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Master's Thesis

# 非洲人類猴痘的地理分布：運用生態棲位模型理解環境變數與自然宿主物種

# Geographic Distribution of Human Mpox in Africa: Understanding Environmental Variables and Reservoir Host Species Using Ecological Niche Modeling

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## MASTER'S THESIS ACCEPTANCE CERTIFICATE
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# Geographic Distribution of Human Mpox in Africa: Understanding Environmental Variables and Reservoir Host Species Using Ecological Niche Modeling

The undersigned, appointed by the Department / Institute of **Master's Program of Biodiversity** on **07/23/2025** have examined a Master's thesis entitled above presented by **Asma Nassor Salim (R10H44008)** candidate and hereby certify that it is worthy of acceptance.

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# Dedication

To my beloved parents, Mom & Dad

This thesis is dedicated to both of you—with profound love, respect, and gratitude.

From the very first day I started school until this very moment, you have been my unwavering pillars of strength. Your dedication to my education has been constant, selfless, and inspiring. You have supported every step of my journey with open hearts and open hands, never once doubting my path, even when it was difficult or uncertain.

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# 摘要

猴痘(mpox) 是一種再現的人畜共通傳染病，目前更在非洲中部和西部地區引發公共健康關注。本研究採用生態棲位模型(ecological niche modeling,ENM）以預測人類猴痘的潛在地理分布，並識別高風險外溢區域。本研究分析2010年至2022年間相關報告確認的人類猴痘病例之550地點，並結合從最初33個環境變數經相關矩陣分析後，篩選出的16個變數進行 最大熵模型( maximum entropy model, MaxEnt)建模分析。這些變數包括氣候資料、土地覆蓋類型、海拔高度、人口數量、人類足跡，以及三種已知囓齒類自然宿主物種（*Cricetomys*、*Funisciurus* 和 *Graphiurus* 屬）的分布情形。最大熵模型建模的表現良好（平均AUC值為0.867），並指出海拔高度、人口數量、最冷季節的降水量（BIO19）、葉面積指數以及*Graphiurus*屬為最具影響力的預測因子。高風險區主要集中在剛果民主共和國、奈及利亞南部、喀麥隆、賴比瑞亞以及獅子山共和國。整合人口資料後發現，剛果民主共和國有超過2,900萬人、奈及利亞有1,300萬人居住於高度適合猴痘傳播的環境區域內。本研究強調將宿主物種納入風險模型的重要性，因為其存在對空間預測結果具有顯著影響。研究結果顯示，結合生態、環境與人口統計數據，有助於識別優先監測區域並制定公共衛生預防措施。

**關鍵詞**：人類猴痘、生態棲位模型、最大熵模型、自然宿主物種、外溢風險。

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# Abstract

Mpox is re-emerging zoonotic disease with increasing public health concern across Central and West Africa. This study used ecological niche modeling (ENM) to predict the potential geographic distribution of human mpox and identify areas at high risk of spillover. A total of 550 confirmed mpox case locations reported between 2010 and 2022 were analyzed using maximum entropy model (MaxEnt), along with 16 environmental variables selected from an initial set of 33 following a correlation matrix analysis. These variables included climate data, land cover types, elevation, population count, human footprint, and distributions of three known rodent reservoir species (*Cricetomys*, *Funisciurus*, and *Graphiurus* spp.). Maxent model performed well (mean AUC = 0.867) and identified elevation, population count, precipitation of the coldest quarter (BIO19), leaf area index and *Graphiurus* spp. as the most influential predictors. High-risk zones were concentrated in the Democratic Republic of the Congo (DRC), southern Nigeria, Cameroon, Liberia, and Sierra Leone. Integrating population data revealed that over 29 million individuals in the DRC and 13 million in Nigeria reside in zones of high environmental suitability for mpox transmission. This study emphasizes the importance of including reservoir host species in risk models, as their presence significantly shaped the spatial predictions. These findings demonstrate the value of combining ecological, environmental, and demographic data to identify priority areas for surveillance and public health intervention.

**Keywords:** human mpox, ecological niche modeling, maximum entropy model, reservoir host species, spillover risk.

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# Chapter 1 Introduction

Zoonotic diseases, transmitted from animals to humans, account for over 60% of emerging infectious diseases globally, with Africa serving as a hotspot due to its rich biodiversity, rapidly changing landscapes, and close human-wildlife interactions (Jones et al., 2008). Among these diseases, monkeypox (mpox)(Damaso, 2023; WHO, 2022), caused by the Monkeypox virus (MPXV), has gained renewed attention following its unprecedented global spread in 2022 (Bunge et al., 2022). Historically endemic to Central and West Africa (Jezek et al., 1983), mpox causes a smallpox-like illness in humans (Petersen et al., 2019), with case fatality rates ranging from 1–10% depending on the viral clade and healthcare access (Vogel, 2022) . While mpox was long considered a neglected tropical disease (Khodakevich et al., 1988), its recent emergence in non-endemic countries underscores the urgent need to understand its ecological drivers to prevent future spillovers (Curaudeau et al., 2023).

The transmission dynamics of mpox are inherently tied to its zoonotic origins (Khodakevich et al., 1987). Although the virus’s natural reservoirs remain unconfirmed, evidence implicates rodents (e.g., rope squirrels *Funisciurus spp*., giant pouched rats *Cricetomys spp*., African dormice *Graphiurus spp.*) as potential hosts (Curaudeau et al., 2023; Parker et al., 2007). Human infections typically occur through direct contact with infected animals or consumption of bushmeat (McCollum & Damon, 2014; Nolen et al., 2015), followed by limited human-to-human transmission (Bunge et al., 2022). However, ecological shifts such as deforestation, agricultural expansion, and climate change are altering wildlife habitats and human exposure risks, potentially expanding the geographic range of mpox (Doshi et al., 2019; Reynolds et al., 2019). Despite these threats, the interplay between environmental variables, reservoir species distributions, and human mpox cases remains poorly quantified.

A key shortcoming lies in the limited integration of reservoir ecology into infection risk assessments. Despite the central role of animal hosts in viral maintenance, the spatial distributions of suspected reservoir species—such as monkeys, squirrels, and ground dwelling rodents hypothesized as primary reservoirs—are rarely incorporated into models, leaving their habitat preferences and overlap with human cases poorly characterized. Furthermore, existing studies often rely on static, coarse-resolution environmental datasets (e.g., WorldClim for climate layers) that fail to capture dynamic anthropogenic pressures like deforestation and urbanization, which are known to escalate human-wildlife contact. Compounding these issues are geographic and temporal biases in surveillance data: case reporting remains disproportionately focused on well-studied regions like the Democratic Republic of Congo (DRC) and Nigeria neglecting underreported areas in West Africa, while ecological studies have yet to account for post-2010 shifts in transmission dynamics, including increased human-to-human spread. Collectively, these gaps hinder the development of spatially explicit risk maps and evidence-based interventions.

This study employs ecological niche modelling (ENM) to bridge critical concerns in understanding mpox transmission dynamics across West and Central Africa. By integrating human case data (2010–2022), environmental variables, and reservoir species distributions, I quantify how abiotic and biotic factors jointly influence spillover risk. The major objectives of this thesis include:

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1. map the geographic distribution of reported human mpox cases in Central and West Africa from 2010-2022.
2. identify abiotic and biotic factors including reservoir species that are strongly associated with mpox occurrence.
3. show high-risk zones of mpox spillover under current environmental conditions

# Chapter 2 Literature Review

## 2.1 Brief historical of mpox

### 2.1.1 Origins and early outbreaks (1958-1970s)

Mpox was first identified in 1958 during outbreaks of a pox-like disease in captive monkeys in a Danish laboratory (Ladnyj et al., 1972; Magnus et al., 1959) . Though initially isolated from monkeys, it was not until 1970 that the first human case was documented in the Democratic Republic of Congo (DRC), in a nine-month-old child (Jezek et al., 1983). This case occurred in the final stages of the global smallpox eradication campaign, which facilitated mpox detection due to active surveillance systems (Ježek et al., 1988). However, clinical similarities between mpox and smallpox led to diagnostic challenges, especially in under-resourced settings ( McCollum & Damon, 2014).

### 2.1.2 Regional endemicity and neglect (1980s-1990s)

During the 1980s and 1990s, mpox was recognized as endemic in parts of Central and West Africa, particularly in countries such as the DRC, CAR, Cameroon, Nigeria, and Gabon (Mandja et al., 2019). Although outbreaks were reported intermittently, the disease received little global attention and was largely considered a rare, rural zoonosis (Gessain et al., 2022; Khodakevich et al., 1988). Research during this period (Khodakevich et al., 1988) focused on describing clinical features and transmission patterns, but limited resources and infrastructure hindered sustained investigations into its ecology and public health impact.

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### 2.1.3 Global emergence and expansion (2000s-2010s)

Mpox entered the global spotlight in 2003 following the first outbreak outside Africa, which occurred in the United States (Cohen, 2022; Reed et al., 2004). The outbreak was linked to imported rodents from Ghana that infected prairie dogs sold as pets, resulting in 47 confirmed human cases across six states (Adler et al., 2022). While no deaths occurred, the incident highlighted the risks posed by the global wildlife trade and the potential for zoonotic viruses to cross continents via commercial networks (Reynolds et al., 2019). Following a period of relative quiescence, Nigeria experienced a dramatic resurgence in 2017-2018 (Arotolu et al., 2022; N. Kumar et al., 2022), reporting approximately 200 cases after nearly four decades without documented outbreaks (Yinka-Ogunleye et al., 2019). This resurgence suggested possible ecological changes or viral adaptations that warranted renewed scientific attention (Reynolds et al., 2019).

### 2.1.4 Current outbreak

In May 2022, mpox spread globally, affecting over 100 countries outside of Africa, with significant outbreaks in Europe and North America (CDC, 2025; WHO, 2022). The epidemic was largely driven by sustained human-to-human transmission, particularly in men who have sex with men (MSM) communities (Thornhill et al., 2022). The World Health Organization declared the outbreak a Public Health Emergency of International Concern (PHEIC) in July 2022 (WHO, 2022). To avoid stigmatization, the term “monkeypox” was officially rebranded as “mpox” in late 2022 (WHO, 2022). However, by 2022, the mpox virus had breached all geographical confines, with a staggering 100,000 confirmed infections globally as of April 2025 (WHO, 2025). This scale of the outbreak was unprecedented, dwarfing previous

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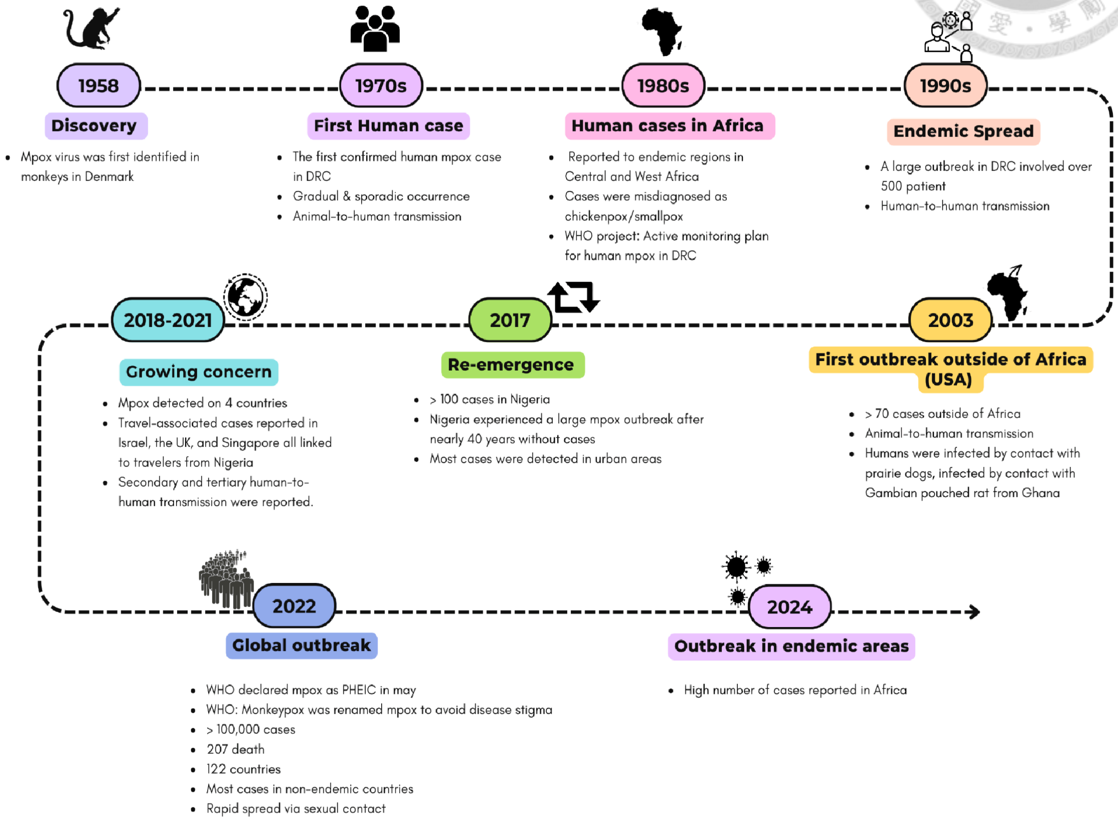
numbers and marking it as the first global outbreak of mpox. A detailed timeline of key outbreak events is presented in Figure 1.



1958
**Discovery**
- Mpox virus was first identified in monkeys in Denmark

1970s
**First Human case**
- The first confirmed human mpox case in DRC
- Gradual & sporadic occurrence
- Animal-to-human transmission

1980s
**Human cases in Africa**
- Reported to endemic regions in Central and West Africa
- Cases were misdiagnosed as chickenpox/smallpox
- WHO project: Active monitoring plan for human mpox in DRC

1990s
**Endemic Spread**
- A large outbreak in DRC involved over 500 patient
- Human-to-human transmission

2003
**First outbreak outside of Africa (USA)**
- > 70 cases outside of Africa
- Animal-to-human transmission
- Humans were infected by contact with prairie dogs, infected by contact with Gambian pouched rat from Ghana

2017
**Re-emergence**
- > 100 cases in Nigeria
- Nigeria experienced a large mpox outbreak after nearly 40 years without cases
- Most cases were detected in urban areas

2018-2021
**Growing concern**
- Mpox detected on 4 countries
- Travel-associated cases reported in Israel, the UK, and Singapore all linked to travelers from Nigeria
- Secondary and tertiary human-to-human transmission were reported.

2022
**Global outbreak**
- WHO declared mpox as PHEIC in may
- WHO: Monkeypox was renamed mpox to avoid disease stigma
- > 100,000 cases
- 207 death
- 122 countries
- Most cases in non-endemic countries
- Rapid spread via sexual contact

2024
**Outbreak in endemic areas**
- High number of cases reported in Africa

**Figure 1** Mpox timeline: From initial discovery (1958) to the ongoing outbreak 2024

## 2.2 Possible drivers of mpox transmission

While mpox is classified as a zoonotic disease, the definitive reservoir host remains unconfirmed (Curaudeau et al., 2023). Nevertheless, multiple studies have implicated rodents such as rope squirrels (*Funisciurus* spp.), giant pouched rats (*Cricetomys* spp.), and African dormice (*Graphiurus* spp.) as probable reservoirs (Doty et al., 2017; Parker et al., 2007). Human infections are often associated with direct contact with infected animals or their body fluids, including through hunting or bushmeat consumption (McCollum & Damon, 2014). Two genetically distinct clades of MPXV have been described: the Central African (Congo Basin) clade, with higher virulence, and the West African clade, associated with lower fatality and transmissibility (S. Kumar et al., 2023; Levine et al., 2007; Reynolds et al., 2019).

The MPXV is endemic to wild rodents and non-human primates in forested regions of West and Central Africa (Forni et al., 2023)(Figure 2), spreading to humans through contact with infected animals or people (Kaler et al., 2022). Its transmission is influenced by multiple factors, including environmental conditions, human behavior, and socioeconomic dynamics (Islam et al., 2023) . Historical outbreaks and recent global spread suggest that cultural practices, land-use changes, healthcare access, and public health policies all play critical roles (Alkhalil et al., 2009; Bunge et al., 2022; Falendysz et al., 2017; Isidro et al., 2022; Khodakevich et al., 1988).

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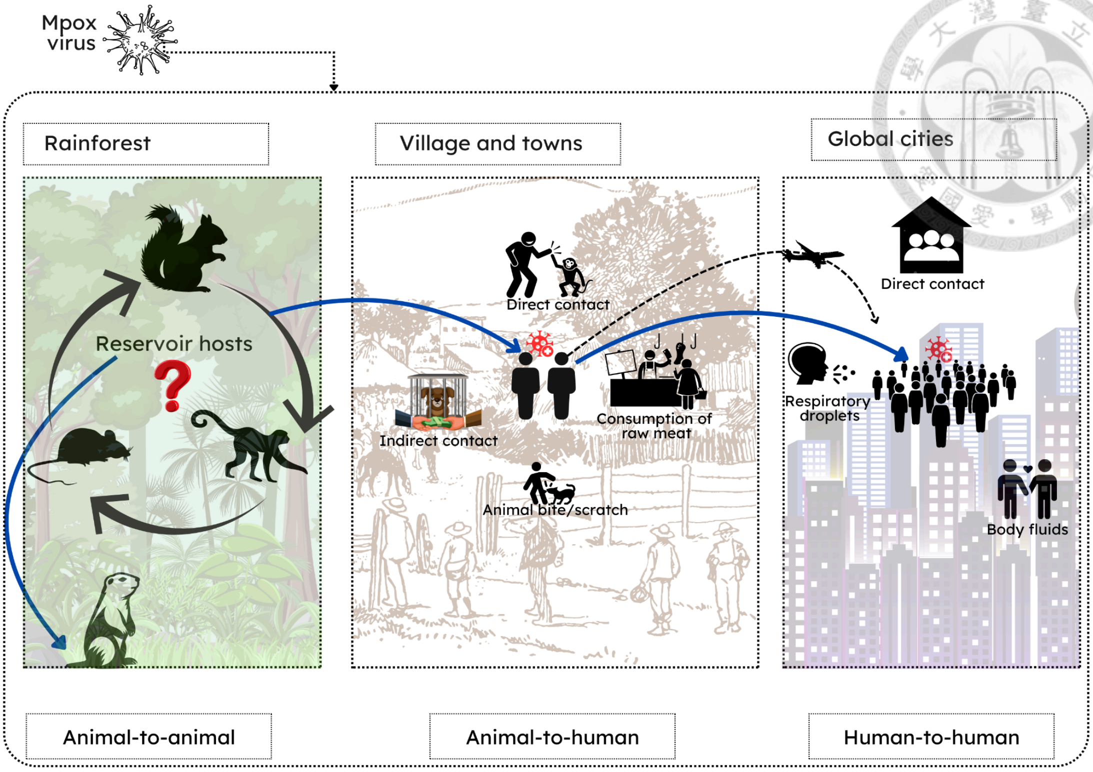

**Figure 2** This figure illustrates the transmission pathways of the mpox virus between animals, humans and the environment (modified from Karagoz et al., 2023).While the natural reservoir of the virus remains unknown, rodents (such as squirrels and rats) and non-human primates in the rainforests of Central and West Africa are recognized as susceptible hosts.Humans can become infected through direct contact with the biological fluids of infected animals or individuals, as well as through environmental exposure in endemic areas. Additional routes of transmission include the handling and consumption of bushmeat. Human-to-human transmission occurs through close physical contact, including within households, healthcare settings, and other close-contact environments. Travel to endemic regions also increases the risk of exposure and subsequent spread of the virus.

