Variables

x population size, later vector of population sizes of different types

x' population sizes at next timestep

t time

x_t population sizes at time t

x_i population size for type i

w growth rate of population per timestep

W matrix of growth rates. Here W is usually diagonal, and $W_{i,i}$ is the growth rate of type i

s fitness. $w = (1 + s)$. s is simply a more convenient way to represent fitness when it is close to 1

μ mutation rate. Rate of switching away from a type per timestep

M mutation matrix. Entry $M_{i,j}$ row i column j is the rate of switching from j to i per timestep

D diagonal matrix

V   Matrix of eigenvectors of $W \times M$. We just find V and D so that $W \times M = V \times D \times V^{-1}$

Eigen example with long genome

L length of genome. Could also be length of a part of the genome that we are considering.

i index for type with i mutations vs. the optimal type.

ν mutation rate per site. Chance of a single site to change in a single timestep. Assuming independence, global rate would be $1 - (1 - \nu)^L$, but I assume it is simply νL.

$p_{i \to i+1}$ Chance to mutate from i mutations to $i+1$, to add one additional mutation

$p_{i \to i-1}$ Chance to mutate from i mutations to $i-1$, to correct one mutation

M mutation matrix. $M_{i,i+1} = p_{i \to i+1}$, $M_{i,i-1} = p_{i \to i-1}$

W fitness matrix for genome. I assume that only the optimal type has fitness>1, so $W_{1,1} = (1+s)$