373812	0.052886	-0.527372	-0.705887	-0.143635	0.119909	-0.0148607	-0.208314	-0.0770573	-0.0488454
ROW5	0.292596	-0.626514	0.0737448	0.0973033	0.124156	-0.029063	-0.152527	-0.210137	0.668102	-0.231282
ROW6	0.241119	0.157119	0.400233	-0.25741	-0.190962	-0.0518058	0.00968822	0.565222	0.0545107	-0.573605
ROW7	0.336902	0.205871	0.255239	0.0758213	-0.104069	0.669786	0.174432	0.0861518	0.298174	0.432456
ROW8	0.313106	0.189176	-0.0796426	0.083734	0.568118	0.0590936	-0.676829	0.206276	-0.142987	0.0740304
ROW9	0.382977	0.0584215	-0.456683	0.557284	-0.433774	-0.194768	0.0141057	0.256996	0.017528	-0.00250029
ROW10	0.293491	-0.618095	0.147377	-0.00899208	-0.0251954	0.155677	0.127194	0.122603	-0.663461	0.115016

TABLE A-10

GER1 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

GERM	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	30.81	27.21	24.79	24.06	16.57	27.14	27.45	22.88	23.67	15.11
ROW2	27.21	46.75	35.18	32.67	20.23	26.63	40.12	31.61	31.17	16.3
ROW3	24.79	35.18	49.94	36.78	22.6	25.34	32.07	39.82	35.58	20.32
ROW4	24.06	32.67	36.78	54.19	23.79	26.53	31.7	36.37	42.97	19.66
ROW5	16.57	20.23	22.6	23.79	44.21	18.23	17.82	22.14	20.56	32.2
ROW6	27.14	26.63	25.34	26.53	18.23	33.9	28.76	24.76	25.31	16.26
ROW7	27.45	40.12	32.07	31.7	17.82	28.76	49.5	30.45	31.06	16.9
ROW8	22.88	31.61	39.82	36.37	22.14	24.76	30.45	47.34	35.69	20.05
ROW9	23.67	31.17	35.58	42.97	20.56	25.31	31.06	35.65	57.17	19.42
ROW10	15.11	18.3	20.32	19.66	32.2	16.26	16.9	20.05	19.42	40.82
LAMBDA										
COL 1										
ROW1	291.567									
ROW2	47.9526									
ROW3	34.0831									
ROW4	21.0319									
ROW5	16.2849									
ROW6	13.1455									
ROW7	9.6566									
ROW8	9.2315									
ROW9	6.98602									
ROW10	4.69097									
EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.259784	0.0668772	-0.31819	-0.218643	-0.459141	-0.0797531	-0.152507	-0.150006	-0.200633	-0.689786
ROW2	0.342581	0.171028	-0.345491	0.126267	0.405566	0.0808555	-0.293131	-0.17412	-0.601278	0.263211
ROW3	0.358371	0.0829988	0.12836	0.584878	-0.146628	-0.0621982	-0.359106	-0.368795	0.463689	0.0279324
ROW4	0.366747	0.096525	0.400488	-0.243591	0.0357224	0.699684	0.263512	-0.26865	-0.00497434	-0.0631141
ROW5	0.248417	-0.66459	-0.0309014	-0.0268295	0.0299174	0.303168	-0.415143	0.472002	0.0755501	-0.0359186
ROW6	0.274055	0.0480242	-0.288258	-0.288825	-0.56268	-0.0155706	0.0942789	0.047211	0.115452	0.644032
ROW7	0.338193	0.239985	-0.449744	-0.0729711	0.430753	-0.0169205	0.289728	0.272077	0.497252	-0.171394
ROW8	0.345543	0.0604324	0.21594	0.496333	-0.21649	-0.12065	0.431427	0.466034	-0.33991	-0.060753
ROW9	0.360997	0.154432	0.515605	-0.445022	0.16893	-0.518451	-0.256351	0.134481	0.00255136	0.0283363
ROW10	0.226508	-0.648838	-0.061064	-0.0312533	0.153211	-0.343349	0.418808	-0.45242	-0.0365691	0.0146175

TABLE A-11

AUS1 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

AUSM1	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	24.11	19.56	16.45	17.18	12.97	20.48	18.62	16.36	18.97	12.32
ROW2	19.56	34.11	23.94	21.22	14.28	19.46	28.88	22.98	22.47	12.46
ROW3	16.45	23.94	37.09	26.48	17.32	17.75	23.64	27.78	27.34	16.6
ROW4	17.18	21.22	26.48	44.76	19.15	17.64	21.24	25.76	33.2	16.99
ROW5	12.97	14.28	17.32	19.15	37.58	13.1	14	16.8	19.41	27.74
ROW6	20.48	19.46	17.75	17.64	13.1	26.52	20.14	17.46	19.36	12.36
ROW7	18.62	28.88	23.64	21.24	14	20.14	35.76	22.81	22.6	13.79
ROW8	16.36	22.98	27.78	25.76	16.8	17.46	22.81	35.64	27.22	15.09
ROW9	18.97	22.97	27.34	33.2	19.41	19.36	22.6	27.22	48.44	17.47
ROW10	12.32	12.96	16.6	16.99	27.74	12.36	13.79	15.09	17.47	33.76

LAMBDA	COL 1
ROW1	217.715
ROW2	39.7111
ROW3	29.2568
ROW4	18.1179
ROW5	13.2593
ROW6	12.6428
ROW7	8.81426
ROW8	7.72301
ROW9	6.26011
ROW10	4.27008

EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
ROW1	0.254532	0.10261	0.266981	-0.451306	-0.0194449	-0.310226	0.0027585	-0.0528742	0.330989	-0.663893
ROW2	0.323363	0.269262	0.330041	0.111128	-0.0360546	0.362361	-0.0845549	-0.229855	0.606957	0.375062
ROW3	0.347751	0.0991518	-0.0851593	0.496097	0.0812975	-0.329423	0.606373	-0.34911	-0.0724007	-0.0770567
ROW4	0.364488	0.00942014	-0.516937	-0.130414	-0.758886	0.062953	-0.0107606	0.0416257	0.0238133	0.0232917
ROW5	0.272635	-0.655346	0.137696	0.024995	-0.00229829	0.0706465	-0.357613	-0.547875	-0.202583	-0.0501752
ROW6	0.265221	0.126514	0.289551	-0.448981	-0.0195608	-0.425783	0.0500654	0.0240856	-0.352617	0.564915
ROW7	0.324837	0.270545	0.366849	0.131875	-0.0873317	0.481306	0.0110427	0.2199	-0.546446	-0.288017
ROW8	0.338145	0.117224	-0.1091	0.427167	0.160919	-0.395431	-0.609083	0.348877	0.0493666	-0.0121353
ROW9	0.385457	0.0530812	-0.51417	-0.342002	0.617402	0.287756	0.0476147	-0.00458858	-0.0269783	0.0162707
ROW10	0.252503	-0.609764	0.177954	0.0426233	0.0266481	0.0535257	0.348245	0.59154	0.221571	0.0841613

TABLE A-12

AUS2 MALE COVARIANCE MATRIX (L5-R1), EIGENVALUES, AND EIGENVECTORS

AUSM2	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
RUN1	27.02	20.66	18.92	21.25	14.96	22.57	19.44	16.97	21.69	13.78
RUN2	20.66	38.16	27.3	25.74	17.63	20.24	27.85	23.78	26.31	15.8
RUN3	18.92	27.3	40.46	28.68	19.29	18.36	22.37	29.37	28	16.7
RUN4	21.25	25.74	28.68	46.15	21.32	20.58	21.87	25.32	35.68	18.7
RUN5	14.96	17.63	19.29	21.32	38.71	14.32	14.19	17.58	19.83	27.78
RUN6	22.57	20.24	18.36	20.58	14.32	27.61	19.33	16.97	20.56	13.54
RUN7	19.44	27.85	22.37	21.87	14.19	19.33	31.64	20.68	22.64	12.87
RUN8	16.97	23.78	29.37	25.32	17.58	16.97	20.68	37.86	27.55	16.51
RUN9	21.69	26.31	28	35.68	19.83	20.56	22.64	27.55	50.63	17.54
RUN10	13.78	15.8	16.7	18.7	27.78	13.94	12.87	16.51	17.54	35.38
				LAMBDA	COL 1					
				ROW1	230.181					
				ROW2	38.3629					
				ROW3	26.3631					
				ROW4	22.0735					
				ROW5	14.2414					
				ROW6	13.133					
				ROW7	9.61307					
				ROW8	8.59376					
				ROW9	6.37925					
				ROW10	4.65894					
EV	COL 1	COL 2	COL 3	COL 4	COL 5	COL 6	COL 7	COL 8	COL 9	COL 10
RUN1	0.269404	0.07276	0.309879	0.363428	0.369671	0.0254541	0.143687	0.000977055	0.0774824	-0.728058
RUN2	0.338562	0.185952	0.349693	-0.143842	-0.530698	-0.0348184	-0.00297829	0.107621	0.642688	0.0181726
RUN3	0.349875	0.126017	-0.0595055	-0.509529	0.173978	0.309709	0.452056	0.468201	-0.219095	0.0280796
RUN4	0.374452	0.0816356	-0.414466	0.259544	-0.133528	0.603465	-0.323663	-0.154987	0.0141339	-0.00661641
RUN5	0.277007	-0.654833	0.00404963	-0.0225216	-0.14	0.0282464	0.482289	-0.488018	0.00469466	0.0524702
RUN6	0.264816	0.0703121	0.353462	0.366015	0.445229	0.0286185	0.0245904	0.0139227	0.0775493	0.678355
RUN7	0.294124	0.209652	0.400861	-0.0210466	-0.35514	-0.118387	-0.176849	-0.197123	-0.705768	-0.00484065
RUN8	0.325317	0.10279	-0.128154	-0.533566	0.419089	-0.256836	-0.36427	-0.427916	0.152517	-0.0426557
RUN9	0.383708	0.189644	-0.54891	0.317217	-0.117644	-0.578852	0.201798	0.147865	-0.0408387	0.0413603
RUN10	0.252464	-0.642921	0.0547671	-0.00302087	0.0132675	-0.135755	-0.482011	0.512831	-0.0606046	-0.0479291

APPENDIX B
ANALYSIS OF VARIANCE TABLES,
REGRESSION STATISTICS,
AND RESIDUAL PLOTS

TABLE B-1

ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC1 (COL1) AND PC2 (COL2)

DEPENDENT VARIABLE: COL1

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.13571551	0.06985775	2.53	0.0908	0.103306	99999.9999
ERROR	44	1.21272425	0.02756191			ROOT MSE	COL 1 MEAN
CORRECTED TOTAL	46	1.35243976				0.16601781	0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.04218769	1.57	0.2173	1	0.12193101	4.42	0.0412
LONG	1	0.09652781	3.50	0.0679	1	0.09652781	3.50	0.0679

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.49443888	2.19	0.0337	0.22557447
LAT	-0.00882567	-2.10	0.0412	0.00419609
LONG	-0.00558367	-1.87	0.0679	0.00298365

DEPENDENT VARIABLE: COL2

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.01485937	0.00742969	0.53	0.5916	0.023579	99999.9999
ERROR	44	0.61533895	0.01398498			ROOT MSE	COL2 MEAN
CORRECTED TOTAL	46	0.63019832				0.11825809	-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.00054835	0.04	0.8439	1	0.00250547	0.18	0.6742
LONG	1	0.01431103	1.02	0.3173	1	0.01431103	1.02	0.3173

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.09074577	0.56	0.5751	0.16068159
LAT	-0.00126513	-0.42	0.6742	0.00298897
LONG	-0.00214995	-1.01	0.3173	0.00212532

TABLE B-2

ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC3 (COL3) AND PC4 (COL4)

DEPENDENT VARIABLE: COL3

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.13556704	0.06778352	4.07	0.0240	0.156006	99999.9999
ERROR	44	0.73341748	0.01666858		ROOT MSE		COL3 MEAN
CORRECTED TOTAL	46	0.86898453			0.12910685		-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.09555768	5.76	0.0207	1	0.13526818	8.12	0.0066
LONG	1	0.03960936	2.38	0.1304	1	0.03960936	2.38	0.1304

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.48688387	2.78	0.0081	0.17542220
LAT	-0.00929652	-2.85	0.0066	0.00326317
LONG	-0.00357678	-1.54	0.1304	0.00232029

DEPENDENT VARIABLE: COL4

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.20913144	0.10456572	7.56	0.0015	0.255714	99999.9999
ERROR	44	0.60870236	0.01383414		ROOT MSE		COL4 MEAN
CORRECTED TOTAL	46	0.81783380			0.11761864		C.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.05753753	4.16	0.0474	1	0.00086301	0.06	0.8039
LONG	1	0.15159391	10.96	0.0019	1	0.15159391	10.96	0.0019

