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The Inheritance of Alcohol Consumption Patterns in a General Population Twin Sample: I. Multidimensional Scaling of Quantity/Frequency Data*

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ABSTRACT. Quantity/frequency data on alcohol consumption were obtained by mailed questionnaire from 2,903 same-sex monozygotic and dizygotic Australian twin pairs. Nonmetric multidimensional scaling was applied to these data. A three-dimensional solution was required to account for the observed pattern of twin concordances for alcohol consumption. These results suggest separate determination of abstinence, frequency of consumption and quantity consumed when drinking, rather than inheritance of a single continuum of overall consumption level. (*J. Stud. Alcohol* 52: 345-352, 1991)

FAMILY STUDIES have found increased risk of alcoholism in the parents, siblings and children of alcoholics (Cotton, 1979; Reich et al., 1988). Studies of adoptees, of half-siblings and of twins are broadly consistent in suggesting a genetic basis for the familial aggregation of alcoholism (e.g., Bohman et al., 1981; Cadoret et al., 1980; Cloninger et al., 1981, 1985; Goodwin et al., 1974; Kaij, 1960; Kaprio et al., 1987; Schuckit et al., 1972), although some small-sample studies have obtained negative results (Murray et al., 1983; Roe and Burks, 1945). Data on the familial transmission of *drinking practices* in general population adult samples are scarce. Nonetheless, surveys of adults that have supplemented self-report data with ratings of parental alcohol consumption patterns have confirmed a high degree of parent-offspring resemblance across the range of alcohol consumption levels (Cahalan et al., 1969; Edwards et al., 1972; see O'Malley et al., 1986, for the validity of such ratings).

Little is known about the contribution of the familial transmission of drinking practices to family resemblance for alcoholism. General population twin studies have usually reported that alcohol consumption patterns are more alike in monozygotic than in dizygotic pairs (e.g., Cederlof et al., 1977; Clifford et al., 1981; Heath et al., 1989; Jardine and Martin, 1984; Kaprio et al., 1981, 1987; Partanen et al., 1966), consistent with a genetic influence on family resemblance for drinking patterns as well as for alcoholism. The evidence is somewhat equivocal, however: some studies have found that the importance of genetic effects on consumption varies with sex or birth cohort (Heath and Martin, 1988; Jardine and Martin, 1984); and several studies have suggested that effects of the social environment on consumption patterns are also important (Clifford et al., 1984; Heath et al., 1989; Jardine and Martin, 1984; Kaprio et al., 1987).

A critical issue concerning the genetic or social inheritance of alcohol consumption patterns, which may help explain some of the inconsistencies between general population genetic studies, is whether different components of drinking behavior are transmitted independently. In some twin studies, researchers have assumed that the determinants of abstinence from alcohol use are quite independent of the determinants of level of consumption in those who drink (Clifford et al., 1981, 1984; Heath et al., 1989; Kaprio et al., 1987), and have excluded abstainers (as defined by criteria that vary between studies) from their analyses. Others have assumed a single liability dimension ranging from abstinence to heavy consumption and have included abstainers (e.g., Jardine and Martin, 1984). If the single liability dimension (SLD) model is correct, exclusion of abstainers will entail sample truncation, which in twin data may lead to overestimation of the importance of genetic factors (Martin and Wilson, 1982; Neale et al., 1989). If the independent liability dimensions (ILD) model is correct, inclusion of drinkers and abstainers in the same analysis may confound two different modes of

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inheritance. For example, if social environmental factors have more effect on abstinence than on consumption level (given that an individual drinks), the importance of genetic effects may be underestimated. Findings from epidemiological surveys suggest that at least some of the factors that distinguish light drinkers from heavy drinkers also discriminate nondrinkers from drinkers (e.g., Cahalan et al., 1969; Clark and Midanik, 1982; Edwards et al., 1972; Encel et al., 1972; Mulford, 1964; Riley and Marden, 1947-48). However, if some, but not all, determinants of abstinence are distinct from the determinants of level of consumption among drinkers, neither SLD nor ILD models will give satisfactory estimates of genetic and environmental influences on drinking pattern.

