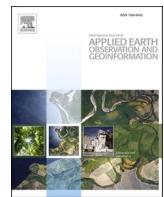


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## Spatiotemporal trends in *Anopheles funestus* breeding habitats

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### ABSTRACT

Effective identification and control of malaria vector larval breeding habitats are crucial for the management and eradication of malaria. Despite its importance, the last decade has seen a decline in data availability and intervention efforts due to reduced attention and prioritization. This study addresses the geographic data scarcity concerning *Anopheles funestus* larval breeding habitats in a malaria-prone region of western Kenya. Employing a two-step methodological approach, we integrated multi-criteria decision analysis (MCDA) and rule-based fuzzy logic analysis to evaluate the spatiotemporal similarity or divergence of these habitats. The analysis spanned a five-year interval, 2008, 2013, and 2018 with 2013 serving as the base year for both hindcast and forecast predictions. The MCDA utilized categorical land use/land cover (LULC) and edaphic variables to identify potential breeding habitats, while climatic and topographic variables and spectral indices were analysed using fuzzy logic to assess the similarity or divergence of these habitats over time. Validation of the MCDA and fuzzy logic models was performed using a flight buffer distance based on adult *An. funestus* presence points ( $n = 136$ ), supplemented by a limited number of larval breeding locations ( $n = 12$ ) respectively. Our findings identified 147 potential *An. funestus* larval breeding habitats across the study area. The fuzzy logic analysis predicted a high degree of similarity (85.03%) in potential breeding habitats between the study years compared to the base year, with a divergence of 14.97%. This study demonstrates the feasibility of using semi-automated methods to detect both permanent and impermanent *An. funestus* breeding habitats under conditions of limited data. The methodologies developed provide a timely, cost-effective tool for enhanced surveillance and management of *An. funestus* mosquito larval breeding, offering valuable insights for stakeholders involved in malaria vector monitoring and control.

### 1. Introduction

Malaria is a deadly vector-borne disease spread by bites from female *Anopheles* mosquitoes carrying the *plasmodium* parasite (WHO, 2021). The disease has claimed many lives globally and resulted in huge costs for its control and management. Between 2017 and 2022, the world witnessed approximately 1.2 billion malaria cases, leading to 3.6 million deaths (WHO, 2023). The burden of the disease heavily falls on Africa, where a vast majority of these cases and deaths occur, underscoring the continent's struggle against malaria. The socio-economic impacts are profound, with billions of dollars spent annually on control and management efforts. These statistics not only highlight the severity of the malaria crisis but also stress the urgent need for effective control

measures to save lives and reduce the economic burden on affected regions (Andrade et al., 2022).

The battle against malaria has been long and arduous, marked by significant milestones since the WHO initiated eradication efforts in 1955. Among the most common strategies, the use of insecticide-treated bed nets and indoor residual spraying have been pivotal in targeting adult malaria vectors (WHO, 2020; WHO, 2022). These approaches have been the cornerstone of global malaria control efforts, credited with saving millions of lives. Recognizing the complexity of malaria transmission which involves both adult mosquitoes and their aquatic larvae, WHO has also advocated for Larval Source Management (LSM) as an integral part of integrated vector management (WHO, 2013). LSM targets the aquatic stages of the malaria vectors, aiming to disrupt the

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lifecycle of mosquitoes before they can become carriers of the disease. While LSM presents a promising avenue for reducing malaria transmission, its implementation has been fraught with challenges. Key among these are weak policies and conflicting interests among stakeholders, which have hampered cohesive and effective action (Innovative Vector Control Consortium, 2017; Gowelo et al., 2020). Additionally, the requirement for intense resources to monitor the spatio-temporal aspects of larval habitats for adequate LSM poses a significant constraint. These challenges underscore the complexity of executing LSM strategies in diverse and often resource-limited settings, highlighting the need for robust policies and coordinated efforts among global health partners. Despite the challenges, there are success stories that showcase the potential of LSM in significantly reducing malaria transmission. Countries like Palestine, Brazil, Egypt, and São Tomé and Príncipe have effectively employed LSM techniques, contributing to the reduction, and in some cases, elimination of malaria (Innovative Vector Control Consortium, 2017; Chen et al., 2019). These LSM efforts have included habitat modification, such as environmental alterations through land reclamation, and habitat manipulation, like clearing vegetation around ponds to disrupt mosquito breeding grounds. Additionally, larvicide which includes the introduction of natural predators like fish to consume mosquito larvae, have proven effective in controlling malaria vectors (WHO, 2013).

The efficacy of LSM strategies in combating malaria hinges on acquiring detailed information about the locations and characteristics of larval breeding habitats (Dambach et al., 2016; Antonio-Nkondjio et al., 2018; Runge et al., 2022). On-field entomological surveys emerge as a pivotal component of LSM, enabling the detailed mapping and characterization of breeding habitats for various *Anopheles* mosquito species. These surveys serve as the cornerstone for designing targeted interventions, making them indispensable in the LSM toolkit. For example, *Anopheles gambiae* s.s., a principal malaria vector, is known to prefer small, temporary water collections like rain puddles, cattle hoofprints, and tyre tracks for breeding (Ndiaye et al., 2020). *An. funestus* another significant vector, opts for more permanent or semi-permanent aquatic environments, both man-made and natural, that have emergent or floating vegetation, such as swamp edges, rivers, and ponds (Nambunga et al., 2020). *An. merus* shows a preference for breeding in saline water habitats (Bartilol et al., 2021), highlighting the species' unique ecological niche. Meanwhile *An. stephensi*, a vector of growing concern due to its adaptation to urban settings, predominantly breeds in artificial water containers, cisterns, and even deep wells (WHO, 2019; Sinka et al., 2020). Notwithstanding, some of these vectors have also been found to share breeding habitats due to factors such as adaptability, seasonal changes and environmental conditions (Jawara et al., 2008; Hinne et al., 2021). Beyond identifying larval breeding habitats, field entomological surveys are crucial for assessing the adult vector population. They provide insights into adult mosquito behaviour, including biting rates, infection rates, and patterns of insecticide resistance (Midega et al., 2012; Tchigossou et al., 2018).

Recent advancements in the study of *Anopheles* larval breeding habitats have employed a variety of methodologies, significantly enhancing our understanding and management strategies for malaria vectors. These methodologies range from traditional field surveys to sophisticated earth observation techniques, each contributing valuable insights for improved LSM efforts. Field surveys remain a fundamental approach, with studies conducting both one-time (Hinne et al., 2021) and time-series surveys (Ndiaye et al., 2020; Forson et al., 2023) to capture temporal variations in habitat availability. However, the labour-intensive nature and time requirements of on-field surveys have led researchers to increasingly rely on earth observation methods. Utilizing geospatial and remote sensing technologies, these methods offer the advantage of covering larger areas and identifying habitat characteristics more efficiently than traditional surveys (Gebreslasie, 2015; Vanhuysse et al., 2023). The characterization of larval breeding habitats through earth observation has incorporated satellite-based analyses of

land use and land cover (LULC), vegetation productivity and dynamics, and digital surface models (Haque, 2007; McCann et al., 2014; Byrne et al., 2021; Jiang et al., 2021; Youssefi et al., 2022a; Vanhuysse et al., 2023). The spatial resolution of the data sets used in these studies varies, ranging from very high (0.5 m Pleiades image, Vanhuysse et al., 2023), to high (5 m Quickbird, Kiszewski et al., 2014, and 5 m SPOT, Haque, 2007), and medium (30 m Landsat 8 image, Jiang et al., 2021).

Ecological niche models (ENM) have majorly been used to establish the suitable habitat of *Anopheles* adults (terrestrial stage). ENM uses various algorithms to predict species (*Anopheles*) distributions based on environmental conditions and *Anopheles* species occurrence data such as machine learning algorithms including Maximum Entropy (MaxEnt) (Kulkarni et al., 2016), Random Forest (RF) (Marston et al., 2023), Artificial Neural Network (ANN) (Gomes et al. 2016), Genetic Algorithm for Rule Set Production (GARP) (Gomes et al. 2016), Boosted Regression Trees (BRT) (Wiebe et al. 2017), Light Gradient Boosting Machine (LightGBM), Decision Tree (DT), Support Vector Machine (SVM) and Multi-Layer Perceptron (MLP) (Javaid et al. 2023). Another algorithm of ENM is BioClimatic envelop model (BioClim) (Kimuyu, 2021). MaxEnt, BioCLim and GARP, use presence-only data of *Anopheles* species while MLP, DT, Light GBM, BRT, ANN, GBM, CART, MDA, MARS, SVM and RF can use presence-absence data. Additionally, MaxEnt, RF, ANN, GARP, GBM, MARS, CART, BRT, LightGBM, DT, SVM and MLP can work with multivariate predictor variables but BioClim only uses climatic variables since it assumes that species (*Anopheles*) distribution is only affected by climatic variables. The requirement of actual larval presence or absence observation data for modelling using these techniques is often a time-consuming and resource-intensive endeavour, especially when covering large geographic areas. This requirement emphasises the ongoing challenge in malaria vector research and control efforts: balancing the need for detailed, accurate habitat characterization with the practical limitations of data collection. However, where sufficient entomological data is available, these data have been coupled with environmental predictors, landscape structures and nearness to landscape features to predict spatial and temporal hot-spots of high abundance *Anopheles* species as a proxy for malaria risk using machine learning techniques (Marston et al., 2023).

To mitigate the challenge of data scarcity in these studies, researchers have turned to techniques such as multi-criteria decision analysis (MCDA), the analytic hierarchy process (AHP) (Vanhuysse et al., 2023) and rule-based methods including expert systems and fuzzy logic algorithm. MCDA facilitates the integration of multiple factors into the decision-making process, allowing for a balanced consideration of all relevant aspects (Taherdoost & Madanchian, 2023). MCDA is particularly useful in scenarios where decision criteria are varied and multi-dimensional, enabling the identification of optimal breeding habitats by evaluating a range of environmental and socio-economic factors (Eastman et al., 1995). On the other hand, AHP focuses on structuring these decision criteria and alternatives into a hierarchical model. It then uses pairwise comparisons to derive preference scales and weightings directly from decision-makers or through expert opinion, providing a quantifiable basis for comparing different habitat characteristics (Taherdoost & Madanchian, 2023). AHP's inclusion of expert judgments and auxiliary ground data for validation ensures that the identified habitats reflect the nuanced understanding of *Anopheles* mosquito breeding preferences and behaviours. Despite the strengths of MCDA and AHP in enhancing the precision of habitat identification, their application is not without challenges. These methods require accurate, reliable, and representative datasets to be effective. Moreover, the inherent limitations of MCDA and AHP in handling a limited range of possibilities restrict their applicability to spatially continuous variables. This limitation heightens the need for careful selection and preparation of decision criteria and the importance of integrating these approaches with other data collection and analysis methods (Greene et al., 2011). Meanwhile, other deductive approaches have been applied to predict malaria risk due to the high cost of collecting entomological field data.

