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MATHEMATICAL MODELING OF DETERMINATION TIME CHARACTERISTICS OF THE FORMATION OF SECOND OTHER TUMORS

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Causes of carcinogenesis are diverse (Aaronson S.A. et al., 1991), but one of the key factors of this phenomenon is damage of certain genes in the tumor cells. Presumably, these genes are responsible for reparation of DNA damage. Thus, the damage to all these genes in the cell is considered a necessary condition for the malignancy of this cell. Proceeding from such a concept, one can construct probabilistic mathematical models that allow calculating the numerical characteristics of the time of formation of other tumors (Adam J.A., 1986), (Batyuk L.V., et al. 2017). Let's proceed from the assumption that the formation of the first and second tumor is an independent random event. Let *t* are be a random variable that is the time of the formation of one tumor, and $F_1(t)$ is the distribution function of this time. The formation of a second tumor for some time is a random event. The probability of formation at the time t of two tumors is a function of the distribution ($F_2(t)$) of the time of formation of these two tumors, and this function is defined by the expression: $F_2(t) = F_1^2(t)$. Expressions for the distribution functions of tumors are dependent on the number of genes that are initially (at birth) contained in the genotype of the individual. Therefore, these characteristics are amounts of this type: $F(t) = \sum_{k=1}^{m}(F_k(t)p_k)$ and $f(t) = \sum_{k=1}^{m}(f_k(t)p_k)$, where *m* is the maximum value of *k*, and p_k is the probability of find encountering an individual with an initial number of genes equal to *k*. The statistics of the time of the formation of the first and second tumors could use to evaluate the values of p_k. If there is sufficient data on the age of the individual at the time of the tumor formation, the above values can be estimated on the basis of such considerations. τ is a period of time equal to one year, *i* is the age (in years) in which the first tumor formed, *j* – the age (in years), in which the second tumor formed and the probability that one of the tumors will appear at age *j*, and the other at age *i* (p (*jτ* and *iτ*)). Let φ_k is a probability to find a human with an initial number of genes equal to *k*. The value (p (*jτ* and *iτ*)) is denoted as p *(i, j)*. Let p (i, j)/k is the probability of the formation in the individual of two tumors in the ages *i* and *j*, provided that in the genotype it originally was *k* number of genes. Then p (i,j) = $\sum_{k=1}^{m}(\varphi_k \cdot p(i,j)/k)$. If the values of p(i, j)/k are calculated and the values of p*(i j)* are determined from the statistical data, then a redefined system of equations is formed, from which it is possible to determine the value of the quantities φ_k.

1. Aaronson S.A. et al. Science Wash. 1991, 254:11460-1153.
2. Adam J.A. Math. Biosci.1986, 81:229-244.
3. Batyuk L.V. et.al. Medical Review. 2017: 4: 46-47.