Regardless of whether they have included or excluded abstainers, general population twin surveys have usually analyzed measures of overall (e.g., weekly) level of alcohol consumption (Clifford et al., 1984; Heath et al., 1989; Jardine and Martin, 1984; Kaprio et al., 1987). It is possible, however, that family resemblance for level of consumption is a consequence of the independent transmission of different components of drinking behavior. Epidemiologists developed Quantity/Frequency and Quantity/Frequency/Variability measures for surveys of alcohol use (Cahalan and Cisin, 1968a,b; Straus and Bacon, 1953) because different drinking styles that produced the same overall level of consumption might nonetheless be associated with different risk-factors. By grouping together those who consume two alcoholic drinks each day, those who consume seven drinks twice a week and those who consume 14 drinks once a week, important underlying differences might be overlooked (Knupfer, 1966). This same issue arises in studies of the social or biological inheritance of drinking behavior. If frequency of alcohol consumption and quantity of alcohol consumed on each occasion that drinking occurs are independently transmitted characters, important information may be lost by considering only overall level of consumption.

Family data, and especially twin data, provide a potentially powerful means of exploring the inheritance of, and relationships between, abstinence, frequency, quantity and total consumption measures of alcohol consumption. If there is independent inheritance of abstinence and of level of consumption (given that an individual is not an abstainer), the average consumption of the drinking co-twin of an abstinent twin should not be different from the consumption of the drinking co-twin of a drinking twin ("independent liability dimensions" model). In contrast, under the "single liability dimension" model, the drinking co-twin of an abstinent twin should be more likely to report a low level of alcohol consumption. If there is strong familial transmission of overall level of consumption, and family resemblance for quantity and frequency measures is only a secondary consequence of this, we would not be surprised to find monozygotic twin pairs where one twin drinks 14 alcoholic drinks once a week and the co-twin drinks two drinks daily. In contrast, we would expect such pairs to be rare if there is separate familial transmission of frequency of consumption and of amount consumed when drinking, and if familial resemblance for overall level of consumption is merely a secondary consequence of the independent transmission of frequency and quantity variables. In this article, we apply nonmetric multidimensional scaling (Kruskal and Wish, 1978) to explore the relationship between the determinants of abstinence, frequency and quantity measures in twin data (see Meyer et al., 1991, for a more detailed and technical discussion of the application of multidimensional scaling to twin data).

Method

Sample

Details of sampling have been described elsewhere (Heath et al., 1989; Jardine, 1985; Jardine and Martin, 1984). Questionnaires were mailed to 5,967 adult volunteer twin pairs enrolled on the Australian National Health and Medical Research Council (NH&MRC) Twin Register. Completed questionnaires were received from both members of 3,810 twin pairs, including 2,903 same-sex pairs (1,233 female monozygotic [MZ], 751 female dizygotic [DZ], 567 male MZ and 352 male DZ pairs). Data from opposite-sex pairs were excluded from the analyses reported in this article. The age of the sample ranged from 18 to 88 years, with a mean (± SD) age of 35.7 ± 14.3 years for female MZ pairs, 35.4 ± 14.3 for female DZ pairs, 34.4 ± 14.0 for male MZ and 32.3 ± 13.9 for male DZ pairs.

Measures

Included in the questionnaire were an item about abstinence from alcohol use ("Have you EVER taken alcoholic drinks?") and standard quantity-frequency questions (Straus and Bacon, 1953). The use of a self-report questionnaire format prevented the inclusion of more detailed questions about the variability of consumption patterns (Cahalan and Cisin, 1968a,b). Frequency of consumption was assessed by the item "Over the last year, about how often have you usually taken any alcoholic drinks," with response categories: every day, 3-4 times each week, about twice a week, about once a week, once or twice a month, less often. Quantity was assessed by the item "On average, how many GLASSES would you drink on each day that you take some alcohol"; the respondents being instructed to report separately their consumption of glasses of beer, wine, spirits and sherry in standard drinks (7 oz for beer, 4 oz for wine, 1 oz for spirits). Respondents were asked to report separately the amount they consumed when they drank on weekdays ("Monday to Friday") and the amount consumed when they drank at weekends. The format of these items is reproduced in Jardine and Martin (1984). We were able to use only the weekend measure, summing across types of drink, to assess quantity, since too few respondents reported weekday consumption levels. Abstinence, quantity and frequency information was combined into a single Quantity/Frequency/Abstinence (Q/F/A) scale (see Table 1) for multidimensional scaling. In constructing the scale, it was necessary to collapse some response categories to avoid very low marginal frequencies for those categories.

