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Global Health

Supplementary appendix 2

This appendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

Supplement to: Local Burden of Disease 2019 Neglected Tropical Diseases Collaborators. The global distribution of lymphatic filariasis, 2000–18: a geospatial analysis. *Lancet Glob Health* 2020; **8:** e1186–94.

Supplementary Appendix 2 for *The changing global distribution of lymphatic filariasis, 2000–2018*

Contents

List of Supplementary Tables

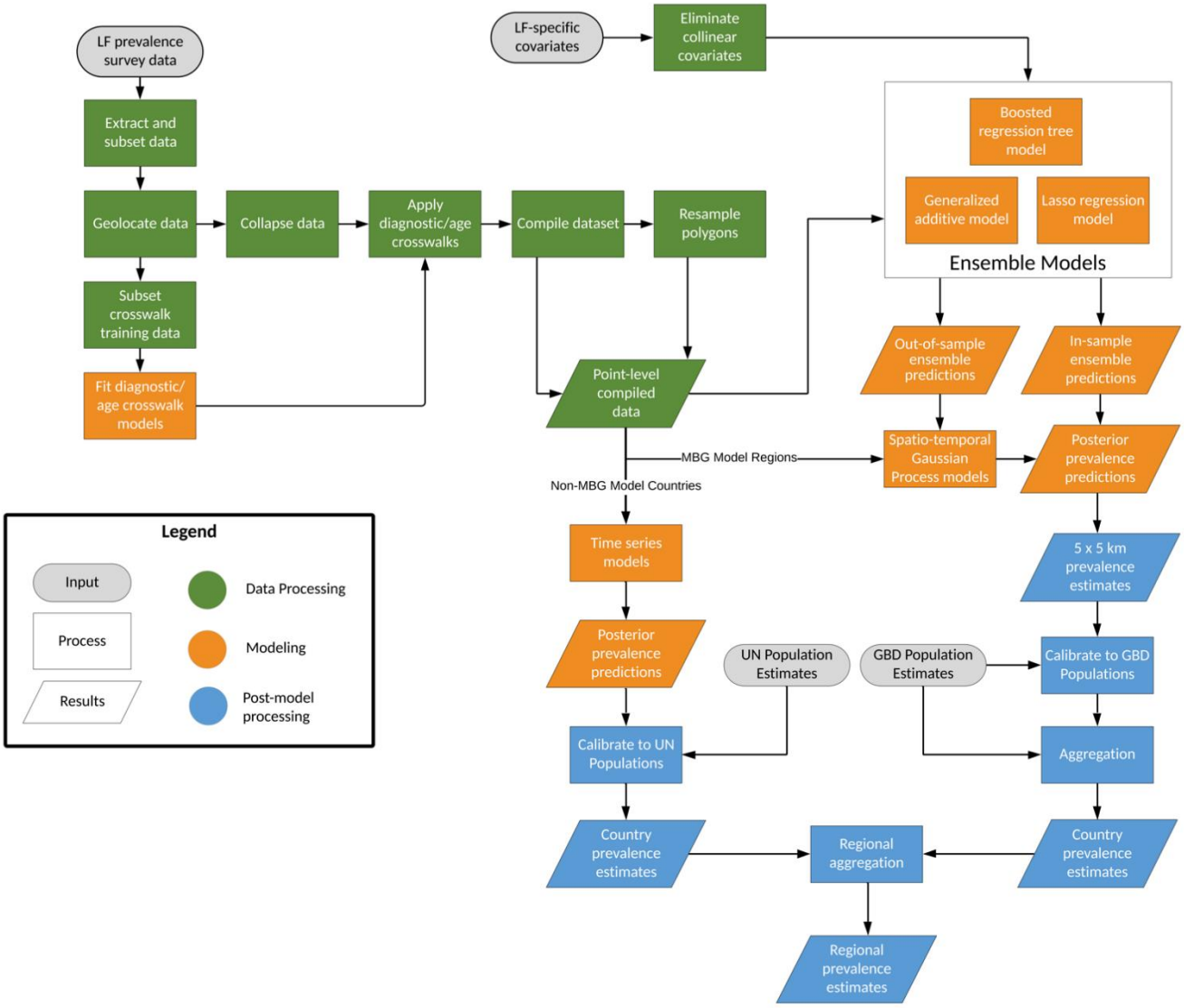
1.0 GATHER compliance

Supplementary Table 1. Guidelines for Accurate and Transparent Health Estimates Reporting (GATHER) checklist

Item #	Checklist item	Reported on page #
Objectives and Funding		
1	Define the indicator(s), populations (including age, sex, and geographic entities), and time period(s) for which estimates were made.	Main text: Introduction
2	List the funding sources for the work.	Main text: Acknowledgments
Data Inputs		
For all data inputs from multiple sources that are synthesized as part of the study:		
3	Describe how the data were identified and how the data were accessed.	Main text: Methods (Epidemiological input data) Supplemental Information: Supplementary data
4	Specify the inclusion and exclusion criteria. Identify all ad-hoc exclusions.	Main text: Methods, (Data, Epidemiological input data) Supplementary Information: 3.0 Supplementary data
5	Provide information on all included data sources and their main characteristics. For each data source used, report reference information or contact name/institution, population represented, data collection method, year(s) of data collection, sex and age range, diagnostic criteria or measurement method, and sample size, as relevant.	Supplementary Information: 3.0 Supplementary data
6	Identify and describe any categories of input data that have potentially important biases (e.g., based on characteristics listed in item 5).	Main text: Discussion (Limitations)
For data inputs that contribute to the analysis but were not synthesized as part of the study:		
7	Describe and give sources for any other data inputs.	Main text: Methods (Geospatial covariates), Supplementary Information: 4.0 Supplementary covariates
For all data inputs:		
8	Provide all data inputs in a file format from which data can be efficiently extracted (e.g., a spreadsheet rather than a PDF), including all relevant meta-data listed in item 5. For any data inputs that cannot be shared because of ethical or legal reasons, such as third-party ownership, provide a contact name or the name of the institution that retains the right to the data.	Available at (GHDx link will be added upon review) Supplementary Information: 3.0 Supplementary data
9	Provide a conceptual overview of the data analysis method. A diagram may be helpful.	Main text: Methods (Data), Supplementary Information: 5.1 Age and diagnostic crosswalk
10	Provide a detailed description of all steps of the analysis, including mathematical formulae. This description should cover, as relevant, data cleaning, data pre-processing, data adjustments and weighting of data sources, and mathematical or statistical model(s).	Main text: Methods (Geospatial analysis), Supplementary Information: 5.3 Geostatistical model
11	Describe how candidate models were evaluated and how the final model(s) were selected.	Main text: Methods (Geospatial analysis), Supplementary Information: 5.4 Model validation
12	Provide the results of an evaluation of model performance, if done, as well as the results of any relevant sensitivity analysis.	Main text: Methods (Geospatial analysis), Supplementary Information: 5.4 Model validation
13	Describe methods for calculating uncertainty of the estimates. State which sources of uncertainty were, and were not, accounted for in the uncertainty analysis.	Main text: Methods (Geospatial analysis), Supplementary Information: 5.3.3. Model description, 5.3.6. Model fitting and prediction
14	State how analytic or statistical source code used to generate estimates can be accessed.	Available at (GHDx link will be added upon review)
Results and Discussion		
15	Provide published estimates in a file format from which data can be efficiently extracted.	Raster files for spatial data and CSVs of estimates available at (GHDx link will be added upon review)
16	Report a quantitative measure of the uncertainty of the estimates (e.g., uncertainty intervals).	Supplementary Information: Supplementary Figures 12–14
17	Interpret results in light of existing evidence. If updating a previous set of estimates, describe the reasons for changes in estimates.	Main text: Discussion (Strengths)
18	Discuss limitations of the estimates. Include a discussion of any modelling assumptions or data limitations that affect interpretation of the estimates.	Main text: Discussion (Limitations)

2.0 Supplementary discussion

This document outlines the major data processing, modelling and validation steps for the analysis described in the main text (Supplementary Figure 1). We present a detailed description of model inputs, with a specific focus on data coverage and covariate sources. We then outline data processing for geo-referencing LF prevalence data and adjusting data to represent all-age ICT prevalence. The geospatial model is outlined along with model validation metrics and a detailed approach to estimating LF prevalence in settings for which geospatial analysis was not feasible.



Supplementary Figure 1. Flowchart of major steps in data processing and modelling of lymphatic filariasis prevalence in endemic areas

3.0 Supplementary data

In the following section, we present a detailed summary of the data inputs used to estimate the global prevalence of LF. Broadly, we aimed to include all published sources of LF infection prevalence, as well as routine programme monitoring data collected to monitor progress toward LF elimination. Data inputs were retained for analysis if they could be accurately geo-referenced.

3.1 Geographical restrictions

Supplementary Table 2 lists all locations in Africa, Central America, South America, the Middle East, Asia, and the Pacific. Europe, North America and Central Asia are excluded as lymphatic filariasis is not endemic to these regions.

Supplementary Table 2. Geographical restrictions, indicating countries that have previously been identified as endemic for lymphatic filariasis, whether elimination targets were verified at the national level, and which countries were included in the global analysis from 2000 to 2018

Location	Evidence of current or historical endemicity?	Local elimination achieved or other evidence supporting classification as non-endemic?	Included in 2000–2018 estimates?
AFRO			
Algeria	No	-	No
Angola	Yes	-	Yes
Benin	Yes	No	Yes
Botswana	No	-	No
Burkina Faso	Yes	No	Yes
Burundi	No[1]	-	No
Cameroon	Yes	-	Yes
Cape Verde	No	-	No
Central African Republic	Yes	No	Yes
Chad	Yes	No	Yes
Comoros	Yes	-	Yes
Republic of the Congo	Yes	No	Yes
Côte d'Ivoire	Yes	No	Yes
Democratic Republic of the Congo	Yes	No	Yes
Equatorial Guinea	Yes	No	Yes
Eritrea	Yes	-	Yes
Eswatini	No	-	No
Ethiopia	Yes	No	Yes
Gabon	Yes	No	Yes
The Gambia	Yes[2]	Yes[3]	Yes
Ghana	Yes	No	Yes
Guinea	Yes	No	Yes
Guinea Bissau	Yes	No	Yes
Kenya	Yes	No	Yes
Lesotho	No	-	No
Liberia	Yes	No	Yes

Madagascar	Yes	No	Yes
Malawi	Yes	Yes	Yes
Mali	Yes	-	Yes
Mauritania	No	No	No
Mauritius	Yes[4]	Yes[5]	No
Mozambique	Yes	No	Yes
Namibia	No	-	No
Niger	Yes	No	Yes
Nigeria	Yes	No	Yes
Rwanda	No[1]	-	No
São Tomé and Príncipe	Yes	No	Yes
Senegal	Yes	No	Yes
Seychelles	Yes[6]	Yes[1]	No
Sierra Leone	Yes	No	Yes
South Africa	No	-	No
South Sudan	Yes	No	Yes
Uganda	Yes	No	Yes
United Republic of Tanzania	Yes	No	Yes
Zambia	Yes	No	Yes
Zimbabwe	Yes	No	Yes
EMRO[7]			
Afghanistan	No	-	No
Bahrain	No	-	No
Djibouti	No	-	No
Egypt	Yes[8]	Yes	Yes
Iran	No	-	No
Iraq	No	-	No
Jordan	No	-	No
Kuwait	No	-	No
Lebanon	No	-	No

Libya	No	-	No
Morocco	No	-	No
Oman	Yes[9]	Yes[10]	No
Pakistan	Yes[11]	Yes	No
Qatar	No	-	No
Saudi Arabia	Yes[7]	Yes	No
Somalia	Uncertain	-	Yes
Sudan	Yes	No	Yes
Syria	No	-	No
Tunisia	No	-	No
United Arab Emirates	No	-	No
Yemen	Yes	Yes	Yes
AMRO			
Antigua and Barbuda	No	-	No
Argentina	No	-	No
Bahamas	No	-	No
Barbados	No	-	No
Belize	No	-	No
Bolivia	No	-	No
Brazil	Yes	No	Yes
Chile	No	-	No
Colombia	No	-	No
Costa Rica	Yes[12]	Yes[1,13]	No
Cuba	No	-	No
Dominica	No	-	No
Dominican Republic	Yes	No	Yes
Ecuador	No	-	No
El Salvador	No	-	No
Grenada	No	-	No
Guatemala	No	-	No

Guyana	Yes[14]	No	Yes
Honduras	No	-	No
Haiti	Yes	No	Yes
Jamaica	No	-	No
Nicaragua	No	-	No
Panama	No	-	No
Paraguay	No	-	No
Peru	No	-	No
Saint Kitts and Nevis	No	-	No
Saint Lucia	No	-	No
Saint Vincent and the Grenadines	No	-	No
Suriname	Yes[15]	Yes[16]	No
Trinidad and Tobago	Yes[17]	Yes[16]	No
Uruguay	No	-	No
Venezuela	No	-	No
SEARO			
Bangladesh	Yes	No	Yes
Bhutan	No	-	No
North Korea	No	-	No
India	Yes	No	Yes
Indonesia	Yes	No	Yes
Maldives	Yes	Yes[18]	Yes
Myanmar	Yes	No	Yes
Nepal	Yes	No	Yes
Sri Lanka	Yes	Yes[18]	Yes
Thailand	Yes	Yes[18]	Yes
Timor-Leste	Yes	No	Yes
WPRO			
American Samoa	Yes	No	Yes

Australia	Yes[19]	Yes[19]	No
Brunei	Yes	No	Yes
Cambodia	Yes	Yes[20]	Yes
China	Yes[21]	Yes[21]	No
Cook Islands	Yes	Yes[22]	Yes
Fiji	Yes[23]	No	Yes
French Polynesia	Yes	No	Yes
Guam	No	-	No
Japan	Yes[24]	Yes[24]	No
Kiribati	Yes	No	Yes
Laos	Yes	No	Yes
Malaysia	Yes	No	Yes
Marshall Islands	Yes	Yes[25]	Yes
Micronesia, Federated States of	Yes[26]	No	Yes
Mongolia	No	-	No
Nauru	No[27]	-	No
New Caledonia	Yes[28]	No	Yes
New Zealand	No	-	No
Niue	Yes	Yes[29]	Yes
Northern Mariana Islands	No[30]	No	No
Palau	Yes	Yes[31]	Yes
Papua New Guinea	Yes	No	Yes
Philippines	Yes	No	Yes
Pitcairn Island	No	No	No
South Korea	Yes[32]	Yes[32]	No
Samoa	Yes	No	Yes
Singapore	No	No	No
Solomon Islands	Yes[33]	Yes[34]	No
Tokelau	No	-	No
Tonga	Yes	No	Yes
Tuvalu	Yes	No	Yes

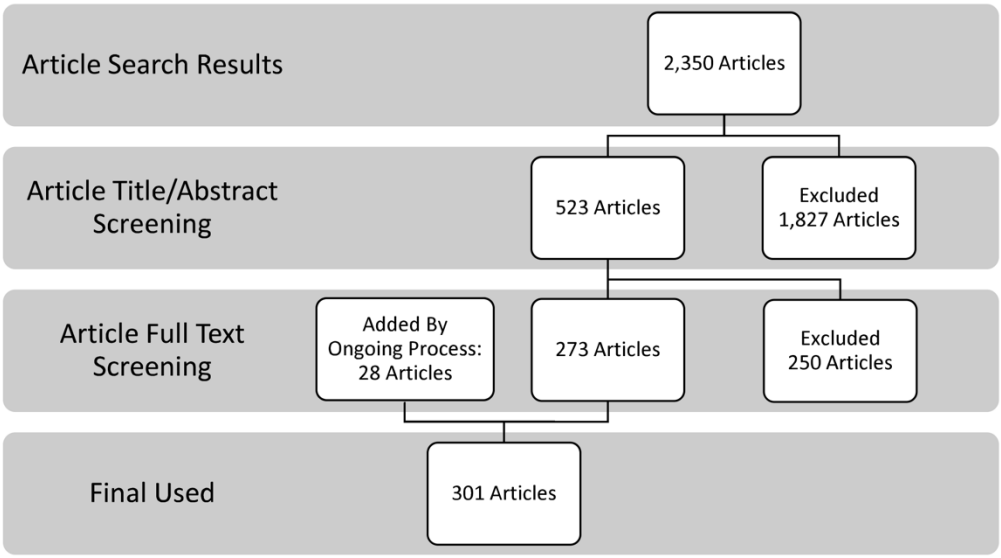
Vanuatu	Yes	No	Yes
Vietnam	Yes	Yes[31]	Yes
Wallis and Futuna	Yes	Yes[31]	Yes

3.2 Systematic review

A systematic review of literature was conducted for all articles published before October 14, 2016 (supplemented with a later search for articles published before October 24, 2018) by searching PubMed, Web of Science, and Scopus with the following keywords: “lymphatic filariasis”, “prevalence”, “incidence”, “mass drug administration”, “coverage”, lymphedema”, “hydrocele”, “transmission assessment survey”, and “mapping”.

3.2.1 Systematic review data processing

The systematic review process is illustrated in Supplementary Figure 2. Throughout the systematic review we excluded publications that met the following criteria: no measurement of LF prevalence, data collected before 1985, case-control studies, qualitative research publications, duplicative data from cohort studies, and publications that did not report the location of data collection. The search identified 2145 publications, which were reduced to 666 after screening titles and abstracts. An additional 190 publications were then excluded because they were duplicative of the 5745 datapoints previously extracted from the Global Atlas of Helminth Infections. A full text review was completed for the 476 remaining publications. The full text review yielded 232 publications which met the inclusion criteria and were extracted. The literature review was updated on October 24, 2018, by searching PubMed with the same search string used in 2016 for articles published after October 14, 2016. The search returned 205 results, which were narrowed to 47 articles after screening titles and abstracts. A full text review resulted in 41 articles that were eligible for extraction. Additional publications were identified outside of the literature review and screened for inclusion by the same criteria, up through March 17, 2020. The final dataset drew from 301 articles. Overall, 2864 datapoints were extracted from 301 publications. Of the extracted datapoints, 2652 were geo-located to the smallest geographical unit possible. Among countries for which data were otherwise not available, ministries of health were contacted directly to request prevalence and intervention monitoring data. Data on the prevalence of clinical disease were not included in the analysis.



Supplementary Figure 2. LF article review and data extraction flowchart

Each step of the extraction process is outlined from article identification and screening to extraction, including the number of articles or records that were processed or removed in each step before reaching the final dataset.

Additional articles outside of the literature review were identified and screened for inclusion ("ongoing process") on an ongoing basis up until March 17, 2020.

3.3 Geo-positioning

LF prevalence data were manually verified and geo-located to ensure accuracy of geographical information. First, data reported from locations smaller than 5 × 5 km were treated as points with coordinates. If lat/long coordinates were provided either in a publication or otherwise available from a data provider, these were mapped to ensure consistency with any other available geographical information (eg, to ensure points were geo-referenced in the correct district or other administrative unit). If coordinates were not provided, locations were manually geo-located and verified comparing results from Google Maps, Open Street Map, Fuzzy Gazetteer, and Humanitarian Data Exchange. Second, prevalence data inputs from locations larger than 5 × 5 km were geo-referenced to the appropriate administrative boundary level (most commonly district or country level), or were geo-referenced to custom boundaries if they represented units of space, such as an Evaluation Unit (EU) used in a Transmission Assessment Survey (TAS) composed of multiple IUs. These inputs were treated as polygon data for the purposes of analysis. In the event that a literature source only included a map of locations sampled without any other information, ArcGIS software was utilised to overlay the map onto existing administrative boundaries, and location coordinates or custom polygons were manually created and recorded. Finally, locations for which LF prevalence was reported that represented administrative areas were assigned to their associated polygons in our administrative shapefile database. If place names were unidentifiable across multiple shapefile libraries or geo-referencing sources, they were excluded from the analysis. National LF programme managers were invited to review results and provide any feedback on accuracy of geo-referencing. We also acknowledge the potential for errors in geo-referencing data inputs by community or IU names. All data inputs were geo-referenced against at least three open-source mapping databases, as well as circulated among national programme managers for accuracy.

3.4 Data processing

A total of 5352 data rows were excluded from the analysis for the following reasons: inability to geo-reference (N = 2,555 observations); missing the year that data collection occurred (N = 371); or missing the number of individuals tested (N = 2426). Duplicate records were identified and excluded (N = 6270); these generally reflected different data sources (eg, literature extraction and ESPEN) which contained the same survey (identical year, location, sample size, and reference when available), although there was some duplication within individual data sources.

Records were identified as outliers and excluded if discordant with published sources of LF programme history (N = 689). When multiple records within a survey series met this criterion, the data quality of the entire series was scrutinised and led to exclusion of the entire survey series. For example, a publication describing baseline survey and monitoring data from Cameroon presents LF prevalence ranging from 1% to 20% for the period 2009–2010. Cameroon data reported via the ESPEN portal for 2003, of which 216 out of 232 surveys exceeded 20% prevalence, was irreconcilable with this publication and outliered. We also chose to exclude prevalence surveys geo-referenced within northern Sahelian areas that likely reflect LF infection in populations that migrate seasonally to LF-endemic locations (northern Niger, northern Chad and northern Mauritania). There is strong evidence against autochthonous transmission here due to the lack of environmental suitability for necessary vector-host interaction.

Supplementary Table 3 provides citations for data sources used in our LF models. The geographical coverage of the final dataset is summarised in Supplementary Figures 3–5.

Supplementary Table 3. Citations for data inputs.

The NID is a unique identifier cataloguing all data inputs in the Global Health Data Exchange (http://ghdx.healthdata.org). Underlying NIDs represent NIDs for primary sources, when data were obtained for this study from a secondary source. Note: Records are listed here in alphabetical order by geography, but some sources provided data for multiple countries; such sources are only listed here once.

NID (underlying NID)	Geographies	Citation
327584	Global	WHO Global Programme for Elimination of Lymphatic Filariasis Database.

NID (underlying NID)	Geographies	Citation
288857	American Samoa	Kroidl I, Saathof E, Maganga L, Clowes P, Maboko L, Hoerauf A, Makunde WH, Haule A, Mviombo P, Pitter B, Mgeni N, Mabuye J, Kowuor D, Mwingira U, Malecela MN, Loescher T, Hoelscher M. Prevalence of Lymphatic Filariasis and Treatment Effectiveness of Albendazole/Ivermectin in Individuals with HIV Co-infection in Southwest-Tanzania. PLoS Negl Trop Dis. 2016; 10(4): e0004618.
289596	American Samoa	Reid EC, Kimura E. Microfilaria prevalence of diurnally subperiodic Wuchereria bancrofti among people having a medical checkup in American Samoa in the past 17 years. J Trop Med Hyg. 1993; 96(2): 118-23.
389386	American Samoa	Sheel M, Sheridan S, Gass K, Won K, Fuimaono S, Kirk M, Gonzales A, Hedtke SM, Graves PM, Lau CL. Identifying residual transmission of lymphatic filariasis after mass drug administration: Comparing school-based versus community-based surveillance - American Samoa, 2016. PLoS Negl Trop Dis. 2018; 12(7): e0006583.
389678	American Samoa	Lau CL, Sheridan S, Ryan S, Roineau M, Andreosso A, Fuimaono S, Tufa J, Graves PM. Detecting and confirming residual hotspots of lymphatic filariasis transmission in American Samoa 8 years after stopping mass drug administration. PLoS Negl Trop Dis. 2017; 11(9): e0005914.
389682	American Samoa	Coutts SP, King JD, Pa'au M, Fuimaono S, Roth J, King MR, Lammie PJ, Lau CL, Graves PM. Prevalence and risk factors associated with lymphatic filariasis in American Samoa after mass drug administration. Trop Med Health. 2017; 45: 22.
143009	American Samoa, Brazil, Ghana, India, Indonesia, Nepal, Sri Lanka	London School of Hygiene and Tropical Medicine. Global Atlas of Helminth Infections - Lymphatic Filariasis. London, United Kingdom: London School of Hygiene and Tropical Medicine.
222546	American Samoa, Dominican Republic, Ghana, Indonesia, Malaysia, Philippines, Sri Lanka, Tanzania, Vanuatu	Chu BK, Deming M, Biritwum NK, Bougma WR, Dorkenoo AM, El-Setouhy M, Fischer PU, Gass K, Gonzalez de Peña M, Mercado-Hernandez L, Kyelem D, Lammie PJ, Flueckiger RM, Mwingira UJ, Noordin R, Offei Owusu I, Ottesen EA, Pavluck A, Pilotte N, Rao RU, Samarasekera D, Schmaedick MA, Settinayake S, Simonsen PE, Supali T, Taleo F, Torres M, Weil GJ, Won KY. Transmission assessment surveys (TAS) to define endpoints for lymphatic filariasis mass drug administration: a multicenter evaluation. *PLoS Negl Trop Dis.* 2013; 7.0(12): e2584.
437961	American Samoa	Graves PM, Sheridan S, Fuimaono S, Lau CL. Demographic, socioeconomic and disease knowledge factors, but not population mobility, associated with lymphatic filariasis infection in adult workers in American Samoa in 2014. Parasites Vectors. 2020; 13(1): 125.
288919	Bangladesh	Shamsuzzaman AKM, Haq R, Karim MJ, Azad MB, Mahmood ASMS, Khair A, Rahman MM, Hafiz I, Ramaiah KD, Mackenzie CD, Mableson HE, Kelly-Hope LA. The significant scale up and success of Transmission Assessment Surveys ñTASî for endgame surveillance of lymphatic filariasis in Bangladesh: One step closer to the elimination goal of 2020. *PLoS Negl Trop Dis*. 2017; 11(1): e0005340.
143009 (270790)	Bangladesh	Samad MS, Itoh M, Moji K, Hossain M, Mondal D, Alam MS, Kimura E. Enzyme-linked immunosorbent assay for the diagnosis of Wuchereria bancrofti infection using urine samples and its application in Bangladesh. Parasitol Int. 2013; 62(6): 564-7.
143009 (271207)	Benin, Burkina Faso, Ghana, Togo	Gyapong JO, Kyelem D, Kleinschmidt I, Agbo K, Ahouandogbo F, Gaba J, Owusu-Banahene G, Sanou S, Sodahlon YK, Biswas G, Kale OO, Molyneux DH, Roungou JB, Thomson MC, Remme J. The use of spatial analysis in maping the distribution of bancroftian filariasis in four West African countries. Ann Trop Med Parasitol. 2002; 96(7): 695-705.

NID (underlying NID)	Geographies	Citation
136401	Brazil	Albuquerque MF, Marzochi MC, Sabroza PC, Braga MC, Padilha T, Silva MC, Silva MR, Schindler HC, Maciel MA, Souza W. Bancroftian filariasis in two urban areas of Recife, Brazil: pre-control observations on infection and disease. Trans R Soc Trop Med Hyg. 1995; 89(4): 373-7.
136494	Brazil	Medeiros Z, Bonfim C, Alves A, Oliveira C, Netto MJE, Aguiar-Santos AM. The epidemiological delimitation of lymphatic filariasis in an endemic area of Brazil, 41 years after the first recorded case. Ann Trop Med Parasitol. 2008; 102(6): 509-19.
136586	Brazil	Medeiros Z, Bonfim C, Brandão E, Netto MJE, Vasconcellos L, Ribeiro L, Portugal J. Using kernel density estimates to investigate lymphatic filariasis in northeast Brazil. *Pathog Glob Health*. 2012; 106(2): 113-7.
288875	Brazil	Brandao E, Bonfim C, Alves A, Oliveira C, Montenegro CE, Costa T, Maciel A, Medeiros Z. Lymphatic filariasis among children and adolescents: spatial identification via socio-environmental indicators to define priority areas for elimination. Int Health. 2015; 7(5): 324-31.
288880	Brazil	Netto MJ, Bonfim C, Brandao E, Aguiar-Santos AM, Medeiros Z. Burden of lymphatic filariasis morbidity in an area of low endemicity in Brazil. Addict Behav Rep. 2016; 163: 54-60.
388976	Brazil	Ramesh A, Cameron M, Spence K, Hoek Spaans R, Melo-Santos MAV, Paiva MHS, Guedes DRD, Barbosa RMR, Oliveira CMF, Sá A, Jeffries CL, Castanha PMS, Oliveira PAS, Walker T, Alexander N, Braga C. Development of an urban molecular xenomonitoring system for lymphatic filariasis in the Recife Metropolitan Region, Brazil. *PLoS Negl Trop Dis*. 2018; 12(10): e0006816.
414527	Brazil	Secretariat of Health Surveillance, Ministry of Health (Brazil). Brazil Lymphatic Filariasis Transmission Assessment Survey and MDA Coverage Data 2002-2016.
437951	Brazil	Xavier A, Oliveira H, Aguiar-Santos A, Barbosa Júnior W, da Silva E, Braga C, Bonfim C, Medeiros Z. Assessment of transmission in areas of uncertain endemicity for lymphatic filariasis in Brazil. PLoS Negl Trop Dis. 2019; 13(11): e0007836.
143009 (136399)	Brazil	Aguiar-Santos AM, Medeiros Z, Bonfim C, Rocha AC, Brandão E, Miranda T, Oliveira P, Sarinho ESC. Epidemiological assessment of neglected diseases in children: lymphatic filariasis and soil-transmitted helminthiasis. *J Pediatr (Rio J)*. 2013; 89(3): 250-5.
143009 (136404)	Brazil	Braga C, Dourado I, Ximenes R, Miranda J, Alexander N. Bancroftian filariasis in an endemic area of Brazil: differences between genders during puberty. Rev Soc Bras Med Trop. 2005; 38(3): 224-8.
143009 (136431)	Brazil	Maciel MA, Marzochi KB, Silva EC, Rocha A, Furtado AF. [Comparative studies on endemic areas of bancroftian filariasis in Greater Recife, Brazil]. Cad Saude Publica. 1994; 10(Suppl 2): 301-9.
143009 (136473)	Brazil	Brandão E, Bonfim C, Cabral D, Lima JL, Aguiar-Santos AM, Maciel A, Medeiros Z. Mapping of Wuchereria bancrofti infection in children and adolescents in an endemic area of Brazil. *Addict Behav Rep*. 2011; 120(1-2): 151-4.
143009 (136479)	Brazil	Bonfim C, Netto MJE, Pedroza D, Portugal JL, Medeiros Z. A socioenvironmental composite index as a tool for identifying urban areas at risk of lymphatic filariasis. Trop Med Int Health. 2009; 14(8): 877-84.
143009 (136514)	Brazil	Bonfim C, Lessa F, Oliveira C o, Evangelista MJ, do Espírito Santo M, Meireles E, Pereira JC, Medeiros Z. [The occurrence and distribution of lymphatic filariasis in Greater Metropolitan Recife: the case of an endemic area in Jaboatão dos Guararapes, Pernambuco, Brazil]. *Cad Saude Publica*. 2003; 19(5): 1497-505.

