Prediction of mosquito vector abundance for three species in the *Anopheles gambiae* complex

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Abstract

Background: The dynamics of vector borne disease transmission depend on the abundances of vectors. The dominant malaria vector species complex of *Anopheles gambiae* sensu lato is a target of vector control strategies designed to reduce and eliminate malaria transmission. The three most widely distributed dominant malaria vectors within the species complex are *An. arabiensis*, *An. coluzzii* and *An. gambiae* sensu stricto.

Methods: Previous studies across the extent of the species complex range have been restricted to annual predictions of species occurrence or relative abundance. This study incorporated relative abundance data at the species level and abundance data at the species complex level to estimate and predict daily carrying capacities of each species. Statistical models with interpretable parameters were used to gain insight into how factors such as meteorological conditions, insecticide treated net use, and human density affect the spatial and temporal predictions. The statistical models were used to predict daily equilibrium vector abundance that is an important factor in indices of malaria transmission such as the basic reproduction number and vectorial capacity.

Results: At the continental scale, precipitation and temperature were important predictors of these three malaria vector species in Africa. Insecticide treated net use was negatively associated with per capita vector abundance of the *An. gambiae* species complex and the ratio of *An. gambiae* s.s. to *An. arabiensis*. A predicted increasing interannual trend for *An. coluzzii* was possibly caused by changing species identification methods over the observational period.

Conclusion: The predicted equilibrium abundances of the three species showed potentially high levels of geographical overlap, niche overlap, and evidence for stable coexistence despite substantial interspecific competition. Improving collection of longitudinal species abundance data across the spatial range of the *An. gambiae* species complex will facilitate future explorations of causal hypotheses that relate vector abundance to control measures, malaria interventions and climate conditions.
Keywords: interspecific competition, generalised linear model, maturation delay, Leslie-Gower model, stability

Background

The reduction of mosquito vector abundance and the number of infectious bites on humans through vector control measures is an effective means to lower or eliminate human malaria [1–3]. Shifts in species abundances of mosquito vectors induce concomitant changes in behaviour and susceptibility to vector control that require adjustment of available intervention strategies such as insecticide treated nets, indoor residual spraying, larval source management, screening house, baited traps or novel techniques such as genetically modified vector suppression and replacement strategies [4–6]. The evaluation of conventional and potential novel vector control strategies on disease transmission dynamics thus benefits from prediction and estimation of vector abundances [7, 8]. Mathematical models of long term or equilibrium vector abundance, for example, have long served as useful guides for vector control and malaria interventions [9]. Equilibrium vector abundance is the theoretical population size that would be attained if birth rates matched death rates at a given location. Equilibrium abundance is a useful concept allowing for the possibility that the true or actual abundance of a species may diverge from carrying capacity because of local environmental or anthropogenic perturbations, dispersal, source-sink meta-population dynamics or through interspecific competition [10–12]. For example, vector populations fluctuate around the equilibrium in response to seasonal changes in birth and death rates, and a range of other factors.

Applications with a time-varying basic reproduction number ($\mathcal{R}_0$) that depends on the ratio of vector abundance to human hosts, and derived indices such as time-varying vectorial capacity, are examples of an equilibrium based analysis. $\mathcal{R}_0$ is defined at the disease free equilibrium composed of completely susceptible vector and human populations in the standard Ross-Macdonald model [1, 2, 13] and related mathematical models of malaria transmission by anophelines [14]. The canonical basic reproduction number $\mathcal{R}_0$ corresponds to the number of malaria infections that arise from a single infectious case introduced into a completely susceptible population at the disease free equilibrium [15]. Macdonald acknowledges that the changing vector abundance and transmission parameters that define $\mathcal{R}_0$ suggest that "... the degrees of equilibrium seen in nature should make a continuous series ..." (p. 34 in [2]). The equilibrium index $\mathcal{R}_0$, for example, can be modelled as a continuous function of temperature and precipitation mediated by the average vector population at a climatically determined equilibrium [16]. The influential Garki model [9, 17, 18] accounts for seasonal malaria transmission in Nigeria via an interpolated function of time-varying vector population size that determines the vector population's contribution to $\mathcal{R}_0$ through the vectorial

capacity [19]. Recent statistical analysis of the Garki data from the 1970s suggests that the equilibrium vector population size of *An. gambiae* s.l. defined by an environmentally driven carrying capacity approximately tracks weekly precipitation [20]. An analysis of seasonal malaria transmission in Burkina Faso suggests that average vector population size of *An. gambiae* is proportional to weekly precipitation [21].

Despite the important contribution of the vector abundance-to-human host ratio to the standard indices of malaria transmission risk such as the basic reproduction number $\mathcal{R}_0$ and vectorial capacity, mosquito vector abundance data are rarely collected in Africa [22]. The species complex *Anopheles gambiae* sensu lato (s.l.) is an important vector of malaria in Africa [23]. *An. gambiae* s.l. is estimated to have caused at least half of the 241 million malaria deaths of children under five years old in sub-Saharan Africa between 3000 BCE and 2000 CE [6]. The three primary malaria vector member or sibling species of the *An. gambiae* complex [6] that have the broadest geographical distribution [24] are *An. arabiensis*, *An. coluzzii* and *An. gambiae* sensu stricto (s.s.). However, longitudinal abundance data for species in the *An. gambiae* complex are rare. Species identification in field collections is often limited because the member species are not morphologically distinguishable, and so molecular identification from subsamples of field collections is required. Longitudinal count data for *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. are therefore uncommon, and most predictive studies at the continental scale rely only on species occurrence data [24–27].

Predictions of the probability of species occurrence from species distribution models link the distributions of species in the *An. gambiae* complex to environmental covariates such as annual indices of meteorological conditions and climate [24–26]. Alternatively, climatological covariates may be used to predict relative abundance or species composition [28] based on species occurrence data [27, 29]. Sinka et al. [27] suggest that the consideration of relative abundance may defray some of the difficulties associated with the estimation of 'true' abundance that is spatially and temporally variable, and use species occurrence data to predict that the relative abundance of *An. arabiensis* versus the aggregate of the two species *An. coluzzii* and *An. gambiae* s.s. increases with insecticide treated net intervention. Tene Fossog et al. [29] use relative species frequencies of *An. coluzzii* and *An. gambiae* s.s. to predict relative probabilities of occurrence in western Africa based on climatic and geographical covariates with species specific responses determined by elevation and distance from coastline. Pombi et al. [30] find high niche overlap among *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. in certain regions based on an index that is a function of relative abundance data [31]. Niche overlap is sometimes suggested as an index of the strength of interspecific competition [32], although this correlative index that is based on species relative abundances may diverge from underlying competitive relationships among species [31].

However, malaria transmission dynamics are driven by the abundance of mosquito species and not just relative abundance or the probability of species occurrence. This study therefore sought to estimate spatiotemporal abundance of *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. by collating data both on relative abundance at the species level (identified genotypically) and longitudinal population counts at the species complex level (identified morphologically) across the geographic range of *An. gambiae* s.l. The difficulty in acquiring such data should not be underestimated or understated. Regular vector surveillance is typically conducted to support operational activities, which in the African entomological context is overwhelmingly in support of malaria intervention through insecticide treated bed-

net (ITN) deployment or indoor residual spray (IRS) activity. Indeed, much of the regular surveillance is focused on determining local species present and their localised behaviours (e.g., measures of anthropophily, endophily, and biting time) to determine appropriate vector interventions [33]. Unlike some regions that employ weekly or daily surveillance to identify mosquito control action thresholds for vector suppression operations such as insecticidal fogging, the operational timescales for African ITN distributions or IRS operations are not based on the weekly or monthly status of mosquito species abundance. Hence, such data are less likely to be collected. This fact is highlighted in a recent global meta-analysis of mosquito control action thresholds [34], where none are listed from Africa. Longitudinal surveillance of *Anopheles* mosquito populations is performed in Africa, particularly for research purposes. However, most of the longitudinal studies investigated in this study either did not use genetic methods (e.g., polymerase chain reaction, PCR) to identify field collections to the species level or instead did not resolve changes in species diversity and relative abundance within a year, thus negating the ability to detect seasonal changes in species composition. Nonetheless, the species identified data collated by this study expand on previous efforts [24] by including finer scale temporal information on the sample collection time that thereby allows incorporation of seasonally varying environmental conditions into the analysis. Importantly, this data acquisition effort also currently represents the largest collation of publicly available longitudinal abundance data for the *An. gambiae* species complex. These data investigation and collation efforts both highlight and help bridge a significant gap in available data for African malaria mosquito biology.

Using these assembled data, the equilibrium abundances of *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. were predicted across sub-Saharan Africa from 2002 to 2020. The species equilibrium abundances are not directly observable and were inferred from empirical observations as responding to known spatial and spatiotemporal covariates. Statistical relationships were estimated for established environmental and geographical factors, such as precipitation, temperature and human population density [16, 20, 21, 35], to enable spatiotemporal predictions of *An. gambiae* s.l. abundance. Previous relative abundance analyses for pairs of species in *An. gambiae* s.l. [27–29] were extended to account for daily varying climatological predictors to allow seasonally varying predictions of relative abundance for *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. The analysis of relative abundance data available at the sibling species level was combined with the longitudinal abundance analysis at the species complex level to predict potential sibling species abundance across sub-Saharan Africa. The predicted equilibrium abundances of *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. were then connected to the equilibrium of an underlying dynamic model that suggests the potential for strong interspecific competition but also stable coexistence among the three vector species.