Data summary

For each twin group, a two-way contingency table was computed, cross-classifying the consumption pattern of the first twin, assessed using the Q/F/A scale, by that of the second twin (Table 2). Twins were assigned as first or second member of a twin pair on the basis of birth order, where this information was available, or otherwise at random. From each contingency table a "similarity matrix" was computed (Table 3), by dividing the raw cell frequencies of the contingency table by the product of the corresponding marginal row and column frequencies, to yield a "similarity index," $r_{i,j} = f_{i,j} / (f_{i.}\ f_{.j})$, where $f_{i,j}$ is the observed frequency of pairs where the first twin falls into category i and the second twin into category j; $f_{i.}$ is the frequency of first twins in category i; and $f_{.j}$ is the frequency of second twins in category j. Researchers have sometimes tried to use raw cell frequencies as a measure of familial concordance (e.g., Harburg et al., 1982). This can be seriously misleading, however, whenever there are differences in frequency between response categories. For example, more twins in the Australian sample fall into the abstinent category (category A in Table 1) than any other category. From the raw cell frequencies (expressed as percentages in Table 2), it appears that female dizygotic twins who are infrequent light drinkers (category B) are more likely to have a co-twin who is abstinent than a co-twin who is also an infrequent light drinker. However, when the data are converted to a similarity metric, there is a greater excess, over what would be predicted from the marginal frequencies alone, of first twins in category B who have co-twins also falling in category B than of B first twins who have A co-twins (Table 3).

Multidimensional scaling

Nonmetric multidimensional scaling (MDS) was performed separately for each similarity matrix using the SAS Alscal procedure (SAS, 1986; Young and Lewyckyj, 1980). MDS uses proximity (or similarity) data to estimate the coordinates in multidimensional space of a set of variables. It provides information about the number of dimensions needed to represent the spatial (similarity) relationships between the variables. MDS has, for example, been applied to the matrix of airline distances between major U.S. cities to provide a graphical representation of the relative positions of those cities in two-dimensional space (Kruskal and Wish, 1978). In the application of MDS to twin quantity/frequency/abstinence data, we sought a graphical representation of the relative positions of the categories of the Q/F/A scale, using as a measure of proximity (rather than distance) the similarity matrices of Table 3. If the value of the i,j-th cell is large (or small), this indicates a higher (or lower) proportion of twin pairs where the first twin falls in category i and the co-twin in category j than would be expected from the marginal frequencies under the hypothesis of no association. High values indicate proximity of categories and low values indicate distance; thus we used a "similarity" metric, in contrast to the airline distance data which are "dissimilarity" data. The data are ordinal rather than interval and asymmetric rather than symmetric, so we used nonmetric asymmetric rather than metric symmetric multidimensional scaling.

Different theories about the determinants of alcohol consumption patterns generate different predictions for the outcome of multidimensional scaling. The "single liability dimension" model predicts that it will be possible to represent the Q/F/A categories in a single dimension. The "independent liability dimensions" model predicts that a three-dimensional solution will be needed, with separate abstinence, quantity and frequency dimensions. Two statistics permit assessment of the goodness-of-fit of solutions of different dimensionality: a STRESS index (Kruskal and Wish, 1978) and an R^2 index (Young and Lewyckyj, 1980). The former may be interpreted as the "square root of the proportion of the total sum of squares of the optimally scaled data which is not accounted for by the model"; the latter as the "proportion of variance of the optimally scaled data that is accounted for by the model" (Young and Lewyckyj, 1980). Thus high STRESS values, or low R^2 values, indicate a poor fit (Kruskal and Wish, 1978).