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	-0.13770383	-0.86	0.3935	0.15981275
LAT	0.00074250	0.25	0.8039	0.00297281
LONG	0.00695736	3.31	0.0019	0.00211383

TABLE B-3

ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC5(COL5) AND PC6 (COL6)

DEPENDENT VARIABLE: COL5

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.06743705	0.00371853	0.13	0.8776	0.005916	99999.9999
ERROR	44	1.24958441	0.02839965		ROOT MSE		COL5 MEAN
CORRECTED TOTAL	46	1.25702146			0.16852194		0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.00298754	0.11	0.7472	1	0.00003641	0.00	0.9716
LONG	1	0.00444951	0.16	0.6941	1	0.00444951	0.16	0.6941

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.01052691	0.05	0.9635	0.22897693
LAT	0.00015251	0.04	0.9716	0.00425938
LONG	-0.00119881	-0.40	0.6941	0.00302865

DEPENDENT VARIABLE: COL6

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.03914608	0.01957304	1.55	0.2245	0.065658	99999.9999
ERROR	44	0.55706378	0.01266054		ROOT MSE		COL6 MEAN
CORRECTED TOTAL	46	0.55620986			0.11251907		-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.01355237	1.07	0.3065	1	0.00000624	0.00	0.9824
LONG	1	0.02559371	2.02	0.1621	1	0.02559371	2.02	0.1621

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.03938272	0.26	0.7979	0.15288377
LAT	6.3123266E-05	0.02	0.9824	0.00284391
LONG	-0.00287515	-1.42	0.1621	0.00202218

TABLE B-4

ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC7(COL7) AND PC8 (COL8)

DEPENDENT VARIABLE: COL7

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.09014459	0.04507229	2.38	0.1044	0.097597	99999.9999
ERROR	44	0.83349618	0.01894310			ROOT MSE	COL7 MEAN
CORRECTED TOTAL	46	0.92364077			0.13763392		-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.01527477	0.81	0.3741	1	0.06705875	3.54	0.0665
LONG	1	0.07486982	3.95	0.0530	1	0.07486982	3.95	0.0530

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.37820279	2.02	0.0492	0.18700823
LAT	-0.00654708	-1.88	0.0665	0.00347869
LONG	-0.00491753	-1.99	0.0530	0.00247354

DEPENDENT VARIABLE: COL8

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.01959629	0.00979815	0.89	0.4198	0.038687	99999.9999
ERROR	44	0.48694446	0.01106692			ROOT MSE	COL8 MEAN
CORRECTED TOTAL	46	0.50654075			0.10519943		-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.00251269	0.23	0.6361	1	0.00120160	0.11	0.7433
LONG	1	0.01708360	1.54	0.2207	1	0.01708360	1.54	0.2207

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.07550713	0.53	0.6000	0.14293831
LAT	-0.00087613	-0.33	0.7433	0.00265891
LONG	-0.00234900	-1.24	0.2207	0.00189063

TABLE B-5

ANOVA TABLES AND REGRESSION STATISTICS FOR FEMALE PC9 (COL9) AND PC10 (COL10)

DEPENDENT VARIABLE: COL9

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.01205389	0.00602694	0.39	0.6768	0.017591	99999.9999
ERROR	44	0.67319002	0.01529977		ROOT MSE		COL9 MEAN
CORRECTED TOTAL	46	0.68524391			0.12369225		-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.00533228	0.35	0.5580	1	0.00014844	0.01	0.9220
LONG	1	0.00672161	0.44	0.5109	1	0.00672161	0.44	0.5109

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.00731034	0.04	0.9655	0.16806518
LAT	0.00030794	0.10	0.9220	0.00312632
LONG	-0.00147343	-0.66	0.5109	0.00222298

DEPENDENT VARIABLE: COL10

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.01534449	0.00767225	0.37	0.6948	0.016417	99999.9999
ERROR	44	0.91930285	0.02089325		ROOT MSE		COL10 MEAN
CORRECTED TOTAL	46	0.93464735			0.14454496		0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.01038211	0.50	0.4846	1	0.01534245	0.73	0.3961
LONG	1	0.00496238	0.24	0.6284	1	0.00496238	0.24	0.6284

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	-0.16486739	-0.84	0.4058	0.19639853
LAT	0.00313067	0.86	0.3961	0.00365337
LONG	0.00126601	0.49	0.6284	0.00259774

TABLE B-6

ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC1 (COL1) AND PC2 (COL2)

DEPENDENT VARIABLE: COL1								
SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.	
MODEL	2	0.02475542	0.01237771	0.67	0.5166	0.028924	99999.9999	
ERROR	45	0.83111115	0.01846914			ROOT MSE	COL1 MEAN	
CORRECTED TOTAL	47	0.85586657				0.13590120	0.00000000	
SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.01207455	0.65	0.4230	1	0.02395334	1.30	0.2608
LONG	1	0.01268087	0.69	0.4117	1	0.01268087	0.69	0.4117
PARAMETER	ESTIMATE	T FOR HO: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE				
INTERCEPT	0.21225040	1.15	0.2559	0.18442221				
LAT	-0.00391080	-1.14	0.2608	0.00343404				
LONG	-0.00201756	-0.83	0.4117	0.00243486				
DEPENDENT VARIABLE: COL2								
SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.	
MODEL	2	0.05131796	0.02565898	0.75	0.4768	0.032385	99999.9999	
ERROR	45	1.53330129	0.03407336			ROOT MSE	COL2 MEAN	
CORRECTED TOTAL	47	1.58461925				0.18458971	-0.00000000	
SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.04742803	1.39	0.2443	1	0.02005179	0.59	0.4470
LONG	1	0.00388913	0.11	0.7371	1	0.00388913	0.11	0.7371
PARAMETER	ESTIMATE	T FOR HO: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE				
INTERCEPT	0.15091153	0.60	0.5499	0.25049405				
LAT	-0.00357815	-0.77	0.4470	0.00466434				
LONG	0.00111732	0.34	0.7371	0.00330719				

TABLE B-7

ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC3 (COL3) AND PC4 (COL4)

DEPENDENT VARIABLE: COL3

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.37394822	0.18697411	11.62	0.0001	0.340590	99999.9999
ERROR	45	0.72399429	0.01608876			ROOT MSE	COL3 MEAN
CORRECTED TOTAL	47	1.09794251				0.12684148	-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.23304926	14.49	0.0004	1	0.37321668	23.20	0.0001
LONG	1	0.14089896	8.76	0.0049	1	0.14089896	8.76	0.0049

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.81971752	4.76	0.0001	0.17212788
LAT	-0.01543701	-4.82	0.0001	0.00320512
LONG	-0.00672520	-2.96	0.0049	0.00227255

DEPENDENT VARIABLE: COL4

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.05930095	0.04965048	3.54	0.0373	0.135954	99999.9999
ERROR	45	0.63110110	0.01402447			ROOT MSE	COL4 MEAN
CORRECTED TOTAL	47	0.73040205				0.11042495	-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.03200316	2.28	0.1379	1	0.00001665	0.00	0.9727
LONG	1	0.06729779	4.80	0.0337	1	0.06725779	4.80	0.0337

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	-0.07271090	-0.45	0.6531	0.16070630
LAT	0.00010310	0.03	0.9727	0.00299244
LONG	0.00464785	2.19	0.0337	0.00212175

TABLE B-8

ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC5 (COL5) AND PC6 (COL6)

DEPENDENT VARIABLE: COL5

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.07196036	0.03598018	2.60	0.0858	0.103411	99999.9999
ERROR	45	0.62390479	0.01386455		ROOT MSE		COL5 MEAN
CORRECTED TOTAL	47	0.69586515			0.11774783		C.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	CF	TYPE III SS	F VALUE	PR > F
LAT	1	0.06640032	0.46	0.5003	1	0.00685722	0.49	0.4855
LONG	1	0.06556005	4.73	0.0350	1	0.06556005	4.73	0.0350

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	-0.16480544	-1.03	0.3079	0.15978751
LAT	0.00209246	0.70	0.4855	0.00297533
LONG	0.00456745	2.17	0.0350	0.00210962

DEPENDENT VARIABLE: COL6

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.07697166	0.03848583	1.48	0.2380	0.061803	99999.9999
ERROR	45	1.16646378	0.02596586		ROOT MSE		COL6 MEAN
CORRECTED TOTAL	47	1.24343545			0.16113926		-C.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	CF	TYPE III SS	F VALUE	PR > F
LAT	1	0.00034282	0.01	0.9090	1	0.02102002	0.81	0.3731
LONG	1	0.07662884	2.95	0.0927	1	0.07662884	2.95	0.0927

PARAMETER	ESTIMATE	T FOR H0: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	-0.24366884	-1.11	0.2711	0.21867105
LAT	0.00366352	0.90	0.3731	0.00407178
LONG	0.00495961	1.72	0.0927	0.00288704

TABLE B-9

ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC7 (COL7) AND PC8 (COL8)

DEPENDENT VARIABLE: COL7

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.11782900	0.05891450	4.33	0.0190	0.161408	99999.9999
ERROR	45	0.61217904	0.01360398		ROOT MSE		COL7 MEAN
CORRECTED TOTAL	47	0.73000804			0.11663610		-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.04715069	3.47	0.0692	1	0.10949118	8.05	0.0068
LONG	1	0.07067831	5.20	0.0274	1	0.07067831	5.20	0.0274

PARAMETER	ESTIMATE	T FOR HO: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.46035794	2.91	0.0056	0.15827885
LAT	-0.00836127	-2.84	0.0068	0.00294724
LONG	-0.00476315	-2.28	0.0274	0.00208970

DEPENDENT VARIABLE: COL8

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.15310588	0.07655254	5.58	0.0050	0.210018	99999.9999
ERROR	45	0.57590845	0.01279797		ROOT MSE		COL8 MEAN
CORRECTED TOTAL	47	0.72901433			0.11312809		0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.02108707	1.65	0.2058	1	0.10797405	8.44	0.0057
LONG	1	0.13201881	10.32	0.0024	1	0.13201881	10.32	0.0024

PARAMETER	ESTIMATE	T FOR HO: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.48315524	3.15	0.0029	0.15351838
LAT	-0.00830314	-2.90	0.0057	0.00285860
LONG	-0.00650983	-3.21	0.0024	0.00202665

TABLE B-10

ANOVA TABLES AND REGRESSION STATISTICS FOR MALE PC9 (COL9) AND PC10 (COL10)

DEPENDENT VARIABLE: COL9

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.01050685	0.00525342	0.38	0.6853	0.016653	99999.9999
ERROR	45	0.62040859	0.01378686		ROOT MSE		COL9 MEAN
CORRECTED TOTAL	47	0.63091544			0.11741745		-0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.00008544	0.01	0.9376	1	0.00265186	0.19	0.6631
LONG	1	0.01042140	0.76	0.3892	1	0.01042140	0.76	0.3892

PARAMETER	ESTIMATE	T FOR HO: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	-0.08753301	-0.55	0.5855	0.15933917
LAT	0.00130124	0.44	0.6631	0.00296698
LONG	0.00182900	0.87	0.3892	0.00210370

DEPENDENT VARIABLE: COL10

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PR > F	R-SQUARE	C.V.
MODEL	2	0.02283067	0.01141533	0.87	0.4247	0.037350	99999.9999
ERROR	45	0.58843949	0.01307643		ROOT MSE		COL10 MEAN
CORRECTED TOTAL	47	0.61127016			0.11435223		0.00000000

SOURCE	DF	TYPE I SS	F VALUE	PR > F	DF	TYPE III SS	F VALUE	PR > F
LAT	1	0.01839894	1.41	0.2418	1	0.00520713	0.40	0.5312
LONG	1	0.00443172	0.34	0.5634	1	0.00443172	0.34	0.5634

PARAMETER	ESTIMATE	T FOR HO: PARAMETER=0	PR > T	STD ERROR OF ESTIMATE
INTERCEPT	0.06779801	0.44	0.6643	0.15517958
LAT	-0.00182340	-0.63	0.5312	0.00288953
LONG	0.00119272	0.58	0.5634	0.00204878