Methods

The study area is defined as the geographic range of *An. gambiae* s.l. [24, 36] in sub-Saharan Africa. The genotype data, abundance data, spatial covariates and spatiotemporal covariates are described below with further details provided in the supplementary R package **AgslPredict** for this paper [37]. The code for analyses and graphical results of relative

abundance predictions, abundance predictions and competition estimates are also available in **AgslPredict**.

Genotype and Abundance Datasets

The two sets of data, species level genotype data and species complex level abundance data, have been made publicly available at VectorBase.org and are each discussed in turn. The genotype data of the three species *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. were downloaded from VectorBase.org [38, 39] and spatially subsetted to the study area. Some samples of the *An. gambiae* s.l. species complex were identified by chromosomal form to species. Species recorded as "Anopheles gambiae chromosomal form Bamako" and "Anopheles gambiae chromosomal form Savanna" were assigned to "Anopheles gambiae sensu stricto", and "Anopheles gambiae chromosomal form Mopti" was assigned to "Anopheles coluzzii" [40]. The three species retained for analysis were "Anopheles arabiensis", "Anopheles coluzzii" and "Anopheles gambiae sensu stricto". Samples for which information on date of collection was missing were filtered out of the dataset. Information on time of collection varied across the remaining samples but could include durations of a single day, month, year or multiple years. The start and end dates of each collection were extracted. Samples with collection dates reported only to the month were assigned start and end dates that corresponded to the start and end dates of the reported month. Samples with reported durations greater than 31 days were filtered out of the dataset. *An. coluzzii* and *An. gambiae* s.s. were not distinguished prior to 2001 [30] and samples with earlier initial dates were omitted. Samples were then identified by project ID, latitude and longitude, collection date and collection protocol to define the sample unit of analysis. The frequency counts of the three species identified for each unit sample were then recorded for use in analyses of species relative abundance (species composition) described in the next section. Sample units with shared collection dates and collection methods were aggregated to 5 km $\times$ 5 km grid cells across the spatial extent, which resulted in 1,738 samples of relative abundance. The 5 km $\times$ 5 km grid cell resolution was chosen to capture the home range of a female mosquito since most mosquitoes disperse less than 5 km based on mark release recapture experiments [41] and for comparison with previous spatial analyses of genotyped data for *An. gambiae* species that also used 5 km $\times$ 5 km grid cell resolution [23, 24, 27, 29]. The collated records extended from 2001 to 2021 and are summarised in Table S1 and Figure S1.

The abundance data for *An. gambiae* s.l. were downloaded from VectorBase.org [38, 42] and spatially subsetted to the study area. Whereas the relative abundance data are typically derived from genotyped subsamples of field collections, the abundance data recorded from a field collection are most often counts of individuals morphologically identified to the level of the *An. gambiae* species complex. The observed counts of *An. gambiae* s.l. were treated as the response variable for the abundance analysis. Observation methods that could be categorised to specific collection methods were retained for analysis. The level of sampling effort was defined as the daily number of field collections by observation method in each grid cell. Records were then subsetted to samples identified as adult female mosquitoes. The available records extended from 1997 to 2021. Sites with long term longitudinal observations often also included long periods without observations. About 2% of the remaining samples had indeterminate sampling dates and were excluded from the analysis. Observations were

aggregated to the each grid cell by day and observation method, which resulted in 9,105 samples of abundance after excluding collection methods that targeted larvae or had low information content due to very few samples collected (less than ten records). The collated records are summarised in Table S2. These *An. gambiae* s.l. abundance records were sparsely distributed across sub-Saharan Africa (Figure S2).

Covariate Datasets

Precipitation, temperature and humidity are meteorological predictors of *An. gambiae* distribution [24, 26, 43]. Spatiotemporal meteorological data for daily precipitation totals, average daily temperature and average daily relative humidity were obtained from the National Aeronautics and Space Administration (NASA) Langley Research Center (LaRC) Prediction of Worldwide Energy Resource (POWER) Project funded through the NASA Earth Science/Applied Science Program [44] using the R package **nasapower** [45, 46]. These data are provided at a resolution of 0.625° longitude by 0.5° latitude. The meteorological covariates of a meteorological grid cell were assigned to all those 5 km × 5 km grid cells with centroids that occurred within the corresponding meteorological grid cell. In the Supplementary Information, the meteorological data are visualised by annual average (Figures S3, S4, S5), quarterly average (Figures S6, S7, S8) and anomalies with respect to the average over the timespan 2002–2020 (Figures S9, S10, S11) used for the prediction period.

The dates listed in the filtered VectorBase.org genotype data typically included a single day for each record, but some records were assigned a duration of up to a month (see previous section). The meteorological covariates for spatially and temporally varying precipitation, temperature and relative humidity used for the relative abundance analyses were constructed as follows. Thirty day averages were constructed from the daily meteorological observations that preceded both the first and last dates of the collection period for a sample. These two thirty day averages, which coincide for collections with a single day duration, were then averaged together. Distances to nearest coast and river, elevation, longitude, latitude and human population are proposed spatial predictors of *An. gambiae* distribution [24, 29, 35]. Spatial covariates were constructed using distances from 5 km × 5 km grid cell centroids to the nearest coast (Figure S12) and river (Figure S13) using data provided by Natural Earth and obtained with the R packages **rnaturalearth** [47] and **rnaturalearthdata** [48]. Elevation data at 15 arcseconds resolution were obtained from the National Centers for Environmental Information, National Oceanic and Atmospheric Administration [49], and averaged to obtain mean elevation for each 5 km × 5km grid cell (Figure S14). Human population data in 2015 at 30 arcseconds resolution were obtained from Landscan [50], and averaged to obtain mean human population density for each 5 km by 5 km grid cell (Figure S15).

Annual vector intervention data for ITN percent use by individuals and IRS percent coverage of households is available for the study area across the years 2000–2022 [51, 52]. The intervention data were averaged to the 5 km × 5 km grid cells to derive spatiotemporal covariates of intervention effort. Caution is required for assessment of intervention efficacy on the basis of observational studies [53]. For example, intervention effort may increase for locations and times with high vector densities. A spurious positive association could then be induced between vector populations and intervention effort that thereby masks an

expected negative causal impact of the intervention. Such an outcome could even be likely where interventions are selectively applied, but possibly less likely or severe for broadly applied interventions with deployment decisions that are less sensitive to vector population abundance. Universal coverage is recommended for ITNs [54], whereas effective vector control intervention by IRS should exceed 30% coverage of households [55] with recommended levels greater than 80% [56]. The ITN covariate shows a geographically broad increasing trend across much of sub-Saharan Africa with values that often exceed 10% in 2020 (Figure S16), whereas non-negligible IRS covariate values are comparatively limited in recent years (Figure S17). Across all samples, the maximum ITN covariate value by grid cell exceeded 10% in 18% of cells with observed genotype data and 86% of cells with observed abundance data. In contrast, the maximum IRS covariate value exceeded 10% in only 3% of grid cells with observed genotype or abundance data. The observational analyses of intervention was therefore restricted to ITNs that exhibited broad geographic deployment of non-negligible interventions. A single abundance study that occurred prior to 2000 was assigned ITN covariate values derived from contemporaneous ITN use data for the study location [57].

Analysis of Relative Species Abundance

Sinka et al. [27] use multinomial generalised additive models of genotype data to predict relative abundance (or composition) of *An. funestus*, *An. arabiensis* and the combination of the two species *An. coluzzii* + *An. gambiae* s.s. based on a habitat suitability index [23] and vector intervention data. Here, in contrast to [27], the VectorBase.org data genotyped to species were used to i) model each of the three species *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s., which is suggested as a potential avenue for exploration by Sinka et al. [27], and ii) include intra-annually varying predictors for the relative abundances of these species. The analysis included covariates of temperature, precipitation and relative humidity that varied daily in contrast to previous studies [24, 27–29]. ITN use is linked to selective pressure against *An. gambiae* s.s. and in favour of *An. arabiensis* [58, 59] and was also included as a covariate. Collection method was not explicitly included as a covariate. Genotype data for the three species of interest often do not distinguish between outdoor and indoor collection methods [24] that can affect interpretation of intervention efficacy [27]. For example, 27% of genotype samples in this study reported the collection method as "catch of live specimens" (collection method was incorporated into the analysis for the abundance data, see next section). The collected samples represent a mix of indoor and outdoor locations, which may help mitigate biased estimates [27]. Geographical covariates included distances to rivers and coasts, elevation, human population density, longitude and the absolute value of latitude as a measure of insolation. The year of collection was included to account for changes in species composition change due to increasing capacity for taxonomic discrimination at the species level for genotype data [60].

Multinomial logit generalised linear models (GLMs), see [61], were analysed using R package **nnet** [62] with the covariates scaled between zero and one based on the observed ranges. Let $m \in \{Aa, Ac, Ag\}$ indicate the three species of *An. arabiensis* (Aa), *An. coluzzii* (Ac) and *An. gambiae* s.s. (Ag) that occur with probability $p_m(s,t)$ at grid cell s and time t. Let $\boldsymbol{\nu}(s,t)$ denote the set of covariates at s and time t. *An. arabiensis* was chosen as the baseline or reference category of the multinomial logit GLM. The logarithm of the odds

$p_{m'}(s,t)/p_{Aa}(s,t)$ in favour of *An. coluzzii* ($m' = Ac$) or *An. gambiae* s.s. ($m' = Ag$) and against *An. arabiensis* were related to the covariates by the unknown parameter vector $\boldsymbol{\gamma}$. The statistical model is

$$\boldsymbol{z}(s,t) \sim \text{Multinomial}(\boldsymbol{p}(s,t), n(s,t))$$
$$\log \frac{p_{m'}(s,t)}{p_{Aa}(s,t)} = \boldsymbol{\nu}(s,t)^\top \boldsymbol{\gamma}, \quad m' \in \{Ac, Ag\},$$

where $\boldsymbol{z}(s,t)$ is the vector of counts of each species, given by $z_m(s,t)$ for species m, which sums to total observed abundances $n(s,t)$, and has corresponding probabilities $\boldsymbol{p}(s,t)$. The parameter vector $\boldsymbol{\gamma}$ was estimated by maximum likelihood. Backwards stepwise model selection was initiated from a quadratic surface model using the R package **MASS** based on the Bayesian information criterion (BIC) [62]. The quadratic surface model was a second order approximation based on the meteorological and geographical covariates, that is, each of these covariates appeared as a squared term, and a linear term, along with all pairwise interactions of the latter. ITN use and year were included as linear terms. The model with the lowest BIC value was chosen as the final model.