### 2.2.1 Ecological and environmental drivers

#### 2.2.1.1 Climate and ecological change

Mpox virus transmission is strongly linked to the humid, lowland tropical forests of Central and West Africa, particularly in the Congo Basin and countries like Nigeria, Ghana, and Sierra Leone (Levine et al., 2007). These endemic regions share key features, especially high annual rainfall that support both viral persistence and its animal reservoirs (Nakazawa et al., 2013). However, rapid environmental changes have reshaped these landscapes over the past four decades. Deforestation, agricultural expansion, urbanization, and climate shifts have fragmented habitats, forcing wildlife and humans into closer contact (Hansen et al., 2008; WHO, 2022).

A critical example is the rope squirrel (*Funisciurus spp.*), whose dependence on oil palm forests brings it into frequent contact with human settlements (Fuller et al., 2011). Such overlap creates spillover opportunities, highlighting how ecological disruption amplifies zoonotic risks. These changes suggest that mpox distribution is not static but evolving alongside anthropogenic pressures on ecosystems (Karagoz et al., 2023).

### 2.2.2 Biological and zoonotic drivers

#### 2.2.2.1 Trapping, hunting and consumption of bushmeat

The MPXV has been detected in various animal species throughout central and western Africa (Alkhalil et al., 2009). Human infection with mpox is most commonly reported in endemic regions, particularly in small villages situated near forests where residents trap and hunt small wild animals, such as squirrels, which are subsequently brought into their homes for consumption (Khodakevich et al., 1988). An epidemiological investigation revealed that 64.5% of patients had contact with monkeys at the time presumed to have been infected, while 11.8% had contact with both squirrels and antelopes (Arita et al., 1985).

#### 2.2.2.2 Animal trade

The importation of animals from endemic countries to non-endemic countries is a significant driver of mpox transmission (Reynolds et al., 2019). A report highlighted an outbreak in the Midwestern US involving 71 individuals, which was attributed to the activities of prairie dog distributors who had imported an infected Gambian giant rat from Ghana in 2003 (Reed et al., 2004). The subsequent infection of humans underscores the potential risks associated with the movement of animals across international borders (Reed et al., 2004).

### 2.2.3 Human behavioral and social drivers

#### 2.2.3.1 Travelling and large scale events

Cases of mpox were reported in the United Kingdom, Israel, and Singapore in 2019 among individuals who had recently traveled to Nigeria (Angelo et al., 2019). Similarly, in 2022, an outbreak was linked to a traveler who returned from Nigeria to the United Kingdom (WHO, 2022). During international travel and large-scale gatherings, individuals may be exposed to the MPXV through close contact with infected humans or animal carriers (Khodakevich et al., 1988). One of the earliest clusters in the 2022 global outbreak was linked to a festival held in the Canary Islands of Spain, suggesting that mass gatherings may have played a significant role in the rapid international spread of the virus (Martínez et al., 2022).

#### 2.2.3.2 Transmission within household

Mpox has also been shown to spread through close contact within households, especially among family members or individuals sharing the same living space (Nolen et al., 2015). According to WHO estimates, approximately 65.7% of human-to-human mpox transmissions are linked to direct physical contact, with a striking 95.2% of these occurring in intra-household settings (WHO, 2022). Several factors contribute to household transmission risk, including the absence of home-based isolation measures, sharing sleeping arrangements such as rooms or beds, and the use of common household items between infected and non-infected individuals (Nolen et al., 2015).

#### 2.2.3.3 Human behavioural transmission

It has been reported that the mpox virus has been detected in semen (Lapa et al., 2022) . Furthermore, it can be transmitted through sexual contact with an individual who has an active rash (WHO, 2022). A majority of the cases during the 2022 outbreak had a history of sexual contact, which is commonly referred to as MSM (Islam et al., 2023). However, there haven't been any cases discussed in African countries (Kumar et al., 2023)

### 2.2.4 Healthcare and public health drivers

#### 2.2.4.1 Healthcare settings

It has been observed that multiple outbreaks within healthcare facilities suggest that medical professionals are particularly susceptible to mpox (Angelo et al., 2019). This susceptibility may result from either late or incorrect diagnosis of mpox cases and inadequate use of personal protective equipment (PPE) (Angelo et al., 2019). Moreover, inadequate healthcare infrastructure, lack of quarantine areas, and limited resources for diagnosing and treating potential cases, especially those with negative outcomes, can contribute to the spread of the virus to uninfected individuals (Islam et al., 2023).

### 2.2.5 Immunological and historical drivers

#### 2.2.5.1 Decline in smallpox vaccine immunity

The smallpox vaccine has demonstrated a high level of efficacy in preventing the mpox, with a reported 85% effectiveness (Arita et al., 1985; Kisalu & Mokili, 2017). Following the declaration of eradication in 1972, vaccination against smallpox was

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discontinued (Rimoin et al., 2010; Jezek et al., 1988). However, the resulting decline in smallpox vaccine immunity, also known as herd immunity, has led to a decline in the protection against the disease (Nguyen et al., 2021). A 2016 survey found that only 10.1% of the total Nigerian population had antibodies against smallpox (Nguyen et al., 2021). Additionally, before the 2017 outbreak, the estimated population immunity in Nigeria was only 2.6% in 2016, and individual-level immunity declined at a rate of 1.29% per year (Nguyen et al., 2021). This decline in herd immunity for smallpox may contribute to the current mpox outbreak, as cross-protective immunity is also reduced (Nguyen et al., 2021). As the number of non-vaccinated people increases, combined with the gradual decline in immunity against smallpox, the population is becoming increasingly susceptible to mpox (Nguyen et al., 2021). All of these were summarized in Figure 3

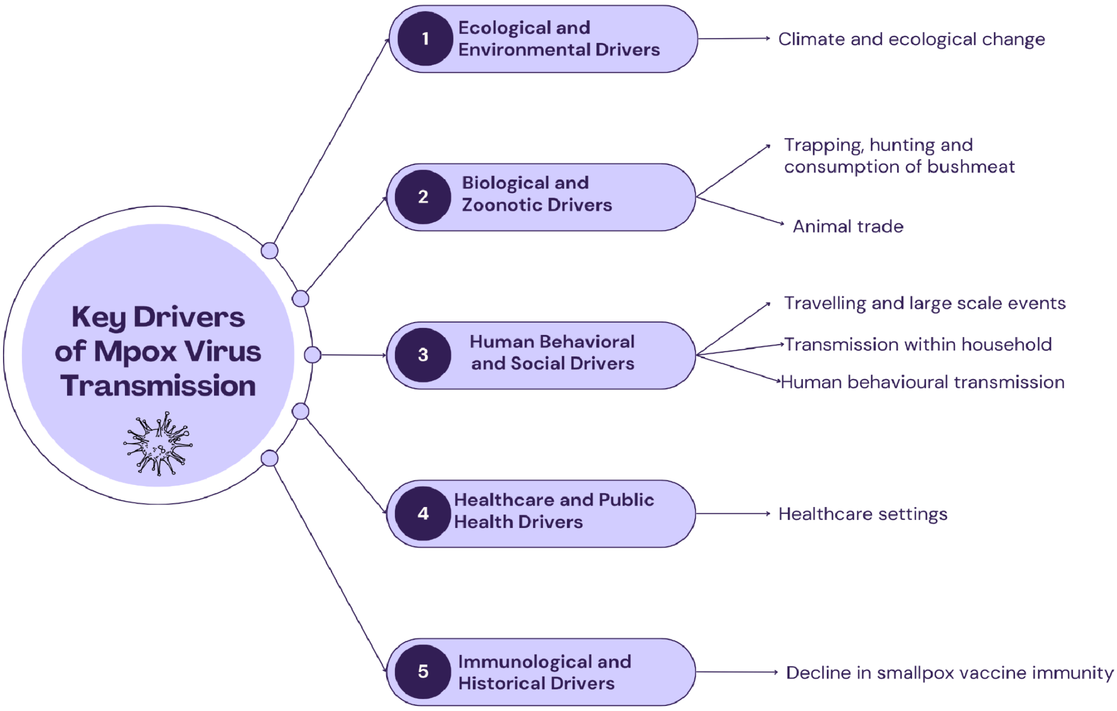

**Figure 3** Potential drivers of mpox spread; animal, human and environmental drivers

### 2.3 Reservoir host

The MPXV is widely recognized as a zoonotic pathogen, with extensive evidence supporting its ability to infect a broad range of mammalian hosts (Curaudeau et al., 2023). Over fifty animal species, including non-human primates, insectivores, domestic dogs, and various rodents such as squirrels, have been identified as susceptible to MPXV infection (Curaudeau et al., 2023; Islam et al., 2023) . While many of these species may act as incidental hosts, certain rodents are increasingly implicated as potential reservoirs due to their ability to harbor the virus without showing clinical signs of illness (Cohen, 2022).

To date, no definitive animal reservoir has been identified outside of Africa (Seang et al., 2022). However, several African rodent species are frequently cited in the literature as strong candidates for natural reservoirs (Mauldin et al., 2022). These include the Gambian pouched rat (*Cricetomys gambianus*), rope squirrels (*Funisciurus spp.*), sun squirrels (*Heliosciurus spp.*), and African dormice (*Graphiurus spp.*), which are commonly found in Central and West African forest ecosystems (Curaudeau et al., 2023; Reynolds et al., 2019; CDC, 2003). These species are considered likely reservoirs not only because of their geographic overlap with human mpox cases, but also due to their asymptomatic infection patterns, which enable them to maintain and transmit the virus over time (Doty et al., 2017) . Human exposure to MPXV from these animals often occurs through direct contact during hunting, handling, or consumption of bushmeat (Mauldin et al., 2022; Reynolds et al., 2019).

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## 2.4 Environmental and climate influences

Environmental factors play a crucial role in the transmission of zoonotic diseases like mpox (Yinka-Ogunleye et al., 2019). As urban areas expand into natural habitats, the interaction between humans and potential disease carriers grows, especially in regions like West and Central Africa where mpox reservoirs are endemic (Reynolds et al., 2019). This is particularly notable in areas transitioning between urban and agricultural spaces (Nolen et al., 2016). Communities with lower socioeconomic status, heavily reliant on bushmeat and engaged in hunting or farming, are more vulnerable to the disease due to reduced access to advanced healthcare (Jagadesh et al., 2023; WHO, 2022).

The global wildlife trade has been identified as a catalyst for disease outbreaks (Van Vliet et al., 2019; Karesh et al., 2005). Though not directly linked to the 2022 outbreak, this trade increases human exposure to potential disease carriers at different stages - from capture to sale. An example of this impact is the establishment of the invasive Gambian pouched rat population in Florida (Falendysz et al., 2015, 2017). Such introductions heighten the risk of new endemic areas forming, even in regions with higher socioeconomic status.

Regions such as the Congo Basin, Central Africa, Guinea, Nigeria, Ivory Coast, Sierra Leone, Ghana, and Togo are potential hotspots for mpox spread, further exacerbated by significant environmental and geographical changes in the past few decades (Levine et al., 2007; Reynolds et al., 2019). Factors like increased human population, urbanization, deforestation, and climate change have altered human-animal dynamics, escalating the threat of emerging diseases (WHO, 2025; Nakazawa et al., 2013).

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Climate plays a defining role in disease dynamics (Bunge et al., 2022). Temperature fluctuations impact both the survival of the mpox pathogen and the behavior of its vectors (Fuller et al., 2011; Islam et al., 2023). Literature confirms the pivotal role of temperature in pathogen survival and vector behavior (Altizer et al., 2013; Patz et al., 2005) . Humidity, another key climatic factor, warrants further study in understanding its effects on mpox transmission (Fuller et al., 2011). As urban expansion and deforestation progress, they reshape the ecological landscape of diseases by altering habitats suitable for vectors or hosts (Swati & Saxena, 2023). This transformation could lead to a shift in the epidemiology of diseases like mpox (Bunge et al., 2022; Mauldin et al., 2022).

With global temperatures on the rise, climate change poses a significant concern (Mandja et al., 2019). It can extend the endemic range of reservoir species and increase the seasonal exposure duration (Muzemil et al., 2018). Climate change-related stressors, including temperature variations and habitat encroachment, elevate zoonotic disease risks (Durski, 2018).

Research using ecological niche modeling (ENM) highlights the significance of factors like precipitation and altitude in mapping infectious diseases' spread. These factors can be instrumental in forecasting potential outbreaks or changes in disease dynamics like some examples in mpox (Curaudeau et al., 2023; Ellis et al., 2012; Fuller et al., 2011; Levine et al., 2007; Nakazawa et al., 2013;  Peterson, 2006). Hence these findings reaffirm that climate variables play a crucial role in shaping the spatial distribution of mpox, supporting their inclusion in predictive modeling for future outbreak preparedness.

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## 2.5 Ecological niche modeling

Ecological niche models (ENMs) has gained considerable attention in understanding the distribution of species and their response to environmental variables (Escobar, 2020; A. Peterson, 2006). This modeling approach, particularly in the context of disease spread and epidemiology, is pivotal in understanding how diseases like mpox might spread geographically and ecologically. Epidemiological studies often use geospatial and ecological tools to map the spread of diseases and provide valuable insights into disease surveillance and prevention (Peterson, 2014). While traditional geospatial methods can help visualize general spatial patterns, they may be biased and overlook complex interactions between hosts, vectors, and pathogens (Peterson et al., 2008). ENM addresses this issue by integrating species occurrence data with environmental factors to determine habitat suitability and the underlying ecological factors that influence disease distribution (Escobar & Craft, 2016). As a result, ENM has transformed epidemiology, allowing for the prediction of disease outbreaks and guiding disease control measures (Johnson et al., 2019).

### 2.5.1 Ecological niche concept

The ecological niche concept, as formalized by Hutchison (1957) (Takola & Schielzeth, 2022), defines the abiotic and biotic conditions required for a species—or in this case, a pathogen—can persist (Peterson, 2014). In disease ecology, this framework extends to pathogens and their hosts, where the niche represents the intersection of environmental drivers (e.g., climate, land cover), host-reservoir interactions, and human activities that mediate spillover (Johnson et al., 2019). For human mpox—a zoonotic disease endemic to Central and West Africa—the niche is shaped by three interdependent components: (1) abiotic factors such as tropical rainforest climates with

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high humidity and seasonal rainfall, which sustain habitats for rodent reservoirs (e.g., Funisciurus squirrels); (2) biotic interactions, including reservoir host density and behavior that facilitate viral maintenance; and (3) socioecological shifts like deforestation or bushmeat hunting, which increase human-wildlife contact (Arotolu et al., 2022; Escobar, 2020;  Peterson, 2014). By quantifying these multidimensional relationships, ENM provides a mechanistic understanding of where and why mpox outbreaks occur.

### 2.5.2 A practical framework of ENM

ENM translates niche theory into actionable insights through a structured workflow. First, georeferenced occurrence data—such as human mpox case reports and reservoir host presence points—are compiled alongside environmental variables (e.g., WorldClim bioclimatic layers, NDVI vegetation indices, and land-use maps) (Peterson, 2012). These variables are carefully selected to minimize multicollinearity and ensure biological relevance; for example, annual precipitation may reflect rainforest habitat suitability for reservoirs, while temperature seasonality could influence viral survival (Escobar, 2020). Next, machine learning algorithms like Maxent correlate occurrence data with environmental predictors to generate spatially explicit suitability maps (Phillips et al., 2006). Model validation, using techniques like spatial cross-validation, area under curve (AUC) ensures robustness, while projections under future climate or land-use scenarios identify regions at risk of emerging outbreaks (Arotolu et al., 2022; Pigott et al., 2015). For mpox in Africa, this framework helps disentangle the relative contributions of environmental stability (e.g., intact forests), ecological disturbance (e.g., agricultural expansion), and reservoir ecology to spillover risk (Ellis et al., 2012; Mandja et al., 2022).

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### 2.5.3 Application of ENM in mpox research

ENM has proven transformative in mapping zoonotic disease risks, particularly in data-limited regions like Africa (Johnson et al., 2019; Peterson et al., 2008). Applied to mpox, ENM can: (1) delineate high-risk zones where environmental conditions overlap with reservoir distributions and human populations, such as the rainforest-agriculture ecotones of the Congo Basin (Fuller et al., 2011); (2) identify potential reservoir species by statistically linking human case clusters to the niches of candidate wildlife hosts (Curaudeau et al., 2023); (3) guide surveillance by prioritizing areas where model-predicted suitability aligns with gaps in health infrastructure (Islam et al., 2023); and (4) forecast geographic shifts in transmission under climate change, such as increased suitability in highland regions as temperatures rise (Bunge et al., 2022; Reynolds et al., 2019; Yinka-Ogunleye et al., 2019).

