Supplementary Information

Yellow fever surveillance suggests zoonotic and anthroponotic emergent potential

Alisa Aliaga-Samanez[1], Raimundo Real[1,2], Marina Segura[3], Carlos Marfil-Daza[1], Jesús Olivero[1,2]

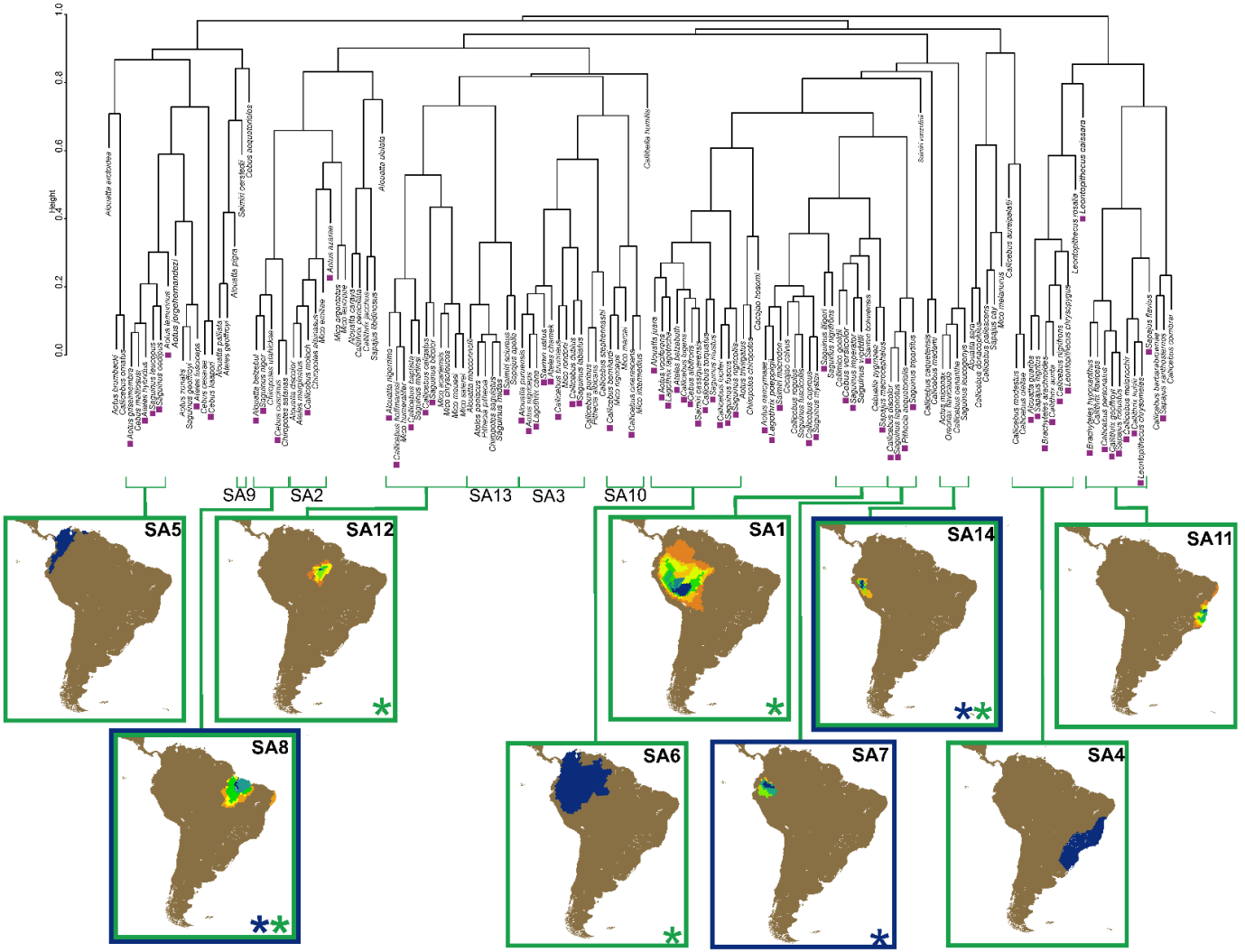
[1]Grupo de Biogeografía, Diversidad y Conservación, Departamento de Biología Animal, Facultad de Ciencias, Universidad de Málaga, 29071 Malaga, Spain