Uncertainty about the equivalence of the Q/F/A categories in the two sexes compelled us to exclude opposite-sex twin pairs and perform separate analyses for twin pairs of each sex. In applying multidimensional scaling to twin data, we are using within-pair *differences* to provide information about the relative positions of the Q/F/A categories in multidimensional space. If twin pairs were perfectly correlated, there would be no information about the rankings of the Q/F/A categories. For monozygotic twins, who share 100% of their genes in common, these differences must be environmental in origin. For dizygotic twins, these differences will reflect both within-pair differences in environmental experiences and genetic segregation within families. In principle, it would be possible to obtain different solutions for monozygotic versus dizygotic

TABLE 1. Percentage of respondents falling into each category of the Quantity/Frequency/Abstinence scale (quantity refers to average quantity per occasion at weekends)

Response category		Men	Women
A	Abstinent or drinks less than once a month	22.3	36.8
B	Drinks once or twice a month, or once or twice a week, and takes 2 or fewer drinks/occasion	15.9	21.8
C	Drinks once or twice a month, or once or twice a week, and takes 3-4 drinks/occasion	10.0	11.7
D	Drinks once or twice a month, or once or twice a week, and takes 5-6 drinks/occasion	8.1	5.6
E	Drinks once or twice a month, or once or twice a week, and takes 7 or more drinks/occasion	11.8	5.0
F	Drinks at least 3-4 times a week and takes 2 or fewer drinks/occasion	6.3	8.4
G	Drinks at least 3-4 times a week, and takes 3-4 drinks/occasion	5.9	5.0
H	Drinks at least 3-4 times a week, and takes 5-6 drinks/occasion	5.1	2.7
I	Drinks at least 3-4 times a week, and takes 7 or more drinks/occasion	14.7	2.9

TABLE 2. Twin-pair concordance for position on Quantity/Frequency/Abstinence scale, by sex and zygosity. For each sex and zygosity group, the percentage of pairs falling into each cell of the two-way Q/F/A table is given (see Table 1 for definition of scale).

	FEMALE MONOZYGOTIC PAIRS								
	Second twin								
	A	B	C	D	E	F	G	H	I
First twin									
A	24.9	6.5	1.7	0.7	0.6	1.7	0.2	0.2	0.2
B	7.1	6.9	3.5	0.8	0.9	1.8	1.2	0.2	0.4
C	2.7	2.6	3.0	1.0	0.8	0.5	0.4	0.2	0.1
D	0.8	1.0	1.5	0.9	0.6	0.1	0.4	0.3	0.2
E	0.6	0.7	0.6	0.5	1.7	0.2	0.0	0.1	0.3
F	1.1	1.5	0.6	0.2	0.0	2.4	1.1	0.4	0.2
G	0.7	0.6	0.3	0.2	0.0	1.2	1.1	0.5	0.5
H	0.2	0.6	0.2	0.8	0.2	0.2	0.6	0.6	0.7
I	0.2	0.2	0.2	0.2	0.5	0.2	0.3	0.2	0.8
	FEMALE DIZYGOTIC PAIRS								
	A	B	C	D	E	F	G	H	I
A	19.7	7.9	3.7	0.9	1.1	2.8	0.9	0.1	0.1
B	6.7	5.3	3.1	1.2	1.3	2.3	1.2	0.4	0.1
C	2.3	3.2	2.4	0.9	0.9	0.9	0.4	0.1	0.3
D	0.9	0.9	1.6	0.9	0.7	0.4	0.4	0.3	0.3
E	0.3	1.6	0.1	0.7	0.8	0.1	0.0	0.1	0.4
F	1.9	1.6	0.9	0.7	0.3	1.9	0.8	0.3	0.3
G	1.1	1.2	0.7	0.4	0.1	0.9	0.5	0.1	0.1
H	0.8	0.5	0.4	0.1	0.3	0.3	0.1	0.0	0.3
I	0.8	0.4	0.1	0.1	0.4	0.3	0.0	0.1	0.4
	MALE MONOZYGOTIC PAIRS								
	A	B	C	D	E	F	G	H	I
A	14.1	3.9	1.1	0.9	1.1	0.0	0.2	0.0	0.7
B	4.6	4.4	2.7	1.1	1.1	0.7	0.9	0.2	0.5
C	1.4	1.8	1.8	1.6	1.6	0.4	0.4	0.2	0.7
D	0.9	1.8	1.1	1.4	0.7	0.4	0.5	0.4	0.7
E	0.7	1.1	1.4	0.7	4.2	0.0	0.4	0.7	2.3
F	0.4	2.3	0.9	0.2	0.0	1.2	1.4	0.2	1.1
G	0.9	0.7	0.9	0.2	0.4	1.1	0.2	0.7	1.4
H	0.5	0.2	0.4	0.0	0.4	0.5	0.9	1.4	1.9
I	0.9	0.7	0.2	0.4	1.8	0.5	1.8	0.7	6.2
	MALE DIZYGOTIC PAIRS								
	A	B	C	D	E	F	G	H	I
A	11.4	3.4	1.1	1.1	0.3	1.1	0.3	0.0	2.0
B	4.3	2.0	3.1	1.1	1.1	0.6	0.6	1.1	1.4
C	1.7	1.4	1.1	1.7	1.4	0.6	0.3	0.6	1.4
D	0.0	1.4	2.6	2.3	1.4	0.9	0.0	0.3	0.6
E	1.7	0.9	1.1	2.0	4.0	0.3	0.0	0.0	2.6
F	0.3	2.0	0.0	0.3	0.0	0.9	0.9	0.9	1.1
G	0.3	1.4	0.0	0.3	0.3	0.6	1.4	0.6	1.7
H	0.9	0.3	0.3	0.3	1.4	0.6	0.0	0.0	1.4
I	0.6	2.0	0.6	1.1	2.6	1.1	0.3	0.9	4.8

