Malaria in Madagascar

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Supplementary Figure 2: Map of Madagascar showing the regions sampled and some climatic characteristics
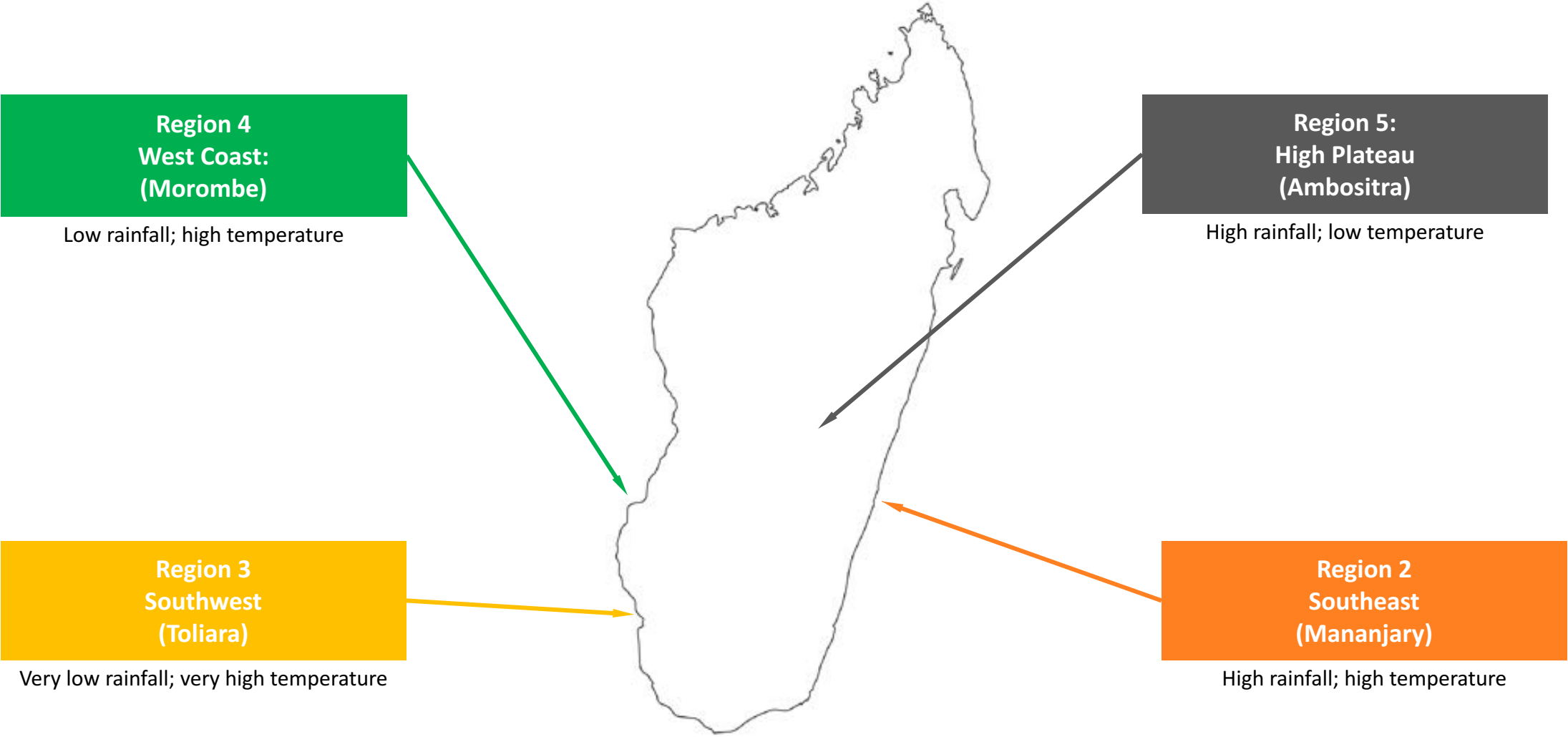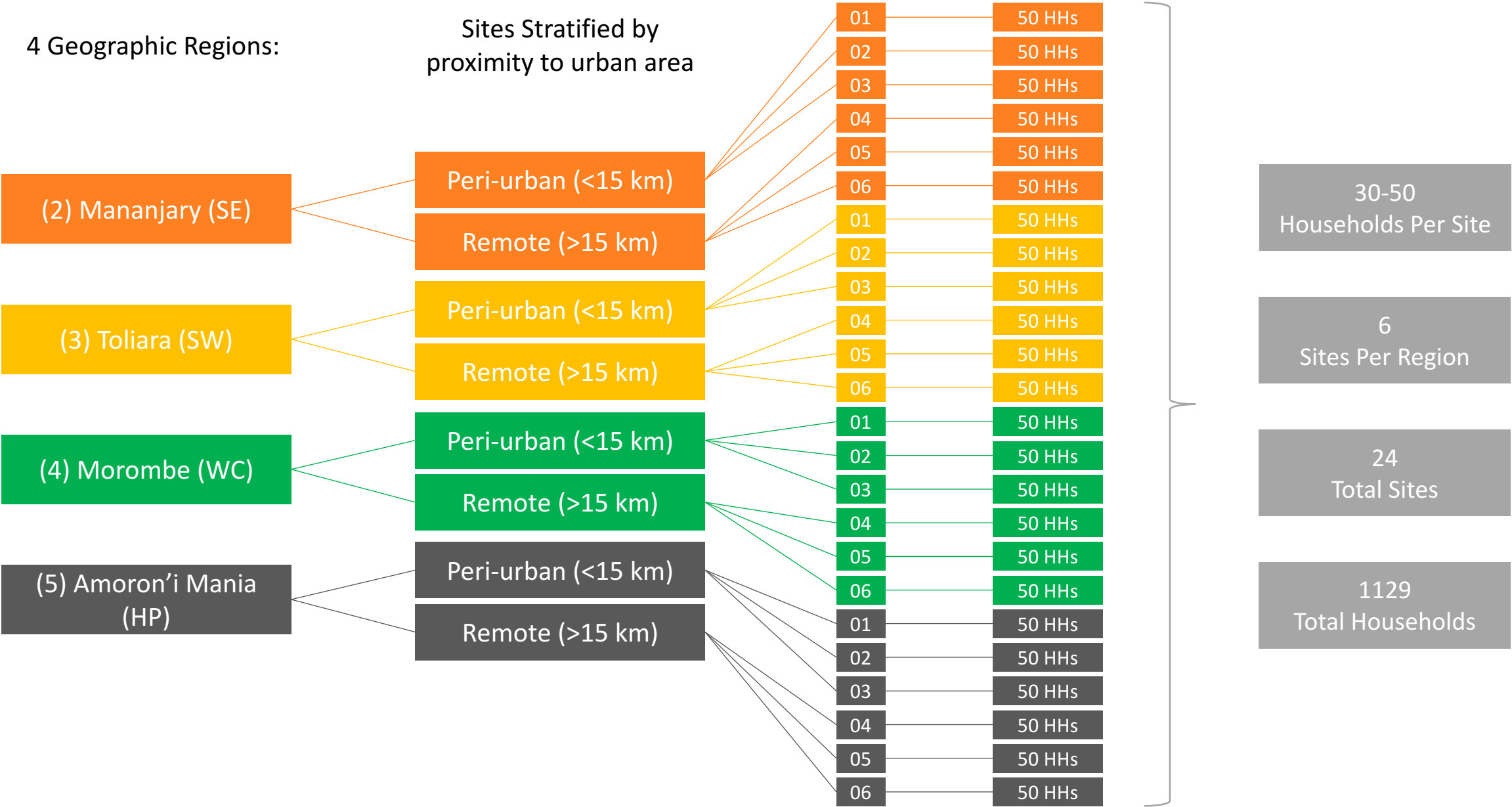