[2]Instituto IBYDA, Centro de Experimentación Grice-Hutchinson, Malaga, Spain

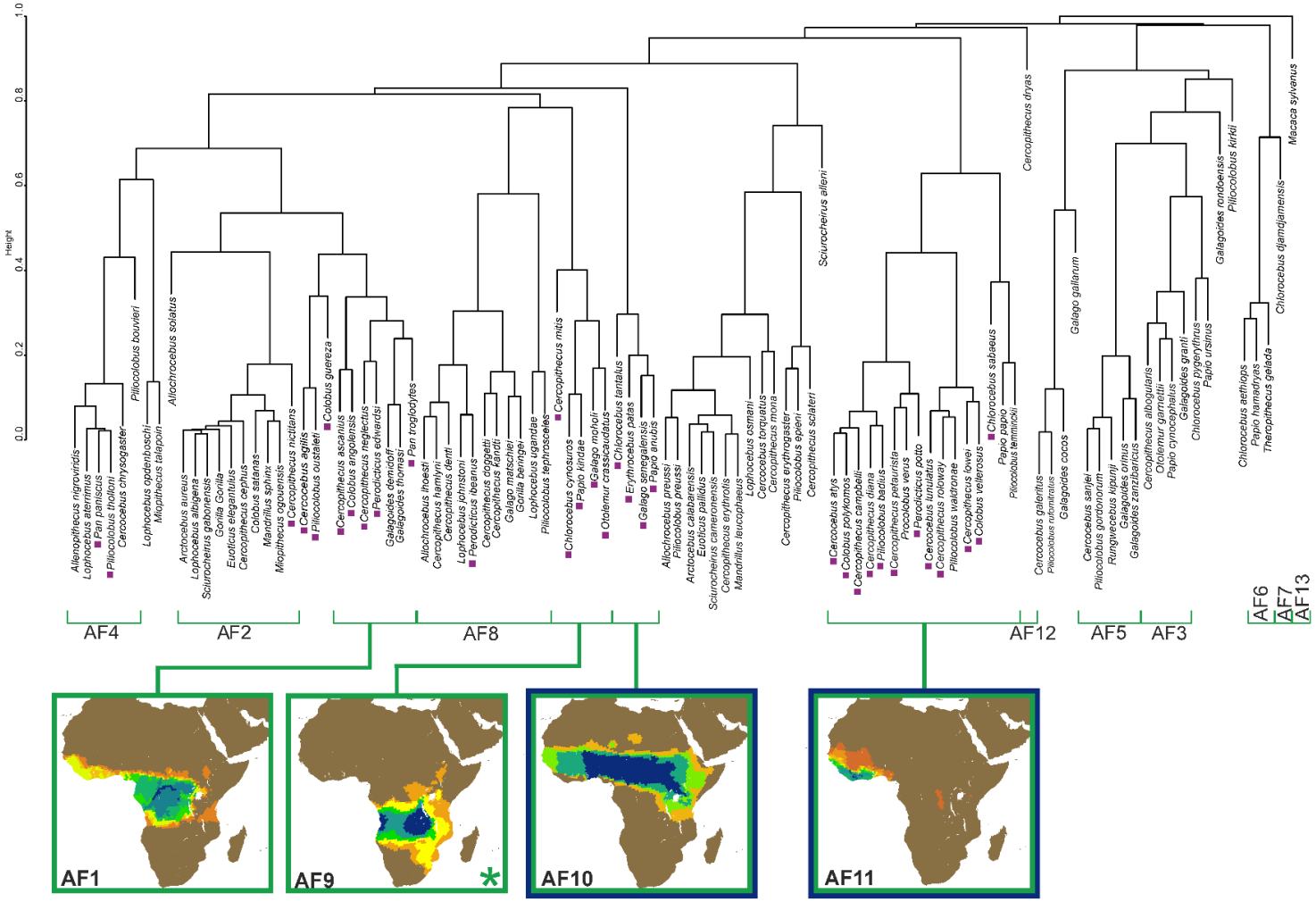
[3]Centro de Vacunación Internacional, Ministerio de Sanidad, Consumo y Bienestar Social, Estación Marítima, Recinto del Puerto, Muelle 3, 29001 Malaga, Spain

The following sections include:

- **Supplementary Figs. 1 – 2**
- **Supplementary Tables 1 – 3**
- **Supplementary Methods**



Supplementary Fig. 1: Classification dendrograms of primate distributions in America. Blue rectangles: chorotypes significantly related to the distribution of the late 20th-century yellow fever cases according to a forward-stepwise logistic regression. Green rectangles: chorotypes significantly related only to the distribution of the 21st-century cases. Chorotypes that were finally included in disease models are highlighted with a blue asterisk for the late 20th century, and with a green asterisk for the 21st century. American chorotype names are coded as SA1 to SA14. Violet square: species belonging to chorotypes significantly related to the yellow fever distribution (degree of membership ≥ 0,5).



Supplementary Fig. 2: Classification dendrograms of primate distributions in Africa. Blue rectangles: chorotypes significantly related to the distribution of the late 20th-century yellow fever cases according to a forward-stepwise logistic regression. Green rectangles: chorotypes significantly related only to the distribution of the 21st-century cases. Chorotypes that were finally included in disease models are highlighted with a blue asterisk for the late 20th century, and with a green asterisk for the 21st century. American chorotype names are coded as AF1 to AF13. Violet square: species belonging to chorotypes significantly related to the yellow fever distribution (degree of membership ≥ 0,5).

Supplementary Table 1: Non-human primate genera included in the chorotypes that were significantly related to the distribution of yellow fever cases in the late 20th century and the early 21st century. SA: South-American chorotype; AF: African chorotype. See the classification dendrograms of primate distributions in South-America and Africa in Supplementary Fig. 1 and 2.