### 2.5.4 Maxent: A robust tool for modelling mpox distribution

Maxent (Maximum Entropy) is widely regarded as the gold standard for ENM in disease ecology, particularly for systems like mpox with sparse or presence-only occurrence data (Phillips et al., 2006). Its advantages include: (1) performance with limited data, critical in Africa where mpox case reporting is patchy (Pearson et al., 2007); (2) transparency, through response curves and jackknife tests that clarify how variables like forest cover or temperature shape predictions (Johnson et al., 2019); (3) bias correction, which accounts for uneven sampling effort (e.g., healthcare access disparities); and (4) probabilistic outputs, which quantify suitability gradients rather than binary presence-absence thresholds (Simoes et al., 2020). For example, Maxent can reveal how intermediate rainfall levels (1200–1800 mm/year) in West African savanna-forest mosaics create optimal conditions for both reservoir rodents and human

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exposure (Bunge et al., 2022; Reynolds et al., 2010). By integrating these features, Maxent outperforms traditional regression models in capturing the complex, non-linear relationships defining mpox's ecological niche (Johnson et al., 2019).

# Chapter 3 Materials and Methods

Combining niche theory and ENM methodologies offers a powerful approach to unraveling mpox's spatial ecology (Peterson, 2014). A workflow of this study (Figure 4) includes: (1) compiling human mpox cases from health centers reports and reservoir occurrence data from GBIF, processing variables like bioclimate factor, elevation, land covers, human footprints and population count; (2) performing and calibrating a Maxent model to select hotspots of suitable environmental and biotic parameters; and (3) identify suitable risk area of mpox in central and west Africa.

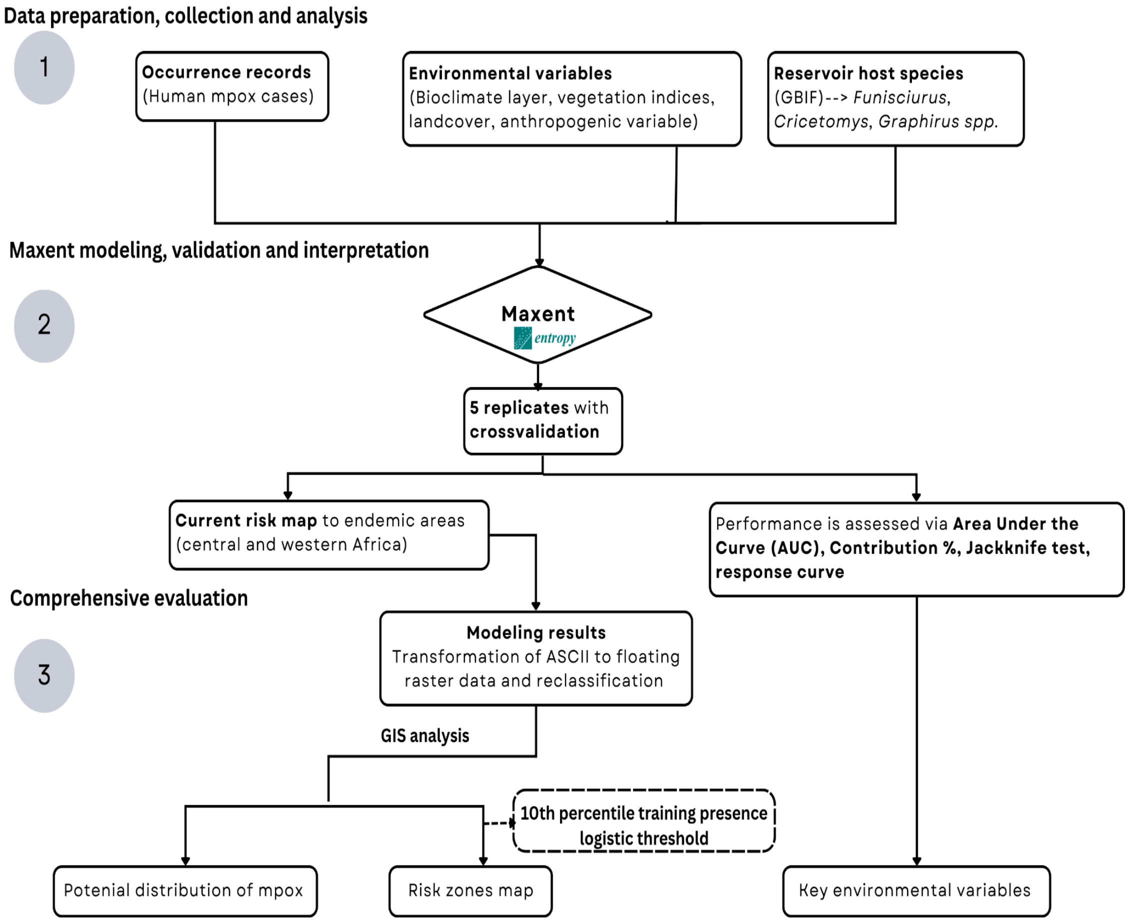

**Figure 4** Flowchart of the ecological niche modeling process for human mpox using maxent model analysis

## 3.1 Study area

This study focuses on the geographic range of mpox incidence across Central and West Africa, specifically covering 12  countries: **Democratic Republic of the Congo (DRC), Republic of the Congo, Nigeria, Central African Republic (CAR), South Sudan, Gabon, Cameroon, Liberia, Sierra Leone, Côte d'Ivoire, Benin, and Ghana** (Figure 5)**.** These countries represent regions with historically high and/or emerging mpox case burdens. The region spans diverse ecological zones, ranging from humid tropical rainforests in the Congo Basin to savannas and coastal ecosystems in West Africa.

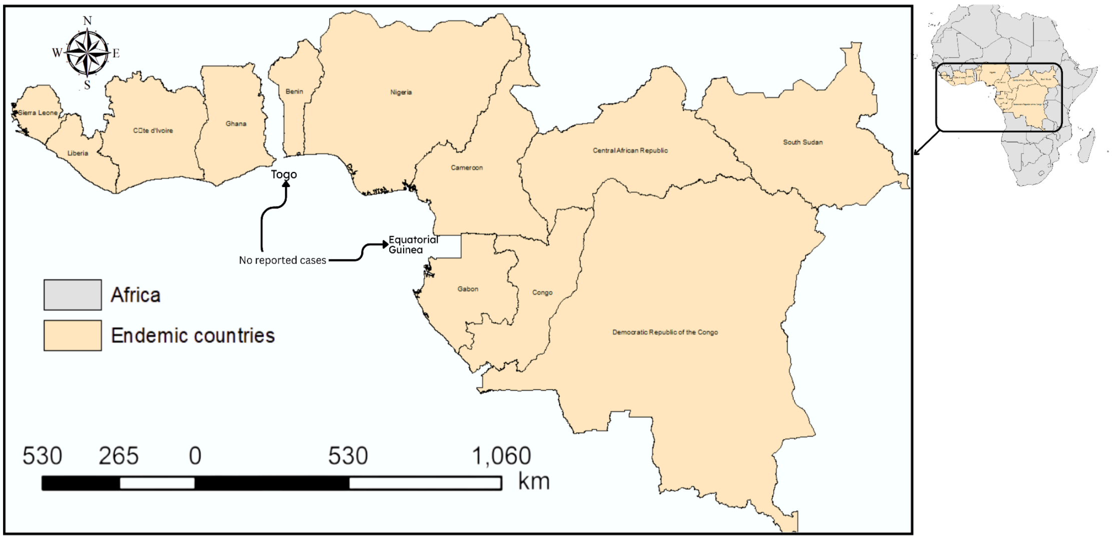

**Figure 5** Location of the study area

## 3.2 Data collection

### 3.2.1 Human mpox cases data

Data on human mpox cases were collected from locations in Central and Western Africa that reported infections between January 2010 and December 2022. Sources were searching from English-language search engines such as Google Scholar, Science Direct, Web of Science (WOS) and PubMed, as well as grey literature from government and professional organizations, including the World Health Organization

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(WHO), U.S. Centers for Disease Control and Prevention (CDC), and Nigeria Centre for Disease Control (NCDC).

A systematic search was conducted using the keywords: “monkeypox”, “monkey pox”, “mpox”, and “orthopoxvirus”. Titles and abstracts of retrieved records were screened independently. The extracted data primarily included studies that reported geographic information such as location and coordinates, year of occurrence, and clinical details confirming human mpox cases for spatial analysis.

From the eligible studies, 550 unique location points were extracted. Each record included geographic coordinates,when coordinates were not directly reported, locations were georeferenced manually using google map. Duplicate entries were excluded. The final dataset was compiled into a CSV file (Appendix 1) and visualized using ArcGIS Desktop 10.8 for spatial analysis.

### 3.2.2 Reservoir host occurrence

To account for the potential role of animal hosts in mpox transmission dynamics, this study focused on three rodent genera with documented susceptibility to MPXV : *Graphiurus* spp., *Funisciurus* spp., and *Cricetomys* spp. These species were selected based on previous serological evidence and virus isolation studies that have confirmed their exposure to or infection with MPXV. Moreover, they represent two ecologically distinct rodent groups: **arboreal rodents** (*Graphiurus* and *Funisciurus*), which interact with human environments through tree canopies and elevated structures, and **terrestrial rodents** (*Cricetomys*), which are more commonly associated with ground-level human activity and rural household settings (Appendix 2). These differing

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habitat preferences are important, as they imply distinct pathways for human–animal interactions and potential zoonotic spillover.

Occurrence records for these three genera were obtained from the Global Biodiversity Information Facility (GBIF)(https://www.gbif.org/), covering the same temporal span as the human case data from **2010 to 2022** (Table 1). To ensure data quality, preliminary cleaning procedures were applied prior to inclusion in the ecological niche modeling. These steps includes; removal of duplicate records, exclusion of records lacking geographic coordinates, and filtering out observations falling in oceans or outside study area (Figure 6). Only georeferenced, reliable presence records were retained for modeling.

**Table 1** Number and source of host genera occurrence records extracted from the GBIF

| Genus | Downloaded Records | After Cleaning | DOI |
|---|---|---|---|
| *Funisciurus* spp. | 193 | 172 | https://doi.org/10.15468/dl.rgkcfh |
| *Cricetomys* spp. | 506 | 381 | https://doi.org/10.15468/dl.jd3hkg |
| *Graphiurus* spp. | 63 | 31 | https://doi.org/10.15468/dl.b4hhr2 |

*Note: Only records classified as "Human observation" or "Preserved specimen" were retained.*

To integrate reservoir host species as biotic environmental predictors in the MaxEnt model, occurrence data for the three suspected host genera were obtained from cleaned CSV files containing geographic coordinates. These datasets were projected to the GCS_WGS 1984 coordinate system and visualized as point features in ArcMap. Kernel Density Estimation (KDE) was applied to each dataset to generate continuous raster surfaces representing the spatial density of each species. KDE was selected for its ability to convert occurrence points into smoothed probability surfaces, thus serving as biotic variables in the modeling process.

The resulting KDE rasters were prepared to ensure spatial alignment with other environmental layers and exported in ASCII (.asc) format for use in MaxEnt. This procedure was repeated for all three host genera, facilitating the inclusion of biotic factors alongside abiotic variables in modeling the potential distribution of human mpox. The overall workflow for processing host genera occurrence data is illustrated in Figure 6. To visually support the modeling inputs, Figure 7A presents the combined occurrence points of all three host genera, while Figures 7B–7D display the corresponding KDE-derived density surfaces for each genus. These figures collectively illustrate both the spatial distribution of raw records and the processed biotic layers used in the ecological niche modeling framework.

[ GBIF Occurrence Data (2010–2022) ]
↓
[ Filter and Clean (Valid types, Coordinates, Duplicates) ]
↓
[ Final Cleaned CSV ]
↓
[ Display in ArcMap (WGS 1984) ]
↓
[ Generate KDE Raster ]
↓
[ Align with Bioclim Layers ] → correlation matrix
↓
[ Export as ASCII (.asc) ]
↓
[ Use in MaxEnt Model ]

**Figure 6** Workflow for processing host genera occurrence data into environmental layers for Maxent modeling

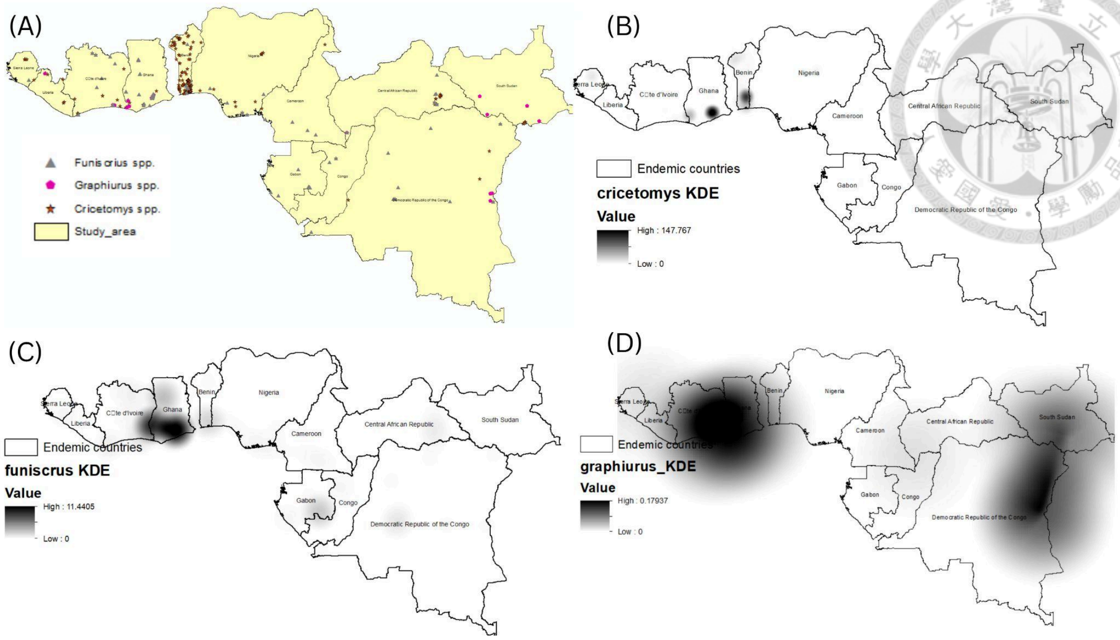

**Figure 7 (A)** Combined point occurrences of all three rodent reservoir genera (*Cricetomys* spp., and *Funisciurus* spp., *Graphiurus* spp.) used in the modeling process.**(B-D)**. Kernel Density Estimation (KDE) raster outputs showing estimated density distributions for each genus, respectively.

### 3.2.3 Environmental variables

A total of 33 variables were hypothesized to be potentially associated with the occurrence of the MPXV in Africa. These include 26 abiotic variables (environmental-related), 4 anthropogenic variables (human-related), and 3 associated with reservoir hosts presence (Table 2). The selection of variables was based on previous studies on zoonotic diseases, ecological niche modeling (ENM), and environmental suitability assessments (see Appendix 3). All variables were obtained in raster format at a spatial resolution of 30 arc-seconds (~1 km²) and were standardized to the geographic extent of the study area using ArcGIS to ensure spatial alignment across datasets. The temporal extent for data collection spans from 2010 to 2022 to capture recent environmental and human activity pattern relevant to MPXV transmission as shown on Table 3.

To reduce multicollinearity and improve model reliability, a pairwise Pearson correlation analysis was conducted in R among the 33 variables, using a threshold of $|r| \geq 0.7$. In cases of strong correlation, the variable with greater ecological relevance to MPXV dynamics was retained. This process resulted in the selection of 16 variables for final modeling. These included two bioclimatic variables (BIO3 and BIO19), seven land cover classes (forest, savanna, grassland, wetlands, cropland, urban, and others), leaf area index, elevation, human footprint, population count, and the predicted distributions of *Cricetomys* spp., *Funisciurus* spp., and *Graphiurus* spp. The correlation matrix is illustrated in Figure 8. All selected layers were converted to ASCII (.asc) format for integration into the MaxEnt modeling framework used to predict the ecological suitability of human mpox occurrence

**Table 2** Description of 33 technical information on the variable used in Maxent model

| Code | Description and Unit | Type |
|---|---|---|
| ***Environment*** | | |
| BIO1 | Annual mean temperature (℃) | Continuous |
| BIO2 | Mean diurnal range (Mean of monthly (max temp-min temp)) (℃) | Continuous |
| BIO3 | Isothermality (BIO2/ BIO7) (*100) | Continuous |
| BIO4 | Temperature seasonality (standard deviation*100) | Continuous |
| BIO5 | Max temperature of warmest month (℃) | Continuous |
| BIO6 | Min temperature of coldest month (℃) | Continuous |
| BIO7 | Annual range of temperature (BIO5- BIO6) (℃) | Continuous |
| BIO8 | Mean temperature of wettest quarter (℃) | Continuous |
| BIO9 | Mean temperature of driest quarter (℃) | Continuous |
| BIO10 | Mean temperature of warmest quarter (℃) | Continuous |
| BIO11 | Mean temperature of coldest quarter (℃) | Continuous |
| BIO12 | Annual precipitation (mm) | Continuous |
| BIO13 | Precipitation of wettest month (mm) | Continuous |
| BIO14 | Precipitation of driest month (mm) | Continuous |
| BIO 15 | Precipitation seasonality (Coefficient of variation) | Continuous |
| BIO16 | Precipitation of wettest quarter (mm) | Continuous |
| BIO17 | Precipitation of driest quarter (mm) | Continuous |
| BIO18 | Precipitation of warmest quarter (mm) | Continuous |
| BIO19 | Precipitation of coldest quarter (mm) | Continuous |
| Leaf area index | Area of leaves ($m^2$) over a unit of land ($m^2$) | Continuous |
| Elevation | Average elevation (m) | Continuous |
| Forest | Percentage coverage | Categorical |
| Savanna | Percentage coverage | Categorical |
| Grasslands | Percentage coverage | Categorical |
| Wetlands | Percentage coverage | Categorical |
| Cropland | Percentage coverage | Categorical |
| Urban | Percentage coverage | Categorical |
| Others | Percentage coverage | Categorical |
| ***Human activity*** | | |
| Population count | Estimated total number of people per grid-cell | Continuous |
| Human footprint | Annual records of the global human footprint (0-50) | Continuous |
| ***Animal*** | | |
| *Graphiurus* spp. | | Continuous |
| *Funiscurus* spp. | | Continuous |
| *Cricetomys* spp. | | Continuous |