NID (underlying NID)	Geographies	Citation
143009 (136521)	Brazil	Braga C, Dourado MI, Ximenes RA de A, Alves L, Brayner F, Rocha A, Alexander N. Field evaluation of the whole blood immunochromatographic test for rapid bancroftian filariasis diagnosis in the northeast of Brazil. Rev Inst Med Trop Sao Paulo. 2003; 45(3): 125-9.
143009 (136552)	Brazil	Braga C, Ximenes RA, Albuquerque M, Souza WV, Miranda J, Brayner F, Alves L, Silva L, Dourado I. [Evaluation of a social and environmental indicator used in the identification of lymphatic filariasis transmission in urban centers]. Cad Saude Publica. 2001; 17(5): 1211-8.
143009 (147783)	Brazil	Medeiros Z, Alves A, Brito JA, Borba L, Santos Z, Costa JP, do Espírito Santo ME, Netto MJE. The present situation regarding lymphatic filariasis in Cabo de Santo Agostinho, Pernambuco, Northeast Brazil. Rev Inst Med Trop Sao Paulo. 2006; 48(5): 263-7.
143009 (222121)	Brazil	Oliveira P, Braga C, Alexander N, Brandão E, Silva A, Wanderley L, Aguiar AM, Diniz G, Medeiros Z, Rocha A. Evaluation of diagnostic tests for Wuchereria bancrofti infection in Brazilian schoolchildren. *Rev Soc Bras Med Trop*. 2014; 47.0(3): 359-66.
423159	Brunei	World Health Organization Regional Office for the Western Pacific (WPRO-WHO). First Mekong-Plus Programme Managers Workshop on Lymphatic Filariasis and Other Helminthiasis - March 2009. Manila, Philippines: World Health Organization Regional Office for the Western Pacific (WPRO-WHO), 2009.
338762	Burkina Faso	Expanded Special Project for Elimination of Neglected Tropical Diseases (ESPEN), Ministry of Health (Burkina Faso), World Health Organization Regional Office for Africa (WHO-AFRO). Burkina Faso Lymphatic Filariasis Site Level Map Data - ESPEN. Geneva, Switzerland: World Health Organization (WHO), 2018.
143009 (147765)	Burkina Faso	Kyelem D, Medlock J, Sanou S, Bonkoungou M, Boatin B, Molyneux DH. Short communication: impact of long-term (14 years) bi-annual ivermectin treatment on Wuchereria bancrofti microfilaraemia. Trop Med Int Health. 2005; 10(10): 1002-4.
338755	Burundi	Expanded Special Project for Elimination of Neglected Tropical Diseases (ESPEN), Ministry of Public Health (Burundi), World Health Organization Regional Office for Africa (WHO-AFRO). Burundi Lymphatic Filariasis Site Level Map Data - ESPEN. Geneva, Switzerland: World Health Organization (WHO), 2018.
288839	Cambodia	Leang R, Socheat D, Bin B, Bunkea T, Odermatt P. Assessment of disease and infection of lymphatic filariasis in Northeastern Cambodia. Trop Med Int Health. 2004; 9(10): 1115-20.
288853	Cameroon	Gounoue-Kamkumo R, Nana-Djeunga HC, Bopda J, Akame J, Tarini A, Kamgno J. Loss of sensitivity of immunochromatographic test (ICT) for lymphatic filariasis diagnosis in low prevalence settings: consequence in the monitoring and evaluation procedures. BMC Infect Dis. 2015; 15: 579.
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389696	Haiti	Knipes AK, Lemoine JF, Monestime F, Fayette CR, Direny AN, Desir L, Beau de Rochars VE, Streit TG, Renneker K, Chu BK, Chang MA, Mace KE, Won KY, Lammie PJ. Partnering for impact: Integrated transmission assessment surveys for lymphatic filariasis, soil transmitted helminths and malaria in Haiti. PLoS Negl Trop Dis. 2017; 11(2): e0005387.
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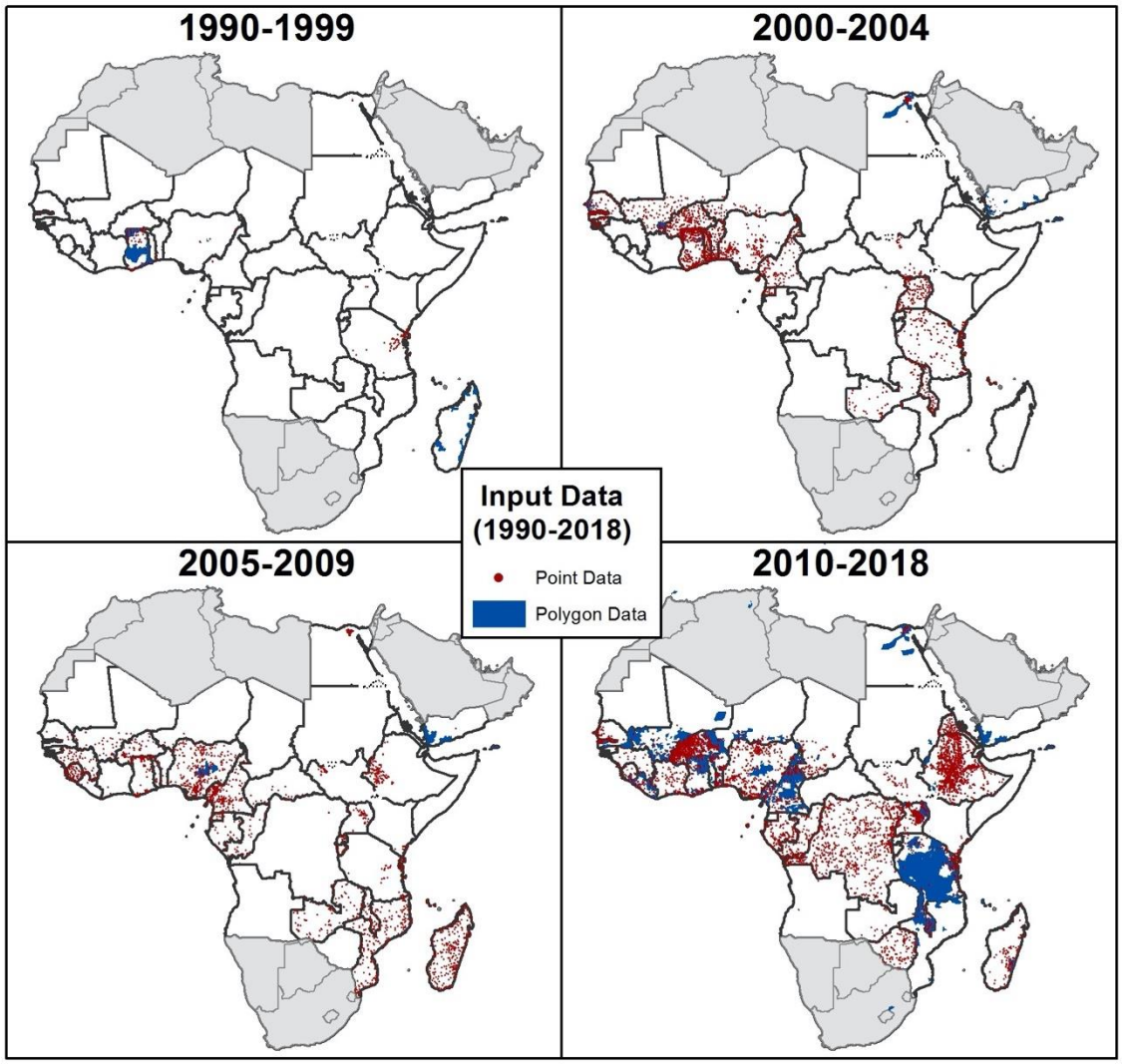
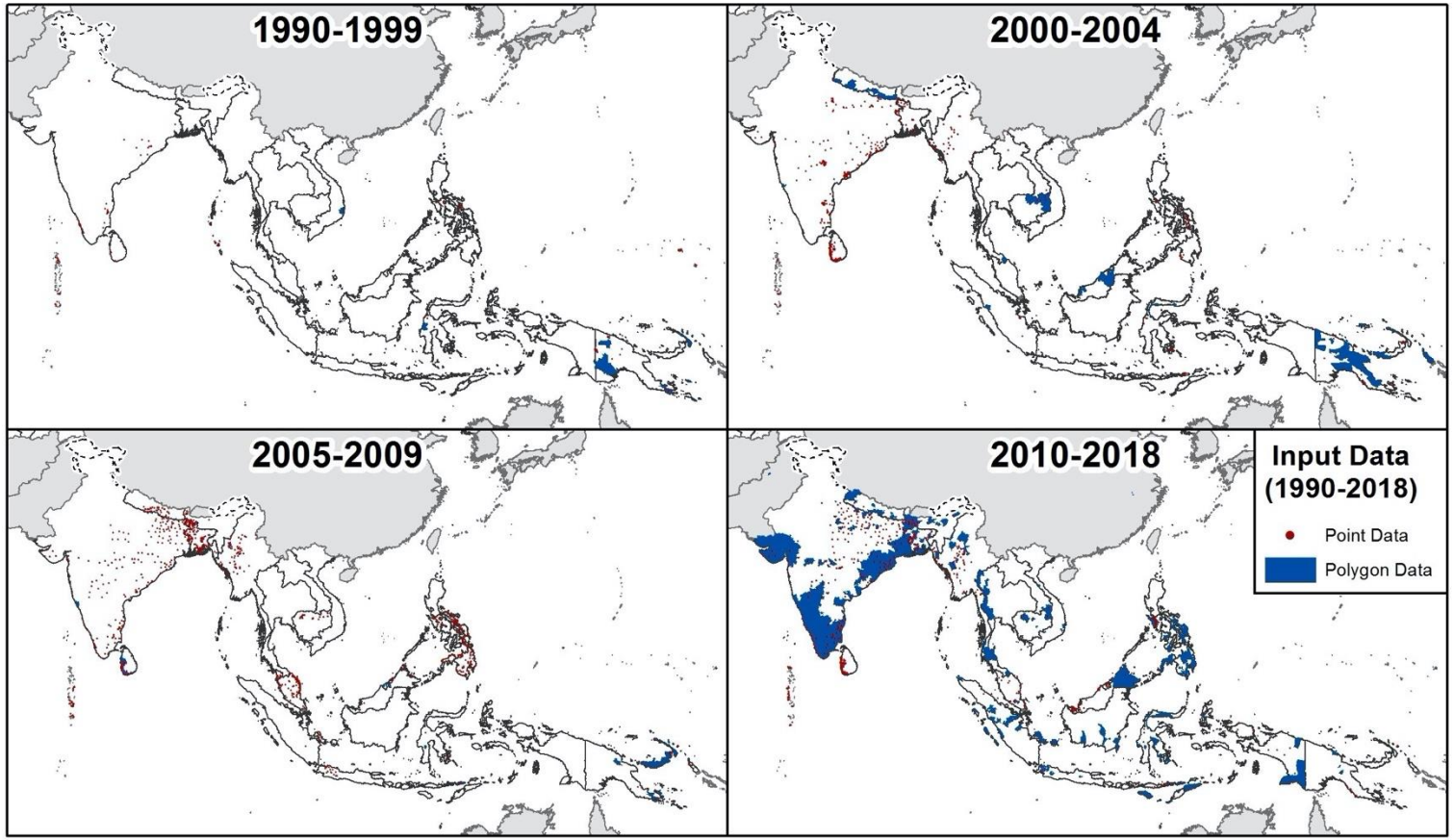
143009 (136507)	Vanuatu	Fraser M, Taleo G, Taleo F, Yaviong J, Amos M, Babu M, Kalkoa M. Evaluation of the program to eliminate lymphatic filariasis in Vanuatu following two years of mass drug administration implementation: results and methodologic approach. Am J Trop Med Hyg. 2005; 73(4): 753-8.
136435	Vietnam	Meyrowitsch DW, Nguyen DT, Hoang TH, Nguyen TD, Michael E. A review of the present status of lymphatic filariasis in Vietnam. Addict Behav Rep. 1998; 70(3): 335-47.
437811	Wallis and Futuna	Pezzoli L, Kim SH, Mathelin JP, Hennessey K, Eswara Aratchige P, Valiakolleri J. An Expanded Transmission Assessment Survey to Confirm the Interruption of Lymphatic Filariasis Transmission in Wallis and Futuna. Am J Trop Med Hyg. 2019; 101(6): 1325-1330.
288871	Yemen	Al-Kubati AS, Al Qubati Y, Ismail W, Laney SJ, El-Setouhy M, Gad AM, Ramzy RMR. Impact of polystyrene beads as a mosquito control measure to supplement lymphatic filariasis elimination activities in Socotra Island, Yemen. East Mediterr Health J. 2011; 17(7): 560-4.
339565	Zambia	Expanded Special Project for Elimination of Neglected Tropical Diseases (ESPEN), Ministry of Health (Zambia), World Health Organization Regional Office for Africa (WHO-AFRO). Zambia Lymphatic Filariasis Site Level Map Data - ESPEN. Geneva, Switzerland: World Health Organization (WHO), 2018.
143009 (222129)	Zambia	Mwase ET, Stensgaard AS, Nsakashalo-Senkwe M, Mubila L, Mwansa J, Songolo P, Shawa ST, Simonsen PE. Mapping the geographical distribution of lymphatic filariasis in Zambia. PLoS Negl Trop Dis. 2014; 8.0(2): e2714.
143009 (222540)	Zambia	Shawa ST, Mwase ET, Pedersen EM, Simonsen PE. Lymphatic filariasis in Luangwa District, South-East Zambia. Parasites Vectors. 2013; 6.0(1): 299.



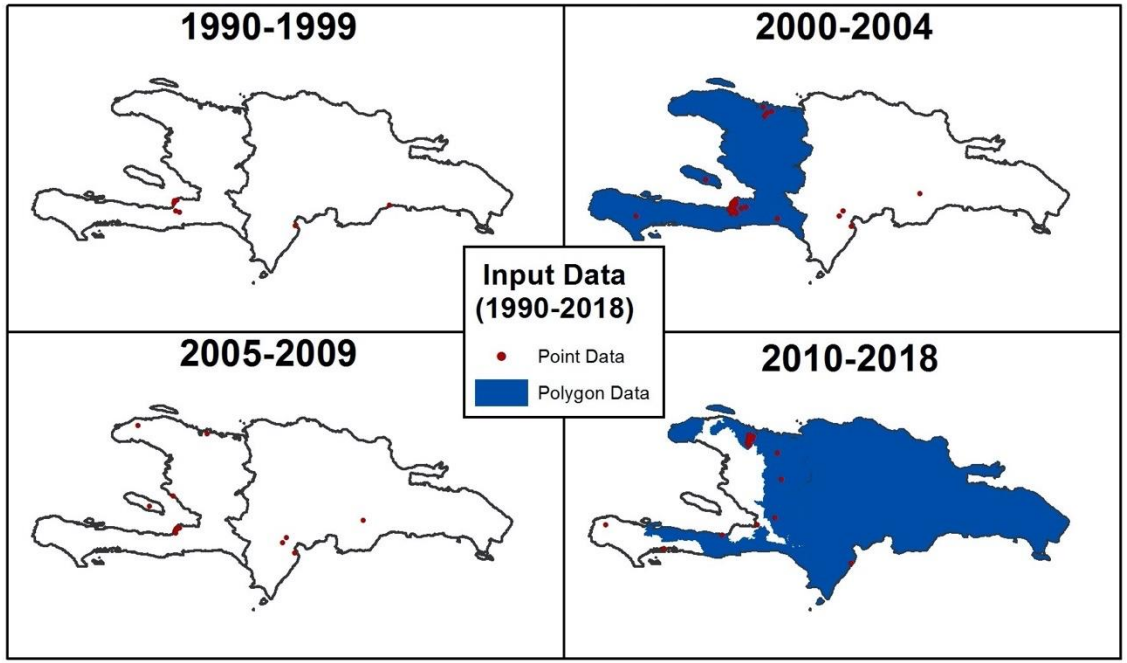
Supplementary Figure 3. Africa and Yemen data maps, 1990–1999, 2000–2004, 2005–2009, 2010–2018

Locations of the unique point and polygon data used in modelling, grouped by year



Supplementary Figure 4. South and Southeast Asia data maps, 1990–1999, 2000–2004, 2005–2009, 2010–2018

Locations of the unique point and polygon data used in modelling, grouped by year



Supplementary Figure 5. Hispaniola data maps, 1990–1999, 2000–2004, 2005–2009, 2010–2018

Locations of the unique point and polygon data used in modelling, grouped by year

4.0 Supplementary covariates

A variety of socioeconomic and environmental variables were used to predict all-age LF prevalence. Where available, the finest spatiotemporal resolution of gridded datasets were used. Data from the nearest year available were used if covariate coverage did not extend to 2018 or prior to 2000. All covariates were resampled to a standard 5 × 5-km raster resolution. Due to unavailability of some covariates in certain regions and to differences in covariate collinearity, the final number of covariates differed among regional models: 23 covariates for Africa, 22 covariates for South Asia, 21 covariates for Southeast Asia, and 21 covariates for Hispaniola (Haiti and the Dominican Republic).

4.1 Pre-existing covariates considered for analysis

Supplementary Table 4 contains a full list of covariates considered in our analysis. In order to provide a standard spatial resolution for prediction, raw covariate rasters were resampled to a 5 × 5-km grid-cell resolution.

4.2 Creation of MDA covariate

Data were obtained from WHO[35] on the years during which LF MDA was conducted, by administrative unit. The names of IUs were fuzzy-matched to geographies using administrative-level shapefiles for GAUL and GADM geographies. Among countries for which GAUL or GADM shapefiles did not represent IU boundaries, the NTD Implementation Unit Shapefile maintained by the Task Force for Global Health[36] was also used. The fuzzy matching algorithm tested polygon names through ascending order of spatial hierarchy (region, district, and lower-level units) on a country-by-country basis, typically matching to second- and third-order administrative-level boundaries. In the case of programmes in which MDA was implemented at the community level, these IU names were matched to community names where possible and a 5-km buffer radius was assigned to each location to represent the population under intervention. The MDA covariate value was set as a binary value by year (MDA yes/no) as well as cumulative number of rounds (defined as total number of rounds implemented) for the entire IU, and then converted into a raster file for use in geospatial analysis.

Supplementary Table 4. Covariates considered for modelling, 1990–2018

Covariate	Temporal resolution	Source	Reference
Travel time to nearest settlement >50,000 inhabitants	Static	Malaria Atlas Project, Big Data Institute, Nuffield Department of Medicine, University of Oxford	Weiss, D. J. et al. A global map of travel time to cities to assess inequalities in accessibility in 2015. Nature 533, 333-336 (2018).
Aridity	Annual	Climatic Research Unit Time-Series (CRUTS)	Harris, I., Jones, P. d., Osborn, T. j. & Lister, D. h. Updated high-resolution grids of monthly climatic observations – the CRUTS3.10 dataset. Int. J. Climatol. 34, 623–642 (2014) University of East Anglia. Climatic Research Unit TS v. 3.24 dataset. Available at: https://crudata.uea.ac.uk/cru/data/hrg/cru_ts_3.24.0 1/. (Accessed: 24th July 2017).
Average daily mean temperature	Annual	CRUTS	Harris, I., Jones, P. d., Osborn, T. j. & Lister, D. h. Updated high-resolution grids of monthly climatic observations – the CRU TS3.10 dataset. Int. J. Climatol. 34, 623–642 (2014). University of East Anglia. Climatic Research Unit TS v. 3.24 dataset. Available at: https://crudata.uea.ac.uk/cru/data/hrg/cru_ts_3.24.0 1/. (Accessed: 24th July 2017).

Covariate	Temporal resolution	Source	Reference
Wet day frequency	Annual	CRUTS	Harris, I., Jones, P. d., Osborn, T. j. & Lister, D. h. Updated high-resolution grids of monthly climatic observations – the CRU TS3.10 dataset. Int. J. Climatol. 34, 623–642 (2014). University of East Anglia. Climatic Research Unit TS v. 3.24 dataset. Available at: https://crudata.uea.ac.uk/cru/data/hrg/cru_ts_3.24.0 1/. (Accessed: 24th July 2017).
Distance to rivers	Static	Natural Earth Data (derived)	Natural Earth. Rivers and lake centerlines dataset. Available at: http://www.naturalearthdata.com/downloads/10mphysical-vectors/10m-rivers-lake-centerlines/. (Accessed: 24th July 2017)
Distance to rivers and lakes	Static	Natural Earth Data (derived)	Natural Earth. Rivers and lake centerlines dataset. Available at: http://www.naturalearthdata.com/downloads/10mphysical-vectors/10m-rivers-lake-centerlines/. (Accessed: 24th July 2017)
Distance to rivers >25m wide	Static	Natural Earth Data (derived)	Andreadis KM, Schumann GJ-P, Pavelsky T. A simple global river bankfull width and depth database. Water Resources Research. 2013;49(10):7164–8.
Distance to floodplains	Static	GFPLAIN250m	Nardi, F, Annis A, Di Baldassarre G, *et al*. 2019. GFPLAIN250m, a global high-resolution dataset of Earth's floodplains. *Sci Data* **6,** 180309. https://doi.org/10.1038/sdata.2018.309
Nighttime lights	Annual	AVHRR	NASA & NOAA. Advanced Very High Resolution Radiometer (AVHRR) Normalized Difference Vegetation Index (NDVI) dataset. Available at: https://nex.nasa.gov/nex/projects/1349/. (Accessed: 25th July 2017)
Elevation	Static	NOAA/NCEI	Young, A. H., K. R. Knapp, A. Inamdar, W. B. Rossow, and W. Hankins, 2017: "The International Satellite Cloud Climatology Project, H-Series Climate Data Record Product", Earth System Science Data, in preparation.
Enhanced Vegetation Index (EVI)	Annual	MODIS	Huete, A., Justice, C. & van Leeuwen, W. MODIS vegetation index (MOD 13) algorithm theoretical basis document. (1999). USGS & NASA. Vegetation indices 16-Day L3 global 500m MOD13A1 dataset. Available at: https://lpdaac.usgs.gov/dataset_discovery/modis/modis_products_table/mod13a1. (Accessed: 25th July 2017) Weiss, D. J. et al. An effective approach for gapfilling continental scale remotely sensed timeseries. Isprs J. Photogramm. Remote Sens. 98, 106–118 (2014). C. Schaaf, Z. Wang. (2015). MCD43A1 MODIS/Terra+Aqua BRDF/Albedo Model Parameters Daily L3 Global - 500m V006. NASA EOSDIS Land Processes DAAC. http://doi.org/10.5067/MODIS/MCD43A1.006

Covariate	Temporal resolution	Source	Reference
Diurnal temperature range	Annual	CRUTS	Harris, I., Jones, P. d., Osborn, T. j. & Lister, D. h. Updated high-resolution grids of monthly climatic observations – the CRU TS3.10 dataset. Int. J. Climatol. 34, 623–642 (2014). University of East Anglia. Climatic Research Unit TS v. 3.24 dataset. Available at: https://crudata.uea.ac.uk/cru/data/hrg/cru_ts_3.24.0 1/. (Accessed: 24th July 2017).
Population (per 5 x 5-km cell)	Annual	WorldPop	Lloyd, C. T., Sorichetta, A. & Tatem, A. J. High resolution global gridded data for use in population studies. Sci. Data 4, sdata20171 (2017). World Pop. Get data. Available at: http://www.worldpop.org.uk/data/get_data/. (Accessed: 25th July 2017)
Growing season length	Static	FAO	FAO. GAEZ - Global Agro-Ecological Zones data portal. Available at: http://www.fao.org/nr/gaez/about-data-portal/en/. (Accessed: 25th July 2017) FAO. GAEZ - Global Agro-Ecological Zones users guide. (2012).
Irrigation	Static	University of Frankfurt	Goethe-Universität. Generation of a digital global map of irrigation areas. Available at: https://www.unifrankfurt.de/45218039/Global_Irrigation_Map. (Accessed: 25th July 2017)
Urbanicity	Annual	European Commission/GHS	Pesaresi, M. et al. Operating procedure for the production of the Global Human Settlement Layer from Landsat data of the epochs 1975, 1990, 2000, and 2014. (Publications Office of the European Union, 2016).
Tassled cap brightness	Annual	MODIS	USGS & NASA. Nadir BRDF- Adjusted Reflectance Reflectance 16-Day L3 Global 1km dataset. Available at: https://lpdaac.usgs.gov/dataset_discovery/modis/modis_products_table/mcd43b4. (Accessed: 25th July 2017) Strahler, A. H. & Muller, J.-P. MODIS BRDF/Albedo product: algorithm theoretical basis document version 5.0. (1999). Weiss, D. J. et al. An effective approach for gapfilling continental scale remotely sensed timeseries. Isprs J. Photogramm. Remote Sens. 98, 106–118 (2014). C. Schaaf, Z. Wang. (2015). MCD43A1 MODIS/Terra+Aqua BRDF/Albedo Model Parameters Daily L3 Global - 500m V006. NASA EOSDIS Land Processes DAAC. http://doi.org/10.5067/MODIS/MCD43A1.006
Tassled cap wetness	Annual	MODIS	USGS & NASA. Nadir BRDF- Adjusted Reflectance Reflectance 16-Day L3 Global 1km dataset. Available at: https://lpdaac.usgs.gov/dataset_discovery/modis/modis_products_table/mcd43b4. (Accessed: 25th July 2017) Strahler, A. H. & Muller, J.-P. MODIS BRDF/Albedo product: algorithm theoretical basis document version 5.0. (1999).

Covariate	Temporal resolution	Source	Reference
			Weiss, D. J. et al. An effective approach for gapfilling continental scale remotely sensed timeseries. Isprs J. Photogramm. Remote Sens. 98, 106–118 (2014). C. Schaaf, Z. Wang. (2015). MCD43A1 MODIS/Terra+Aqua BRDF/Albedo Model Parameters Daily L3 Global - 500m V006. NASA EOSDIS Land Processes DAAC. http://doi.org/10.5067/MODIS/MCD43A1.006
Multi-source Weighted-Ensemble Precipitation	Annual	Princeton Climate Analytics	Beck, H.E., A.I.J.M. van Dijk, V. Levizzani, J. Schellekens, D.G. Miralles, B. Martens, A. de Roo: MSWEP: 3-hourly 0.25 global gridded precipitation (1979-2015) by merging gauge, satellite, and reanalysis data, Hydrology and Earth System Sciences, 21(1), 589-615, 2017.
Slope for land surfaces	Static	NOAA/NCEI	Young, A. H., K. R. Knapp, A. Inamdar, W. B. Rossow, and W. Hankins, 2017: "The International Satellite Cloud Climatology Project, H-Series Climate Data Record Product", Earth System Science Data, in preparation.
Human Development Index	Annual	UNDP	UNDP. Human Development Index (HDI). New York: United Nations Development Program, 2016. Available from http://hdr.undp.org/en/content/human-development-index-hdi (Cited Aug 12 2017).
Under 5-mortality	Annual	IHME LBD model	Burstein, Roy, Nathaniel J. Henry, Michael L. Collison, Laurie B. Marczak, Amber Sligar, Stefanie Watson, Neal Marquez, et al. "Mapping 123 Million Neonatal, Infant and Child Deaths between 2000 and 2017." *Nature* 574, no. 7778 (October 2019): 353–58. https://doi.org/10.1038/s41586-019-1545-0.
Childhood stunting prevalence	Annual	IHME LBD model	Osgood-Zimmerman, Aaron, Anoushka I. Millear, Rebecca W. Stubbs, Chloe Shields, Brandon V. Pickering, Lucas Earl, Nicholas Graetz, et al. "Mapping Child Growth Failure in Africa between 2000 and 2015." *Nature* 555, no. 7694 (March 2018): 41–47. https://doi.org/10.1038/nature25760.
Childhood underweight prevalence	Annual	IHME LBD model	Osgood-Zimmerman, Aaron, Anoushka I. Millear, Rebecca W. Stubbs, Chloe Shields, Brandon V. Pickering, Lucas Earl, Nicholas Graetz, et al. "Mapping Child Growth Failure in Africa between 2000 and 2015." *Nature* 555, no. 7694 (March 2018): 41–47. https://doi.org/10.1038/nature25760.
Childhood wasting prevalence	Annual	IHME LBD model	Osgood-Zimmerman, Aaron, Anoushka I. Millear, Rebecca W. Stubbs, Chloe Shields, Brandon V. Pickering, Lucas Earl, Nicholas Graetz, et al. "Mapping Child Growth Failure in Africa between 2000 and 2015." *Nature* 555, no. 7694 (March 2018): 41–47. https://doi.org/10.1038/nature25760.
Mean years of education attained (maternal)	Annual	IHME LBD model	Graetz N, Friedman J, Osgood-Zimmerman A, Burstein R, Biehl MH, Shields C, Mosser JF, Casey DC, Deshpande A, Earl L, Reiner RC, Ray SE, Fullman N, Levine AJ, Stubbs RW, Mayala BK, Longbottom J, Browne AJ, Bhatt S, Weiss DJ, Gething PW, Mokdad AH, Lim SS, Murray CJLM, Gakidou E, Hay SI. "Mapping local variation in educational attainment

Covariate	Temporal resolution	Source	Reference
			across Africa." *Nature*. 28 Feb 2018. doi:10.1038/nature25761
Proportion of individuals that slept under an insecticide-treated net (ITN) the night before	Annual	Malaria Atlas Project	Malaria Atlas Project. https://map.ox.ac.uk/
Indoor residual spraying (IRS) coverage	Annual	Malaria Atlas Project	Malaria Atlas Project. https://map.ox.ac.uk/
Access to antimalarial drugs	Annual	Malaria Atlas Project	Malaria Atlas Project. https://map.ox.ac.uk/
Malaria incidence (Pf) (all ages)	Annual	Malaria Atlas Project	Malaria Atlas Project. https://map.ox.ac.uk/
Malaria incidence (Pv) (all ages)	Annual	Malaria Atlas Project	Malaria Atlas Project. https://map.ox.ac.uk/
Malaria prevalence (Pf) (all ages)	Annual	Malaria Atlas Project	Malaria Atlas Project. https://map.ox.ac.uk/
Malaria prevalence (Pv) (all ages)	Annual	Malaria Atlas Project	Malaria Atlas Project. https://map.ox.ac.uk/
LF mass drug administration (MDA) coverage	Annual	WHO (rasters produced in present study: SI section 4.2)	WHO. Global Programme to Eliminate Lymphatic Filariasis. http://www.who.int/lymphatic_filariasis/elimination-programme/en/ (accessed May 29, 2019).

Pf: *Plasmodium falciparum*. Pv: *Plasmodium vivax*.

4.3 Covariate reduction

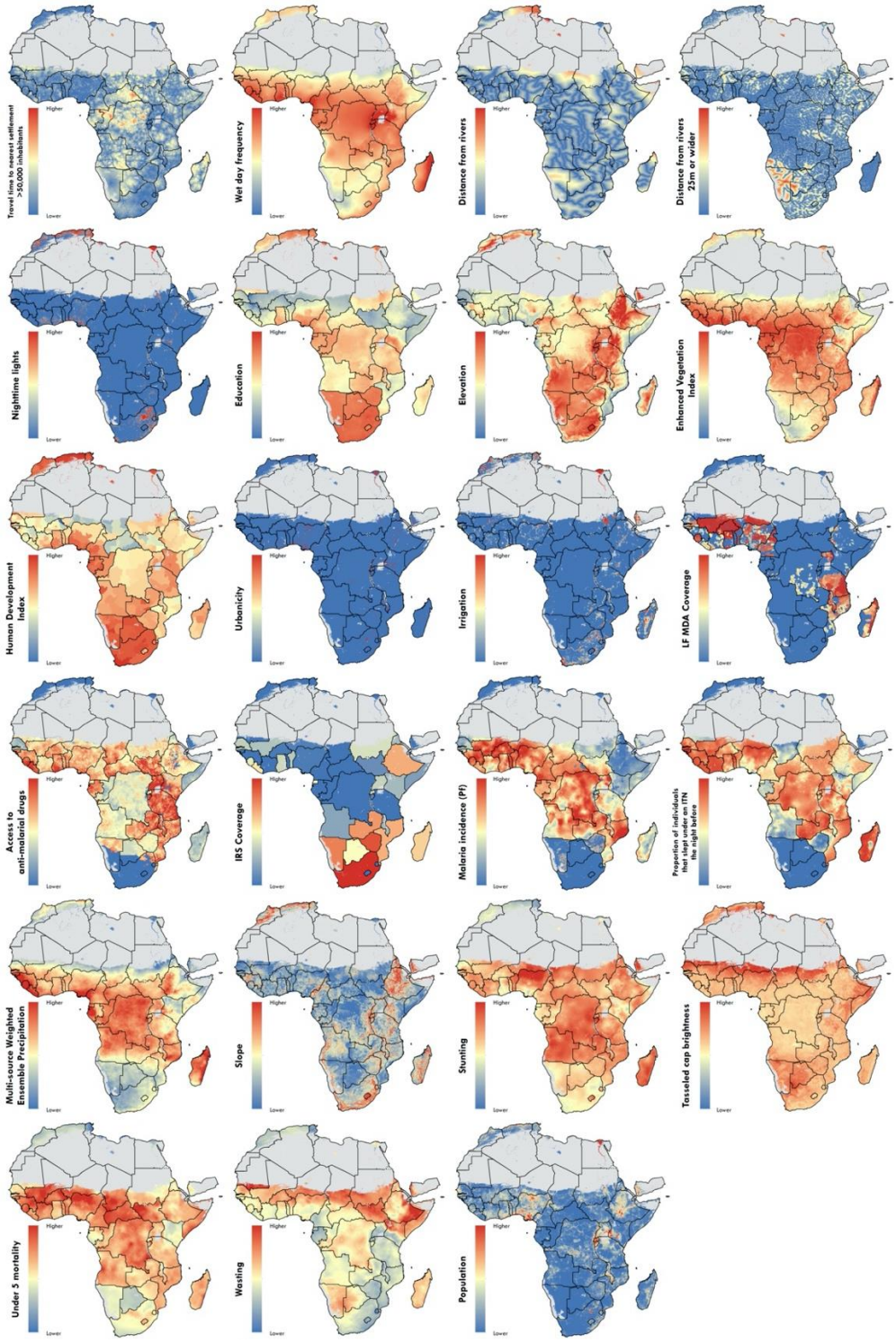
As high inter-correlation (collinearity) among model covariates can contribute to model instability and unreliable predictions,[37,38] we derived reduced covariate sets using variance inflation factor (VIF) analysis. Variance inflation factors quantify the extent to which collinearity among model covariates increases the variance of a model coefficient. Starting with the full covariate set for a given model region, we iteratively removed covariates with the highest VIF values until all remaining covariates had a VIF below 5.0.[38] Reduced covariate sets were used in the fitting of child models via an ensemble model and regression (see Supplementary Section 5.3.2) and for spatiotemporal predictions. Exploratory analyses of LF models for Hispaniola indicated poor model fit with inclusion of the under-5 mortality and *Plasmodium vivax* malaria incidence covariates; these covariates were excluded from the final models for Hispaniola. Supplementary Table 5 summarises the covariates retained for each model region, with representative plots provided for each covariate in Supplementary Figure 6–8.

To better reflect the potential temporal relationship of covariates with LF prevalence, the following variables were modelled with a one-year lag (eg, covariate values from 2000 were associated with LF prevalence in 2001): aridity, temperature, nighttime lights, education, EVI, urbanicity, mass drug administration, diurnal temperature difference, precipitation, stunting, tassel capped brightness, under-5 mortality, wasting, and population. All other variables were modelled without a temporal lag.

The derivation of 5 × 5-km grid-cell-level predictions from our geostatistical models requires complete coverage of covariate data at a given grid cell. Due to minor differences in model coverage between our LF models and some indicators that are used as inputs to our models (eg, under-5 mortality), complete covariate coverage was not available for all 5 × 5-km grid cells. Most notably, covariate data were incomplete for Brunei and for a small proportion of grid cells along coastlines. In order to enable LF model predictions for Brunei, the under-5 mortality and child growth failure covariates were excluded from the Southeast Asia models.

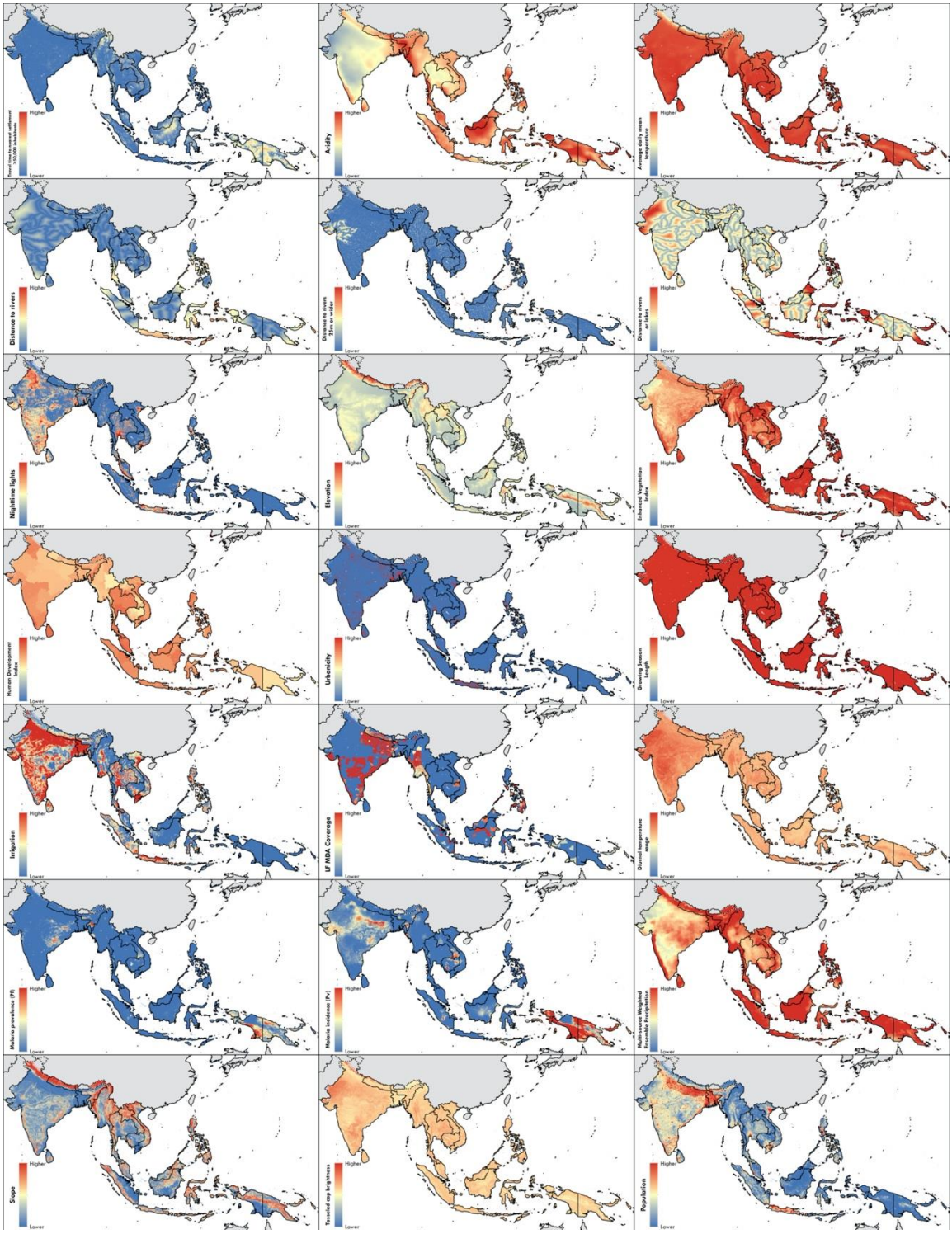
Supplementary Table 5. Covariates used in final MBG models, 1990–2018
Some covariates were available only for some model regions. +/-: Covariate was/was not included in the final model for a given region, after VIF analysis. n/a: Data were unavailable for a given region. Hisp.: Hispaniola.