Model	Chorotype	Genera
20th century	SA7	*Callicebus*, *Pithecia*, *Saguinus*
	SA8	*Alouatta*, *Cebus*, *Chiropotes*
	SA14	*Saguinus*, *Brachyteles*, *Callithrix*, *Callicebus*, *Leontophitecus*
	AF10	*Chlorocebus*, *Erythrocebus*, *Galago*, *Papio*
	AF11	*Colobus*, *Cercopithecus*, *Piliocolobus*, *Cercocebus*, *Perodicticus*, *Procolobus*
21st century*	SA1	*Callimico*, *Cebus*, *Callithrix*, *Saguinus*, *Saimiri*, *Sapajus*
	SA4	*Alouatta*, *Sapajus*, *Brachyteles*, *Callithrix*, *Callicebus*, *Leontophitecus*
	SA5	*Aotus*, *Cebus*, *Ateles*, *Saguinus*
	SA6	*Alouatta*, *Aotus*, *Ateles*, *Callicebus*, *Saguinus*, *Saimiri*
	SA11	*Brachyteles*, *Callithrix*, *Callicebus*, *Sapajus*, *Leontopithecus*
	SA12	*Alouatta*, *Callicebus*, *Mico*, *Saguinus*
	AF1	*Cercopithecus*, *Colobus*, *Perodicticus*, *Galagoides, Pan*
	AF9	*Cercopithecus*, *Chlorocebus*, *Galago*, *Otolemur*, *Papio*

(*) All chorotypes in the 20th-century model are also included in the 21st-century model. Only additional chorotypes are shown here.

Supplementary Table 2: Baseline disease model logit equations (i.e., linear combinations of predictor variables that form part of the logistic-regression equations). B: variable coefficient; SE: standard error; W: Wald parameter; DF: degrees of freedom; S: statistical significance. Variable codes as in Supplementary Table 1.

20th-century model					
Variable	**B**	**SE**	**W**	**DF**	**S**
Bio12	0.096×10^{-3}	0.104×10^{-3}	0.844	1	0.358
Dist_pop	-0.034×10^{-3}	0.005×10^{-3}	55.15	1	0.112×10^{-14}
Slope	0.121	0.048	6.492	1	0.011
DeXS	-2.784	0.947	8.636	1	0.003
Famerica	9.282	0.559	275.365	1	0.769×10^{-63}
Fafrica	6.805	0.422	260.479	1	0.135×10^{-59}
SA7	0.714	0.132	29.274	1	0.628×10^{-9}
SA8	0.334	0.084	16.01	1	0.063×10^{-3}
SA14	0.542	0.187	8.416	1	0.004
Constant	-6.959	0.388	321.032	1	0.863×10^{-73}
Goodness of fit		$\chi^2 = 4.214$; $n = 10$ bins; $p = 0.837$			
21st-century model					
Variable	**B**	**SE**	**W**	**DF**	**S**
Y-20th century	0.012	0.059	0.045	1	0.833
Bio12	0.161×10^{-3}	0.019×10^{-3}	2.165	1	0.141
Bio5	0.016	0.002	44.564	1	0.246×10^{-12}
Bio6	0.007	0.002	7.633	1	0.006
Dist_pop	-0.026×10^{-3}	0.003×10^{-3}	60.015	1	0.941×10^{-16}
Elev	0.001	0.219×10^{-3}	29.283	1	0.625×10^{-9}
DeXS	-2.759	0.688	16.068	1	0.061×10^{-3}
Famerica	7.983	0.605	174.096	1	0.943×10^{-42}
Fafrica	5.479	0.46	141.984	1	0.981×10^{-34}
SA1	0.26	0.047	31.12	1	0.243×10^{-9}
SA6	0.127	0.036	12.215	1	0.474×10^{-3}
SA8	0.625	0.084	55.567	1	0.903×10^{-15}
SA12	0.313	0.108	8.422	1	0.004
SA14	0.548	0.194	7.95	1	0.005
AF9	0.257	0.075	11.658	1	0.001
Constant	-12.354	1.349	83.913	1	0.517×10^{-21}
Goodness of fit		$\chi^2 = 6.499$; $n = 10$ bins; $p = 0.592$			
21st-century enhanced model					
Variable	**B**	**SE**	**W**	**DF**	**S**
Y-20th century	0.115	0.053	4.661	1	0.031
Bio12	0.202×10^{-3}	0.111×10^{-3}	3.303	1	0.069
Bio5	0.015	0.003	36.517	1	0.151×10^{-10}