This also entailed model validation using previously collected entomological data, due to the inaccessibility of appropriate entomological data (Youssefi et al., 2022b).

Elsewhere, rule-based methods such as expert systems and fuzzy logic use predefined rules and knowledge about a phenomenon (Zadeh, 1965). However expert systems require accurate data and provide definitive conclusions while fuzzy logic systems produce a range of outcomes giving room for uncertainty and thus can be useful when little or imprecise data on *Anopheles* species is available. In contrast to the traditional binary logic which relies on absolutes (true or false), fuzzy logic considers the degrees of truth, with values ranging from 0 (false) to 1 (completely true). This flexibility makes it particularly useful in modelling complex systems where information is incomplete or imprecise. In the context of malaria research, fuzzy logic has been utilized to model disease risk, considering the uncertain nature of disease transmission dynamics and recovery rates. Notably, studies have applied fuzzy logic to delineate areas at risk of *Plasmodium falciparum* and *Plasmodium vivax* transmission in India, providing insights into malaria risk patterns under conditions of data vagueness and uncertainty (Sarkar et al., 2019). Additionally, in the Democratic Republic of Congo, fuzzy logic has been employed to analyse the dynamics of malaria transmission, accommodating imprecise estimates of transmission and recovery rates (Mangongo et al., 2021). Despite its successful application in disease risk modelling, the use of fuzzy logic in directly modelling malaria vector larval breeding habitats remains unexplored. However, the approach has been documented in the modelling of other insect species, suggesting its potential applicability in identifying and characterizing malaria vector habitats under conditions of limited or uncertain data (Agboka et al., 2022; Landmann et al., 2023; Agboka et al., 2024). The adaptability of fuzzy logic to handle partial truths and imprecise data presents a promising avenue for advancing our understanding of vector ecology and improving LSM strategies.

The majority of studies on larval breeding habitats have focussed on field surveys observing the nature of the habitat, chemical properties of water, vegetation cover, water temperature, soil type, weather and climate characteristics, agricultural activities and presence and abundance of the mosquitoes in these habitats (Ndiaye et al., 2020). Furthermore, studies on larval habitats mainly used machine learning and statistical methods to analyse the relationship of these landscape environmental predictors and the occurrence and or abundance of mosquito species and demonstrate any of the significant predictor(s). Moreover, ENM models have focussed on the adult stage which is terrestrial and mobile often yielding to the prediction of spatial distribution and abundance at a landscape scale, unlike the larval stage which is immobile, requiring larval breeding habitat analysis with point-specific output which is more useful for larval control strategies.

Therefore, there is a lack of methodologies to monitor and model the changes of larval patterns over time, under the constraints of labour and resource intensiveness of conducting time series entomological surveys to study patterns of *An. funestus* larval breeding habitats, as a case study. Thus, this study proposes a novel methodological framework designed to overcome these challenges by leveraging the strengths of MCDA and fuzzy logic under conditions of data scarcity. The approach is aimed at the following,

- i. characterizing, hindcasting, and predicting the persistence or alteration of potential *An. funestus* larval breeding habitats, in malaria-prone regions of western Kenya. Initially, the method employs MCDA techniques to identify potential *An. funestus* larval breeding habitats. This involves the integration of remotely sensed LULC data with edaphic variables such as soil type, slope, drainage, and pH levels. The MCDA framework facilitates the systematic evaluation of these variables to detect habitats most likely to support *An. funestus* larval breeding.
- ii. The study then applies fuzzy logic modelling to assess the stability or variability of the identified larval breeding habitats over time. This

stage utilizes additional remotely sensed spectral indices alongside climatic and topographic variables to evaluate the similarity (habitats that remain consistent throughout the study period) and divergence (habitats that show impermanence at any study time step compared to the baseline year of 2013) of potential breeding habitats. The fuzzy logic approach, with its capacity to handle partial truths and imprecise data, provides a robust tool for predicting the persistence or changes in *An. funestus* larval breeding habitats under varying environmental conditions.

## 2. Materials and methods

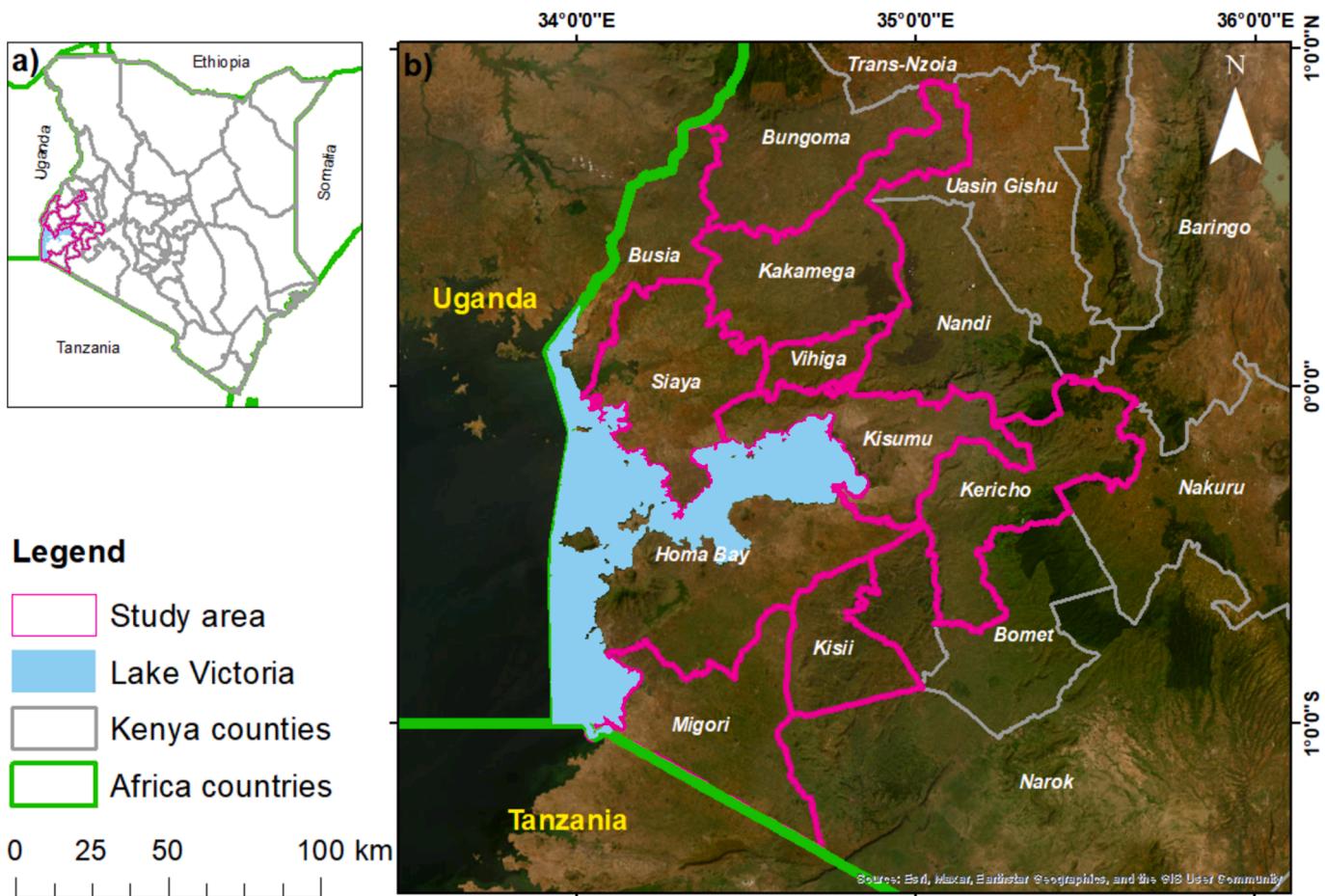
### 2.1. Study area

The focus of this study encompasses various counties within the western region of Kenya (Fig. 1), distinguished by their malaria prevalence rates as either lake-endemic or highland-epidemic areas, according to the Kenya Malaria Indicator Report 2020 (DNMP and ICF, 2021) with observed and georeferenced *An. funestus* species data from readily available data from the Malaria Atlas Project (MAP) and Vector Atlas database. The lake-endemic counties, which include Busia, Vihiga, Kisumu, Migori, Homa Bay, and Siaya, are juxtaposed with the highland-epidemic counties of Kericho and Kisii. Bungoma and Kakamega Counties uniquely straddle both classifications due to their varied geographical and climatic conditions. These regions are characterized by an elevation range of 1,097 m to 2,905 m above sea level (van Zyl, 2001), creating a diverse climate that significantly impacts malaria transmission dynamics. The average temperature fluctuates between 18 °C and 26 °C, with annual rainfall varying from 199.89 mm to 340.25 mm. The relative humidity ranges from very humid (Lakeside) to dry (highland top). In lake-endemic counties, malaria transmission is heavily influenced by climatic factors such as rainfall, temperature, and humidity. These areas experience substantial malaria transmission throughout the year, with *An. gambiae*, a predominant malaria vector, preferring to breed in temporary water accumulations like tyre tracks and cattle hoofprints. The highland-epidemic counties, on the other hand, show marked seasonal and annual variations in malaria transmission. Here, the occurrence of malaria aligns closely with rainfall patterns, peaking during the wet seasons from March to June and from October to November. Even during the dry seasons, malaria transmission persists, primarily through species like *An. funestus*, which prefers to breed in semi-permanent or permanent water bodies (Ndiaye et al., 2020). The economic activities prevalent in these counties, including fishing, rain-fed agriculture, and practices associated with irrigation schemes in Ahero, West Kano, Bunyala, and Bura, inadvertently contribute to the creation of potential breeding habitats for malaria vectors. Such anthropogenic alterations to the environment highlight the intricate relationship between human activity, ecological factors, and the epidemiology of malaria in the region (Rejmánková et al., 2013; Ngenoh et al., 2015). This study specifically focused on Busia, Vihiga, Kisumu, Migori, Homa Bay, Siaya, Kericho, Kisii and Kakamega Counties with readily georeferenced *An. funestus* data from MAP and Vector Atlas database.

### 2.2. Datasets

Our selection of variables for this study was informed by a comprehensive literature review, synthesis, and expert insights on the characteristics of *An. funestus* larval breeding habitats, drawing on key studies (Dambach et al., 2012; Tchigossou et al., 2018; Nambunga et al., 2020). These variables include LULC, edaphic, topographic, climatic and spectral indices. The LULC classification process is in the supplementary section while spectral indices, edaphic, topographic and climatic variables are described below.