Analysis of Abundance of *An. gambiae* s.l.

The recorded collection methods from the VectorBase.org abundance dataset were mapped to covariates that assigned indoor human landing catch as the baseline method. Binary factors were scored for collection methods of light traps, exit traps, pyrethrum spray catches, animal baited traps and pit traps (Table S4), and whether or not a collection method was documented to occur outdoors. Projects with collection methods that were uncertain with respect to indoor or outdoor sampling were assigned a value of 0.5 for outdoors.

The observed abundance $y(s,t)$ of adult female *An. gambiae* s.l. per person at "site" (grid cell) s and time t was assumed to depend on observation method as described above. The equilibrium vector population abundance per indoor human $f(s,t)$ was assumed to be described by the spatially and temporally varying covariates $\boldsymbol{v}(s,t)$ with unknown coefficients $\boldsymbol{\beta}$. The covariate vector $\boldsymbol{v}(s,t)$ incorporated the lagged effect of precipitation on larval habitat. For example, the carrying capacity for *An. gambiae* is related to weekly total precipitation by [21]. Here, the immature phase of the life cycle was assumed to be about 10 days [35]. Thus, for a given day and location, the precipitation covariate was constructed by first calculating the weekly average precipitation that preceded each day of the corresponding 10-day larval period at that location. The weekly running means were then averaged over these 10 days to define the contribution of precipitation to the carrying capacity experienced by *An. gambiae* s.l. mosquitoes during the immature stage of development.

The observation method according to Table S4 was encoded by the covariate vector $\boldsymbol{w}(s,t,k)$ with unknown coefficients $\boldsymbol{\zeta}$ to adjust the mean abundance per indoor human $f(s,t)$ by the multiplicative factor $\rho(s,t,k)$ to produce the observed mean abundance per indoor human $\mu(s,t,k)$ for collection method k. If $\boldsymbol{w}(s,t,k)$ is a zero vector then the corresponding collection method is "man biting catch - indoors" (MBCI, Table S4) with $\rho(s,t,k = MBCI) = 1$ and $\mu(s,t,k = MBCI) = f(s,t)$. The statistical model for vector abundance per indoor human given collection method k was described by a negative binomial

GLM,

$$
\begin{aligned}
y(s,t,k) &\sim \text{NegativeBinomial}\left(\mu(s,t,k)u(s,t,k),\theta\right)\\
\log\mu(s,t,k) &= \log\rho(s,t,k) + \log f(s,t)\\
\log\rho(s,t,k) &= \boldsymbol{w}(s,t,k)^{\top}\boldsymbol{\zeta}\\
\log f(s,t) &= \boldsymbol{v}(s,t)^{\top}\boldsymbol{\beta},
\end{aligned}
$$

with mean and variance

$$
\begin{aligned}
&\mathbb{E}[y(s,t,k) \mid \mu(s,t,k)u(s,t,k),\theta] = \mu(s,t,k)u(s,t,k),\\
&\mathbb{V}[y(s,t,k) \mid \mu(s,t,k)u(s,t,k),\theta] = \mu(s,t,k)u(s,t,k) + [\mu(s,t,k)u(s,t,k)]^2/\theta,
\end{aligned}
$$

where θ is the overdispersion parameter and $u(s,t,k)$ is an offset for the sampling effort for observation method k at cell s on day t as described above (Methods–Genotype and Abundance Datasets).

A second order approximation was considered for the running mean of precipitation so that both a linear and squared term for the precipitation running mean was incorporated. Interactions allowed for modification of the impact of precipitation on adult female *An. gambiae* s.l. abundance. The linear term of precipitation shared linear interactions with the absolute value of latitude as a measure of insolation, elevation that relates to annual average temperature, and the spatially and temporally varying running mean for temperature that was constructed in the same way as the precipitation covariate. These three interacting covariates were less correlated with precipitation (Kendall rank correlation coefficient magnitudes did not exceed 0.25) than relative humidity (Kendall rank correlation of 0.5) that was excluded to reduce multicollinearity. The spatial covariate of human population density was included as a linear term to allow per capita mean vector abundance, as defined relative to indoor human landing catches, to change proportionally as human population density increases. Human population density is a proxy index for anthropogenic habitat modification and urbanisation. For example, the density of houses is negatively associated with larval habitat area for *Anopheles* mosquitoes [63]. Increasing human density not only reduces larval habitat but also reduces per capita malaria exposure [64]. Unknown parameters were estimated by maximisation of the likelihood with the covariates scaled between zero and one based on their ranges. The negative binomial GLM was fit in R v4.4.0 [65] using the R package **glm2** [66] and function `glm.nb` in package **MASS** [62].

Predicted Species Equilibrium Abundance

The equilibrium vector abundances of the three species *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. were predicted for the time period from 1 January 2002 to 31 December 2020 across the potential spatial range of *An. gambiae* s.l. [24, 36]. The predictions of relative abundance for the three species were based on the multinomial logit GLM with the year covariate set to the last year of the prediction period, 2020. The predictions for mean abundance of adult female *An. gambiae* s.l. per human at site (grid cell) s and time (day) t were based on the negative binomial GLM with the collection method set to indoor human landing catch ($MBCI$), such that $f(s,t) = \mu(s,t,k = MBCI)$. Abundance predictions

of *An. gambiae* s.l. are best related to precipitation in regions where temperature is not a limiting factor [67]. A temperature threshold rule was therefore applied. Laboratory experiments suggest that larval emergence of *An. gambiae* s.l. does not occur if water temperatures are less than 18°C or more than 34°C [68]. Air temperatures tend to be lower than water temperatures in *Anopheles gambiae* s.l. larval habitats [69], although the exact relationship between water and air temperatures can vary depending on local environmental factors [70]. About 1% of data observations included average temperatures that were outside the 18°C – 34°C range. Seasonal reproduction could potentially still occur in such areas during favourable months, but such regions were not represented well enough in the abundance sample data to capture such detail in the predictions. Sites where temperatures were outside these temperature tolerances for at least 30 continuous days in each year were filtered out to avoid overextrapolation and were provisionally assigned predictions of zero *An. gambiae* s.l. abundance, such that $\mu(s,t) = 0$ for all t at any site s that exceeded the temperature tolerance for larval emergence.

The negative binomial GLM provided per capita estimates of adult females for the *An. gambiae* species complex based on counts of *An. gambiae* s.l. Species level predictions therefore require incorporation of the multinomial GLM that provides relative abundance estimates for the three species of interest. A complication is that the predicted mean abundance $f(s,t) = \mu(s,t,k = MBCI)$ in the negative binomial GLM is the average daily abundance of adult female *An. gambiae* s.l. per human based on indoor feeding mosquitoes, but the propensity for human feeding among the three species of interest is not the same and adult female mosquitoes do not feed every day. Human feeding rates across the species range of *An. gambiae* s.l. have been elicited from domain experts [71] accounting for species differences among *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. using a prior elicitation method for GLMs [72]. Estimates of the average daily probabilities of an adult female mosquito biting a human are $\boldsymbol{r} = [0.37, 0.49, 0.47]^\top$ for *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s., respectively [71]. These average estimates reflect the greater degree of zoophilic feeding habit of *An. arabiensis* [23], although the human feeding rate will in actuality vary with covariates such as livestock density. The feeding rate adjustment for total adult females of the *An. gambiae* complex specifies that there are more adult female mosquitoes than those that may be observed feeding on humans, and this effect is greater on average for *An. arabiensis* compared to the other two species. Let $\xi(s,t)$ denote the average abundance of adult female *An. gambiae* s.l. per human after this adjustment for the mean daily probability of human feeding. Using the predicted per capita abundance $f(s,t)$ from the negative binomial GLM and the predicted relative abundances $\boldsymbol{p}(s,t)$ from the multinomial logit GLM obtains

$$f(s,t) = \sum_{m \in \{Aa, Ac, Ag\}} \xi(s,t) p_m(s,t) r_m,$$

so that *An. gambiae* s.l. vector abundance per human is

$$\xi(s,t) = f(s,t) \left[\sum_{m \in \{Aa, Ac, Ag\}} p_m(s,t) r_m \right]^{-1}.$$

The predicted species vector abundances $\boldsymbol{x}(s,t)$ were then obtained by again using the

multinomial GLM predictions,

$$x_m(s,t) = h(s)p_m(s,t)\xi(s,t), \quad m \in \{Aa, Ac, Ag\},$$

where $h(s)$ is the human population at site s. Note that the relative abundance of each species based on the total vector abundances is again $p_m(s,t) = x_m(s,t)/\sum_m x_m(s,t)$ as originally predicted by the multinomial GLM. Predictions for equilibrium vector abundance were thresholded to non-urban areas with less than 1500 human inhabitants on average per km^2 [73] because the three species of interest are not important vectors in central urban areas [23, 74].

