A SEMI-MARKOV MODEL FOR THE NATURAL HISTORY OF HUMAN PAPILLOMAVIRUS INFECTION

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We consider the application of a discrete-time semi-Markov model to the natural history of infection with human papillomavirus (HPV), a sexually transmitted infection that is now considered to be a necessary cause of cervical cancer. The model is applied to a screening trial in which data on 38 genetically distinct HPV types were collected on 5060 women every 6 months for 2 years. The model considers prevalent infection, persistence, and incidence as parts of a single process, and each HPV type as a distinct infection nested within women. The probability of persistence is allowed to vary with duration of infection in order to reflect the clinically important distinction between transient and persistent infections. Working in a hierarchical Bayesian framework, we are able to easily extend the model to include individual frailties, and also test for possible biological interaction between different HPV types. Lack of interaction suggests that different HPV types are independent and do not compete for the same ecological niche. This work illustrates the ways in which realistically complex models can address important substantive questions in epidemiology.