#### a) Water-related spectral indices



**Fig. 1.** Illustration of the study's geographical focus within Kenya. a) shows the map of Kenya, highlighting its geographical features, borders, and major cities, b) details the western region of Kenya, identifying the malaria-prone counties specified in the study.

The normalized difference turbidity index (NDTI) is a remotely sensed index used to identify the level of suspended sediments in water, indicating water turbidity (Lacaux et al., 2007). The clarity of water can be reduced with the presence of mud. Thus high level of water turbidity due to mud is negatively associated with the presence of water hence unsuitable for *An. funestus* larval breeding (Dambach et al., 2012). In addition, the normalized difference pond index (NDPI) is a remotely sensed index used to identify surface water bodies (Lacaux et al., 2007). Surface water bodies are potential breeding habitats for *Anopheles* mosquito larvae (Dambach et al., 2012; Ndiaye et al., 2020). Likewise, normalized difference water index McFeeeters (NDWI McFeeeters) utilizes the reflected near-infrared wavelength and visible green light to easily delineate open water features, while reducing the effects of the present soil and earthbound vegetation (McFeeeters, 1996). The NDWI McFeeeters has been demonstrated to be positively correlated with the presence of environmental surface water, which is a conducive habitat for *Anopheles* mosquito larval breeding (Dambach et al., 2012) (Table S3 in supplementary).

#### b) Climatic variables

The climatic variables considered in this study were average temperature, precipitation, day and night land surface temperature, relative humidity, solar radiation, and potential-evapotranspiration. These variables are expounded below and were retrieved from different sources (Table 1).

##### i Average temperature

Temperature is an important component in the growth of *Anopheles* mosquitoes for both egg-laying and development (Charlwood, 2017). For instance, *An. funestus* have been observed to slow-up their return to feeding just after oviposition at temperatures above 26.5 °C. However, with lower temperatures, the female *An. funestus* re-feeds shortly after egg laying (Gillies & Wilkes, 1963).

##### ii Precipitation

Precipitation provides conducive breeding habitats for *Anopheles* mosquitoes to lay their eggs (Alemu et al., 2011). Regions with moderate to low rainfall can provide stable breeding habitats compared to high rainfall thresholds that may wash away the laid eggs (Alemu et al., 2011; McCann et al., 2014).

##### iii Relative humidity

Suitable ranges of relative humidity prolong the survival of the *Anopheles* mosquito (Charlwood, 2017). For instance, when the temperatures are high and relative humidity is very low, there is a high probability of mosquito death. This is due to the disintegration of protein stability and metabolic processes that occur when the *Anopheles* mosquito's body temperature increases (Charlwood, 2017).

##### iv Wind speed

As *Anopheles* mosquitoes lay their eggs in water, strong winds can disturb the water surface. This may impact the behaviour of female mosquitoes when ovipositing and thus affect the stability of larval

**Table 1**

Variables used in the *Anopheles funestus* larval habitat similarity and divergence modelling.

Category	Variables	Resolution	Source/reference	Year
Land	Land use land cover	30 m	Landsat 7 ETM+ from USGS	2013
Edaphic	Soil type	30 m	(ICPAC, 2017)	1997
	Soil pH H <sub>2</sub> O	30 m	(ICPAC, 2017)	1997
	Soil drainage	30 m	(ICPAC, 2017)	1997
Climatic	Soil slope	30 m	(ICPAC, 2017)	1997
	Soil moisture	4 km	(Abatzoglou et al., 2018)	2008, 2013 & 2018
	Relative humidity*	1 km	(Karger et al., 2017)	2008, 2013 & 2018
	Average temperature*	1 km	(Karger et al., 2017)	2008, 2013 & 2018
	Precipitation*	1 km	(Karger et al., 2017)	2008, 2013 & 2018
	Wind speed*	1 km	(Karger et al., 2017)	2008, 2013 & 2018
	Solar radiation*	1 km	(Karger et al., 2017)	2008, 2013 & 2018
	Potential evapotranspiration*	1 km	(Karger et al., 2017)	2008, 2013 & 2018
Topographic	Day Land surface temperature*	1 km	(NASA, 2023)	2008, 2013 & 2018
	Night Land surface temperature*	1 km	(NASA, 2023)	2008, 2013 & 2018
	Elevation*	30 m	SRTM	2008, 2013 & 2018
	Slope*	30 m	SRTM	2008, 2013 & 2018
Spectral indices	Aspect*	30 m	SRTM	2008, 2013 & 2018
	Hillshade*	30 m	SRTM	2008, 2013 & 2018
	Normalized difference vegetation index (NDVI)*	30 m	Calculated from Landsat 7 ETM+	2008, 2013 & 2018
	Normalized difference turbidity index (NDTI)*	30 m	Calculated from Landsat 7 ETM+	2008, 2013 & 2018
	Normalized difference pond index (NDPI)*	30 m	Calculated from Landsat 7 ETM+	2008, 2013 & 2018
	Normalized difference water index (NDWIMcFeeeters)*	30 m	Calculated from Landsat 7 ETM+ (	2008, 2013 & 2018
	Normalized difference water index (NDWI) Gao*	30 m	Calculated from Landsat 7 ETM+	2008, 2013 & 2018
	Distance to settlements	Maximum 500 m	Google Earth Imagery	2013

Note: ICPAC = IGAD Climate Predictions and Applications Centre; SRTM = Shuttle radar topography mission; USGS = United States Geological Survey; ETM+ = Enhanced thematic mapper plus. \* = Variables subjected to exploratory data analysis.

habitats, causing larval mortality or hindering larval development (Midega et al., 2012; Endo & Eltahir, 2018).

#### v Solar radiation

Solar radiation is the energy (electromagnetic radiation) emitted by the sun, affecting atmospheric and climatological processes (Budyko, 1969). The incident solar radiation on the Earth can affect the near-surface water temperatures, which can also affect the suitability of the water surface as a breeding habitat of *Anopheles* (Paaijmans et al., 2008).

#### vi Potential evapotranspiration

This refers to the amount of evaporation that would occur depending on the availability of sufficient water sources. Areas with low potential evapotranspiration have sufficient water sources thus having larger breeding habitats. On the other hand, areas with high potential evapotranspiration have limited water sources, hence breeding habitats of malaria vectors are in small isolated pools of water (Parham et al., 2012).

#### vii Day and night land surface temperature

Land surface temperature (LST) measurement estimates the emission of thermal radiation from the land surface, when energy from the sun interacts with and heats the Earth surface canopy surfaces in vegetated regions (NASA, 2023). Dambach et al., (2012) studied how day and night LST affect *Anopheles* mosquito larval presence and found a positive correlation between night LST and *Anopheles* mosquito larval density.

#### c) Edaphic variables

The composition, texture, water-holding capacity and alkalinity or acidity of soil directly impact adult mosquito breeding and emergence (Multini et al., 2021). Most of the soil dataset used in this study was obtained from ICPAC, and generated by the soil and terrain database for Kenya (KENSOTER), except soil moisture, which was obtained from Terraclimate (Abatzoglou et al., 2018). The attributes of the soil data obtained from ICPAC included soil type (very clayey, clayey, loamy and sandy), soil pH H<sub>2</sub>O (0: strongly acidic to 14: strongly alkaline), soil drainage (poor drainage, well-drained, moderately drained) and soil slope (flat, gentle undulating, steep). These soil datasets available in vector format were rasterized to 30 m by 30 m pixel size resolution to be compatible with the LULC dataset. Soil types such as very clayey and clayey have a high propensity for water retention, unlike sandy soils that have poor water retention capacity, while loam soils can retain water temporarily. Additionally, areas with poorly drained soils and flat slopes also have high water retention capacity, unlike the well-drained, and steep slope areas. The soil pH H<sub>2</sub>O also influences the breeding of *Anopheles* mosquito species. For instance, strongly alkaline soil (pH = 0–3) is best for *An. merus* species, whereas *An. funestus* prefers weakly alkaline (pH = 8–10) or weakly acidic (pH = 4–6) (Nambunga et al., 2020; Bartolol et al., 2021). These edaphic variables affect *Anopheles* larval breeding and have been well documented in the literature (Rejmánková et al., 2013). On the other hand, soil moisture informs the water content available in the pores of the soil. Surface soil moisture was used in this study to retrieve the water content level present in the upper 10 cm of soil, which is the most probable typical surface level of breeding habitats (Patz, 1998).

#### d) Topographic variables

Topographic variables are important drivers in characterizing the potential breeding habitats of malaria vectors including *An. funestus* (Haque, 2007; McCann et al., 2014). They inform on pockets of the land surface that have the potential of water from rain; causing possible

breeding habitats. Topographic variables for this study were obtained from the shuttle radar topography mission at 30 m in the Google Earth Engine (GEE) cloud computing platform.

To ensure spatial compatibility of all the variables, the World Geodetic System 84 (WGS84) reference coordinate represented in latitudes and longitudes was used for all variables. In addition, the climatic and edaphic variables of 1 km x 1 km and 4 km x 4 km spatial resolution were resampled to 30 m x 30 m for compatibility with the spatial resolution of Landsat 7 ETM + satellite imagery LULC and spectral indices datasets. The bilinear resampling method which uses the weighted mean value of the four surrounding area pixels to estimate the ultimate value of a pixel was used (Shivanandappa & Patil, 2018).