Class 100	-752.147	831.976	0.817	1	0.366
Class 110	2.285	0.662	11.906	1	0.001
Class 130	-0.63	0.393	2.563	1	0.109
Class 200	-12.12	5.11	5.626	1	0.018
Dist_pop	-0.023×10^{-3}	0.003×10^{-3}	50.083	1	0.147×10^{-13}
Elev	0.001	0.176×10^{-3}	26.835	1	0.222×10^{-8}
Forest loss	3.967	0.903	19.287	1	0.011×10^{-3}
Famerica	6.845	0.583	137.899	1	0.766×10^{-33}
Fafrica	4.820	0.449	115.32	1	0.670×10^{-28}
SA1	0.265	0.048	30.900	1	0.272×10^{-9}
SA6	0.146	0.038	14.917	1	0.112×10^{-3}
SA8	0.508	0.085	35.764	1	0.223×10^{-10}
SA12	0.337	0.109	9.560	1	0.002
SA14	0.463	0.196	5.576	1	0.018
AF9	0.310	0.074	17.348	1	0.031×10^{-3}
Constant	-10.302	1.195	74.274	1	0.680×10^{-19}
Goodness of fit		χ^2 = 10.818; *n* = 10 bins; p=0.212			

Supplementary Table 3: Independent predictor variables considered for disease, vector, and transmission-risk modelling. Some variables were used only in specific models: *20th century models; ** enhanced 21st century models; ***enhanced 21st century vector models; ****disease models.

Factor	Code	Variable	Source
Climate	*Bio1*	Annual Mean Temperature	Chelsa (http://chelsa-climate.org)
	Bio5	Max Temperature of Warmest Month	
	Bio6	Min Temperature of Coldest Month	
	Bio7	Temperature Annual Range (Bio5-Bio6)	
	Bio12	Annual Precipitation	
	Bio15	Precipitation Seasonality (Coefficient of Variation)	
Human Concentration	*Pop_den*	Population density**	Administrative Centres & Populated Places shapefile at the Relational World Database II (RWDB2) updated in 2000 (http://www.fao.org/geonetwork)
	Dist_pop	Distance to populated places	
Infrastructures**	*Dist_road*	Distance to roads	Vector Map Level 0 at the Digital Chart of the World (DCW,http://worldmap.harvard.edu), updated in 2002
	Dist_rail	Distance to rail-roads	
Livestock***	*Buffaloes*	Density of buffaloes	FAO 2010(http://www.fao.org/livestock-systems/en/)
	Poultry	Density of poultry	
	Goats	Density of small ruminants (goats)	
	Pigs	Density of pigs	
	Sheep	Density of small ruminants (sheep)	
	Cattle	Density of cattle	
Topography	*Slope*	slope	From GTOPO30 (US Geological Survey 1996), using ArcGIS Desktop 10.3.
	Elev	Elevation	GTOPO30 (US Geological Survey 1996).
Hydrography	*Dist_riv*	Distance to rivers	Global Drainage Basin Database GDBD. Released Version 1.0: May 29, 2007 (http://www.cger.nies.go.jp/db/gdbd/gdbd_index_e.html).
Ecoregions*	*MedFWS*	Mediterranean Forest, Woodlands and Scrub	Terrestrial Ecoregions of the World: A New Map of Life on Earth: A new global map of terrestrial ecoregions provides an innovative tool for conserving biodiversity[1]
	TrosubDBF	Tropical and Subtropical Dry Broadleaf Forest	
	TempCF	Temperate Coniferous Forests	
	TempBMF	Temperate Broadleaf and Mixed Forests	
	TrosubCF	Tropical and Subtropical Coniferous Forests	
	DeXS	Deserts and Xeric Shrublands	
	Mangro	Mangroves	
	TrosubMBF	Tropical and Subtropical Moist Broadleaf Forest	
	BorFT	Boreal Forests/Taiga	
	TrosubGSS	Tropical and Subtropical Grasslands, Savannas and Shrublands	
	TempGSS	Temperate Grasslands, Savannas and Shrublands	
	FloGS	Flooded Grassland and Savannas	
	MonGS	Montane Grasslands and Shrublands	
	Tundra	Tundra	

Agriculture	*Class 11-14*	Croplands	GlobCover (GC) Land Cover version 2.3 database for 2009[2]
	Class 20	Mosaic Cropland (50-70%) / Vegetation (grassland, shrubland, forest) (20-50%)**	
	Class 30	Mosaic Vegetation (grassland, shrubland, forest) (50-70%) / Cropland (20-50%)**	
	Equi_irrig	Percentage of area equipped for irrigation***	Global Map of Irrigation Areas (version 4.0.1) around the year 2000 (http://www.fao.org/nr/water)
Ecosystem Types**	*Class 40*	Closed to open (>15%) broadleaved evergreen and/or semi-deciduous forest (>5m)	GlobCover (GC) Land Cover version 2.3 database for 2009[2]
	Class 50	Closed (>40%) broadleaved deciduous forest (>5m)	
	Class 60	Open (15-40%) broadleaved deciduous forest (>5m)	
	Class 70	Closed (>40%) needleleaved evergreen forest (>5m)	
	Class 90	Open (15-40%) needleleaved deciduous or evergreen forest (>5m)	
	Class 100	Closed to open (>15%) mixed broadleaved and needleleaved forest (>5m)	
	Class 110	Mosaic Forest/Shrubland (50-70%) / Grassland (20-50%)	
	Class 120	Mosaic Grassland (50-70%) / Forest/Shrubland (20-50%)	
	Class 130	Closed to open (>15%) shrubland (<5m)	
	Class 140	Closed to open (>15%) grassland	
	Class 150	Sparse (>15%) vegetation (woody vegetation, shrubs, grassland)	
	Class 160	Closed (>40%) broadleaved semi-deciduous and/or evergreen forest regularly flooded - Saline water	
	Class 170	Closed (>40%) broadleaved semi-deciduous and/or evergreen forest regularly flooded - Saline water	
	Class 180	Closed to open (>15%) vegetation (grassland, shrubland, woody vegetation) on regularly flooded or waterlogged soil - Fresh, brackish or saline water	
	Class 200	Bare areas	
	Class 220	Permanent snow and ice	
Forest loss**	*Forest loss*	Non intact forest	High-Resolution Global Maps of 21st-Century Forest Cover Change[3]
Logit equation	*Y-20th century*	20th-century-model logit equation	Linear combinations of predictor variables that form part of the logistic-regression equations
Spatial descriptors	*Fx*	Spatial trend, where "x" represents a continent	Linear combination of spatial variables derived from continental-scale trend surface analyses[4]
Primate chorotypes****	*SAx* and *AFy*	Chorotype species richness. *SAx*: South-American chorotype "x" and *AFy*: African chorotype "y"	Supplementary Figs. 5-7[5]

