

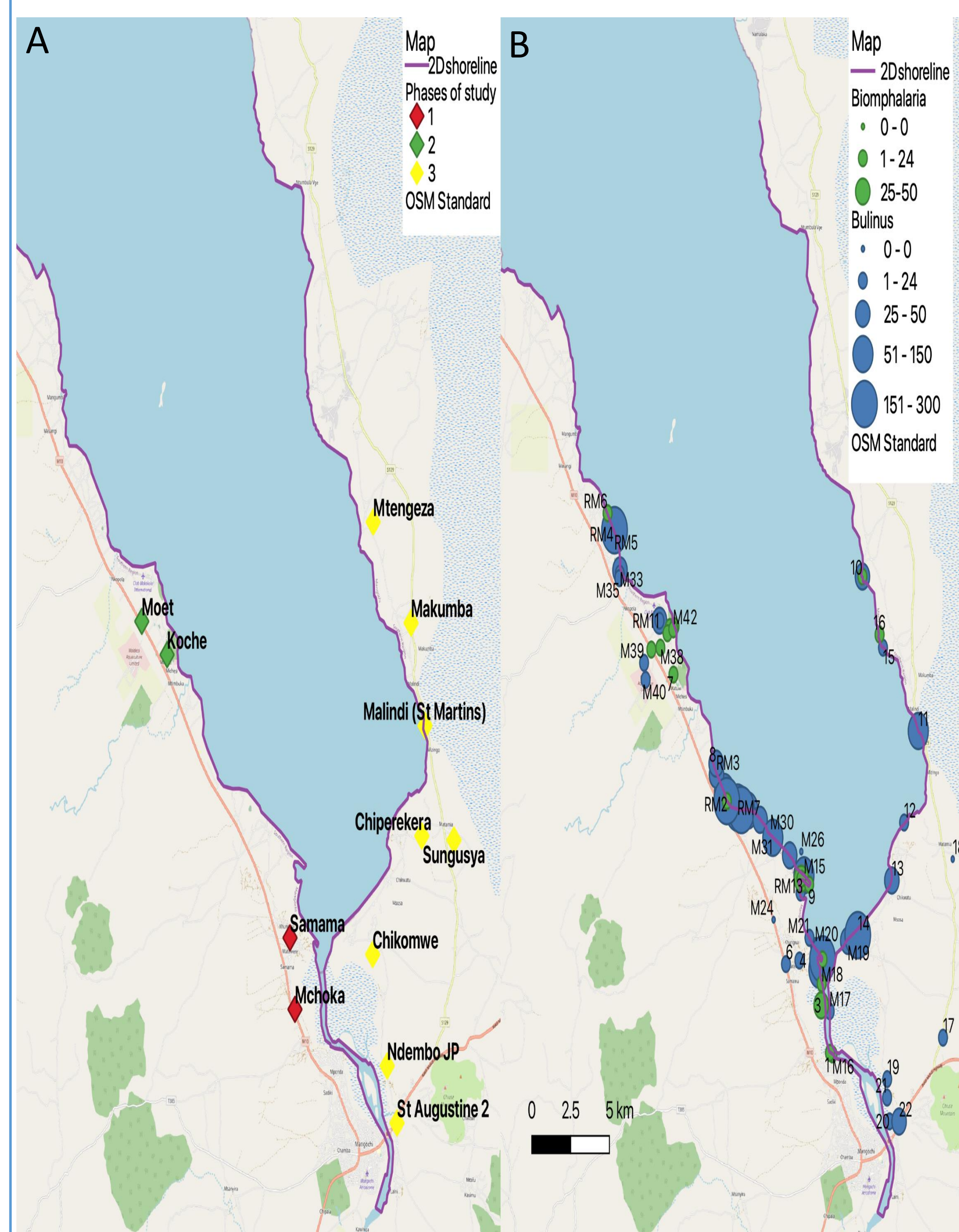
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Background

Schistosomiasis transmission is a water-borne disease and can only occur in the presence of the intermediate host snail. Recently *Biomphalaria spp.* of snail have been discovered along the southern shoreline of Lake Malawi, Mangochi district, cohabiting with *Bulinus spp.* These snail species are intermediate hosts for *Schistosoma mansoni* and *S. haematobium* which cause intestinal (IS) and urogenital schistosomiasis (UGS), respectively.