**Table 3** Detail information about the data used in the study and preprocessing step

| Variables | Dataset | Temporal extent | Spatial resolution | Format | Website |
|---|---|---|---|---|---|
| *Environmental-related* | | | | | |
| Climate data | CHELSA V2.1 | 2011-2019 | 1km | Raster | https://chelsa-climate.org |
| Elevation | EarthEnv-DEM90 digital elevation model | 2010 | 1km | Raster | http://www.earthenv.org/ |
| Leaf area index | MODIS MCD15A2H V6.1 | 2010-2020 | 500m | Raster | https://earthexplorer.usgs.gov/ |
| Land cover | ESA Land Cover Climate Change Initiative | 2010, 2015, 2020 | 300m | Raster | https://climate.esa.int/en/data/#/search |
| *Human-related* | | | | | |
| Population count | WorldPop | 2010, 2015, 2020 | 1km | Raster | https://www.worldpop.org/ |
| Human Footprint | Human Footprint dataset from 2010 to 2022 | 2010-2022 | 1km | Raster | https://doi.org/10.6084/m9.figshare.16571064 |
| Human Mpox occurrence | Confirmed presence points | 2010-2022 | - | CSV (latitude, longitude) | WHO/Surveillance reports/Published source |
| *Animal-related* | | | | | |
| *Funisciurus spp.* | Point location of species occurrence | 2010-2022 | - | CSV/ shapefile | https://doi.org/10.15468/dl.rgkcfh |
| *Cricetomys spp.* | Point location of species occurrence | 2010-2022 | - | CSV/ shapefile | https://doi.org/10.15468/dl.jd3hkg |
| *Graphiurus spp.* | Point location of species occurrence | 2010-2022 | - | CSV/ shapefile | https://doi.org/10.15468/dl.b4hhr2 |

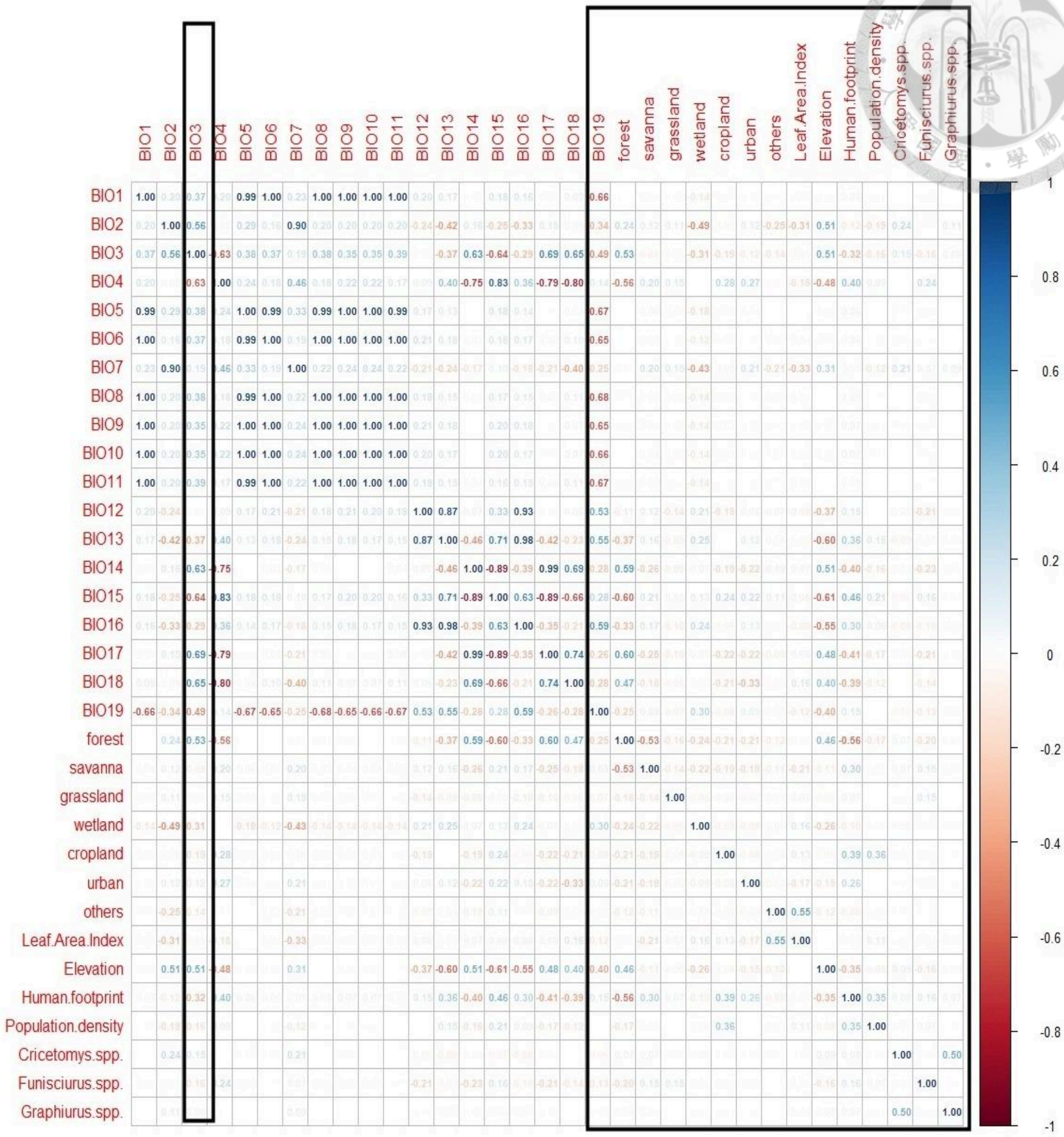

**Figure 8** Heatmap showing the pairwise Pearson correlation coefficients among the 33 environmental variables initially considered in the study. Variables with |r| ≥ 0.7 were considered highly correlated and were screened to reduce multicollinearity. The variables highlighted in the black margin box represent the final 16 predictors selected and used in the MaxEnt model. Blue tones indicate positive correlations, while red tones indicate negative correlations.

#### 3.2.3.1 Climate data

Climate data used in this study were obtained from the CHELSA (Climatologies at High resolution for the Earth’s Land Surface Areas) database, covering the period from 2011 to 2019. Monthly climate layers for precipitation minimum temperature and maximum temperature were downloaded from the CHELSA portal (https://chelsa-climate.org) at a spatial resolution of 30 arc-seconds (~1 km$^2$). These data were selected due to their high spatial resolution and ecological relevance, making them suitable for ecological modeling. The downloaded raster files were imported into R for processing and analysis. Using the 'biovars' function from the ‘dismo’ package in R, the monthly data were used to compute the standard 19 bioclimatic variables (BIO1–BIO19). These variables summarize ecologically meaningful aspects of climate explained in Table 2.

After generating the bioclimatic variables in R, the output raster files were saved as GeoTIFF (.tif) format and imported into ArcGIS 10.8. All layers were reprojected to a uniform coordinate reference system to ensure spatial consistency. These finalized raster datasets were then incorporated as environmental predictors in the ecological niche modeling (ENM) of human mpox distribution.

#### 3.2.3.2 Elevation

Elevation data were sourced from the Shuttle Radar Topography Mission (SRTM) (http://www.earthenv.org/) at 30 arc-second resolution for the year 2010. The data were downloaded from the USGS Earth Explorer, mosaicked to cover the study region, and clipped to the study boundary in ArcGIS.

#### 3.2.3.3 Leaf area index

Leaf area index (LAI) data were obtained from the MODIS MCD15A2H product (https://earthexplorer.usgs.gov/)(8-day composites at 500 m resolution). Monthly layers from 2010 to 2020 were averaged to create a single LAI raster representing overall vegetation density. This average was calculated in ArcGIS by first resampling all rasters to 1 km, then using the “Cell Statistics” tool to compute the mean.

#### 3.2.3.4 Land cover

Land cover data were obtained from the ESA Climate Change Initiative (CCI) (https://climate.esa.int/en/data/#/search) for the years 2010, 2015, and 2020. These categorical rasters (300 m resolution) were first resampled to 1 km resolution using majority resampling. An average categorical map was then created by applying a mode filter using the “Cell Statistics” tool to reflect the dominant land cover type across the three years.

To simplify the land cover for modeling, the data were reclassified into seven broader categories based on ecological relevance to mpox transmission. The categories and their justification are listed on Table 4. After preprocessing, all environmental variables were converted to ASCII (.asc) format.

**Table 4** Land cover reclassification scheme

| New Code | Group Name | Original MODIS Codes | Justification |
|---|---|---|---|
| 1 | Forest | 1, 2, 3, 4, 5 | Rodent and primate habitat (reservoirs) |
| 2 | Savanna | 6, 7, 8, 9 | Wildlife-human interface, transition zones |
| 3 | Grasslands | 10 | Open habitats, reservoir movement |
| 4 | Wetlands | 11 | Disease vector and host habitats |
| 5 | Cropland | 12, 14 | Human-wildlife contact |
| 6 | Urban | 13 | Human population exposure |
| 7 | Others | 0, 15, 16, 254, 255 | Water, snow, unclassified—irrelevant |

#### 3.2.3.5 Population count

Data were downloaded from WorldPop (Population Counts/Unconstrained global mosaic 2000-2020)(https://www.worldpop.org/) for the years 2010, 2015, and 2020. Each raster was resampled to 1 km resolution and averaged using “Raster Calculator” in ArcGIS to obtain a representative human population layer.

#### 3.2.3.6 Human footprint

Human footprint (HFP) data from 2010 to 2022 were used to represent cumulative human pressures across Africa, including population density, built infrastructure, land transformation, and transportation networks. The original raster datasets were in 30 arc-second (~1 km²) spatial resolution, which aligns with the resolution used for other environmental variables in the study. The *Cell Statistics* tool was then applied to compute the pixel-wise average of all 13 yearly rasters, producing a single composite layer. This averaging approach reduces annual variability and highlights long-term human impact patterns.

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### 3.2.3.7 Reservoir host species layers

As described in section 3.2.2, occurrence data for three suspected host species were processed using Kernel Density Estimation (KDE) in ArcGIS to convert point data into continuous rasters. Occurrence records and environmental data from Section 3.2 were used to model the potential distribution of human mpox in Africa.

## 3.3 Ecological niche modeling (ENM)

### 3.3.1 Software and modelling approach

To model the potential geographic distribution of human mpox in Africa, we used the MaxEnt (Maximum Entropy) software, version 3.4.4. MaxEnt is widely adopted for ecological niche modeling using presence-only data and environmental predictors, offering strong performance even with limited occurrence records.

A total of 550 confirmed human mpox cases collected between 2010 and 2022 were used as input, along with 16 environmental predictor variables. These were selected from an original set of 33 raster layers based on Pearson correlation analysis (threshold $|r| \geq 0.7$) conducted in R. The final variables included:

1. Bioclimatic: **BIO3** (Isothermality), **BIO19** (Precipitation of Coldest Quarter)
2. Land Cover Types: **Forest, Savanna, Grassland, Wetlands, Cropland, Urban, Others**
3. Vegetation & Terrain: **Leaf Area Index, Elevation**
4. Human Factors: **Human Footprint (2010–2022 average), Population count**
5. Reservoir Host Species: ***Cricetomys* spp., *Funisciurus* spp., *Graphiurus* spp.**

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All raster data were standardized to 30 arc-second resolution, clipped to the Western and Central Africa, and projected using GCS_WGS_1984. These layers were then imported into MaxEnt for modeling to produce risk maps.

### 3.3.2 Model evaluation

In this study, the ecological niche model was developed using MaxEnt version 3.4.4 with a total of 550 georeferenced human mpox occurrence records. To ensure robust model performance and minimize overfitting, the model was run using five replicates under *k-fold cross-validation* mode. This method divides the occurrence data into five equal subsets (or "folds"), with each replicate using a different fold for testing and the remaining four for training. This process maximizes the use of available data for both training and validation, which is particularly important for presence-only datasets such as this.

The model output was generated in *logistic* format, which provides continuous environmental suitability scores ranging from 0 (unsuitable) to 1 (highly suitable). The *random test percentage* was set to 0%, meaning all 550 occurrence points were used for training in each replicate. This decision was justified because data partitioning was already addressed through cross-validation. Introducing a separate random test split would have reduced the effective training data in each fold, potentially weakening the model's performance, especially in regions with fewer presence records.

Other settings included; the regularization multiplier was set to 1, which is the default value in MaxEnt. This setting helps balance the trade-off between model fit and complexity by penalizing overfitting. Feature types were automatically selected by MaxEnt based on the characteristics of the input data, including the number of

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occurrence records and the nature of the environmental variables. Additionally, 10,000 background points were randomly sampled from within the study extent to represent the range of environmental conditions across Africa. These background points serve as pseudo-absence data, allowing the model to contrast conditions at presence locations with the broader landscape.

Model performance was evaluated using the Area Under the Curve (AUC) of the Receiver Operating Characteristic (ROC), a threshold-independent metric that quantifies the model's ability to distinguish between suitable and unsuitable environments. AUC values range from 0.5 (no better than random) to 1 (perfect discrimination), with higher values indicating better predictive performance.

To interpret the relative importance of each environmental variable, three MaxEnt-based metrics were employed: percent contribution, permutation importance, and jackknife analysis. Percent contribution indicates the proportion of influence each variable had during model training. It is determined based on the model’s internal optimization process and can be affected by correlations among predictors. Permutation importance, in contrast, measures the reduction in model performance (as assessed by AUC) when the values of each variable are randomly permuted. This method is more robust to multicollinearity and offers insight into the model’s actual dependency on individual variables. The jackknife test of variable importance further explores each variable’s unique contribution by running the model with each variable in isolation, and again by excluding each one from the full model. This approach identifies which variables provide the most independent and informative contribution to predicting human mpox distribution.

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### 3.3.3 Risk mapping and interpretation

The final logistic outputs from MaxEnt provided continuous environmental suitability values for human mpox across Africa, ranging from 0 (unsuitable) to 1 (highly suitable). To enhance interpretability and support practical risk assessment, these continuous predictions were reclassified into three discrete risk categories: **low**, **medium**, and **high**. This classification allowed for a clearer understanding of ecological risk zones and their spatial distribution.

In this study, the **10 percentile training presence logistic threshold** was chosen to define the lower boundary of environmental suitability. This thresholding method excludes the lowest 10% of training presence suitability value, accounting for potential spatial uncertainty or environmental noise in occurrence data, an important consideration when modeling zoonotic diseases like human mpox. Reported cases may be mislocated, underreported, or influenced by non-environmental factors such as surveillance bias or human mobility (Liu et al., 2005). By removing the least suitable 10% of occurrence points, the model becomes more conservative, thereby reducing overprediction in areas with only marginal suitability.

So, threshold was calculated for each of the five replicates used in cross-validation. The values ranged from **0.190 to 0.198**, with an average threshold of **0.193**. This mean threshold was used to define the cut-off for low-risk areas, with suitability values below this point considered environmentally unsuitable for mpox occurrence. To further distinguish between medium and high-risk zones, a value of 0.6 was used as an upper threshold. This medium-to-high cut-off was chosen based on the distribution of logistic outputs and visual interpretation of suitability maps, representing areas with strongly favorable environmental conditions for mpox transmission.

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Hence the suitability ranges were defined as ;

1. low risk: suitability < 0.193,
2. medium risk: 0.193 to 0.6
3. high risk: > 0.6

# Chapter 4 Results and Discussion

This chapter presents and interprets the key findings from the ENM of human mpox distribution across Central and West Africa. Results are discussed in direct alignment with the three research objectives: (1) mapping the geographic distribution of reported human mpox cases (2010–2022), (2) identifying key abiotic and biotic predictors of mpox occurrence, and (3) delineating areas of elevated spillover risk under current environmental conditions.

## 4.1 Geographic distribution of human mpox cases (2010–2022)

Figure 9 displays the geographic distribution of human mpox occurrence records across Central and West Africa between 2010 and 2022. A total of 550 confirmed cases were compiled and spatially verified, shown on the map as red points. The densest concentration of reported cases appears in the Democratic Republic of the Congo (DRC), particularly in its central, western and northern regions. This pattern aligns with mpox's established endemic zones, particularly within the Congo Basin's forested environments. Other noticeable clusters are seen in southern Nigeria, the Republic of the Congo, Central African Republic, suggesting areas of sustained transmission or more comprehensive surveillance coverage.

Smaller case clusters also occur in Cameroon, Gabon, Ghana, Côte d'Ivoire, and Liberia, potentially reflecting localized transmission events or imported cases. In contrast, countries such as Benin, South Sudan, and Sierra Leone show few reported cases during the study period. These gaps may indicate either true absence or reflect insufficient surveillance systems and underreporting in those areas.

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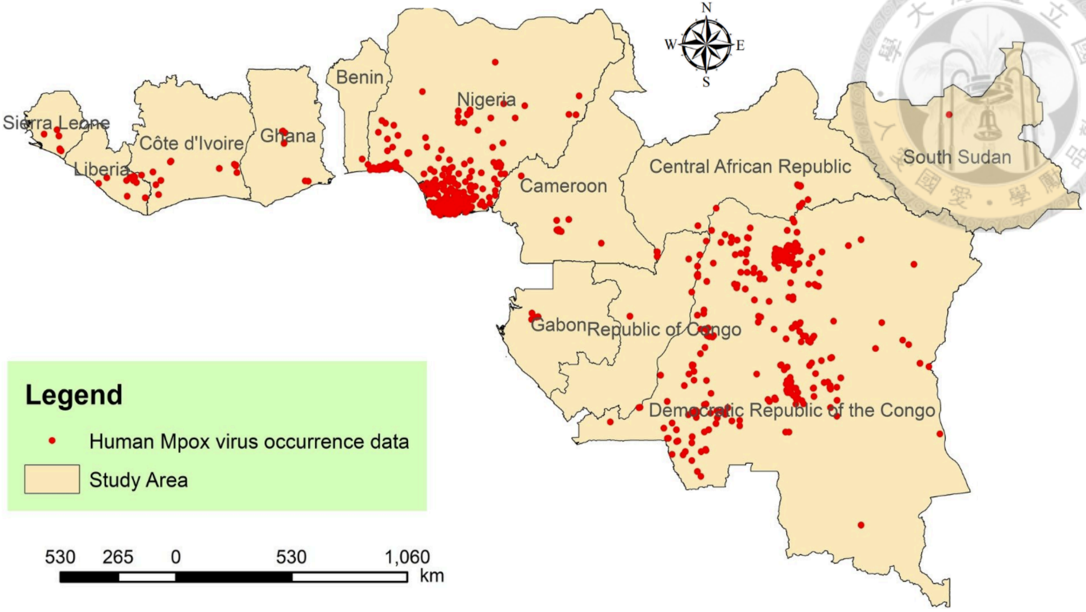

**Figure 9** Reported 550 human mpox cases locations across the study area (2010-2022). The red dots represent confirmed human mpox occurrence points compiled from literature sources. The map includes 12 countries in Central and West Africa.

