2. *The First Eigenvalues of an Operator Related to Selection in Population Genetics*

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1. Introduction. Among the diffusion approximations of 2-allelic gene frequency models in population genetics, one of the simplest is described by the Kolmogorov equation

$$\frac{\partial u}{\partial t}=\frac{x(1-x)}{4N}\frac{\partial^2 u}{\partial x^2}+sx(1-x)\frac{\partial u}{\partial x}. \tag{1}$$

Here we are taking account only of the selection force. x is the space variable running over the interval $0\leq x\leq 1$. x and $1-x$ denote genetically the gene frequencies of 2 allels, say A and A' respectively. t is, genetically the generation, time variable running over the positive real line. $2N$ and s are independent of (t,x). $2N$ (population size) is a large positive integer, and s is a real number ($|s|$ is small). $1+s$ and 1 are relative fitnesses of A and A' respectively. Hence, A is advantageous to A' if $s\geq 0$, and contrarily if $s\leq 0$.

The stochastic process $x(t,\omega)$ starting from $0<x(0,\omega)<1$ reaches almost surely in a finite time to one of the boundary points $x=0$ or $x=1$. If we consider the eigenvalue problem

$$\begin{cases}\dfrac{x(1-x)}{4N}\dfrac{d^2u}{dx^2}+sx(1-x)\dfrac{du}{dx}+\mu u=0, & \text{in } 0<x<1,\\ u(0)=u(1)=0,\end{cases} \tag{2}$$

the first eigenvalue μ_1 is the rate of the absorption to the boundary (see [2] and [3]).

Hence it is of interest to know the magnitude of μ_1 as a function of $2N$ and s. If we change the parameters $(2N,s)$ by

$$4Ns=\sigma \quad\text{and}\quad 4N\mu=\lambda, \tag{3}$$

(2) becomes an equation for spheroidal wave functions ([1])

$$x(1-x)\frac{d^2u}{dx^2}+\sigma x(1-x)\frac{du}{dx}+\lambda u=0, \qquad \text{in } 0<x<1, \tag{4}$$

$$u(0)=u(1)=0. \tag{5}$$

In this note, we will estimate $\mu_1=\mu_1(2N,s)=\lambda_1(4Ns)/(4N)$ as $4Ns$ is large. But the method being the same, we will treat the first $2m$ eigenvalues $\{\lambda_p(\sigma)\}_{p=1}^{2m}$ of (4)–(5), supposing that σ is large (m is arbitrary but fixed). The result will be stated in § 3.

2. Gene frequency model. The original model corresponding