Covariate	Shortname	Africa	S Asia	SE Asia	Hisp.
Antimalarial drug access	map_antimalarial	+	n/a	n/a	n/a
Aridity	crutsard	-	+	+	+
Daily average temperature	crutstmp	-	+	+	+
Distance to rivers	distrivers	+	+	+	+
Distance to rivers >25 m wide	distrivers25m	+	+	+	+
Distance to rivers and lakes	distrivers_lakes	-	+	+	+
Elevation	elevation	+	+	+	+
Enhanced Vegetation Index (EVI)	evi	+	+	+	+
Growing season length	growingseason	-	+	+	+
Human Development Index	gdl_hdi	+	-	+	-
Indoor residual spraying (IRS) coverage	map_irs	+	n/a	n/a	n/a
Insecticide-treated net (ITN) use	mapitncov	+	n/a	n/a	n/a
Irrigation	irrigation	+	+	+	+
Malaria incidence (*P. falciparum*)	map_pf_incidence	+	-	-	-
Malaria incidence (*P. vivax*)	map_pv_incidence	-	+	+	-
Malaria prevalence (*P. falciparum*)	map_pf_prevalence	-	+	+	+
Mass drug administration (MDA) for LF	lfmda	+	+	+	+
Maternal education	education	+	-	-	-
Nighttime lights	dmspntl	+	+	+	+
Population	worldpop	+	+	+	+
Precipitation	mswep	+	+	+	+
Slope	slope	+	+	+	+
Stunting prevalence	stunting_mod_b	+	-	-	+
Tassled cap brightness	tcb	+	+	+	+
Tassled cap wetness	tcw	-	-	-	-
Temperature range (diurnal)	lstdiurnaldiff	-	+	+	+
Travel time to nearest city	access2	+	+	+	+
Under-5 mortality probability	u5m	+	+	-	-
Underweight prevalence	underweight	-	-	-	-
Urbanicity	ghslurbanicity	+	+	+	+
Wasting prevalence	wasting_mod_b	+	+	-	+
Wet day frequency	crutswet	+	-	-	-
Total covariates used		23	22	21	21



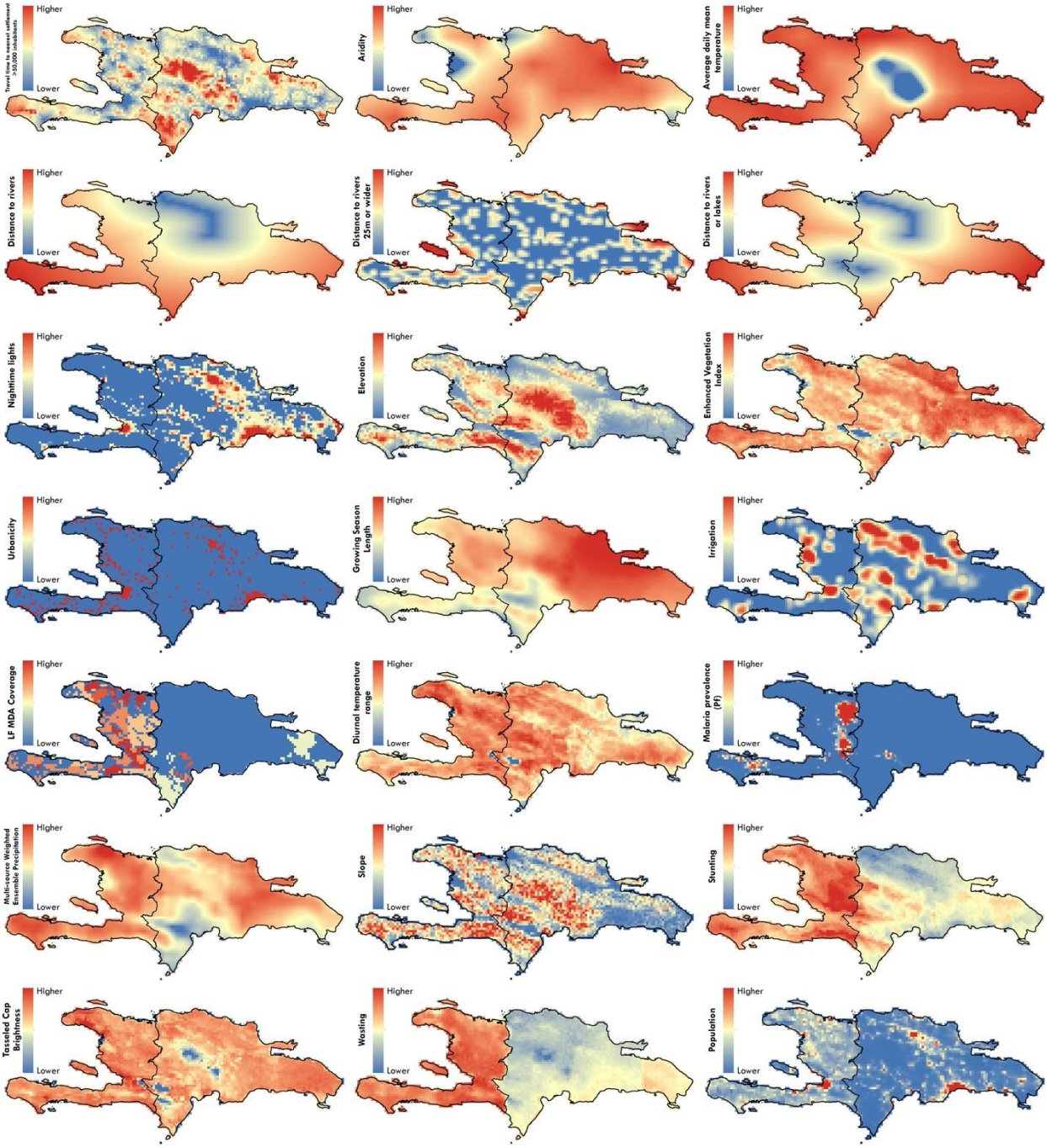
Supplementary Figure 6. Africa and Yemen covariate values

Twenty-three socioeconomic and environmental variables were used as inputs for the stacking modelling process for Africa and Yemen. Time-varying covariates are presented here for the year 2015 (except for nighttime lights, for which values are shown from 2013 due to more limited data availability). Please refer to Supplementary Table 4 for the corresponding citations for each covariate.



Supplementary Figure 7. South and Southeast Asia covariate values

Twenty-three socioeconomic and environmental variables were used as inputs for the stacking modelling process for South or Southeast Asia. Time-varying covariates are presented here for the year 2015 (except for nighttime lights, for which values are shown from 2013 due to more limited data availability). Please refer to Supplementary Table 4 for the corresponding citations for each covariate.



Supplementary Figure 8. Hispaniola covariate values

Twenty-one covariate layers of possible socioeconomic and environmental correlates of LF prevalence were used as inputs for the stacking modelling processes for Hispaniola. Time-varying covariates are presented here for the year 2015. Please refer to Supplementary Table 4 for the corresponding citations for each covariate.

5.0 Supplementary methods

5.1 Age and diagnostic crosswalks

Studies on LF prevalence have differed in both their sampled age ranges and in the diagnostic tests they utilised. For example, surveys have variously targeted population-representative samples or focused on restricted age ranges, such as 6–7 year olds in many TAS surveys. In order to derive a consistent outcome measure for modelling, we adjusted survey data to represent all-age ICT prevalence by developing age and diagnostic crosswalk models. We fit a prevalence-by-age model for ICT and FTS antigen tests, and a separate prevalence-by-age model for microfilaraemia. If age groups were not reported in the input data, we assumed the age sampling occurred per programme monitoring guidelines (eg, TAS implemented among children ages 6-7 years).

Most LF survey data used by our spatiotemporal prevalence models were derived from observations of microfilariae (mf) or detection of adult worm antigens. We developed a crosswalk model relating age-specific ICT prevalence with mf prevalence. Due to limited data available to model a similar relationship between the Filariasis Test Strip (FTS, which was broadly adopted by programmes as of 2016) and ICT, prevalence measures obtained using FTS were considered equivalent to ICT for our geostatistical model. Until recently, antigen surveys mainly utilised the ICT test, which has now been supplanted by FTS. Age-specific ICT and FTS results in the same study populations have only been published in one study to date (Yahathugoda and colleagues 2015[39]), although multi-site all-age comparisons have been published showing that FTS is generally more sensitive in low-prevalence settings with overall agreement between the tests,[40] particularly among children.[41] We have assumed that these tests share a common prevalence-by-age relationship (ie, that relative age-specific sensitivity and specificity profiles do not differ between these antigen tests). For areas in which both Bancroftian and Brugian LF co-circulate, we only estimated prevalence of Bancroftian LF. Among areas with LF transmission of *Brugia* species only, we rely on MF prevalence measures to represent infection. Since national programmes in *Brugia* settings often use the Brugia Rapid ® point of care antibody test to monitor impact of MDA, we did not crosswalk Brugia Rapid results.

As individual-level infection data were unavailable, we relied on published within-study comparisons reporting mf, ICT, or FTS prevalence (age crosswalks), or both ICT and mf prevalence (diagnostic crosswalk), for more than one age group in the same study population. We identified 47 unique survey populations from 25 studies for the ICT age crosswalk, 126 unique survey populations from 72 studies for the mf age crosswalk, and 18 unique survey populations from 11 studies for the diagnostic crosswalk; these studies are summarised in Supplementary Table 6. The crosswalk training data set is available upon request.

Supplementary Table 6. Data used in estimation of age and diagnostic crosswalks

Note that studies may have reported data for additional diagnostic tests that were not used in crosswalk model fitting.

Countries	Survey years	Diagnostic data
American Samoa[42]	2016 (post-MDA)	FTS
Bangladesh[43]	1968–1969 (pre-MDA)	mf
Benin[44]	1983, 1994 (pre-MDA; only data from 1983 used for crosswalk)	mf
Brazil[45]	1999 (pre-MDA)	ICT, mf
Brazil[46]	1991 (pre-MDA)	mf
Brazil[47]	2000 or earlier (pre-MDA)	mf
Brazil[48]	2000–2002 (pre-MDA)	mf
Brazil[49]	2002 (pre-MDA)	mf

Cameroon[50]	2000 (pre-MDA)	Mf
Egypt[51]	1999 or earlier (pre- and post-MDA; only pre-MDA data used for crosswalk)	mf
Federated States of Micronesia[26]	2003 (pre-MDA)	ICT, mf
Ghana[52]	2008 (post-MDA)	ICT, mf
Ghana[53]	2016–2017 (pre- and post-MDA)	FTS
Ghana[54]	1992 (pre-MDA)	mf
Ghana[55]	1994 (pre-MDA)	mf
Ghana[56]	1994–1995 (pre-MDA)	mf
Ghana[57]	1995–1996 (pre-MDA)	mf
Ghana[58]	2000, 2002, 2004 (pre-MDA)	mf
Ghana[59]	2004 (post-MDA)	mf
Haiti[60]	2003 (pre-MDA)	ICT
Haiti[61]	2008 (post-MDA)	ICT, mf
Haiti[62]	1994 or earlier (pre-MDA)	mf
India[63]	1971 (pre-MDA)	mf
India[64]	1977 or earlier (pre-MDA)	mf
India[65]	1986 (pre-MDA)	mf
India[66]	1986–1988 (pre- and post-MDA; only pre-MDA data used in crosswalk)	mf
India[67]	1988 (pre-MDA)	mf
India[68]	2003 or earlier (pre-MDA)	mf
India[69]	2006 or earlier (pre-MDA)	mf
India[70]	2009 (post-MDA)	mf
Indonesia[71]	1974, 1976 (pre-MDA)	mf
Indonesia[72]	2001 or earlier (pre-MDA)	mf
Indonesia[73]	2001 (pre-MDA)	mf
Indonesia[74]	2003 or earlier (pre-MDA)	mf
Indonesia[75]	2011–2014 (longitudinal, pre- and post-MDA; only first survey in each village was used for crosswalk)	mf
Indonesia, Sri Lanka[39]	2014 (post-MDA)	FTS, mf
Kenya[76]	2002–2004, 2007, 2009 (post-MDA)	ICT, mf

Kenya[77]	2004 (pre-MDA)	ICT, mf
Kenya[78]	1976 or earlier (pre-MDA)	mf
Kenya[79]	1999 or earlier (pre-MDA)	mf
Kenya[80]	2001 (pre-MDA)	mf
Kenya, Tanzania[81]	1998 (pre-MDA)	mf
Kenya, Tanzania[82]	1998 (pre-MDA)	mf
Madagascar[83]	2016 (post-MDA)	FTS
Malawi[84]	2000 (pre-MDA)	ICT, mf
Mali[85]	2005 or earlier (pre-MDA)	mf
Myanmar[86]	2015 (post-MDA)	ICT
New Zealand (Cook Islands)[87]	1975 (pre-MDA), 1992 (post-MDA)	mf
Nigeria[88]	1998 (pre-MDA)	ICT
Nigeria[89]	2003 (pre-MDA), 2009 (post-MDA)	ICT, mf
Nigeria[90]	2009 (pre-MDA)	ICT
Nigeria[91]	2010 (pre-MDA)	ICT
Nigeria[92]	2015 (post-MDA)	ICT
Nigeria[93]	1989 (pre-MDA)	mf
Nigeria[94]	1990–1991 (pre-MDA)	mf
Nigeria[95]	2002 (pre-MDA)	mf
Nigeria[96]	2006 (pre-MDA)	mf
Nigeria[97]	2007 (pre-MDA)	mf
Nigeria[98]	2008–2009 (pre-MDA)	mf
Nigeria[99]	2009 (pre-MDA)	mf
Niue[29]	1999 (pre-MDA)	ICT
Papua New Guinea[100]	2001–2006 (longitudinal time series; pre-MDA data used for crosswalk)	ICT
Papua New Guinea[101]	1985 (pre-MDA)	mf
Papua New Guinea[102]	1986 (pre-MDA)	mf
Papua New Guinea[103]	1987 (pre-MDA)	mf
Papua New Guinea[104]	1994 (pre-MDA)	mf
Philippines[105]	1991 (pre-MDA)	mf

Republic of the Congo[106]	2012 (pre-MDA)	ICT, mf
Sierra Leone[107]	2011 (post-MDA)	mf
Sri Lanka[108]	1999 (pre-MDA)	ICT, mf
Sri Lanka[109]	2016–2017 (post-MDA)	mf
Tanzania[110]	1991–1992 (some sites pre-MDA, some post-MDA)	mf
Tanzania[111]	1990 (pre-MDA)	mf
Tanzania[112]	1992 (pre-MDA)	mf
Tanzania[113]	1992 (pre-MDA)	mf
Tanzania[114]	1994 or earlier (pre-MDA)	mf
Tanzania[115]	2000 or earlier (pre-MDA)	mf
Tanzania[116]	2001 (pre-MDA)	mf
Tanzania[117]	2006 (pre-MDA), 2006–2008 (post-MDA); only pre-MDA data used in crosswalk	mf
Thailand[118]	1998 (pre-MDA)	ICT, mf
Thailand[119]	2001 or earlier (pre-MDA)	mf
Uganda[120]	1998 (pre-MDA)	ICT, mf
Vanuatu[121]	1997 (pre-MDA)	ICT
Yemen[35]	2007 (pre-MDA)	mf

We obtained Global Burden of Disease (GBD)[122] population estimates by age-year for the country and year of each survey, and assumed that the age distribution ($P(A)$, or probability of age A) within a survey sample matched that in the country and year of the survey:

$$P(A)_{study} = P(A)_{country}$$

We estimated prevalence-by-age models ($P(D|A)$, or the probability of disease, D, at age A) from birth through age 94 years, the maximum individual age-year modelled by GBD. We used the GBD age distributions to estimate the likelihood of observing the reported number of cases in each surveyed age bin, given a logistic (binomial) regression model of the average prevalence-by-age relationship across surveys:

$$\text{logit}\big(P(D|A1 \leq A < A2)\big) = \beta_0 + f(A) + \alpha_i$$

LF prevalence within a given age range ($P(D|A1 \leq A < A2)$) was modelled in logit space as a linear combination of an intercept, β_0, which was set at logit(0.00001) (ie, very close to zero); $f(A)$, a basis spline (fda R package[123]) on age to accommodate non-linear relationships; and α_i, cohort-level fixed effects (dummy variables identifying the study cohort in the training dataset) for cohort *i*, to account for differences in study populations and survey designs. This model formed the basis of the age crosswalks.

The diagnostic crosswalk model used mf prevalence in a given age range and study as a predictor of ICT prevalence in the same age range and study, with an age-dependent basis spline on the (logit) mf prevalence:

$$\text{logit}(P(D|A1 \leq A < A2)_{\text{ICT}}) = f\big(\text{logit}(P(D|A1 \leq A < A2)_{\text{mf}})\big)$$

As sample sizes may differ between mf and ICT surveys in the same age range and study, ICT and mf cases were standardised to a sample size reflecting the geometric means of their individual sample sizes, retaining their original prevalence values, prior to the estimation of the diagnostic crosswalk. Due to the sensitivity of the diagnostic crosswalk model to assumptions about how to crosswalk observations of zero cases, data rows reporting zero mf, ICT, or FTS cases were excluded from the diagnostic crosswalk training dataset. The age crosswalk models did not exhibit the same sensitivity, and zero-case data were retained in the respective age crosswalk training datasets.

In both the age and diagnostic crosswalk models, spline knot placements were first identified by spacing four internal knots evenly by quantile in the training data. Additional knots were placed at ages 3 and 6 to improve model flexibility, given evidence of rapid increases in prevalence in early childhood[124,125] and the generally low resolution of age bins. An additional spline knot was placed at age 65 in an attempt to address model instability at the right tails of the crosswalk curves, which resulted from the small sample sizes, wide age bins, and low population fractions for older adults. However, as model estimates continued to be unreliable at the right tail in the ICT age crosswalk, we constrained the ICT age crosswalk to be constant above age 65. Due to a sparsity of age-resolved data in young children, initial maximum likelihood estimates for the mf model implausibly suggested high but decreasing prevalence in very young children, before prevalence again increased. We therefore constrained the mf prevalence-by-age curve to be increasing between ages 0 and 3 years. The diagnostic crosswalk was unstable at both tails, for similar reasons, and the diagnostic crosswalk model was constrained to be constant below age 5 and above age 65. Starting values for all spline and cohort-level coefficients were randomly drawn from uniform distributions, in the interval [-5, 5] for age crosswalks and [-30, 30] for the diagnostic crosswalk. Models were estimated with maximum likelihood optimisation using the conjugate gradients method[126] in the optim function (R stats package[127]).

Adjustment of input data was performed using maximum likelihood coefficient estimates, with mf data first crosswalked to ICT prevalence, and ICT/FTS or mf prevalence then crosswalked to all-age prevalence. Adjustments for the diagnostic crosswalk were calculated by applying the estimated spline coefficients to reported mf prevalences in logit space, and then back-transforming to probability space to obtain corresponding ICT estimates. An analogous approach was used to crosswalk ICT to corresponding mf estimates. Age crosswalks were applied by estimating the difference (in logit space) between reported and baseline prevalence across the survey age range to derive a scaling factor, α:

$$\alpha = \text{logit}\big(P(D|A1 \leq A < A2)_{sample}\big) - \text{logit}(P(D|A1 \leq A < A2)_{baseline})$$

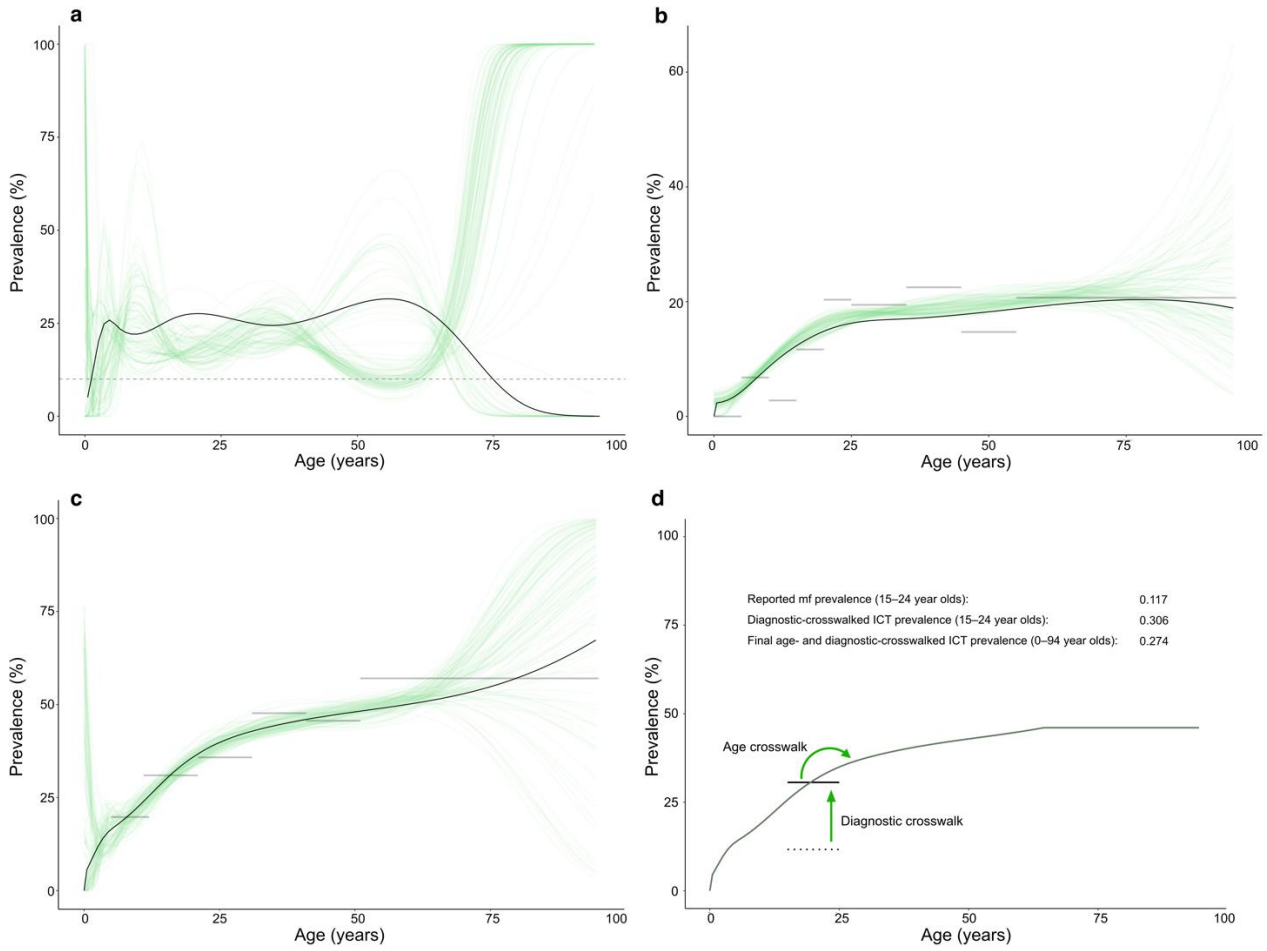
Here, baseline prevalence is taken from the estimated prevalence-by-age curve in the absence of cohort-level effects. The scaling factor is then added (in logit space) to all-age baseline prevalence to derive a final all-age prevalence estimate for each study sample:

$$\text{logit}\big(P(D|0 \leq A < 95)_{sample}\big) = \alpha + \text{logit}(P(D|0 \leq A < 95)_{baseline})$$

In order to quantify uncertainty in the crosswalk models, 100 bootstrap replicates were generated and analysed for each model. Bootstrap samples were produced by sampling, with replacement, an equal number of study cohorts as were in the full dataset. Resampling was performed at the level of cohorts rather than individual surveyed age bins to better account for inter-population variability. As cohorts differed in the number of age bins they sampled, bootstrap replicates contained varying numbers of data rows. Each of the three crosswalk models (ICT prevalence-by-age, mf prevalence-by-age, and ICT:mf ratio-by-age) were fit to separate sets of bootstrap samples, with spline knot placements and coefficients determined for each sample as previously described for the full dataset. Due to the computational demands of the conjugate gradients likelihood optimiser, we switched to the quasi-Newton method with box constraints[128] in the optim function (although no constraints were specified) for fitting bootstrapped crosswalk models, yielding more tractable computational performance. In order to visualise the bootstrapped results for a given survey, the scaling parameter (α) was calculated for each bootstrap replicates using maximum likelihood optimisation, with spline coefficients fixed to the values estimated for that bootstrap replicate.

Sample plots for the final crosswalk models, including bootstrapped estimates, are provided in Supplementary Figure 9. The diagnostic crosswalk model displays decreases in the ICT:mf ratio among young children and older

adults. The lower ratio among young children is inconsistent with the different nematode life stages targeted by these tests: ICT detects the presence of adult worms, which are a prerequisite for the production and presence of microfilariae. Given zero prevalence at birth and the lengthy maturation time for adult worms, we expect that very young children are more likely to display antigenaemia without microfilaraemia than older age groups. This pattern is also supported by the generally lower intensity of infection in young children, which reduces the sensitivity of diagnosis based on microfilaraemia.[124] Given this biological implausibility and the dearth of high-resolution age-based data in very young children, we constrained the ICT:mf ratio to be constant below age 5 years. Although the general shapes of our inferred antigenaemia-by-age models are qualitatively consistent with previously reported prevalence-by-age models,[129] the sparcity of age-resolved data in older adults also led to unreliable estimates above age 65 in the diagnostic and ICT age crosswalks, and these were similarly constrained above age 65 when applying the crosswalk. Note that prevalence at birth is shown in Supplementary Figure 9 panels **b**–**c** as forced to zero, for display purposes only; actual crosswalked prevalence at birth was a function of both the intercept (close to zero) and the cohort-specific scaling factor. The plots of bootstrapped estimates in Supplementary Figure 9 illustrate the instability (uncertainty) of the age crosswalk models for ICT and mf in older adults, of the ICT model in young children (the ICT model was not constrained to be increasing in very young children as in the mf model), and of the diagnostic crosswalk in both young children and older adults. The diagnostic-specific crosswalk models otherwise show low uncertainty. The ICT:mf diagnostic crosswalk model is more variable across bootstrap samples. One possible consequence of using a different maximum likelihood optimisation process for bootstrapping is that these models may have converged on different coefficient optima than the original full crosswalk models, which may be reflected in the mismatch between the bootstrap intervals and the full models in Supplementary Figure 9 (most notable in the ICT:mf diagnostic crosswalk). However, the bootstrapped estimates serve to illustrate the areas and patterns of relative uncertainty in the crosswalk models and support our decisions to constrain model behaviour in certain age ranges, as described.



Supplementary Figure 9. Diagnostic and age crosswalks

Example plots from diagnostic and age crosswalk models. (**a**) ICT prevalence-by-age curve (solid black line) at a hypothetical constant mf prevalence of 10% (horizontal dotted line), illustrating the age-specific ICT:mf ratio. Green lines indicate each of 100 independent bootstrap. Prior to application of this crosswalk, ratios below age 5 years were assumed to be identical to that at age 5, and values above 65 years were assumed to be identical to that at age 65. (**b**) The predicted mf prevalence-by-age relationship (solid black line), including cohort-level effect, for a survey population from India[63] that was included in the crosswalk training dataset. Horizontal bars represent reported values in a given age range. Green lines represent bootstrap replicates. (**c**) The predicted ICT prevalence-by-age relationship (solid black line), including cohort-level effect, for a survey population from Kenya that was included in the crosswalk training dataset.[76] Horizontal bars and green lines are as in the preceding panels. (**d**) An illustration of the diagnostic- and age-crosswalk applied to a cohort of 15–24 year olds surveyed in Tanzania[111] in 1990. This group had a reported mf prevalence of 0.117 (dotted line), which was crosswalked to an ICT prevalence of 0.306 among 15–24 year olds (solid bar), and then to an all-age ICT prevalence of 0.274 (the corresponding prevalence-by-age curves is shown as a solid curve). The latter value would be the prevalence measure used in the final MBG models.

Our models represent the first application, to our knowledge, of both age and diagnostic crosswalks to geospatial estimates of lymphatic filariasis prevalence. By harmonising survey data with differing age and diagnostic coverage, we are able to integrate a more comprehensive dataset for geospatial modelling than was previously tractable. However, we recognise several important limitations to our crosswalk approach. First, we assume that the shapes of the prevalence-by-age and ICT:mf relationships are constant at all sites and years, a necessary simplifying assumption given the sparsity of available training data. However, both actual and reported age-structured

antigenaemia and microfilaraemia prevalence patterns are likely to be strongly affected by local ecological and sociodemographic factors, the history and effectiveness of LF interventions, and variations in diagnostic accuracy and logistical survey constraints. Perhaps most notably, we have not incorporated the impact of MDA or other interventions on prevalence in the crosswalk models, despite the effects of MDA on antigenaemia and microfilaraemia. The more immediate and pronounced microfilaricidal activity of anti-filarial drugs, relative to their impacts on adult worm mortality, suggests that ICT and mf prevalence profiles are likely to differ among populations in pre-, post-, and early-MDA scenarios.[130–132] In addition, reduction or cessation of parasite transmission as a result of MDA should be reflected in progressively reduced antigenaemia prevalence in young children, while prevalence declines more slowly in individuals infected prior to initiation of MDA, within whom adult worm clearance relies on natural senescence and weak or moderate macrofilaricidal drug effects. We intend to pursue development of an expanded crosswalk methodology that explicitly includes the effects of MDA for future model updates.

We were also limited by the varying availability and precision of age information among data sources. When surveys reported only broad age categories for their survey populations, we made assumptions prior to conducting the age crosswalk: "children" were assumed to represent ages 0–14 years; "adults" or mapping surveys without specified age ranges were assumed to represent ages 15–94 years; any surveys reporting prevalence among both children and adults were assumed to represent 0–94 years; TAS surveys without specified age ranges were assumed to represent ages 6–7 years; sentinel site and spot check surveys were assumed to represent ages 2–94 (pre-2011) or 5–94 (2011–2017) years; and any remaining surveys without reported age range, age category or programmatic stage were assumed to represent ages 0–94 years (ie, no age crosswalk was performed). It is possible that some data inputs may have been misclassified as all-age data and are therefore biased in an unknown direction and extent. Similarly, the absence of individual-level data on LF prevalence precluded full age standardisation, as we could rely only on an assumed age distribution within the survey population. The absence of finely resolved age bins among older adults also prevented reliable model fitting above age 65 years, and we therefore assumed constant ICT:mf ratios and age-specific relative prevalence above that age. While these assumed relationships could introduce bias in our crosswalk models, older adults represent small population proportions in most LF-endemic settings, and the degree of bias in our all-age prevalence estimates is therefore likely to be small.

Our crosswalk models are inferred and applied outside of the broader MBG prevalence modelling framework, and we do not currently have a computationally feasible method to propagate uncertainty from the crosswalk models into the MBG models, or to fit the crosswalk models as part of the MBG process. We intend to explore future model developments that include incorporation of the crosswalk directly into the INLA MBG models. Finally, our crosswalks do not currently account for the sensitivity and specificity of mf, ICT and FTS diagnostic tests, and crosswalk uncertainty is therefore likely to be underestimated.

