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Stochastic Models of Heredity Rhesus Factor

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Abstract: We consider linear and nonlinear stochastic models of transmission Rhesus factor from parents to their offspring and show that in long run behavior the frequency of Rhesus factor be the same.

Key words: Markov Chain; Quadratic Stochastic Operator; Rhesus factor; Heredity.

INTRODUCTION

Blood groups are the distinguishing of blood by their antigenic properties. These properties are determined by the substances found on the surface of the red blood cells. There are approximately 200 blood group substances identified and categorized into 19 distinct systems. The most common system is the ABO system. The human ABO blood group was discovered by Karl Landsteiner in 1900[4], and its mode of inheritance as multiple alleles at a single generic locus was established by Felix Bernstein[1] a quarter century later.

The ABO blood group antigens appear to have been important throughout our evolution because the frequencies of different ABO blood types vary among different populations, suggesting that a particular blood type conferred a selection advantage.

The Rhesus system is the second most significant blood group system in human blood transfusion. Individuals either have, or do not have, the Rhesus factor (or Rh D antigen) on the surface of their red blood cells. This is usually indicated by Rh^+ (does have the RhD antigen) or Rh^- (does not have the antigen) suffix to the ABO blood type.

A child inherits two rhesus genes, one from each parent, where gene *D* corresponds to positive rhesus factor and gene *d* corresponds to negative rhesus factor.

Table 1: Offspring's Rhesus genes

Offspring's Rhesus genes		Rhesus gene inherited from the mother	
		D	*d*
Rhesus gene inherited from the father	*D*	(*D*,*D*)	(*D*, *d*)
	d	(*D*, *d*)	(*d*, *d*)

Offspring is rhesus negative if they have inherited a *d* gene from each parent (*d*,*d*) and offspring is rhesus positive if they inherited a *D* gene from both parents. If offspring have inherited a rhesus positive gene *D* and a rhesus negative gene *d* , they are most likely to be rhesus positive as the *D* gene is more dominant as compared to the *d* gene. Hence it is possible to have a rhesus negative child and a rhesus positive father.

Table 2: Offspring's Rhesus factor

Offspring's Rhesus factor		Mother's Rhesus factor	
		Rh^+	Rh^-
Father's Rhesus factor	Rh^+	Rh^+ or Rh^-	Rh^+ or Rh^-
	Rh^-	Rh^+ or Rh^-	Rh^-

It is well known that blood groups and rhesus of parents do not determine unambiguously their offspring's blood group and rhesus (see Table 2). The transmission of blood groups and its rhesus from parents to their offspring is a random events. To study these transmissions we consider two type of stochastic modeling:

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(*i*) Markov chains;
(*ii*) Quadratic stochastic operators.

The theory of Markov chains is well known. It is naturally the model that described by Markov chain call linear model

In the next part we briefly introduce a nonlinear model that is described by nonlinear transformation, namely, a quadratic stochastic operator.

In this paper we consider models of transmission Rhesus factor. To study models of transmission of blood type is the subject of the second part.

1. Quadratic Stochastic Operators:

Quadratic stochastic operator was first introduced in [1].Such operator frequently arises in many models of mathematical genetics[1-6].Consider a biological population, that is a community of organisms closed with respect to reproduction. Assume that each individual in this population belongs to precisely one species 1,…, *m* . Below we consider the scale of blood rhesus with *m* = 2. The scale of species is such that the species of the parents *i* and *j* unambiguously determines the probability of every species *k* for the first generation of direct descendants. Denote this probability, that is to be called the heredity coefficient, by $p_{ij,k}$. It is then obvious that $p_{ij,k} \geq 0$ and $\sum_{k=1}^{m} p_{ij,k} = 1$. Assume that the population is so large that frequency fluctuations can be neglected. Then the state of the population can be described by the *m*-tuple $(x_1,x_2,\ldots,x_m)$ of species probabilities, that is x_k is the fraction of the species *k* in the total population. In the case of panmixia (random interbreeding) the parent pairs *i* and *j* arise for a fixed state $x=(x_1,x_2,\ldots,x_m)$ with probability x_ix_j. Hence the total probability of the species *k* in the first generation of direct descendants is defined by

$$x_k' = \sum_{i,j=1}^{m} p_{ij,k} x_i x_j \quad , k=1,\ldots,m \tag{1}$$

Let $S^{m-1} = \{x = (x_1,\ldots,x_m) \in R^m : x_i \geq 0 \ \ for\ any\ i = 1,\ldots,m\ and\ \sum_{i=1}^{m} x_i = 1\}$ be the (*m*-1) - dimensional canonical simplex in R^m. The transformation $V : S^{m-1} \to S^{m-1}$ is called a quadratic stochastic operator if

$$V : (Vx)_k = \sum_{i,j=1}^{m} p_{ij,k} x_i x_j \quad , k=1,\ldots,m \tag{2}$$

where *a*) $p_{ij,k} \geq 0$; *b*) $p_{ij,k} = p_{ji,k}$; and *c*) $\sum_{k=1}^{m} p_{ij,k} = 1$ for arbitrary *i,j,k*=1,…,*m*.