Supplementary References:

1. Olson DM, Dinerstein E, Wikramanayake E, Burgess ND, Powell G, Underwood E, et al. Terrestrial Ecoregions of the World: A New Map of Life on Earth: A new global map of terrestrial ecoregions provides an innovative tool for conserving biodiversity. Bioscience. 2001; 51: 933–938.
2. Bontemps S. GLOBCOVER 2009 Products Description and Validation Report. 2011.
3. Hansen MC. High-resolution global maps of 21st-century forest cover change. Science. 2013;342: 850–853
4. Legendre P. Spatial autocorrelation: Trouble or New Paradigm? Ecology. 1993;74: 1659–1673
5. Olivero J, Real R, Márquez AL. Fuzzy chorotypes as a conceptual tool to improve insight into biogeographic patterns. Syst Biol. 2011;60: 645–660. doi:10.1093/sysbio/syr026

Supplementary methods

Methodological explanations for the variables and outputs shown in Fig. 4 of the main text. These variables and outputs are related to the following sections through letter codes (A – F).

A. Independent variables: Environment

1. Preselection of environmental variables potentially influencing the distribution of the item to be modelled (i.e., a mosquito species, yellow fever cases). Variable sources and descriptions are shown in Supplementary Table 3.

B. Independent variables: Space

1. Selection of the geographic context: A spatial independent variable was made for each continent (*x*).
2. Logistic regression: It provides a probability value (P_x), based on spatial descriptors, of the analysed item to occur in each hexagon:
   a. Dependent variable: Presences (1) and absences (0) of the item to be modelled.
   b. Initial independent variables: Spatial descriptors consisting on polynomial combinations of longitude (X) and latitude (Y) up to the third degree: X, Y, XY, X^2, Y^2, X^2Y, XY^2, X^3, and Y^3.
   c. Selection of independent variables: Conditional backward-stepwise procedure.
   d. Estimation of variable coefficients: machine-learning iterative process based on the maximum log-likelihood criterion.
   e. Model evaluation: Hosmer & Lemeshow's goodness of fit.

SPSS syntax for the logistic regression

```
LOGISTIC REGRESSION VARIABLES Dependent_variable
  /METHOD=BSTEP(COND) List_of_spatial_descriptors
  /SAVE=PRED
  /CRITERIA=PIN(.05) POUT(.10) ITERATE(20) CUT(.5).
```

3. A spatial independent variable is defined by the spatial favourability (F_x), where *x* represents a continent. F_x provides a value of the degree to which spatial descriptors favour the occurrence of the analysed item in each hexagon.

$$F_x = \frac{P_x}{1 - P_x} \Big/ \left(\frac{n_1}{n_0} + \frac{P_x}{1 - P_x}\right)$$

where n_1 = number of presences, and n_0 = number of absences of the item to be modelled.

C. Independent variables: Primate zoogeography

1. Initial data: IUCN range maps of the American and African non-human primates.
2. For every continent, building of a matrix of presence (1) / absence (0) of every primate species (columns) in every hexagon (rows): "primate_data"
3. Hierarchical classification of the species ranges, separately for every continent, through the analysis of the 1/0 matrix using the Baroni-Urbani & Buser´s similarity index and the UPGMA classification method.
4. Chorotype variables: Definition of chorotypes through the evaluation of the statistical significance of all clusters in the hierarchical classification using RMacoqui 1.0 software (http://rmacoqui.r-forge.r-project.org/). For every chorotype, quantification, in each hexagon, of the number of species belonging to each chorotype.