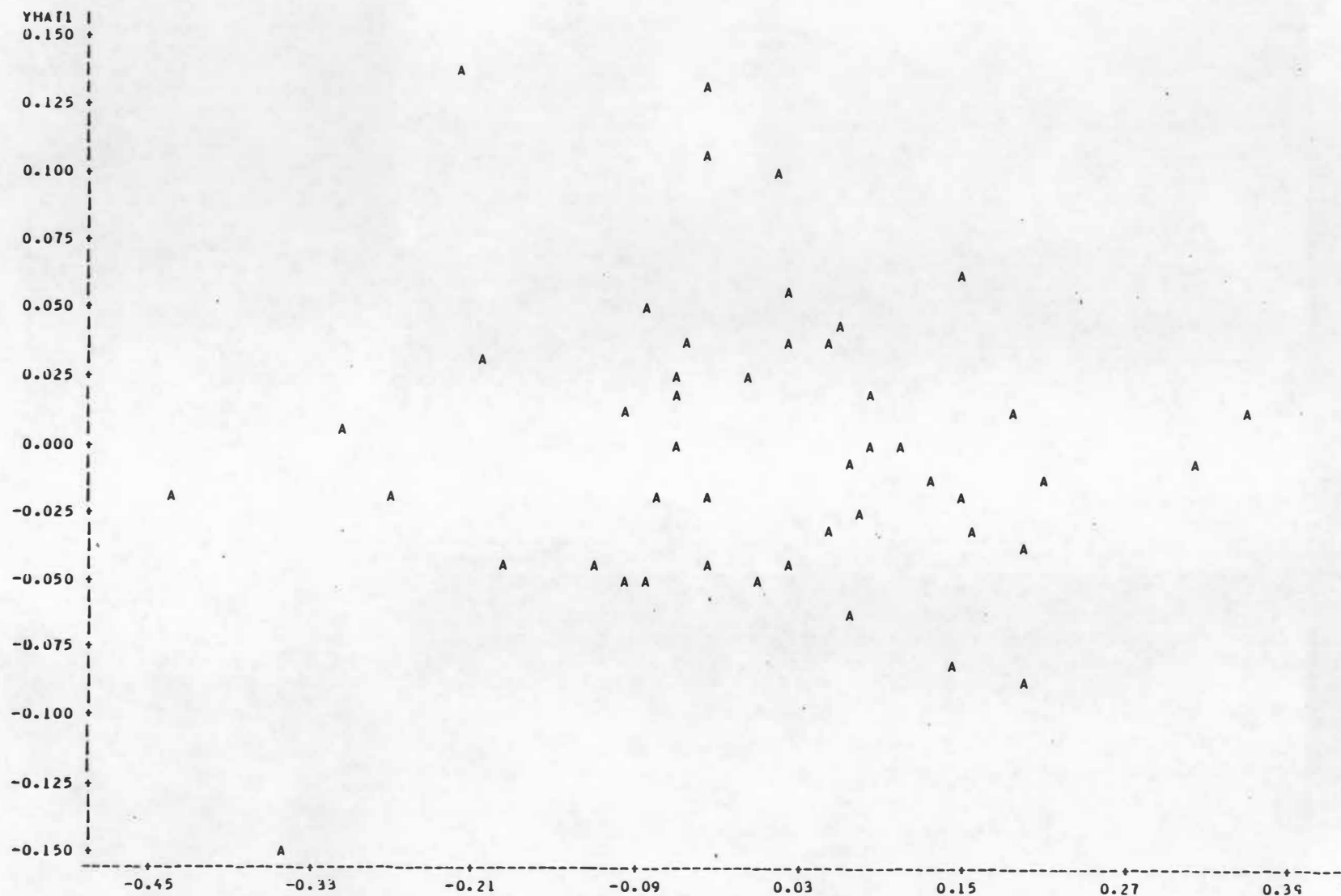


Figure B-1. Plot of female PC1 residuals (X-axis) against fitted values.

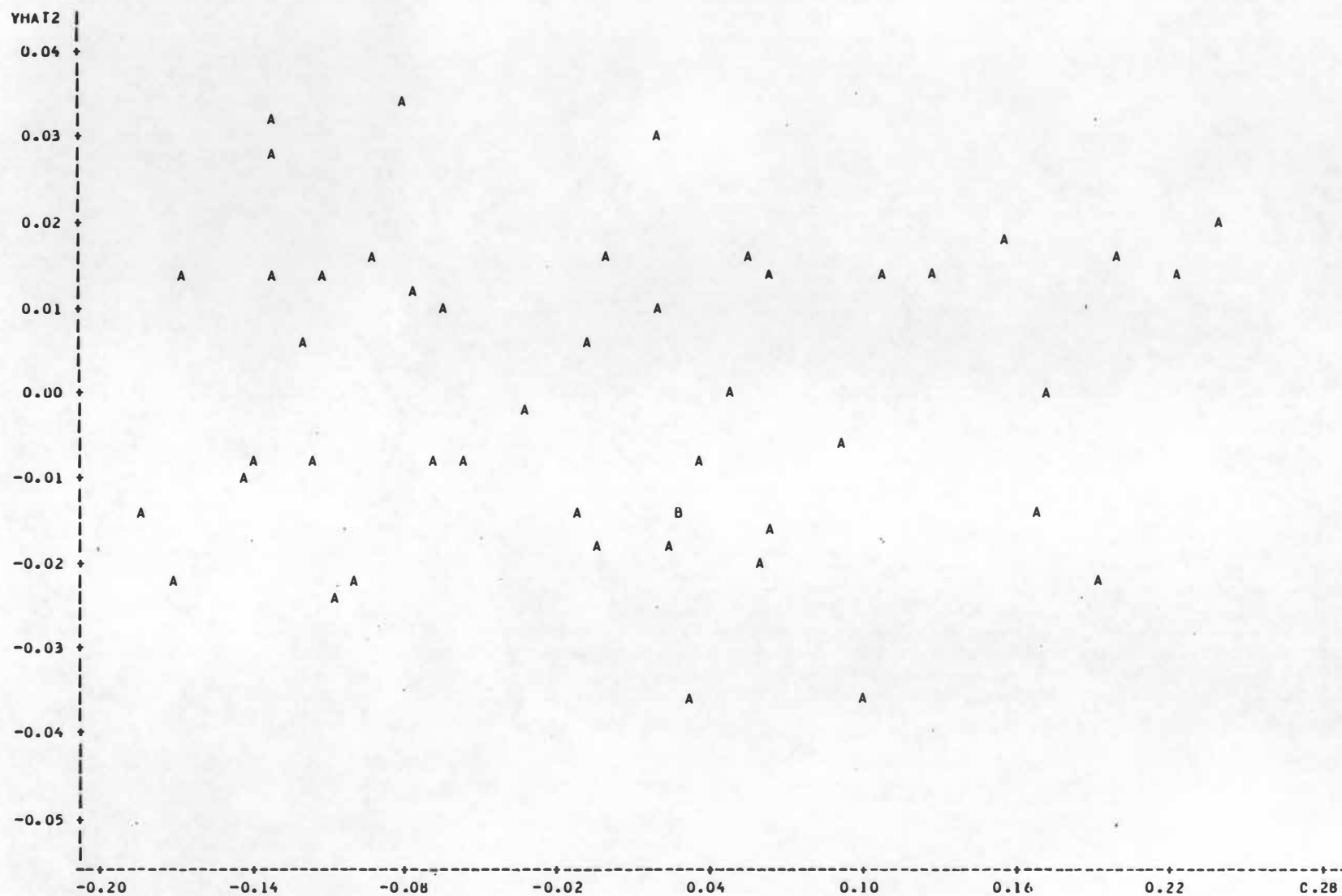


Figure B-2. Plot of female PC2 residuals (X-axis) against fitted values.

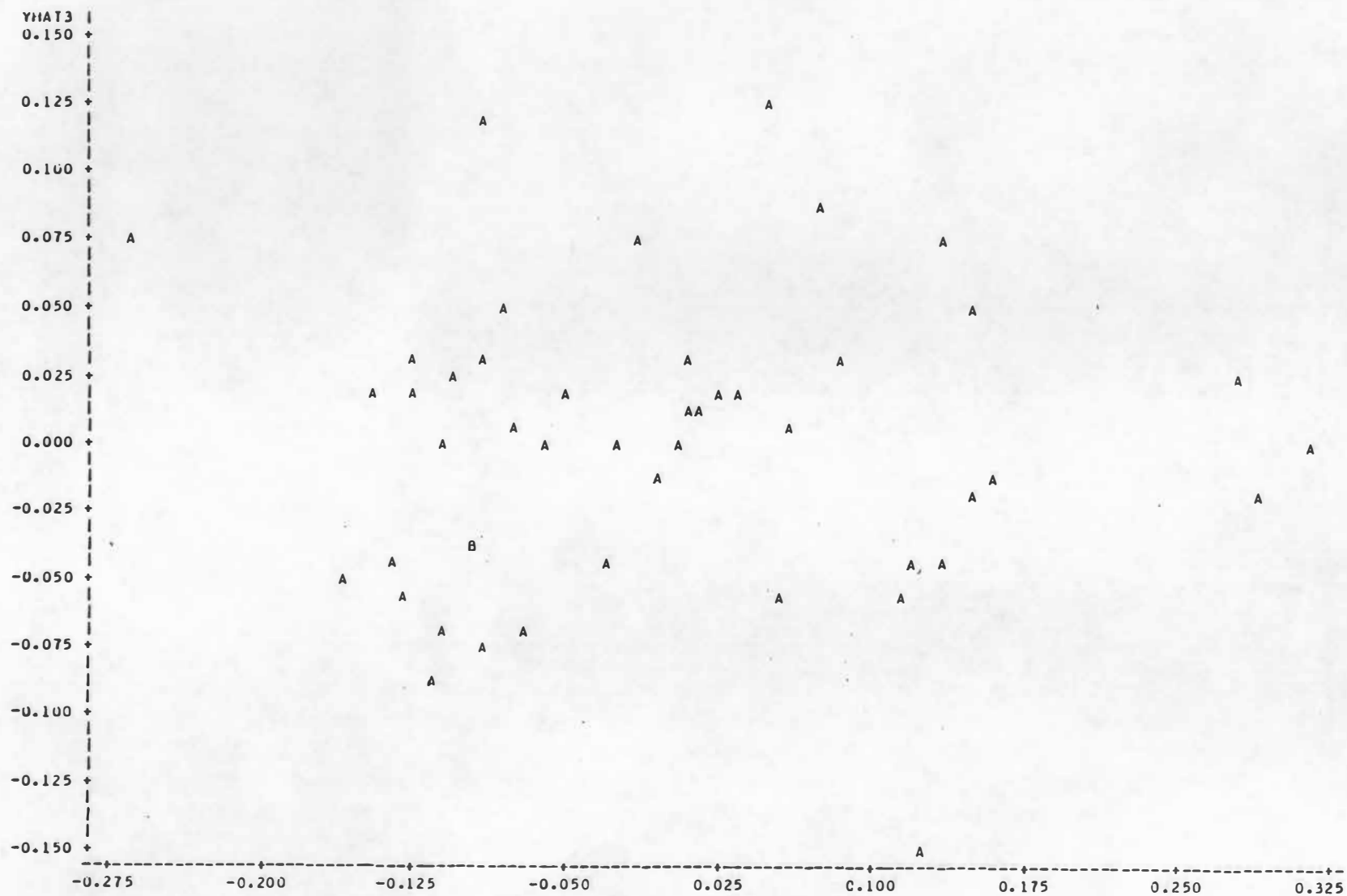


Figure B-3. Plot of female PC3 residuals (X-axis) against fitted values.

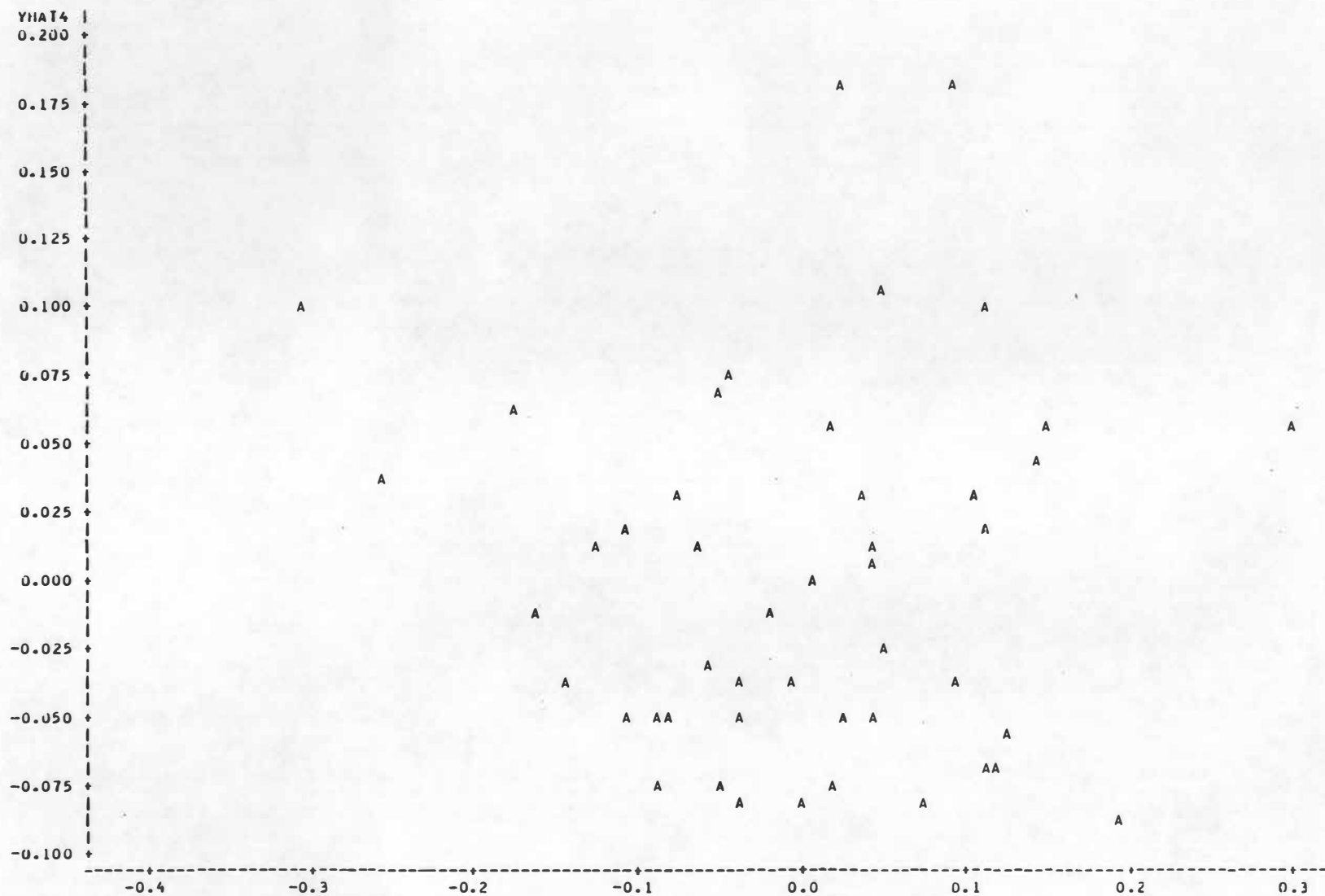


Figure B-4. Plot of female PC4 residuals (X-axis) against fitted values.