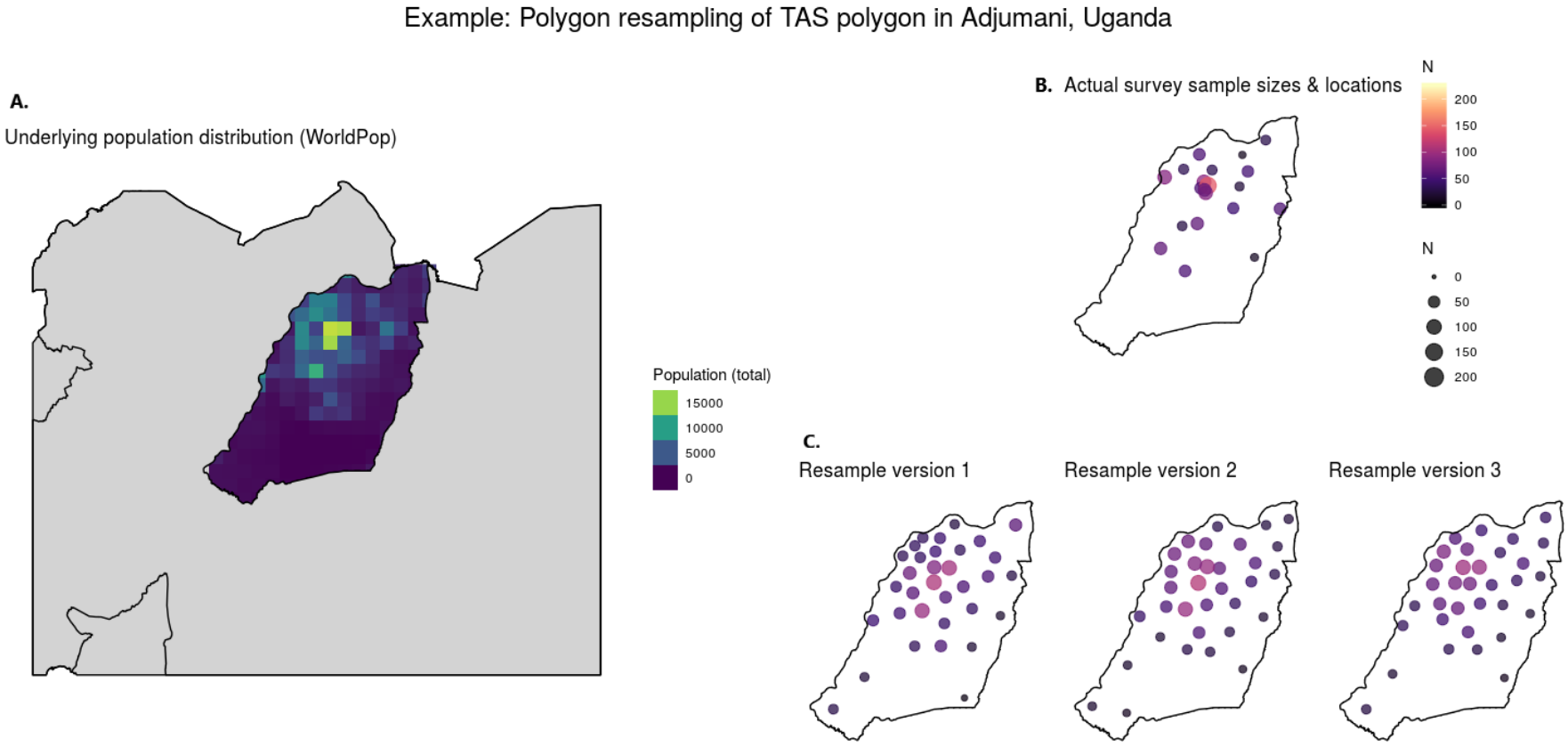
Previous studies have modelled the relationship between LF antigenaemia and microfilaraemia either directly as a function of prevalence itself, or via models that explicitly incorporate parameters describing aspects of the filarial life cycle. To highlight some examples, Irvine and colleagues explored the ICT:mf relationship in pre- and post-MDA settings using a model of worm burden, microfilariae production and diagnostic sensitivity, with empirical data from Kenya and Sri Lanka.[133] Jambulingam and colleagues employed the LYMFASIM microsimulation model[134] to examine associations of antigenaemia and microfilaraemia under a range of values for vector exposure, baseline prevalence, MDA efficacy, duration and coverage, and diagnostic sensitivity, using data from India. Berg Soto and colleagues[135] used regression models to relate microfilaraemia and antigenaemia prevalence in Papua New Guinea, accounting for MDA. We sought to address possible age-specific differences in the ICT:mf relationship, which we considered a potential biasing factor in our geospatial model given the high variability of age ranges sampled across our dataset. Our simple diagnostic crosswalk model (Supplementary Figure 9a) predicts an average ICT prevalence around 25% across most ages when mf prevalence is 10%, consistent with the range of antigenaemia to microfilaraemia ratios estimated by each of the cited studies (e.g., see figures 2 and 3 in Irvine and colleagues, figure 1 in Jambulingam and colleagues, figures 2 and 3 in Berg Soto and colleagues), which employed different methodologies and estimated from different datasets. We therefore consider our model to provide a reasonable generalised estimate of this relationship.

5.2 Polygon resampling

Prevalence records within our analysis dataset can be representative of a point location or an area defined by a polygon. Our geostatistical approach requires use of point data only, requiring polygon data to first be converted to a

representative collection of point data. This process, referred to as “polygon resampling,” generates candidate point locations based on the underlying population distribution of the polygon area, assuming use of population-based survey designs (although some baseline LF mapping surveys employed purposive sampling to explicitly bias survey site selection toward locations deemed likely to be endemic).

This polygon resampling methodology is consistent with the method used in geospatial modelling of under-5 mortality[136] (illustrated in Supplementary Figure 10). For each polygon-level observation, 10,000 points were randomly sampled from within the polygon (regardless of the polygon’s area) using the WorldPop total population raster to weight the locations of the draws. K-means clustering was performed on the candidate points to generate integration points used in the modelling. Integration points were generated at a density of 1 per 1,000 grid cells, except when this yielded fewer than ten integration points (ie, when polygons are small), whereby density was iteratively increased by a factor of ten until this minimum threshold was met. Weights were assigned to each integration point proportionally to the number of candidate points that entered into the k-means cluster, such that the weight of each point represented the number of population-sampled locations contained within the K-means cluster location, divided by the number of sampled points generated (10,000). Each point generated by this process is assigned the prevalence of LF observed from the survey for that polygon. These sample weights were used in model fitting.



Supplementary Figure 10. Polygon resampling

The process of polygon resampling uses (a) an underlying population distribution surface to probabilistically generate pseudo-clusters from a representative polygon record. Here, an example is presented to allow comparison of (b) actual cluster-level surveys from Adjumani, Uganda in 2015[137] to (c) pseudo-clusters generated through polygon resampling. Three versions are presented to illustrate the probabilistic nature of the process. Actual cluster-level surveys were aggregated to create a representative polygon for this example.

5.3 Geostatistical model

5.3.1 Model geographies

Model-based geostatistical (MBG) methods were used to generate estimates of all-age LF prevalence for four distinct modelling regions: (1) Africa plus Yemen; (2) South Asia; (3) Southeast Asia; and (4) the island of Hispaniola. These regions were modelled separately due to (1) computational constraints with running larger models, (2) differences in covariate availability, and (3) likely regional differences in prevalence–covariate relationships. South and Southeast Asia were modelled separately due also to unreliability of the spatiotemporal model in South Asia, for which a time-stationary geospatial model was ultimately used.

The Africa model region consisted of Angola, Benin, Burkina Faso, Burundi, Cameroon, Central African Republic, Chad, Comoros, Côte d'Ivoire, the Democratic Republic of the Congo, Djibouti, Egypt, Equatorial Guinea, Eritrea, Ethiopia, Gabon, The Gambia, Ghana, Guinea, Guinea-Bissau, Kenya, Liberia, Madagascar, Malawi, Mali, Mauritania, Mozambique, Niger, Nigeria, Republic of the Congo, Rwanda, Senegal, Sierra Leone, São Tomé and Príncipe, Somalia, South Sudan, Sudan, Tanzania, Togo, Uganda, Yemen, Zambia, and Zimbabwe. The South Asia model region consisted of India, Bangladesh, Nepal, and Sri Lanka, while the Southeast Asia model region was composed of Myanmar, Thailand, Vietnam, Laos, Cambodia, Malaysia, Indonesia, Papua New Guinea, Philippines, Timor-Leste and Brunei. The island of Hispaniola was treated as a distinct model region in order to model Haiti and the Dominican Republic.

The modelling region is defined as the geographies included in the spatial extent of the geospatial model. For countries such as Rwanda or Burundi that are known to be non-endemic, but for which they are bordered by LF-endemic areas, we included them in the modelling region.

Due to their small geographical area and inconsistent availability of geospatial covariates, estimates of infection prevalence for the following LF endemic settings were generated using simple time series analyses of reported data: Palau, Marshall Islands, Vanuatu, Kiribati, American Samoa, Samoa, Cook Islands, Niue, Wallis and Futuna, Tonga, Maldives, New Caledonia, Tuvalu, Fiji, and French Polynesia. Similar time series analyses were also performed for Guyana and Brazil, given the focal nature of LF endemicity in those countries.

5.3.2 Stacked generalisation

We incorporated the predictive ability of the selected environmental, sociodemographic, and public health covariates using stacked generalisation, a method of model ensembling. Our strategy follows the approach previously described by Bhatt and colleagues[138] and subsequent studies of under-5 mortality.[136] Briefly, we estimated child models of LF prevalence using multiple distinct modelling frameworks. Cross-validated predictions from these child models were then used as predictors in the full Bayesian geostatistical models described below. The geostatistical models for each region employed three child models: a generalised additive model (GAM), a gradient boosting machine (GBM, specifically boosted regression trees, or BRT), and a penalised regression model using lasso. GBMs were fit using a Poisson likelihood model, the GAMs used binomial likelihoods, and lasso models were fit using a Gaussian likelihood and empirical logit-transformed outcomes. GAM models accommodate possible non-linear effects, while GBM enables non-linearity and complex covariate interactions; lasso regression converges on a reduced covariate subset to minimise overfitting. Models were fit using the mgcv,[139] dismo,[140] and glmnet[141] R packages.

5.3.3 Model description

We modelled LF infection prevalence using a spatially and temporally explicit Bayesian generalised linear mixed effects regression model:

$$Y_{i,t} \sim \text{Binomial}\left(p_{i,t}, N_{i,t}\right)$$

$$\text{logit}\left(p_{i,t}\right) = \beta_0 + \beta X_{i,t} + \gamma_{c[i]} + Z_{i,t} + \epsilon_{i,t}$$

$$\sum \beta = 1$$

$$\gamma_{c[i]} \sim N\left(0, \sigma^2_{country}\right)$$

$$Z_{i,t} \sim \text{GP}(0, \Sigma_{space} \otimes \Sigma_{time})$$

$$\epsilon_{i,t} \sim N\left(0, \sigma^2_{nug}\right)$$

We modelled the number of LF-infected individuals ($Y_{i,t}$) among a sample ($N_{i,t}$) in location *i* and year *t* as a binomial variable. This model specified logit-transformed LF prevalence ($p_{i,t}$) as a linear combination of an intercept for the modelling region (β_0); child model (stacker) random effects ($\beta X_{i,t}$) with a sum-to-one constraint across coefficients; country random effects ($\gamma_{c[i]}$); spatially and temporally correlated spatial random fields ($Z_{i,t}$); and an uncorrelated error term or nugget effect ($\epsilon_{i,t}$; a random effect at the level of unique observations). In this model, the spatiotemporal random field ($Z_{i,t}$) was modelled as a Gaussian process with mean 0 and a covariance matrix given by the Kronecker product of a spatial Matérn covariance function (Σ_{space}) and a temporal first-order autoregressive (AR1) covariance function (Σ_{time}) on model calendar year.

To evaluate the performance of the spatiotemporal model relative to an analogous time-stationary model, we also conducted in- and out-of-sample analyses of time-stationary models for each model region. In these models, the AR1 temporal correlation structure on the spatial random field was excluded, but the model was otherwise structured identically to the spatiotemporal models. In this alternative modelling framework, the spatial fields reflect the average spatial effects in a location over time, with temporal variability being driven by variation in the covariates. The time-stationary model was constructed as follows:

$$Y_{i,t} \sim \text{Binomial}\left(p_{i,t}, N_{i,t}\right)$$

$$\text{logit}\left(p_{i,t}\right) = \beta_0 + \beta X_{i,t} + \gamma_{c[i]} + Z_i + \epsilon_{i,t}$$

$$\sum \beta = 1$$

$$\gamma_{c[i]} \sim N\left(0, \sigma^2_{country}\right)$$

$$Z_i \sim \text{GP}(0, \Sigma_{space})$$

$$\epsilon_{i,t} \sim N\left(0, \sigma^2_{nug}\right)$$

For each model region, a final model was selected between competing spatiotemporal and time-stationary models through comparison of WAIC, out-of-sample validation metrics, and consideration of possible sources of bias and implausibility of model results. Spatiotemporal models were selected as final models for Africa, Southeast Asia, and Hispaniola, but the time-invariant model was selected for South Asia; model results in the sections that follow reflect these final model selections. Validation results and further discussion of model comparisons are provided in Supplementary Section 5.4.

5.3.4 Priors

We specified minimally informative priors for INLA hyperparameters, as detailed in Supplementary Table 7. Priors for the spatial hyperparameters τ and κ were derived automatically by R-INLA based on the finite elements mesh, and therefore varied by region.

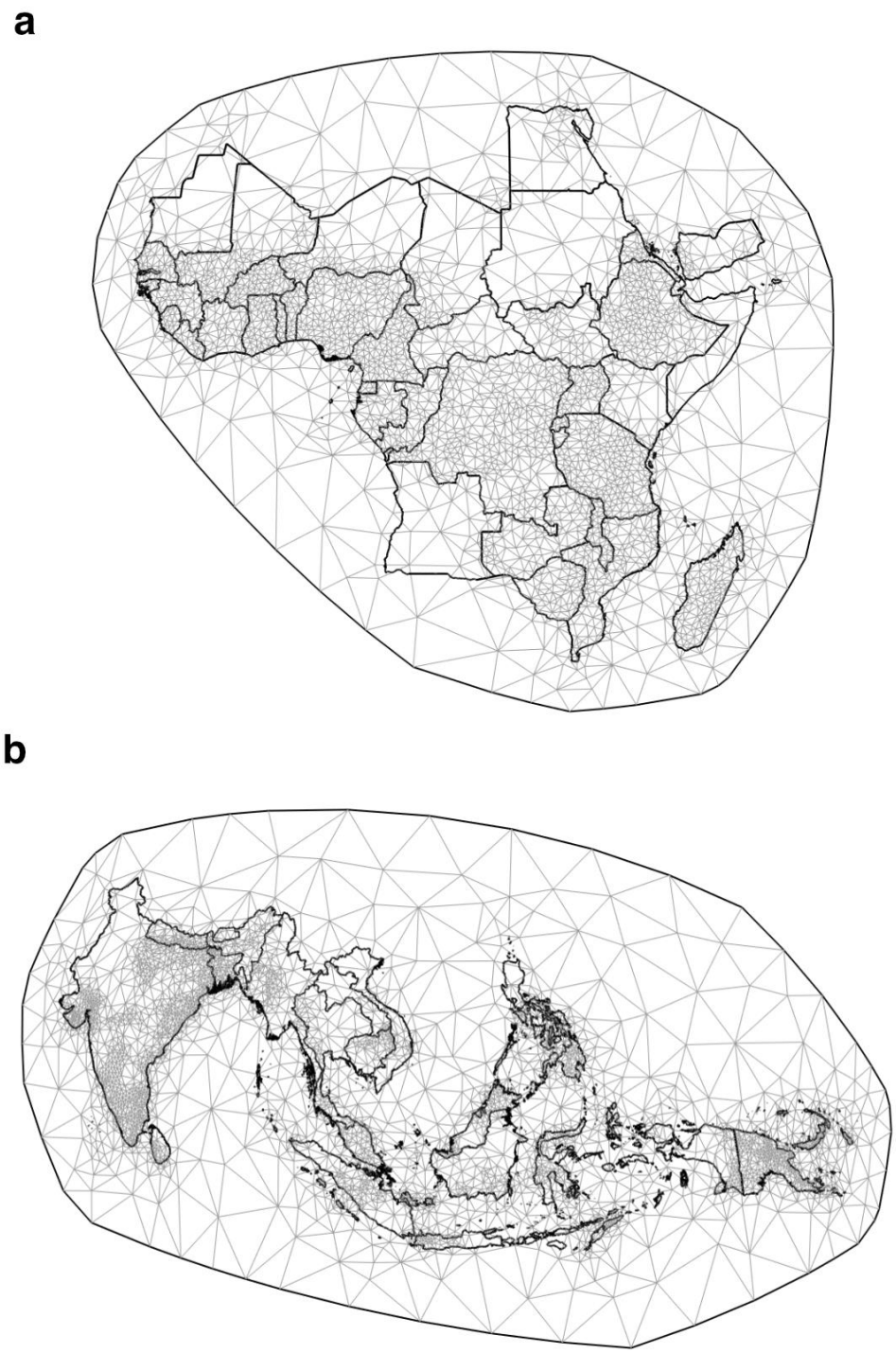
Supplementary Table 7. INLA model priors.

Parameter	Description	Prior
β_0	Intercept	$\mathrm{N}(\mu = 0, \sigma^2 = 3^2)$
$\left(\frac{1}{\sigma^2_{country}}\right)$	Precision for country random effects (i.i.d.)	$\mathrm{gamma}(a = 1, b = 0.00005)$
$\left(\frac{1}{\sigma^2_{nug}}\right)$	Precision for nugget effect (i.i.d)	$\mathrm{gamma}(a = 1, b = 0.00005)$
PACF1	Partial autocorrelation function, lag 1, for AR(1) models	$\mathrm{pc.cor0}(0.5, 0.5)$[1]
$\theta_1 = \log(\tau)$	Variance-control parameter for SPDE model	
	Africa	$\mathrm{N}(\mu = -3.70, \sigma^2 = 10)$
	S Asia	$\mathrm{N}(\mu = -4.34, \sigma^2 = 10)$
	SE Asia	$\mathrm{N}(\mu = -3.90, \sigma^2 = 10)$
	Hispaniola	$\mathrm{N}(\mu = -5.20, \sigma^2 = 10)$
$\theta_2 = \log(\kappa)$	Scale parameter (related to range) for SPDE model	
	Africa	$\mathrm{N}(\mu = 2.43, \sigma^2 = 10)$
	S Asia	$\mathrm{N}(\mu = 3.08, \sigma^2 = 10)$
	SE Asia	$\mathrm{N}(\mu = 2.64, \sigma^2 = 10)$
	Hispaniola	$\mathrm{N}(\mu = 3.93, \sigma^2 = 10)$

[1] PC prior for correlation, ρ, with $\rho = 0$ base-model (see INLA documentation for implementation details).

5.3.5 Mesh construction

We modelled continuous spatial random effects using stochastic partial differential equations (SPDE) representations of Gaussian-Markov random field (GMRF) approximations of a spatially autocorrelated Gaussian process, using triangular finite element meshes as implemented in the R-INLA R package.[142–144] Due to the large geographical size of the African and Asian model regions, spherical (S2) meshes were constructed in order to minimise distance distortions across spatial domains. Minimum and maximum edge lengths for all regions except Africa were set to 25 and 1,000 km, respectively, yielding sparser mesh vertices in data-poor areas. Due to computational limitations, 50-km minimum and 1,000-km maximum edge lengths were used for Africa. A 500-km external buffer was used to avoid edge effects. Spatial meshes for Africa and Asia are illustrated in Supplementary Figure 11.



Supplementary Figure 11. Spatial mesh construction.

Two-dimensional projections of spherical refined Delaunay triangulation meshes used in estimating spatial random fields in (a) Africa and (b) Asia, with national boundaries (bold lines). Meshes feature greater vertex density in data-rich locations. Note: Separate meshes were produced for South and Southeast Asia model regions, respectively; the mesh provided in this figure for Asia represents the analogous mesh produced when these model regions are considered together, for ease of display.

5.3.6 Model fitting and estimation generation

Models were fit using the integrated nested Laplace approximation (INLA) algorithm in R-INLA. Fitted models for each region were used to generate 1,000 random samples from the joint posterior distributions of model parameters, yielding mean and uncertainty estimates for LF prevalence.

5.3.7 Model results

Model parameter estimates from regional MBG models are summarised in Supplementary Table 8. Nominal range is the distance (in km) at which spatial correlation has declined to about 0.1 and is approximated by $\sqrt{8}/\kappa$, while nominal spatial variance, in logit space, is approximated by $1/4\pi\kappa^2\tau^2$.

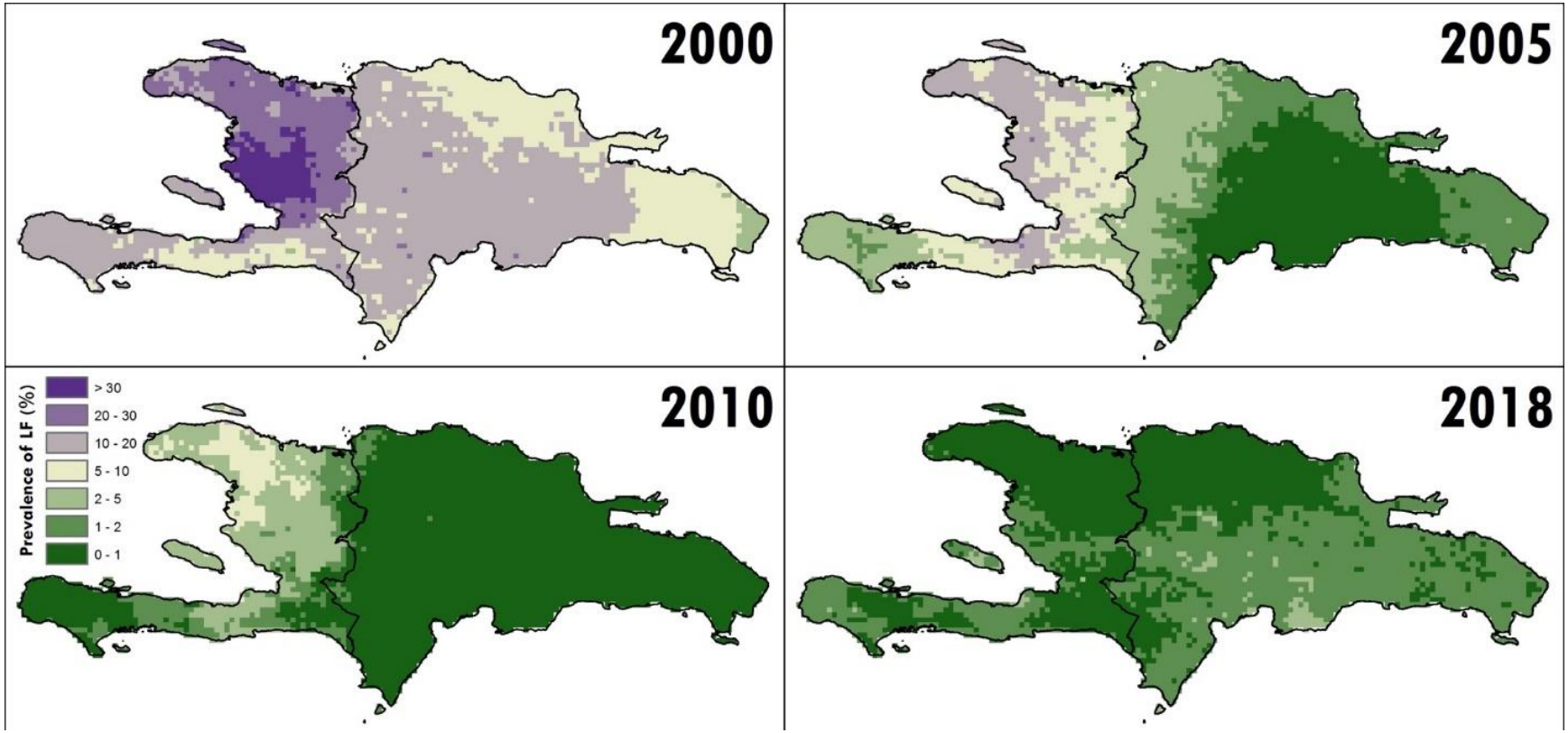
Estimated mean LF prevalence is plotted for Hispaniola in Supplementary Figure 12, and mean LF prevalence and absolute uncertainty (range of upper and lower 95% UI) are plotted jointly at 5 × 5-km resolution by region in Supplementary Figures 13–15, for 2000, 2005, 2010, and 2018. Supplementary Figures 16–20 display estimated posterior probabilities that LF prevalence is below 1% or 2% in 2018 for each model region. Supplementary Figures 21–23 show estimates of LF microfilaraemia prevalence for 2010, 2005, 2010, and 2018 by model region.

To estimate the number of infected individuals from the 5 × 5-km model predictions, the total number of cases per country was calculated by multiplying grid-cell-level prevalence by the grid-cell-level population estimate produced by WorldPop[145], then aggregating those case estimates to national boundaries by draw. Aggregate population estimates were raked to population estimates generated by the Global Burden of Disease (GBD) study[146]. We first masked all final model outputs for which land cover was classified as "barren or sparsely vegetated" on the basis of 2013 Moderate Resolution Imaging Spectroradiometer satellite data[147] (the most recent year available), as well as areas in which total population density was less than ten individuals per 1 × 1-km grid cell in 2015. The mean total cases infected was calculated across the 1000 posterior samples of case totals and the UI was constructed from the 2·5th and 97·5th percentile. Totals by WHO regions were produced by aggregating up to regional boundaries, also by posterior sample. Mean case estimates from the non-MBG locations were produced by applying the model-predicted national prevalence (mean, 2·5th percentile, and 97·5th percentile values) to GBD population estimates or the United Nations' national population estimates if GBD estimates were unavailable[148]. Sensitivity analyses were performed to examine the effect of excluding high-population grid cells from the total numbers infected, due to limited data on prevalence in urban areas and the potential biasing effects of rural prevalence estimates. These sensitivity analyses are presented in Appendix Section 5.5.

Supplementary Table 8. Parameter estimates from in-sample MBG models, by region

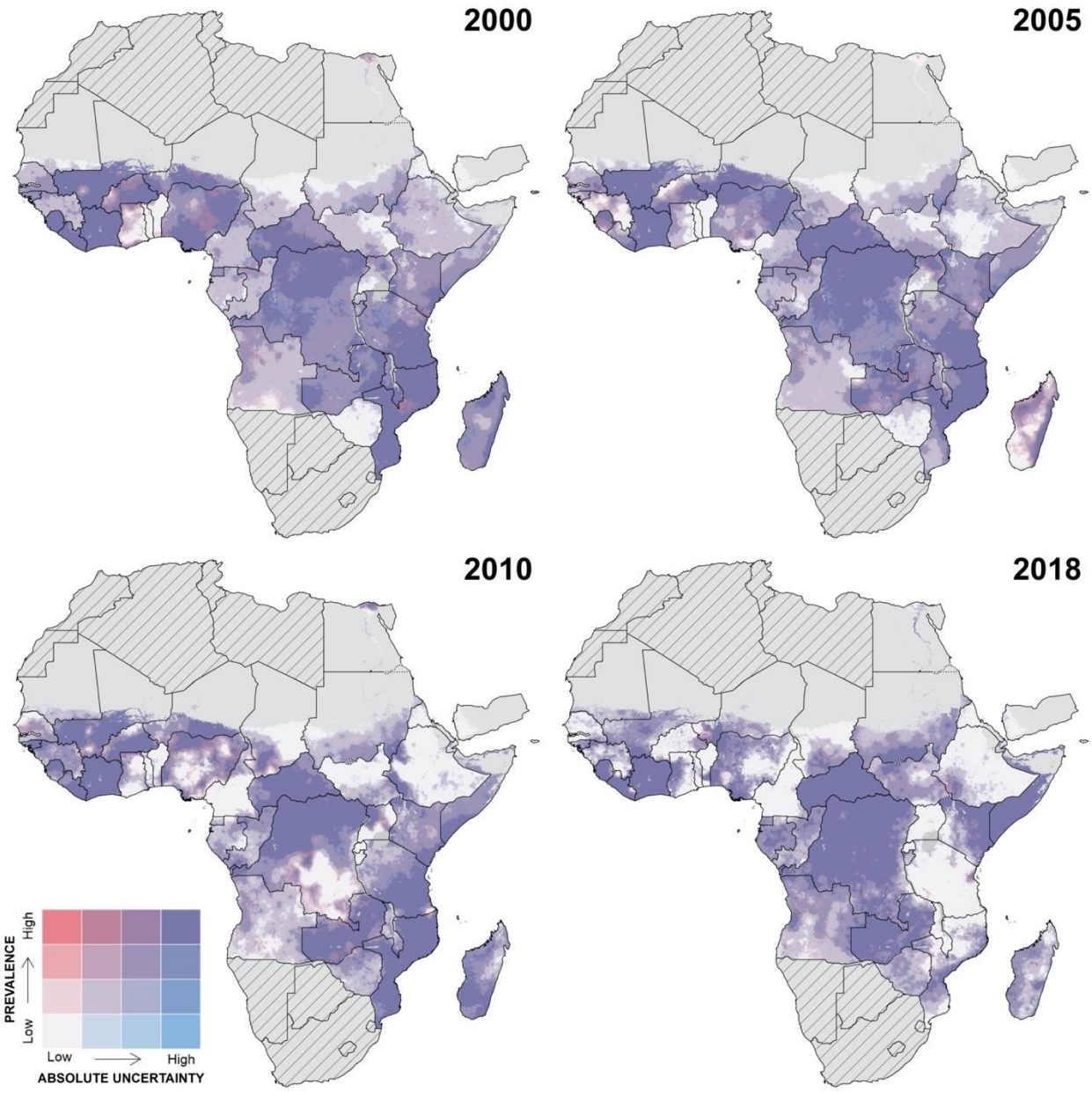
Estimates are given as *median (95% UI)*. GAM: Generalised additive model. GBM: Gradient boosted machine. GP: Gaussian process. PACF: Coefficient of partial autocorrelation function.

Parameter	Africa	S Asia	SE Asia	Hispaniola
Intercept	-1.59 (-1.91, -1.27)	-1.00 (-1.31, -0.69)	-1.48 (-1.91, -1.04)	-1.08 (-1.96, -0.21)
Child model: GAM	-0.01 (-0.07, 0.05)	-0.01 (-0.11, 0.08)	-0.01 (-0.09, 0.08)	0.05 (-0.04, 0.14)
Child model: GBM	0.55 (0.47, 0.63)	0.96 (0.88, 1.04)	0.28 (0.20, 0.36)	0.47 (0.26, 0.67)
Child model: Lasso	0.46 (0.37, 0.56)	0.04 (-0.05, 0.15)	0.73 (0.62, 0.83)	0.48 (0.27, 0.69)
GP nominal range	279 (255, 312)	161 (129, 209)	477 (410, 571)	231 (147, 396)
GP nominal variance	3.57 (3.29, 3.92)	1.27 (0.98, 1.69)	5.68 (4.65, 7.29)	3.41 (2.09, 5.73)
PACF1 (AR1)	0.59 (0.52, 0.65)	n/a	0.69 (0.59, 0.77)	0.74 (0.53, 0.86)
Nugget precision	1.09 (1.03, 1.14)	0.76 (0.69, 0.81)	2.72 (2.42, 3.15)	2.65 (2.07, 3.39)
Country precision	1.76 (0.87, 3.74)	74.8 (11.0, 550.6)	13 517 (1 268, 68 128)	13 242 (1 266, 67 358)



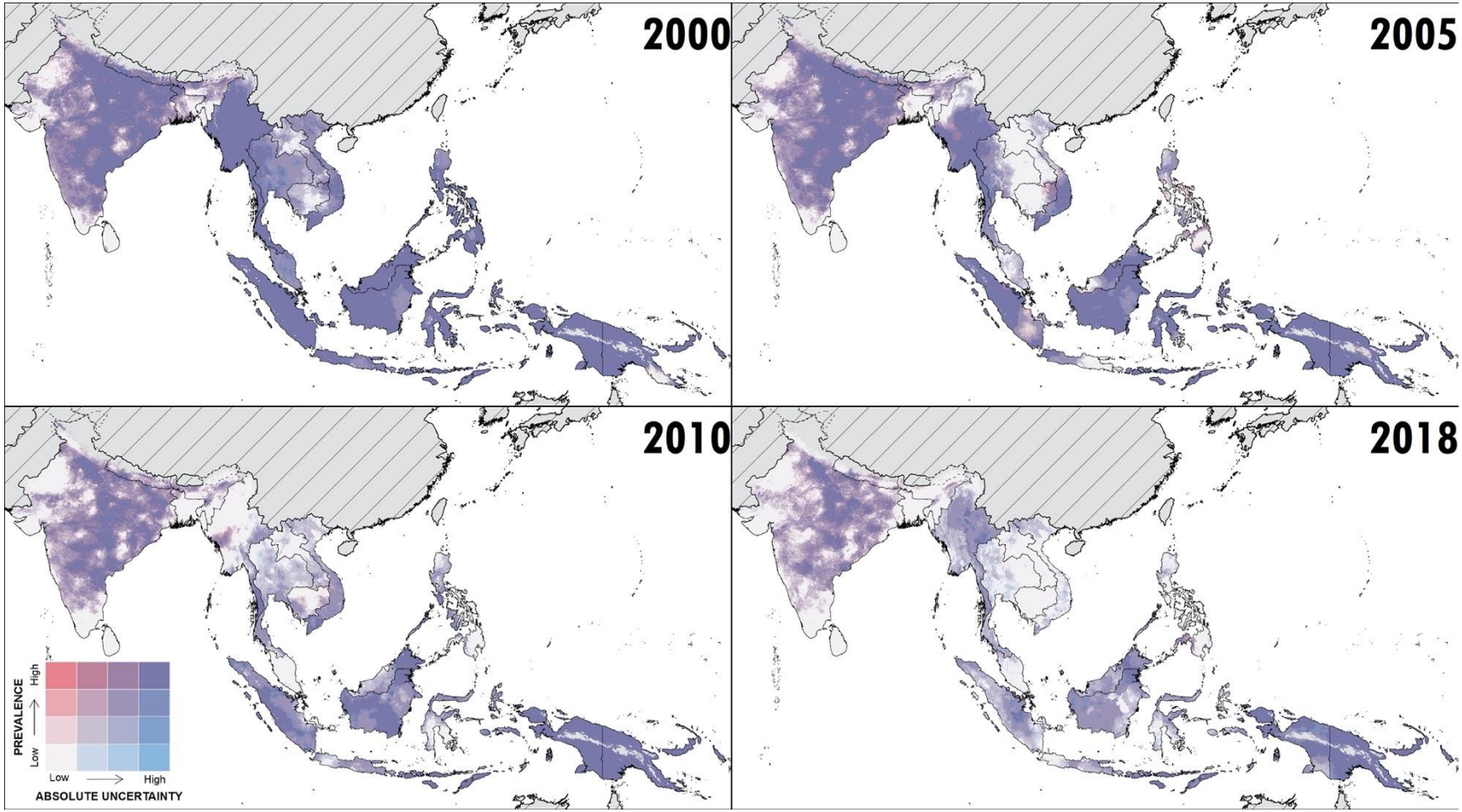
Supplementary Figure 12. Prevalence of lymphatic filariasis antigenaemia in Hispaniola at the 5 × 5-km level: 2000, 2005, 2010, and 2018

Mean predictions of LF antigenaemia (infection) prevalence from the Bayesian geostatistical model for 2000, 2005, 2010, and 2018 in Hispaniola (Haiti and the Dominican Republic), as measured by the immunochromatographic test (ICT). Areas for which prevalence exceeded 1% in 2000 would have resulted in the implementation unit (typically a district) qualifying for MDA. Hatch-marks indicate countries for which estimates are not produced; grey areas are masked based on sparsely-populated areas (fewer than ten people per 1 × 1-km grid cell) and barren landscape classification. Interactive visualisation tool at https://vizhub.healthdata.org/lbd/lf.