R script for the package "RMacoqui" (https://rmacoqui.r-forge.r-project.org/)

```
## The data set was a presences/absences matrix for primates of a continent.

data(primate_data)
macoquires <- macoqui(primate_data)

## Friendly 'macoqui' results. Output of interest: "Chorotype Report".

ver.matRmacoqui(macoquires)

## Parameters for chorotype variable quantification. Output of interest: "Chorotypes in
Localities". The SR (species richness) result was used.

locs <- locCorot(macoquires)
ver.matRmacoqui(locs)
```

5. Logistic regression: The objective is to choose the set of chorotype variables to be considered henceforth. The study area is global, and so both African and American chorotypes are included in the analysis.
    a. Dependent variable: Presences (1) and absences (0) of yellow fever cases
    b. Independent variables: African and American chorotype variables.
    c. Selection of independent variables: Conditional forward-backward stepwise procedure.
    d. Estimation of variable coefficients: machine-learning iterative process based on the maximum log-likelihood criterion.
    e. Only the chorotype variables selected by the stepwise logistic regression were considered to be "primate zoogeography" variables henceforth.

SPSS syntax for the logistic regression

```
LOGISTIC REGRESSION VARIABLES Dependent_variable
  /METHOD=FSTEP(COND) List_of_chorotype_variables
  /SAVE=PRED
  /CRITERIA=PIN(.05) POUT(.10) ITERATE(20) CUT(.5).
```

D. Vector models

D1. 20th-century model for urban vector species *Aedes aegypti* and *Ae. albopictus*

1. Control of the Type I error using the False Discovery Rate (FDR):
    a. RAO´s score test of all environmental variables (respect to the presences and absences of the mosquito species between 1970 and 2000) to get the *p* values.
    b. Pre-selection of variables for which $p < i \times q / v$ [i = position of the variable, arranged in increasing p order; q = 0.05; v = total number of environmental variables]. Only these pre-selected variables are considered henceforth.
2. Logistic regression: It provides a probability value (P_{um20}), based on environment and space variables, of the urban mosquito (*um*) species to occur in each hexagon during the late 20th century.
    a. Dependent variable: Presences (1) and absences (0) of the mosquito species between 1970 and 2000. *Ae. aegypti* and *Ae. albopictus* are modelled separately.
    b. Independent variables: environment (**A**) and space (**B**) variables.
    c. Selection of independent variables: Conditional forward-backward stepwise procedure.
    d. Estimation of variable coefficients: machine-learning iterative process based on the maximum log-likelihood criterion.
    e. Model evaluation: Hosmer & Lemeshow's goodness of fit.

SPSS syntax for the logistic regression
LOGISTIC REGRESSION VARIABLES *Dependent_variable*
/METHOD=FSTEP(COND) *List_of_environment_and_space_variables*
/SAVE=PRED
/CRITERIA=PIN(.05) POUT(.10) ITERATE(20) CUT(.5).

3. Control for excessive multicollinearity:
   a. Identification of variables with Spearman correlation coefficient > 0.8 among the variables selected by the logistic regression.
   b. This being the case, deletion of the least significant correlated variable according to the RAO´s score test, and repetition of the logistic regression.
4. Favourability (F_{um20}) values are calculated, based on the probability (P_{um20}) values provided by the logistic regression:

$$F_{um20} = \frac{P_{um20}}{1 - P_{um20}} \Big/ \left(\frac{n_1}{n_0} + \frac{P_{um20}}{1 - P_{um20}}\right)$$

where n_1 = number of presences, and n_0 = number of absences of the modelled mosquito species

D2. 21st-century model for urban vector species *Aedes aegypti* and *Ae. albopictus*

1. Control of the Type I error using the False Discovery Rate (FDR):
   a. RAO´s score test of all environmental variables (respect to the presences and absences of the mosquito species between 2001 and 2017) to get the *p* values.
   b. Pre-selection of variables for which $p < i \times q/v$ [i = position of the variable, when arranged in increasing p order; q = 0.05; v = total number of environmental variables]. Only these pre-selected variables are considered henceforth.
2. Logistic regression: It provides a probability value (P_{um21}), based on environmental and spatial variables, of the urban mosquito (*um*) species to occur in each hexagon during the early 21st century.
   a. Dependent variable: Presences (1) and absences (0) of the mosquito species between 2001 and 2017. *Ae. aegypti* and *Ae. albopictus* are modelled separately.
   b. Independent variables: environment (**A**) and space (**B**) variables, and the "updating variable", that is the value for the logit equation of this mosquito's 20th-century model (**D1**). The logit equation is the linear combination of variables selected in section D1.2c (see above).
   c. Selection of independent variables: A two-blocks approach is employed. The updating variable is forced to enter in the model in the first block; environment and space variables are selected in the second block using a conditional forward-backward stepwise procedure.
   d. Estimation of variable coefficients: machine-learning iterative process based on the maximum log-likelihood criterion.
   e. Model evaluation: Hosmer & Lemeshow's goodness of fit.

SPSS syntax for the logistic regression
LOGISTIC REGRESSION VARIABLES *Dependent_variable*
/METHOD=ENTER *20th-century_model_logit*
/METHOD=FSTEP(COND) *List_of_environment_and_space_variables*
/SAVE=PRED
/CRITERIA=PIN(.05) POUT(.10) ITERATE(20) CUT(.5).