The multinomial and negative binomial GLMs each accounted for various environmental and human factors that affect the average carrying capacities of the three species. For prediction, the models were interpreted to track potential equilibrium vector abundances determined by the running averages of the meteorological covariates, rather than actual abundances, subject to local conditions not accounted for in the continent-wide spatial and temporal covariates used in this analysis. The predicted equilibrium vector abundance at a given site may not be realised for many important ecological factors not considered in this model, for example, immigration or emigration due to metacommunity dynamics (see [71] for an elaborated model to address these considerations including wind-assisted advection, sensu [75]). The predicted species abundances $\boldsymbol{x}(s,t)$ were therefore considered predictions of equilibrium species vector abundances across the various sites and times. An underlying dynamic model that allows for stable coexistence and competing species at equilibrium is presented in the next section.

Estimated Niche Overlap and Interspecific Competition

Pombi et al. [30] estimate the niche overlap among the three species *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. in Burkina Faso. The pairwise estimates of niche overlap α_{ij} between species i and species j use the method of Pianka [31]. Applying this method to the equilibrium predictions over all days and grid cells, the niche overlap was estimated from the predicted mean proportion $\bar{p}_m(s) = \bar{x}_m(s)/\sum_m \bar{x}_m(s)$ of each species m with average vector abundance $\bar{x}_m(s)$ at a site s to obtain

$$\alpha_{ij} = \sum_s \bar{p}_i(s)\bar{p}_j(s) \left(\sum_s \bar{p}_i(s)^2 \sum_s \bar{p}_j(s)^2 \right)^{-1/2}, \quad i,j \in \{Aa, Ac, Ag\}.$$

The resulting niche overlap matrix is positive definite and symmetric with unit entries on the main diagonal [32]. The niche overlap index has been suggested as a measure of interspecific competition [32], although Pianka [31] lists limitations with this interpretation.

A contrasting approach estimates interspecific competition by identifying an underlying dynamic model [76] that is a multispecies version of the Beverton-Holt population model [77] or two-species Leslie-Gower model [78] with the added inclusion of a maturation delay. Envision a model for adult female mosquitoes given by

$$x_i(s,t+1) = \sigma_i x_i(s,t) + \frac{\lambda_i x_i(s,t)}{1 + q_i(s,t)\sum_j A_{ij} x_j(s,t-\delta)}, \quad i \in \{Aa, Ac, Ag\}.$$

The dynamics of the set of competing species are described at each day t with immature life history stages of duration $\delta = 10$ days. The dynamic model allows for competitive effects among immature individuals of species j on species i as mediated by $A_{ij} \geq 0$ that emerge as reproductive adults after the conclusion of the immature life history stage. It is assumed that $A_{ii} = 1$ so that strength of intraspecific competition is defined by $q_i(s,t)$. The density independent per-capita growth rate is λ_i. The probability of daily adult survival is σ_i. The positive parameter $q_i(s,t) > 0$ varies through space and time to set the equilibrium level of species i.

If $\boldsymbol{q}(s,t)$ is held constant, then from [76] the resulting equilibrium is

$$\boldsymbol{x}^*(s,t) = \boldsymbol{A}^{-1}\text{diag}\left[\boldsymbol{\lambda} - \mathbf{1} + \boldsymbol{\sigma}\right]\text{diag}[\mathbf{1} - \boldsymbol{\sigma}]^{-1}\boldsymbol{q}(s,t).$$

Let $\boldsymbol{q}(s,t)$ have spatial and temporal average $\mathbb{E}[\boldsymbol{q}(s,t)] = \bar{\boldsymbol{q}}$. The predicted average equilibrium is then defined by the spatial and temporal average,

$$\hat{\boldsymbol{x}}^* = \mathbb{E}\left[\boldsymbol{x}^*(s,t)\right] = \boldsymbol{A}^{-1}\text{diag}\left[\boldsymbol{\lambda} - \mathbf{1} + \boldsymbol{\sigma}\right]\text{diag}[\mathbf{1} - \boldsymbol{\sigma}]^{-1}\bar{\boldsymbol{q}}.$$

Given the above model, if it is assumed that the average vector abundance $\bar{x}_m$ of species m over all sites and times is an approximation of its predicted equilibrium vector abundance, such that $\bar{\boldsymbol{x}} \approx \hat{\boldsymbol{x}}^*$, then following [76] a minimisation problem can be constructed that seeks to shift the bottom of the "bowl" formed by the basin of attraction towards the estimated equilibrium $\bar{\boldsymbol{x}}$ while increasing the magnitude of interspecific competition described by the off-diagonal entries in $\boldsymbol{A}$. The underlying premise is that species "seek" to maximise available resources, thus increasing competition, and are more likely to be observed near an equilibrium that is stable. Stability is measured by the spectral radius, or largest eigenvalue by magnitude, of the linearised system around the equilibrium [76]. If the spectral radius is less than one, then the system is locally stable such that species abundances will eventually return to equilibrium after a small perturbation. The symmetric positive definite structure of the niche overlap method is retained for $\boldsymbol{A}$ in this approach.

The estimate used the ten day immature stage duration ($\delta_m = 10$ days) with fecundity rate of $\lambda_m = 9/2$ female adults estimated in [35] for *An. gambiae* and adjusted for equal sex ratio. See also [76] for an example using the empirical results of Pombi et al. [30] for Burkina Faso only. Adult daily survival probabilities across the species range of *An. gambiae* s.l. were elicited from domain experts [71] accounting for species differences among *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. using a prior elicitation method for GLMs [72]. The average predicted survival probabilities of $\boldsymbol{\sigma} = [0.85, 0.84, 0.84]^\top$ for the species *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s., respectively, were obtained from [71]. The estimate of competition does not depend on $\boldsymbol{q}$ in the method of [76], so that the above assumptions allowed estimation of the interspecific density dependent coefficients A_{ij} with $i \neq j$.

Results

Relative Abundance and Per Capita Abundance GLMs

The coefficient estimates and standard errors of the best fitting model for the log odds of *An. coluzzii* and *An. gambiae* s.s. against *An. arabiensis* as the baseline or reference

category are presented in Table S3. The backwards stepwise selection resulted in a best fitting final model having a BIC value of 50,534 compared to 50,625 for the initial full model. The meteorological covariates of precipitation, temperature and relative humidity were all retained as quadratic relationships, with both linear and quadratic terms retained as useful predictors of relative abundance, in the best fitting model. The estimated coefficients of covariates for relative abundance also indicated a strong increasing annual trend in the relative abundance of *An. coluzzii*. The relative abundances of both *An. coluzzii* and *An. gambiae* s.s. showed a decreasing trend with higher latitudes. Due to interactions, this latitudinal trend was diminished by increasing elevation but enhanced by human population density. Human population density was evidently an important predictor as it also showed a negative interaction with longitude for the log odds of *An. coluzzii* and *An. gambiae* s.s. ITN use was negatively associated with the log odds of *An. gambiae* s.s. versus *An. arabiensis*.

Predictions from the multinomial GLM are averaged through time and presented across the spatial scope in Figure S21. The associated predicted variance on the linear predictor scale is presented in Figure S22. Higher relative abundance was predicted for *An. coluzzii* relative to *An. arabiensis* in coastal West Africa. Greater relative abundance was predicted for *An. gambiae* s.s. versus *An. arabiensis* in coastal West Africa and some regions near Lake Victoria. With less certainty, higher relative abundance for *An. gambiae* s.s. was predicted in northern and central Madagascar whereas *An. arabiensis* was more prevalent elsewhere on the island. High uncertainty accompanied predictions of higher relative abundance for *An. gambiae* s.s. versus *An. arabiensis* in the Horn of Africa and the Sahara. These regions of prediction with high uncertainty lacked relative abundance data sources (Figure S1).

The parameter estimates for the negative binomial GLM are provided in Table S5. Observed counts were strongly affected by observation method. For example, outdoor pit traps were much less efficient compared to indoor human landing catch ($MBCI$). Precipitation was a strong predictor with per capita vector abundance peaking at an intermediate value within the range of observed precipitation: the linear coefficient for precipitation was 15.1 and the corresponding squared term was -12.7. The quadratic relationship with precipitation in the absence of interactions was therefore concave with peak per capita abundance predicted at 0.6, which was above the midpoint of the precipitation covariate that was scaled between 0 and 1 by its observed range. ITN use was negatively associated with per capita abundance. Negative interactions were estimated between precipitation and temperature, which also varied both spatially and temporally along with precipitation, and also the spatial covariates of elevation and distance from the equator. A negative association was suggested between per capita mosquito female abundance and human population density (estimated coefficient of -0.58), which was expected because generally less *An. gambiae* s.l. habitat is available in urbanised areas [23, 74]. Although negative, this coefficient was greater than -1, which indicated a positive relationship between total vector population density and human population that is expected because *An. gambiae* s.l. exhibits anthropophily. The highest overall per capita abundance was predicted near the equator (Figure S23a) with some areas of high uncertainty (Figure S23b) located in regions with comparatively few abundance data sources (Figure S2).