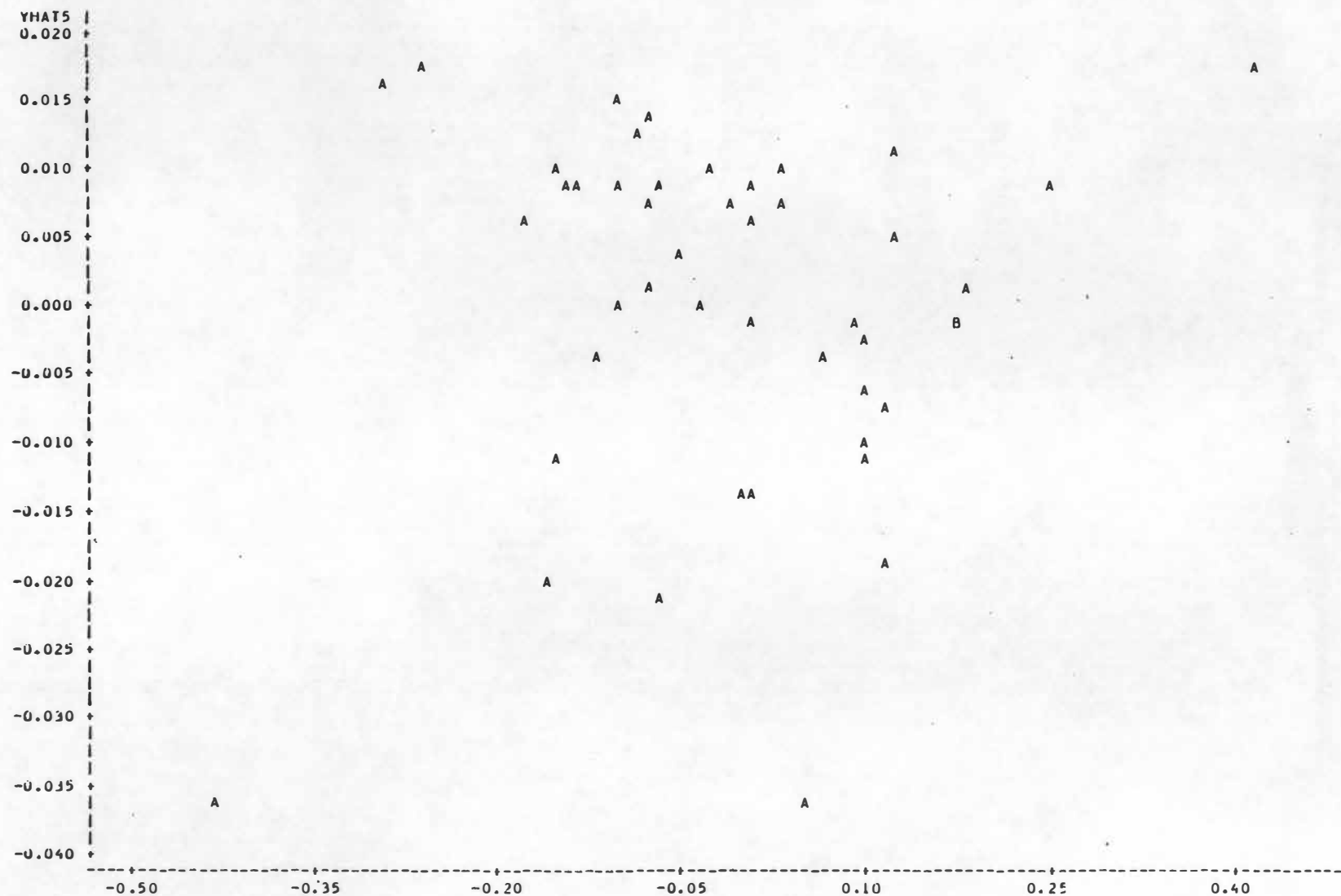


Figure B-5. Plot of female PC5 residuals (X-axis) against fitted values.

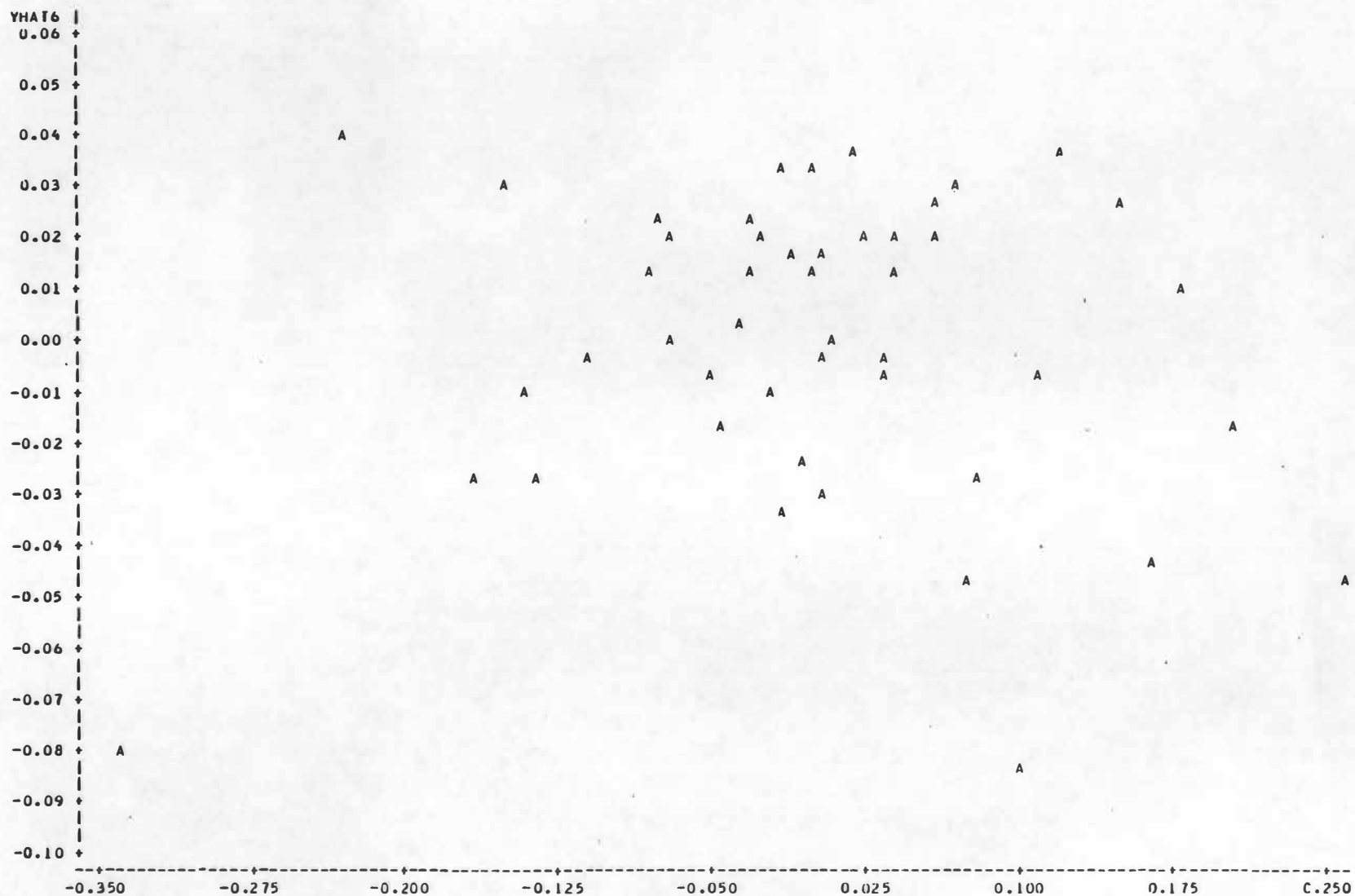
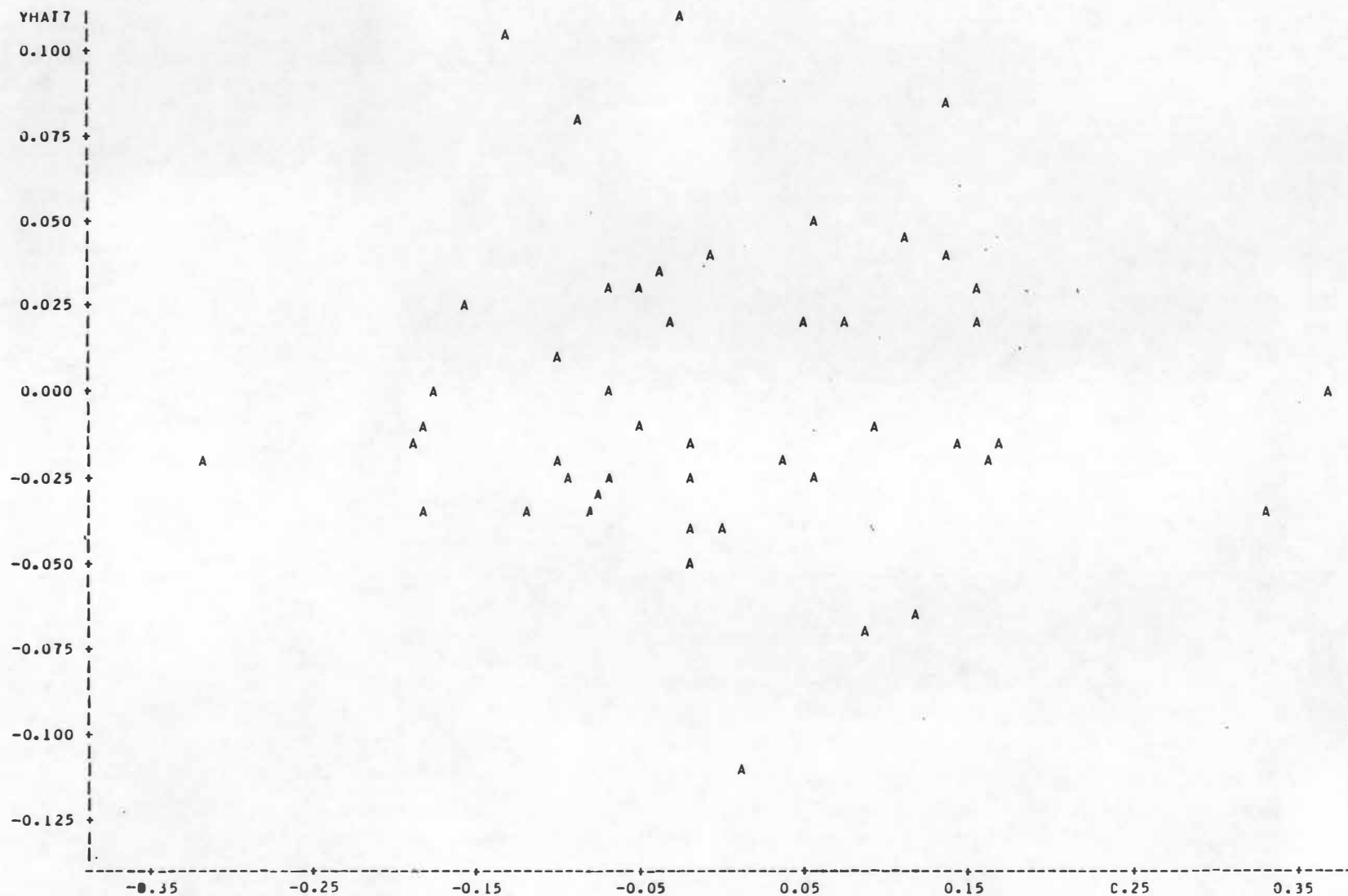


Figure B-6. Plot of female PC6 residuals (X-axis) against fitted values.