### 2.3. Methods

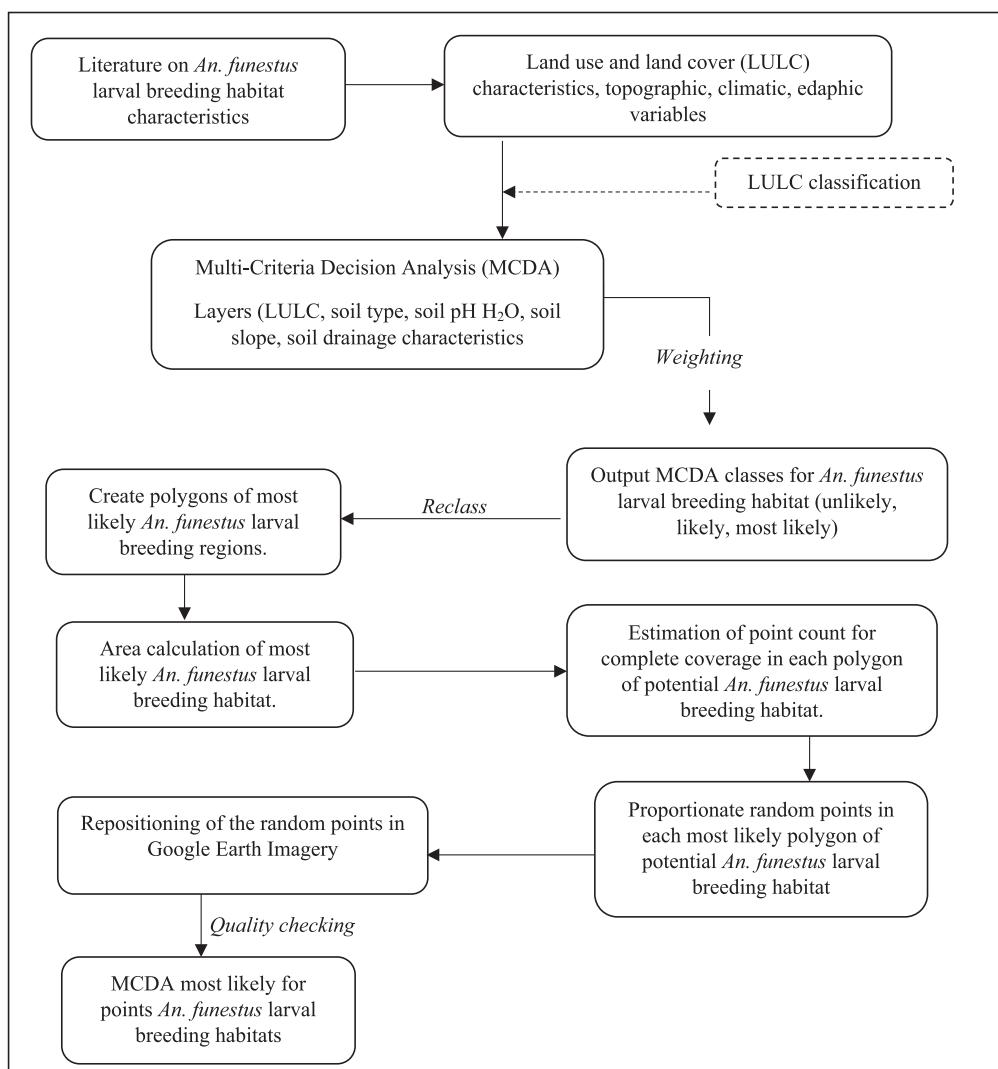
**Fig. 2a** and **Fig. 2b** presents the adopted methodological framework for evaluating the similarities and/or divergence in larval breeding habitats of *An. funestus* during the dry season. This study focused exclusively on the dry season to pinpoint semi-permanent and permanent breeding habitats preferred for *An. funestus*, which are easily findable, utilizing freely accessible remote sensing imagery. In contrast, temporary and smaller breeding habitats mostly appearing in the rainy season, were excluded from this analysis. Meanwhile, permanent habitats are identified as those persisting throughout both the dry and wet

seasons and can be monitored over time.

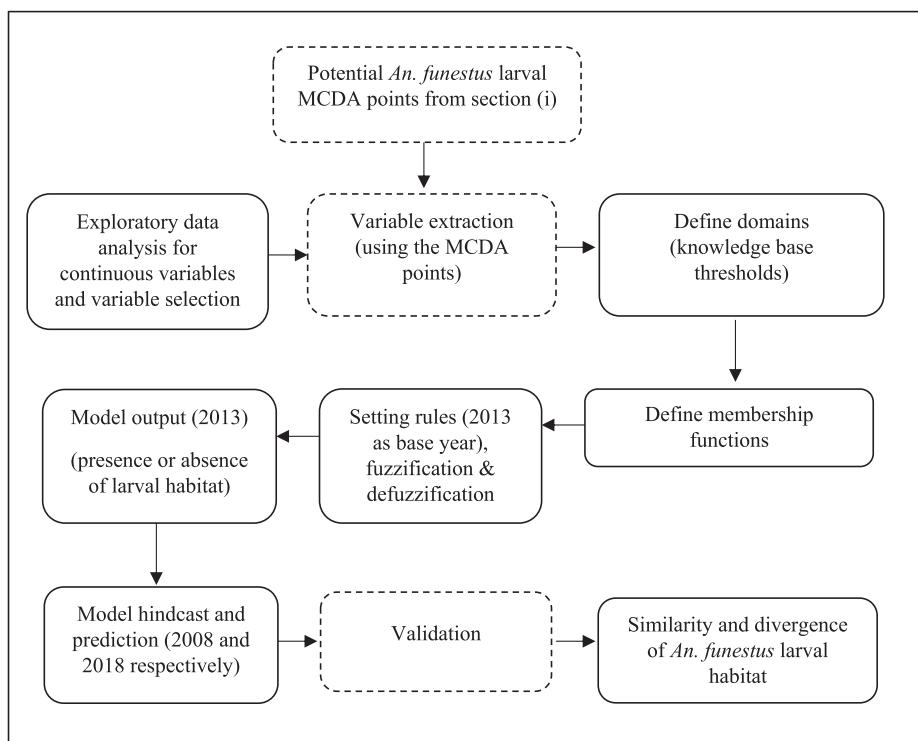
#### 2.3.1. Multi-criteria decision analysis (MCDA)

In this study, MCDA was applied to evaluate the suitability of various environments for *An. funestus* larval breeding. The analysis incorporated variables such as LULC, soil type, soil slope, soil pH H<sub>2</sub>O, and soil drainage. Each variable was assigned a class reflecting its potential to support larval breeding: 1 (unlikely), 2 (likely), and 3 (most likely). These classifications are detailed in **Table 2**. A weighted average of these predictor variables was calculated using the 'raster calculator' tool in QGIS version 3.28.6 ([QGIS.org](#), QGIS 2022). Weights were assigned based on inferred expert knowledge (Nambunga et al., 2020; Ndiaye et al., 2020). For instance, LULC received the highest weight of 0.4 due to its significant influence on mosquito survival, such as providing blood meal sources (human settlements or built-up) and breeding grounds (water bodies and emergent vegetation). Each soil variable was equally weighted at 0.15 with the assumption that each soil characteristic is equally important. Thus, all variables summed up to a total of 1 (100%). To enhance the practical applicability and accuracy of the MCDA output, the class values were rescaled to:

- 1 – 1.75 for 'unlikely'
- 1.75 – 2.55 for 'likely'
- 2.55 – 3 for 'most likely'



**Fig. 2a.** Section (i) methodological approach adopted for the multi-criteria decision analysis (MCDA) for potential *Anopheles funestus* larval breeding habitats.



**Fig. 2b.** Section (ii) methodological approach adopted for the characterization of *Anopheles funestus* larval breeding habitats similarity and divergence using fuzzy logic approach. MCDA = multi-criteria decision analysis.

**Table 2**

Variables and classes assigned for the potential *Anopheles funestus* larval breeding habitats using the multi-criteria decision analysis (MCDA).

Variable	Most likely characteristics	Most likely class assigned	Likely characteristics	Likely class assigned	Unlikely characteristics	Unlikely class assigned
Soil type	Clay, very clayey	3	Loamy	2	Sandy	1
Soil drainage characteristics	Poor drainage, very poor drainage,	3	Imperfectly drained	2	Well drained, moderately drained	1
Soil slope characteristics	Flat, flat-wet	3	Gently undulating,	2	Steep, moderately steep,	1
Land use land cover (LULC)	Croplands, shrublands, natural vegetation, water bodies	3	Bare land,	2	Buildings	1
Soil pH H <sub>2</sub> O	Weakly alkaline, weakly acidic	3	Alkaline	2	Acidic,	1

This rescaling addresses the need for flexibility and precision in the analysis, as well as providing a realistic and inclusive identification of potential breeding habitats for *An. funestus*.

To identify precise locations for potential *An. funestus* larval breeding habitats, we initially generated polygons representing the most likely regions for breeding based on the MCDA outcomes (Fig. S1 in Supplementary). For accurate spatial analysis, these polygons were converted from the World Geodetic System 1984 (WGS84) to the Universal Transverse Mercator (UTM) Zone 37S projection system. This transformation facilitates precise area calculations necessary for subsequent steps. We then calculated the total area of each polygon in square kilometres (km<sup>2</sup>). Proportional random points were then generated within these polygons to identify specific potential breeding habitats. The number of points per polygon was proportional to its area, with a ratio determined by the initial spatial resolution of the climatic variables used in the study (one point per 1 km<sup>2</sup>). For instance, a polygon covering an area of 1 km<sup>2</sup> contained only one point, while larger polygons could contain up to 15 points, resulting in a total of 255 random points.

These points were subsequently overlaid on high-resolution (0.5 m) Google Earth imagery (Google Earth, 2013) to verify their accuracy and relevance. This verification process ensured that each point corresponded to areas identified as suitable *An. funestus* larval breeding

habitats in previous studies, such as those reported by Youssefi et al. (2022a). Considering ecological requirements, each point was evaluated based on its proximity to human settlements—a maximum distance of 500 m was maintained as a proxy for *An. funestus*' blood meal sources (Nambunga et al., 2020; Ndiaye et al., 2020). This assessment refined the selection from the initial 255 points to 184 points deemed suitable for *An. funestus* breeding. A subsequent quality check eliminated redundant points (more than one point within a 1 km<sup>2</sup> area), narrowing the selection down to 147 suitable locations.

### 2.3.2. Validation of multi-criteria decision analysis (MCDA) analysis

Due to the limited availability of observed larval habitat data across the study area, we employed an alternative validation method based on the known flying distances of adult *An. funestus* mosquitoes. This approach leverages adult mosquito presence points to assess the predictive accuracy of our MCDA results. From the Malaria Atlas Project website (<https://malariaatlas.org>), we obtained 136 presence points for adult *An. funestus*. Based on existing entomological research, the maximum flying distance for most *Anopheles* mosquitoes, including *An. funestus*, is generally considered to be 2 km (US EPA, 2013). Accordingly, we generated a 2-km radius buffer around each of these presence points to reflect this typical dispersal range. Additionally, we recognized

the potential for adult mosquitoes to travel further under favourable wind conditions (Kamau et al., 2002; Verdonschot & Besse-Lototskaya, 2014). Thus, we also created a 7-km buffer to account for the maximum downwind flying distance of *An. funestus*. This extended buffer was specifically intended to cover any suitable breeding polygons that might not fall within the standard 2-km range. We hypothesized that the overlap of these buffer zones (2 km or 7 km) with the polygons identified as the most likely larval breeding regions by the MCDA, would indicate the accuracy of our spatial analysis (Equation 1). This intersection provides a crucial validation point: if the polygons where breeding is deemed most likely also correspond to areas within the flying range of adult mosquitoes, it reinforces the predictive validity of our MCDA approach. The results of this validation process are fundamental in confirming the effectiveness of the MCDA method in identifying critical breeding habitats under conditions of data scarcity, thereby supporting targeted malaria vector control interventions.

$$\text{MCDA validation} = \left( \frac{a}{b} \right) * 100 \quad (1)$$

where  $a$  is the total *An. funestus* adult points within the 2 km and 7 km flight buffer distance zones that overlapped/intersected with the most likely *An. funestus* larval habitats polygons/ regions, and  $b$  is the total number of adult *An. funestus* data.

