Table A4: Bayesian binomial model with random noises fitted to the DCO data

Sources of variation	**Mean**	**SD**	**2.5%**	**50%**	**97.5%**
Prevalence of infection					
(Intercept)	1.076	0.076	0.925	1.076	1.226
ben_ppp	-0.286	0.136	-0.553	-0.287	-0.015
bio12_wc30s	0.333	0.522	-0.703	0.335	1.359
bio16_wc30s	-0.578	0.645	-1.848	-0.579	0.700
dst_coastlin	0.380	0.408	-0.429	0.381	1.183
dst_waterway	0.158	0.127	-0.093	0.158	0.410
landcover	-0.075	0.096	-0.265	-0.075	0.113
pet_wc30s	-0.275	0.271	-0.809	-0.275	0.260
srtm_slope	0.065	0.089	-0.110	0.065	0.239
Precision τ_v	5.682	1.835	2.888	5.415	10.020
Prevalence of cases					
(Intercept)	-0.671	0.101	-0.868	-0.671	-0.471
ben_ppp	-0.113	0.136	-0.383	-0.113	0.155
bio4_wc30s	0.257	0.163	-0.064	0.256	0.579
bio12_wc30s	0.441	0.278	-0.107	0.440	0.990
dst_waterway	0.300	0.198	-0.089	0.299	0.692
miaq_wc30s	-0.125	0.149	-0.419	-0.125	0.168
mimq_wc30s	-0.298	0.319	-0.929	-0.298	0.333
srtm_slope	-0.015	0.115	-0.242	-0.015	0.213
srtm_topo	0.195	0.198	-0.196	0.195	0.587
landcover	0.126	0.129	-0.129	0.126	0.380
Precision τ_v	2.841	0.804	1.538	2.749	4.671

Table A4 showed the estimates of the effects of malaria determinants in the DCO health district using Bayesian GLMM (generalized linear mixed models) without spatial component. In the presence of village-specific random effects, only the population density showed a significant effect on the malaria infection. No covariate has significant effect on the malaria clinical cases in the DCO region since the credibility interval of all estimates contain zero.