Region 4
West Coast:
(Morombe)

Low rainfall; high temperature

Region 5:
High Plateau
(Ambositra)

High rainfall; low temperature

Region 3
Southwest
(Toliara)

Very low rainfall; very high temperature

Region 2
Southeast
(Mananjary)

High rainfall; high temperature

Figure 1: Schematic of nested study design where individuals were sampled within households at 6 sites per region for 4 regions

4 Geographic Regions:

Sites Stratified by proximity to urban area

(2) Mananjary (SE)
- Peri-urban (<15 km)
- Remote (>15 km)

(3) Toliara (SW)
- Peri-urban (<15 km)
- Remote (>15 km)

(4) Morombe (WC)
- Peri-urban (<15 km)
- Remote (>15 km)

(5) Amoron'i Mania (HP)
- Peri-urban (<15 km)
- Remote (>15 km)

01 — 50 HHs
02 — 50 HHs
03 — 50 HHs
04 — 50 HHs
05 — 50 HHs
06 — 50 HHs

30-50 Households Per Site

6 Sites Per Region

24 Total Sites

1129 Total Households

Summary of data set analyzed

Regions	4
Sites	24
Households	1129
Individuals	6293
Mean household size (number of individuals)	5.57
Household size range	(2-19)
Individuals with valid malaria result	5544
Percent of individuals with a malaria result (%)	88.1
Number of malaria positive individuals	776
Malaria prevalence (overall) (%)	13.99
Mean age of individuals (years)	17.34

Southeast:
Vatovavy Fitovinany
(Mananjary)

R2V4

January-March 2017
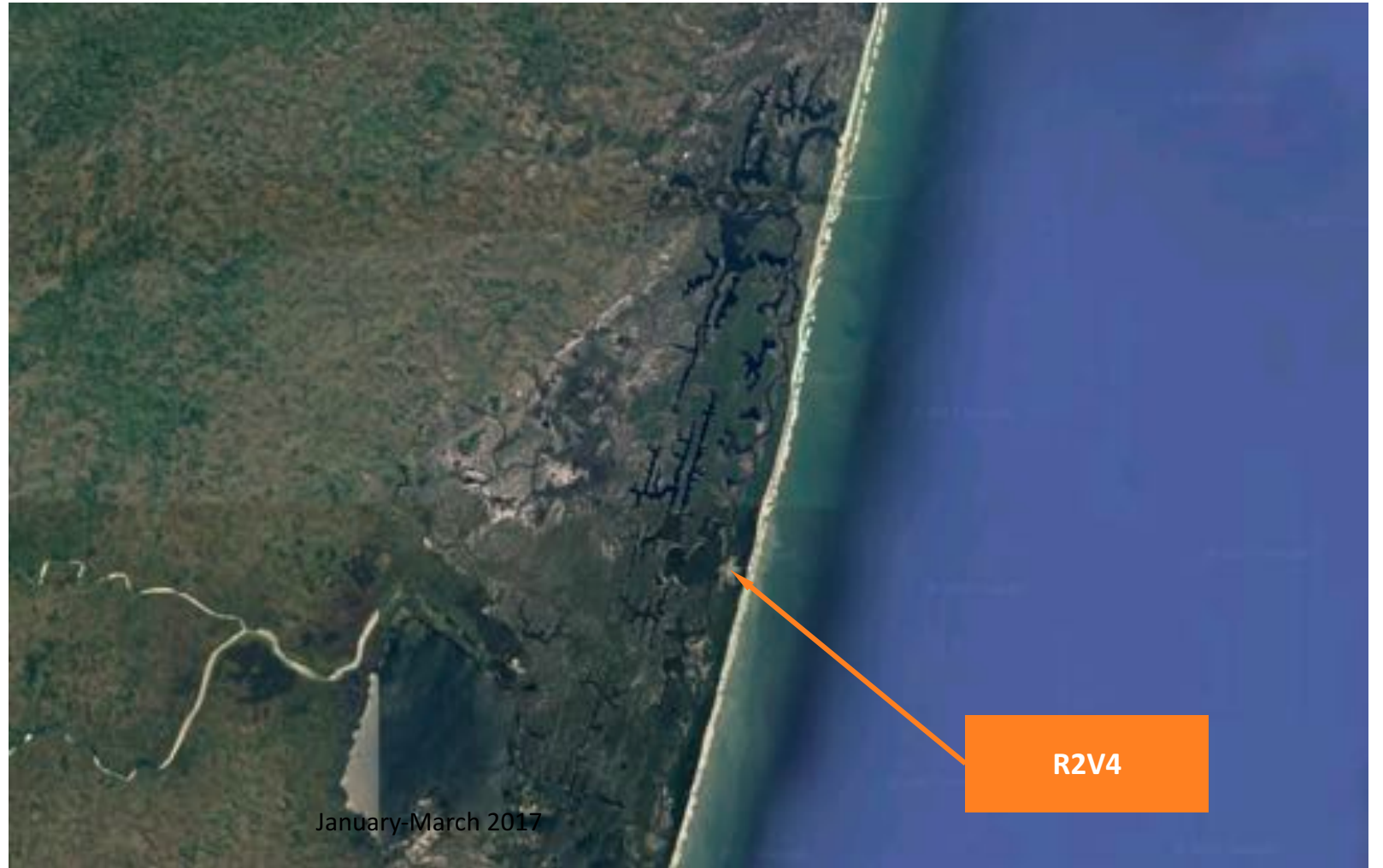
Spatial Clustering Example: Site R2V4