twin pairs. This might occur, for example, if genetic effects on consumption were acting along a single continuum but there were separate environmental determinants of abstinence, quantity and frequency. For this reason, multidimensional scaling was performed separately for each zygosity group.

Results

Table 1 gives the percentages of male and female respondents falling into each category of the Q/F/A scale. Even though a relatively small proportion of this sample were life-long abstainers (Heath and Martin, 1988), no less than 36.8% of women and 22.3% of men report drinking alcohol either not at all or less than once a month. A much higher proportion of men than women report that they are regular heavy drinkers: for category I (drinks at least 3-4 times a week and takes on average 7 or more drinks per occasion [at weekends]), the sex-ratio is over 5 : 1.

Table 2 gives the concordances for each twin group for position on the Q/F/A scale. Table 3 gives the corresponding similarity matrices for each twin group. In the raw frequency data (Table 2), the high proportion of twin pairs who are concordant for abstinence is striking. However, once marginal frequency differencies between categories are taken into account (Table 3), it is apparent that there is also an excess of concordant twin pairs, over what would be predicted under the hypothesis of no association, for most other Q/F/A categories. There are more than the expected number of pairs falling into the same frequency class (once or twice a month or once or twice a week [B,C,D,E] versus daily or at least 3-4 times a week [F,G,H,I]). Within each frequency class, similarity indices decrease with increasing difference in quantity consumed, implying that twins may vary along a dimension of quantity of alcohol consumed when drinking, even after controlling for frequency of consumption. Note also that within a frequency class similarity is generally higher the greater the quantity consumed.

Table 4 compares the results of one-, two-, three- and four-dimensional MDS solutions. For all twin groups, a one-dimensional solution gave a very poor fit to the data: stress values of greater than 0.15 are considered large enough to reject a one-dimensional solution (Kruskal and Wish, 1978). Two-dimensional solutions gave a much better fit and in every twin group identified separate quantity and frequency dimensions. Three-dimensional solutions gave a further substantial improvement in fit and identified a third dimension, abstinence. Including a fourth dimension produced a much smaller improvement in fit, and no interpretation of the fourth dimension could be found that was consistent across either sex or zygosity groups. In particular, we did not, as we might have expected, obtain a fourth dimension distinguishing the very heavy drinkers in the sample (e.g., those in category I) from the rest. This suggests that three dimensions are adequate to account for the observed twin Q/F/A concordances.