Aim

In this poster, a secondary analysis is carried out on malacological survey data collected along the shoreline. We aim to create a map of snail abundance (SNA) along the shoreline based on the sampled collected data, and a set of covariate data measured along the shoreline which allows us to identify spatial heterogeneities in where school-aged-children (SAC) are most likely exposed to *Schistosoma*.



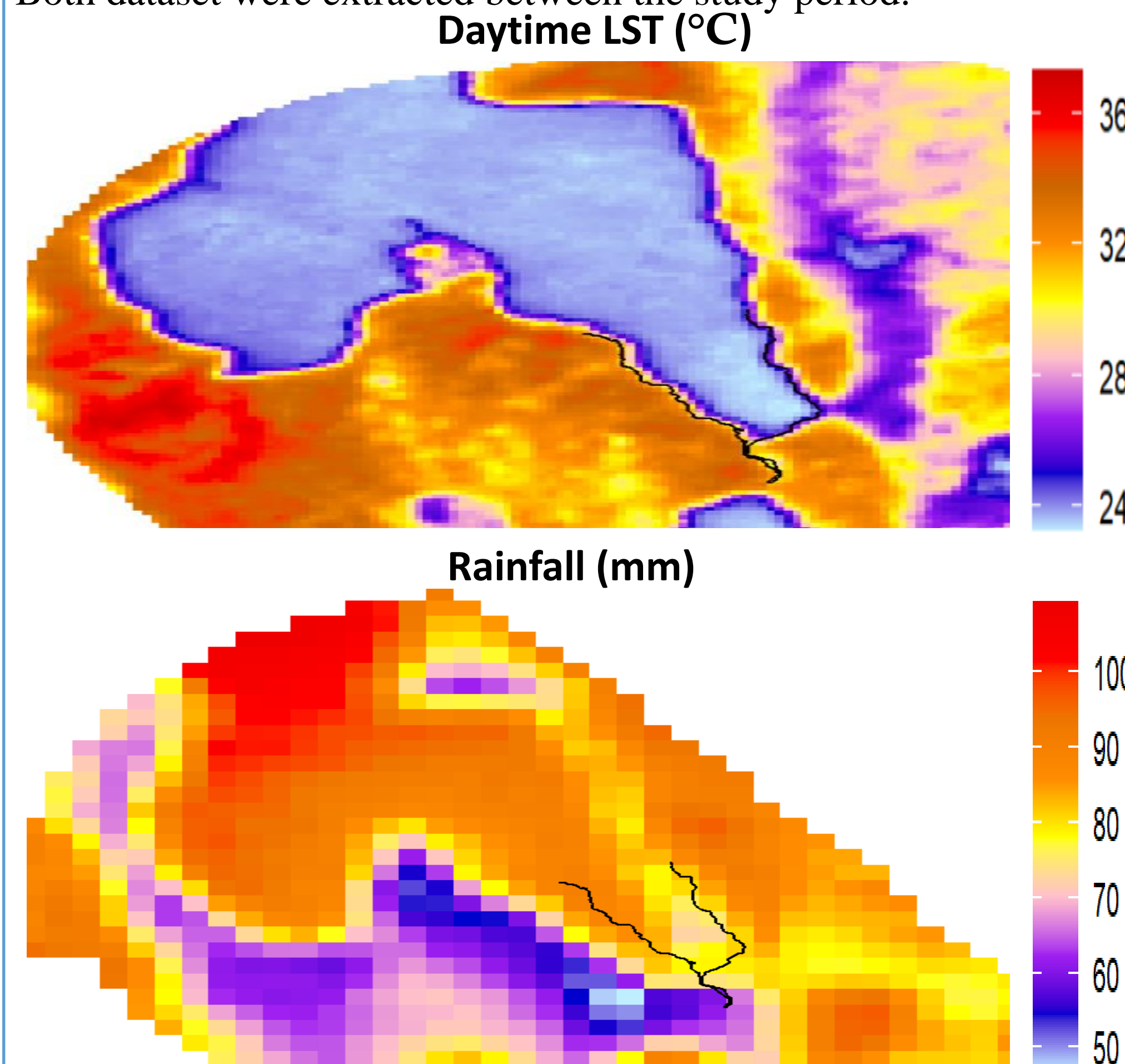
Map of southern part of Lake Malawi. A) School locations sampled in years 2017-2019. B) Number of snails spp. Observed. Green dots: *Biomphalaria* Blue dots: *Bulinus*

