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<u>Entitled</u> MATHEMATICAL MODELING OF AN EPIDEMIC IN SCALE-FREE NETWORK WITH IMPERFECT VACCINATION

> <u>by</u> Heba Hameed <u>Faculty Advisor</u> Abdessamad Tridane, Department of Science College of Mathematics <u>Date & Venue</u> 1:00pm Thursday, 13 of June 2024 Room 234, Building-F3

## <u>Abstract</u>

In light of the recent COVID-19 pandemic, the mathematical epidemiological model has proven to be essential for understanding the disease dynamic and finding the best control tool to help contain the disease and minimize its impact. This thesis investigates the dynamics of an infectious disease spread with latent infection and vaccination. The aim is to study this model's dynamic in a network that reflects the heterogeneity of the environment where the disease spreads. The vaccination is assumed to be not perfect, which means that vaccinated persons are likely to be infected and that the vaccinated person could lose their immunity, i.e., the waning rate of the vaccination. Using an extended version of the SEIR model with an additional vaccination compartment model, we first studied the single patch model, and we showed the basic properties in terms of the existence of a solution and its feasibility, as well as the basic reproduction number and stability results. The study was extended to scale-free networks to model the non-uniform connectivity of real-world populations, reflecting the varied susceptibility and contact rates among different groups. The findings highlight the critical thresholds for disease control and emphasize the complex interplay between network topology and disease dynamics. This study advances our understanding of epidemic control and underscores the importance of considering network structures in public health strategies.

**Keywords:** COVID-19 pandemic, Mathematical epidemiological model, Disease dynamics, Infectious disease spread, Latent infection, Vaccination, Heterogeneity, SEIR model, Vaccination compartment, Single patch model, Basic reproduction number, Stability results, Scale-free networks, Non-uniform connectivity, Real-world populations, Susceptibility, Contact rates, Disease control, Network topology, Public health strategies.