Note that the condition b) $p_{ij,k} = p_{ji,k}$ is not overloaded, since otherwise one can determine new heredity coefficients $q_{ij,k} = \frac{p_{ij,k} + p_{ji,k}}{2}$ with preserving the operator V

$$V : (Vx)_k = \sum_{i,j=1}^{m} q_{ij,k} x_i x_j \quad , k=1,\ldots,m \tag{3}$$

Thus the transformation (2) or (3), which describes a model of heredity is a quadratic stochastic operator.

A model of heredity is uniquely determined by heredity coefficients $p_{ij,k}$ or $q_{ij,k} = \frac{p_{ij,k} + p_{ji,k}}{2}$ for

i,j,k=1,…,*m.*

Assume $\{V^k(x)$: k=0,1,2,…$\}$ is the trajectory of the initial point $x \in S^{m-1}$, where $V^{k+1}(x) = V(V^k(x))$ for all k=0,1,2,… with $V^0(x)=x$.

To investigate limit behavior of trajectories and fixed points of quadratic stochastic operator V (2) play important role in many applied problems.

A fixed point of a quadratic stochastic operator V is a point **x** = **a** where V(**a**) = **a.**

A quadratic stochastic operator V is called regular if for each initial point $x \in S^{m-1}$ the limit

$$\lim_{n\to\infty} V^n(x)$$

exists.

Note that the limit point be a fixed point of a quadratic stochastic operator V.

Thus the fixed points of a quadratic stochastic operator describe limit or long run behavior the trajectories of any initial points.

A quadratic stochastic operator describes the transmission of the same scales from pair of parents to their offspring.

2. Rhesus Factor Transmission:

Firstly we consider linear model of transmission, namely, Markov chain. A Markov chain describes transmission of some scale from one of parents to their offspring of the same gender. Note that only for such Markov chains one can study their limiting distribution or long run behavior. Below we consider two Markov chains: first Markov chain describes a transmission of rhesus factor from fathers to their sons and second one describes transmission of rhesus factor from mothers to their daughters. For collected data let $N_S(F_X)$ be the number of sons of fathers F_X ,that is fathers with rhesus factor X and $N_S^Y(F_X)$ be the number of sons with rhesus factor$Y$ of fathers F_X where $X, Y \in \{+,-\}$. Then $N_S(F_X)= N_S^+(F_X) + N_S^-(F_X)$.

To describe the transmission of factor rhesus from fathers to their sons we need to find the probabilities P_{XY} that from a father with factor rhesus X his son heredities factor rhesus Y, where X,Y Î {+,-}. It is naturally to put $P_{XY} = \dfrac{N_S^Y(F_X)}{N_S(F_X)}$.

Then according collected data the transition probalities matrix of the first Markov chain has form

(Son)

$$\Pi(F,S) = \begin{array}{c} \\ \text{(Father)} \\ \\ \end{array} \begin{array}{c} \begin{array}{cc} \quad^{+} & \quad^{-} \end{array} \\ \begin{vmatrix} 0.970 & 0.030 \\ 0.508 & 0.492 \end{vmatrix} \end{array} \begin{array}{l} \\ + \\ - \end{array} \qquad (4)$$

and the transition probalities matrix of the second Markov chain, which describes the transmission of rhesus factor from mother to her daughters, has form

(Daughter)

$$\Pi(M,D) = \begin{array}{c} \\ \text{(Mother)} \\ \\ \end{array} \begin{array}{c} \begin{array}{cc} \quad^{+} & \quad^{-} \end{array} \\ \begin{vmatrix} 0.969 & 0.031 \\ 0.510 & 0.490 \end{vmatrix} \end{array} \begin{array}{l} \\ + \\ - \end{array} \qquad (5)$$

Both Markov chains are regular with limiting distribution

$\pi_+ = 0.944, \quad \pi_- = 0.056$

for first Markov chain and with limiting distribution

$\pi_+ = 0.943, \quad \pi_- = 0.057$

for second one.

