Population models for sexually transmitted diseases are typically based on an infection transmission model that is better suited for the flu by including only the risk that a susceptible partner can be infected as the probability per sexual act with an inherent partnership length of zero. We overcome this weakness by developing a model that can account for the possibilities of an infection from either a casual sexual partner or a longtime partner who was uninfected at the start of the partnership. The model allows for multiple longterm partnerships, which adds the advantage that network models have, the means to include serially monogamous and concurrent relationships, within the traditional strengths of a population model for computational speed and understanding of how each parameter affects the disease spread in an analytic reproduction number. We develop a model with longterm partnerships using a SIR model with differential infectivity and present a new treatment for contact numbers, the average number of sexual partners per year, in disease transmission rates which will result in a more realistic number of lifetime partners. Results include models for homogeneous and heterogeneous groups, along with reproduction numbers, and numerical simulations using HIV and HSV-2 data. (Received August 13, 2018)