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Computational approaches to parameter estimation and model selection in immunology.

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Summary: One of the significant challenges in biomathematics (and other areas of science) is to formulate meaningful mathematical models. Our problem is to decide on a parametrized model which is, in some sense, most likely to represent the information in a set of observed data. We illustrate the computational implementation of an information-theoretic approach (associated with a maximum likelihood treatment) to modelling in immunology.

The approach is illustrated by modelling lymphocytic choriomeningitis virus (LCMV) infection using a family of models based on systems of ordinary differential and delay differential equations. The models (which use parameters that have a scientific interpretation) are chosen to fit data arising from experimental studies of virus-cytotoxic T lymphocyte kinetics; the parametrized models that result are arranged in a hierarchy by the computation of Akaike indices. The practical illustration is used to convey more general insight. Because the mathematical equations that comprise the models are solved numerically, the accuracy in the computation has a bearing on the outcome, and we address this and other practical details in our discussion.

MSC:

[92C50](#) Medical applications (general)

[62P10](#) Applications of statistics to biology and medical sciences; meta analysis

[65C20](#) Probabilistic models, generic numerical methods in probability and statistics

[92C30](#) Physiology (general)

Cited in **9** Documents

Keywords:

[computational modelling](#); [Parameter estimation](#); [Numerical accuracy](#); [Maximum likelihood](#); [Parsimony](#); [Immune response](#); [Experimental LCMV infection](#); [ordinary differential equations](#)

Software:

[LANCELOT](#); [nag](#); [NAG](#)

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