Predicted Equilibrium Species Abundances

The multinomial and negative binomial GLMs were used to predict the daily equilibrium abundances of adult female *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. in each 5 km $\times$ 5 km grid cell across the range of *An. gambiae* s.l. in Africa after accounting for temperature tolerances, daily probabilities of human feeding, and human population density. The average equilibrium vector abundances of each species are presented in Figure 1. The predicted equilibrium vector abundance of *An. arabiensis* was highest in eastern Africa, the Sahelian region and Madagascar, with low areal densities in central Africa. The predicted equilibrium vector abundance of *An. coluzzii* was highest in western Africa. The highest predicted equilibrium vector abundance for *An. gambiae* s.s. occurred in western Africa, central Africa, the Lake Victoria basin and Madagascar. Seasonal predicted vector abundances are visualised in Figures S18, S19 and S20.

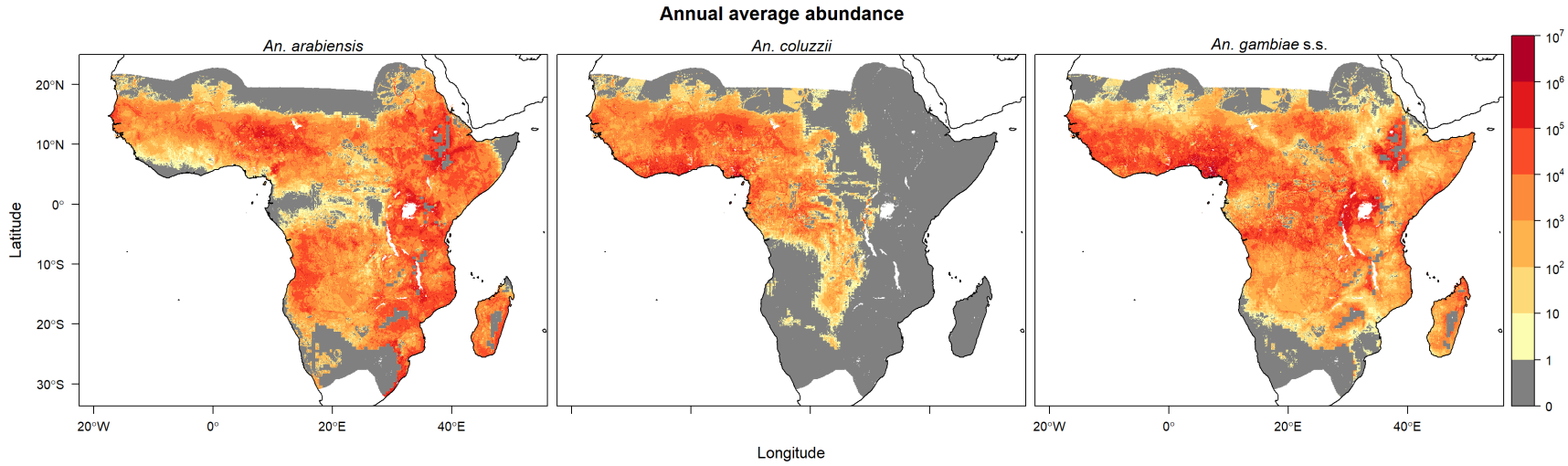


Figure 1: Annual average of predicted equilibrium vector abundances of dominant malaria vector species of *An. gambiae* s.l. per 25 square kilometres over years 2002–2020. Predictions are masked to the potential range of *An. gambiae* s.l. [24] provided by the Malaria Atlas Project (`https://malariaatlas.org/`) under the terms of a Creative Commons Attribution 4.0 International License available at `https://creativecommons.org/licenses/by/4.0/`. Note logarithmic scale.

The negative association of ITN use and per capita vector abundance (Table S5) led to predictions of decreasing overall vector abundance in general because of the widespread increase of ITN use over the prediction period 2002–2020 (Figure S16). Broad geographical decreases in vector abundance were therefore predicted for all three species with the greatest decreases occurring in areas with high ITN use (Figures 2, 3, 4). Across four years separated by six year intervals between 2002–2020, the areal density of *An. arabiensis* was predicted to increase in north-eastern Africa, but overall decreases were predicted (Figure 2). The equilibrium vector abundance of *An. coluzzii* was generally predicted to decrease (Figure 3). Predictions for *An. gambiae* s.s. suggested decreases in most areas of its range, except for areas east and northeast of Lake Victoria (Figure 4) that exhibited lesser increases in ITN use compared to the western areas surrounding Lake Victoria (Figure S16).

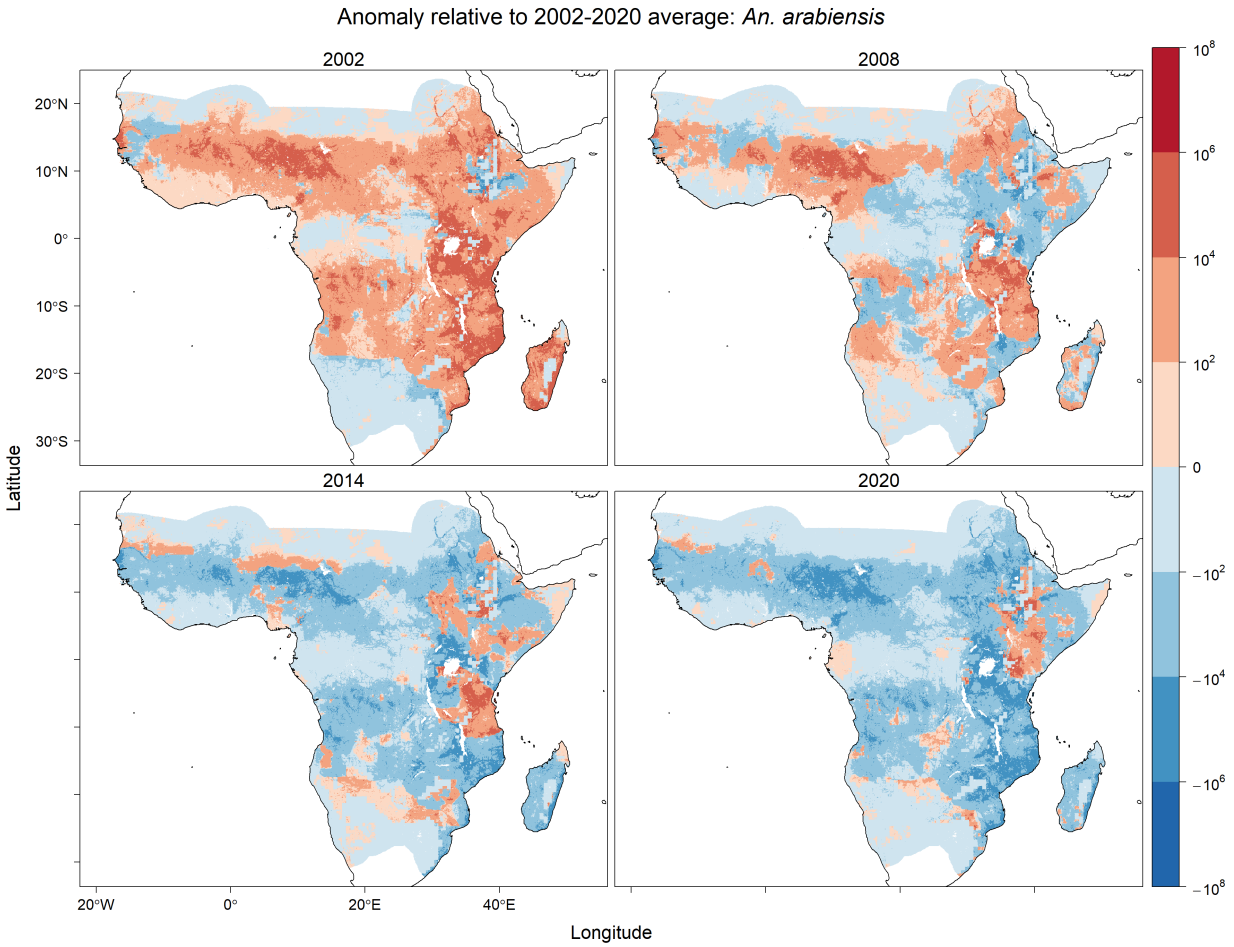


Figure 2: Annual average anomalies of total potential equilibrium vector abundance of *An. arabiensis* relative to its predicted average per 25 square kilometres over years 2002–2020. Predictions are masked to the potential range of *An. gambiae* s.l. [24] provided by the Malaria Atlas Project (`https://malariaatlas.org/`) under the terms of a Creative Commons Attribution 4.0 International License available at `https://creativecommons.org/licenses/by/4.0/`.