R2V4 RDT Outcomes	n (+)	Total	%
Malaria	44	276	15.94
Malaria | HH	44	144	30.55

Figure 3: Density plots of age for all individuals, those infected with malaria, and uninfected with malaria (n = 5533)
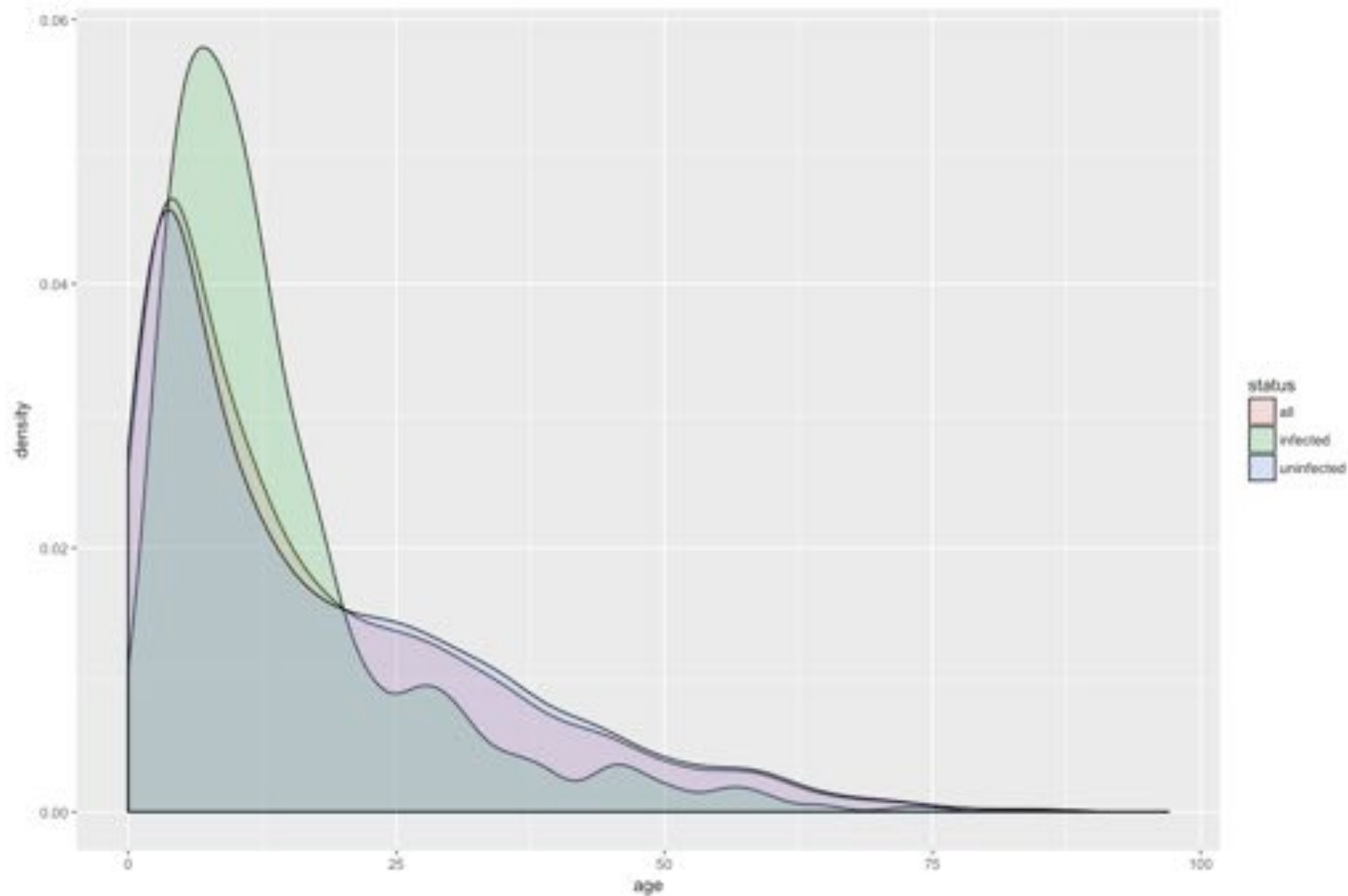
Figure 2: Variation in the percentage of individuals