



# Library Indian Institute of Science Education and Research Mohali



**DSpace@IISERMohali (/jspui/)**  
**/ Publications of IISER Mohali (/jspui/handle/123456789/4)**  
**/ Research Articles (/jspui/handle/123456789/9)**

Please use this identifier to cite or link to this item: <http://hdl.handle.net/123456789/2738>


Title:	A Realistic Host-Vector Transmission Model for Describing Malaria Prevalence Pattern
Authors:	Mandal, S. (/jspui/browse?type=author&value=Mandal%2C+S.) Sinha, Somdatta (/jspui/browse?type=author&value=Sinha%2C+Somdatta) Sarkar, R.R. (/jspui/browse?type=author&value=Sarkar%2C+R.R.)
Keywords:	Malaria continues Disease Biology Policies
Issue Date:	2013
Publisher:	Springer Link
Citation:	Bulletin of Mathematical Biology, 75(12), pp. 2499-2528.
Abstract:	Malaria continues to be a major public health concern all over the world even after effective control policies have been employed, and considerable understanding of the disease biology have been attained, from both the experimental and modelling perspective. Interactions between different general and local processes, such as dependence on age and immunity of the human host, variations of temperature and rainfall in tropical and sub-tropical areas, and continued presence of asymptomatic infections, regulate the host-vector interactions, and are responsible for the continuing disease prevalence pattern. In this paper, a general mathematical model of malaria transmission is developed considering short and long-term age-dependent immunity of human host and its interaction with pathogen-infected mosquito vector. The model is studied analytically and numerically to understand the role of different parameters related to mosquitoes and humans. To validate the model with a disease prevalence pattern in a particular region, real epidemiological data from the north-eastern part of India was used, and the effect of seasonal variation in mosquito density was modelled based on local climatic data. The model developed based on general features of host-vector interactions, and modified simply incorporating local environmental factors with minimal changes, can successfully explain the disease transmission process in the region. This provides a general approach toward modelling malaria that can be adapted to control future outbreaks of malaria.
URI:	<a href="https://link.springer.com/article/10.1007/s11538-013-9905-7">https://link.springer.com/article/10.1007/s11538-013-9905-7</a> ( <a href="https://link.springer.com/article/10.1007/s11538-013-9905-7">https://link.springer.com/article/10.1007/s11538-013-9905-7</a> ) <a href="http://hdl.handle.net/123456789/2738">http://hdl.handle.net/123456789/2738</a> ( <a href="http://hdl.handle.net/123456789/2738">http://hdl.handle.net/123456789/2738</a> )
Appears in	Research Articles (/jspui/handle/123456789/9)
Collections:	

## Files in This Item:

File	Description	Size	Format
Need to add pdf.odt (/jspui/bitstream/123456789/2738/1/Need%20to%20add%20pdf.odt)		8.63 kB	OpenDocument Text

[View/Open \(/jspui/bitstream/123456789/2738/1/Need%20to%20add%20pdf.odt\)](#)

Show full item record (</jspui/handle/123456789/2738?mode=full>)

 (</jspui/handle/123456789/2738/statistics>)

Items in DSpace are protected by copyright, with all rights reserved, unless otherwise indicated.