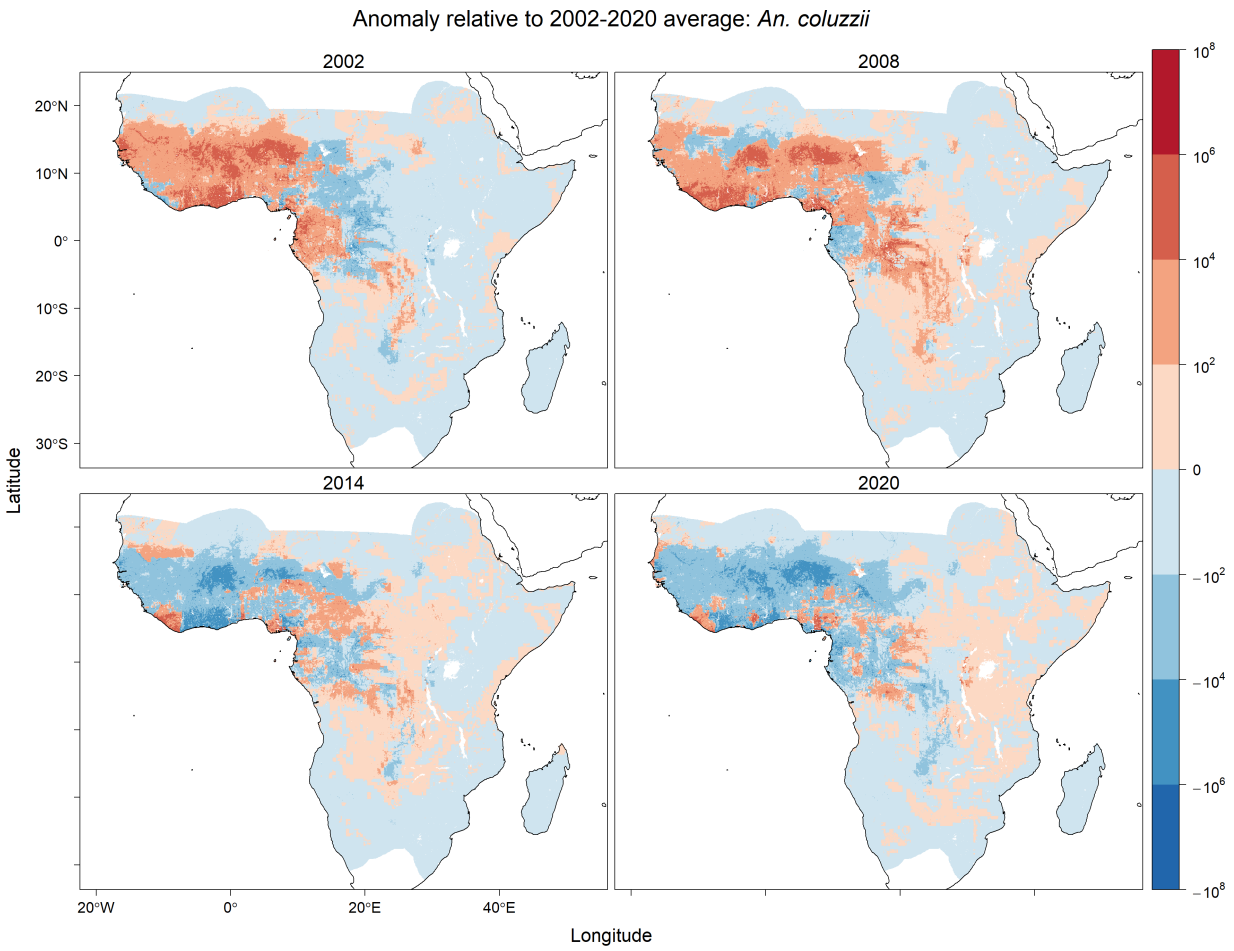


Figure 3: Annual average anomalies of total potential equilibrium vector abundance of *An. coluzzii* relative to its predicted average per 25 square kilometres over years 2002–2020. Predictions are masked to the potential range of *An. gambiae* s.l. [24] provided by the Malaria Atlas Project (`https://malariaatlas.org/`) under the terms of a Creative Commons Attribution 4.0 International License available at `https://creativecommons.org/licenses/by/4.0/`.

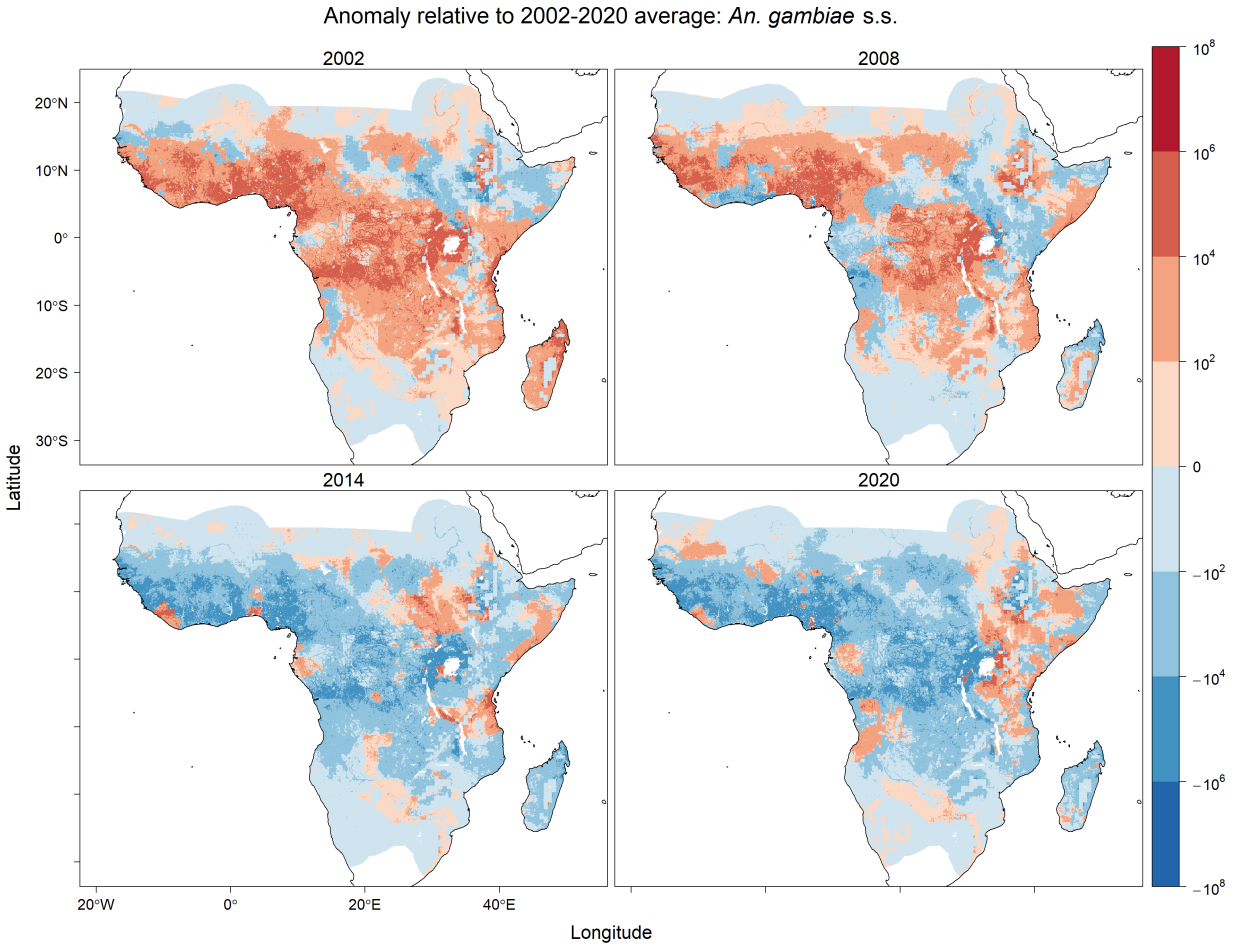


Figure 4: Annual average anomalies of total potential equilibrium vector abundance of *An. gambiae* s.s. relative to its predicted average per 25 square kilometres over years 2002–2020. Predictions are masked to the potential range of *An. gambiae* s.l. [24] provided by the Malaria Atlas Project (`https://malariaatlas.org/`) under the terms of a Creative Commons Attribution 4.0 International License available at `https://creativecommons.org/licenses/by/4.0/`.

Comparative Evaluation of Equilibrium Abundance Predictions

The predicted daily species equilibrium vector abundances were evaluated by comparison to previous empirical analyses of large spatial scale prediction of species in the *An. gambiae* species complex from four distinct perspectives: i) species distribution models of species occurrence, ii) relative abundance models, iii) observed entomological inoculation rate (EIR) and iv) effective population size estimates from genotype data. Studies in i) and ii) that incorporate species occurrence data may not be entirely independent of the data used for the multinomial GLM model of species relative abundance in this study. However, the comparisons iii) and iv) provide independent empirical comparisons. None of these studies allow for intra-annually varying covariates, and so comparisons considered only the mean equilibrium vector abundance (Figure 1) averaged over daily, and seasonal (e.g., Figures S18, S19 and S20), variation for the 2002–2020 prediction period.

i) Species Distribution Models. Species distribution models based on species occurrence do not estimate abundance but instead "potential distribution" [26] or the relative probability of presence (e.g., [24]) and so are not directly comparable with this study. Qualitative comparison is still possible for the several species distribution models applied within the *An. gambiae* complex [22, 24, 26, 79, 80]. Of these, only Wiebe et al. [24] predict relative probabilities of presence for all three species based on annually varying covariates. The species distribution model predictions in that study [24] are clipped to independently derived species range limits, but comparison within the limits suggests broad qualitative agreement with the average equilibrium vector abundance predictions of Figure 1: *An. arabiensis* estimates are highest in the northern, eastern and southern regions (see also [22, 26, 80]); *An. coluzzii* estimates are highest in western Africa; and *An. gambiae* s.s. estimates are highest in western Africa and near Lake Victoria with high estimates also occurring in central Africa. The range limits imposed by Wiebe et al. [24] exclude *An. gambiae* s.s. from the northeastern portion of the range for *An. gambiae* s.l. In this region, Figure 1 shows low densities extending into the Horn of Africa (the Somali Peninsula and eastern Ethiopia), although as noted above the predictions of relative abundance are highly uncertain (Figure S22). Species distribution models that permit predictions into the Horn of Africa suggest either presence [22, 79] or absence [80] of *An. gambiae* s.s.

