

MODEL-BASED DESIGN AND ANALYSIS OF LIFE TABLE EXPERIMENTS FOR INSECT VECTORS OF DISEASE

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Life tables can help identify physiological differences in distinct development stages and detect potential vulnerabilities for conservation or control. However, cataloguing mortality, development, and fecundity by following each individual could be challenging due to interweaving generations and development stages in insects. Therefore, the information needed for life tables depend heavily on carefully designed experiments concentrating on a single development stage at a time.

Here, we propose the use of age- and stage- structured population dynamics modelling to aid in the design and analysis of life table experiments [1]. We use a hypothetical case, a simulated population with known life parameters, to demonstrate that model-based inference can correctly identify life parameters from the longitudinal observations of laboratory-reared insect populations. The analysis reveals not only the differential physiological behaviour of each development stage, but also identifies the degree to which each parameter can be inferred from the data. We validate this method against the traditional approach by inferring correctly the life table of a well-studied disease vector, *Culex quinquefasciatus*, from the unprocessed experimental observation of its population dynamics [2].

In this study, we present a novel model-based approach to identify life table parameters from incomplete longitudinal observations. We demonstrate that the method is effective, robust, and easily adjustable to fit the specific requirements of different species and experimental setups.

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References

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