TABLE 3. Similarity matrices for each twin group for quantity/frequency/abstinence data. Raw cell frequencies have been divided by the corresponding row and column marginal frequencies and then multiplied by 100 for ease of interpretation.

	A	B	C	D	E	F	G	H	I
FEMALE MONOZYGOTIC PAIRS (*Second twin*)									
First twin									
A	178	86	40	39	29	56	12	17	19
B	81	147	132	78	74	95	100	40	50
C	63	113	231	191	137	53	68	54	20
D	36	81	228	336	184	17	[illegible]	208	117
E	32	77	106	232	699	42	0	66	197
F	36	99	64	70	0	386	278	199	89
G	34	56	57	72	0	297	398	368	276
H	18	79	60	51	132	84	304	608	587
I	22	28	49	189	325	69	214	320	801
FEMALE DIZYGOTIC PAIRS	A	B	C	D	E	F	G	H	I
A	154	93	77	42	49	76	57	22	16
B	90	109	109	93	105	106	126	116	27
C	58	123	160	136	139	83	79	73	103
D	42	64	192	243	178	63	142	261	184
E	19	171	25	269	330	33	0	202	428
F	64	83	84	130	53	222	213	196	138
G	60	102	98	128	44	182	233	160	113
H	83	84	109	79	163	97	108	0	421
I	87	66	38	83	256	101	0	313	663
MALE MONOZYGOTIC PAIRS	A	B	C	D	E	F	G	H	I
A	265	106	47	64	44	0	12	0	21
B	117	164	161	104	59	92	84	25	21
C	60	109	178	258	147	76	56	41	47
D	47	136	133	286	82	95	104	103	59
E	25	55	120	97	332	0	47	140	129
F	19	180	114	37	0	342	285	53	90
G	57	66	136	44	50	350	43	252	143
H	35	17	56	0	51	180	219	518	203
I	28	32	13	43	122	85	207	123	305
MALE DIZYGOTIC PAIRS	A	B	C	D	E	F	G	H	I
A	261	111	55	54	11	84	37	0	56
B	132	88	205	72	59	57	100	174	54
C	79	94	112	163	111	85	75	130	81
D	0	103	274	237	121	139	0	71	36
E	65	46	91	156	255	35	0	0	120
F	22	215	0	44	0	209	369	320	107
G	21	147	0	43	35	133	589	204	153
H	79	38	56	54	222	170	0	0	163
I	19	97	41	80	147	125	55	144	204

Figures 1-4 plot the three-dimensional solutions obtained for monozygotic female, dizygotic female, monozygotic male and dizygotic male pairs. Results are broadly consistent across groups. Separate frequency, quantity and abstinence dimensions can clearly be identified. In each figure, the horizontal axis corresponds to the quantity dimension which distinguishes light drinkers (right) from heavy drinkers (left of the figure); the vertical axis corresponds to the abstinence dimension which distinguishes abstainers (top) from drinkers (bottom of the figure); and the third axis is a frequency dimension which distinguishes infrequent (front) from regular drinkers (rear of the figure). However, for dizygotic men, the smallest group in terms of sample size, the quantity and abstinence dimensions are less clearly defined than for the other groups (Figure 4).

Conclusions

The results of the multidimensional scaling analyses did not support the "single liability dimension" model for the inheritance of alcohol consumption levels. In each twin group an abstinence dimension was found that was distinct from the dimensions determining consumption level in those who were not abstainers. These results also imply that analyses of overall level of consumption might be potentially misleading, even if abstainers were excluded. It appears rather that there is separate determination of frequency of alcohol consumption and quantity consumed on each occasion that alcohol is taken. However, we cannot exclude totally the possibility that genetic effects determine differences in overall level of consumption, acting in a different manner than environmental effects. The similarity of the results that we obtained for both monozygotic and dizygotic pairs could still arise if the effects of genetic segregation on within-pair differences in dizygotic pairs were weak, and the results of multidimensional scaling for dizygotic pairs consequently were dominated by environmental effects. Parametric genetic analyses would make it possible to reject this explanation.