Snail survey data

Malacological surveys were carried out during i) Nov 2017 – pilot surveillance data identified *Biomphalaria* and *Bulinus spp.* along the shoreline, ii) May/June 2018 and iii) 2019 where repeated locations and new sites were selected based on there surrounding environment suitable for breeding sites to confirm the emergence and outbreak of IS. The number of snails was counted for each snail spp. and covariate data only at sampled locations of snails.

Extracted covariate data

Daytime Land Surface Temperature (LST), was from Land Processes Distribution Active Archive Center. Rainfall was extracted from TAMSAT version 3.1 Monthly at 4km resolution. Both dataset were extracted between the study period.



Model Formulation

We used a Bayesian log-linear Gaussian Process (GP) model to smooth observations of SNA along the shoreline. Our study observed the number of snails y_i at sampling locations x_i expressed as distance along the shoreline relative to an arbitrary reference point. In addition, we have two covariates, Daytime LST and rainfall, which we express as the design matrix Z . We then model y_i as

$$y_i \sim \text{Poisson}(\mu_i),$$

with

$$\log(\mu_i) = \alpha + Z^T \beta(x_i) + s_i.$$

s is modelled using a 1-dimensional GP with exponential correlation function with variance σ , length scale $\phi = 1$ an additional uncorrelated variance term τ . Priors were placed on our unknown model parameters,

$$\begin{aligned} \alpha &\sim \text{Normal}(0,10), \\ \beta &\sim \text{Normal}(0,10), \\ \sigma &\sim \text{Gamma}(1,1), \\ \tau &\sim \text{Gamma}(0.1,0.1) \end{aligned}$$

The STAN probabilistic programming language was used to fit the model, allowing us to project the GP onto a fine grid of points, along the shoreline to create predictions of SNA at arbitrary points in our study region. Mean number of snails were attained by finding the mean of the Poisson distribution variables,

$$\log(\hat{u}_i) = \hat{\alpha} + Z^T(x_i^*)\hat{\beta} + \hat{s}(x_i^*),$$

where \hat{u}_i is our GP prediction of the number of snails present, x_i^* is the covariate values for each prediction point, where $i=1, \dots, N$.