3. Nonlinear Model of Rhesus Factor Transmission:

Now consider nonlinear model of transmission, namely quadratic stochastic operators. Let a set of species be a set of factor rhesus {1, 2}, where 1 denote positive rhesus and 2 denote negative rhesus. To describe the transmission of factor rhesus from parents to their offspring we need to find the probability $P_{XY,Z}$ that from a father with factor rhesus X and a mother with factor rhesus Y their child receives factor rhesus Z, where $X,Y,Z \in \{1,2\}$. Let $N(F_X,M_Y)$ be the number of offspring of fathers F_X and mothers M_Y ,that is fathers with factor rhesus X and mothers with factor rhesus Y and $N^Z(F_X,M_Y)$ be the number of offspring with factor rhesus Z of fathers F_X and mothers M_Y. Then the transmission probability $P_{XY,Z}$ is defined as

$$P_{XY,Z} = \frac{N^Z(F_X,M_Y)}{N(F_X,M_Y)} \tag{6}$$

Let $q_{ij,k} = \frac{P_{ij,k} + P_{ji,k}}{2}$ be the heredity coefficients for $i,j,k \in \{1,2\}$.

For collected data according (6) we have following:

$$q_{11,1} = 0.985,\ q_{12,1} = 0.652,\ q_{22,1} = 0.092$$
$$q_{11,2} = 0.015,\ q_{12,2} = 0.348,\ q_{22,2} = 0.908$$

and corresponding quadratic stochastic operator has form

$$\begin{aligned} x_1' &= 0.985x_1^2 + 1.305x_1x_2 + 0.092x_2^2 \\ x_2' &= 0.015x_1^2 + 0.695x_1x_2 + 0.908x_2^2 \end{aligned} \tag{7}$$

where x_1 is the fraction of the population with positive rhesus factor and x_2 is the fraction of the population with negative rhesus factor.

The transformation (7) has single fixed point

$$x_1^* = 0.954, x_2^* = 0.046 \tag{8}$$

The Jacobian of the quadratic stochastic operator (6) at the fixed point has following form

$$J(0.954, 0.046) = \begin{Vmatrix} 1.939 & 1.253 \\ 0.061 & 0.746 \end{Vmatrix}$$

with eigen values $\lambda_1 = 0.685$ and $\lambda_2 = 2$. The eigen vector corresponding to eigen value $\lambda_2 = 2$ is fixed

vector (8) and the eigen vector corresponding to eigen value $\lambda_1 = 0.685$ does not belong to simplex S^1.

The fixed point (8) is stable and any trajectory of quadratic stochastic operator (7) converge to fixed point (8). Thus the quadratic stochastic operator (7) is a regular.

4. Discussion and Conclusion:

From our considerations follow that frequencies of Rhesus factor among men and women are the same, that is there is no significant association between sex and Rhesus factor. Secondary, probability that a son (daughter) of a father (respectively a mother) with negative Rhesus factor will inherit positive rhesus factor is equal to 0.5.

Now consider the received heredity coefficients:

$$q_{11,1} = 0.985,\ q_{12,1} = 0.652,\ q_{22,1} = 0.092$$
$$q_{11,2} = 0.015,\ q_{12,2} = 0.348,\ q_{22,2} = 0.908$$

One can see that there are instances when the chart of Table 2 is not accurate, since $q_{22,1}$=0.092 means that a child of parents with negative rhesus factor receives positive rhesus factors with probability 0.092. . In the case of a mutation, the factor rhesus typing may not hold true in the question of parentage.

Finally note since the data collected at two regions of Malaysia, probably our results are valid within a national, regional, or ethnic group.

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REFERENCES

Bernstein, F., 1925. Zusammenfassende Betrachtungen uber die erblichen Blutstrukturen des Menschen. Z. Indukt. Abstammungs.Vererbungsl., 37: 237-370.

Bernstein, S.N., 1924. Solution of a mathematical problem connected with the theory of heredity, Ann.Sci. de l'Ukraine, 1: 83- 114.

Ganikhodjaev, N.N., 1999. An application of the theory of Gibbs distributions to Mathematical Genetics, Doklady Mathematics, 61(3): 13-16.

Jenks, R.D., 1969. Quadratic Differential Systems for Interactive Population Models, J.Diff.Eqs., 5: 497-514.

Kesten, H., 1970. Quadratic transformations: a model for population growth .I, II, Adv. Appl. Prob., 2: 1-82, 179-228.

Landsteiner, K., 1900. Zur Kenntnis der antifermentativen, lytischen und agglutinierenden Wirkungen des Blutserums und der Lymphe. Centralblatt für Bakteriologie, Parasitenkunde und Infektionskrankheiten. Originale, 27: 357-362.

Lyubich Yu, I., 1971. Basic concepts and theorems of the evolution genetics of free populations, Russian Math. Surveys, 26(5): 51-116.

Reed, M.L., 1997. Algebraic structure of genetic inheritance, Bulletin of AMS, 34(2): 107-130.