3. Control for excessive multicollinearity:
    a. Identification of variables with Spearman correlation coefficient > 0.8 among the variables selected.
    b. This being the case, deletion of the least significant correlated variable according to the RAO´s score test, and repetition of the logistic regression.
4. Favourability (F_{um21}) values are calculated, based on the probability (P_{um21}) values provided by the logistic regression:

$$F_{um21} = \frac{P_{um21}}{1 - P_{um21}} / \left(\frac{n_1}{n_0} + \frac{P_{um21}}{1 - P_{um21}}\right)$$

where n_1 = number of presences, and n_0 = number of absences of the modelled mosquito species.

D3. Model for every sylvatic vector species

1. Control of the Type I error using the False Discovery Rate (FDR):
    a. RAO´s score test of all environmental variables (respect to the presences and absences of the mosquito species between 1970 and 2017) to get the *p* values.
    b. Pre-selection of variables for which $p < i \times q/v$ [*i* = position of the variable, when arranged in increasing *p* order; *q* = 0.05; *v* = total number of environmental variables]. Only these pre-selected variables are considered henceforth.
3. Logistic regression: It provides a probability value (P_{sm}), based on environmental and spatial variables, of the sylvatic mosquito (*sm*) species to occur in each hexagon
    a. Dependent variable: Presences (1) and absences (0) of the mosquito species between 1970 and 2017. *Haemagogus janthinomys*, *H. leucocelaenus, Sabethes chloropterus*, *Ae. africanus*, and *Ae. vittatus* are modelled separately.
    b. Independent variables: environment (**A**) and space (**B**) variables.
    c. Selection of independent variables: Conditional forward-backward stepwise procedure.
    d. Estimation of variable coefficients: machine-learning iterative process based on the maximum log-likelihood criterion.
    e. Model evaluation: Hosmer & Lemeshow's goodness of fit.

SPSS syntax for the logistic regression
LOGISTIC REGRESSION VARIABLES *Dependent_variable*
/METHOD=FSTEP(COND) *List_of_environment_and_space_variables*
/SAVE=PRED
/CRITERIA=PIN(.05) POUT(.10) ITERATE(20) CUT(.5).

4. Control for excessive multicollinearity:
    a. Identification of variables with Spearman correlation coefficient > 0.8 among the variables selected.
    b. This being the case, deletion of the least significant correlated variable according to the RAO´s score test, and repetition of the logistic regression.
5. Favourability (F_{sm}) values are calculated, based on the probability (P_{sm}) values provided by the logistic regression:

$$F_{\mathrm{sm}} = \frac{P_{sm}}{1 - P_{sm}} / \left(\frac{n_1}{n_0} + \frac{P_{sm}}{1 - P_{sm}}\right)$$

where n_1 = number of presences, and n_0 = number of absences of the modelled mosquito species.

D4. Integration of individual vector models using fuzzy logic

1. **20th-century vector model:** Application of the fuzzy union (U) between the models of the seven mosquito species considered (**D1** and **D3**); i.e., in each hexagon, the maximum value shown by any of the mosquito species models is selected. The 20th-century models are used for *Ae. aegypti* and *Ae albopictus*.

SPSS syntax for fuzzy union between mosquito models, late 20th century

```
COMPUTE 20_century_vector_model =MAX(Fum20_Ae_aegypti,
Fum20_Ae_albopictus, Fsm_H_janthinomys, Fsm_H_leucocelaenus,
Fsm_S_chloropterus, Fsm_Ae_africanus, Fsm_Ae_vittatus).
EXECUTE.
```

2. **21st-century vector model:** Application of the fuzzy union (U) between the models of the seven mosquito species considered (**D2** and **D3**); i.e., in each hexagon, the maximum value shown by any of the mosquito species models is selected. The 21st-century models are used for *Ae. aegypti* and *Ae albopictus*.

SPSS syntax for fuzzy union between mosquito models, early 21st century

```
COMPUTE 21_century_vector_model =MAX(Fum21_Ae_aegypti,
Fum21_Ae_albopictus, Fsm_H_janthinomys, Fsm_H_leucocelaenus,
Fsm_S_chloropterus, Fsm_Ae_africanus, Fsm_Ae_vittatus).
EXECUTE.
```

E. Baseline disease models:

E.1. 20th-century disease model

1. Control of the Type I error using the False Discovery Rate (FDR):
   a. RAO´s score test of all environmental variables (respect to the presences and absences of yellow fever cases between 1970 and 2000) to get the *p* values.
   b. Pre-selection of variables for which $p < i \times q/v$ [i = position of the variable, when arranged in increasing p order; q = 0.05; v = total number of environmental variables]. Only these pre-selected variables are considered henceforth.
2. Logistic regression: It provides a probability value (P_{dis20}) based on environmental and spatial variables, of yellow fever disease cases (*dis*) to occur in each hexagon during the late 20th century.
   a. Dependent variable: Presences (1) and absences (0) of yellow fever cases between 1970 and 2000.
   b. Independent variables: environment (**A**), space (**B**) and primate zoogeography (**C**) variables.
   c. Selection of independent variables: A two-blocks approach is employed. Environment and space variables are selected the first block; primate zoogeography variables are selected the second block. For this selection, a conditional forward-backward stepwise procedure is used.
   d. Estimation of variable coefficients: machine-learning iterative process based on the maximum log-likelihood criterion.
   e. Model evaluation: Hosmer & Lemeshow's goodness of fit.