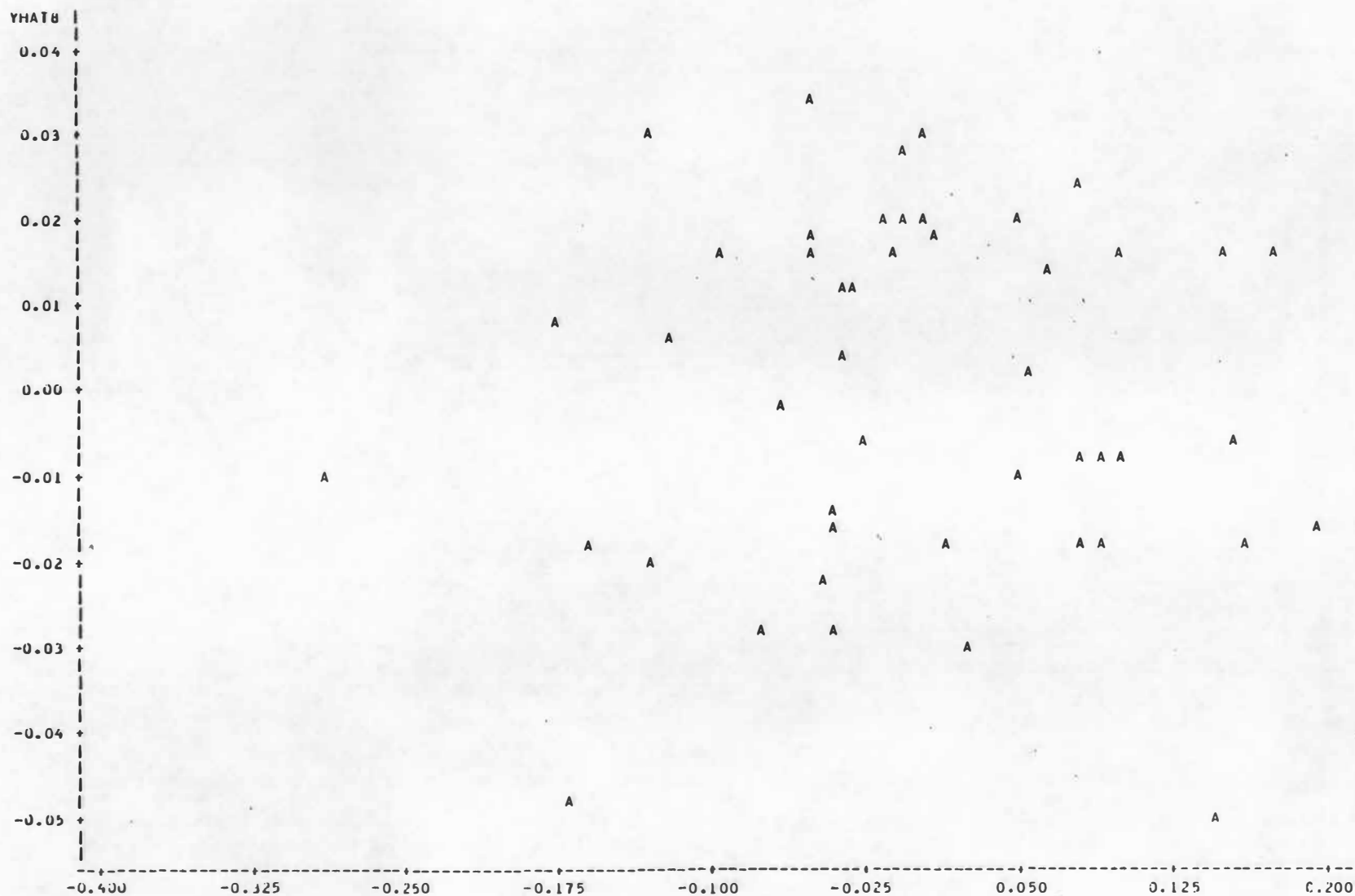


Figure B-8. Plot of female PC8 residuals (X-axis) against fitted values.

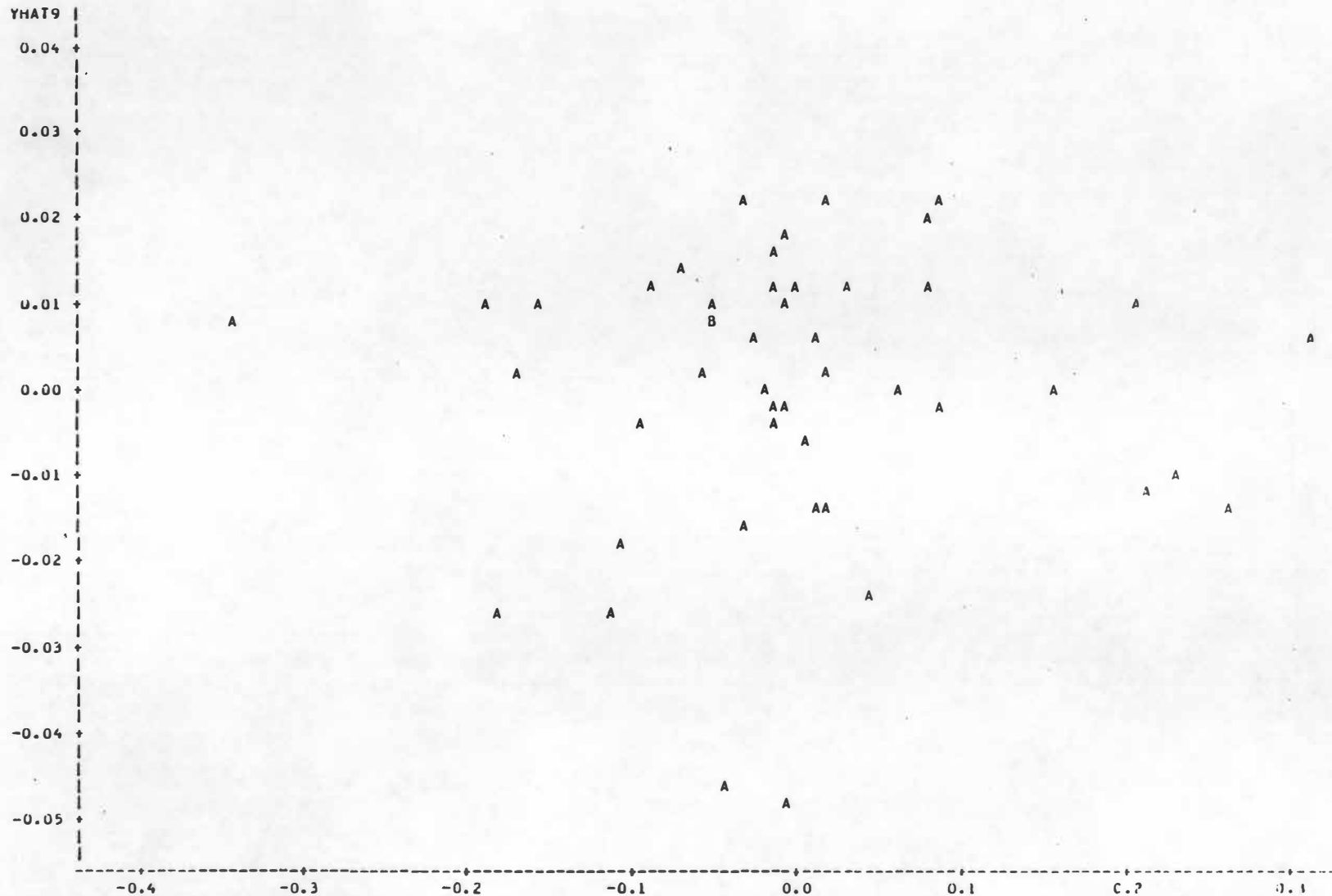


Figure B-9. Plot of female PC9 residuals (X-axis) against fitted values.

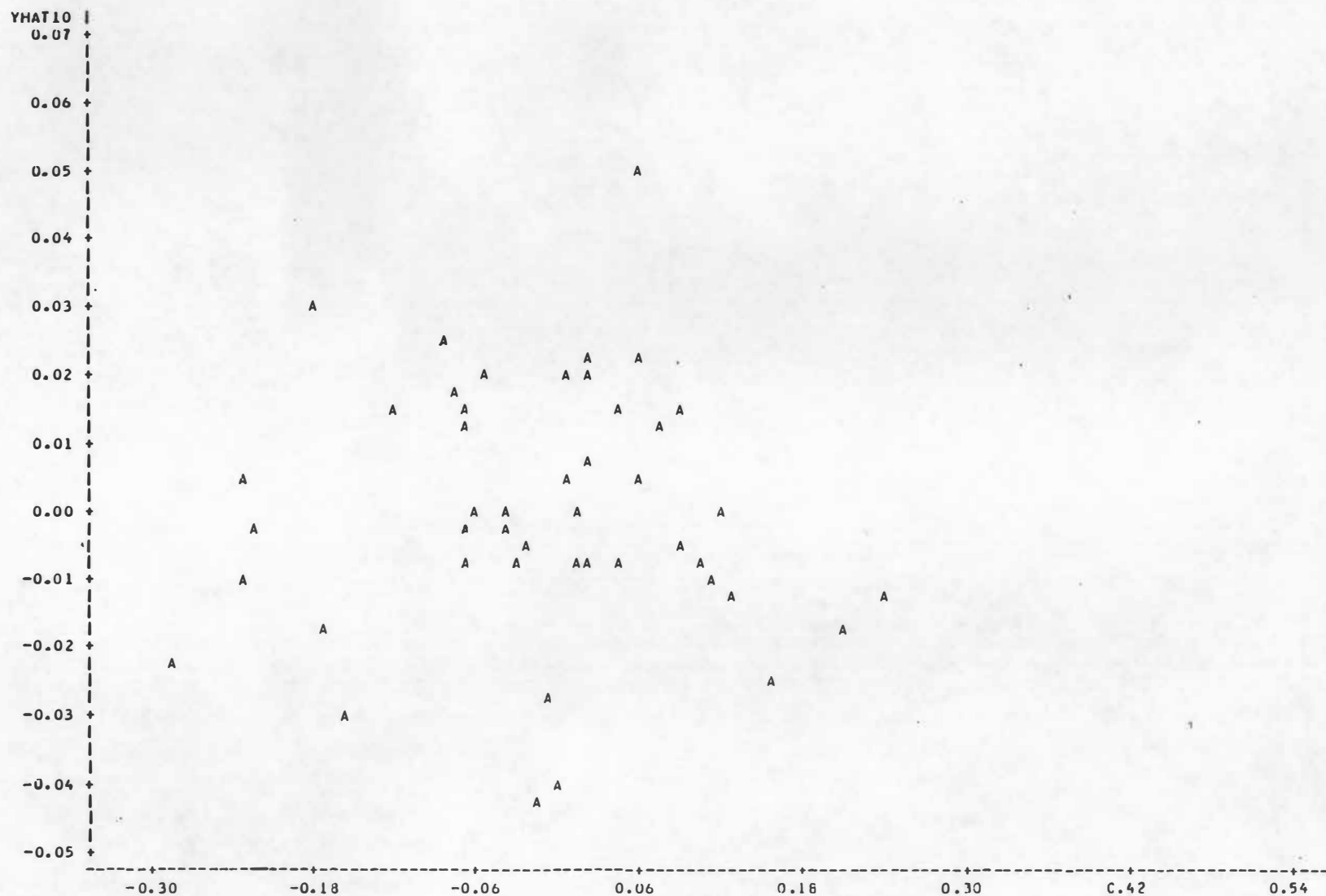


Figure B-10. Plot of female PC10 residuals (X-axis) against fitted values.

