Quantifying heterogeneity in acquisition of infectious diseases using frailty models

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December 2, 2015, 16:00 Uhr s.t.
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Frailty models are often used in survival analysis to model multivariate timeto-event data. In infectious disease epidemiology, frailty models have been proposed to model heterogeneity in the acquisition of infection and to accommodate for association in the occurrence of multiple infections. More traditional frailty models in infectious disease epidemiology rely on the assumption of lifelong immunity after recovery (Farrington et al. (2001)). In Abrams and Hens (2014) refinements have been made to account for reinfections with the same pathogen. Farrington et al. (2012) and Unkel et al. (2014) introduced and applied time-varying shared frailty models to paired bivariate serological data. Abrams, Wienke and Hens (submitted) extended the proposed frailty methodology to account for age-dependency in individual heterogeneity through the use of age-dependent shared and correlated gamma frailty models extending also previous work by Hens et al. (2009). More recently, overdispersed frailty models have been investigated (Abrams et al., in prep).
In this talk an overview of these developments will be given. The methodology will be illustrated using bivariate current status data on parvovirus B19 and varicella zoster virus, and Hepatitis A and B.