### 4.2 Environmental and host variable importance in mpox distribution

The MaxEnt model performed well, with an average AUC value of 0.867 across five replicates (standard deviation = 0.013), indicating strong model performance in distinguishing between suitable and unsuitable areas for human mpox occurrence Figure 10.

Among the 16 environmental predictors used in the model, elevation emerged as the most influential, contributing 32.6% to the model and showing the highest standalone predictive power in the jackknife test. Other major contributors included population count (23.9%), precipitation of the coldest quarter (BIO19, 14.2%), leaf area index (11.2%), and the distribution of *Graphiurus* spp. (8.6%). These variables also had high permutation importance, reinforcing their unique roles in predicting mpox suitability Table 5.

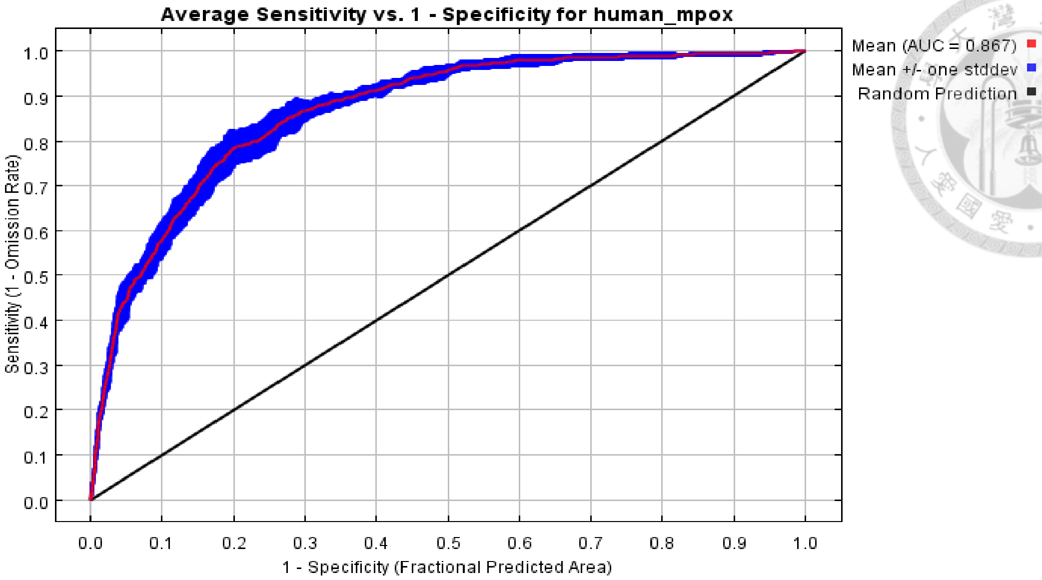

**Figure 10** Receiver operating characteristic (ROC) curve and Area Under Curve (AUC) for the MaxEnt model predicting human mpox distribution. The average AUC across five replicated MaxEnt runs was 0.867, indicating good predictive accuracy of the model in distinguishing suitable and unsuitable areas for human mpox occurrence.

**Table 5** Contribution of biotic and abiotic variables to the final suitability model

| Variable | Percent contribution | Permutation importance | Units |
|---|---|---|---|
| Elevation | 32.6 | 24.1 | Meters above sea level (m) |
| Human population count | 23.9 | 13.6 | No. of individuals |
| Precipitation of coldest quarter | 14.2 | 20.9 | Millimeter (mm) |
| Leaf area index | 11.2 | 5.0 | Ratio |
| *Graphiurus* spp. | 8.6 | 20.8 | Unitless |
| Isothermality | 3.6 | 9.2 | Percentage (%) |
| *Funisciurus* spp. | 3.5 | 2.7 | Unitless |
| Human footprint | 1.7 | 2.9 | Index scale from 0-50 |
| Others (land cover) | <1 | Very Low | % |

Note: *Percent contribution and permutation importance values reflect how much each variable influenced the final model. While percent contribution indicates how often a variable was used during model training, permutation importance measures how sensitive the model's predictions are to that variable. Higher values in either metric denote stronger influence on the predicted environmental suitability for human mpox*

The jackknife analyses affirm that **elevation** is the strongest predictor of human mpox distribution, likely due to its control over climate, vegetation type, and habitat structure (Figure 11). ***Funisciurus* spp.** emerges as a significant biotic predictor, likely due to its ecological role as a reservoir. Its predictive power overlaps with vegetation indicators like **leaf area index**, which reflect its forest-dependent habitat. ***Graphiurus* spp.**, while less impactful individually, still contributes to model performance and likely shares spatial and ecological patterns with other variables.

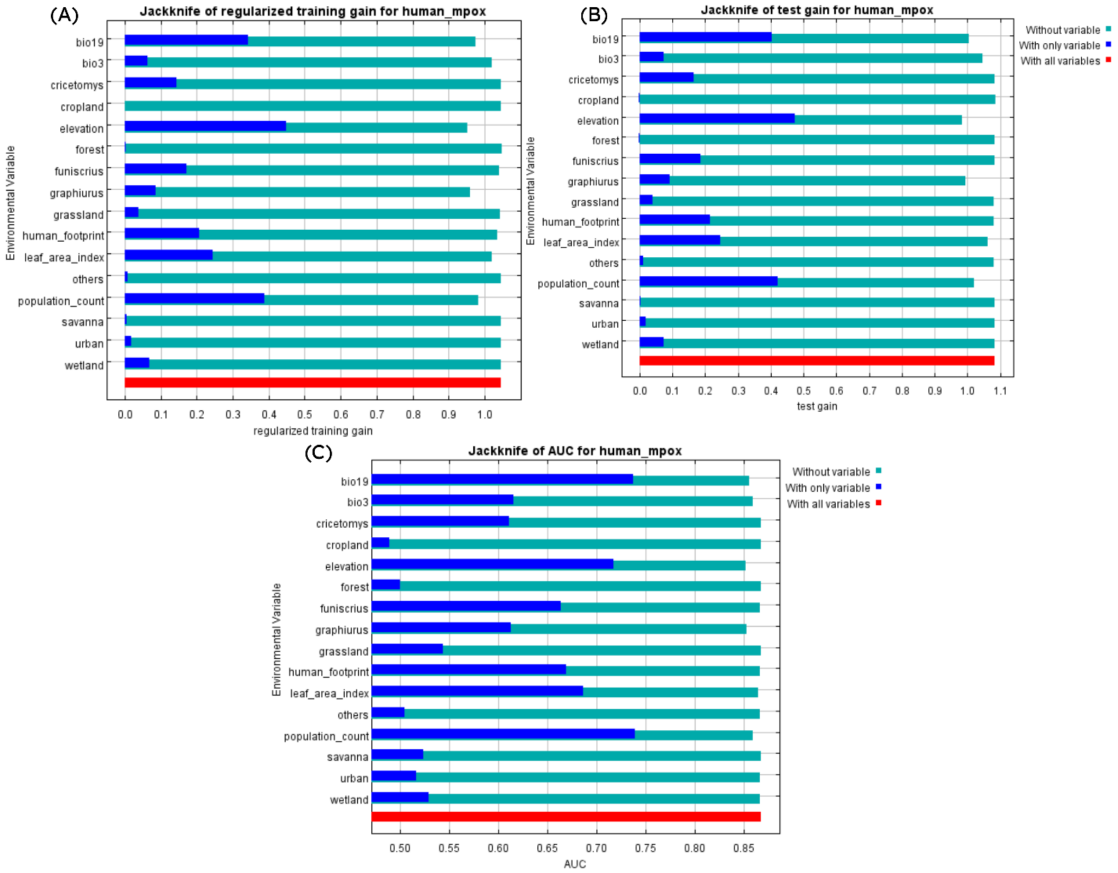

**Figure 11** Jackknife test of variable importance in the MaxEnt model for human mpox occurrences.This figure shows the individual contribution of each environmental and biotic variable to model performance, using (A) training gain, (B) test gain, and (C) AUC when used in isolation and when omitted. The blue bars represent the model gain when the variable is used in isolation, indicating how much useful information the variable provides on its own. The light green bars show the model gain when the variable is omitted, illustrating how much unique information is lost when that variable is excluded. The red bars indicate the gain when all variables are used together. Variables with tall blue bars contribute strong predictive power independently, while those with short green bars contain information not present in other variables.

Figure 12 (a-g) The response curves from the MaxEnt model illustrate how various environmental, anthropogenic, and biotic factors individually influence the predicted suitability for human mpox occurrence across the study area. Elevation (Fig.12 a) shows a negative relationship with suitability, where lower elevations (particularly below 500 meters) are associated with higher mpox suitability, likely reflecting the ecological characteristics of tropical lowland forests where both human activity and reservoir species are more common. Population count (Fig.12b) exhibits a positive association with suitability, increasing steadily up to around 40,000 people per km², which suggests that densely populated areas provide more opportunities for zoonotic transmission and human-to-human spread. Similarly, the leaf area index (Fig. 12d), a proxy for forest density, is positively correlated with mpox suitability, indicating that dense vegetation likely supports reservoir habitats conducive to virus maintenance and transmission. Climatic variables also played a significant role in shaping mpox distribution. Precipitation of the coldest quarter (BIO19) (Fig.12c) shows that suitability peaks around 10,000 mm and declines thereafter, suggesting that moderate to high rainfall during colder months may promote suitable ecological conditions for the virus and its hosts. Isothermality (BIO3) (Fig.12f), which reflects temperature stability, shows a rising trend beyond 7.5%, implying that environments with more consistent temperature patterns may support mpox persistence. The response of biotic variables provides insight into reservoir hosts contributions. *Funisciurus* spp. (Fig.12g), is strongly associated with high suitability values across most KDE density ranges, supporting its role. In contrast, *Graphiurus* spp. (Fig.12e) shows an inverse relationship, where higher KDE densities correspond to decreased suitability, potentially due to ecological niche segregation or spatial mismatches between *Graphiurus* presence and human mpox cases. Lastly, the human footprint (Fig.12h), an index of anthropogenic disturbance,

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shows a strong positive relationship with suitability, with the highest values nearing the maximum of the scale.These findings emphasize the multifactorial nature of mpox risk, where topographic, climatic, human, and biological factors jointly determine the risk landscape across Central and West Africa.

Interestingly, among the three host species modeled in this study, *Funisciurus* spp. showed a positive association with the ecological suitability of human mpox, whereas *Graphiurus* spp. and *Cricetomys* spp. demonstrated a negative relationship. This variation may be attributed to differences in ecological behavior and habitat preferences. *Funisciurus*, being diurnal and more arboreal, frequently occupies ecotones and disturbed habitats near human settlements, thereby increasing the likelihood of human contact and potential spillover (Kingdon, 2015; Omifolaji et al., 2022). In contrast, *Graphiurus* and *Cricetomys* may occupy more specialized or less disturbed habitats, and their interaction with humans could be more limited or context-specific, reducing their apparent contribution to human mpox risk (Lang et al., 2020; Vesey-Fitzgerald, 1966).

Furthermore, the interaction between human population count and the human footprint index varied across the study area. In countries like the DRC, despite having a large population, the human footprint index was relatively low. This discrepancy may be explained by several factors. First, infrastructure development and global connectivity in DRC remain limited due to poor socio-economic conditions and longstanding political instability (World Bank, 2023; ENACT Africa, 2021), which in turn may constrain internal mobility and reduce the scale of environmental disturbance typically associated with urbanization. Consequently, the opportunities for widespread human-wildlife interaction that often drive zoonotic transmission may be lower in such settings.

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Moreover, DRC has historically borne the highest burden of mpox but remains relatively isolated from international travel corridors. Rigorous border health screenings and containment strategies for individuals traveling from endemic regions, especially natives, have likely helped limit the external spread of the disease (Bunge et al., 2022; WHO, 2023). These layers of geographic and socio-political insulation could explain the weak correlation between human footprint and population count in high-endemic but low-footprint areas like DRC. It underscores that while population pressure is often a driver of zoonotic disease emergence, its impact is modulated by infrastructural, economic, and governance contexts, which in turn shape the patterns of disease transmission and reporting.

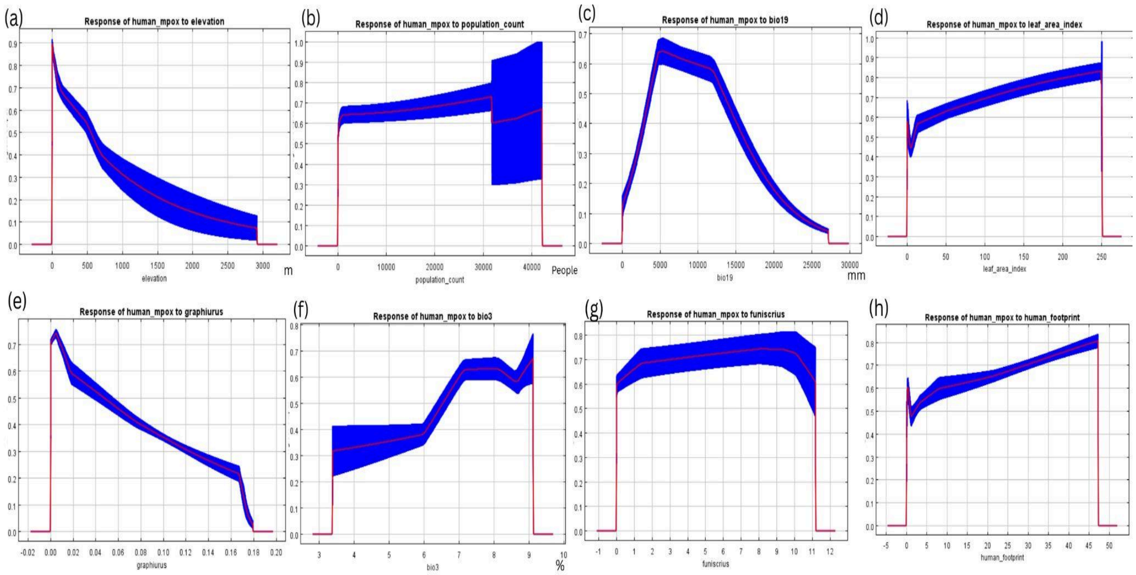

**Figure 12** Responsive curve of predictive continuous variables.Each curve represents how the predicted environmental suitability for human mpox changes in response to a single variable, while keeping all others at their average value. The **red line** shows the **mean logistic prediction**, and the **blue shaded area** represents the **standard deviation**, indicating the uncertainty across replicated model runs. ((a)elevation (m), (b)population count (people), (c) precipitation of the coldest (BIO19, mm) (d) leaf area index, (e) *Graphiurus* spp. (f) isothermality (BIO3, (%))(g) *Funiscrius* spp. (h)human footprint

### 4.3 Predicted suitability and high-risk zones

Using the final logistic outputs from MaxEnt, environmental suitability predictions were classified into **three risk categories** (low, medium, high) based on the 10th percentile training presence threshold. This allowed for classification of ecological risk zones under current conditions.

The resulting map (Figure 13) reveals that **high-risk zones** (in red) are concentrated primarily in the central, western and northern regions of the Democratic Republic of the Congo (DRC), with notable extensions into the southern Central African Republic, northern Republic of the Congo. In West Africa, southeastern Nigeria, southern Benin, and parts of Liberia, Sierra Leone and Côte d'Ivoire also exhibit high suitability. These areas align with tropical rainforest and forest-savanna ecotones, which are known to support both the ecological requirements of the virus and the distribution of key host species.

**Medium-risk zones** (in orange) appear across parts of central Nigeria, interior Gabon, southern Cameroon, and northern Liberia and Sierra Leona and a huge part of Benin, Ghana and Cote d'Ivoire, representing transitional savanna-forest with partial suitability. These regions may still appear disease emergence under shifting climatic or land use patterns.

**Low-risk zones** (in blue) dominate northern West Africa, South Sudan, northeastern Central African Republic, and high-altitude plateaus in the eastern DRC. These regions are typically drier, more sparsely vegetated, absence of reservoir host , or more urbanized, and lack suitable environmental or biological conditions to sustain mpox transmission.

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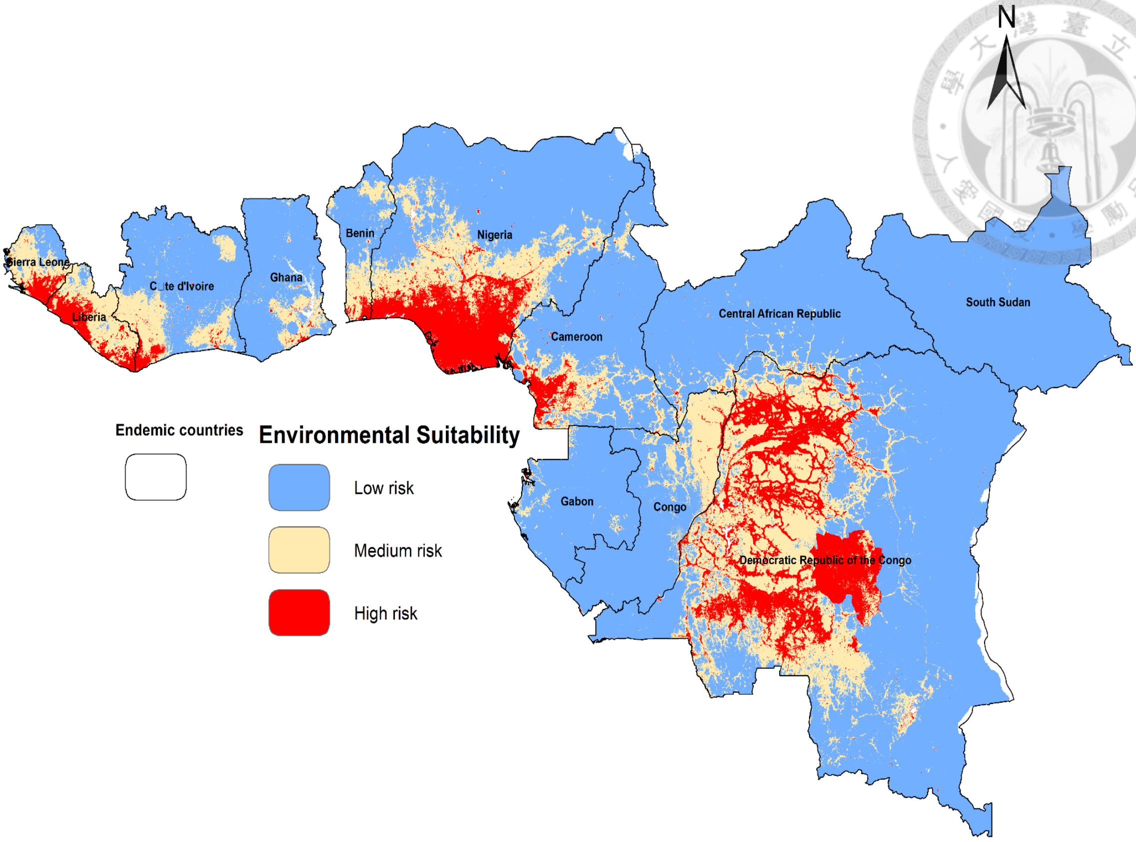

**Figure** 13 Predicted environmental suitability map for human mpox in West and Central Africa. Based on MaxEnt model results, classified into low (blue), medium (orange), and high (red) risk zones. High-risk zones occur primarily in the Congo Basin and forested parts of West Africa, where environmental conditions, reservoir species presence, and moderate human activity converge to support zoonotic spillover of mpox.

