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Modeling vector-borne interactions have often been based on well-mixed models that make it difficult to address effectively the role of host mobility on vector borne disease dynamics. Here, we consider a Lagrangian framework where hosts' dispersal is modeled via the proportion of time that individuals, residents, spend in different environments. We consider a general *SIS* framework to account for the host dynamics and an *SI* framework to account for the vector dynamics. The transmission terms take a modified frequency-dependent incidence that accounts for the effective density of infected hosts within each patch at any time generated by the residence time matrix $\mathbb{P} = (p_{ij})_{\substack{1 \leq i \leq n, \\ 1 \leq j \leq m}}$, where the p_{ij} denotes the proportion of time the host of group i spends in environment j . We compute the basic reproduction number $\mathcal{R}_0^2(\mathbb{P}, m, n)$ for the general host-vector mode. We derive conditions under which either the disease free equilibrium or a unique endemic equilibrium is globally asymptotically stable (GAS). The approach include both when hosts' structure is the same as vectors's structure. (Received September 22, 2015)