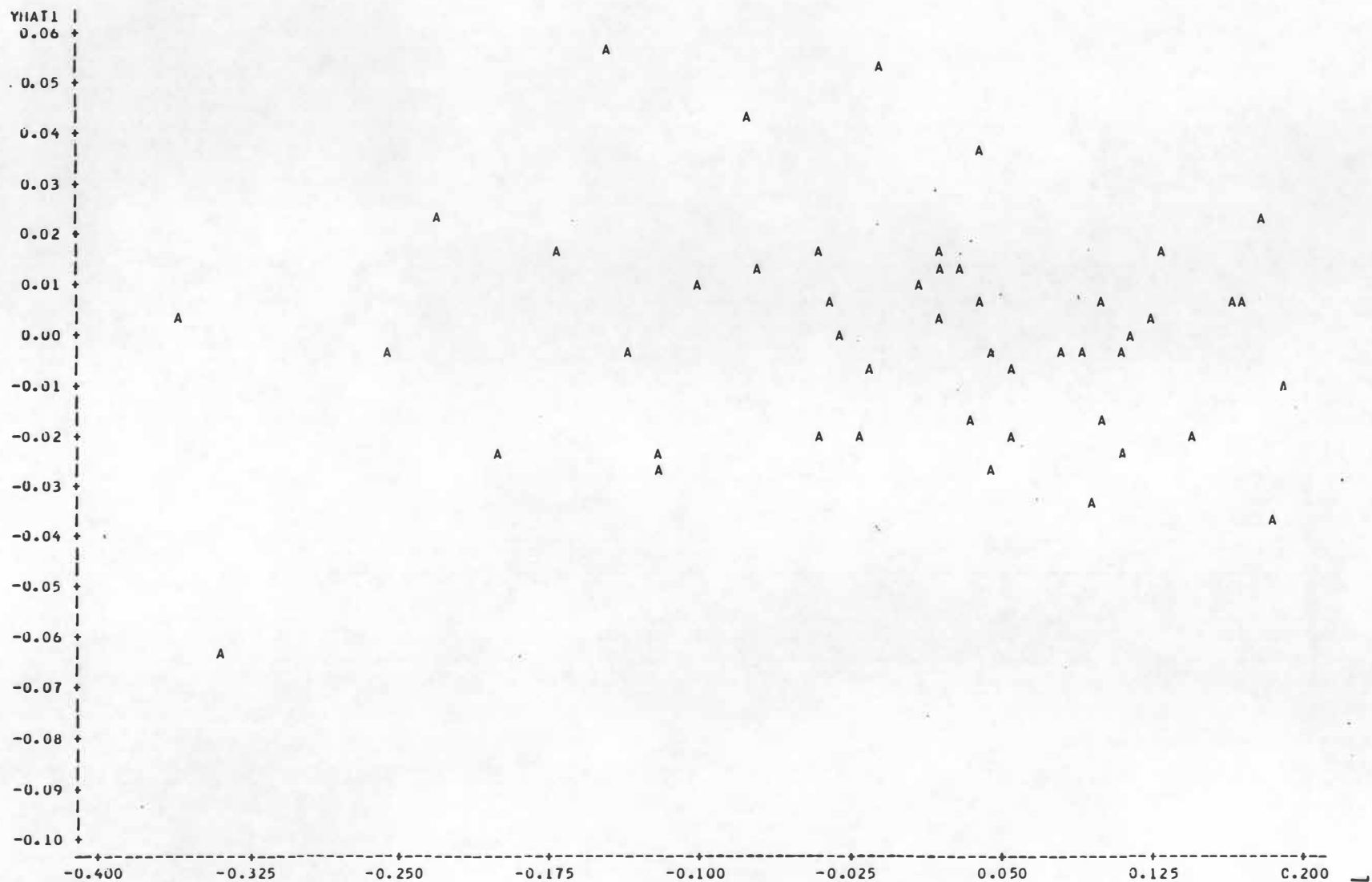


Figure B-11. Plot of male PC1 residuals (X-axis) against fitted values.

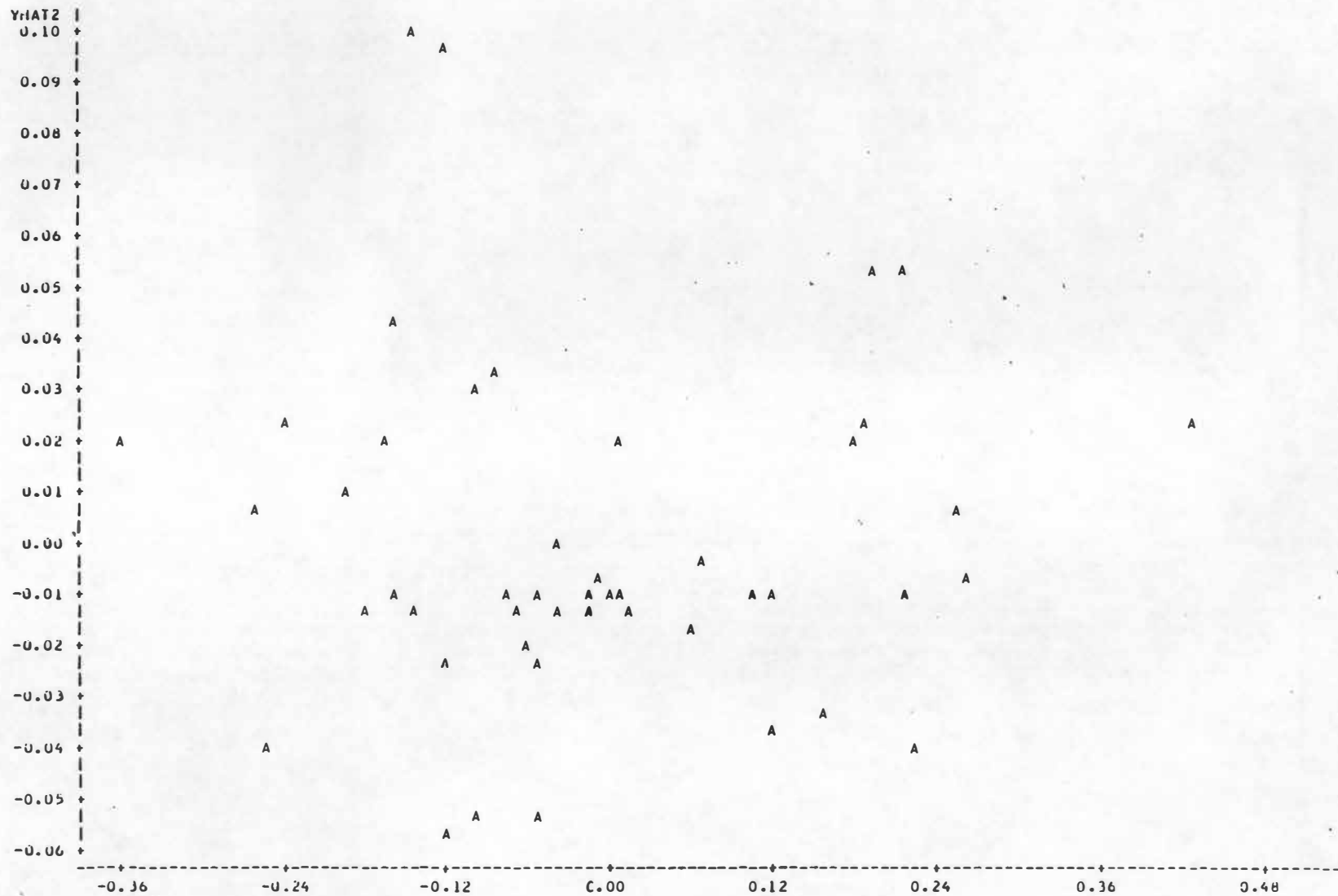


Figure B-12. Plot of male PC2 residuals (X-axis) against fitted values.

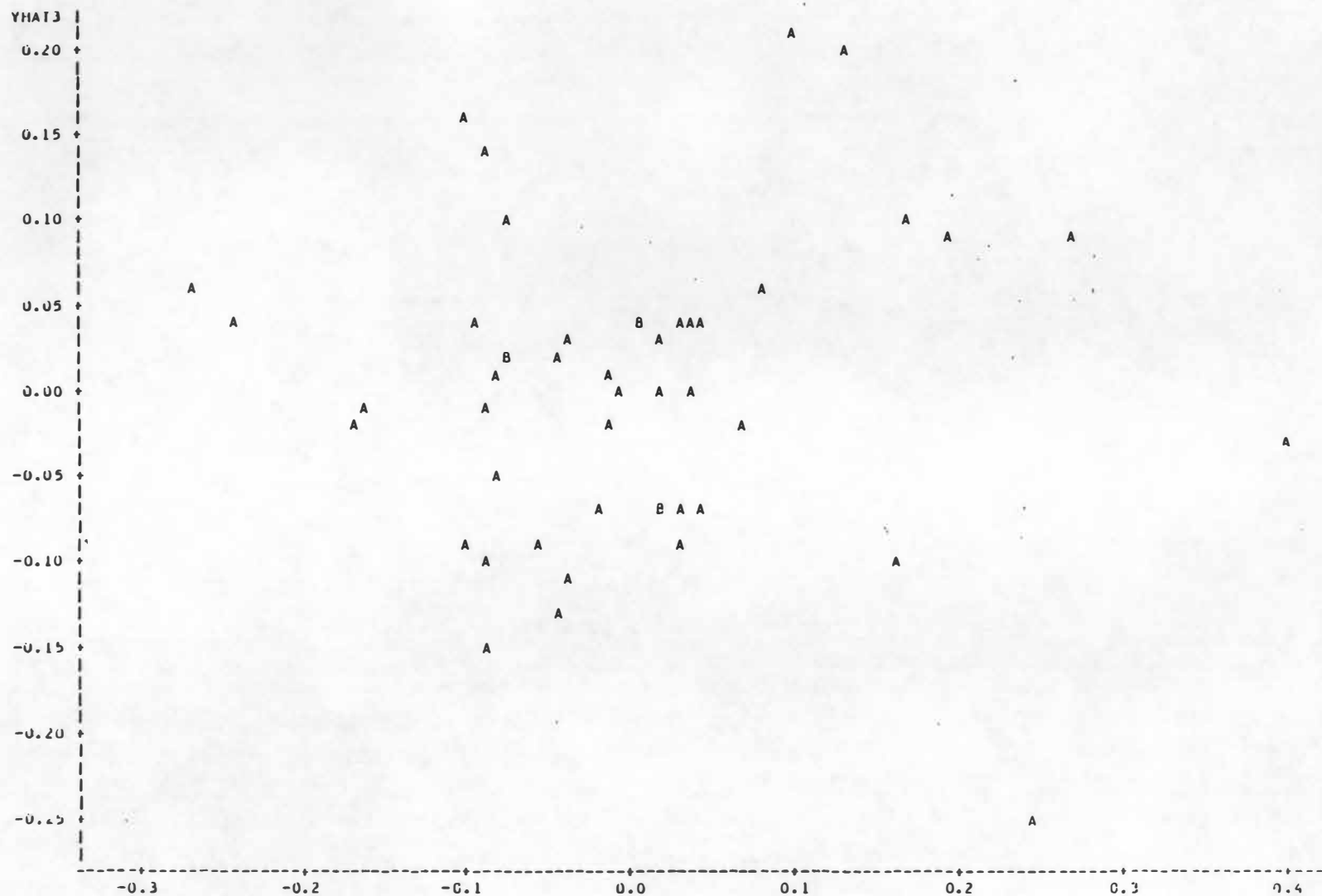


Figure B-13. Plot of male PC3 residuals (X-axis) against fitted values.

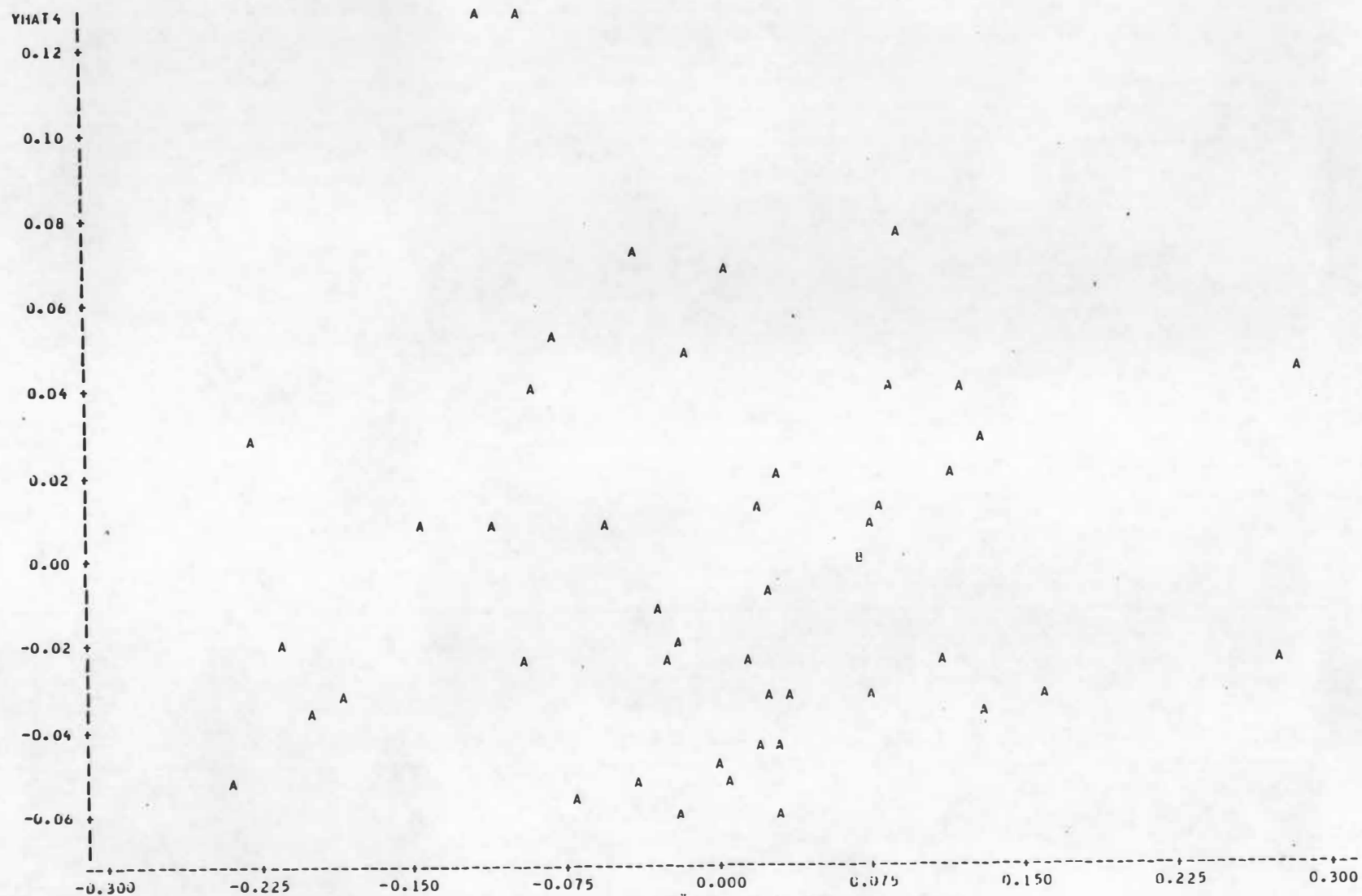


Figure B-14. Plot of male PC4 residuals (X-axis) against fitted values.