The prediction of mpox spread in Central and Western Africa reveals significant concerns for countries in proximity to endemic regions, notably Togo and Equatorial Guinea, which currently show no confirmed cases. These nations, given their geographic location, ecological characteristics, and lack of prior exposure, remain highly vulnerable to future outbreaks. Contributing to this risk, accelerated tropical deforestation, projected to increase by approximately 30% by 2030 (Bedair et al., 2023), and intensive land-use changes are expected to exacerbate climate change impacts significantly in tropical Africa (Bedair et al., 2023). Climate models predict an average temperature rise of 1.5 to 2.0°C by 2030, alongside a 10-15% reduction in precipitation during dry seasons, and intensified rainfall by up to 20% during wet seasons (https://www.uneca.org/acpc). These climatic extremes are likely to amplify wildfires, with estimates suggesting wildfire occurrences could increase by over 25% in the coming decades (Wimberly et al., 2024). Such environmental disruptions will lead to habitat degradation and increased human-wildlife interactions, substantially raising the potential for zoonotic disease transmission, including mpox (Esposito et al., 2023). Additionally, shifting climatic conditions are expected to expand suitable habitats for reservoirs and vectors of the virus, increasing the risk of disease emergence in previously unaffected regions. For countries with low or moderate risk, such as Cote d'Ivore, South Sudan, Gabon, Congo and Ghana, climate-related concerns include increased flooding risks due to extreme rainfall, drought-induced agricultural stress, and potential displacement of populations (Bedair et al., 2023). These factors could further strain healthcare resources and undermine public health infrastructure, indirectly elevating their vulnerability to mpox outbreaks. This scenario underscores the urgent need for proactive public health measures, disease surveillance, and ecological management strategies in vulnerable countries to mitigate the anticipated rise in mpox incidence driven by climate and environmental changes.

### 4.4 Population exposure and public health implications

To assess the population under mpox exposure risk, 2020 population count data from WorldPop 2020 were overlaid with the risk map to estimate population exposure by country and risk class (Figure 14). The analysis revealed that **Democratic Republic of the Congo (DRC)** exhibited the highest population at risk, with approximately **110 million people** in low-risk areas, **~49 million** in medium-risk areas, and **~29 million** residing in high-risk zones. Other countries with significant at-risk populations include **South Sudan** (notably in low-risk zones), **Nigeria**, and **Cameroon**, all showing millions of people residing within medium to high suitability regions. Although

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countries like **Benin**, **Gabon**, **Liberia**, and **Sierra Leone** showed comparatively lower absolute populations at risk, the presence of high and medium risk zones within their territories indicates potential localized hotspots for spillover events.

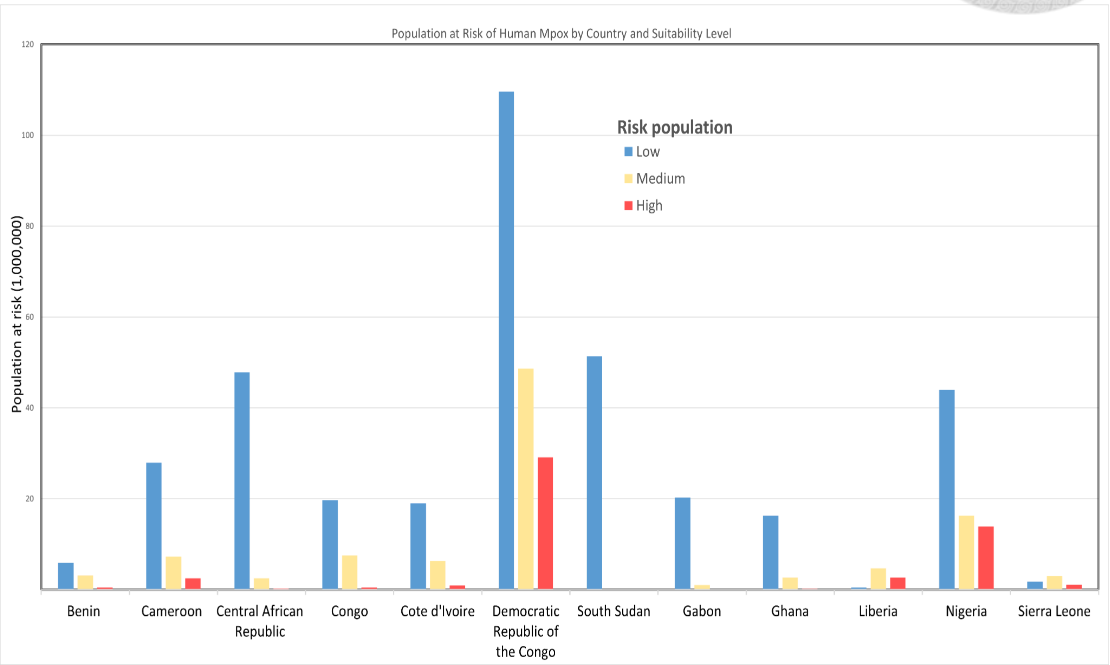

**Figure 14** Estimated population at risk of human mpox by risk class and country. Bar chart expresses the estimated population (in millions) residing in low (blue), medium (orange), and high (red) suitability zones across 12 African countries based on environmental risk modeling. Population data derived from WorldPop 2020.The Democratic Republic of the Congo (DRC) and Nigeria exhibit the highest total populations exposed to high environmental suitability zones, exceeding 29 million and 13 million people, respectively.

## 4.5 Limitations and uncertainties

While the MaxEnt modeling framework provides a valuable spatial tool for estimating environmental suitability for human mpox, several limitations and assumptions must be acknowledged when interpreting the results.

First, the study is constrained by the **quality and completeness of human mpox occurrence data**, which depend heavily on national surveillance and reporting systems. While MaxEnt is well-suited to handling presence-only data, the availability of such data remains uneven across the study region. Most occurrence records come from countries with stronger health infrastructure and ongoing surveillance programs—such as the Democratic Republic of the Congo, Nigeria, and the Central African Republic. This results in **geographic bias**, as areas with limited case reporting (e.g., South Sudan, and Sierra Leone) may appear free of disease despite possible underreporting or diagnostic challenges. Thus, gaps in reporting—not model limitations—may partly explain discrepancies between predicted suitability and observed cases..

Second, the environmental variables used in this study were aggregated or averaged over multiple years, particularly for layers like human footprint (2010–2022), precipitation (BIO19), population count, and vegetation indices. This approach was taken to align the environmental data with the temporal range of mpox case records (2010–2022). While averaging helps account for inter-annual variability and missing data, it also introduces uncertainty by smoothing out short-term fluctuations that might be important for mpox emergence in specific years. Additionally, does not currently account for seasonality, which could play a role in viral transmission dynamics.

Third, the study used **proxy measures for biotic factors**, particularly host reservoir distributions. Kernel density estimation (KDE) was applied to GBIF presence data for *Funisciurus, Graphiurus*, and *Cricetomys* spp. to generate relative habitat suitability maps. However, these proxies do not represent actual host abundance, infection prevalence, or confirmed involvement in mpox transmission. Additionally, spatial sampling effort varies between regions and species, which may introduce further uncertainty in interpreting biotic-environmental interactions..

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Finally, the model represents a static snapshot of current environmental conditions and does not incorporate future scenarios such as land-use change, deforestation, urbanization, or climate change. Given that many of the ecological drivers of mpox transmission are dynamic, future work should explore spatiotemporal modeling frameworks and scenario-based forecasting to assess how risk patterns may evolve over time.

### 4.6 Strengths of this study

This study demonstrates several strengths when compared to previous ecological niche modeling[1] efforts of human mpox (Table 6). In terms of geographic scope, while earlier studies often focused on single countries or subregions, this research expands the coverage to multiple endemic countries across Central and West Africa, providing a more comprehensive regional assessment. Unlike many past studies that relied solely on abiotic environmental variables, the present study integrates a diverse set of predictors, including human demographic data and reservoir species distributions, thereby enhancing ecological realism. Additionally, the use of recent confirmed mpox cases from 2010 to 2022 offers a more up-to-date representation of disease distribution compared to prior studies that primarily used historical records from the 1970s and 1980s. Methodologically, although various models have been used in the literature including GLMs, GAMs, RF, and BRT this study exclusively applies MaxEnt, which is well-suited for presence-only data and widely accepted in ecological niche modeling. Importantly, this study advances public health relevance by directly incorporating population data to estimate potential human exposure, moving beyond general ecological conclusions to inform targeted surveillance and preparedness efforts.

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[1] Refer to Appendix 3 for the full list of cited studies (n = 19) on ecological modeling.

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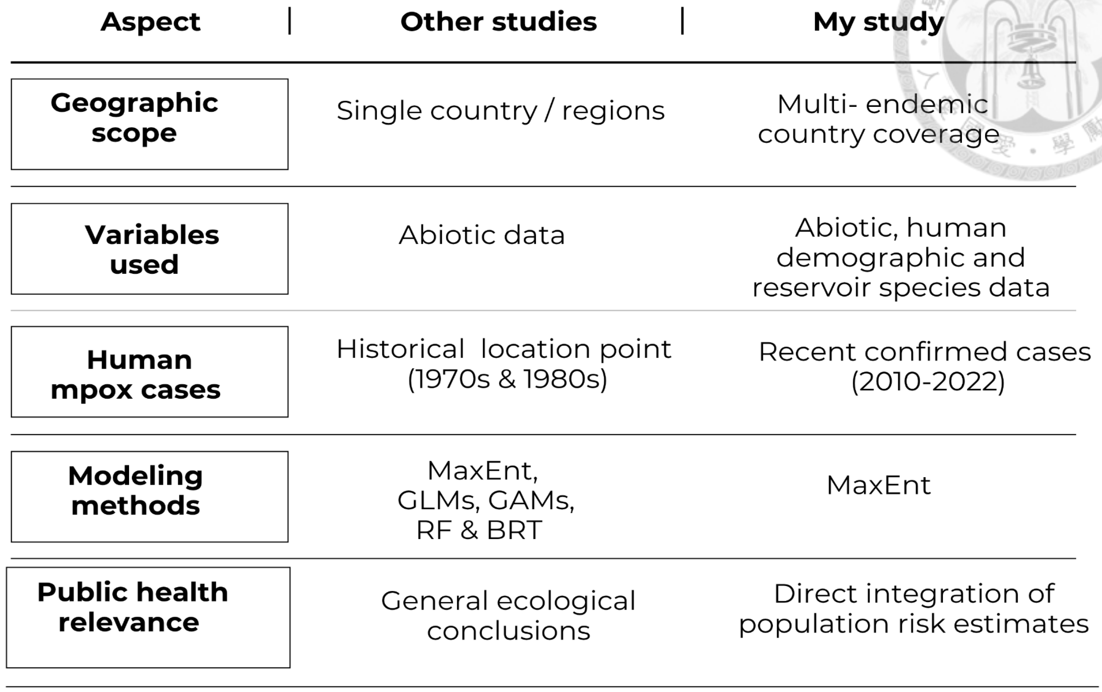
**Table 6** Summary comparison between this study and previous ecological studies on human mpox in Africa



| Aspect | Other studies | My study |
|---|---|---|
| **Geographic scope** | Single country / regions | Multi- endemic country coverage |
| **Variables used** | Abiotic data | Abiotic, human demographic and reservoir species data |
| **Human mpox cases** | Historical location point (1970s & 1980s) | Recent confirmed cases (2010-2022) |
| **Modeling methods** | MaxEnt,<br>GLMs, GAMs,<br>RF & BRT | MaxEnt |
| **Public health relevance** | General ecological conclusions | Direct integration of population risk estimates |

# Chapter 5 Conclusion

This study applied ENM to estimate the environmental suitability and spatial spillover risk of human mpox across Central and West Africa. By integrating 550 confirmed human mpox occurrence records (2010–2022) with 16 carefully selected abiotic, biotic, and anthropogenic variables, a well-performing MaxEnt model (mean AUC = 0.867) was developed. The areas with high risk of mpox are related to elevation, precipitation in the coldest quarter (BIO19), leaf area index, population count, and the presence of reservoir species, especially *Funiscurus* and *Graphiurus* spp.

The model's predictions highlighted that high-risk zones are concentrated in the central, western and northern regions of the Democratic Republic of the Congo (DRC), southern Central African Republic (CAR), southern Nigeria, southern Benin and Sierra Leone. These areas represent ecological settings with favorable conditions for mpox transmission and host persistence. In contrast, low-risk zones were located in drier northern regions and high-altitude plateaus, where ecological conditions are less suitable for the virus and its reservoirs.

To enhance understanding of potential human risk, population data from WorldPop (2020) were overlaid with the predicted risk zones. Results revealed that the DRC and Nigeria host the largest populations within high-suitability areas, with DRC alone having more than 29 million people residing in high-risk zones. Cameroon, Côte d'Ivoire,Liberia and Ghana also showed significant populations exposed to medium- and high-risk areas. Even countries with smaller populations, such as Benin and Sierra Leone, demonstrated notable localized vulnerability. This demographic overlay reinforces the urgent need for targeted surveillance, health infrastructure, and One

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Health interventions, especially in peri-urban and rural communities where ecological risk and human presence converge.

Nonetheless, the findings provide critical insight into the geography of mpox risk in Africa. This model serves as a baseline for future research and supports policy-making in the context of zoonotic surveillance. Future work should explore temporal dynamics, climate change scenarios, and socioecological drivers that may shift mpox distribution over time.

In conclusion, this study demonstrates that ecological suitability, host presence, and human exposure are all interlinked in shaping the distribution of mpox. By combining ecological niche modeling with population data, it identifies spatial hotspots of potential spillover and helps prioritize regions for future One Health–focused interventions and disease preparedness.