infected (prevalence) between sites within regions and between regions
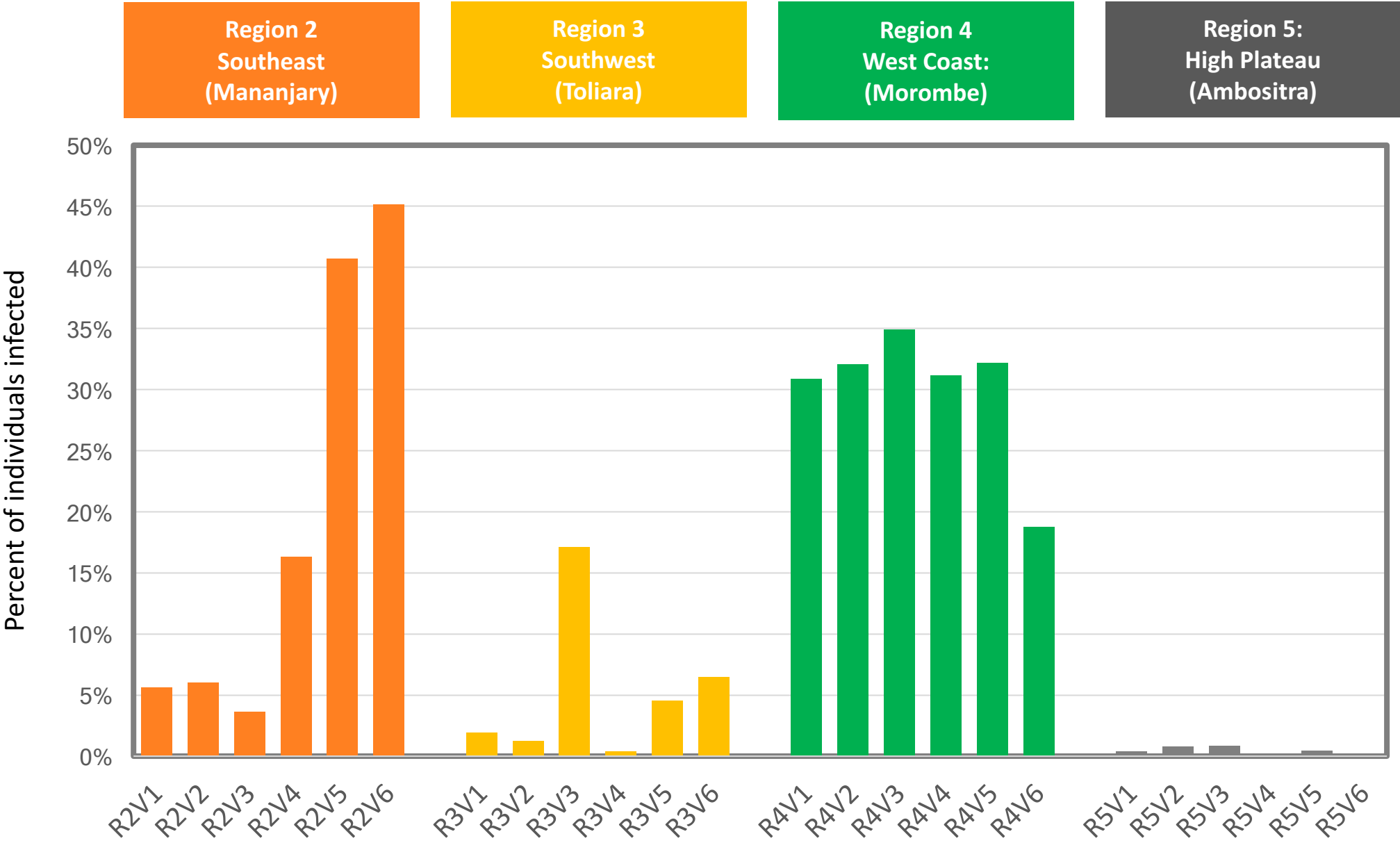
Table 2: Using a simple generalized linear model of four site-specific predictors of malaria prevalence to demonstrate the need for accounting for inter-regional differences