SPSS syntax for the logistic regression

```
LOGISTIC REGRESSION VARIABLES Dependent_variable
/METHOD=FSTEP(COND) List_of_environment_and_space_variables
/METHOD=FSTEP(COND) Primate_zoogeography_variables
/SAVE=PRED
/CRITERIA=PIN(.05) POUT(.10) ITERATE(20) CUT(.5).
```

3. Control for excessive multicollinearity:

a. Identification of variables with Spearman correlation coefficient > 0.8 among the variables selected.
b. This being the case, deletion of the least significant correlated variable according to the RAO´s score test, and repetition of the logistic regression.

4. Favourability (F_{dis20}) values are calculated, based on the probability (P_{dis20}) values provided by the logistic regression:

$$F_{dis20} = \frac{P_{dis20}}{1 - P_{dis20}} / \left(\frac{n_1}{n_0} + \frac{P_{dis20}}{1 - P_{dis20}} \right)$$

where n_1 = number of presences, and n_0 = number of absences of yellow fever cases during the late 20th century.

E.2. 21st-century disease model

1. Control of the Type I error using the False Discovery Rate (FDR):
   a. RAO´s score test of all environmental variables (respect to the presences and absences of yellow fever cases between 2001 and 2017) to get the *p* values.
   b. Pre-selection of variables for which $p < i \times q / v$ [*i* = position of the variable, when arranged in increasing *p* order; *q* = 0.05; *v* = total number of environmental variables]. Only these pre-selected variables are considered henceforth.
2. Logistic regression: It provides a probability value (P_{dis21}) based on environmental and spatial variables, of yellow fever disease cases (*dis*) to occur in each hexagon during the late 21st century.
   a. Dependent variable: Presences (1) and absences (0) of yellow fever cases between 2001 and 2017.
   b. Independent variables: environmental variables (**A**), spatial variables (**B**), primate zoogeography (**C**) variables, and the "updating variable", that is the value for the logit equation of the 20th-century disease model (**E1**). The logit equation is the linear combination of variables selected in section E1.2c (see above).
   c. Selection of independent variables: A three-blocks approach is employed. The updating variable is forced to enter in the model in the first block; environment and space variables are selected in the second block; primate zoogeography variables are selected in the third block. For this selection, a conditional forward-backward stepwise procedure is used.
   d. Estimation of variable coefficients: machine-learning iterative process based on the maximum log-likelihood criterion.
   e. Model evaluation: Hosmer & Lemeshow's goodness of fit.

SPSS syntax for the logistic regression
LOGISTIC REGRESSION VARIABLES *Dependent_variable*
/METHOD=ENTER *20_century_disease_model_logit*
/METHOD=FSTEP(COND) *List_of_environment_and_space_variables*
/METHOD=FSTEP(COND) *Primate_zoogeography_variables*
/SAVE=PRED
/CRITERIA=PIN(.05) POUT(.10) ITERATE(20) CUT(.5).

5. Control for excessive multicollinearity:
   a. Identification of variables with Spearman correlation coefficient > 0.8 among the variables selected.
   b. This being the case, deletion of the least significant correlated variable according to the RAO´s score test, and repetition of the logistic regression.
6. Computation of favourability (F_{dis21}) values based on the probability (P_{dis21}) values provided by the logistic regression:

$$F_{dis21} = \frac{P_{dis21}}{1 - P_{dis21}} / \left(\frac{n_1}{n_0} + \frac{P_{dis21}}{1 - P_{dis21}} \right)$$

where n_1 = number of presences, and n_0 = number of absences of yellow fever cases during the early 21st century.

F. Transmission risk models:

1. **20th-century transmission risk model:** Application of the fuzzy intersection (∩) between the 20th-century vector model (**D4.1**) and the 20th-century disease model (**E1**); i.e., in each hexagon, the minimum value shown by any of these models is selected.

SPSS syntax for fuzzy intersection between the vector and disease models, late 20th century

```
COMPUTE 20_century_transmission_model=MIN(20_century_vector_model,
20_century_disease_model).
EXECUTE.
```

2. **21st-century transmission risk model:** Application of the fuzzy intersection (∩) between the 21st-century vector model (**D4.2**) and the 21st -century disease model (**E2**); i.e., in each hexagon, the minimum value shown by any of these models is selected.

SPSS syntax for fuzzy intersection between the vector and disease models, late 21st century

```
COMPUTE 21_century_transmission_model=MIN(21_century_vector_model,
21_century_disease_model).
EXECUTE.
```