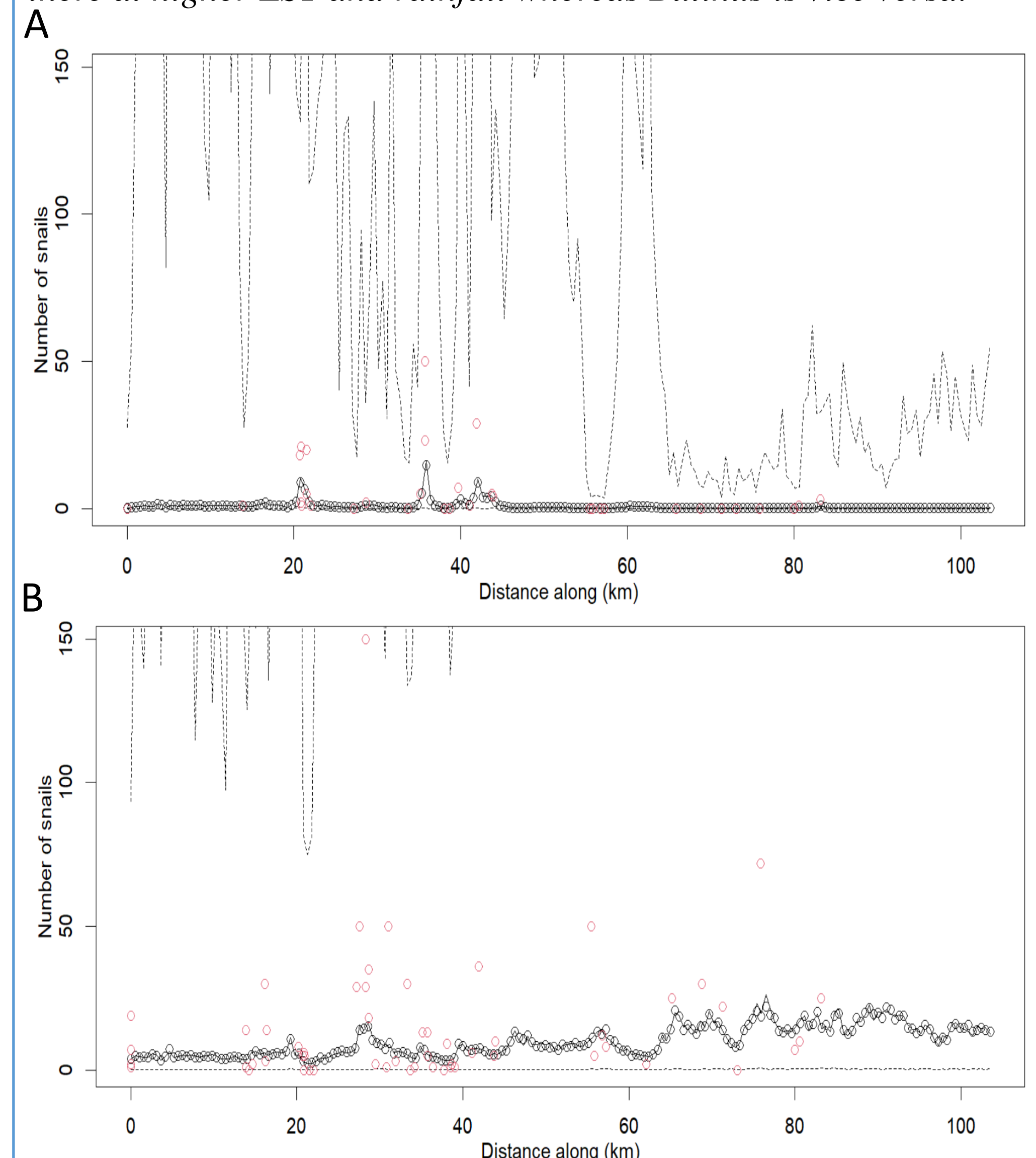
Method

1. Create high-resolution linestring along Lake Malawi shoreline.
2. Map each snail prediction location to its nearest vertex on the linestring.
3. Calculate distance from the end of the line of each mapped snail prediction location (1D distance).
4. Run Bayesian model using the predicted locations and observed data.
5. Project fitted GP onto all other vertices in the linestring to create prediction.
6. Calculate the mean, 95% confidence interval (CI) and standard deviation (SD)
7. Plot the exponential mean, CI and SD on the 2D prediction points – matching up the 1D to 2D.