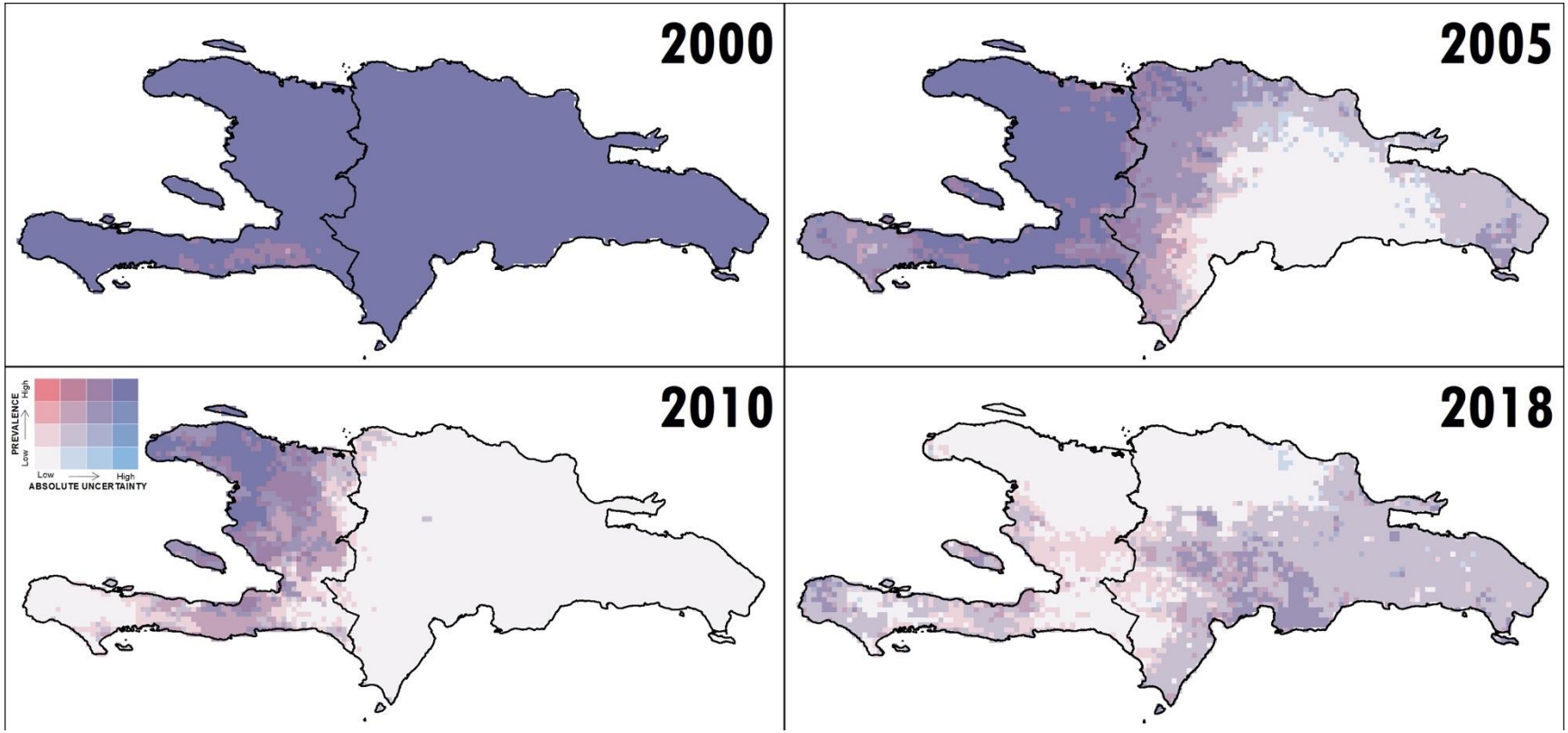
Supplementary Figure 13. Africa and Yemen ICT model uncertainty

Simultaneous plots of mean and absolute uncertainty (measured as the range, or difference between, the upper and lower 95% UI) in LF ICT prevalence estimates in Africa, for 2000, 2005, 2010 and 2018. Quantile breakpoints for plotted categories are 0.009 (25th percentile), 0.016 (50th percentile), and 0.036 (75th percentile) for mean prevalence, and 0.056, 0.108 and 0.248 for range. Interactive visualization tool at (https://vizhub.healthdata.org/lbd/lf).



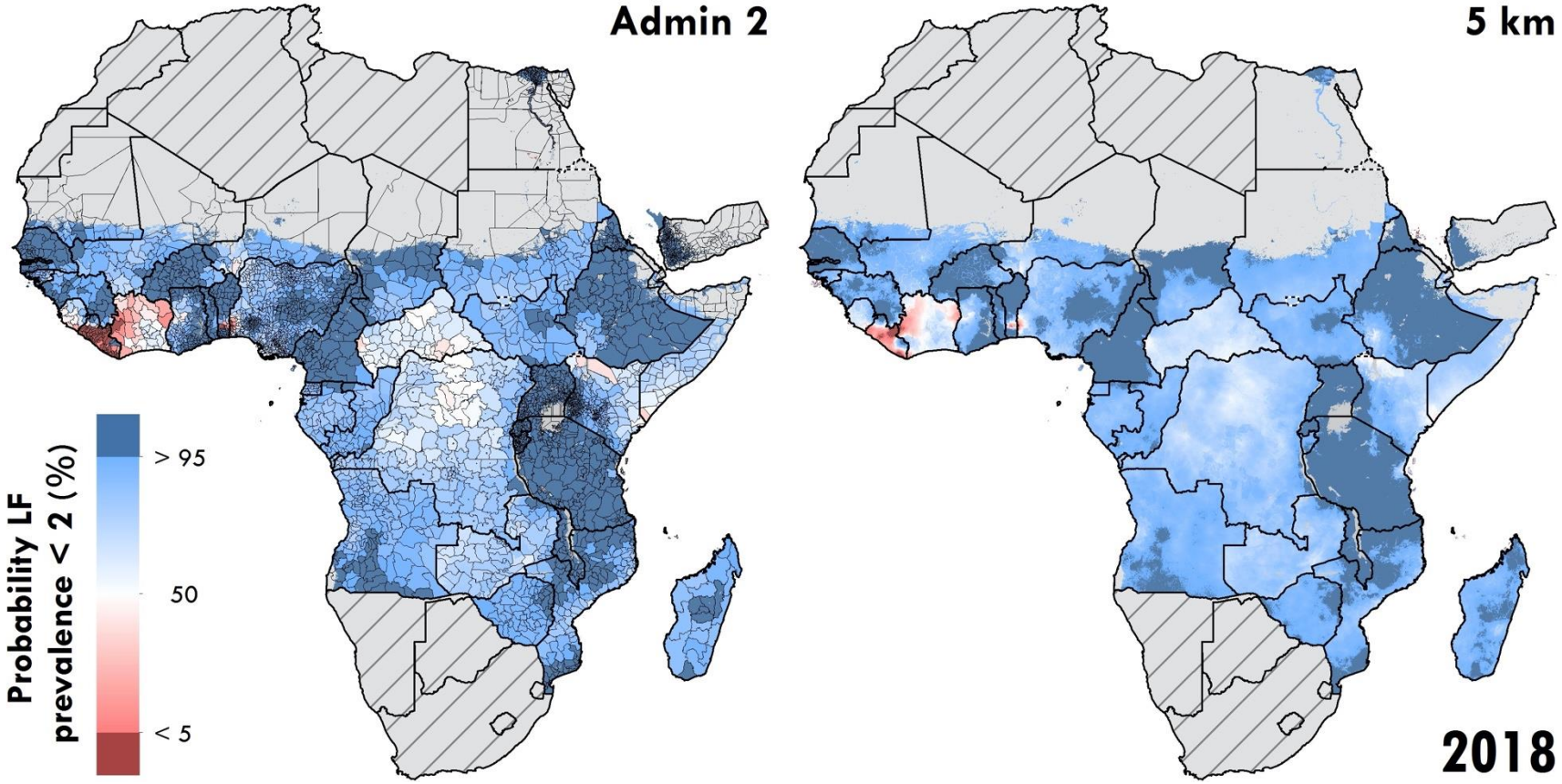
Supplementary Figure 14. South Asia and Southeast Asia ICT model uncertainty

Simultaneous plots of mean and absolute uncertainty (measured as the range, or difference between, the upper and lower 95% UI) in LF ICT prevalence estimates in Asia, for 2000, 2005, 2010 and 2018. Quantile breakpoints are as in Supplementary Figure 13. Interactive visualization tool (https://vizhub.healthdata.org/lbd/lf).



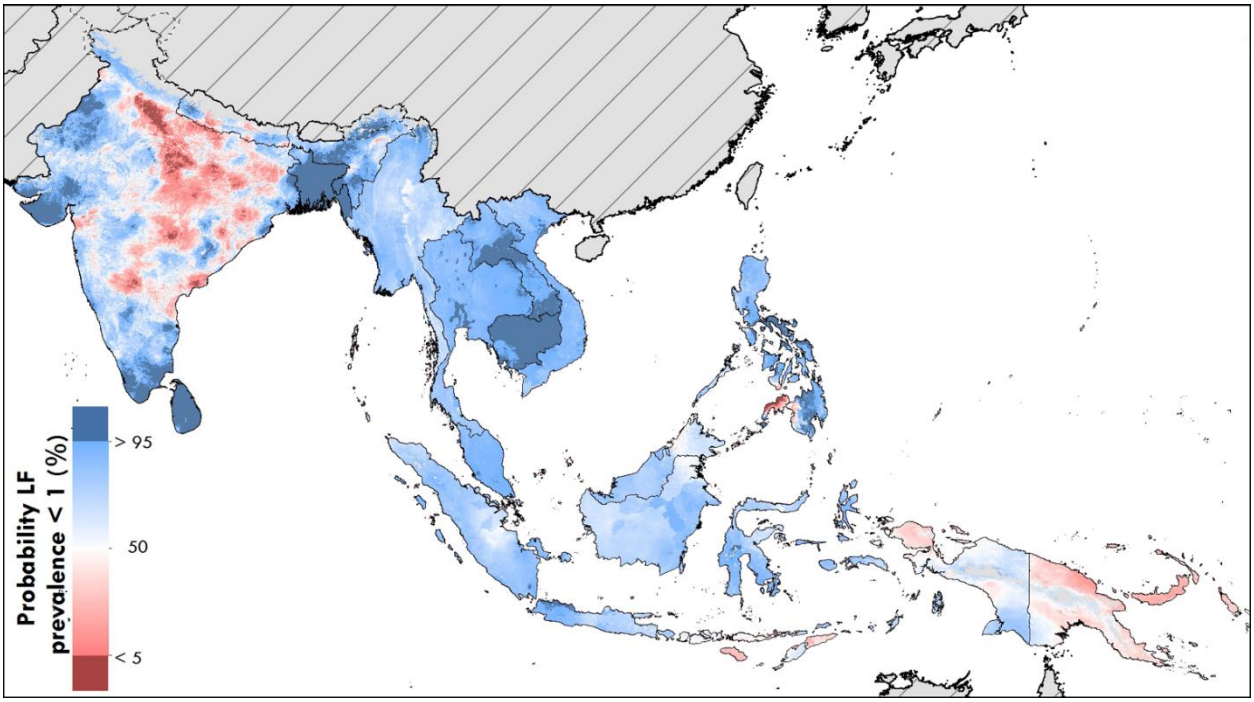
Supplementary Figure 15. Hispaniola ICT model uncertainty

Simultaneous plots of mean and absolute uncertainty (measured as the range, or difference between, the upper and lower 95% UI) in LF ICT prevalence estimates in Hispaniola, for 2000, 2005, 2010, and 2018. Quantile breakpoints are as in Supplementary Figure 13.



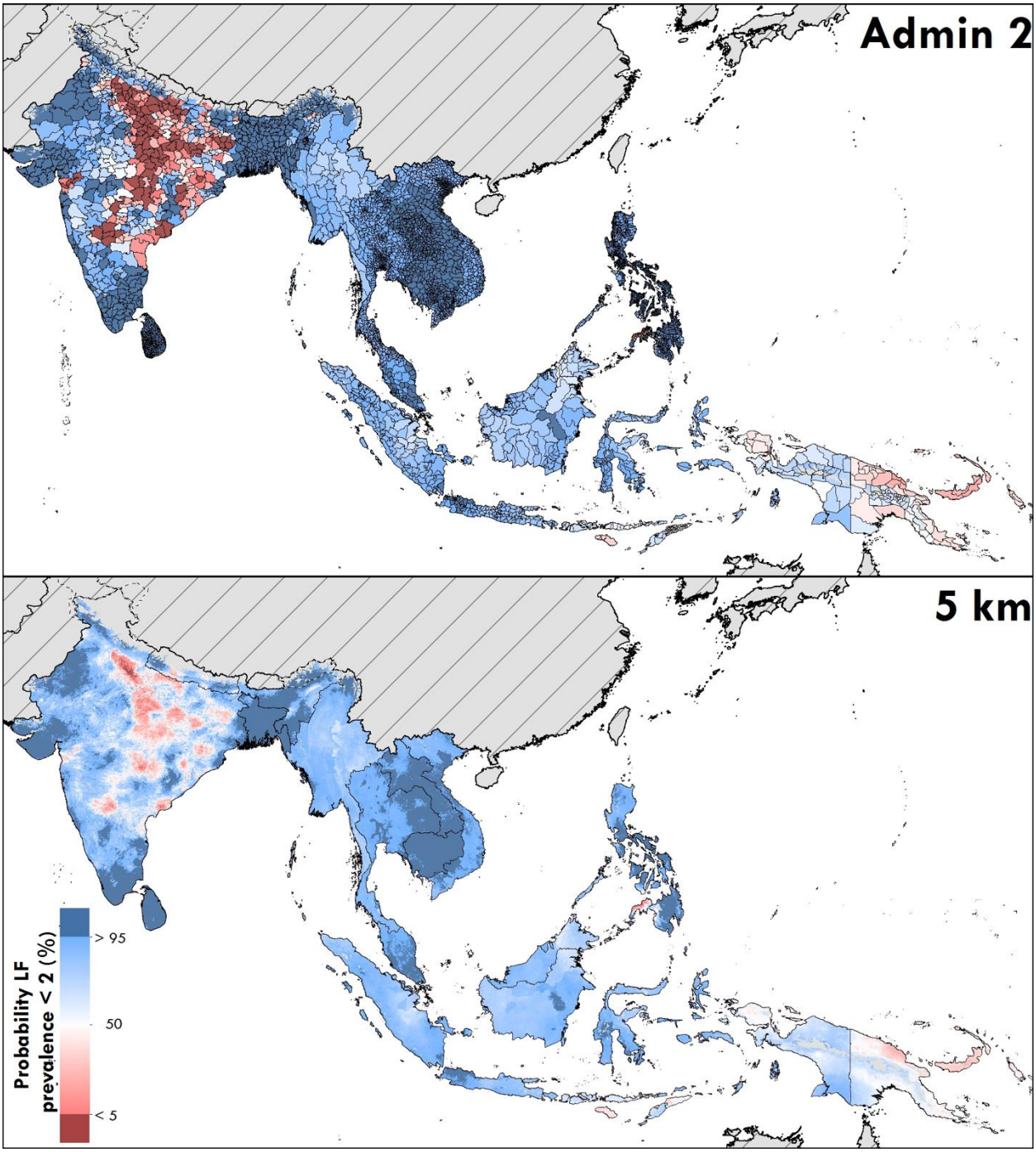
Supplementary Figure 12. Africa and Yemen 2% probability plots

Posterior probability that LF ICT prevalence is below 2% in 2018, at the second administrative level and at the 5 × 5-km resolution, in Africa. Hatch-marks indicates countries for which estimates are not produced; grey areas are masked based on sparsely populated areas (fewer than ten people per 1 × 1-km) and barren landscape classification.



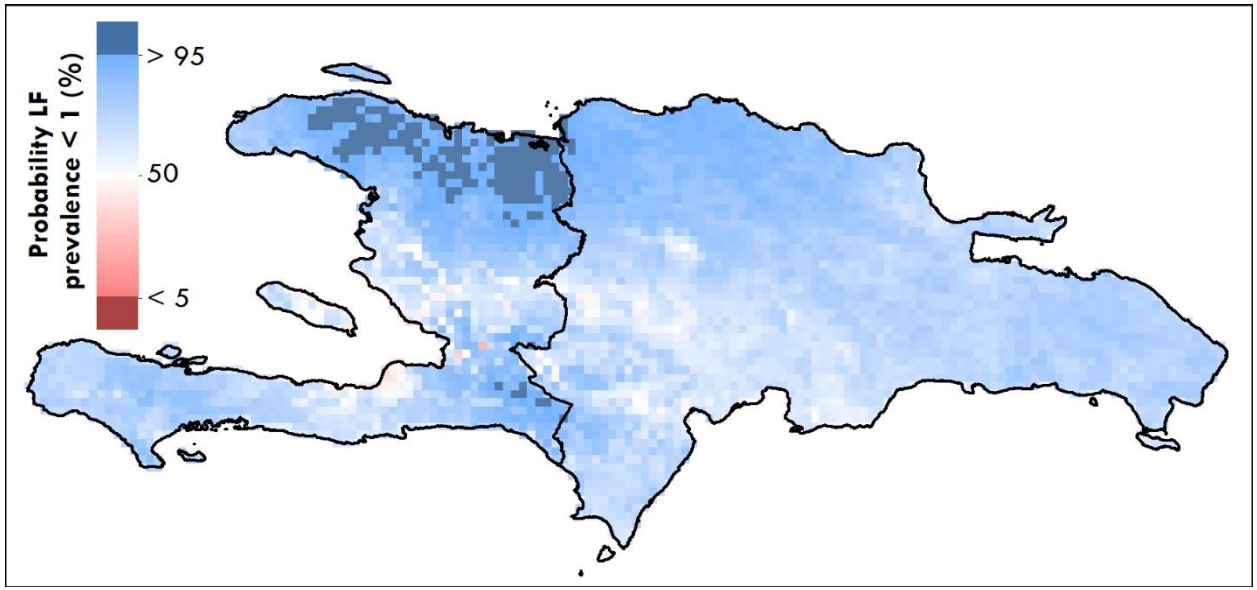
Supplementary Figure 17. Posterior probability that all-age lymphatic filariasis antigenaemia prevalence was below 1% in a given 5 × 5-km grid cell in 2018, in South and Southeast Asia

Mean predictions of posterior probability that all-age LF antigenaemia (infection) prevalence was below 1% in a given 5 × 5-km grid cell from the Bayesian goestatistcal model for 2018 in South and Southeast Asia, as measured by the immunochromatographic test (ICT). Hatch-marks indicate countries for which estimates are not produced; grey areas are masked based on sparsely-populated areas (fewer than ten people per 1 × 1-km grid cell) and barren landscape classification. Interactive visualisation tool at https://vizhub.healthdata.org/lbd/lf.



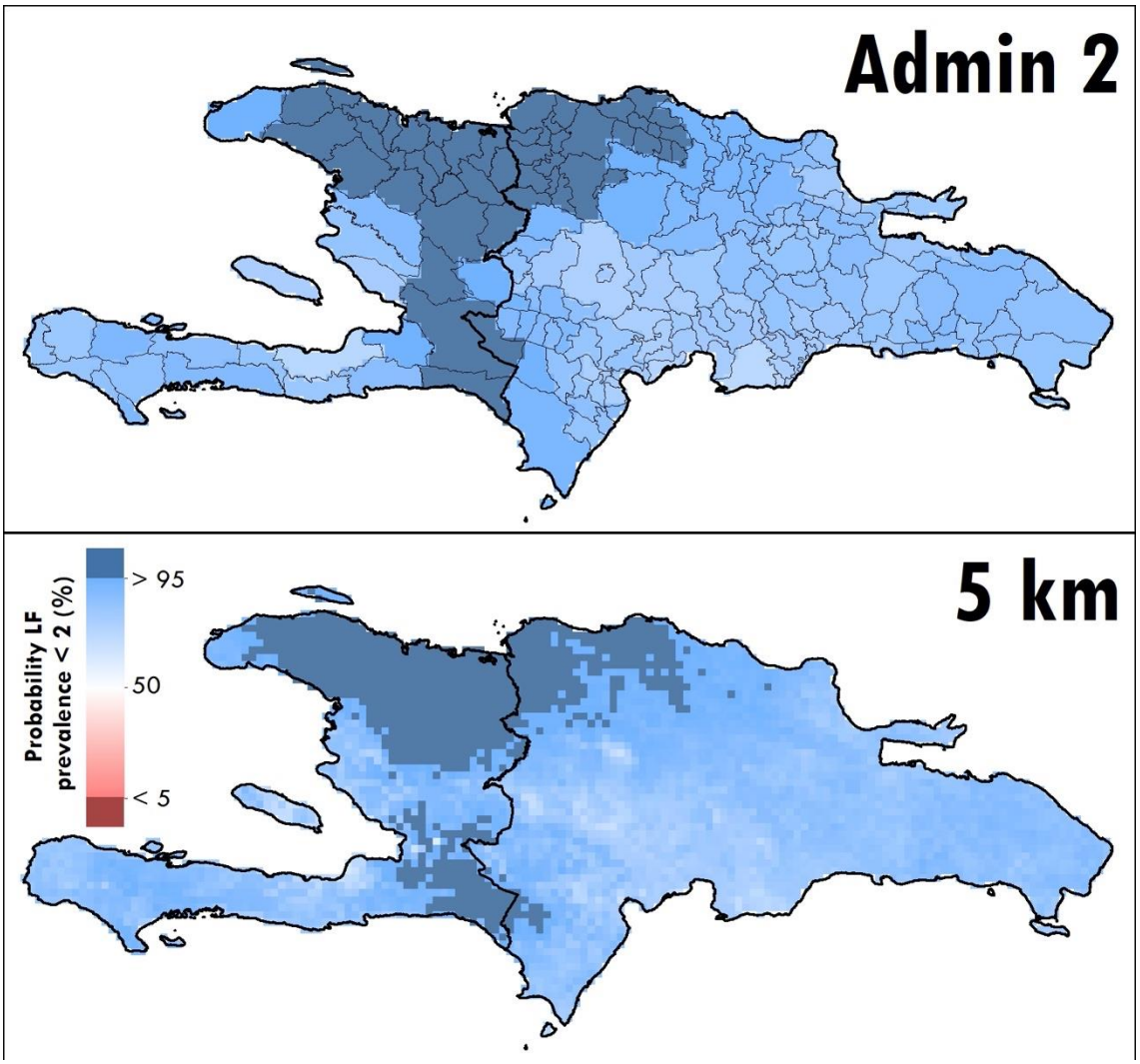
Supplementary Figure 18. Asia 2% probability plots

Posterior probability that LF ICT prevalence was below 2% in 2018, at the second administrative level and at the 5 × 5-km resolution, in Asia. Hatch-marks indicates countries for which estimates are not produced; grey areas are masked based on sparsely populated areas (fewer than ten people per 1 × 1-km) and barren landscape classification.



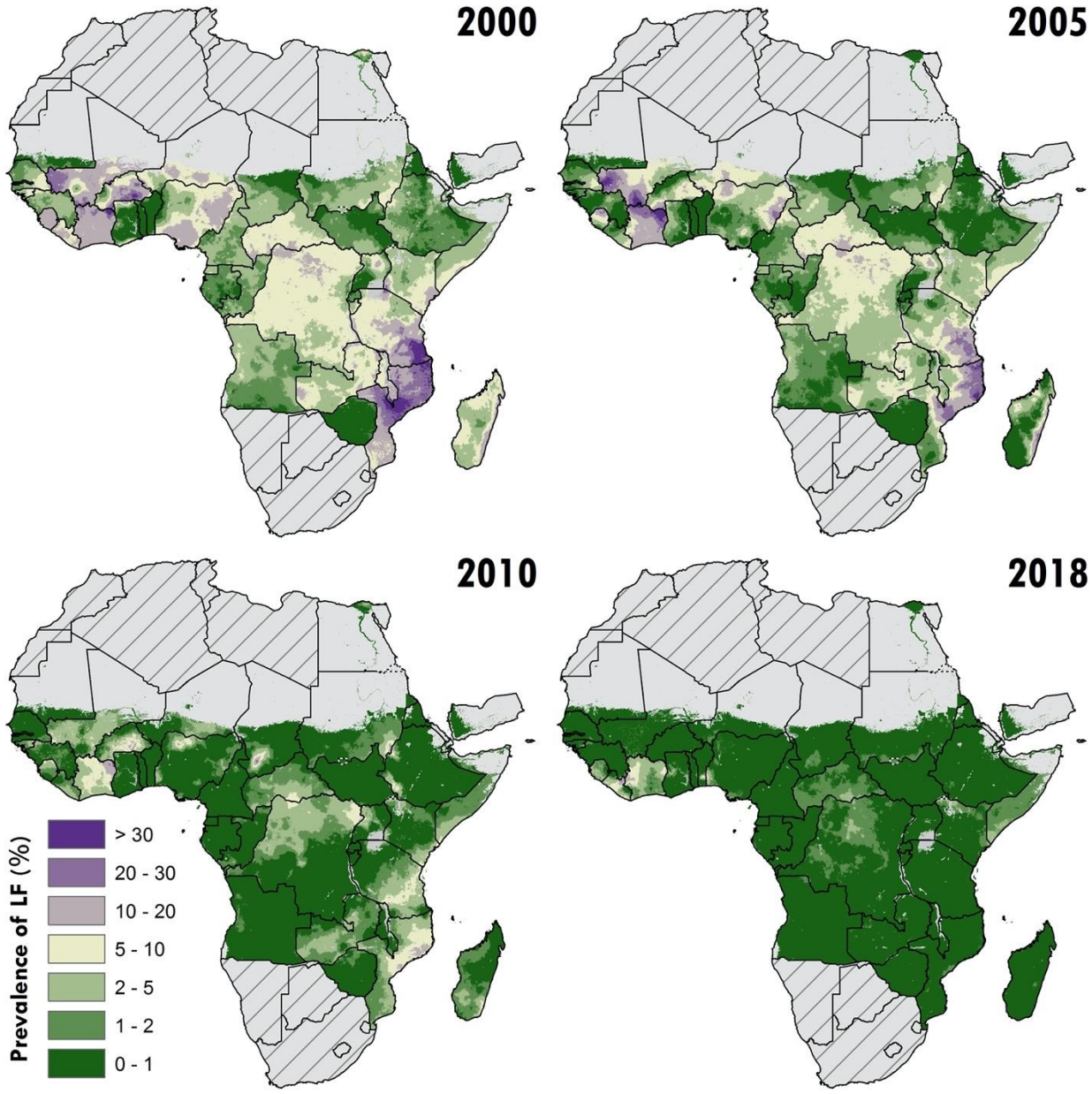
Supplementary Figure 19. Posterior probability that all-age lymphatic filariasis antigenaemia prevalence (as measured by the ICT test) was below 1% in a given 5 × 5-km grid cell in 2018, in Hispaniola

Mean predictions of posterior probability that all-age LF antigenaemia (infection) prevalence was below 1% in a given 5 × 5-km grid cell from the Bayesian goestatistcal model for 2018 in Hispaniola (Haiti and the Dominican Republic), as measured by the immunochromatographic test (ICT). Interactive visualisation tool at https://vizhub.healthdata.org/lbd/lf.



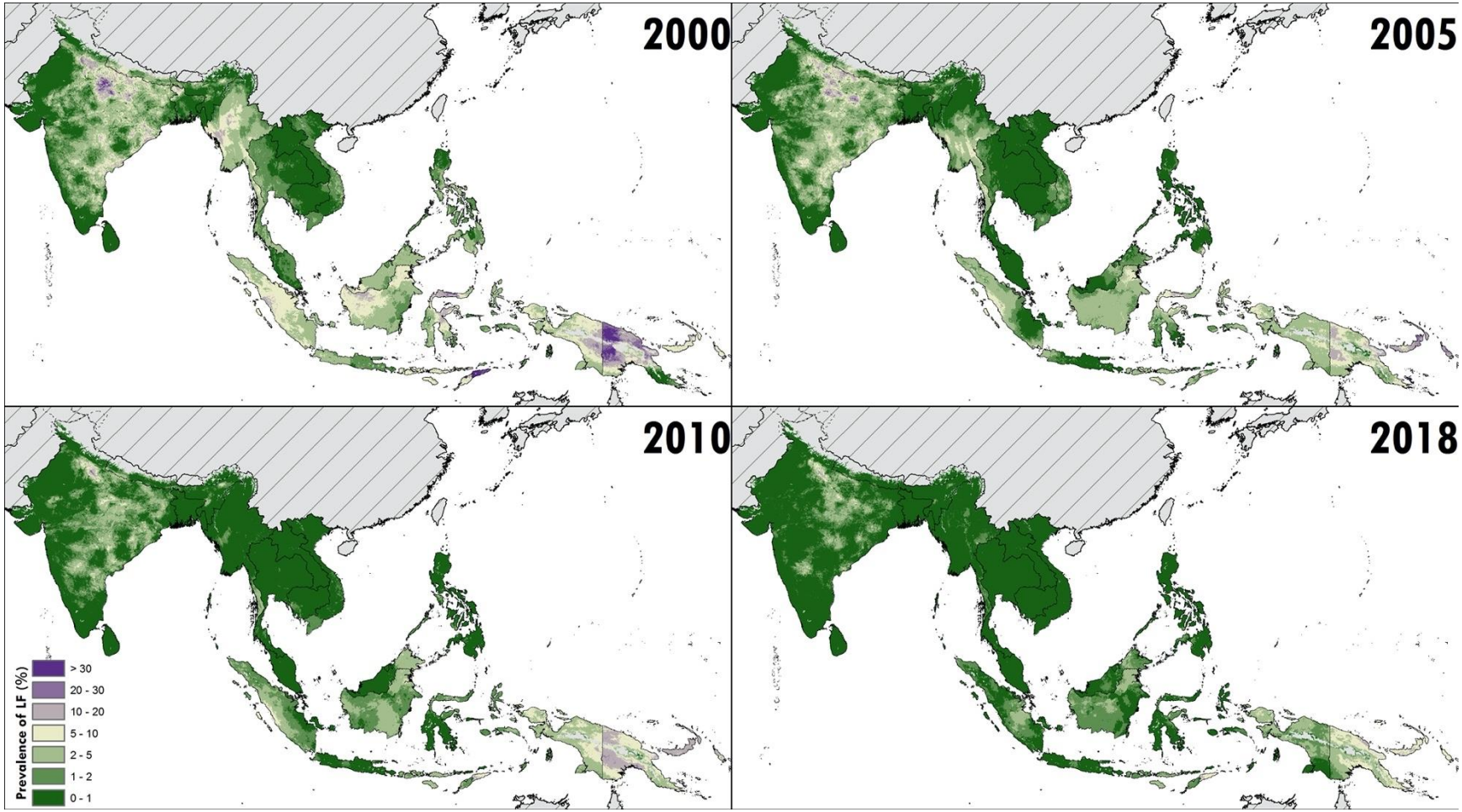
Supplementary Figure 20. Hispaniola 2% probability plots

Posterior probability that LF ICT prevalence was below 2% in 2018, at the second administrative level and at the 5 × 5-km resolution, in Hispaniola.



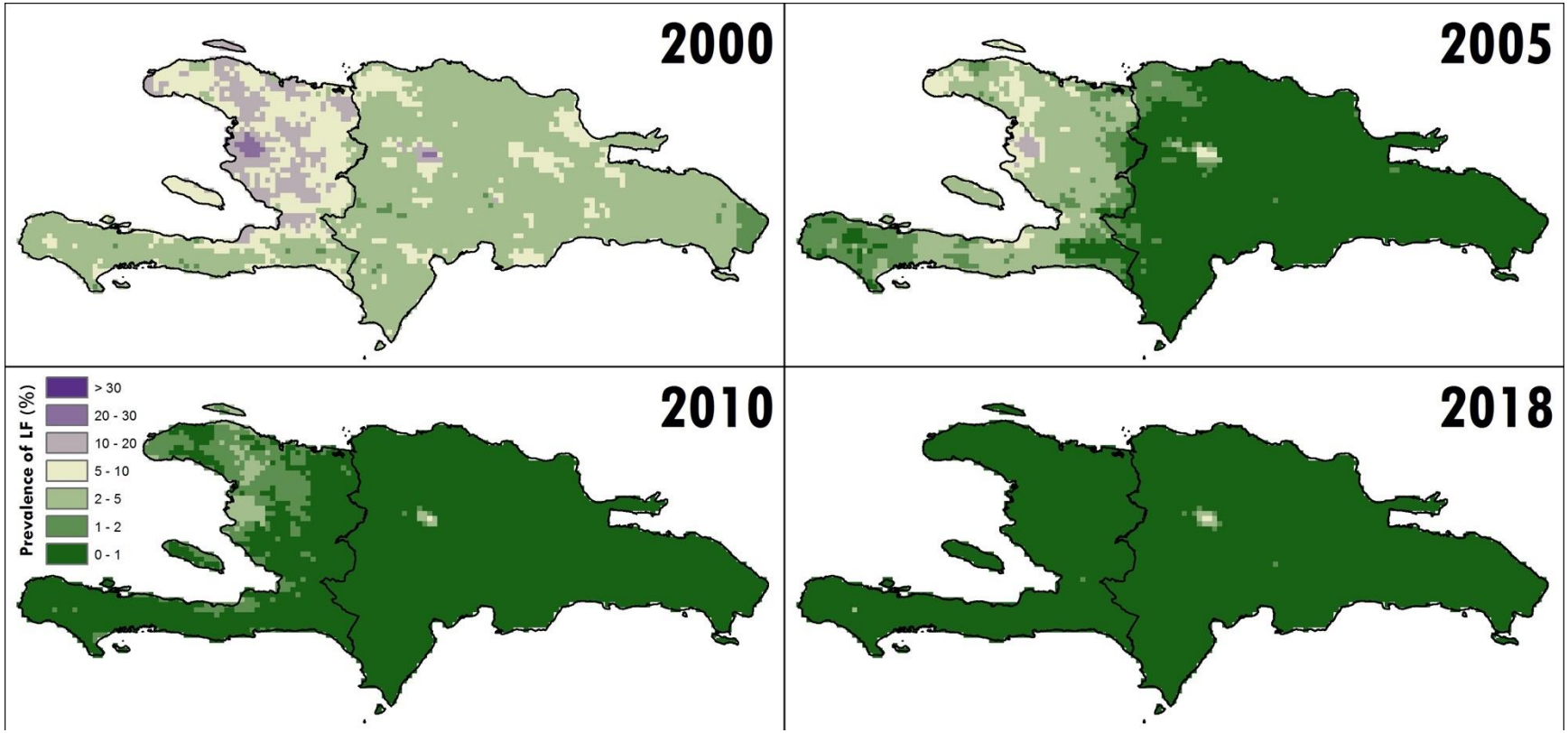
Supplementary Figure 13. Prevalence of lymphatic filariasis microfilaraemia in Africa and Yemen at the 5 × 5-km level: 2000, 2005, 2010, and 2018

Mean predictions of antigenaemia (infection) prevalence from the Bayesian geostatistical model for 2000, 2005, 2010, and 2018 in Africa and Yemen, as measured by detection of microfilariae.