**2.3.3. Exploratory data analysis for fuzzy logic predictor variable selection**  
Exploratory data analysis was undertaken to assess the strength and significance of 17 predictor variables (Table 1) for fuzzy logic modelling. We utilized two primary methods: Principal Component Analysis (PCA) and cluster dendograms. These approaches helped in reducing data dimensionality and understanding the interrelationships among variables. The PCA was employed to reduce the dataset's dimensionality, enabling us to identify which variables contributed most significantly to variance within the dataset (initially, 15 points were identified i.e., five in each category of MCDA class prior to rescaling the MCDA output class values, hence the use of PCA in reducing data dimensionality against the 17 variables). This method is crucial for isolating the most impactful variables in large datasets (Shlens, 2014). Concurrently, a cluster dendrogram was used to discern the hierarchical relationships among the variables, further informing our selection by highlighting groupings based on similar characteristics (Forina et al., 2002). This hierarchical clustering helps in understanding how variables are related at different levels of aggregation and is instrumental in identifying potential redundancy due to collinearity. The key variables identified through PCA (illustrated in Fig. S2 in the supplementary material) were cross-referenced with the cluster groups shown in the dendrogram (Fig. S3 in supplementary). This cross-validation ensures that selected variables are not only significant in explaining the variance but also representative of different clusters, thereby minimizing bias from collinearity and enhancing model accuracy (Barker & MacIsaac, 2022). Despite their varying contributions in the PCA, essential climatic variables known to affect *An. funestus* larval development—such as temperature, precipitation (moisture), and relative humidity—were retained for further analysis. This decision is based on their known biological importance in *An. funestus* rearing conditions in laboratory settings (Tchigossou et al., 2018). Ultimately, the most contributing and non-collinear variables selected for the fuzzy logic modelling experiment to assess potential *An. funestus* larval breeding habitat similarity and divergence included elevation, soil moisture, NDVI, average temperature, precipitation, relative humidity, and solar radiation. (Fig. S3 in the supplementary material).

#### 2.3.4. Fuzzy logic modelling approach

To evaluate potential similarities and or divergences in *An. funestus* larval breeding habitats, a fuzzy logic model was employed, following the principles outlined by Zadeh (1965). This model interprets phenomena on a probability scale from 0 to 1, capturing degrees of truth and

vagueness. The implementation, conducted in a Python Jupyter Notebook environment (version 6.4.8), involved several key steps: defining variable thresholds to categorize larval presence probabilities as unlikely (low conditions), most likely (optimum conditions), or unlikely (high conditions); establishing membership functions to assign fuzzy values to these probabilities; creating rules for applying these functions to classify habitat characteristics; executing fuzzification to convert crisp inputs into fuzzy values and defuzzification to revert fuzzy outputs to precise conclusions; assessing model performance through training and validation; and finally, analysing the similarity and divergence in habitat characteristics. This comprehensive approach allowed for nuanced interpretations of larval habitat data, providing a robust framework for understanding *An. funestus* breeding patterns and informing vector control strategies.

##### a) Defining variable thresholds

To further refine the fuzzy logic model for assessing *An. funestus* larval breeding habitats, a detailed analysis of the selected seven variables was conducted using boxplots in R (version 4.2.2, R Core Team 2022). This step involved visualizing the distribution of the variables' values at the potential breeding habitats identified earlier through the MCDA process. The boxplots provided a clear depiction of the lower and upper bounds for each of the seven variables. Based on the distribution observed in the boxplots, all values lying between the lower and upper bounds were classified as representing optimum conditions for *An. funestus* larval breeding (Table 3). The extremes of these ranges' values below the lower bounds and above the upper bounds were categorized to reflect extreme conditions less conducive to *An. funestus* larval breeding. Specifically, values ranging from the global minimums of the 2013 dataset to the lower bounds observed in the boxplots were classified as low, indicating potentially inadequate conditions for breeding. Conversely, values exceeding the observed upper bounds up to the global maximums of the dataset were classified as high uncondusive, potentially representing excessively harsh conditions. For instance, within the 2013 global dataset, temperature extremes ranged from  $-49.5^{\circ}\text{C}$  to  $35.9^{\circ}\text{C}$ , solar radiation from  $0\text{ W/m}^2$  to  $460.7\text{ W/m}^2$ , precipitation from  $0\text{ mm}$  to  $1769.41\text{ mm}$ , and relative humidity from 27.09% to 100%. Elevation extremes were from sea level to 8,424 m above sea level. NDVI values, which range from  $-1$  to  $1$ , were also standardized to match this framework. These categorizations and visualizations facilitated a detailed understanding of environmental variables affecting *An. funestus* breeding habitats, enabling precise threshold settings for the fuzzy logic model used in subsequent analyses.

##### b) Defining linguistic variables and membership functions

Membership functions are a fundamental component of fuzzy logic models, used to quantify the uncertainty in evaluating the similarity and

**Table 3**

Variable thresholds of potential *Anopheles funestus* larval breeding habitats for the base year of 2013.

Variable	Low (Unconducive)	Optimum (Conducive)	High (Unconducive)
Elevation (m)	$0 - 1,134$	$1,134 - 1,913$	$1,913 - 8,424$
Soil moisture ( $\text{m}^3\text{m}^{-3}$ )	$0 - 31.06$	$31.06 - 102.09$	$102.09 - 654.50$
NDVI	$-1 - 0.17$	$0.17 - 0.75$	$0.75 - 1$
Average temperature ( $^{\circ}\text{C}$ )	$-49.5 - 18.67$	$18.67 - 24.68$	$24.68 - 35.90$
Precipitation (mm)	$0 - 28.64$	$28.64 - 118.05$	$118.05 - 1769.41$
Relative humidity (%)	$27.09 - 50.84$	$50.84 - 62.04$	$62.04 - 100$
Solar radiation ( $\text{Wm}^{-2}$ )	$0 - 210.60$	$210.60 - 236.50$	$- 460.70$

or divergence of potential *An. funestus* larval breeding habitats. These functions graphically represent the degree of truth as a value between 0 and 1 for each data point within the dataset, as established by Zadeh (1965). Triangular membership function was chosen for its simplicity and effectiveness in categorizing data into defined classes (Pedrycz, 1993). The triangular membership function is characterized by three parameters: the lower and upper bounds, which define the edges of the triangle, and the midpoint, which represents the peak or the point of maximum membership. This setup is particularly useful for modelling phenomena where data points are expected to peak around a central value. In our model, these functions were applied to the environmental variables influencing *An. funestus* larval breeding, with a 50% overlap between adjacent categories of 'low' (uncoductive) 'optimum' conducive and 'high' uncoductive thresholds to ensure a smoother transition between categories. The applied triangular membership functions for each variable are visually represented in Fig. S4 in the [supplementary materials](#). This illustration provides insights into the fuzziness of the habitat suitability classification for *An. funestus* breeding.

#### c) Formulation of Fuzzy logic rules for selected variables

In the fuzzy logic model, rules were specifically formulated for the seven selected variables critical to determining the potential *An. funestus* larval breeding habitats. These rules incorporate different logical connectives to cater to varying levels of inference strictness, which directly affects the model's sensitivity and specificity. The rules included ORs only (very flexible), a combination of ANDs and ORs (flexibility and strictness) and ANDs only (very strict) logical connectives. The specific rules applied within the model are summarized in Table 4, which outlines the parameters and conditions associated with each rule set. For a more detailed representation and further elaboration of these rules, refer to Table S4 in the [supplementary materials](#).

#### d) Fuzzification and defuzzification

The model development involved two critical processes: fuzzification and defuzzification, essential for transforming numeric data into actionable insights. Fuzzification is the transformation of crisp (numeric) variable values into linguistic terms (e.g., unlikely (low conditions), unlikely (high conditions), and most likely (optimum conditions)) that describe the probability of *An. funestus* larval breeding habitat suitability. This step converts quantitative measurements into qualitative descriptors, which are more suitable for fuzzy logic analysis.

**Table 4**  
Summary of fuzzy logic rules and their definition.

	Threshold	Elevation			Soil moisture			NDVI			Average temperature			Precipitation			Relative humidity			Solar radiation			
		L <sup>U</sup>	H <sup>U</sup>	O	L <sup>U</sup>	H <sup>U</sup>	O	L <sup>U</sup>	H <sup>U</sup>	O	L <sup>U</sup>	H <sup>U</sup>	O	L <sup>U</sup>	H <sup>U</sup>	O	L <sup>U</sup>	H <sup>U</sup>	O	L <sup>U</sup>	H <sup>U</sup>	O	
Elevation	L <sup>U</sup>					-	-		-	-		-	-		-	-		-	-		-	-	
	H <sup>U</sup>				-		-	-		-	-		-	-		-	-		-	-		-	-
Soil moisture	Optimum																						
	L <sup>U</sup>	&	-	-																			
	H <sup>U</sup>	-	&	-																			
NDVI	Optimum	-	-	&																			
	L <sup>U</sup>	&	-	-																			
	H <sup>U</sup>	-	&	-																			
NDVI	Optimum	-	-	&																			
	L <sup>U</sup>	&	-	-																			
	H <sup>U</sup>	-	&	-																			
Average temperature	Optimum	-	-	&																			
	L <sup>U</sup>	&	-	-																			
	H <sup>U</sup>	-	&	-																			
Precipitation	Optimum	-	-	&																			
	L <sup>U</sup>	&	-	-																			
	H <sup>U</sup>	-	&	-																			
Relative humidity	Optimum	-	-	&																			
	L <sup>U</sup>	&	-	-																			
	H <sup>U</sup>	-	&	-																			
Solar radiation	Optimum	-	-	&																			
	L <sup>U</sup>	&	-	-																			
	H <sup>U</sup>	-	&	-																			

Note: | = OR, & = AND, L<sup>U</sup> = Low uncoductive, H<sup>U</sup> = High uncoductive, O = optimum conducive, NDVI = Normalized difference vegetation index. No rules are applied on the grey shaded regions with diagonal line and areas cells with dash (-).

Once the data is fuzzified, the output, which is in linguistic form, must be converted back into a numeric value, a process known as defuzzification. Several methods (centre of gravity (COG), weighted average, and maxima methods, centre of sums (COS), centre of area/bisector of area (BOA)); are utilized for defuzzification, each with specific applications and advantages. For our purposes, the Centroid of Area method was selected due to its ease of interpretation and broad applicability. This method effectively balances the contributions of all parts of the membership function, providing a well-rounded output that reflects the composite influence of all input variables (Agboka et al., 2022; Landmann et al., 2023).