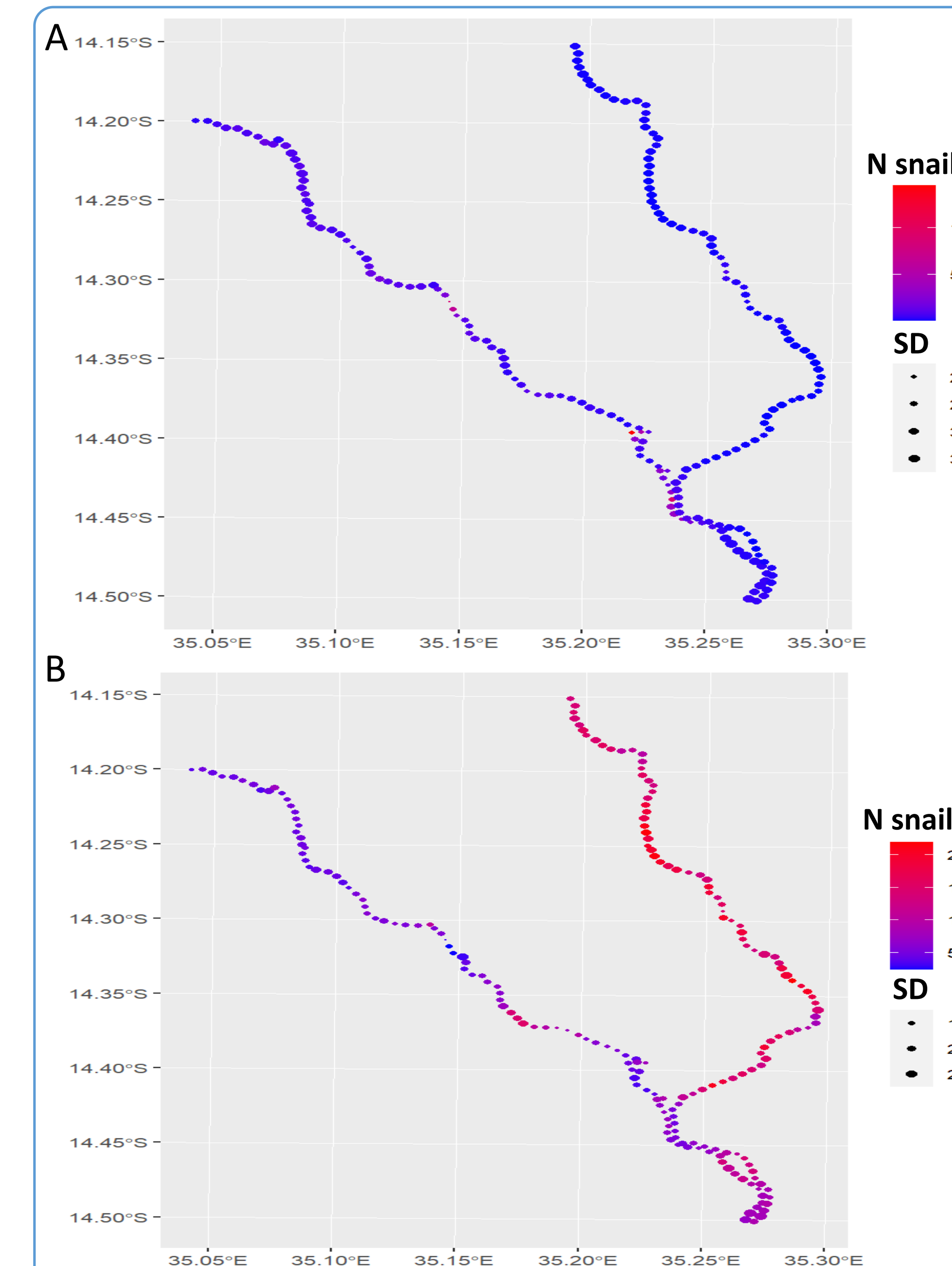
Results

Parameter	<i>Biomphalaria</i>			<i>Bulinus</i>		
	mean	SD	95% CI	mean	SD	95% CI
α	-0.96	0.83	[-2.76,0.37]	1.86	0.29	[1.31,2.40]
β_1 (LST)	0.05	0.11	[-0.17,0.27]	-0.03	0.05	[-0.13,0.05]
β_2 (Rainfall)	0.04	0.31	[-0.20,1.08]	-0.20	0.14	[-0.49,0.05]

No significant association of *Biomphalaria* snails increase where there at higher LST and rainfall whereas *Bulinus* is vice versa.



Distances from origin of shoreline A) *Biomphalaria* B) *Bulinus*



Number of snails, \hat{u}_i A) *Biomphalaria* B) *Bulinus* SD of GP prediction with size of dots.

Summary of Results

- Shoreline predicted to have higher number of *Biomphalaria spp.* present close by to Koche, Moet, Samama and Mchoka.
- Shoreline predicted *Bulinus spp.* was present along the entire shoreline (known to be true), however predicted there were higher number of *Bulinus spp.* snails on east side of the shoreline.
- There is no significant values and a varying degree of uncertainty in locations as shown from the SD result.
- Presence predicted near sampled locations, not necessarily the true abundance.

Conclusions

Our study shows **substantive heterogeneities** in snail distributions along the lake, providing essential information for developing a future **statistically-grounded dynamical infection model** to find the main determinants of infection within SAC.

Acknowledgements

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