The SI model is described by 2 differential equations:

$$\frac{dS}{dt}=\frac{-\beta SI}{N} \quad \text{and} \quad \frac{dI}{dt}=\frac{\beta SI}{N}$$

That implies in another 2 equations:

$$\frac{dS}{dt}+\frac{dI}{dt}=0 \quad \text{and} \quad N=S(t)+I(t)$$

And, using N equation and differential equations, we discover S(t) and I(t):

$$I(t)=\int \frac{dI}{dt}dt=\frac{\beta SI}{N}t+n \qquad S(t)=N-I(t)=N-(\frac{\beta SI}{N}t+n)=N-n-\frac{\beta SI}{N}$$

Where n means, in this case, the initial population infected by the pathogen.

We could specify the differential equations by each group based on β_1 and β_2 transmission rates. As the pathogen can be transmitted only from a node of one type to a node of the other type, we could infer that the pathogen is transmitted for each type after 2 rounds of rates β_1 and β_2, implying $\beta \simeq \beta_1 \beta_2$ for both types M and F:

$$\frac{dS_M}{dt}=\frac{-\beta_1\beta_2 S_M I_M}{N_M} \quad \text{and} \quad \frac{dI_M}{dt}=\frac{\beta_1\beta_2 S_M I_M}{N_M} \quad \text{for M;}$$
$$\frac{dS_F}{dt}=\frac{-\beta_1\beta_2 S_F I_F}{N_F} \quad \text{and} \quad \frac{dI_F}{dt}=\frac{\beta_1\beta_2 S_F I_F}{N_F} \quad \text{for F.}$$

Since $f(t)=\frac{I_F(t)}{N_F}$ and $m(t)=\frac{I_M(t)}{N}$, your differential equations governing the growth over time are:

$$\frac{df}{dt}=\frac{1}{N_F}\times\frac{dI_F}{dt}=\frac{1}{N_F}\times\frac{\beta_1\beta_2 S_F I_F}{N_F}=\frac{\beta_1\beta_2 S_F I_F}{{N_F}^2}$$

$$\frac{dm}{dt}=\frac{1}{N}\times\frac{dI_M}{dt}=\frac{1}{N}\times\frac{\beta_1\beta_2 S_M I_M}{N_M}=\frac{\beta_1\beta_2 S_M I_M}{N\times N_M}$$