#### e) Training performance assessment of fuzzy logic classification model

An overall training performance assessment of the fuzzy logic rules was performed using equation (2) (Bartholomew, 2011).

$$\text{Training performance} = \left( \frac{c}{d} \right) * 100 \quad (2)$$

where  $c$  is the number of habitats correctly classified by the model as the most potential *An. funestus* larval breeding habitats from the defuzzified output for the years under study i.e., 2008 and 2018 and  $d$  is the total number of potential *An. funestus* larval breeding habitats considered for training as obtained from the base year 2013.

#### f) Similarity and divergence of *Anopheles funestus* larval breeding habitat characteristics

Defuzzified values for the potential *An. funestus* breeding habitats with 2008 and 2018 variable values which related to most likely (optimum conditions) (0.55–1) were pronounced to have similar characteristics with respect to the base year potential *An. funestus* breeding habitats points. However, defuzzified values for the potential *An. funestus* breeding habitats with 2008 and 2018 variable values of unlikely (low conditions) (0–0.35) or unlikely (high conditions) (0.35–0.55) were classified as divergent in relation to the base year. Furthermore, the similarities and or differences of the minimum and maximum variable thresholds were compared between the base year 2013 and the 2008 and 2018 thresholds.

#### g) Fuzzy logic model validation

To validate the fuzzy logic model used to assess potential *An. funestus*

larval breeding habitats, we sourced validation data from published malaria research accessible via the Malaria Atlas Project (<https://malariaatlas.org>). The selection criteria targeted studies conducted during the dry season, specifically in January, from 2000 to 2023. This period was chosen to align with the seasonal timing used in our fuzzy logic modelling, ensuring consistency in environmental variables across both datasets. The dry season and specifically the month of January was selected to be consistent with the month and season used for the fuzzy logic modelling experiment. Inspection of these studies yielded sampled locations of *An. funestus* larval breeding habitats in 2004 ( $n = 7$ ) and 2007 ( $n = 5$ ) from Howard et al. (2007), Howard & Omlin (2008) and Fillinger et al. (2009). The centroid points of these areas were available from MAP database with a georeferenced accuracy of 25 km – 100 km. Thus, appropriate buffer for each centroid were created. Consequently likely *An. funestus* breeding habitats points within the buffered zones were positioned as validation points. Thereafter, validation of the fuzzy rules on similarity and/or divergence of most likely potential *An. funestus* larval breeding habitat points between 2008 and 2018 against the base year were carried out using equation (3) (Bartholomew, 2011). The rule with the best performance of flexibility and strictness with accuracy equal to or greater than 70% across all the years under study was selected.

$$\text{Validation accuracy} = \left( \frac{g}{h} \right) * 100 \quad (3)$$

where  $g$  is the number of breeding habitats in the validation data set that were correctly classified by the fuzzy logic model as *An. funestus* larval breeding habitats and  $h$  is the total number of breeding habitats considered for validation, for the years 2004 and 2007.

#### h) Spatial visualization

To further analyse the performance of the selected fuzzy rule, maps were created to visually represent the patterns of most likely potential *An. funestus* larval breeding habitat points. These maps illustrated both similarity and divergence from the best-performing rule in the years 2008 and 2018 compared to the base year of 2013. This spatial visualization helps in understanding the spatial distribution and temporal consistency of the model predictions, providing a clear visual representation of areas where the model performed well and areas where discrepancies occurred.

### 3. Results

#### 3.1. Land use and land cover (LULC) classification

The overall accuracy (OA) of the LULC classification was found to be 90.31%, which indicates a high level of accuracy in the classification process. Additionally, the Quantity and Allocation Disagreement Index (QADI) was calculated to be 0.17, suggesting a moderate level of disagreement or uncertainty in the classification (Figures and tables referenced are included in supplementary materials: Fig. S5, Table S5, and Table S6). The classified data reveals a diverse landscape composition within the study area, with cropland being the most prevalent type of land cover, accounting for 39.02% of the area. This is followed by trees/forest, which cover 29.57% of the area, and water bodies, which make up 16.64% (Table S7 in supplementary). The results highlight the significant presence of ecological features that could influence the distribution and breeding of *An. funestus*, providing essential insights for vector control strategies.

#### 3.2. Multi-criteria decision analysis (MCDA)

The MCDA successfully identified 147 points as the most likely potential *An. funestus* larval breeding habitats. Analysis of the geographic distribution of these points shows they are primarily located in varying

aquatic environments: swampy areas accounted for 26 points, river beds comprised the majority with 73 points, and ponds represented 48 points. These habitats included both natural and man-made water bodies. Spatial analysis revealed that the highest concentrations of potential breeding habitats were predominantly in the northern and central parts of the study area (Fig. 3). Importantly, a significant portion of the larval habitats identified through MCDA overlapped with locations from the validation dataset: out of 136 points in the validation dataset, 82 (60.29%) were situated within the polygons predicted as most likely breeding habitats by the MCDA. This overlap indicates a substantial agreement between the MCDA model predictions and the observed data, emphasizing the effectiveness of the MCDA approach in pinpointing potential larval breeding habitats.

#### 3.3. Fuzzy logic model

##### 3.3.1. Training performance assessment

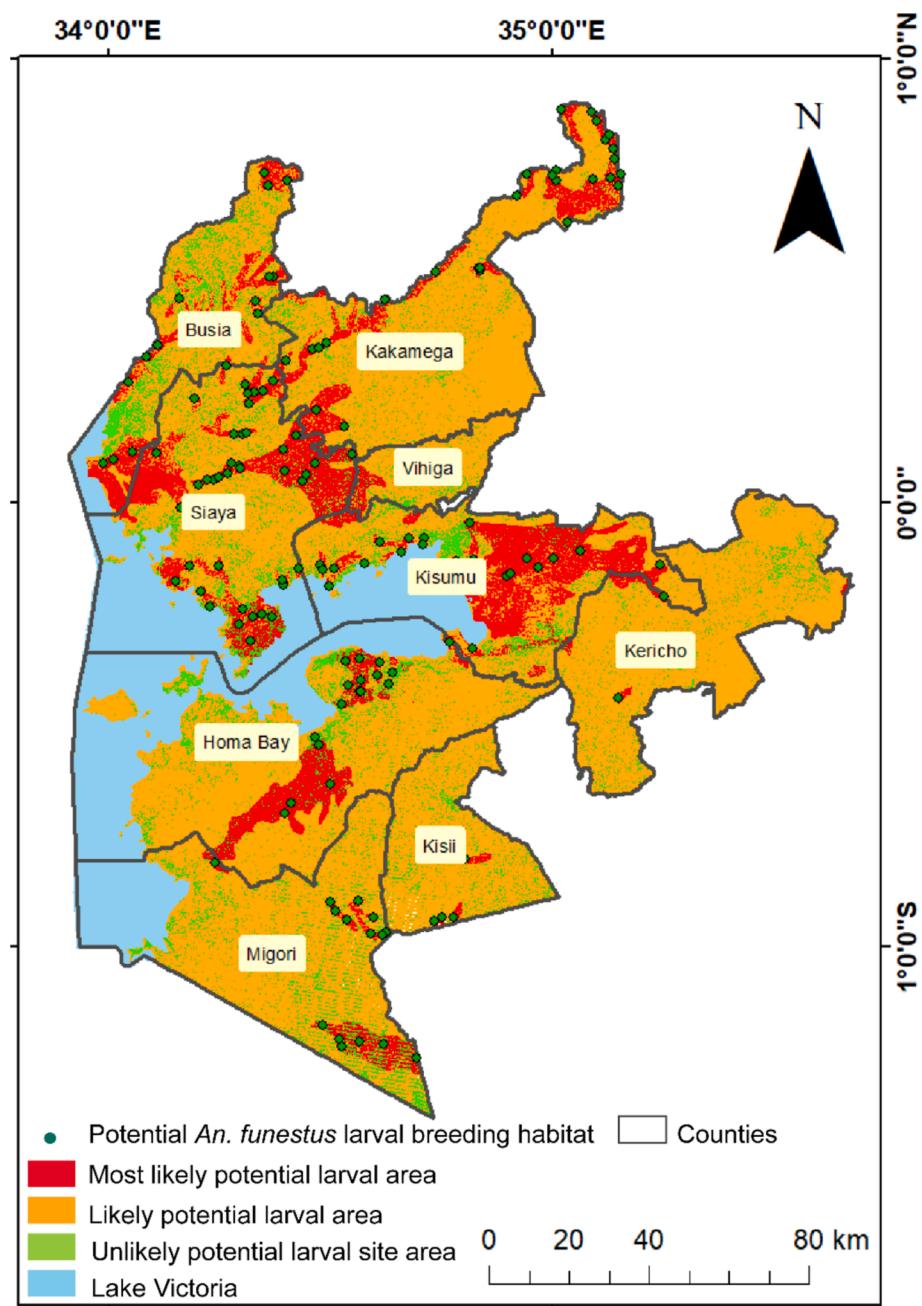
In the analysis of the fuzzy logic model, the defuzzified outputs for Rule option no. 0, 1, and 2 showed a 100% classification rate for locations as the most likely *An. funestus* larval breeding habitats. Conversely, Rule no. 6 demonstrated significantly different results, with less than 5% of its defuzzified values classified as the most likely breeding habitats for the years 2008 and 2018. This stark contrast highlights the variability in rule performance and highlights the importance of rule selection based on specific model goals and data characteristics. It is important to note that the results for the base year of 2013 are not included in this summary. The 2013 data were used to establish the initial thresholds for the fuzzy logic process, serving as a reference point for evaluating the effectiveness of the rules in subsequent years. These results are detailed further in Table 5, which presents a comprehensive overview of the defuzzification outcomes across different rules and assessment years.

##### 3.3.2. Validation of fuzzy logic model rules

The assessment of the fuzzy logic rules revealed consistent and highly effective results for the year 2004, with all rules achieving a 100% accuracy rate in identifying existing *An. funestus* larval breeding habitats. This indicates that the chosen parameters and conditions for the fuzzy logic model were highly suitable for the data from this year. In contrast, the performance varied in the year 2007. Only rules numbered 0, 1, and 2 maintained a 100% success rate, mirroring their effectiveness as observed in 2004. However, rule number 6, characterized by its use of all ANDs which represents a very strict approach, showed the lowest performance, underscoring the potential limitations of applying overly stringent criteria in variable ecological conditions. Rule option no. 3, designed to balance strictness with flexibility, demonstrated robust performance with an 80% accuracy rate in 2007. This rule's relatively high success rate highlights the efficacy of a balanced approach in fuzzy logic rule design, especially in fluctuating or less predictable environmental settings. These results are detailed in Table 6.