Table 2A: All regions combined ($n = 24$ sites)

Predictor	Coefficient	Confidence interval
Travel time by foot to nearest doctor (hours) (continuous)	-0.73	[-2.31, 0.85]
Road access (binary)	-10.64	[-23.15, 1.87]
Coastal versus inland (binary)	15.56	[2.25, 28.87]
Distance to nearest hospital (km) (integer)	0.31	[-0.099, 0.73]

Table 2B: Excluding Region 5 ($n = 18$ sites)

Predictor	Coefficient	Confidence interval
Travel time by foot to nearest doctor (hours) (continuous)	-0.93	[-3.0684, 1.2084]
Road access (binary)	-13.73	[-29.2334, 1.7734]
Coastal versus inland (binary)	11.72	[-5.506, 28.946]
Distance to nearest hospital (km) (integer)	0.28	[-0.215, 0.775]

Supplementary Table 2: Parameter values: Empirically derived, chosen simulation inputs or simulation outputs for the intercepts, coefficients, and residual standard deviations show

	Empirical estimate	Simulation (1X)* Inputs	Simulation (1X) Outputs (mean)	Simulation (2X)* Inputs	Simulation (2X) Outputs (mean)
Intercept	14.09	14	5.64	14	18.72
Travel time by foot to nearest doctor (hours)	-0.72	-0.70	-0.71	-1.50	-1.49
Distance to nearest hospital (km)	0.14	0.13	0.13	0.26	0.26
Residual sd	15.61	15	14.84	7.30	7.18

*In the "2X" simulation scenario the coefficients (i.e. slopes) were increased approximately by a factor of two and the residual sd was decreased by approximately a fact of two (intercept unchanged). For both simulation scenarios, the proportion of repetitions in which the simulation returned parameter estimates with confidence intervals that covered the inputted parameter values were recorded. For both coefficients in both simulation scenarios, the proportions were above 0.93.

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Table 3: Mean household size as a site predictor – not enough sites to have sufficient statistical power		
Model: $Pr(infection) = \alpha + \beta^*(mean\ household\ size) + error$		
Model parameter estimates	All regions included*	Region 5 excluded*
α	38.089 [1.20, 74.97]	7.44 [-76.01, 90.89]
β	-4.301 [-10.749, 2.14]	2.04 [-13.58, 17.66]
Residual sd	15.03	15.65

*95% confidence intervals shown in brackets next to parameter estimates

Figure 2: Variation in the percentage of individuals infected (prevalence) between sites within regions and between regions

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