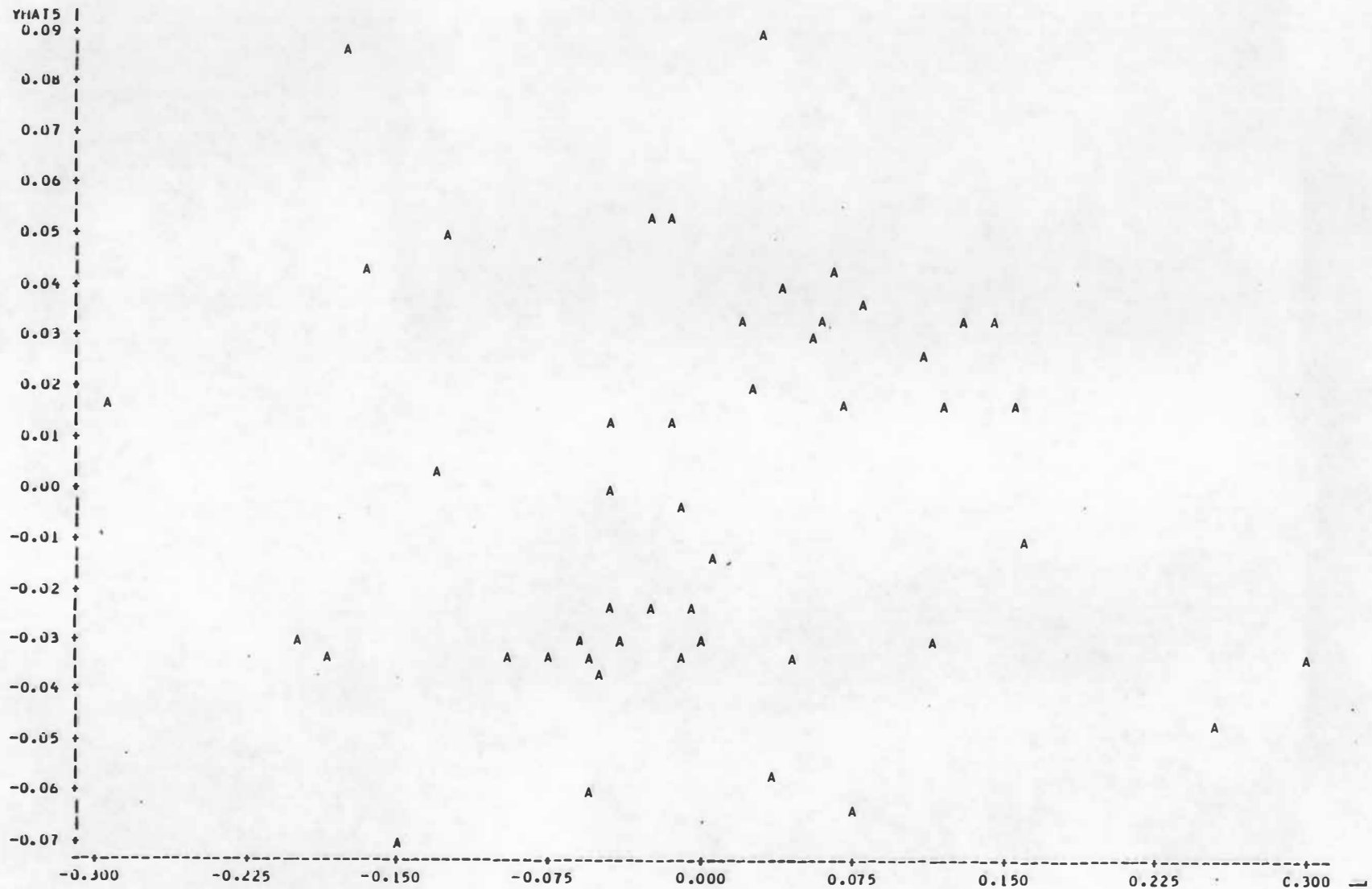


Figure B-15. Plot of male PC5 residuals (X-axis) against fitted values.

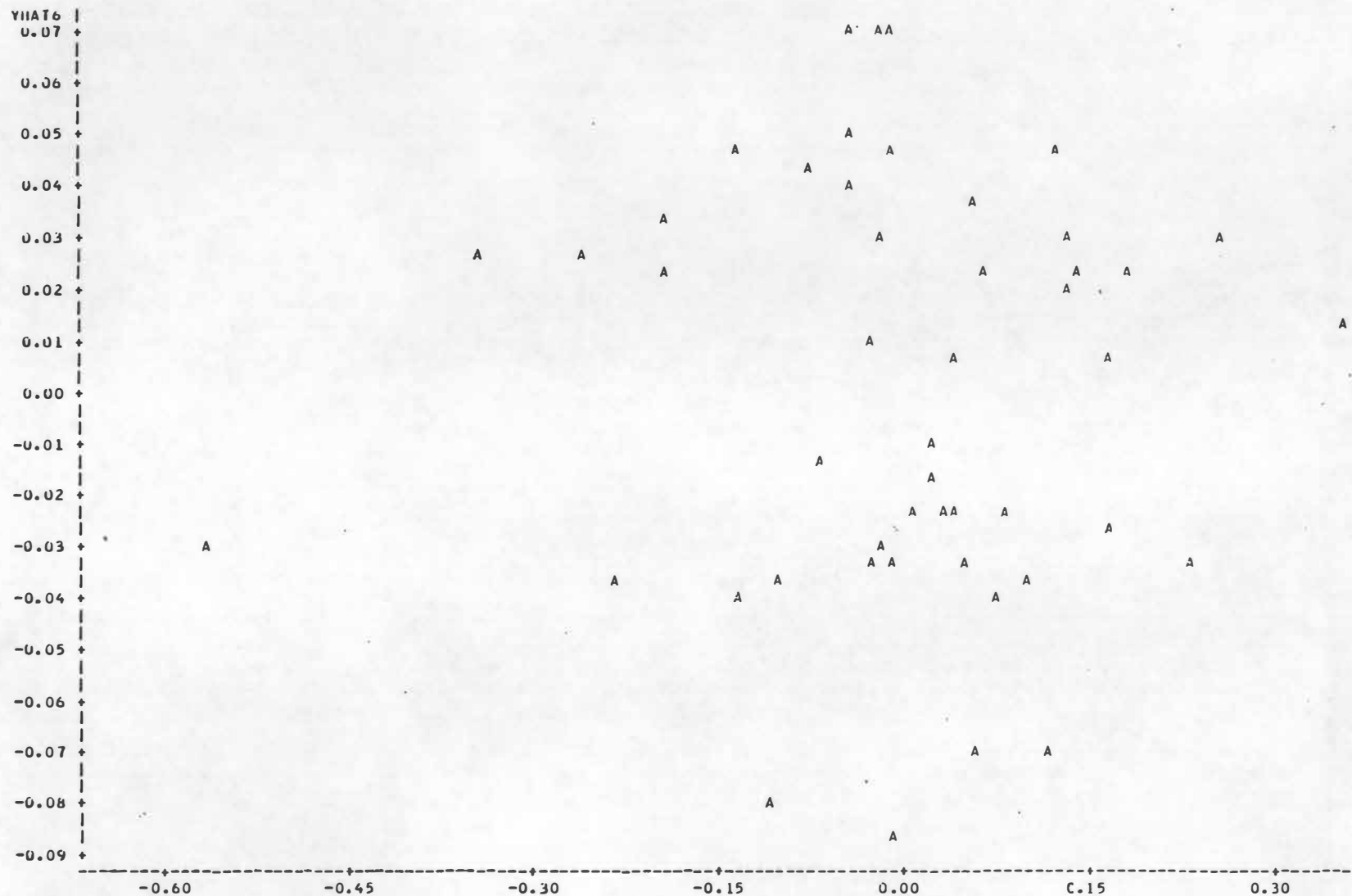
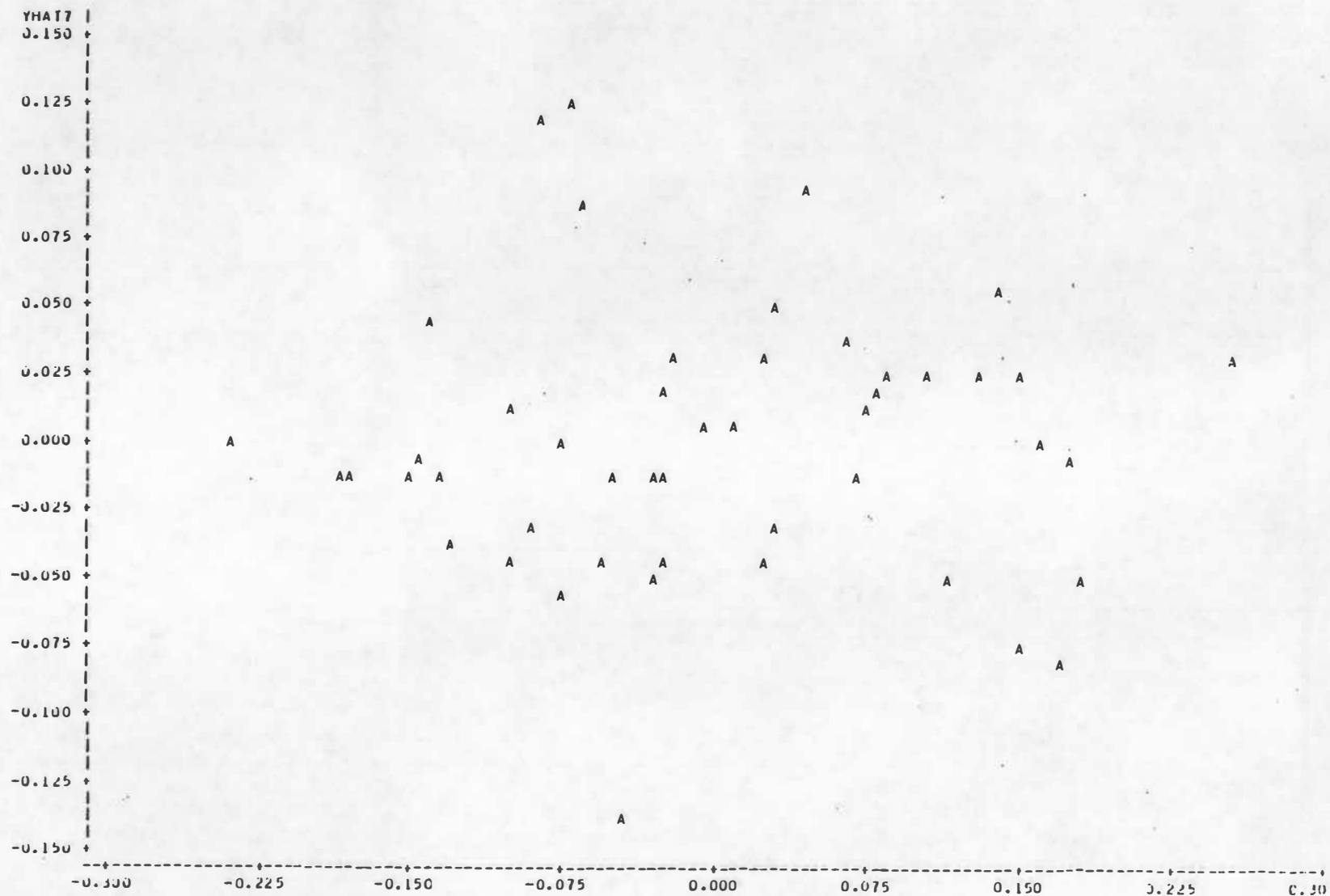
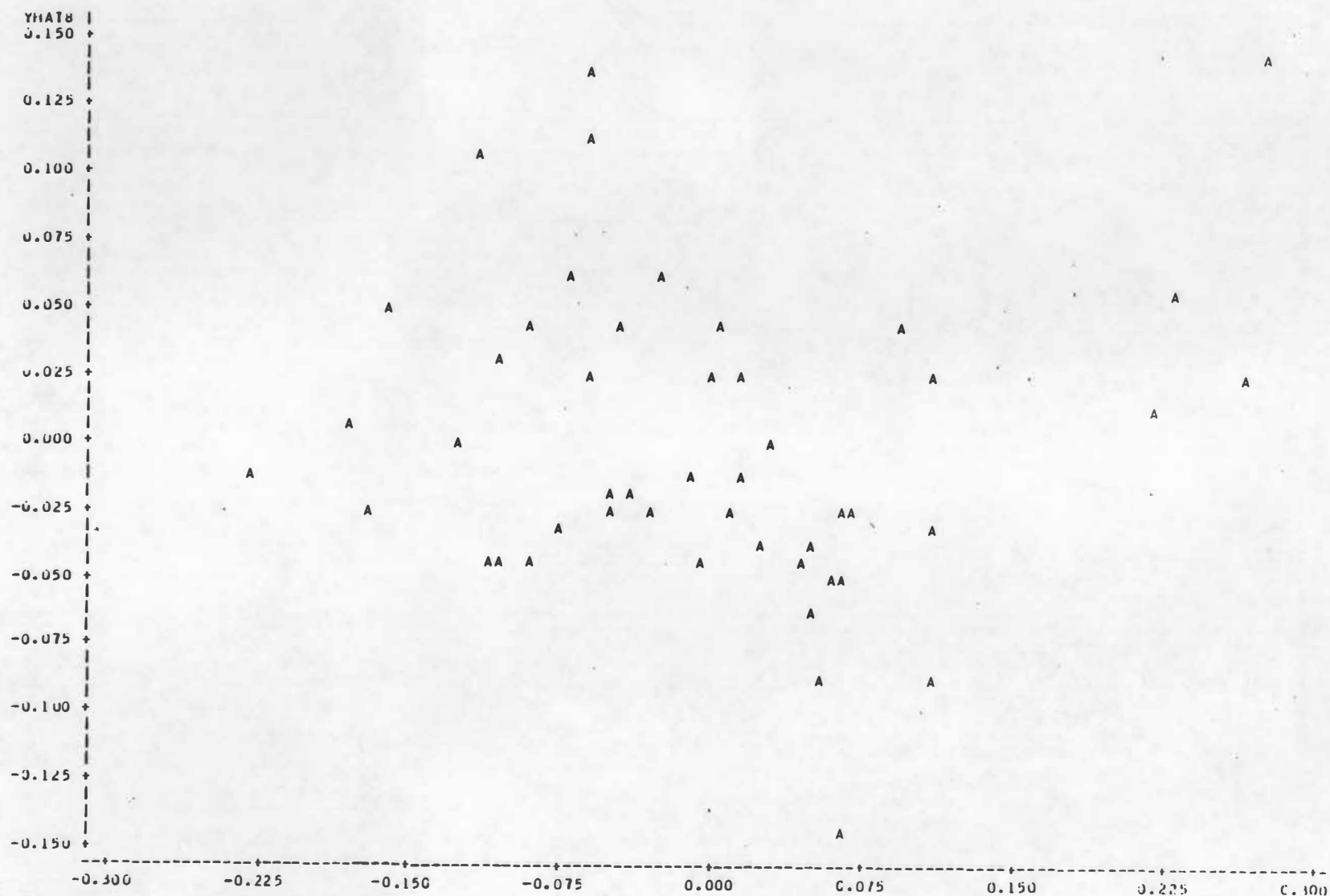