#### 3.4. Similarity and divergence of *Anopheles funestus* larval breeding habitat characteristics

In examining spatiotemporal patterns of potential *An. funestus* larval breeding habitats across 2008, 2018, and the base year 2013, we found that 125 habitats displayed similar environmental characteristics, adhering to the thresholds established in 2013. Conversely, 22 larval habitats in 2008 and 2018 diverged from these base-year thresholds. Specifically in 2008, habitats with similar characteristics exceeded the maximum threshold for solar radiation, while the minimum for soil moisture, precipitation and NDVI fell below the base year's figures. In 2018, similar larval habitats only breached the minimum soil moisture below the 2013 threshold, with maximum values for NDVI and solar radiation surpassing those of the base year. Divergent habitats in 2008 showed minimum values for soil moisture, NDVI, precipitation, and relative humidity below 2013 thresholds, with solar radiation exceeding



**Fig. 3.** The most likely, likely and unlikely areas for *An. funestus* larval breeding habitats in malaria-prone counties in the western region of Kenya obtained from the multi-criteria decision analysis (MCDA) overlaid with Lake Victoria.

**Table 5**

Summary of fuzzy rules and the model training performance evaluation. The total number of data points was 147.

Rule option No.	Correctly classified 2008 (%)	Correctly classified 2013 base year (%)	Correctly classified 2018 (%)
0	147 (100%)	147 (100%)	147 (100%)
1	147 (100%)	147 (100%)	147 (100%)
2	147 (100%)	147 (100%)	147 (100%)
3	125 (85.03%)	146 (99.31%)	125 (85.03%)
4	132 (89.79%)	146 (99.31%)	125 (85.03%)
5	109 (74.14%)	145 (98.63%)	18 (12.24%)
6	1 (0.59%)	114 (77.55%)	6 (4.08%)

**Table 6**

Validation of fuzzy rules for 2004 and 2007 data points and classification performance.

Rule No.	Total points (2004)	Classification performance (2004)	Total points (2007)	Classification performance (2007)
0	7	7 (100%)	5	5 (100%)
1	7	7 (100%)	5	5 (100%)
2	7	7 (100%)	5	5 (100%)
3	7	7 (100%)	5	4 (80%)
4	7	7 (100%)	5	2 (40%)
5	7	7 (100%)	5	1 (20%)
6	7	0	5	0

them. In 2018, divergent characteristics included precipitation minimum and minimum relative humidity alongside higher maximum solar radiation. In the divergent breeding habitats, minimum solar radiation for 2008 and both minimum and maximum solar radiation for 2018 exceeded the maximum threshold of the base year 2013.

Geographically, similar breeding habitats between January 2008 and 2018 compared to 2013 were mostly located in counties such as Migori, Busia, Kericho, Kisumu, Siaya, Vihiga, and Kisii, while habitats showing divergence were predominantly in Kakamega County. This spatial and temporal analysis of habitat characteristics informs targeted malaria control strategies and is detailed in Table 7 and visualized in Fig. 4.

## 4. Discussion

### 4.1. Overview of the study

This study undertook a comprehensive analysis of the similarity and divergence among potential *An. funestus* larval breeding habitats as a focused use case. With the emphasis on the critical need for efficient surveillance methods in malaria vector control, our research highlights the utility of resource-friendly and time-saving approaches like MCDA and fuzzy logic algorithms. These methodologies proved instrumental in identifying potential breeding habitats and examining their changes over time offering valuable insights for LSM strategies. The use of MCDA allowed for the systematic evaluation of various environmental variables to pinpoint locations most likely to support *An. funestus* larval development. Following this, the fuzzy logic algorithm facilitated an assessment of how these habitats have evolved or remained consistent over time, factoring in ecological variables known to influence *An. funestus* breeding success. This dual-approach not only enhances the precision of habitat identification but also adjusts for spatiotemporal ecological variations that could impact LSM efforts. The variables selected for analysis were those most critical to the ecology of *An. funestus*, ensuring that the habitats identified are both ecologically relevant and likely to be true breeding grounds. The integration of these ecological factors into our model experiments reinforces the importance of tailored surveillance and control measures that adapt to the ecological realities of malaria vectors.

### 4.2. Multi-criteria decision analysis (MCDA) and fuzzy logic modelling approaches

The study has successfully delineated the most likely potential larval breeding habitats for *An. funestus*, predominantly located in the northern and central regions of the study area, which include counties such as Migori, Busia, Kericho, Kisumu, Siaya, Vihiga, Kakamega, and Homa Bay, with additional habitats in the southern and south-eastern sections like Kisii and Kericho. These regions are characterized by ecologically

favourable conditions such as cropland, irrigation areas, and predominantly clay soils, which facilitate mosquito larval development. This finding aligns with Rejmánková et al. (2013) who reported similar characteristics conducive to mosquito breeding. Moreover, the identified potential habitats were typically situated in swampy areas, riverbeds, and ponds encompassing both natural and man-made water bodies. This corresponds with field observations from larval habitat studies in Tanzania and Ethiopia as documented by Getachew et al. (2020) and Kahamba et al. (2024), emphasizing the ecological consistency across different geographic locations. These habitats are significantly influenced by the proximity to Lake Victoria and the presence of multiple irrigation schemes and rivers such as Nyando, Yala, Sio, Sondu Miriu, and Migori. Other geographical features contributing to these habitats include areas with poorly draining soils and regions with flat or gentle slopes, which are ideal for sustaining water pools necessary for mosquito larvae (Minakawa et al., 2012; Ndiaye et al., 2020). Conversely, areas identified as less suitable for *An. funestus* breeding typically featured sandy-textured soils, which are highly permeable and thus less likely to retain water, rendering them unsuitable for sustaining mosquito larvae (Ndiaye et al., 2020). Furthermore, to minimize potential autocorrelation and enhance the integrity of the data analysis, this study intentionally limited the inclusion of potential breeding habitats to one per 1 x 1 km area. This decision, while necessary to reduce redundancy and potential bias, means that the identified 147 habitat points do not represent an exhaustive list but rather a strategic sampling, emphasizing the study's focused approach to identifying and analysing potential *An. funestus* larval breeding habitats.

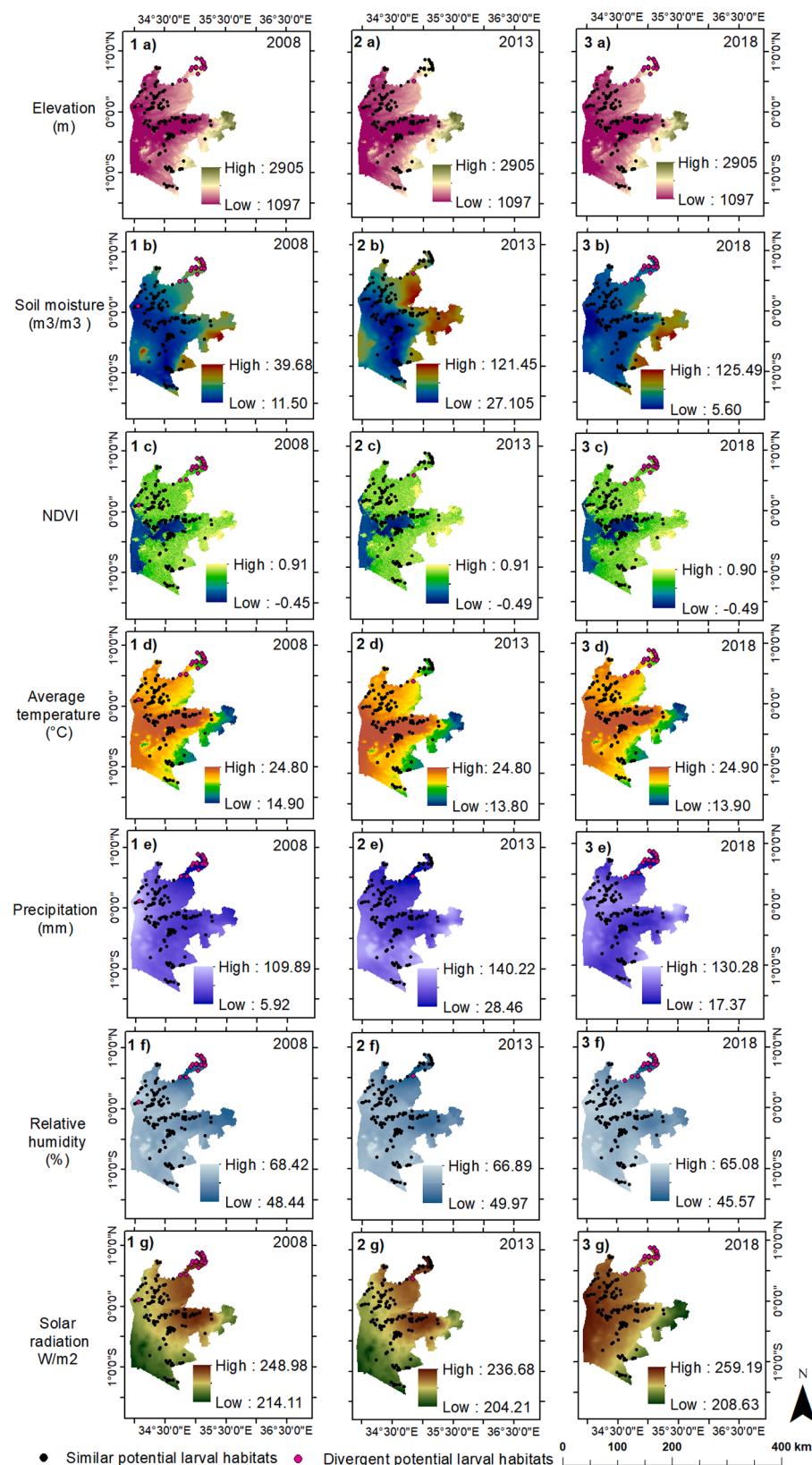
The application of a buffer based on the flight distance of *An. funestus* adults served as a pragmatic validation approach for our MCDA model, given the limited availability of directly surveyed larval breeding habitats data. This method yielded a validation accuracy of 60.29%. Although this figure may not represent an exceptionally high level of precision, the performance of MCDA model is robust since, we deliberately avoided extending the MCDA scales to prevent generalization and potential overfitting, which could distort the true efficacy of the model. Furthermore, we recognize that the methods used to sample the adult *An. funestus* population such as preferential or purposeful sampling might compromise the diversity and representativeness of the larval data. These sampling strategies are often dictated by the constraints of time and available resources, which may bias the outcomes. In contrast, employing systematic sampling designs could potentially offer a more comprehensive view of the *An. funestus* population and their breeding habitats. This approach would likely enhance the accuracy and reliability of our estimations concerning larval breeding habitats, facilitating more effective and targeted vector control strategies. Where quality georeferenced field data on larval population is available, future studies can explore the use of other methodologies of evaluating risks of larval habitat breeding such as Weights of Evidence and Statistical index models to further improve the modelling results. Weights of Evidence

**Table 7**

Summary of minimum and maximum thresholds of similar and divergent *Anopheles funestus* potential larval breeding habitat points obtained from fuzzy rule option no. 3: Elevation AND Soil moisture AND NDVI AND Average temperature OR Precipitation OR Relative humidity OR Solar radiation.