ii) Relative Abundance Models. Extrapolations from relative abundance estimates of *An. arabiensis* versus the aggregate of *An. coluzzii* and *An. gambiae* s.s. collated for Nigeria, Niger and the Senegambia [28] suggest strong similarities with Figure 1. The latter two species are relatively more abundant in western coastal Africa, central Africa and western Ethiopia. A discrepancy is noted in southern Tanzania, where the relative abundance of *An. arabiensis* is higher than suggested by Figure 1 that is more closely in agreement with Sinka et al. [27]. On the other hand, the predictions of Sinka et al. [27], unlike [28] and Figure 1, do not suggest higher estimates of *An. gambiae* s.s. in western Ethiopia, which accords with empirical observations of *An. arabiensis* rather than *An. gambiae* s.s. in this area [81]. The predicted equilibrium vector abundances in western Ethiopia shown in Figure 1, however, were accompanied by high uncertainty for species relative abundances (Figure S22) and per capita vector abundance (Figure S23b). Although restricted to comparisons of *An. coluzzii*

and *An. gambiae* s.s. relative abundance based on species occurrence data from western and central Africa, Tene Fossog et al. [29] similarly predict higher estimates of the former species across the Sahel and higher estimates of *An. gambiae* s.s. in the West Sudanian savannah. The predictions by Tene Fossog et al. [29] suggest higher relative abundance of *An. gambiae* s.s. compared to *An. coluzzii* across central Africa outside of a narrow coastal margin, whereas Figure 1 places higher estimates of *An. coluzzii* in a region centred around Gabon. Both studies predict higher relative abundance for *An. gambiae* s.s. across most of central Africa.

iii) Entomological Inoculation Rate. Outside of areas with highly successful vector control and malaria case intervention, Rogers et al. [22] suggest a strong relationship between vector abundance and the entomological inoculation rate (EIR) that is equal to the vector abundance multiplied by the human feeding and sporozoite rates divided by the human population. Proceeding therefore with the predicted species equilibrium vector abundances, where ITN use is incorporated, allows comparison with observations of EIR across East Africa before (years 2000–2010) and after (years 2011–2022) widespread increases in ITN use [82]. For this comparison, EIR is estimated from the predicted species equilibrium vector abundances (Figure 1) averaged over 2002–2020 in each grid cell east of 30°E longitude with human feeding rates estimated from the daily feeding probabilities reported in the Methods and median sporozoite rates *An. gambiae* s.l. reported for both time periods by Msugupakulya et al. (2023) [82]. There is substantial variability in these estimates and also the EIR observations [82] that include uncertainty in the sporozoite rate and proportion of EIR attributable to various vector species. Comparisons are therefore based on central 0.80 probability intervals constructed from estimates of the 0.10 and 0.90 quantiles. Using observations of EIR [82], the central 0.80 interval for annualised EIR attributable to *An. gambiae* s.l. in East Africa is (0.15, 175) for the 2000–2010 period and (0, 20) for the 2011–2022 period (see Supplementary Information in [82]). The corresponding 0.80 central intervals for annualised EIR based on the predicted species equilibrium vector abundances were (90, 241) in 2002 and (15, 100) in 2020. It should be noted that occurrences of zero sporozoite rates, which are observed for *An. gambiae* s.l. [82], will underestimate vector abundance based on observed EIR. The equilibrium based estimates of EIR, which assumed median sporozoite rates, were indeed somewhat higher than observed EIR. Despite the requisite assumptions and caveats, the studies suggest overlapping 0.80 central intervals for EIR in each time period with decreasing upper and lower bounds since widespread increases in ITN use.

iv) Effective Population Size. A pan-African estimate of mean total effective population size for *An. coluzzii* and *An. gambiae* s.s. obtained from allele frequency data is between 1.6×10^9 and 3.1×10^9 after accounting for seasonal fluctuations [83]. The genetic study uses genotype data collected between 2000 and 2012 with the majority of samples collected since 2009 [84]. In 2011, ITN use was widely increasing in East Africa, as noted in iii) above. Regarding the predicted overall equilibrium vector abundance aggregated over the entirety of the *An. gambiae* s.l. species range across sub-Saharan Africa, multiplying the predicted average daily aggregate vector equilibrium abundances for *An. coluzzii* and *An. gambiae* s.s. by a factor of two to allow for a roughly equal sex ratio suggested a total population average

daily estimate that more than halved from 6.0×10^{10} individuals in 2002 to 2.85×10^{10} individuals in 2014 (Figures 3 and 4 depict the 2002 and 2014 anomalies from Figure 1 for *An. coluzzii* and *An. gambiae* s.s.). Assuming a ratio of total to effective population size of 0.10 [85] suggests an effective population size of 2.85×10^9 based on the combined predicted equilibrium abundances of *An. coluzzii* and *An. gambiae* s.s. in 2014, which is within the estimated range for the mean effective population size.

Estimated Niche Overlap and Interspecific Competition

The species with the greatest niche overlap was *An. gambiae* s.s. (Table 1). The strongest interspecific competition was estimated between *An. arabiensis* and *An. gambiae* s.s. (Table 1), which exhibited the greatest degree of spatial overlap (Figure 1). The two remaining pairwise relationships of optimised interspecific competition estimates were of similar magnitude. The equilibrium that maximised stability was further away from the observed equilibrium $\bar{\boldsymbol{x}}$ for the Pianka niche overlap estimates (Figure 5a) compared to the optimised competition estimates (Figure 5b). For the optimised estimate ($\hat{\boldsymbol{A}}$), the observed equilibrium approximately corresponded to the most stable species composition.

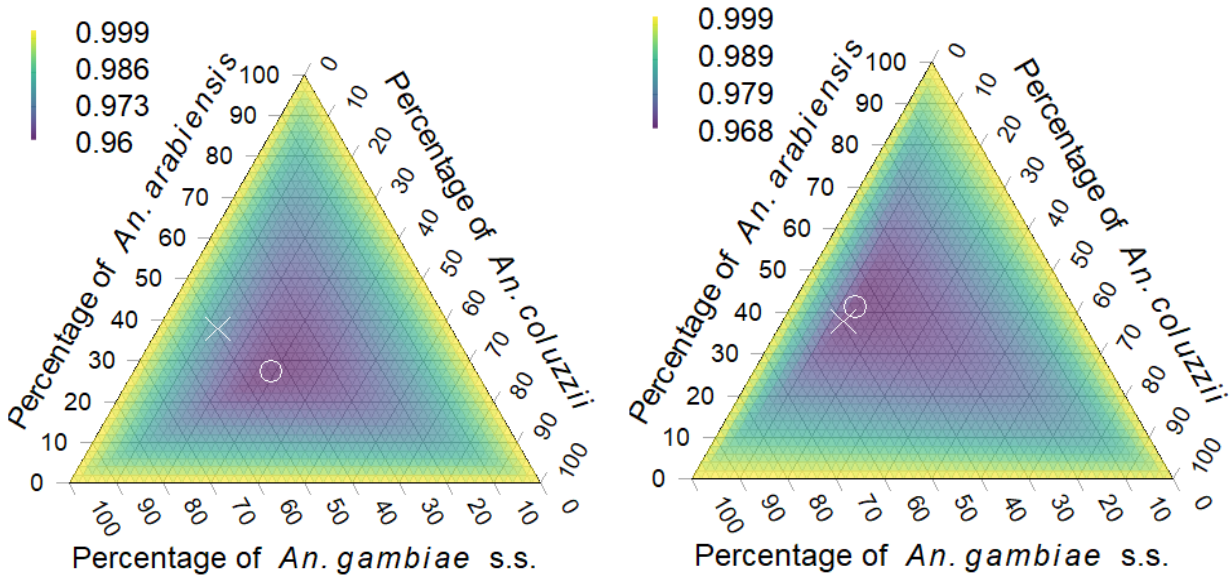
Table 1: Estimated competitive interactions over the species range of *An. gambiae* s.l. for the years 2002–2020 using the Pianka niche overlap ($\boldsymbol{\alpha}$) and optimised ($\hat{\boldsymbol{A}}$) methods: *An. arabiensis* (Aa) versus *An. coluzzii* (Ac), *An. arabiensis* versus *An. gambiae* s.s. (Ag), and *An. coluzzii* versus *An. gambiae* s.s.

	Aa vs Ac	Aa vs Ag	Ac vs Ag
Niche overlap ($\boldsymbol{\alpha}$)	0.16	0.23	0.26
Competition ($\hat{\boldsymbol{A}}$)	0.16	0.38	0.18

Discussion

Management of malaria requires knowledge of the abundance of important vector species [1, 86] such as members of the *An. gambiae* s.l. species complex [6] to allow efficient malaria control by conventional methods [8] or potential new technologies including genetic biocontrol [7]. The spatiotemporal distribution of vector species abundances, and hence threat of malaria, will change with environmental factors [70] and hence potentially also with climate change [26]. Here, statistically estimated environmental relationships are used to give insights into the predicted abundances of the three important malaria vectors of *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. across their combined ranges of sub-Saharan Africa, and also evaluate the potential for interspecific interactions through niche overlap or competition.

Climatological factors such as precipitation and temperature, geographical factors such as elevation and human population density, and deployment of insecticide treated nets (ITNs) were linked to the relative abundances of *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. and the per capita abundance of *An. gambiae* s.l. These analyses of species relative abundance from species occurrence data and abundance of *An. gambiae* s.l. from count



(a) $\boldsymbol{A} = \boldsymbol{\alpha}$.

(b) $\boldsymbol{A} = \hat{\boldsymbol{A}}$.