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# Appendices

## **Appendix 1** Human mpox case locations used in ENM

| No. | Positive Hosts | Longitude | Latitude | No. | Positive Hosts | Longitude | Latitude |
|---|---|---|---|---|---|---|---|
| 1 | human mpox | -8.37 | 6.07 | 276 | human mpox | 5.66 | 5.31 |
| 2 | human mpox | -1.27 | 8.16 | 277 | human mpox | 5.70 | 5.41 |
| 3 | human mpox | -0.20 | 5.91 | 278 | human mpox | 5.87 | 5.34 |
| 4 | human mpox | 18.08 | 1.67 | 279 | human mpox | 5.98 | 5.26 |
| 5 | human mpox | 21.93 | 2.39 | 280 | human mpox | 5.62 | 4.93 |
| 6 | human mpox | 22.24 | 2.91 | 281 | human mpox | 5.77 | 4.91 |
| 7 | human mpox | 24.23 | -3.48 | 282 | human mpox | 5.99 | 4.93 |
| 8 | human mpox | -1.24 | 8.18 | 283 | human mpox | 5.60 | 4.80 |
| 9 | human mpox | -8.19 | 6.13 | 284 | human mpox | 5.77 | 4.76 |
| 10 | human mpox | -6.45 | 6.81 | 285 | human mpox | 5.87 | 4.72 |
| 11 | human mpox | -3.43 | 6.60 | 286 | human mpox | 5.77 | 4.67 |
| 12 | human mpox | 4.63 | 7.19 | 287 | human mpox | 6.10 | 5.03 |
| 13 | human mpox | 7.38 | 5.05 | 288 | human mpox | 6.17 | 5.05 |
| 14 | human mpox | 11.52 | 3.68 | 289 | human mpox | 6.34 | 5.16 |
| 15 | human mpox | 11.73 | 3.61 | 290 | human mpox | 6.37 | 5.12 |
| 16 | human mpox | 16.18 | 2.69 | 291 | human mpox | 6.42 | 5.15 |
| 17 | human mpox | 18.81 | 2.17 | 292 | human mpox | 6.40 | 5.31 |
| 18 | human mpox | 18.37 | 0.04 | 293 | human mpox | 6.18 | 4.99 |
| 19 | human mpox | 17.87 | -2.46 | 294 | human mpox | 6.24 | 4.93 |
| 20 | human mpox | 17.67 | -2.87 | 295 | human mpox | 6.28 | 4.95 |
| 21 | human mpox | 18.56 | -0.78 | 296 | human mpox | 6.34 | 4.88 |
| 22 | human mpox | 18.62 | -1.17 | 297 | human mpox | 6.20 | 4.84 |
| 23 | human mpox | 18.83 | -1.12 | 298 | human mpox | 6.12 | 4.81 |
| 24 | human mpox | 18.47 | -4.23 | 299 | human mpox | 6.24 | 4.80 |
| 25 | human mpox | 18.08 | -4.59 | 300 | human mpox | 6.21 | 4.68 |
| 26 | human mpox | 19.33 | -4.62 | 301 | human mpox | 6.15 | 4.68 |
| 27 | human mpox | 18.59 | -5.40 | 302 | human mpox | 6.17 | 4.61 |
| 28 | human mpox | 18.47 | -6.34 | 303 | human mpox | 6.14 | 4.56 |
| 29 | human mpox | 18.23 | -7.52 | 304 | human mpox | 6.09 | 4.60 |
| 30 | human mpox | 17.81 | -6.80 | 305 | human mpox | 5.98 | 4.60 |
| 31 | human mpox | 17.40 | -6.54 | 306 | human mpox | 5.94 | 4.62 |
| 32 | human mpox | 17.10 | -5.94 | 307 | human mpox | 5.98 | 4.67 |
| 33 | human mpox | 16.72 | -5.79 | 308 | human mpox | 5.81 | 4.50 |
| 34 | human mpox | 20.04 | -5.22 | 309 | human mpox | 5.94 | 4.52 |
| 35 | human mpox | 21.02 | -0.28 | 310 | human mpox | 5.99 | 4.45 |
| 36 | human mpox | 22.19 | -1.27 | 311 | human mpox | 6.09 | 4.35 |
| 37 | human mpox | 24.41 | -0.47 | 312 | human mpox | 6.38 | 4.43 |
| 38 | human mpox | 24.27 | -2.14 | 313 | human mpox | 6.45 | 4.41 |
| 39 | human mpox | 24.57 | -4.06 | 314 | human mpox | 6.55 | 4.40 |
| 40 | human mpox | 21.35 | -4.03 | 315 | human mpox | 6.66 | 4.47 |
| 41 | human mpox | 21.70 | -4.03 | 316 | human mpox | 6.77 | 4.40 |
| 42 | human mpox | 23.01 | -4.22 | 317 | human mpox | 6.81 | 4.49 |
| 43 | human mpox | 22.75 | -3.98 | 318 | human mpox | 6.85 | 4.45 |
| 44 | human mpox | 22.31 | -3.71 | 319 | human mpox | 6.67 | 4.74 |
| 45 | human mpox | 22.66 | -3.51 | 320 | human mpox | 6.57 | 4.61 |
| 46 | human mpox | 22.40 | -3.35 | 321 | human mpox | 6.52 | 4.60 |
| 47 | human mpox | 22.39 | -3.02 | 322 | human mpox | 6.43 | 4.59 |
| 48 | human mpox | 22.90 | -1.41 | 323 | human mpox | 6.52 | 4.67 |
| 49 | human mpox | 23.04 | -1.14 | 324 | human mpox | 6.59 | 4.66 |
| 50 | human mpox | 23.49 | -1.14 | 325 | human mpox | 6.48 | 4.72 |
| 51 | human mpox | 23.32 | -1.42 | 326 | human mpox | 6.40 | 4.81 |
| 52 | human mpox | 22.68 | -0.70 | 327 | human mpox | 6.51 | 4.92 |
| 53 | human mpox | 22.86 | -0.53 | 328 | human mpox | 6.57 | 4.80 |
| 54 | human mpox | 20.72 | 0.50 | 329 | human mpox | 6.64 | 5.02 |
| 55 | human mpox | 20.34 | 2.58 | 330 | human mpox | 6.71 | 5.05 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 56 | human mpox | 20.39 | 2.79 | 331 | human mpox | 6.71 | 5.12 |
| 57 | human mpox | 20.39 | 3.34 | 332 | human mpox | 6.74 | 5.21 |
| 58 | human mpox | 23.41 | 2.44 | 333 | human mpox | 6.81 | 5.14 |
| 59 | human mpox | 23.59 | 1.16 | 334 | human mpox | 6.80 | 5.06 |
| 60 | human mpox | 22.51 | 0.53 | 335 | human mpox | 6.81 | 4.98 |
| 61 | human mpox | 22.40 | 1.28 | 336 | human mpox | 6.92 | 4.92 |
| 62 | human mpox | 21.68 | 2.37 | 337 | human mpox | 6.82 | 4.87 |
| 63 | human mpox | 22.56 | 1.85 | 338 | human mpox | 6.90 | 4.78 |
| 64 | human mpox | 22.75 | 2.12 | 339 | human mpox | 6.98 | 4.76 |
| 65 | human mpox | 21.94 | 2.68 | 340 | human mpox | 7.04 | 4.70 |
| 66 | human mpox | 26.65 | -0.53 | 341 | human mpox | 7.17 | 4.86 |
| 67 | human mpox | 22.86 | 2.73 | 342 | human mpox | 7.13 | 4.84 |
| 68 | human mpox | 22.64 | 3.09 | 343 | human mpox | 7.21 | 4.84 |
| 69 | human mpox | 22.25 | 2.55 | 344 | human mpox | 7.15 | 4.92 |
| 70 | human mpox | 22.56 | 2.77 | 345 | human mpox | 7.13 | 5.02 |
| 71 | human mpox | 28.15 | 2.12 | 346 | human mpox | 7.03 | 5.04 |
| 72 | human mpox | -1.18 | 7.65 | 347 | human mpox | 6.98 | 5.11 |
| 73 | human mpox | -8.14 | 6.09 | 348 | human mpox | 6.92 | 5.19 |
| 74 | human mpox | -7.82 | 6.17 | 349 | human mpox | 6.74 | 5.33 |
| 75 | human mpox | -6.48 | 6.78 | 350 | human mpox | 6.95 | 4.56 |
| 76 | human mpox | -3.43 | 6.60 | 351 | human mpox | 7.29 | 4.84 |
| 77 | human mpox | 4.58 | 7.19 | 352 | human mpox | 7.29 | 4.75 |
| 78 | human mpox | 7.43 | 5.11 | 353 | human mpox | 7.22 | 4.69 |
| 79 | human mpox | 7.33 | 4.93 | 354 | human mpox | 7.34 | 4.71 |
| 80 | human mpox | 12.07 | 4.16 | 355 | human mpox | 7.29 | 4.63 |
| 81 | human mpox | 11.60 | 3.71 | 356 | human mpox | 7.26 | 4.59 |
| 82 | human mpox | 11.71 | 3.61 | 357 | human mpox | 7.27 | 4.50 |
| 83 | human mpox | 10.36 | -0.10 | 358 | human mpox | 7.31 | 4.51 |
| 84 | human mpox | 10.34 | -0.39 | 359 | human mpox | 7.50 | 4.67 |
| 85 | human mpox | 10.56 | -0.29 | 360 | human mpox | 7.55 | 4.73 |
| 86 | human mpox | 16.21 | 2.68 | 361 | human mpox | 7.61 | 5.05 |
| 87 | human mpox | 18.09 | 3.87 | 362 | human mpox | 7.30 | 5.16 |
| 88 | human mpox | 18.73 | 3.66 | 363 | human mpox | 7.25 | 5.19 |
| 89 | human mpox | 19.16 | 3.12 | 364 | human mpox | 7.63 | 5.19 |
| 90 | human mpox | 18.07 | 2.04 | 365 | human mpox | 7.66 | 5.21 |
| 91 | human mpox | 18.08 | 1.56 | 366 | human mpox | 7.75 | 5.19 |
| 92 | human mpox | 18.50 | 1.34 | 367 | human mpox | 7.18 | 5.40 |
| 93 | human mpox | 19.92 | 3.22 | 368 | human mpox | 7.00 | 5.37 |
| 94 | human mpox | 20.44 | 3.31 | 369 | human mpox | 6.95 | 5.37 |
| 95 | human mpox | 20.37 | 2.79 | 370 | human mpox | 6.82 | 5.43 |
| 96 | human mpox | 20.09 | 2.62 | 371 | human mpox | 6.66 | 5.42 |
| 97 | human mpox | 19.83 | 2.56 | 372 | human mpox | 6.64 | 5.51 |
| 98 | human mpox | 20.33 | 2.22 | 373 | human mpox | 6.58 | 5.56 |
| 99 | human mpox | 20.08 | 1.76 | 374 | human mpox | 6.91 | 5.72 |
| 100 | human mpox | 20.38 | 1.75 | 375 | human mpox | 6.78 | 5.80 |
| 101 | human mpox | 20.68 | 1.73 | 376 | human mpox | 7.26 | 5.87 |
| 102 | human mpox | 21.18 | 1.46 | 377 | human mpox | 7.47 | 5.61 |
| 103 | human mpox | 20.97 | 1.46 | 378 | human mpox | 7.52 | 5.71 |
| 104 | human mpox | 19.92 | 1.19 | 379 | human mpox | 7.72 | 5.66 |
| 105 | human mpox | 18.36 | -0.12 | 380 | human mpox | 7.95 | 4.84 |
| 106 | human mpox | 18.06 | -0.19 | 381 | human mpox | 8.03 | 4.96 |
| 107 | human mpox | 22.25 | 3.66 | 382 | human mpox | 8.15 | 4.76 |
| 108 | human mpox | 22.50 | 4.18 | 383 | human mpox | 8.38 | 5.16 |
| 109 | human mpox | 22.72 | 2.99 | 384 | human mpox | 8.07 | 5.55 |
| 110 | human mpox | 22.83 | 2.72 | 385 | human mpox | 7.46 | 6.08 |
| 111 | human mpox | 23.27 | 2.15 | 386 | human mpox | 7.55 | 6.35 |
| 112 | human mpox | 22.80 | 2.15 | 387 | human mpox | 8.00 | 6.28 |
| 113 | human mpox | 22.54 | 2.15 | 388 | human mpox | 7.21 | 6.68 |
| 114 | human mpox | 22.48 | 2.46 | 389 | human mpox | 7.49 | 6.84 |
| 115 | human mpox | 22.61 | 2.70 | 390 | human mpox | 8.58 | 6.75 |
| 116 | human mpox | 22.40 | 2.95 | 391 | human mpox | 8.83 | 6.75 |
| 117 | human mpox | 21.91 | 2.75 | 392 | human mpox | 8.92 | 6.65 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 118 | human mpox | 21.82 | 2.51 | 393 | human mpox | 8.89 | 6.54 |
| 119 | human mpox | 21.66 | 2.16 | 394 | human mpox | 8.70 | 6.56 |
| 120 | human mpox | 21.84 | 1.95 | 395 | human mpox | 8.91 | 6.23 |
| 121 | human mpox | 22.18 | 2.40 | 396 | human mpox | 9.10 | 6.23 |
| 122 | human mpox | 22.23 | 2.69 | 397 | human mpox | 8.61 | 6.00 |
| 123 | human mpox | 22.51 | 0.64 | 398 | human mpox | 8.76 | 5.78 |
| 124 | human mpox | 21.40 | 0.43 | 399 | human mpox | 8.65 | 5.47 |
| 125 | human mpox | 22.50 | 0.52 | 400 | human mpox | 8.66 | 5.25 |
| 126 | human mpox | 20.90 | -0.51 | 401 | human mpox | 8.65 | 11.31 |
| 127 | human mpox | 21.64 | -0.83 | 402 | human mpox | 10.03 | 9.33 |
| 128 | human mpox | 18.77 | -1.19 | 403 | human mpox | 9.04 | 9.42 |
| 129 | human mpox | 18.52 | -1.13 | 404 | human mpox | 8.44 | 8.77 |
| 130 | human mpox | 18.48 | -0.84 | 405 | human mpox | 9.58 | 8.77 |
| 131 | human mpox | 18.22 | -0.83 | 406 | human mpox | 7.48 | 9.14 |
| 132 | human mpox | 18.42 | -1.66 | 407 | human mpox | 7.48 | 9.02 |
| 133 | human mpox | 22.83 | -0.59 | 408 | human mpox | 7.36 | 8.92 |
| 134 | human mpox | 22.83 | -0.93 | 409 | human mpox | 7.20 | 8.56 |
| 135 | human mpox | 22.99 | -1.13 | 410 | human mpox | 6.93 | 8.57 |
| 136 | human mpox | 23.42 | -1.23 | 411 | human mpox | 6.91 | 8.83 |
| 137 | human mpox | 23.23 | -1.35 | 412 | human mpox | 6.93 | 9.10 |
| 138 | human mpox | 23.24 | 1.21 | 413 | human mpox | 7.85 | 8.21 |
| 139 | human mpox | 23.76 | 1.73 | 414 | human mpox | 9.01 | 7.63 |
| 140 | human mpox | 23.70 | 1.12 | 415 | human mpox | 8.53 | 7.44 |
| 141 | human mpox | 23.53 | 1.21 | 416 | human mpox | 12.41 | 8.92 |
| 142 | human mpox | 23.87 | 2.69 | 417 | human mpox | 12.08 | 8.93 |
| 143 | human mpox | 22.57 | 4.04 | 418 | human mpox | 12.56 | 9.78 |
| 144 | human mpox | 25.69 | 3.24 | 419 | human mpox | 6.32 | 5.48 |
| 145 | human mpox | 24.32 | -2.12 | 420 | human mpox | 6.23 | 5.52 |
| 146 | human mpox | 23.39 | -2.36 | 421 | human mpox | 6.26 | 5.69 |
| 147 | human mpox | 23.29 | -2.48 | 422 | human mpox | 6.15 | 5.77 |
| 148 | human mpox | 24.56 | -3.47 | 423 | human mpox | 22.73 | 5.74 |
| 149 | human mpox | 24.25 | -3.39 | 424 | human mpox | 22.76 | 5.70 |
| 150 | human mpox | 24.26 | -3.55 | 425 | human mpox | 22.80 | 5.70 |
| 151 | human mpox | 23.48 | -3.50 | 426 | human mpox | 22.85 | 5.68 |
| 152 | human mpox | 24.56 | -4.78 | 427 | human mpox | 22.86 | 5.70 |
| 153 | human mpox | 22.94 | -4.08 | 428 | human mpox | 22.88 | 5.68 |
| 154 | human mpox | 22.65 | -4.23 | 429 | human mpox | 22.86 | 5.66 |
| 155 | human mpox | 22.67 | -4.00 | 430 | human mpox | 22.95 | 4.90 |
| 156 | human mpox | 22.54 | -3.85 | 431 | human mpox | 22.81 | 4.77 |
| 157 | human mpox | 22.33 | -3.70 | 432 | human mpox | 22.83 | 4.77 |
| 158 | human mpox | 22.46 | -3.46 | 433 | human mpox | 22.81 | 4.74 |
| 159 | human mpox | 22.42 | -3.21 | 434 | human mpox | 22.84 | 4.73 |
| 160 | human mpox | 22.25 | -3.16 | 435 | human mpox | 19.65 | 3.35 |
| 161 | human mpox | 21.66 | -3.95 | 436 | human mpox | 19.63 | 3.11 |
| 162 | human mpox | 21.42 | -4.11 | 437 | human mpox | 20.71 | 1.94 |
| 163 | human mpox | 20.83 | -2.87 | 438 | human mpox | 20.29 | 1.00 |
| 164 | human mpox | 18.49 | -3.16 | 439 | human mpox | 21.71 | 2.83 |
| 165 | human mpox | 17.83 | -2.51 | 440 | human mpox | 21.67 | 2.61 |
| 166 | human mpox | 17.91 | -3.15 | 441 | human mpox | 21.66 | 2.46 |
| 167 | human mpox | 17.46 | -3.39 | 442 | human mpox | 21.88 | 2.30 |
| 168 | human mpox | 18.39 | -4.26 | 443 | human mpox | 22.01 | 2.38 |
| 169 | human mpox | 19.48 | -4.40 | 444 | human mpox | 22.13 | 2.46 |
| 170 | human mpox | 18.97 | -4.54 | 445 | human mpox | 22.12 | 2.28 |
| 171 | human mpox | 18.68 | -4.65 | 446 | human mpox | 22.24 | 2.32 |
| 172 | human mpox | 18.01 | -4.84 | 447 | human mpox | 22.32 | 2.17 |
| 173 | human mpox | 17.83 | -4.63 | 448 | human mpox | 22.32 | 0.62 |
| 174 | human mpox | 18.93 | -5.12 | 449 | human mpox | 23.11 | -1.14 |
| 175 | human mpox | 19.67 | -5.00 | 450 | human mpox | 17.82 | -2.45 |
| 176 | human mpox | 20.04 | -4.97 | 451 | human mpox | 23.57 | -2.85 |
| 177 | human mpox | 18.39 | -5.50 | 452 | human mpox | 22.11 | -2.67 |
| 178 | human mpox | 18.45 | -6.29 | 453 | human mpox | 22.20 | -3.32 |
| 179 | human mpox | 18.06 | -7.30 | 454 | human mpox | 22.29 | -3.49 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 180 | human mpox | 17.50 | -6.39 | 455 | human mpox | 22.50 | -3.48 |
| 181 | human mpox | 16.89 | -6.52 | 456 | human mpox | 22.22 | -3.60 |
| 182 | human mpox | 17.16 | -5.91 | 457 | human mpox | 22.42 | -3.74 |
| 183 | human mpox | 16.67 | -5.79 | 458 | human mpox | 27.91 | -1.53 |
| 184 | human mpox | 16.66 | -4.11 | 459 | human mpox | 17.91 | -2.75 |
| 185 | human mpox | 15.34 | -4.39 | 460 | human mpox | 18.70 | -3.75 |
| 186 | human mpox | 16.35 | -2.92 | 461 | human mpox | 17.64 | -4.72 |
| 187 | human mpox | 22.33 | -5.51 | 462 | human mpox | 17.09 | -5.40 |
| 188 | human mpox | 28.85 | -2.53 | 463 | human mpox | 17.82 | -5.72 |
| 189 | human mpox | -1.24 | 8.17 | 464 | human mpox | 18.24 | -6.39 |
| 190 | human mpox | -8.13 | 6.07 | 465 | human mpox | 8.41 | 4.89 |
| 191 | human mpox | -6.45 | 6.81 | 466 | human mpox | 7.38 | 4.96 |
| 192 | human mpox | -0.05 | 5.90 | 467 | human mpox | 3.63 | 7.28 |
| 193 | human mpox | 4.57 | 7.16 | 468 | human mpox | -3.38 | 6.29 |
| 194 | human mpox | 7.31 | 5.01 | 469 | human mpox | -7.65 | 5.15 |
| 195 | human mpox | 11.51 | 4.12 | 470 | human mpox | -8.06 | 5.84 |
| 196 | human mpox | 10.65 | -0.26 | 471 | human mpox | -8.49 | 5.22 |
| 197 | human mpox | 18.05 | 1.62 | 472 | human mpox | -9.44 | 6.06 |
| 198 | human mpox | 19.79 | 1.22 | 473 | human mpox | -1.13 | 8.09 |
| 199 | human mpox | 22.20 | 2.80 | 474 | human mpox | 22.17 | -5.51 |
| 200 | human mpox | 20.91 | -0.24 | 475 | human mpox | 24.26 | -4.39 |
| 201 | human mpox | 23.84 | -2.26 | 476 | human mpox | 22.25 | -2.55 |
| 202 | human mpox | 21.94 | -2.47 | 477 | human mpox | 18.99 | -4.85 |
| 203 | human mpox | 23.97 | -3.25 | 478 | human mpox | 17.81 | -5.99 |
| 204 | human mpox | 24.15 | -3.23 | 479 | human mpox | 22.47 | -0.77 |
| 205 | human mpox | 23.49 | -3.89 | 480 | human mpox | 18.21 | -1.94 |
| 206 | human mpox | 22.74 | -3.71 | 481 | human mpox | 26.36 | -1.71 |
| 207 | human mpox | 22.26 | -3.71 | 482 | human mpox | 28.43 | -2.38 |
| 208 | human mpox | 19.20 | -4.57 | 483 | human mpox | 19.89 | 1.05 |
| 209 | human mpox | 24.74 | -3.04 | 484 | human mpox | 22.69 | 2.11 |
| 210 | human mpox | 2.83 | 6.42 | 485 | human mpox | 25.10 | 2.97 |
| 211 | human mpox | 2.99 | 6.45 | 486 | human mpox | 20.53 | 3.77 |
| 212 | human mpox | 2.98 | 6.51 | 487 | human mpox | 19.35 | 3.47 |
| 213 | human mpox | 3.05 | 6.48 | 488 | human mpox | 13.59 | 3.08 |
| 214 | human mpox | 3.11 | 6.43 | 489 | human mpox | 7.01 | 4.82 |
| 215 | human mpox | 3.26 | 6.56 | 490 | human mpox | 3.87 | 7.45 |
| 216 | human mpox | 3.33 | 6.53 | 491 | human mpox | -4.20 | 6.48 |
| 217 | human mpox | 3.26 | 6.42 | 492 | human mpox | -8.52 | 5.93 |
| 218 | human mpox | 3.43 | 6.51 | 493 | human mpox | -1.19 | 7.62 |
| 219 | human mpox | 3.41 | 6.45 | 494 | human mpox | 7.35 | 8.96 |
| 220 | human mpox | 3.48 | 6.45 | 495 | human mpox | 7.03 | 4.75 |
| 221 | human mpox | 3.61 | 6.46 | 496 | human mpox | 23.22 | 5.06 |
| 222 | human mpox | 3.59 | 6.55 | 497 | human mpox | 18.18 | 2.55 |
| 223 | human mpox | 3.51 | 6.59 | 498 | human mpox | 18.48 | 3.17 |
| 224 | human mpox | 3.45 | 6.60 | 499 | human mpox | 22.70 | 3.57 |
| 225 | human mpox | 3.53 | 6.64 | 500 | human mpox | 20.97 | 1.70 |
| 226 | human mpox | 3.59 | 6.68 | 501 | human mpox | -11.56 | 7.28 |
| 227 | human mpox | 3.65 | 6.64 | 502 | human mpox | 17.80 | 0.86 |
| 228 | human mpox | 3.73 | 6.61 | 503 | human mpox | 3.56 | 6.53 |
| 229 | human mpox | 3.81 | 6.61 | 504 | human mpox | 23.46 | -3.51 |
| 230 | human mpox | 4.23 | 6.43 | 505 | human mpox | 6.11 | 4.77 |
| 231 | human mpox | 4.15 | 6.50 | 506 | human mpox | 9.86 | 6.14 |
| 232 | human mpox | 4.04 | 6.49 | 507 | human mpox | 27.63 | -1.33 |
| 233 | human mpox | 3.99 | 6.56 | 508 | human mpox | 29.36 | -5.59 |
| 234 | human mpox | 4.04 | 6.59 | 509 | human mpox | 16.89 | -5.09 |
| 235 | human mpox | 4.02 | 6.66 | 510 | human mpox | -11.62 | 7.32 |
| 236 | human mpox | 3.96 | 6.69 | 511 | human mpox | -11.76 | 8.24 |
| 237 | human mpox | 4.03 | 6.76 | 512 | human mpox | 25.69 | -9.73 |
| 238 | human mpox | 3.21 | 8.12 | 513 | human mpox | 22.63 | -0.60 |
| 239 | human mpox | 3.63 | 7.82 | 514 | human mpox | -8.21 | 5.94 |
| 240 | human mpox | 3.54 | 8.54 | 515 | human mpox | -9.82 | 5.80 |
| 241 | human mpox | 3.37 | 8.66 | 516 | human mpox | -12.36 | 8.04 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 242 | human mpox | 3.93 | 8.44 | 517 | human mpox | 7.51 | 5.45 |
| 243 | human mpox | 4.12 | 7.98 | 518 | human mpox | -3.50 | 6.67 |
| 244 | human mpox | 5.26 | 9.97 | 519 | human mpox | 22.11 | 2.49 |
| 245 | human mpox | 5.40 | 7.88 | 520 | human mpox | 16.50 | -5.33 |
| 246 | human mpox | 5.47 | 7.46 | 521 | human mpox | 14.01 | -5.05 |
| 247 | human mpox | 6.15 | 7.32 | 522 | human mpox | 18.94 | 4.67 |
| 248 | human mpox | 6.01 | 6.95 | 523 | human mpox | 21.81 | 2.77 |
| 249 | human mpox | 6.52 | 6.87 | 524 | human mpox | 22.47 | 2.18 |
| 250 | human mpox | 6.65 | 6.53 | 525 | human mpox | 15.40 | -4.38 |
| 251 | human mpox | 6.56 | 6.48 | 526 | human mpox | 17.99 | -4.52 |
| 252 | human mpox | 6.28 | 6.46 | 527 | human mpox | 19.36 | -4.70 |
| 253 | human mpox | 6.49 | 6.30 | 528 | human mpox | 14.92 | -0.24 |
| 254 | human mpox | 6.20 | 6.18 | 529 | human mpox | 21.97 | -2.45 |
| 255 | human mpox | 6.50 | 6.08 | 530 | human mpox | 4.60 | 7.17 |
| 256 | human mpox | 6.68 | 6.02 | 531 | human mpox | -7.15 | 5.74 |
| 257 | human mpox | 6.52 | 5.87 | 532 | human mpox | -7.03 | 5.29 |
| 258 | human mpox | 6.36 | 5.93 | 533 | human mpox | -7.29 | 6.32 |
| 259 | human mpox | 6.95 | 6.24 | 534 | human mpox | -6.92 | 5.94 |
| 260 | human mpox | 5.64 | 6.44 | 535 | human mpox | -7.15 | 5.74 |
| 261 | human mpox | 5.80 | 6.33 | 536 | human mpox | 16.21 | 2.50 |
| 262 | human mpox | 5.33 | 6.23 | 537 | human mpox | -3.43 | 6.63 |
| 263 | human mpox | 5.86 | 5.97 | 538 | human mpox | 7.51 | 5.45 |
| 264 | human mpox | 5.75 | 5.84 | 539 | human mpox | 22.45 | -3.46 |
| 265 | human mpox | 5.64 | 5.69 | 540 | human mpox | 11.58 | 3.63 |
| 266 | human mpox | 5.47 | 5.81 | 541 | human mpox | 22.30 | 2.98 |
| 267 | human mpox | 5.25 | 5.67 | 542 | human mpox | 22.30 | 2.98 |
| 268 | human mpox | 5.85 | 5.68 | 543 | human mpox | 22.48 | 2.78 |
| 269 | human mpox | 5.90 | 5.73 | 544 | human mpox | 16.19 | 2.47 |
| 270 | human mpox | 5.93 | 5.59 | 545 | human mpox | -11.63 | 7.37 |
| 271 | human mpox | 5.39 | 5.50 | 546 | human mpox | -11.67 | 7.96 |
| 272 | human mpox | 5.48 | 5.48 | 547 | human mpox | 17.66 | 2.36 |
| 273 | human mpox | 5.63 | 5.48 | 548 | human mpox | 29.79 | 8.93 |
| 274 | human mpox | 5.58 | 5.42 | 549 | human mpox | 2.72 | 6.66 |
| 275 | human mpox | 5.54 | 5.31 | 550 | human mpox | 2.45 | 6.91 |