	Similar potential <i>An. funestus</i> larval breeding habitats						Divergent potential <i>An. funestus</i> larval breeding habitats					
	Minimum threshold			Maximum threshold			Minimum threshold			Maximum threshold		
	2008	2013	2018	2008	2013	2018	2008	2013	2018	2008	2013	2018
Elevation (m)	1134	1134	1134	1866	1913	1788	1145	1134	1323	1913	1913	1913
Soil moisture ( $m^3 m^{-3}$ )	<b>12.45</b>	31.06	<b>8.06</b>	29.32	102.09	85.83	<b>13.73</b>	31.06	31.74	29.02	102.09	38.67
NDVI	<b>0.15</b>	0.17	0.17	0.75	0.75	0.78	<b>0.14</b>	0.17	0.17	0.68	0.75	0.65
Average temperature (°C)	18.93	18.67	18.67	24.60	24.68	24.59	19.68	18.67	19.76	23.50	24.68	23.57
Precipitation (mm)	<b>9.30</b>	28.64	33.88	105.85	118.05	91.25	<b>5.951</b>	28.64	<b>17.85</b>	98.49	118.05	33.22
Relative humidity (%)	51.51	50.84	51.53	61.71	62.04	60.47	<b>49.57</b>	50.84	<b>45.73</b>	61.61	62.04	50.84
Solar radiation ( $Wm^{-2}$ )	219.59	210.60	222.65	<b>245.78</b>	236.50	<b>256.09</b>	228.36	210.60	<b>241.47</b>	<b>248.88</b>	236.50	<b>248.04</b>

Note: The bold italic values are out of range of minimum or maximum thresholds of potential *An. funestus* larval breeding habitats in 2008 and 2018 vis-à-vis the minimum and maximum thresholds of the base year of 2013.



**Fig. 4.** Similar and divergent potential *Anopheles funestus* larval breeding habitats of fuzzy rule option no. 3 (Elevation AND Soil moisture AND NDVI AND Average temperature OR Precipitation OR Relative humidity OR Solar radiation) in 2008 and 2018 variables against variables of the base year (2013). NDVI = normalized difference vegetation index.

and Statistical index models techniques have been successfully used to model groundwater potential and predict wild fire risk with ground observation data (Khoshtinat et al. 2019; Salavati et al. 2022).

Elevation, soil moisture, NDVI, average temperature, precipitation, relative humidity and solar radiation were methodically selected for this study. This selection corroborates some of the variables that depicted the peak *Anopheles* presence period in Youssefi et al. (2022b), i.e., precipitation, NDVI and soil moisture. Likewise, precipitation and soil moisture were among the critical variables in malaria vector abundance and malaria risk prediction in Marston et al. (2023). The selection of a fuzzy logic rule-based method for this study was particularly advantageous due to its effectiveness in environments where data is either scarce or of poor quality, as well as its capability to process approximate or incomplete data sets (Zadeh, 1965). This attribute is critical, as fuzzy logic accommodates degrees of truth instead of binary true/false outcomes, thus enabling decision-making under conditions of uncertainty or ambiguity. This flexibility is particularly crucial in ecological studies where precise data may be lacking (Zadeh, 1965). Among the various fuzzy logic rules tested, rule option no. 3, which combines multiple ecological factors (Elevation AND soil moisture AND NDVI AND average temperature OR precipitation OR relative humidity OR solar radiation), proved to be the most robust. It maintained a balance between flexibility and strictness, yielding a validation accuracy exceeding 80% across various scenarios. This rule successfully identified 125 (85.03%) of the 147 potential breeding habitats in 2008 and 2018 that had characteristics like those observed in 2013. Notably, many of these habitats were located within ecosystems such as Lake Victoria, known for its persistent ecological features conducive to harbouring malaria vectors like *An. gambiae* as well as irrigation areas that consistently provide favourable conditions for larval breeding (Minakawa et al., 2012; Mwangangi et al., 2010). These irrigation areas allude to the effect of agricultural areas on malaria vector breeding habitats.

Approximately 15% of the habitats (22 out of 147), primarily situated in the northern regions of Kakamega County, displayed characteristics in 2008 and 2018 that diverged significantly from the 2013 baseline. These divergences were largely found in riverbeds and ponds, where environmental changes such as drying can significantly impact habitat suitability. The unexpected divergence in habitats along the perennial River Nzoia was attributed to reduced stream flow during dry seasons, leading to dry river beds (Odira et al., 2010; Asare et al., 2016). Moreover, the similarity or divergence of the field larval habitat survey can also be affected by malaria vector control methods such as LSM and insecticide use as well as human population changes. Nonetheless, LSM efforts have not been consistently implemented while insecticide resistance of the malaria vectors has been reported in the study area (MoH, 2019). In addition, the human population changes proxied by built-up areas were assumed not to have significant changes over the five-year time step of our modelling. Thus, the dynamics of malaria intervention and human population changes did not significantly impact our results. In addressing the issue of data scarcity in malaria vector studies, this present study corroborates Youssefi et al. (2022b) who predicted high-risk times for growth and survival of malaria vectors using environmental factors in GEE and validated with previous entomological data.

This study successfully demonstrates an innovative approach to identifying patterns of *Anopheles* mosquito larval breeding habitat similarity and divergence, particularly under conditions of data scarcity. By enabling the efficient mapping of potential breeding habitats, this methodology conserves time and resources for entomologists and malaria health experts, allowing them to focus on validating the presence of larvae and their abundance in these pre-identified habitats. This efficiency is crucial for enhancing targeted LSM. Significantly, the findings of this study can greatly enhance the surveillance of *Anopheles* mosquito larval breeding habitats. For instance, the results support targeted LSM efforts such as the sustainable removal, of water hyacinth from Lake Victoria, which has been used creatively in the production of

mushrooms (Djègbè et al., 2020). This study also acknowledges the complexities of implementing intermittent flooding in rice irrigation areas, a strategy that, while effective at reducing vector breeding, could negatively impact rice production and thus food security (Eriksen et al., 1985). This highlights the need for sustainable solutions that balance vector control with agricultural productivity. Moreover, the success of LSM strategies hinges on sustained funding, commitment, and continuous monitoring (Innovative Vector Control Consortium, 2017). While this study provides a robust methodological framework for under-resourced settings, it also reaffirms the critical role of comprehensive on-field entomological surveys. Accurate collection of data, including the geolocation of *An. funestus* breeding habitats and water physiochemical properties is essential for refining and enhancing the predictive accuracy of future models. Thus, while advancing artificial intelligence and modelling techniques for predicting breeding habitats, the integration of detailed field data remains indispensable for the holistic understanding and management of malaria vector habitats.

#### 4.3. Limitations

Although shared larval breeding habitats of some malaria vectors can be modelled using our approach, incorporating the distinct breeding characteristics of some malaria vector species (e.g., larval breeding salinity levels for *An. merus* and *An. funestus*) into a generalized model is inherently complex (Rejmánková et al., 2013). Additionally, the use of freely available datasets with spatial resolutions ranging from medium (30 m) to coarse (4 km) has potentially limited the accuracy of point-specific variable observations at potential *An. funestus* larval breeding habitats. This resolution disparity may impact the precision with which these habitats are identified and characterized. Wind direction was not incorporated in our model, with the assumption that wind direction also influences temperature of the landscape. While wind direction may be changed very rapidly due to sea breeze within Lake Victoria (Ssebuggwawo et al., 2024), we are convinced that the wind direction at the time of the entomological survey conducted by previous studies was favourable to avail capturing of larval and adult vectors. However, future studies can explore the direct impact of wind direction on the breeding habitats to further improve the model representation.

Notwithstanding, the study made concerted efforts to utilize the best available data and methodologies to develop a robust model for analysing the similarity and divergence of potential *An. funestus* larval breeding habitats under conditions of data scarcity. With the adaption to the constraints imposed by available resources and data, this research contributes significantly to the field of vector control and malaria management, offering a strategic approach to address gaps in knowledge and capabilities in resource-limited settings. Our methodology not only enhances our understanding of *An. funestus* vector breeding habitats but also aids in refining strategies for effective larval source management for *An. funestus*, thereby supporting broader efforts to combat malaria.

#### 5. Conclusions

This study has developed a robust methodology for modelling the similarity and divergence of potential *Anopheles funestus* mosquito larval breeding habitats, in the context of data scarcity within lake endemic and highland epidemic malaria regions in Kenya. This approach enables the semi-automatic monitoring of potential larval breeding habitats over time, facilitating more focused and resource-efficient field entomological surveys of *Anopheles* mosquito larvae. The ability to pinpoint potential breeding habitats with greater precision is crucial for enhancing surveillance and informing LSM strategies, which are pivotal in the broader effort to control and eliminate malaria. The findings from this study provide essential guidance for ongoing and future surveillance initiatives, ensuring that interventions are well-targeted and based on the most current and relevant data. Looking forward, it is recommended that future research endeavours utilize larval abundance data and larval

survival rates, where available, to further refine the accuracy and applicability of malaria risk models. Such enhancements will improve the predictive capabilities of these models, offering more nuanced insights into the dynamics of malaria vector populations and contributing significantly to the global fight against this disease.

### CRediT authorship contribution statement

**Grace R. Aduvukha:** Writing – original draft, Writing – review & editing, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Elfati M. Abdel-Rahman:** Writing – review & editing, Validation, Supervision, Methodology, Investigation, Conceptualization. **Bester Tawona Mudereri:** Writing – review & editing, Validation, Methodology, Investigation, Conceptualization. **Onisimo Mutanga:** Writing – review & editing, Validation, Supervision, Methodology, Investigation. **John Odindi:** Writing – review & editing, Validation, Supervision, Methodology, Investigation. **Henri E.Z. Tonnang:** Writing – review & editing, Validation, Supervision, Resources, Project administration, Methodology, Investigation, Funding acquisition, Conceptualization.

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### Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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### Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.jag.2024.104351>.

### Data availability

All data used will be made available upon request.

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