Supplementary Figure 22. Prevalence of lymphatic filariasis microfilaraemia in South and Southeast Asia at the 5 × 5-km level: 2000, 2005, 2010, and 2018

Mean predictions of antigenaemia (infection) prevalence from the Bayesian geostatistical model for 2000, 2005, 2010, and 2018 in South and Southeast Asia, as measured by detection of microfilariae.



Supplementary Figure 23. Prevalence of lymphatic filariasis microfilaraemia in Hispaniola at the 5 × 5-km level: 2000, 2005, 2010, and 2018

Mean predictions of antigenaemia (infection) prevalence from the Bayesian geostatistical model for 2000, 2005, 2010, and 2018 in Hispaniola, as measured by detection of microfilariae.

Supplementary Table 9. Estimate of lymphatic filariasis microfilaraemia cases, by World Health Organization region: 2000, 2005, 2010, and 2018

For comparison against historical estimates of global infection prevalence, we estimated global mf prevalence by replicating the diagnostic and age adjustments, setting mf as the reference diagnostic.

	2000		2005		2010		2018	
Region	**Mean**	**95% UI***	**Mean**	**95% UI***	**Mean**	**95% UI***	**Mean**	**95% UI***
AFRO	36 895 078	27 194 124– 49 679 454	24 187 718	17 604 137– 32 588 770	8 655 400	6 345 893– 12 213 219	4 266 576	2 587 729– 6 972 649
AMRO	1 214 547	601 903– 2 309 001	507 055	265 498– 906 058	175 606	95 568– 333 085	126 610	59 737– 232 781
EMRO	1 956 094	988 040– 4 252 387	645 586	141 948– 2 436 124	820 818	302 904– 2 307 129	464 455	77 415– 1 600 381
SEARO	44 217 535	36 881 192– 56 645 698	33 679 430	29 056 708– 40 981 642	18 672 932	15 477 506– 23 737 626	13 509 376	11 011 676– 17 437 256
WPRO	3 074 931	1 098 093— 7 714 714	1 754 801	851 862– 4 455 283	1 587 687	607 295– 4 066 275	1 088 751	460 094– 2 544 894
Total	**88 147 726**	**74 774 162– 105 680 535**	**61 323 562**	**52 329 202– 72 625 996**	**30 140 587**	**25 453 956– 36 552 262**	**19 765 739**	**16 167 906– 25 026 914**

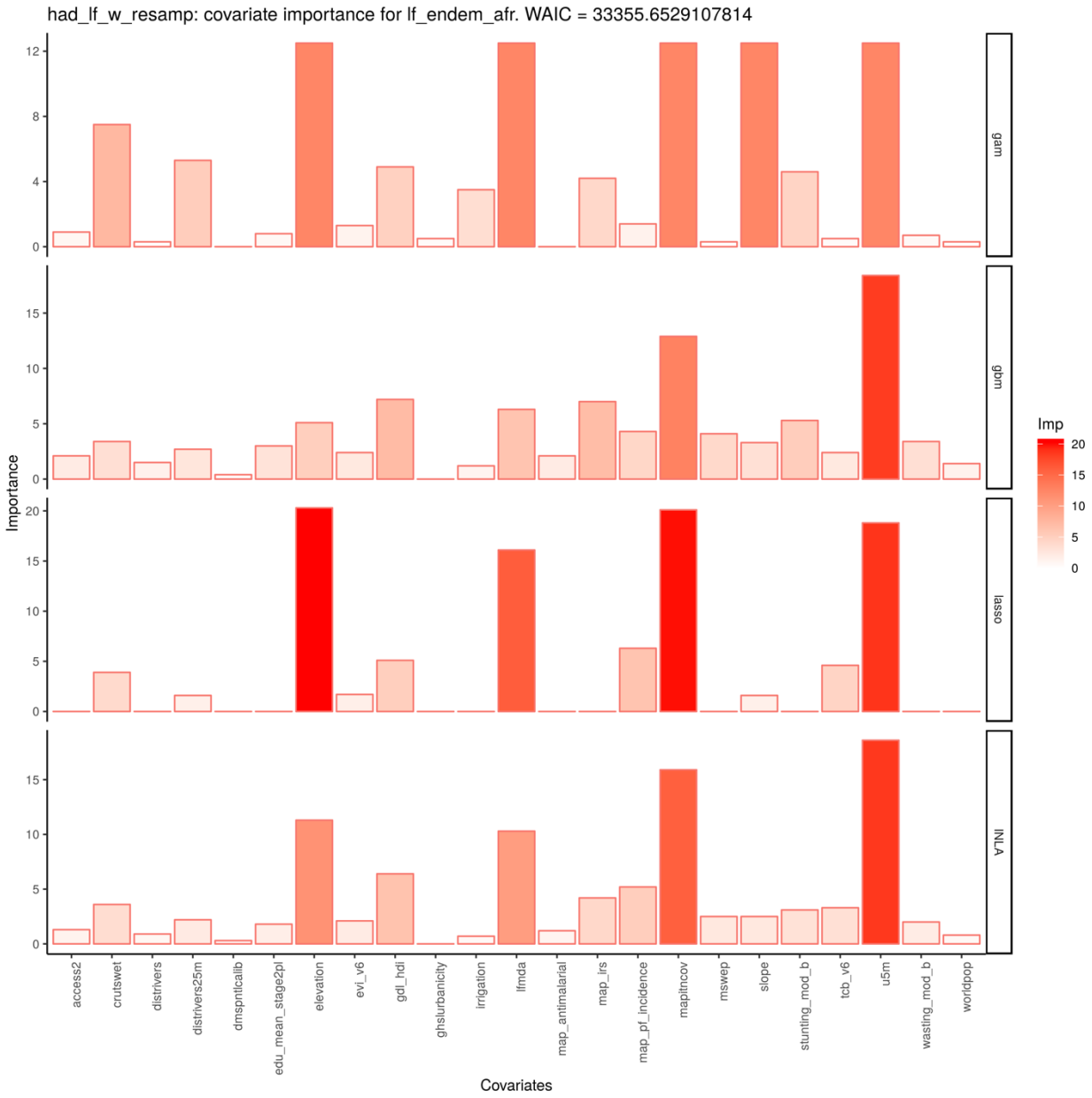
World Health Organization regions include AFRO: African Region, AMRO: Region for the Americas, EMRO: Eastern Mediterranean Region, SEARO: South-East Asia Region, and WPRO: Western Pacific Region. We do not estimate filariasis-infected individuals for the European Region.
*UI: Uncertainty interval.

5.3.8 Covariate importance

LF prevalence predictions from each of the covariate ensemble sub-models (GAM, boosted regression trees, and lasso regression) were used as predictors in the final geostatistical model, in lieu of the covariates themselves. This approach accommodates complex and non-linear covariate interactions in order to improve predictive performance, but complicates inferential analysis of covariate-prevalence relationships. Some covariates themselves represent modelled quantities, and the models used to produce these spatial estimates utilise some of the same covariates that are included in the LF prevalence models. While analyses attempting to infer which covariates drive LF prevalence in the geospatial models should therefore be interpreted with caution, the relative importance of each covariate within each component of the ensemble model can provide insight into which covariates are most influential in the overall model.

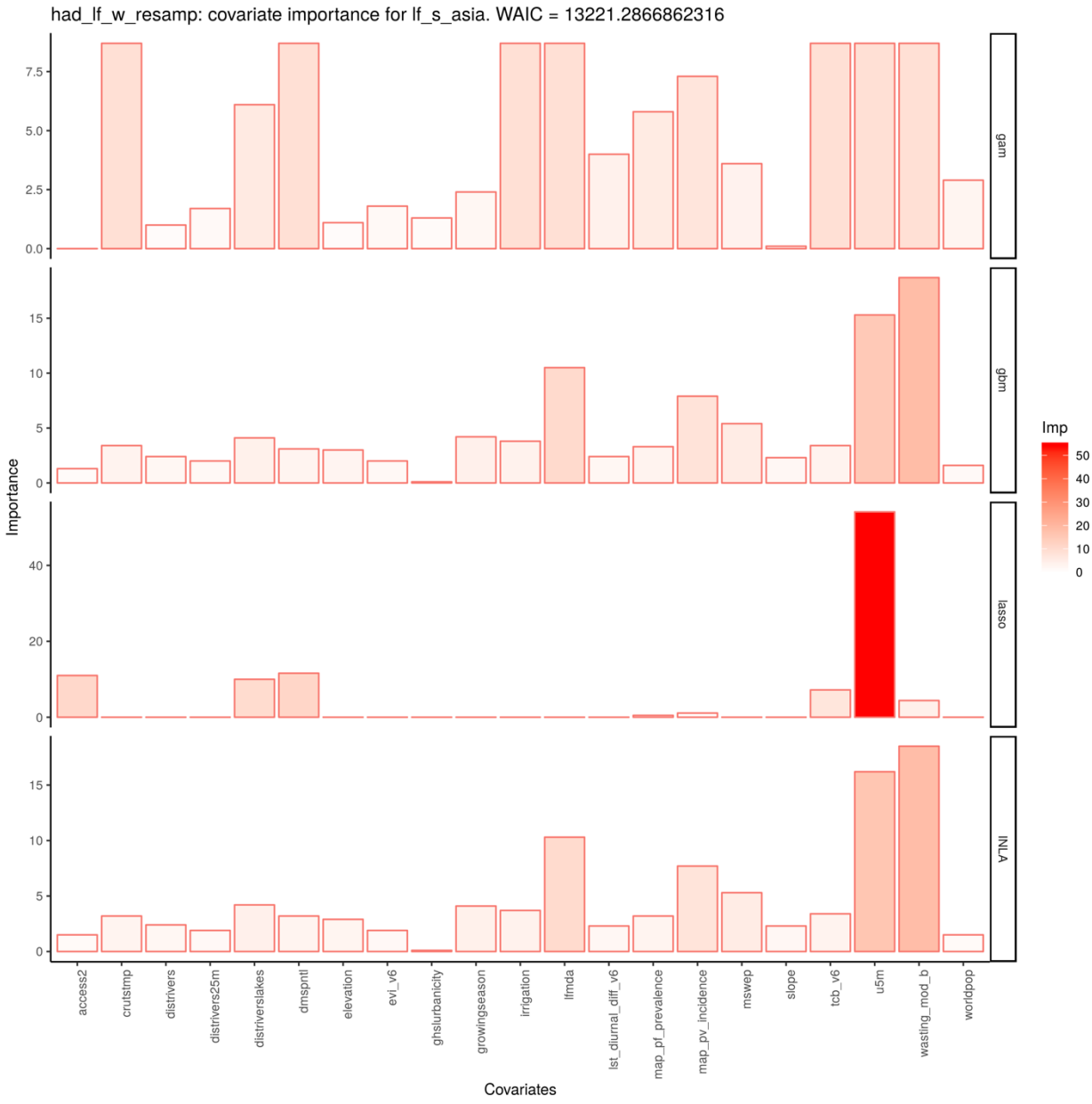
A measure of covariate importance was calculated for each of the three sub-models used in the ensemble modelling process: negative logs of covariate *p*-values for GAM models; frequency of covariate inclusion in regression tree samples (GBM); and the Agresti method of generating standardised coefficients, for lasso regression.[149] These relative importance metrics were normalised to sum to one within each sub-model, and a weighted average of these sub-model-specific relative importance values was calculated for each covariate, using the beta coefficients for each sub-model in the final INLA model as weights.

Supplementary Figures 24–27 illustrate the relative influence of each modelled covariate in the stacker child models and the full INLA model, by region. The estimated associations between LF prevalence and the most influential covariates in the GBM models are plotted in Supplementary Figures 28–31; Supplementary Figures 32–35 display these estimated relationships for the GAM child models, and Supplementary Table 9 provides coefficients from the lasso child models.



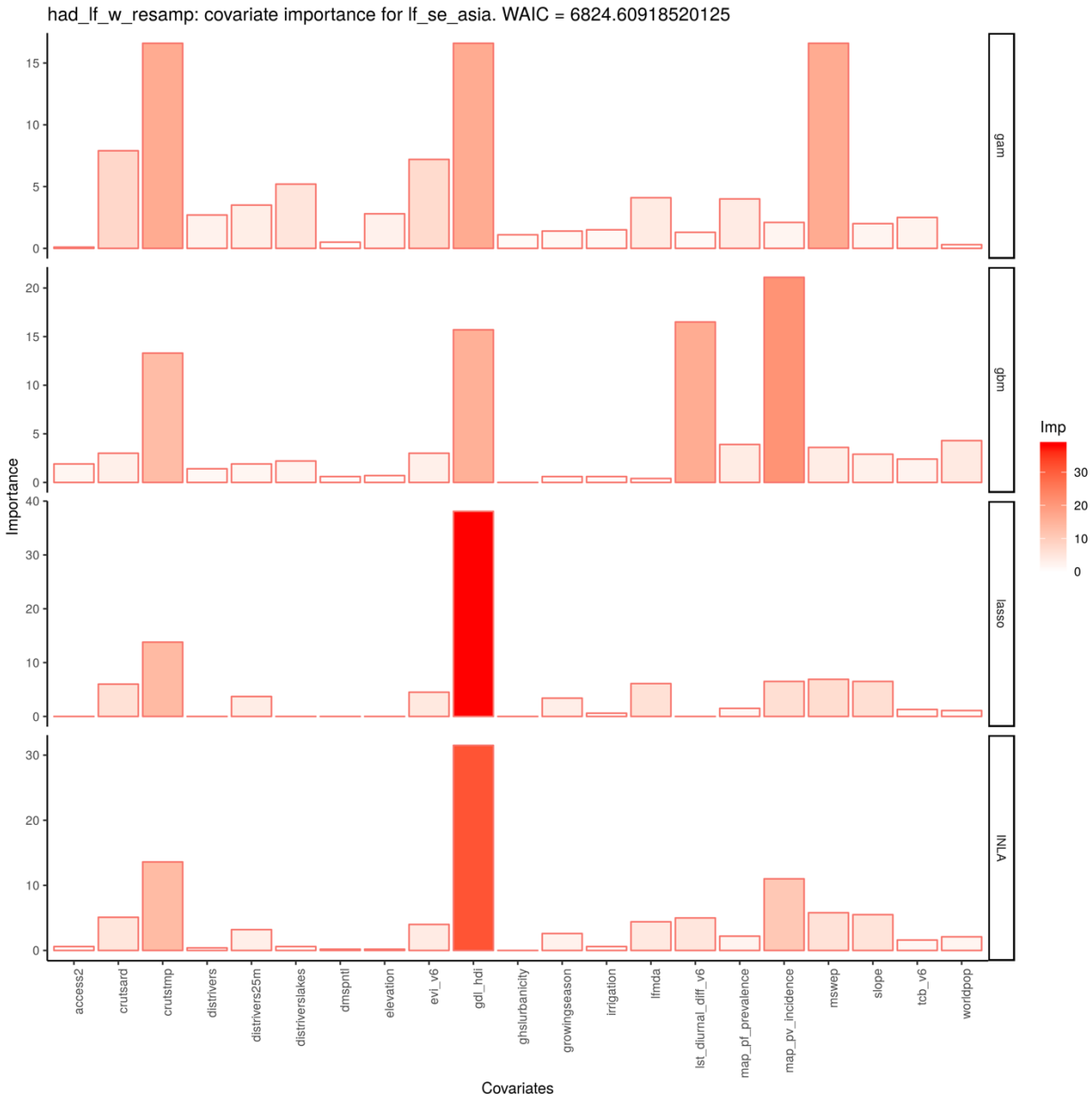
Supplementary Figure 24. Africa and Yemen stacker and covariate influence plots

Relative contributions of each covariate in the stacker child models and in the final MBG INLA model, for the Africa model region. Covariate names are as in Supplementary Table 5.



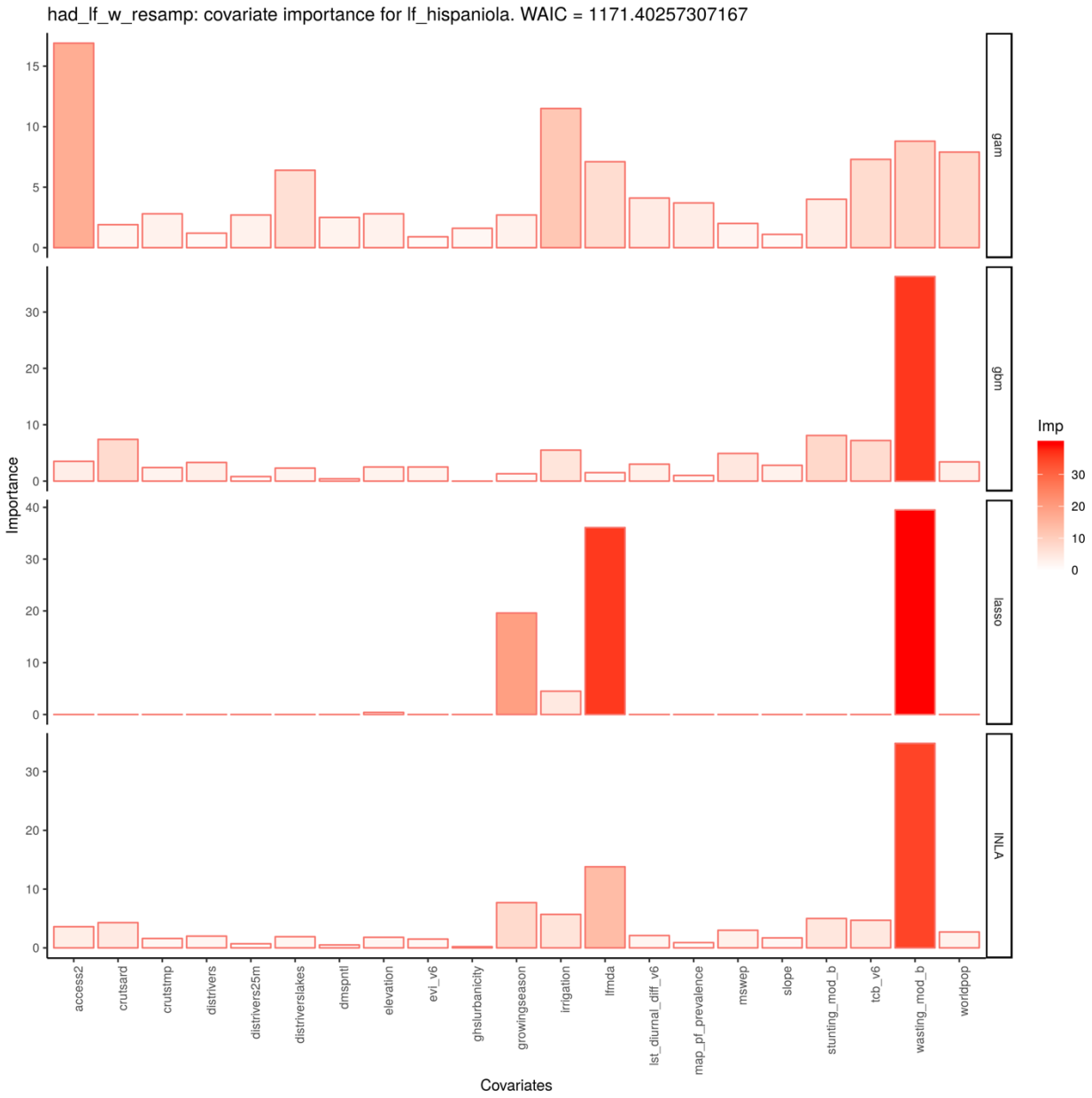
Supplementary Figure 25. South Asia stacker and covariate influence plots

Relative contributions of each covariate in the stacker child models and in the final MBG INLA model, for the South Asia model region. Interpretation is as for Supplementary Figure 22. Covariate names are as in Supplementary Table 5.



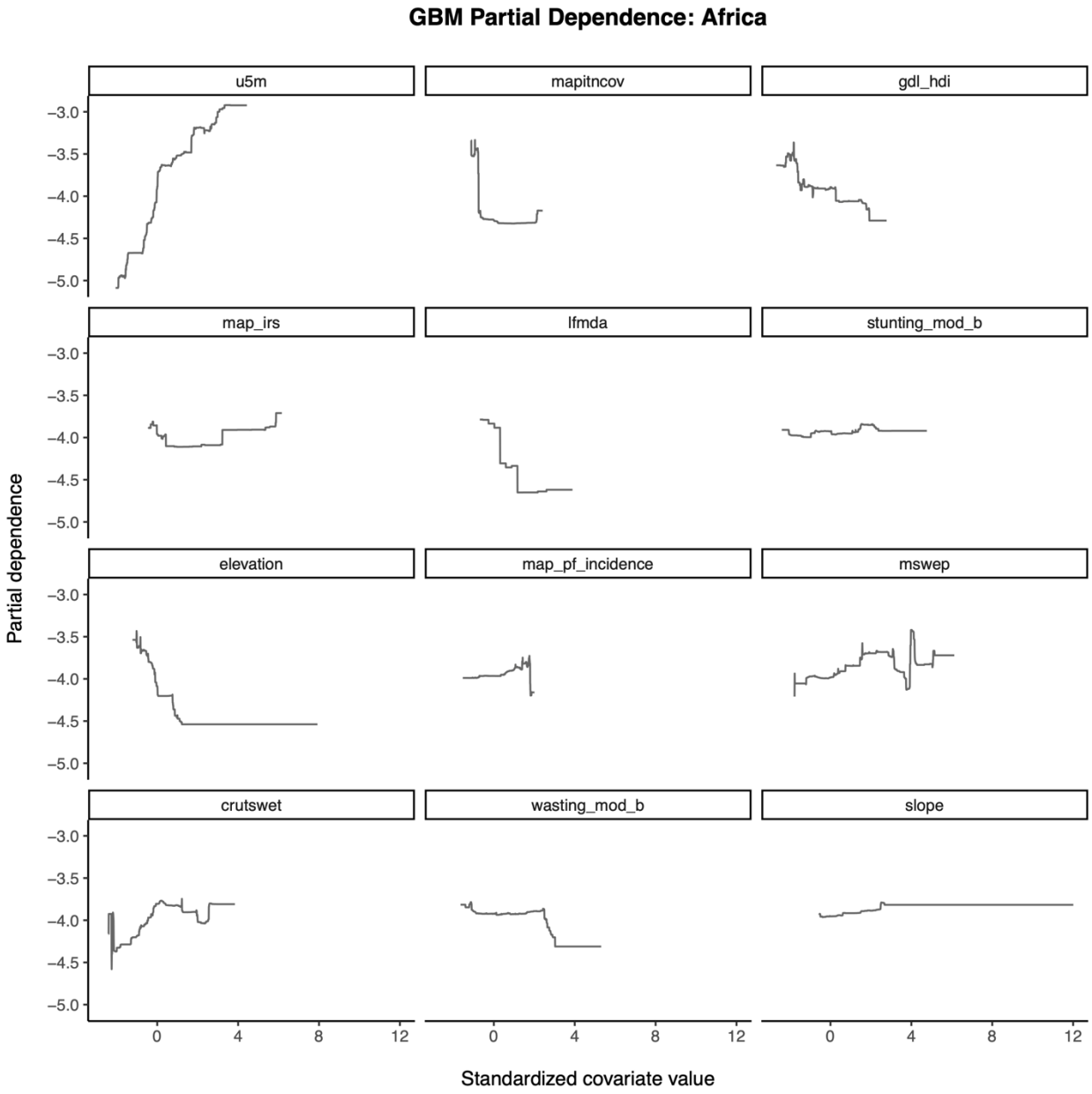
Supplementary Figure 26. Southeast Asia stacker and covariate influence plots.

Relative contributions of each covariate in the stacker child models and in the final MBG INLA model, for the Southeast Asia model region. Interpretation is as for Supplementary Figure 22. Covariate names are as in Supplementary Table 5.



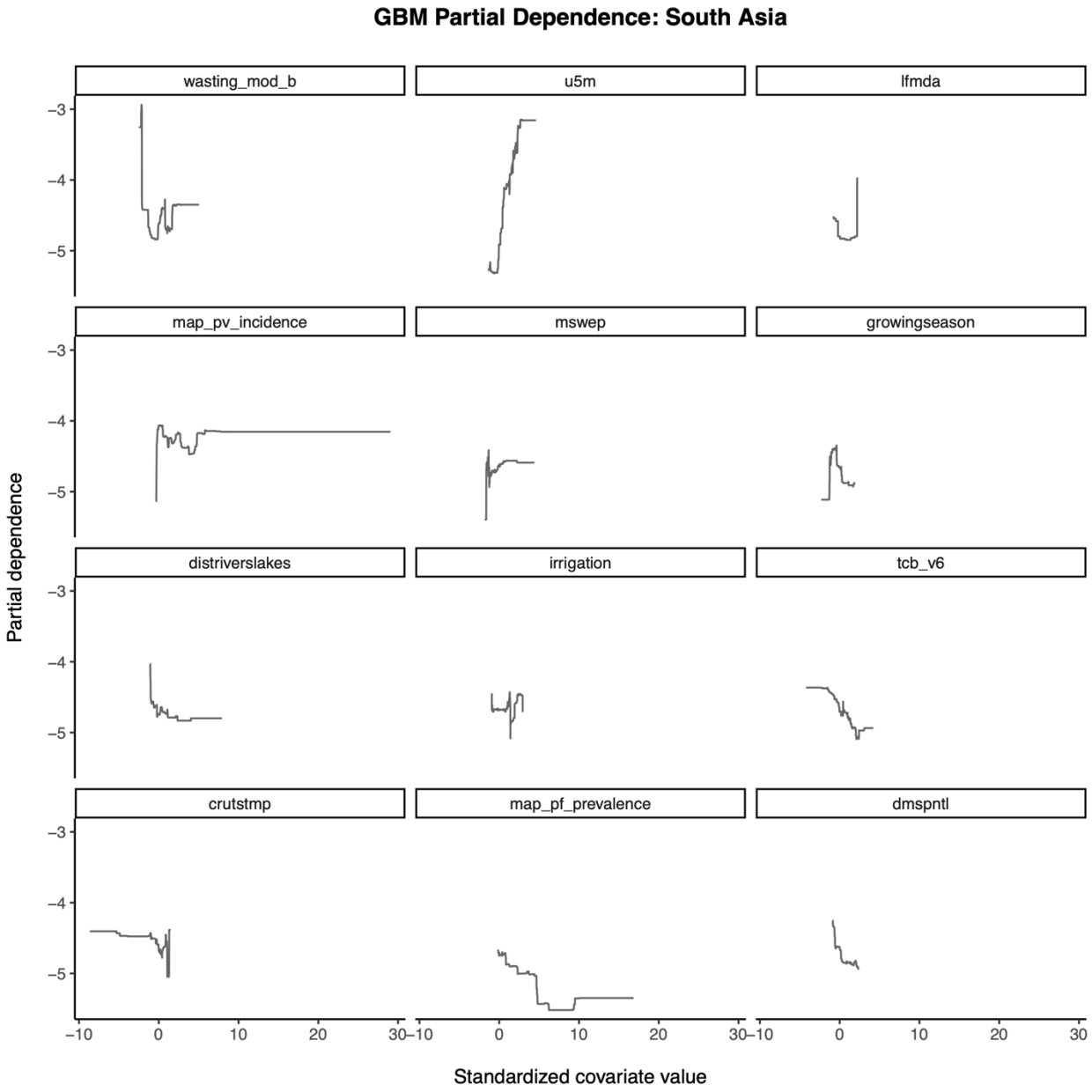
Supplementary Figure 27. Hispaniola stacker and covariate influence plots

Relative contributions of each covariate in the stacker child models and in the final MBG INLA model, for the Hispaniola model region. Interpretation is as for Supplementary Figure 22. Covariate names are as in Supplementary Table 5.



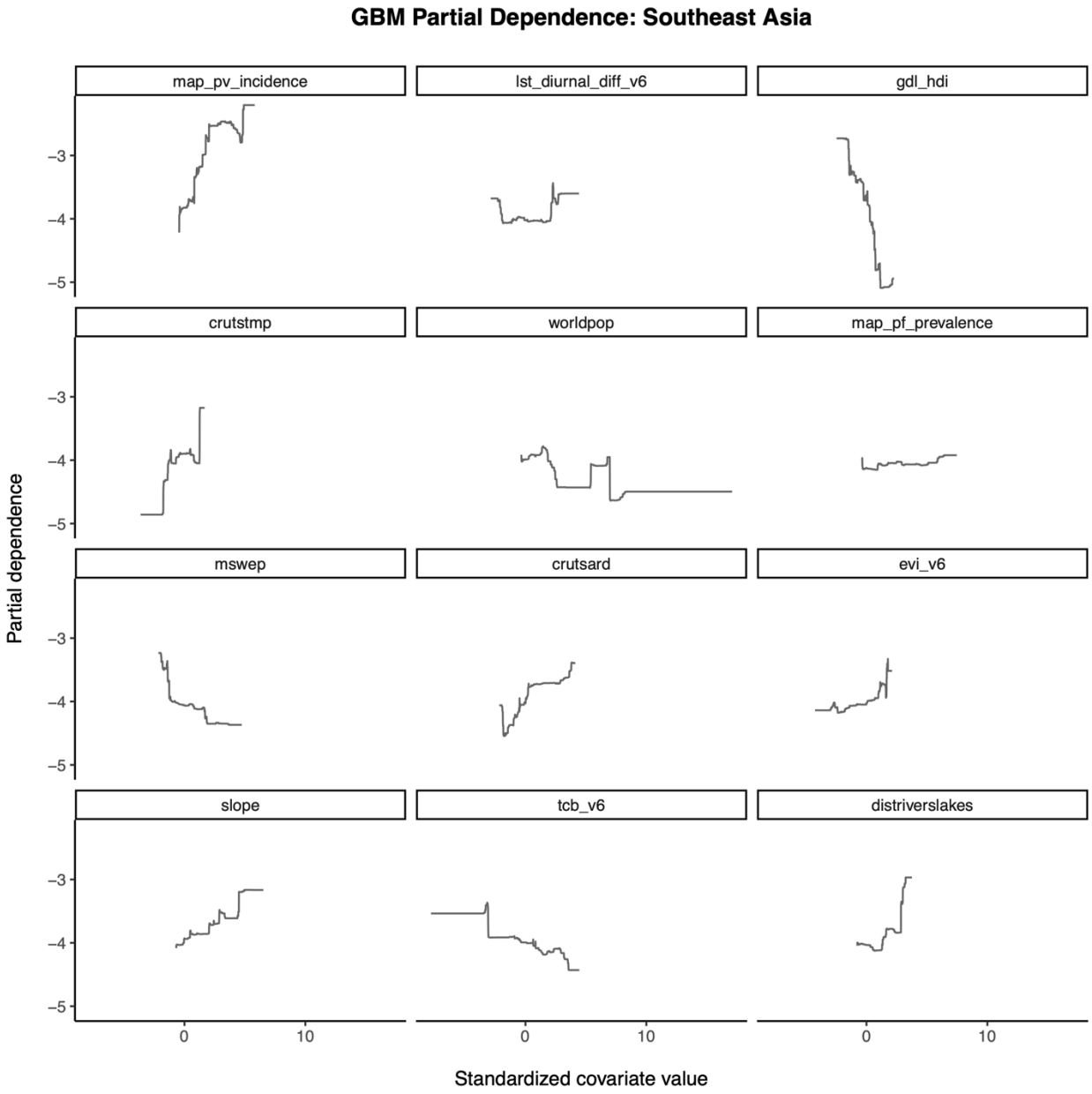
Supplementary Figure 28. Africa and Yemen GBM covariate plots

Partial dependence plots of the most influential covariates in the Africa GBM stacker model (not including country fixed effects). Plots illustrate the inferred associations between individual covariates and LF prevalence from post-burnin regression trees; values on the x-axis represent standardised covariate values, while the y-axis represents associations with LF prevalence in log space. Covariate names are as in Supplementary Table 5.



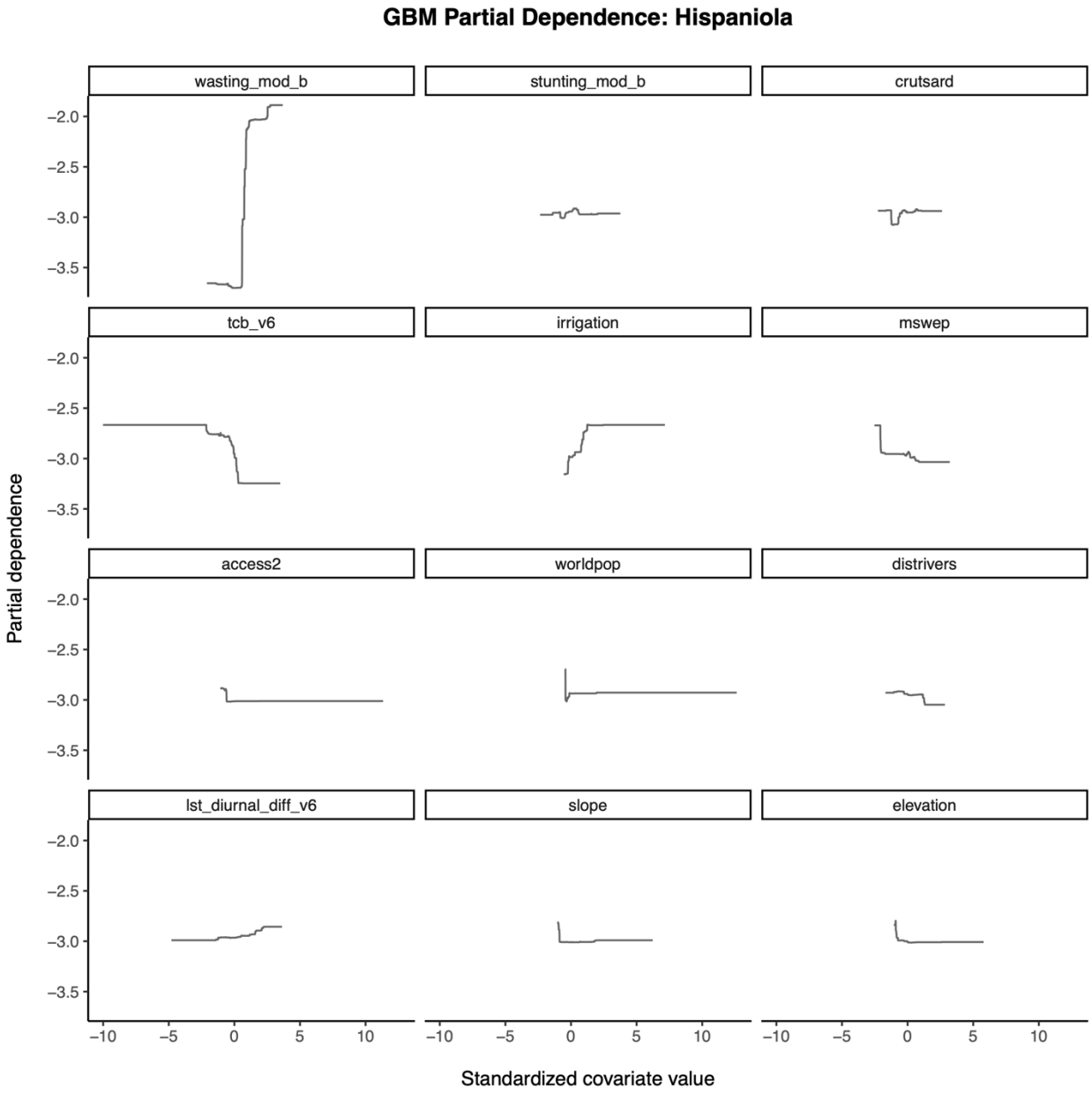
Supplementary Figure 14. South Asia GBM covariate plots

Partial dependence plots of the most influential covariates in the South Asia GBM stacker model (not including country fixed effects). Plots illustrate the inferred associations between individual covariates and LF prevalence from post-burnin regression trees; values on the x-axis represent standardised covariate values, while the y-axis represents associations with LF prevalence in log space. Covariate names are as in Supplementary Table 5.