Figure 5: Spectral radius for all possible interior equilibrium species abundances given (a) Pianka niche overlap estimate $\boldsymbol{A} = \boldsymbol{\alpha}$ and (b) optimised estimate $\boldsymbol{A} = \hat{\boldsymbol{A}}$ for the interspecific competitive interactions. Points show the location of species equilibrium with lowest spectral radius (∘) and the location of the predicted overall equilibrium (×). Note change in colour scale for (a) versus (b).

data were combined to produce joint predictions of daily vector equilibrium abundances for the years 2002–2020 (Figure 1). ITN coverage by household in sub-Saharan Africa increased from 5% in 2000 to 70% in 2022 [3], and areas with increasing ITN use (Figure S16) suggested decreases in vector equilibrium abundances across the prediction period (Figure 2, 3 and 4). Increased equilibrium abundances for *An. arabiensis* and *An. gambiae* s.s. were predicted in some regions northeast of Lake Victoria with relatively low ITN use in 2020. Such increases are attributable to the climatological covariates because all temporal changes in predicted vector equilibrium abundances were attributable to either ITN use or the meteorological covariates of precipitation, temperature and relative humidity. The relative abundance of *An. coluzzii* was predicted to increase across years at the expense of *An. arabiensis*. The trend of increasing *An. coluzzii* relative abundance could be caused in part to climatic or land use factors, but it could also be explained by the relatively recent species characterisation of *An. coluzzii* and *An. gambiae* s.s. combined with improved genotyping capabilities of the *An. gambiae* species complex [29, 30, 40]. For example, the occurrence of *An. coluzzii* in northwestern Kenya has recently been shown using whole genome sequencing of historical samples dated from 2006 and 2019, where taxonomic characterisation based on previous molecular methods limited to identification of alternative species would have missed detection of *An. coluzzii* [60].

The predicted equilibrium vector abundance at a given site is a potential abundance that may not be realised for many important ecological factors not considered in this model due

to local conditions not accounted for in this continental scale analysis. Predictions were therefore comparatively evaluated against four alternative empirical modelling perspectives with general agreement: i) species distribution models based on species occurrence records [22, 24, 26, 79, 80], ii) relative abundance models [27–29], iii) entomological inoculation rate (EIR) estimates in eastern and southern Africa [82] and iv) effective population size estimates from genotype data [83]. Overall, results showed qualitatively similar patterns, although it should be noted that none of the comparisons in i)-ii) provide species-specific estimates of vector abundances. The comparisons iii) and iv), however, provide independent empirical estimates of EIR and vector abundances that are not dissimilar from estimates based on predicted species vector equilibrium abundances.

Analyses suggested that the three species can coexist (Figure 5) despite evidence of substantial niche overlap and interspecific competition (Table 1) across the shared species range. The estimates for niche overlap among the three species (Table 1) were, in comparison, less than those reported by Pombi et al. [30] in a study that derived the estimates from field observations in a region of Burkina Faso where all three species coexist. In contrast, the niche overlap estimates from this study included the whole of the range of *An. gambiae* s.l. in regions where not all species were predicted to occur with non-negligible abundances. As a consequence, the niche overlap estimates were lower in this study because of its broader geographic scale. The interspecific competition estimates (Table 1) suggested that the three species exhibited substantial interspecific competition while maintaining stable coexistence at the overall predicted vector equilibrium abundances.

Ideally, daily times series of species-level abundances collected over long durations would be available from many sites geographically dispersed across sub-Saharan Africa. Then the delayed density dependent model proposed by [76] and described in the Methods could be implemented within a state space modelling framework to estimate the parameters of interest while allowing for non-equilibrium dynamics. Without daily time series data, this study used smoothed moving average covariates of the meteorological covariates that determine the environmental carrying capacities and equilibrium abundances of the species. The predicted equilibrium is spatially and temporally varying due to changing environmental conditions that modify the Grinellian niche of the constituent species [87], which in turn is modified by interspecific competition to produce the realised niche [88]. However, the predicted equilibrium is only a measure of potential abundance: the species may be limited by dispersal capability or source-sink metapopulation dynamics such that it is either above or below the predicted equilibrium abundance over the long run [11, 89]. Moreover, species abundances do not exactly attain potential equilibrium due to changing environment, dispersal and immigration. The proposed density dependent model may be elaborated to account for immigration and emigration, see [12] for a non-delayed example, as well as delayed maturation with introgression among the constituent species of a species complex such as *An. gambiae* s.l. [71].

Given the sparse data available for this study across the broad spatial and temporal scope of interest, and predicted changes of species abundance both within and among years, sophisticated analyses for causal attribution among cumulative effects were commensurately limited. Higher quality longitudinal abundance data at the species level of sufficient sub-seasonal temporal frequency would greatly help statistical evaluation of competing causal hypotheses, such as vector control, malaria interventions, land use and climate. The pre-

dictions and results of this study accounted for intra-annual shifts in species composition, but could not explicitly control for many important covariates. For example, factors such as land use impact not only larval habitat but also the feeding habit of *An. arabiensis* that feeds on livestock to a greater degree than *An. coluzzii* and *An. gambiae* s.s. [23]. Inclusion of spatiotemporal covariates of livestock density in particular would assist predictions of *An. arabiensis* that exhibits greater zoophily biting habit. Improved estimation of the relationship between species abundances and human feeding rates would also require abundance data for each of the three species, whereas most of the spatially extensive and longitudinal data available for this study were limited to counts for the entire species complex. Although the ecologically important and spatially and temporally varying covariate of livestock density was not explicitly represented, the lower probability of human host feeding by *An. arabiensis* compared to the other species was incorporated into the predictions. The abundance estimates also accounted for collection methods, but the analysis of the relative abundance data did not incorporate sampling effects because species identification by genotyping were often based on samples collected from the field by multiple methods that did not document, for example, indoor versus outdoor collection. Hence, predictions of *An. arabiensis* relative abundance must be interpreted cautiously and particularly so in regional areas with high livestock density relative to human inhabitant density.

The modelling approach used here elaborated previous relative abundance models [27–29] to consider the three species of *An. arabiensis*, *An. coluzzii* and *An. gambiae*. Daily varying climatological covariates were used to predict the relative abundances of these species and also the per capita vector abundance of *An. gambiae* s.l. across sub-Saharan Africa for the first time. These statistical models used covariate and response data collated to a grid of 5 km $\times$ 5 km cells for analysis and prediction at the continental scale. Other regional and continental scale studies use this same resolution [23, 24, 27, 29] as a suitable choice for the ecology and dispersal of species in the *An. gambiae* species complex [23, 29]. At finer resolutions, climatological factors such as precipitation and temperature can for some locales be more important predictors of *An. gambiae* s.s. abundance counts than microscale covariates such as the number of occupants per home or distance to larval habitat [90]. Climatological factors remain important predictors for resolutions that are coarser than the choice of 5 km $\times$ 5 km cells [26, 28]. The choice of 5 km $\times$ 5 km resolution, however, does not deny the known importance of microscale habitat variability to the risk of malaria transmission [63], and is more suitable for interpretation at coarser national or sub-national levels [24].

Conclusion

Meteorological factors such as precipitation and temperature were found at the continental scale to be important spatially and temporally varying predictors of vector equilibrium abundances of the primary malaria vector species within the *Anopheles gambiae* s.l. species complex: *An. arabiensis*, *An. coluzzii* and *An. gambiae* s.s. Precipitation and temperature were important contributors to substantial variation in the seasonal levels of the three species. Insecticide treated net use was negatively associated with per capita vector abundance of the *An. gambiae* species complex and the ratio of *An. gambiae* s.s. to *An. arabiensis*. A

longer term trend of increasing relative abundance of *An. coluzzii* was also found, and was possibly attributable to advances in genetic methods of species identification within the *An. gambiae* species complex that occurred over the observational period. Human population density was also an important predictor that was negatively associated with per capita vector abundance. Across sub-Saharan Africa, the observational analyses suggested evidence for niche overlap and competitive interactions among the three species. Additional time series data of mosquito vector species abundance, collected at fine temporal resolutions of monthly sampling intervals or higher frequencies and across broad geographical regions, are necessary to improve discernment of ecological interactions among species and the effectiveness of vector control interventions designed to measurably reduce the burden of mosquito-borne disease.

Supplementary information

The reproducible code, data sources and licenses are summarised in the R package **AgslPredict** [37] provided as a supplement for this article.

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Declarations

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- Conflict of interest/Competing interests. The authors declare no conflicts of interest.

- Ethics approval and consent to participate. This article incorporates elicited information with participants providing their consent to participate under ethics approval by the CSIRO Social Science Human Research Ethic Committee (approval number 136/19).

- Consent for publication. The authors provide their consent for publication.

- Data availability. The data sources and licenses are summarised in the R package **AgslPredict** [37] provided as a supplement for this article.

- Materials availability. Not applicable.

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- Author contribution. **G. R. Hosack:** Conceptualization, data curation, formal analysis, funding acquisition, investigation, methodology, project administration, software, visualization, writing–original draft, writing–review and editing. **M. El-Hachem:** Conceptualization, data curation, investigation, methodology, software, validation, visualization, writing–review and editing. **A. Ickowicz:** Conceptualization, investigation, methodology, writing–review and editing. **N. J. Beeton:** Conceptualization, investigation, visualization, writing–review and editing. **A. Wilkins:** Conceptualization, writing–review and editing. **K. R. Hayes:** Conceptualization, funding acquisition, visualization, writing–review and editing. **S. S. C. Rund:** Data curation, writing–review and editing. **S. A. Kelly:** Data curation, writing–review and editing. **M. A. McDowell:** Data curation, writing–review and editing.

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