Figure B-16. Plot of male PC6 residuals (X-axis) against fitted values.





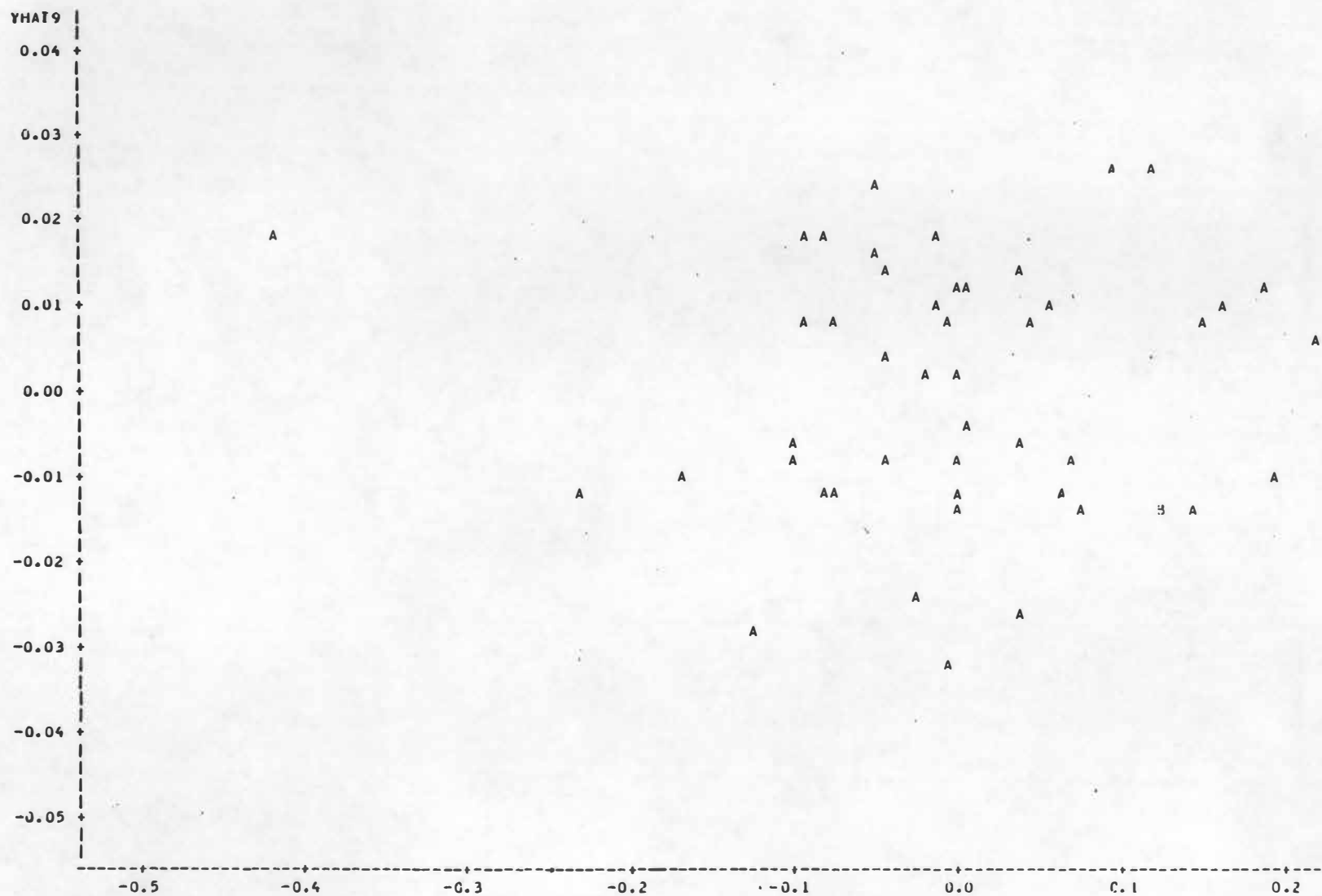


Figure B-19. Plot of male PC9 residuals (X-axis) against fitted values.

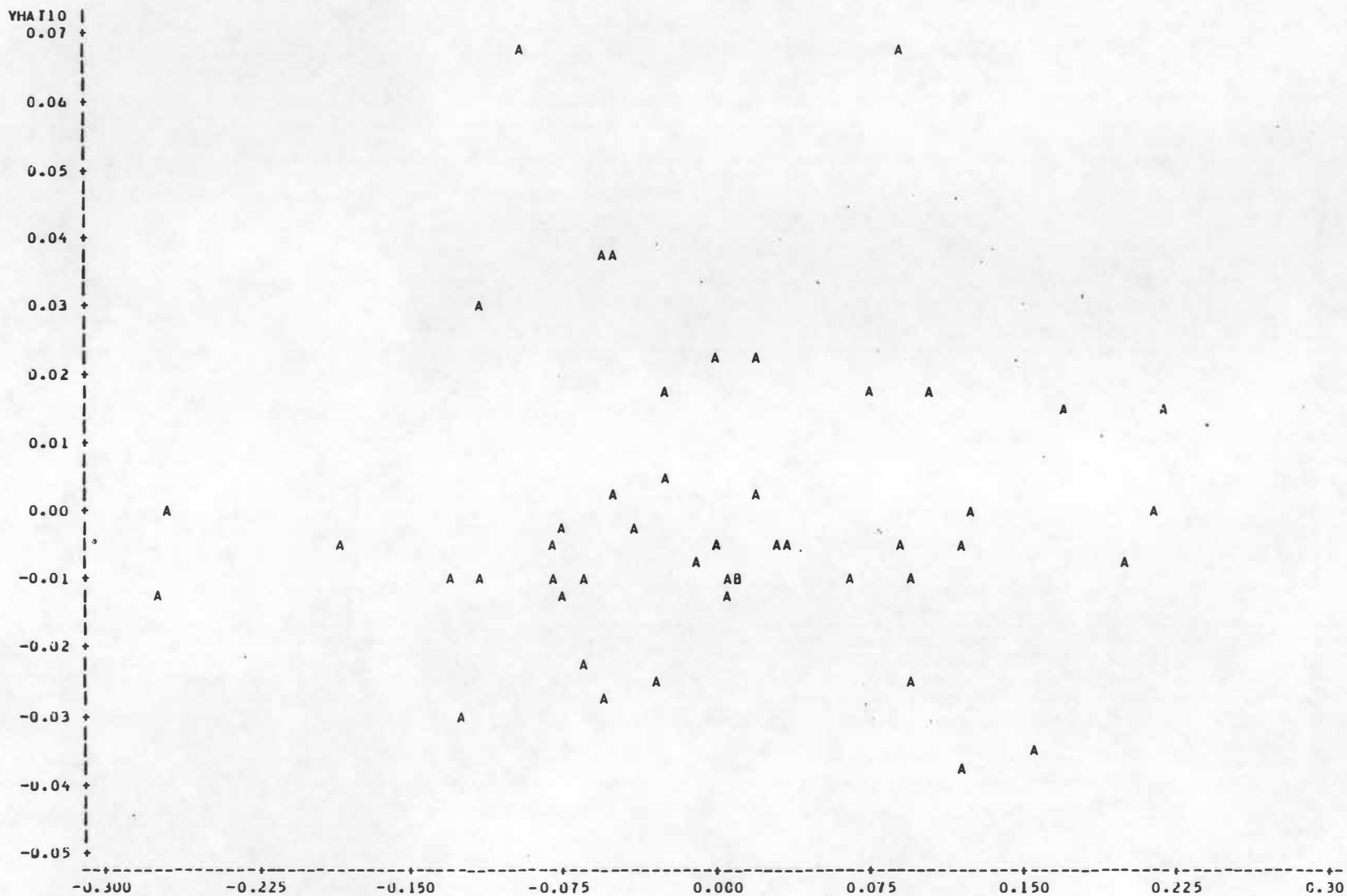


Figure B-20. Plot of male PC10 residuals (X-axis) against fitted values.

VITA

Kenneth M. Binkley received his undergraduate degree in the physical and biological sciences from Indiana State Teachers College in June 1959. Following graduation, he served in the United States Naval Air Force and thereafter pursued an aviation career until returning to academic life in 1975. He received the Master of Science degree in anthropology from Florida State University in August 1976. After five years of experience as an archaeologist with the University of Mississippi's Center for Archaeological Research, he entered the doctoral program in physical anthropology at The University of Tennessee, Knoxville. He received the Doctor of Philosophy degree in anthropology in August 1985.

The author is a member of the American Association of Physical Anthropologists, American Dermatoglyphics Association, Human Biology Council, and the National Pilots' Association. He is married to the former Deborah Kenece King of Oxford, Mississippi.