Over the years, population models of sexually transmitted infections have included several approaches to modeling concurrency, i.e. overlapping sexual partnerships, and its effect of disease spread. In 2017, Kretzschmar and Heijne published a primer on pair formation models that considered monogamous pairs of different durations. They acknowledged that the difficulties of pair formation models are the inability to capture concurrency except through brief casual sexual partnerships and the rapidly increasing number of differential equations needed when adding heterogeneity to the population. In this talk we compare results from non-exclusive pair formation models to results from a non-pair model that instead incorporates the added infection from non-monogamous longterm partners to the rate of infection. Our model allows for multiple longterm partnerships, which adds the advantage of network models, 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. The model can be further diversified by including populations divided by sexual behavior, age, and/or race/ethnicity. (Received September 23, 2018)