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A MODEL FOR INTRA-FAMILIAL DISTRIBUTION OF AN INFECTIOUS DISEASE (CHAGAS' DISEASE)

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A probabilistic model for intra-familial distribution of infectious disease is proposed and applied to the prevalence of positive serology for Trypanosoma cruzi *infection in a Northeastern Brazilian sample.*

This double binomial with one tail excess model fits satisfactorily to the data and its interpretation says that around 51% of these 982 families are free of infection risk; among those that are at risk, 3% have a high risk (0.66), probably due to high domestic infestation of the vector bug; while 97% show a small risk (0.11), probably due to accidental, non-domestic transmission.

Key words: intra-familial distribution – infectious disease – Chagas' disease – double binomial

Several statistical models have been proposed for the dynamics of infectious disease (Bailey, 1975; Anderson & May, 1979), considering both spatial and/or temporal trends. It is rather infrequent the development of models that take into account the variability within families, for this class of nosological entities. This apparent lack of importance is probably due to the little interest on familial causes for the explanation of both endemic dynamics and on the physiopathology of this group of diseases.

The present paper is an attempt to propose simple probabilistic models and to study the distribution of *Trypanosoma cruzi* infection within families from the Brazilian Northeastern region.

METHODS AND SAMPLE

A general model (double binomial with one-tail excess) is proposed, in order to explain the distribution of affected individuals within families.

The model is as follows:

$$L_{s,r} = P(s,r = 0) = T + (1-T)\{(1-w)(1-m)^s + w(1-p-m+mp)^s\}$$

or

$$L_{s,r} = P(s,r > 0) = (1-T)\binom{s}{r}\{(1-w)(1-m)^{s-r} m^r + w(1-p-m+mp)^{s-r}(p+m-mp)^r\},$$

where r is the number of affected individuals in a family with s members; m is the baseline low risk affection probability; $p + m - mp$ is the larger risk affection probability; w is the proportion of families with high risk of affection, among those with probability larger than zero; and T is the proportion of families without risk of affection.

By fixing some of the above parameters, it is possible to arrive to some different models. By fixing $T = 0$, the double binomial is obtained. By fixing $w = 0$, we arrive at the single binomial with one-tail Excess. Finally, fixing both $T = 0$ and $w = 0$, the single binomial is obtained.

Miximum likelihood techniques were employed in order to achieve parameter's estimations. In other words, by iterative non-linear optimization procedures (Fletcher & Powell, 1963), a parameter vector θ was attained in order to minimize the vector of Maximum likelihood scores, with elements $\partial \ln L_{S,R} / \partial \theta_i$,

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where θ_i is the ith parameter. Usual likelihood ratio tests were applied, in order to test the model validity.

The utilized sample comprises 982 rural Northeastern Brazilian families whose data was collected between September of 1969 and August of 1970 (Penalva da Silva & Krieger, 1983; Cabello et al., 1988). Although the study was mainly concerned with genetic variability, frozen sera samples from these families were tested, by indirect immunofluorescent techniques (Camargo, 1966) for the presence of anti-*T. cruzi* antibodies.

RESULTS AND DISCUSSION

The familial distribution of *T. cruzi* infection is showed in Table I. It should be mentioned that one family with 11 members, being six affected was excluded from the sample, as a clear outlier, since it contributes disproportionately to the goodness-of-fit χ^2 in all of the tested models. The estimated parameters as well as the statistical inferences are shown in Table II. As can be seen, only the double binomial with one-tail excess model fits rather satisfactorily to the data ($\chi^2_{42} = 59.85$), while none of the other tested models fit to the data.

It should be remembered that the double binomial with one-tail excess is a derivation of the double binomial one, which was applied successfully to the distribution of congenital malformations (Mi et al., 1965) and to fetal deaths (Krieger, 1972).

The *T. cruzi* infection in rural populations, as the present one, is due almost exclusively to the transmission of the parasite by Triatomidae bugs, while among the more urban populations, blood transfusion is an important source of new infection (Brener, 1979). It seems reasonable to interpret the present findings in the sense that among the analyzed sample, around 50% of the families live in such conditions that *T. cruzi* infection is practically impossible. Among the remained families, 97% show a low probability (0.115) of infection, probably due to accidental non-domestic infection; while 3% show a high probability (0.659) of being infected, being their household infested by infected Triatomidae bugs. Although this interpretation is rather consistent with previous knowledge, the possibility of quantification of the size of the various groups as well as their respective risks may provide new insights on both the epidemiology and on the efficiency of future prophylactic measures.

It is obvious that some other distribution (negative binomial, for example), would also fit to this data. However, the clear epidemiological interpretation of the parameters in situ-

TABLE I

Familial distribution of *Trypanosoma cruzi* serology in Northeastern Brazil

Family size (s)	Number of affected individuals within the family (r)	Number of families ($N_{S,R}$)
1	0	43
1	1	3
2	0	7
2	1	2
3	0	55
3	1	8
3	2	3
4	0	186
4	1	33
4	2	8
4	3	2
5	0	139
5	1	41
5	2	8
5	3	1
6	0	112
6	1	33
6	2	9
6	3	3
6	4	1
6	5	1
7	0	81
7	1	19
7	2	9
7	3	2
7	4	2
7	6	1
8	0	67
8	1	12
8	2	5
8	3	3
8	6	1
8	7	1
9	0	26
9	1	8
10	0	16
10	1	4
10	2	2
11	0	5
11	1	5
11	3	1
12	0	6
12	4	1
13	0	5
13	4	1
14	0	1

TABLE II

General description of the models, their correspondent goodness of fit (χ^2) tests and parameter estimates

Model	Goodness of fit χ^2	D.F.	Estimated parameters and standard errors T	S.E.	w	S.E.	m	S.E.	p	S.E.
Double binomial with one-tail excess	59.85	42	0.5134	0.0474	0.0267	0.0143	0.1146	0.0143	0.6152	0.1341
Double binomial	131.35	43			0.1049	0.0242	0.0331	0.0042	0.2920	0.0317
Single binomial with one-tail excess	2511.71	44	0.5882	0.0282			0.1531	0.0094		
Simple binomial	452818.24	45					0.0621	0.0025		

ations where the risk is heterogeneous among families (Down's syndrome has a similar population distribution) makes the present model an attractive alternative.

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