



Analyzing observed or hidden heterogeneity on survival and mortality in an isogenic *C. elegans* cohort

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It is generally difficult to understand the rates of human mortality from biological and biophysical standpoints because there are no cohorts or genetic homogeneity; in addition, information is limited regarding the various causes of death, such as the types of accidents and diseases. Despite such complexity, Gompertz's rule is useful in humans. Thus, to characterize the rates of mortality from a demographic viewpoint, it would be interesting to research a single disease in one of the simplest organisms, the nematode *C. elegans*, which dies naturally under identically controlled circumstances without predators. Here, we report an example of the fact that heterogeneity on survival and mortality is observed through a single disease in a cohort of 100% genetically identical (isogenic) nematodes. Under the observed heterogeneity, we show that the diffusion theory, as a biophysical model, can precisely analyze the heterogeneity and conveniently estimate the degree of penetrance of a lifespan gene from the biodemographic data. In addition, we indicate that heterogeneity models are effective for the present heterogeneous data.

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