

**Li, Bang-he.** Describing DNA sequences by 2-dimensional walks. *Acta Analysis Functionalis Applicata*, 6(1), 1-4, 2004.

**Abstract:** In the literature, DNA sequences were described as 1-dimensional walks and 3-dimensional walks. In the former case, one walk corresponds to many DNA sequences; and in the latter case, the walks and the DNA sequences are in one-to-one correspondence. We find that in the 3-dimensional walks  $(x_n, y_n, z_n)$ , the 2-dimensional walks given by any ordered two of  $x_n, y_n$  and  $z_n$ , are already in one-to-one correspondence with the DNA sequences, and the remained 1-dimensional walks are determined completely by the 2-dimensional walks. Therefore, it seems that, 2-dimensional walks are the most suitable model for describing DNA sequences. There are  $4!=24$  orderings of the four bases A, C, G and T. Any such ordering gives a description of DNA sequences by 2-dimensional walks. Two walks  $(x'_n, y'_n)$  and  $(x''_n, y''_n)$  are regarded to be equivalent if  $(x'_n, y'_n) = (\varepsilon x''_n, \delta y''_n)$  or  $(\varepsilon y''_n, \delta x''_n)$ , where  $\varepsilon = \pm 1$ , and  $\delta = \pm 1$ . Then the 24 types of walks are divided into 3 equivalence classes with representatives  $(x_n, y_n)$ ,  $(y_n, z_n)$  and  $(x_n, z_n)$  respectively, where  $(x_n, y_n, z_n)$  are exact the 3-dimensional walks of Zhang and Zhang.

**Keywords:** DNA sequence; 2-dimensional walk