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The risk matrix of vector-borne diseases in metapopulation networks and its relation with local and global R_0

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1 The risk matrix of vector-borne diseases in
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15 **Abstract**

The basic reproduction number R_0 is an index worldwide commonly used by public health organizations as a key estimator of the severity of a given epidemic. In this work we use a Lagrangian approach to model vector-borne diseases (SIR-SI) into a metapopulation network in order to derive an expression of the basic reproduction number and we analyze its dependency on human mobility. We prove that this index can be computed by evaluating the spectral radius of the risk matrix W , whose entries W_{ij} are the number of secondary cases in patch j produced by the inclusion of a single infected human in patch i . Based on the risk matrix, we propose a risk index which locally describes the epidemic vulnerability, while R_0 give us an estimation of the global vulnerability. Further, we numerically analyze the effect of human mobility over the values of R_0 in a system composed of two and three patches, and for a network connected in a star topology configuration.

16 *Keywords:* Basic reproduction number, vector-borne disease, metapopulation
 17 networks, human mobility.

18 **1. Introduction**

19 Vector-borne diseases, particularly those transmitted by mosquitoes, are one
 20 of the most important concerns in public health, mainly due to its growing im-
 21 pact and fast spreading in endemic areas. In particular, Dengue (DEN), Zika
 22 (ZIKV) and Chikungunya (CHIKV) are the main three arboviruses that are
 23 transmitted to humans via the bite of two mosquito species (among the 3500

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