Although the multidimensional scaling analyses separated out abstainers from drinkers on a third dimension, it

TABLE 4. Comparison of goodness-of-fit of MDS solutions of different dimensionality

	Solution							
	1-dimensional		2-dimensional		3-dimensional		4-dimensional	
Twin group	STRESS	R^2	STRESS	R^2	STRESS	R^2	STRESS	R^2
Monozygotic female	0.40	0.60	0.17	0.87	0.11	0.94	0.09	0.95
Monozygotic male	0.37	0.64	0.20	0.83	0.15	0.89	0.10	0.95
Dizygotic female	0.39	0.59	0.25	0.74	0.16	0.87	0.13	0.92
Dizygotic male	0.46	0.47	0.25	0.75	0.20	0.78	0.15	0.87

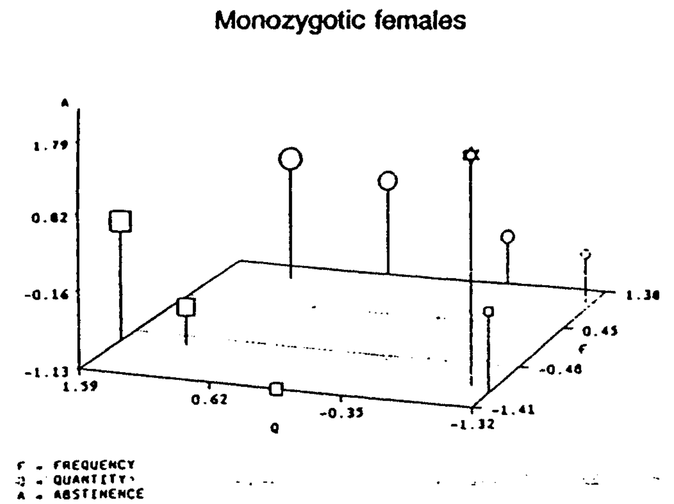

FIGURE 1. Plot of three-dimensional MDS solution: monozygotic females. Abstainers are indicated by a star, infrequent drinkers by a square and frequent drinkers by a circle. Increasing quantity consumed when drinking occurs is indicated by increasing magnitude of the circle or square.

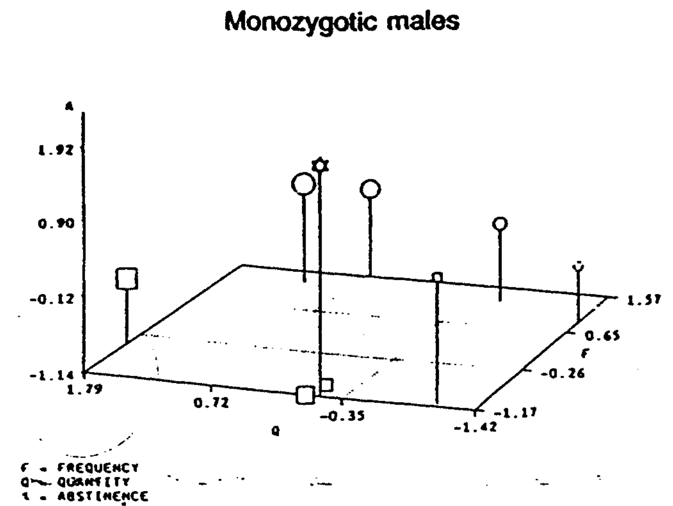

FIGURE 3. Plot of three-dimensional MDS solution: monozygotic males. Abstainers are indicated by a star, infrequent drinkers by a square and frequent drinkers by a circle. Increasing quantity consumed when drinking occurs is indicated by increasing magnitude of the circle or square.