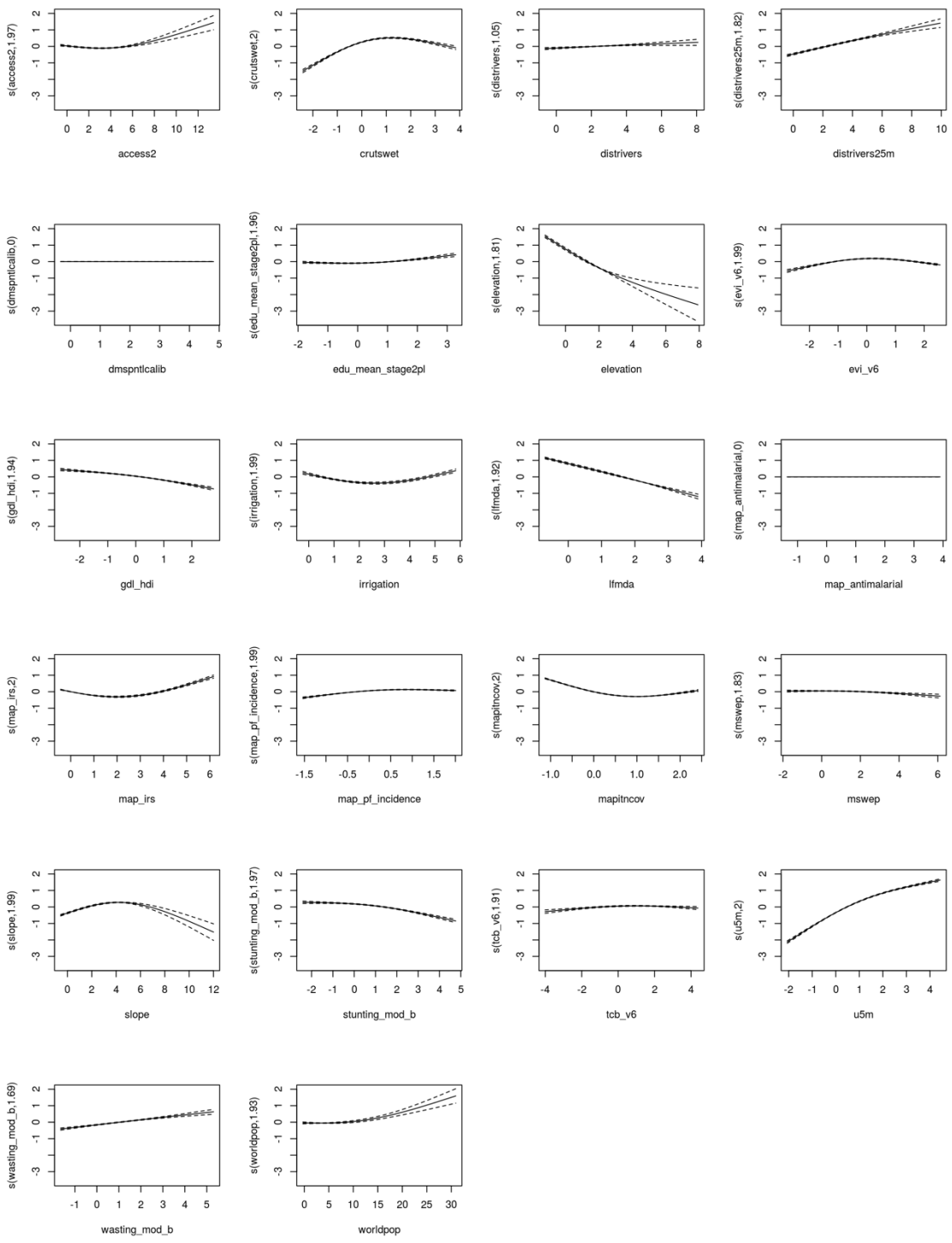
Supplementary Figure 150. Southeast Asia GBM covariate plots

Partial dependence plots of the most influential covariates in the Southeast Asia GBM stacker model (not including country fixed effects). Plots illustrate the inferred associations between individual covariates and LF prevalence from post-burnin regression trees; values on the x-axis represent standardised covariate values, while the y-axis represents associations with LF prevalence in log space. Covariate names are as in Supplementary Table 5.



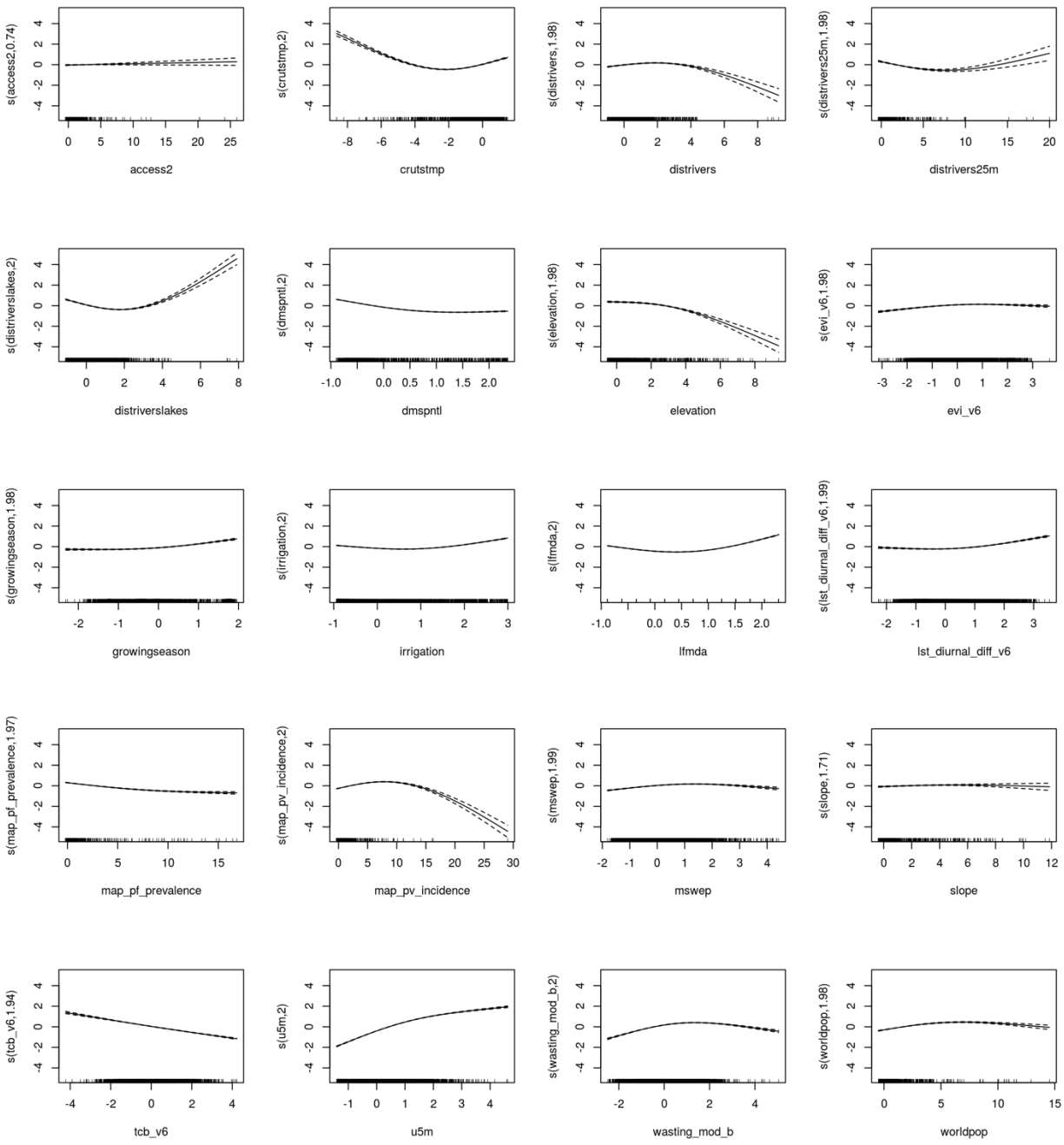
Supplementary Figure 31. Hispaniola GBM covariate plots

Partial dependence plots of the most influential covariates in the Hispaniola GBM stacker model (not including country fixed effects). Plots illustrate the inferred associations between individual covariates and LF prevalence from post-burnin regression trees; values on the x-axis represent standardised covariate values, while the y-axis represents associations with LF prevalence in log space. Covariate names are as in Supplementary Table 5.



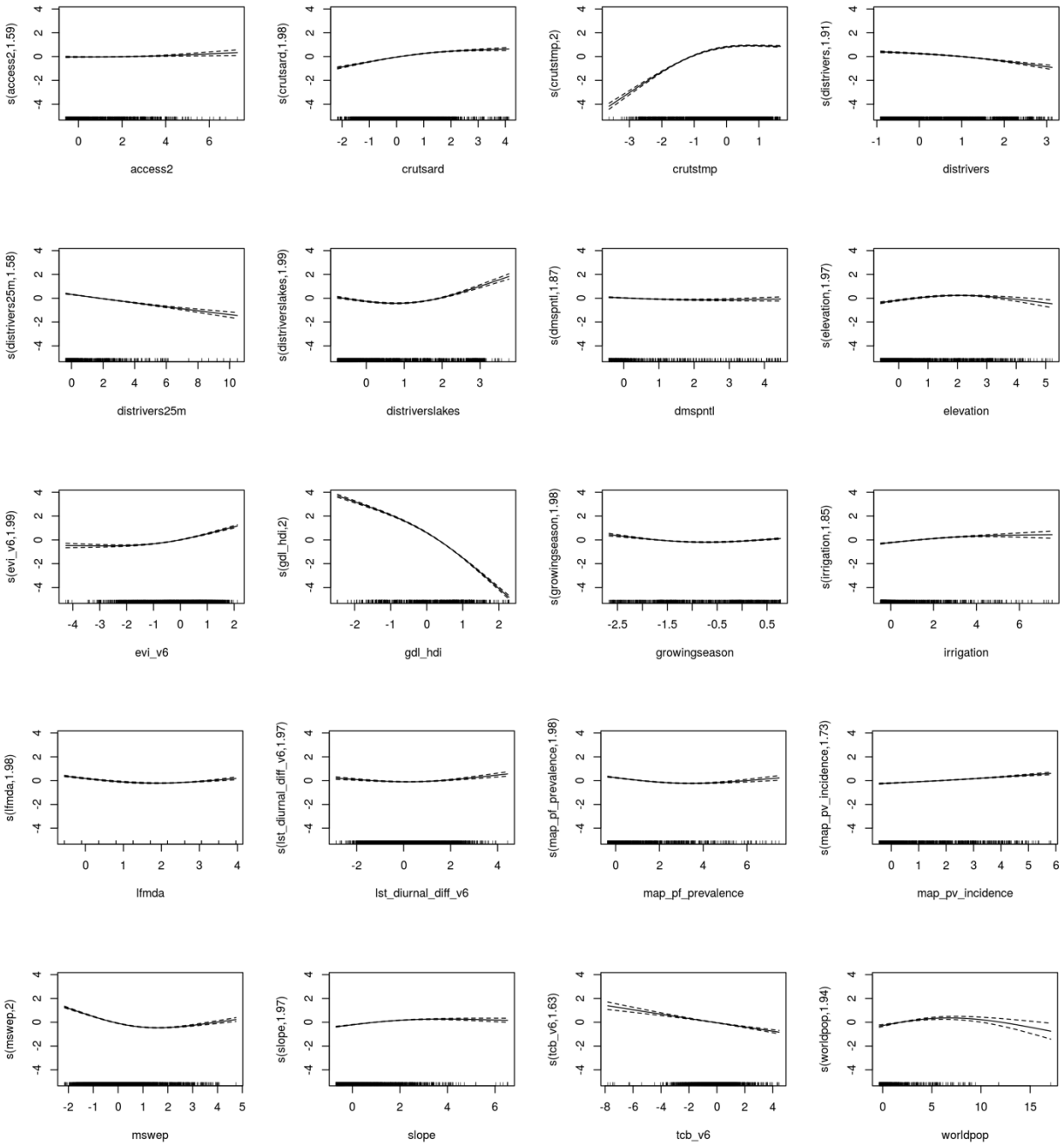
Supplementary Figure 32. Africa and Yemen GAM covariate plots

Covariate term plots from the Africa GAM stacker model (not including country fixed effects). Plots illustrate the smoothed associations between individual covariates and LF prevalence; values on the x-axis represent standardised covariate values, while the y-axis represents associations with LF prevalence in logit space. Covariate names are as in Supplementary Table 5.



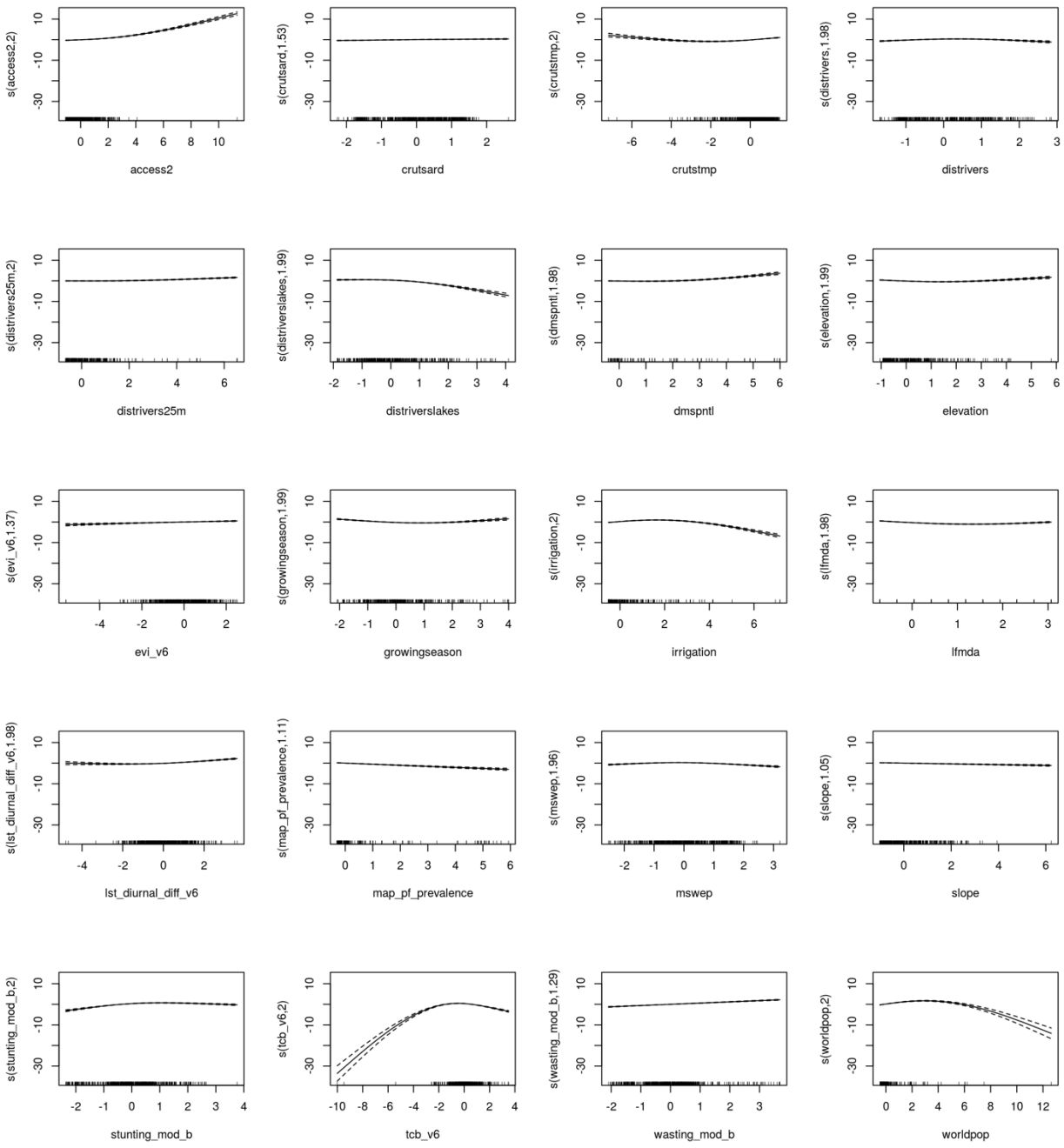
Supplementary Figure 33. South Asia GAM covariate plots

Covariate term plots from the South Asia GAM stacker model (not including country fixed effects). Plots illustrate the smoothed associations between individual covariates and LF prevalence; values on the x-axis represent standardised covariate values, while the y-axis represents associations with LF prevalence in logit space. Covariate names are as in Supplementary Table 5.



Supplementary Figure 34. Southeast Asia GAM covariate plots

Covariate term plots from the Southeast Asia GAM stacker model (not including country fixed effects). Plots illustrate the smoothed associations between individual covariates and LF prevalence; values on the x-axis represent standardised covariate values, while the y-axis represents associations with LF prevalence in logit space. Covariate names are as in Supplementary Table 5.



Supplementary Figure 35. Hispaniola GAM covariate plots

Covariate term plots from the Hispaniola GAM stacker model (not including country fixed effects). Plots illustrate the smoothed associations between individual covariates and LF prevalence; values on the x-axis represent standardised covariate values, while the y-axis represents associations with LF prevalence in logit space. Covariate names are as in Supplementary Table 5.

Supplementary Table 10. Coefficients for covariates (standardised scale) in lasso child models, by region, selected with the cross-validated value of lambda (penalty coefficient).

Covariate names are as in Supplementary Table 5. Country-level fixed effects are not shown. Covariates with a coefficient of 0.0000 were eliminated by the lasso model. -: Covariate was not included in stacker models.

Covariate	Africa	S Asia	SE Asia	Hispaniola
access2	0.0000	0.1373	0.0000	0.0000
crutsard	-	-	0.1999	0.0000
crutstmp	-	0.0000	0.4577	0.0000
crutswet	0.1031	-	-	-
distrivers	0.0000	0.0000	0.0000	0.0000
distrivers25m	0.0426	0.0000	-0.1266	0.0000
distriverslakes	-	-0.1192	0.0000	0.0000
dmspntl	0.0000	-0.1321	0.0000	0.0000
education	0.0000	-	0.0000	-
elevation	-0.5313	0.0000	0.0000	-0.0024
evi	0.0441	0.0000	0.1525	0.0000
gdl_hdi	-0.1346	-	-1.2742	-
ghslurbanicity	0.0000	0.0000	0.0000	0.0000
growingseason	-	0.0000	-0.1142	-0.1346
irrigation	0.0000	0.0000	0.0199	0.0310
lfmda	-0.4227	0.0000	-0.2055	-0.2482
lstdiurnaldiff	-	0.0000	0.0000	0.0000
mapitncov	-0.5273	-	-	-
map_antimalarial	0.0000	-	-	-
map_irs	0.0000	-	-	-
map_pf_incidence	0.1643	-	-	-
map_pf_prevalence	-	-0.0059	-0.0502	0.0000
map_pv_incidence	-	0.0121	0.2172	-
mswep	0.0000	0.0000	-0.2302	0.0000
slope	0.0417	0.0000	0.2174	0.0000
stunting_mod_b	0.0000	-	-	0.0000
tcb	-0.1209	-0.0825	-0.0436	0.0000
tcw	-	-	-	-
u5m	0.4926	0.6191	-	-
underweight_mod_b	-	-	-	-
wasting_mod_b	0.0000	0.0499	-	0.2711
worldpop	0.0000	0.0000	0.0361	0.0000

5.4 Model validation

5.4.1 Metrics of predictive validity

In order to assess the predictive validity of our estimates, we validated our ICT models using spatially stratified ten-fold out-of-sample cross-validation. To construct each spatial fold, we used a modified bi-tree algorithm to spatially aggregate datapoints. This algorithm recursively partitions two-dimensional space, alternating between horizontal and vertical splits on the weighted data sample size medians, until the data contained within each spatial partition are of a similar sample size. The depth of recursive partitioning is constrained by the target sample size within a partition and the minimum number of clusters or pseudo-clusters allowed within each spatial partition (in this case, a minimum sample size of 500 was used). These spatial partitions are then allocated to one of ten folds for cross-validation. Temporal partitioning was unstructured (random).

For validation, each geostatistical model was run five times, each time holding out data from one of the folds, generating a set of out-of-sample predictions for the held-out data. For each indicator, a full suite of out-of-sample predictions over the entire dataset was generated by combining the out-of-sample predictions from the five cross-validation runs. Using these out-of-sample predictions, we then calculated mean error (bias), mean absolute error, 95% coverage of our predictive intervals (the proportion of observed out-of-sample data that fall within our predicted 95% uncertainty intervals), root-mean squared-error (RMSE, which summarises error variance), and the correlation of predicted versus observed prevalence at the level of individual datapoints. Validation metrics were generated for both spatiotemporal and time-stationary models for each model region and are summarised (along with WAIC from in-sample model runs) for each MBG region in Supplementary Tables 11–14. Scatterplots of reported prevalence versus mean out-of-sample predictions are provided in Supplementary Figures 36–43.

Supplementary Table 11. In-sample model fit (WAIC) and out-of-sample validation metrics (ICT) for Africa and Yemen at the level of individual datapoints, from ten-fold cross-validation, for all model regions

Out-of-sample performance was aggregated over 1990–2018 and is also provided for individual model years, and is given for both spatiotemporal and time-stationary model variants. WAIC is only meaningful for the in-sample comparison (all years). Mean abs. error: Mean absolute error. 95% cov.: 95% coverage. Corr.: Correlation.

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
1990	Spatiotemporal	-	0.026	0.187	1.000	0.193	-0.244
	Time-stationary	-	-0.082	0.152	1.000	0.185	0.030
1991	Spatiotemporal	-	0.071	0.091	1.000	0.125	-0.274
	Time-stationary	-	0.086	0.097	1.000	0.136	0.462
1992	Spatiotemporal	-	-0.137	0.224	1.000	0.232	-0.942
	Time-stationary	-	-0.145	0.234	1.000	0.267	-0.900
1993	Spatiotemporal	-	0.290	0.290	0.813	0.312	0.999
	Time-stationary	-	0.270	0.270	0.428	0.290	0.972
1994	Spatiotemporal	-	0.014	0.106	0.853	0.164	0.535
	Time-stationary	-	-0.019	0.139	0.871	0.203	0.481
1995	Spatiotemporal	-	0.109	0.109	1.000	0.109	NA
	Time-stationary	-	0.234	0.234	0.000	0.234	NA

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
1996	Spatiotemporal	-	0.030	0.038	1.000	0.039	0.880
	Time-stationary	-	0.152	0.152	0.983	0.160	0.471
1997	Spatiotemporal	-	0.040	0.116	1.000	0.135	0.205
	Time-stationary	-	0.165	0.190	0.748	0.218	0.228
1998	Spatiotemporal	-	0.017	0.080	1.000	0.121	0.749
	Time-stationary	-	0.063	0.112	0.825	0.172	0.500
1999	Spatiotemporal	-	-0.084	0.128	0.851	0.190	-0.494
	Time-stationary	-	-0.054	0.081	0.885	0.122	0.173
2000	Spatiotemporal	-	-0.012	0.064	0.878	0.103	0.685
	Time-stationary	-	0.011	0.065	0.858	0.112	0.585
2001	Spatiotemporal	-	0.004	0.072	0.871	0.128	0.685
	Time-stationary	-	0.021	0.077	0.877	0.132	0.666
2002	Spatiotemporal	-	0.006	0.053	0.949	0.100	0.792
	Time-stationary	-	0.011	0.066	0.912	0.121	0.676
2003	Spatiotemporal	-	-0.005	0.051	0.948	0.095	0.812
	Time-stationary	-	0.006	0.071	0.888	0.131	0.589
2004	Spatiotemporal	-	-0.003	0.033	0.932	0.071	0.742
	Time-stationary	-	0.002	0.040	0.897	0.083	0.616
2005	Spatiotemporal	-	-0.002	0.043	0.941	0.082	0.748
	Time-stationary	-	-0.003	0.045	0.939	0.078	0.773
2006	Spatiotemporal	-	-0.002	0.064	0.958	0.100	0.756
	Time-stationary	-	0.019	0.074	0.919	0.111	0.680
2007	Spatiotemporal	-	-0.014	0.067	0.906	0.101	0.508
	Time-stationary	-	0.019	0.060	0.924	0.098	0.428
2008	Spatiotemporal	-	-0.004	0.037	0.944	0.072	0.408
	Time-stationary	-	0.002	0.038	0.901	0.071	0.410
2009	Spatiotemporal	-	-0.001	0.034	0.949	0.066	0.532

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
	Time-stationary	-	0.006	0.036	0.930	0.071	0.467
2010	Spatiotemporal	-	-0.002	0.027	0.947	0.056	0.476
	Time-stationary	-	-0.002	0.031	0.921	0.058	0.371
2011	Spatiotemporal	-	0.000	0.026	0.967	0.049	0.580
	Time-stationary	-	-0.002	0.032	0.915	0.064	0.174
2012	Spatiotemporal	-	-0.003	0.016	0.963	0.038	0.649
	Time-stationary	-	0.001	0.020	0.929	0.043	0.426
2013	Spatiotemporal	-	0.001	0.009	0.976	0.029	0.564
	Time-stationary	-	0.001	0.010	0.973	0.030	0.509
2014	Spatiotemporal	-	-0.001	0.007	0.975	0.024	0.375
	Time-stationary	-	-0.001	0.008	0.976	0.024	0.342
2015	Spatiotemporal	-	0.002	0.012	0.967	0.048	0.260
	Time-stationary	-	0.000	0.013	0.963	0.049	0.164
2016	Spatiotemporal	-	-0.001	0.008	0.968	0.025	0.500
	Time-stationary	-	-0.004	0.010	0.948	0.024	0.534
2017	Spatiotemporal	-	0.000	0.001	0.988	0.006	0.780
	Time-stationary	-	-0.004	0.005	0.983	0.009	0.077
2018	Spatiotemporal	-	-0.001	0.002	0.993	0.007	0.958
	Time-stationary	-	-0.003	0.005	0.957	0.013	0.849
1990–2018	Spatiotemporal	33 356	-0.001	0.025	0.959	0.063	0.755
	Time-stationary	35 735	0.002	0.029	0.938	0.070	0.679

Supplementary Table 12. In-sample model fit (WAIC) and out-of-sample validation metrics (ICT) for South Asia at the level of individual datapoints, from ten-fold cross-validation, for all model regions

Out-of-sample performance was aggregated over all model years and is also provided for those individual model years for which prevalence data were available (no prevalence data were present for this region for 1990 and 1997), and is given for both spatiotemporal and time-stationary model variants. WAIC is only meaningful for the in-sample comparison (all years). Mean abs. error: Mean absolute error. 95% cov.: 95% coverage. Corr.: Correlation.

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
1991	Spatiotemporal	-	0.001	0.001	1.000	0.001	NA
	Time-stationary	-	0.043	0.043	1.000	0.043	NA
1992	Spatiotemporal	-	-0.300	0.060	1.000	0.073	-0.671
	Time-stationary	-	0.046	0.046	1.000	0.051	0.588
1993	Spatiotemporal	-	0.053	0.055	0.007	0.067	0.304
	Time-stationary	-	0.044	0.063	0.044	0.079	0.522
1994	Spatiotemporal	-	0.015	0.035	0.897	0.066	0.858
	Time-stationary	-	0.048	0.057	0.882	0.111	0.615
1995	Spatiotemporal	-	-0.011	0.103	1.000	0.125	-1.000
	Time-stationary	-	0.007	0.112	0.819	0.151	-1.000
1996	Spatiotemporal	-	0.135	0.135	1.000	0.135	NA
	Time-stationary	-	0.189	0.189	1.000	0.189	NA
1998	Spatiotemporal	-	0.000	0.007	1.000	0.020	0.997
	Time-stationary	-	0.011	0.011	0.594	0.028	0.914
1999	Spatiotemporal	-	-0.009	0.038	0.964	0.066	0.314
	Time-stationary	-	0.006	0.027	0.934	0.066	0.359
2000	Spatiotemporal	-	-0.022	0.026	0.963	0.039	0.785
	Time-stationary	-	-0.017	0.022	0.999	0.044	0.717
2001	Spatiotemporal	-	-0.005	0.018	0.999	0.042	0.895
	Time-stationary	-	0.002	0.021	0.995	0.044	0.853
2002	Spatiotemporal	-	0.000	0.020	0.948	0.050	0.755
	Time-stationary	-	0.012	0.020	0.947	0.057	0.691
2003	Spatiotemporal	-	-0.017	0.021	0.782	0.036	0.403

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
	Time-stationary	-	-0.004	0.010	0.928	0.017	0.244
2004	Spatiotemporal	-	-0.006	0.016	0.871	0.036	0.796
	Time-stationary	-	-0.005	0.017	0.918	0.042	0.709
2005	Spatiotemporal	-	-0.003	0.008	0.993	0.032	0.695
	Time-stationary	-	-0.002	0.010	0.768	0.024	0.781
2006	Spatiotemporal	-	-0.001	0.014	0.881	0.039	0.584
	Time-stationary	-	0.000	0.013	0.899	0.036	0.605
2007	Spatiotemporal	-	-0.018	0.027	0.801	0.040	0.299
	Time-stationary	-	-0.010	0.023	0.890	0.037	0.279
2008	Spatiotemporal	-	-0.020	0.024	0.770	0.034	0.291
	Time-stationary	-	-0.004	0.007	0.935	0.012	0.448
2009	Spatiotemporal	-	-0.010	0.020	0.851	0.031	0.301
	Time-stationary	-	-0.008	0.019	0.900	0.029	0.292
2010	Spatiotemporal	-	-0.005	0.009	0.901	0.019	0.482
	Time-stationary	-	-0.008	0.012	0.888	0.021	0.328
2011	Spatiotemporal	-	-0.004	0.009	0.946	0.019	0.412
	Time-stationary	-	-0.006	0.011	0.923	0.020	0.370
2012	Spatiotemporal	-	-0.004	0.004	0.531	0.006	0.579
	Time-stationary	-	-0.004	0.005	0.945	0.008	0.474
2013	Spatiotemporal	-	-0.001	0.006	0.850	0.009	0.705
	Time-stationary	-	-0.002	0.007	0.939	0.010	0.672
2014	Spatiotemporal	-	-0.003	0.004	0.821	0.007	0.874
	Time-stationary	-	-0.003	0.004	0.991	0.012	0.567
2015	Spatiotemporal	-	-0.001	0.001	0.997	0.003	0.892
	Time-stationary	-	-0.002	0.003	0.940	0.006	0.696
2016	Spatiotemporal	-	-0.004	0.010	0.985	0.017	0.985
	Time-stationary	-	0.002	0.018	0.971	0.036	0.925

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
2017	Spatiotemporal	-	-0.001	0.001	1.000	0.001	NA
	Time-stationary	-	-0.008	0.008	1.000	0.008	NA
2018	Spatiotemporal	-	-0.001	0.002	0.994	0.002	0.945
	Time-stationary	-	-0.002	0.003	1.000	0.004	0.155
1990–2018	Spatiotemporal	12 422	-0.007	0.013	0.862	0.028	0.720
	Time-stationary	13 221	-0.005	0.013	0.901	0.029	0.648

Supplementary Table 13. In-sample model fit (WAIC) and out-of-sample validation metrics (ICT) for Southeast Asia at the level of individual datapoints, from ten-fold cross-validation, for all model regions
Out-of-sample performance was aggregated over 1990–2018 and is also provided for individual model years, and is given for both spatiotemporal and time-stationary model variants. WAIC is only meaningful for the in-sample comparison (all years). Mean abs. error: Mean absolute error. 95% cov.: 95% coverage. Corr.: Correlation.