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**Appendix 2** Overview of MPXV infection in identified reservoir host species

| **Habitat type** | **Taxa** | **Common name** | **Species** | **Detection methods** | **Reference** |
|---|---|---|---|---|---|
| Terrestrial rodent | *Graphiurus* spp. | African dormouse | *Graphiurus lorraine, Graphiurus crassicaudatus* | PCR | 1. Hutson CL, Lee KN, Abel J, Carroll DS, Montgomery JM, Olson VA, et al. Monkeypox zoonotic associations: insights from laboratory evaluation of animals associated with the multi-state US outbreak. *Am J Trop Med Hyg*. 2007; 76(4): 757-768.<br>2. Fuller T, Thomassen HA, Mulembakani PM, Johnston SC, Lloyd-Smith JO, Kisalu NK, et al. Using remote sensing to map the risk of human monkeypox virus in the Congo Basin. *Ecohealth*. 2011;8(1):14-25. |
| Terrestrial rodent | *Cricetomys* spp. | Giant pouched rat | *Cricetomys gambianus* | PCR | 1. Hutson CL, Lee KN, Abel J, Carroll DS, Montgomery JM, Olson VA, et al. Monkeypox zoonotic associations: insights from laboratory evaluation of animals associated with the multi-state US outbreak. *Am J Trop Med Hyg*. 2007; 76(4): 757-768.<br>2. Falendysz EA, Lopera JG, Lorenzsonn F, Salzer JS, Hutson CL, Doty J, et al. Further assessment of Monkeypox virus infection in Gambian pouched rats (*Cricetomys gambianus*) using in vivo bioluminescent imaging. *PLoS Negl Trop Dis*. 2015; 9(10): e0004130.<br>3. Hutson CL, Nakazawa YJ, Self J, Olson VA, Regnery RL, Braden Z, et al. Laboratory investigations of african pouched rats (*Cricetomys gambianus*) as a potential reservoir host species for Monkeypox virus. *PLoS Negl Trop Dis*. 2015; 9(10): e0004013. |
| Arboreal rodent | *Funisciurus* spp. | Rope squirrel | *Funisciurus anerythrus*, *Funisciurus carruthersi*, *Funisciurus congicus*, *Funisciurus lemniscatus*, *Funisciurus pyrropus*, *Funisciurus bayonii*, *Funisciurus bayonii* | Virus Isolation/PCR | 1. Khodakevich L, Jezek Z, Kinzanzka K. Isolation of Monkeypox virus from wild squirrel infected in nature. *Lancet*. 1986; 1(8472): 98-99.<br>2. Hutson CL, Lee KN, Abel J, Carroll DS, Montgomery JM, Olson VA, et al. Monkeypox zoonotic associations: insights from laboratory evaluation of animals associated with the multi-state US outbreak. *Am J Trop Med Hyg*. 2007; 76(4): 757-768.<br>3. Reynolds MG, Carroll DS, Olson VA, Hughes C, Galley J, Likos A, et al. A silent enzootic of an orthopoxvirus in Ghana, West Africa: evidence for multi-species involvement in the absence of widespread human disease. *Am J Trop Med Hyg*. 2010; 82(4): 746-754.<br>4. Tiee MS, Harrigan RJ, Thomassen HA, Smith TB. Ghosts of infections past: using archival samples to understand a century of monkeypox virus prevalence among host communities across space and time. *R Soc Open Sci*. 2018; 5(1): 171089. |

## **Appendix 3** Summary of ecological factors used in previous mpox modeling studies

| Variable | Reference | Content | Method | Usage and/or result |
|---|---|---|---|---|
| BIO1 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Levine RS, et al. [4] | Monkeypox disease in Africa | Model: GARP | The variable has significant contributions to the transmission of monkeypox disease |
| | Mandja BA, et.al. [5] | Monkeypox disease in the Democratic Republic of the Congo | Model: Bayesian hierarchical generalized linear mixed model | The IRR of the variable is 1.143 (1.028–1.261) in the model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Significant environmental variable |
| | Lash RR, et.al. [7] | Monkeypox disease in Africa | Model: GARP | Used in the monkeypox ecological niche model |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV reservoir species model |
| BIO2 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Levine RS, et al. [4] | Monkeypox disease in Africa | Model: GARP | The variable has significant contributions to the transmission of monkeypox disease |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Significant environmental variable |
| | Lash RR, et.al. [7] | Monkeypox disease in Africa | Model: GARP | Used in the monkeypox ecological niche model |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV reservoir species model |
| BIO3 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| BIO4 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV reservoir species model |
| BIO5 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Significant environmental variable |
| | Lash RR, et.al. [7] | Monkeypox disease in Africa | Model: GARP | Used in the monkeypox ecological niche model |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV reservoir species model |

| Variable | Reference | Content | Method | Usage and/or result |
|---|---|---|---|---|
| BIO6 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Significant environmental variable |
| | Lash RR, et.al. [7] | Monkeypox disease in Africa | Model: GARP | Used in the monkeypox ecological niche model |
| BIO7 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| BIO8 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche mode. |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| BIO9 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| BIO10 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| BIO11 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| BIO12 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Levine RS, et al. [4] | Monkeypox disease in Africa | Model: GARP | The key environmental variable |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Significant environmental variable |
| | Lash RR, et.al. [7] | Monkeypox disease in Africa | Model: GARP | Used in the monkeypox ecological niche model |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV reservoir species model |
| BIO13 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological |

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| Variable | Reference | Content | Method | Usage and/or result |
|---|---|---|---|---|
| | | | | niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Lash RR, et.al. [7] | Monkeypox disease in Africa | Model: GARP | Used in the monkeypox ecological niche model |
| BIO14 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Lash RR, et.al. [7] | Monkeypox disease in Africa | Model: GARP | Used in the MPXV reservoir species model |
| BIO15 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| BIO16 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV reservoir species model |
| BIO17 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Contributed 47% in the model, and precipitation of the driest quarter (15–25 mm) could most affect monkeypox ecological suitability. |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Significant environmental variable |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV reservoir species model |
| BIO18 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| BIO19 | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Used in the monkeypox ecological niche model |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Ellis CK, et.al. [6] | Monkeypox disease in Africa | Model: MaxEnt | Used in the monkeypox ecological niche model |
| Leaf area index | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |

| Variable | Reference | Content | Method | Usage and/or result |
|---|---|---|---|---|
| Elevation | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Contributed 26% in the model |
|  | Levine RS, et al. [4] | Monkeypox disease in Africa | Model: GARP | The variable has significant contributions to the model |
|  | Mandja BA, et.al. [5] | Monkeypox disease in the Democratic Republic of the Congo | Model: Bayesian hierarchical generalized linear mixed model | Used in the monkeypox ecological niche model |
|  | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV reservoir species model |
| Forest | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | The most important ecological variable for determining the ecological niche of the monkeypox virus |
|  | Mandja BA, et.al. [5] | Monkeypox disease in the Democratic Republic of the Congo | Model: Bayesian hierarchical generalized linear mixed model | The IRR of the variable is 1.034 (1.029-1.040) in the model |
|  | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Land cover was used in the analysis of monkeypox infections in humans in Sankuru |
| Shrubland | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Land cover was used in the analysis of monkeypox infections in humans in Sankuru |
| Grassland | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Land cover was used in the analysis of monkeypox infections in humans in Sankuru |
| Water body | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Land cover was used in the analysis of monkeypox infections in humans in Sankuru |
| Cropland | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Land cover was used in the analysis of monkeypox infections in humans in Sankuru |
| Urban construction land | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Land cover was used in the analysis of monkeypox infections in humans in Sankuru |
| Population count | Arotolu TE, et al. [1] | Monkeypox disease in southern Nigeria | Model: MaxEnt | Contributed 17% in the model, and human population count (10 people/$km^2$) can influence monkeypox transmission |
|  | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
|  | Mandja BA, et.al. [5] | Monkeypox disease in the Democratic Republic of the Congo | Model: Bayesian hierarchical generalized linear mixed model | Used in the monkeypox ecological niche model |
| Human footprint | Gallardo B, et.al. [10] | The global distribution of invaders | Model: MaxEnt | Factors related to the human footprint explained a substantial amount (23% on average) of species distributions |
|  | Skinner EB, et.al. [11] | The vector-borne diseases | Model: RF | Human footprint is an important predictor of local occurrence and that its nonlinear effects vary predictably with the transmission ecology of each vector-borne diseases |
| *Funisciurus* spp. | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | *Funisciurus anerythrus* and *Funisciurus pyrropus* ranked first and third based on a niche overlap analysis between MPXV and mammal species, respectively |
|  | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | The second important ecological variable for determining the ecological |

| Variable | Reference | Content | Method | Usage and/or result |
|---|---|---|---|---|
| | | | | niche of the MPXV |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | *Funisciurus anerythrus* and *Funisciurus* congicus were the most important variables in the model |
| | Khodakevich L, et.al. [14] | Laboratory testing of MPXV | Testing: isolation | MPXV was isolated from *Funisciurus anerythrus* |
| | Tiee MS, et.al. [15] | Laboratory testing of MPXV | Testing: PCR | Historical distribution and prevalence of MPXV in *Funisciurus* spp. collected across Central Africa |
| | Hutson CL, [16] | Laboratory testing of MPXV | Testing: PCR | Potential animal host of MPXV |
| *Graphiurus* spp. | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Hutson CL, et.al. [16] | Laboratory testing of MPXV | Testing: PCR | Potential animal host of MPXV |
| | Reynolds MG, et.al. [17] | Laboratory testing of Orthopoxvirus (OPXV) | Testing: PCR | Susceptible to natural OPXV infection |
| | Curaudeau M, et al. [2] | MPXV in Africa | Model: MaxEnt | *Graphiurus lorraineus* ranked second based on a niche overlap analysis between MPXV and mammal species |
| *Cricetomys* spp. | Fuller T, et.al. [3] | Monkeypox disease in the Congo Basin | Model: Logistic regression and MaxEnt | Used in the monkeypox ecological niche model |
| | Thomassen HA, et.al. [8] | Monkeypox disease in Central Africa | Model: MaxEnt | Used in the MPXV ecological niche model |
| | Hutson CL, et.al. [16] | Laboratory testing of MPXV | Testing: PCR | Potential animal host of MPXV |
| | Reynolds MG, et.al. [17] | Laboratory testing of OPXV | Testing: PCR | Susceptible to natural OPXV infection |
| | Falendysz EA, et.al. [18] | Laboratory testing of MPXV | Testing: Animal infection experiment | *Cricetomys gambianus* may play an important role in the transmission of the virus to humans |
| | Hutson CL, et.al. [19] | Laboratory testing of MPXV | Testing: Animal infection experiment | *Cricetomys gambianus* may be involved in the maintenance of MPXV in wildlife mammalian populations |

## **Additional references** based on the **appendix 3**

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