is noteworthy that even in the four-dimensional solutions they did not separate out the heavy drinkers (e.g., those falling in category I) from the other drinkers in our sample. If some of these heavy drinkers were already alcoholics at the time of the survey, or have subsequently progressed to become alcoholics, this would be consistent with a continuum model of alcoholism, with alcoholics being distinguished from moderate drinkers, and moderate drinkers from light drinkers, by their more extreme positions along either or both of two liability continua (corresponding to our frequency and quantity dimensions). Recent work on the genetics of alcoholism (Cloninger, 1987; Cloninger et al., 1981, 1985, 1988) has suggested that there are at least two separately inherited forms of alcoholism: Type I alcoholism, associated with persistent alcohol-seeking behaviors (identified with the gamma alcoholism of Jellinek [1960]); and Type II alcoholism, associated with the ability to abstain from alcohol, but loss of control once drinking has started (the delta alcoholism of Jellinek: Cloninger, 1987). It is possible that these two subtypes correspond to extremes on the same liability dimensions that we are detecting using general population quantity/frequency data. Until follow-up data are obtained on alcoholism in this sample, however, this interpretation must remain speculative.

Nonmetric multidimensional scaling, as applied in this article, is applicable to a broad class of problems in sub-

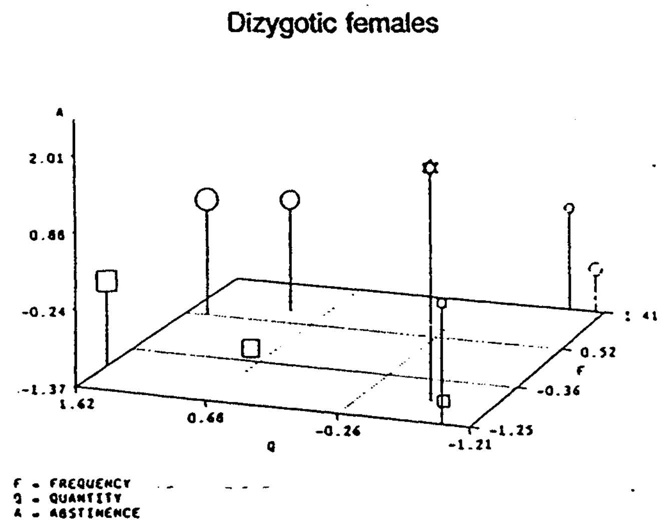

FIGURE 2. Plot of three-dimensional MDS solution: dizygotic females. Abstainers are indicated by a star, infrequent drinkers by a square and frequent drinkers by a circle. Increasing quantity consumed when drinking occurs is indicated by increasing magnitude of the circle or square.

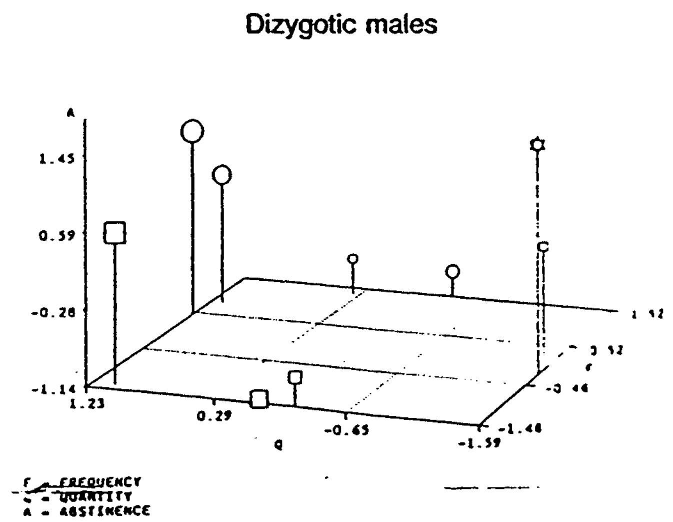

FIGURE 4. Plot of three-dimensional MDS solution: dizygotic males. Abstainers are indicated by a star, infrequent drinkers by a square and frequent drinkers by a circle. Increasing quantity consumed when drinking occurs is indicated by increasing magnitude of the circle or square.

stance abuse research, when twin or family data are available. It is potentially applicable to etiologic questions concerning patterns of multiple drug use, or concerning heterogeneity of diagnostic categories (e.g., Cloninger, 1987). We emphasize its use, however, as an exploratory or hypothesis-generating tool. Parametric model-fitting methods must then be applied to provide rigorous tests of specific hypotheses (Heath et al., in press).

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