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
1990	Spatiotemporal	-	-0.031	0.099	0.912	0.149	0.708
	Time-stationary	-	-0.052	0.098	0.941	0.150	0.721
1991	Spatiotemporal	-	0.031	0.031	1.000	0.041	1.000
	Time-stationary	-	0.117	0.117	0.777	0.147	1.000
1992	Spatiotemporal	-	0.001	0.049	1.000	0.084	0.758
	Time-stationary	-	0.194	0.194	0.817	0.228	0.394
1993	Spatiotemporal	-	-0.013	0.013	1.000	0.013	NA
	Time-stationary	-	-0.152	0.152	1.000	0.152	NA
1994	Spatiotemporal	-	-0.034	0.135	0.501	0.164	0.753
	Time-stationary	-	0.010	0.180	0.521	0.205	0.756
1995	Spatiotemporal	-	-0.020	0.125	0.822	0.168	-0.229
	Time-stationary	-	-0.005	0.110	1.000	0.136	0.237
1996	Spatiotemporal	-	-0.015	0.060	1.000	0.070	0.693
	Time-stationary	-	0.063	0.081	0.771	0.103	0.642
1997	Spatiotemporal	-	0.002	0.047	0.820	0.061	0.949
	Time-stationary	-	0.090	0.130	0.518	0.166	0.639

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
1998	Spatiotemporal	-	0.152	0.226	0.960	0.297	0.287
	Time-stationary	-	0.082	0.146	0.955	0.174	0.912
1999	Spatiotemporal	-	0.038	0.066	1.000	0.104	0.931
	Time-stationary	-	0.021	0.135	0.965	0.164	0.845
2000	Spatiotemporal	-	0.004	0.030	1.000	0.065	0.962
	Time-stationary	-	-0.003	0.057	0.585	0.097	0.939
2001	Spatiotemporal	-	0.000	0.076	0.919	0.131	0.512
	Time-stationary	-	-0.009	0.094	0.779	0.150	0.336
2002	Spatiotemporal	-	-0.019	0.093	0.875	0.129	0.761
	Time-stationary	-	0.056	0.122	0.573	0.188	0.344
2003	Spatiotemporal	-	-0.011	0.059	0.870	0.097	0.686
	Time-stationary	-	-0.017	0.069	0.747	0.102	0.630
2004	Spatiotemporal	-	-0.009	0.043	0.800	0.067	0.392
	Time-stationary	-	-0.005	0.042	0.717	0.067	0.449
2005	Spatiotemporal	-	-0.009	0.038	0.828	0.060	0.865
	Time-stationary	-	0.000	0.047	0.779	0.077	0.760
2006	Spatiotemporal	-	-0.001	0.029	0.802	0.074	0.815
	Time-stationary	-	0.000	0.033	0.788	0.074	0.811
2007	Spatiotemporal	-	0.001	0.015	0.734	0.028	0.523
	Time-stationary	-	-0.005	0.019	0.789	0.032	0.387
2008	Spatiotemporal	-	-0.003	0.008	0.944	0.018	0.635
	Time-stationary	-	-0.013	0.019	0.812	0.032	0.215
2009	Spatiotemporal	-	-0.005	0.032	0.793	0.059	0.134
	Time-stationary	-	-0.009	0.039	0.759	0.058	-0.081
2010	Spatiotemporal	-	0.008	0.019	0.928	0.063	0.274
	Time-stationary	-	0.001	0.025	0.750	0.066	0.117
2011	Spatiotemporal	-	-0.006	0.035	0.874	0.071	0.576

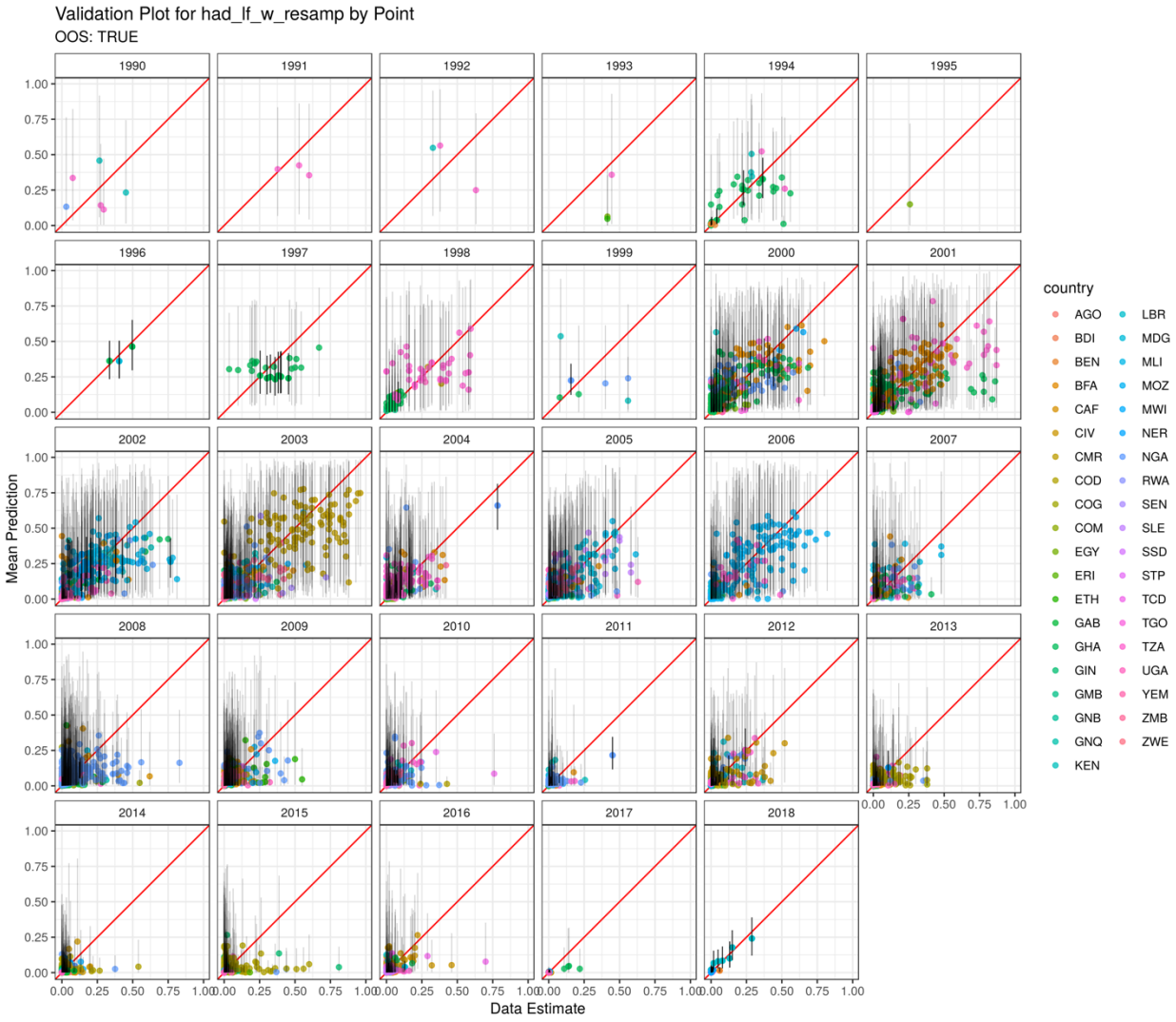
Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
	Time-stationary	-	0.009	0.033	0.711	0.062	0.586
2012	Spatiotemporal	-	-0.005	0.012	0.978	0.028	0.888
	Time-stationary	-	-0.004	0.019	0.855	0.031	0.835
2013	Spatiotemporal	-	-0.004	0.006	1.000	0.013	0.857
	Time-stationary	-	-0.011	0.015	0.793	0.025	0.462
2014	Spatiotemporal	-	-0.002	0.004	0.983	0.009	0.893
	Time-stationary	-	-0.003	0.009	0.883	0.016	0.654
2015	Spatiotemporal	-	-0.002	0.004	0.981	0.015	0.726
	Time-stationary	-	-0.008	0.011	0.826	0.023	0.510
2016	Spatiotemporal	-	-0.002	0.002	1.000	0.005	1.000
	Time-stationary	-	-0.005	0.014	0.770	0.020	0.965
2017	Spatiotemporal	-	-0.001	0.008	0.940	0.014	0.705
	Time-stationary	-	-0.005	0.012	0.929	0.020	0.058
2018	Spatiotemporal	-	-0.001	0.001	1.000	0.003	0.999
	Time-stationary	-	-0.002	0.004	0.826	0.006	0.758
1990–2018	Spatiotemporal	6825	-0.002	0.021	0.897	0.055	0.861
	Time-stationary	7893	-0.002	0.028	0.802	0.061	0.820

Supplementary Table 14. In-sample model fit (WAIC) and out-of-sample validation metrics (ICT) for Hispaniola at the level of individual data points, from ten-fold cross-validation, for all model regions
Out-of-sample performance was aggregated over 1990–2018 and is also provided for those individual model years for which prevalence data were available (no prevalence data were present for this region for 1990, 1992, 1995–1997, 2006, 2009, 2011, and 2013), and is given for both spatiotemporal and time-stationary model variants. WAIC is only meaningful for the in-sample comparison (all years). Mean abs. error: Mean absolute error. 95% cov.: 95% coverage. Corr.: Correlation.

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
1991	Spatiotemporal	-	-0.084	0.084	1.000	0.084	NA
	Time-stationary	-	0.010	0.010	1.000	0.010	NA
1993	Spatiotemporal	-	0.266	0.266	1.000	0.266	NA
	Time-stationary	-	0.398	0.398	0.000	0.398	NA

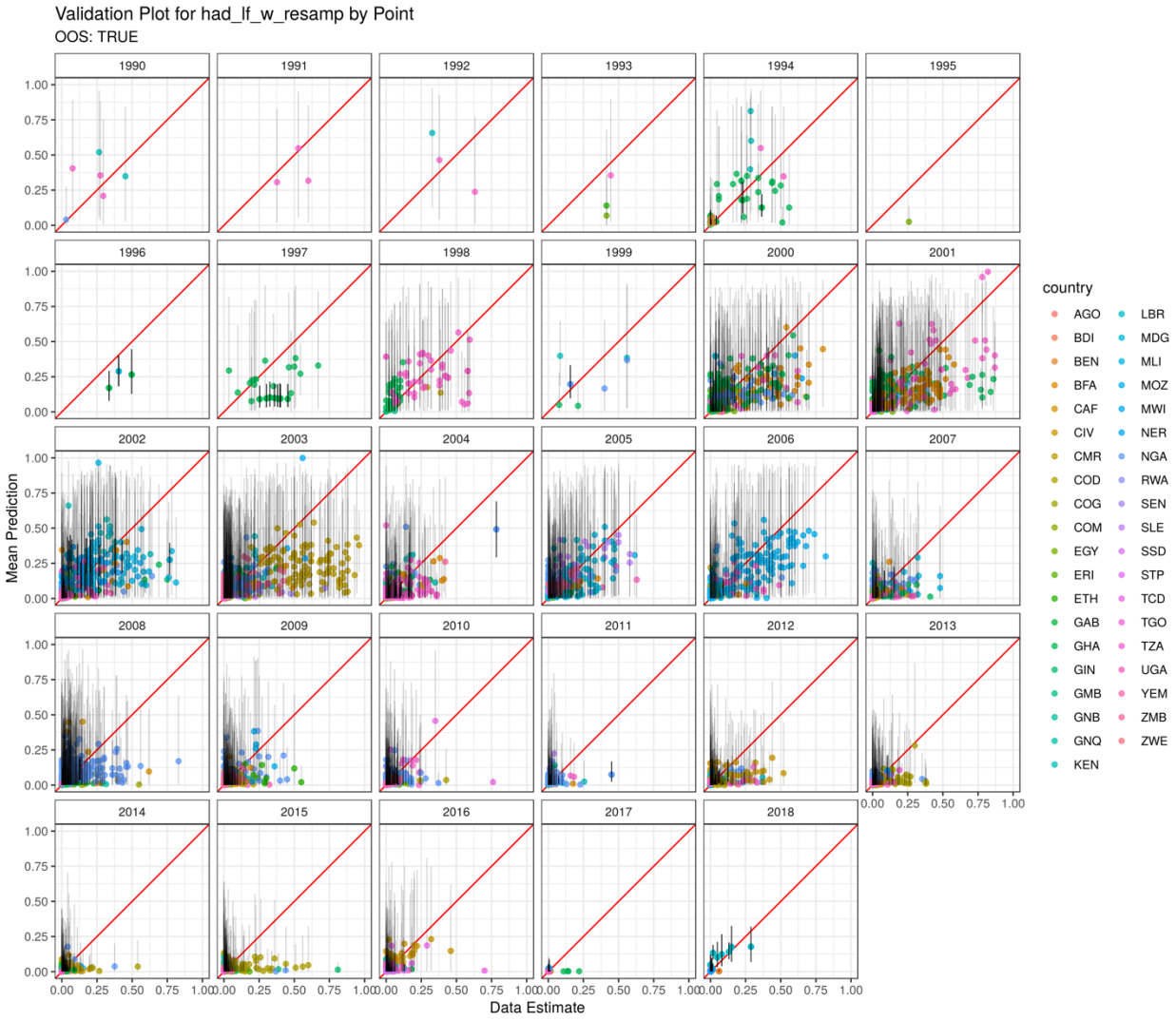
Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
1994	Spatiotemporal	-	0.035	0.092	1.000	0.094	-0.152
	Time-stationary	-	0.021	0.051	1.000	0.056	0.454
1998	Spatiotemporal	-	-0.208	0.251	0.682	0.295	0.205
	Time-stationary	-	-0.003	0.151	0.506	0.173	0.320
1999	Spatiotemporal	-	0.364	0.364	0.000	0.364	Inf
	Time-stationary	-	0.411	0.411	0.000	0.411	NA
2000	Spatiotemporal	-	0.071	0.176	0.410	0.202	0.080
	Time-stationary	-	0.063	0.163	0.956	0.191	0.298
2001	Spatiotemporal	-	-0.022	0.036	1.000	0.044	0.806
	Time-stationary	-	0.041	0.045	0.694	0.053	0.694
2002	Spatiotemporal	-	0.024	0.143	0.925	0.197	0.140
	Time-stationary	-	0.214	0.259	0.458	0.286	0.007
2003	Spatiotemporal	-	-0.005	0.077	0.870	0.097	-0.029
	Time-stationary	-	0.099	0.099	0.687	0.124	0.490
2004	Spatiotemporal	-	0.001	0.063	0.560	0.078	0.500
	Time-stationary	-	-0.019	0.035	1.000	0.045	0.888
2005	Spatiotemporal	-	-0.009	0.055	1.000	0.084	0.499
	Time-stationary	-	0.002	0.040	1.000	0.057	0.713
2007	Spatiotemporal	-	-0.029	0.180	1.000	0.181	-1.000
	Time-stationary	-	0.085	0.085	1.000	0.103	1.000
2008	Spatiotemporal	-	-0.023	0.102	0.809	0.131	-0.198
	Time-stationary	-	-0.009	0.093	1.000	0.101	0.475
2010	Spatiotemporal	-	-0.007	0.012	1.000	0.019	0.703
	Time-stationary	-	-0.029	0.029	0.750	0.042	0.854
2012	Spatiotemporal	-	-0.002	0.002	1.000	0.002	1.000
	Time-stationary	-	-0.009	0.009	1.000	0.009	1.000
2014	Spatiotemporal	-	-0.001	0.004	0.912	0.007	0.801

Year	Model	WAIC	Mean error	Mean abs. error	95% cov.	RMSE	Corr.
	Time-stationary	-	-0.008	0.009	0.947	0.011	0.767
2015	Spatiotemporal	-	-0.001	0.006	0.875	0.009	0.766
	Time-stationary	-	-0.007	0.009	0.991	0.011	0.782
2016	Spatiotemporal	-	-0.026	0.026	1.000	0.029	1.000
	Time-stationary	-	0.046	0.049	0.834	0.053	0.880
2017	Spatiotemporal	-	0.001	0.006	0.904	0.010	0.392
	Time-stationary	-	-0.002	0.006	0.990	0.009	0.592
2018	Spatiotemporal	-	-0.001	0.002	1.000	0.002	0.880
	Time-stationary	-	-0.008	0.009	0.978	0.010	-0.540
1990–2018	Spatiotemporal	1171	-0.001	0.041	0.895	0.086	0.720
	Time-stationary	1322	0.027	0.049	0.863	0.095	0.657



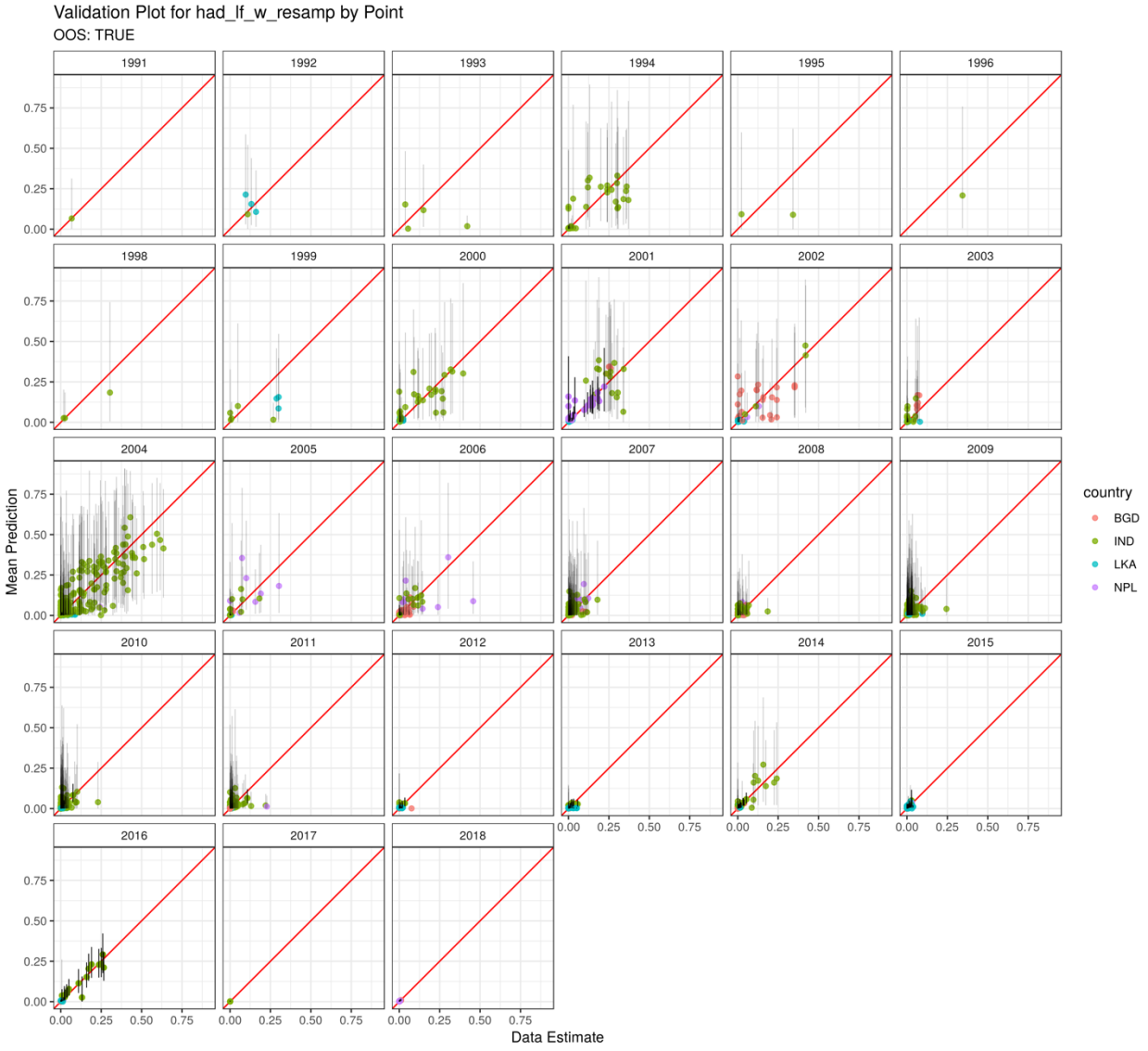
Supplementary Figure 36. Spatiotemporal model validation scatterplots for Africa and Yemen

Reported prevalence (post-crosswalk) versus mean out-of-sample predictions for individual datapoints in Africa, by year and country, from the spatiotemporal model. Vertical bars represent 95% UI, and red lines indicate equivalence.



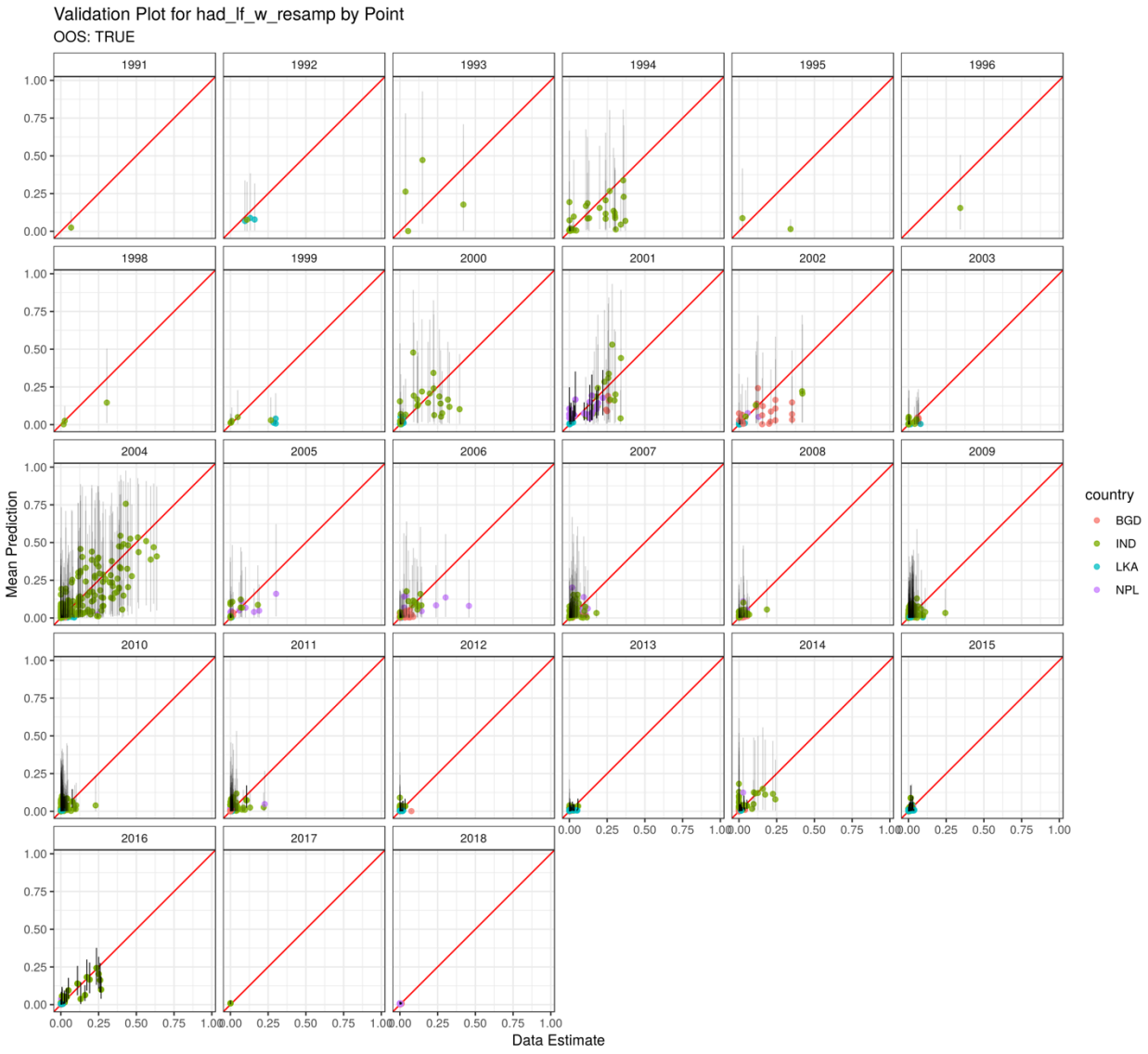
Supplementary Figure 37. Time-stationary model validation scatterplots for Africa and Yemen

Reported prevalence (post-crosswalk) versus mean out-of-sample predictions for individual datapoints in Africa, by year and country, from the time-stationary model. Vertical bars represent 95% UI, and red lines indicate equivalence.



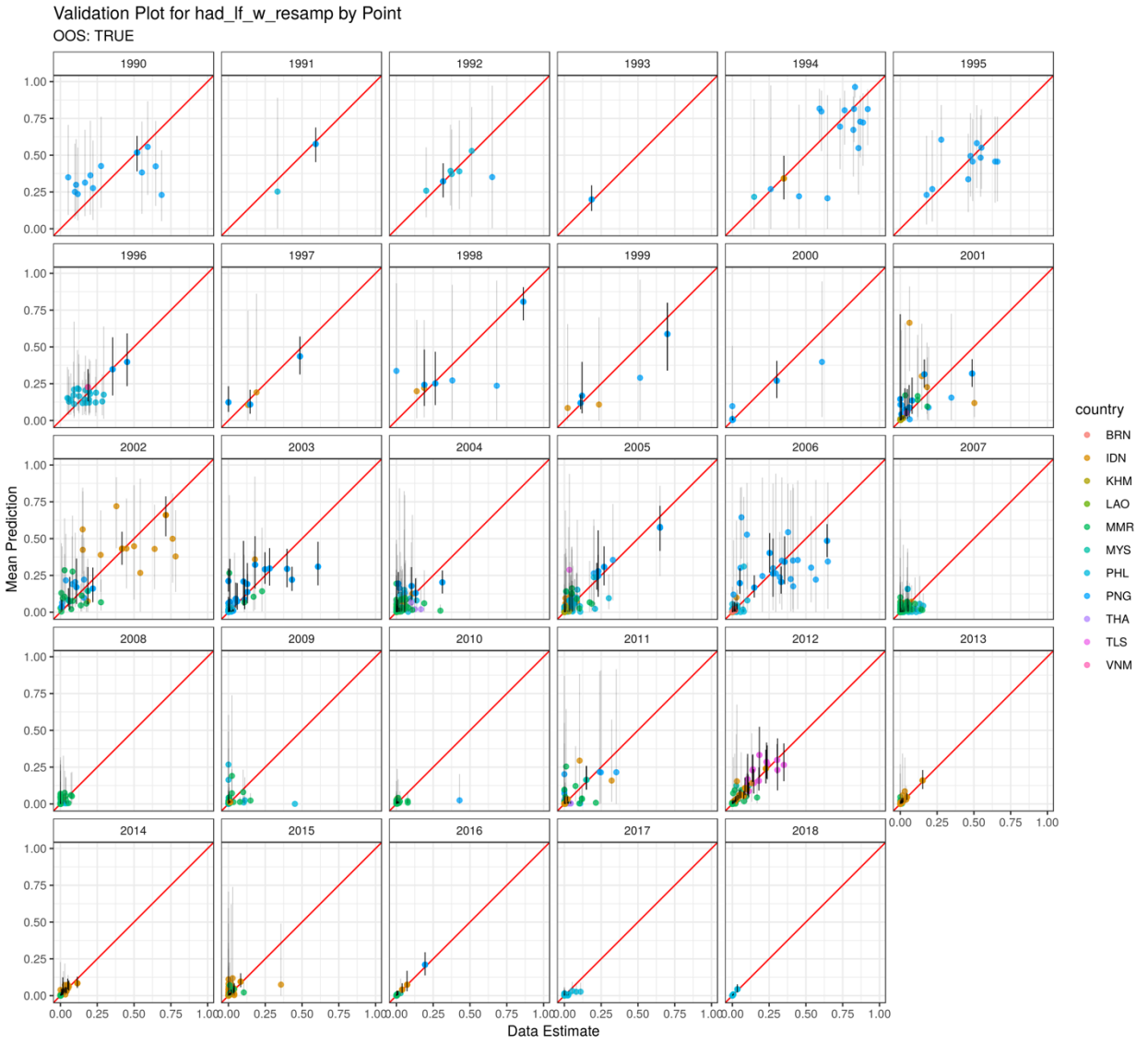
Supplementary Figure 38. Spatiotemporal model validation scatterplots for South Asia

Reported prevalence (post-crosswalk) versus mean out-of-sample predictions for individual datapoints in South Asia, by year and country, from the spatiotemporal model. Vertical bars represent 95% UI, and red lines indicate equivalence.



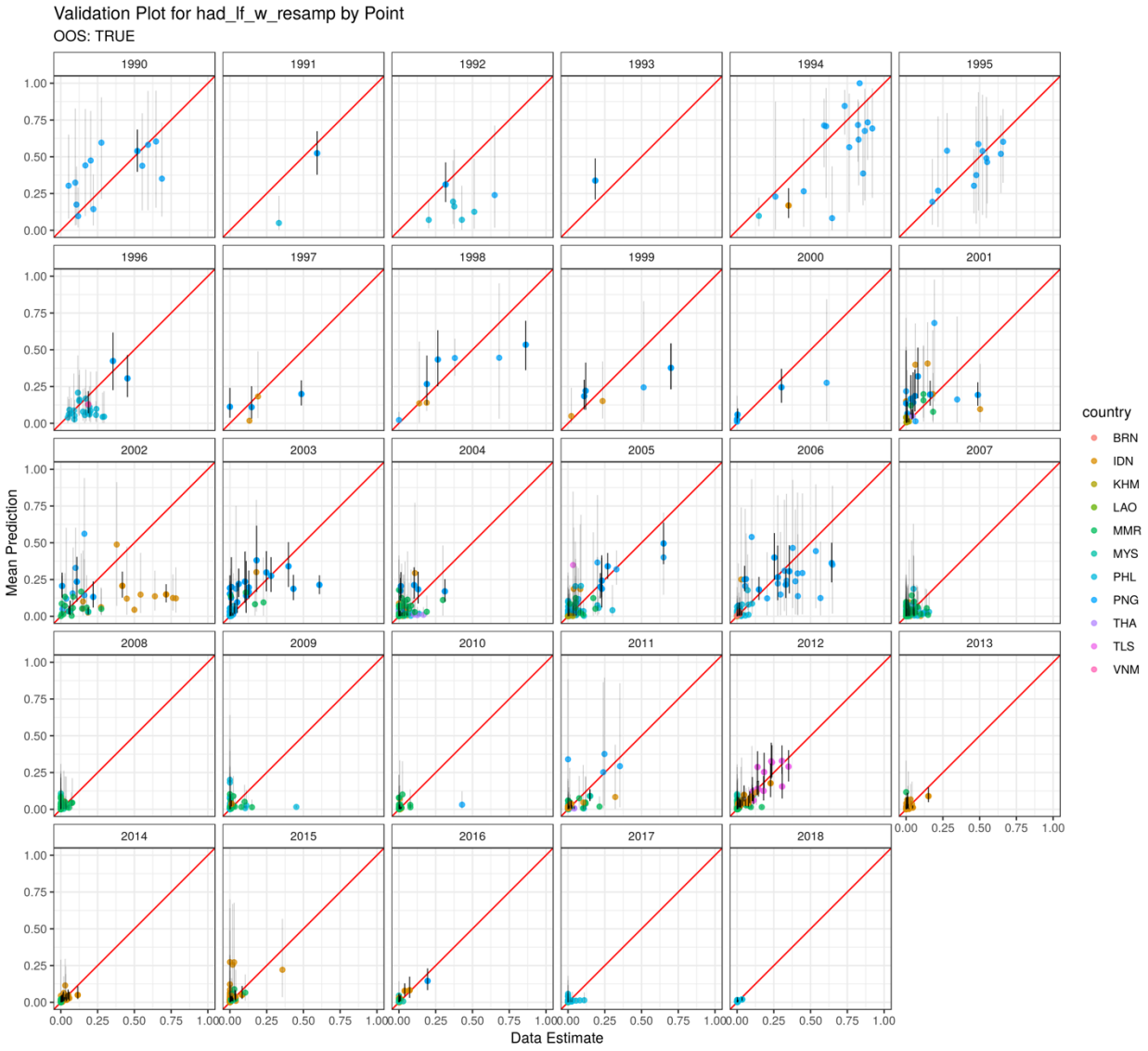
Supplementary Figure 16. Time-stationary model validation scatterplots for South Asia

Reported prevalence (post-crosswalk) versus mean out-of-sample predictions for individual datapoints in South Asia, by year and country, from the time-stationary model. Vertical bars represent 95% UI, and red lines indicate equivalence.



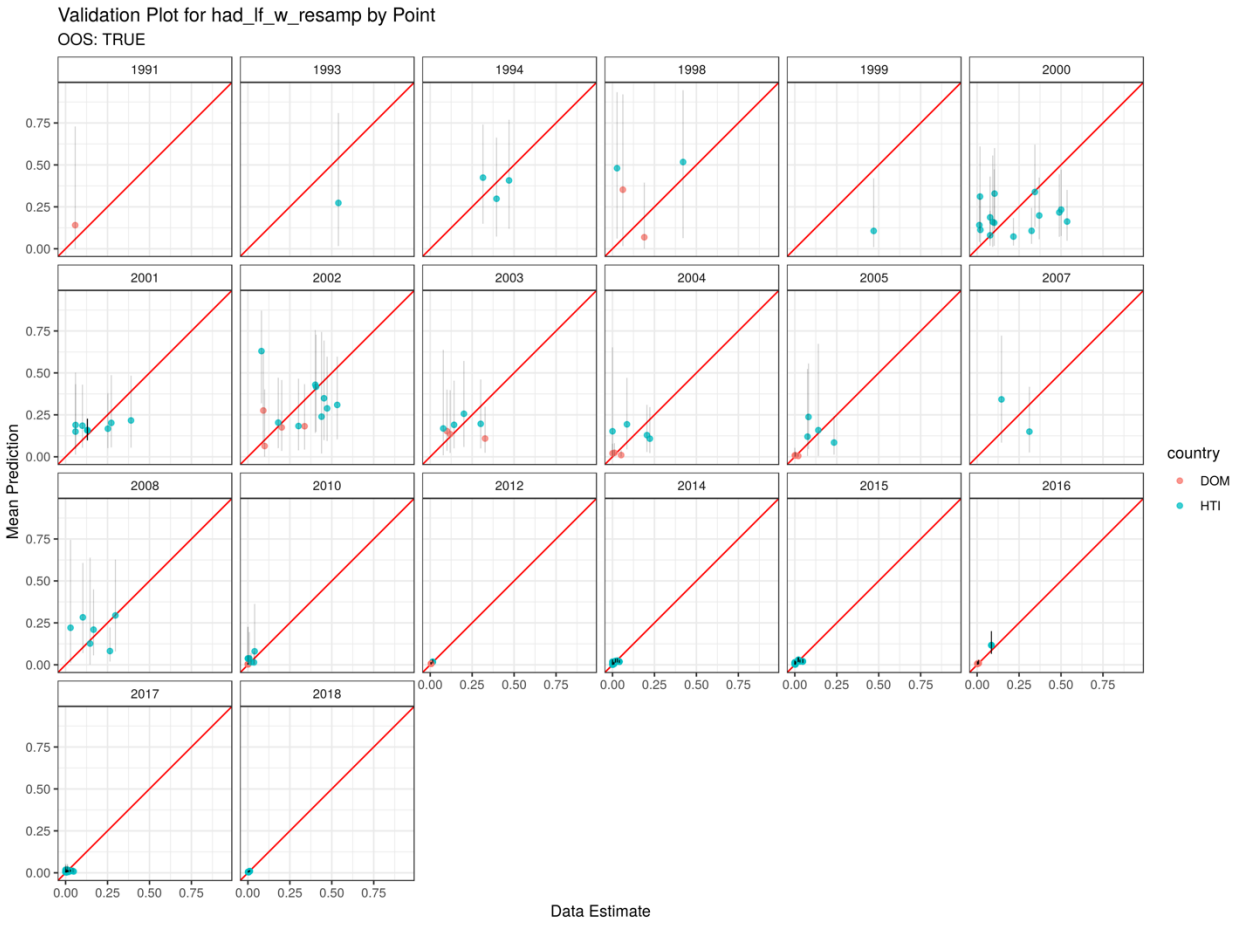
Supplementary Figure 17. Spatiotemporal model validation scatterplots for Southeast Asia

Reported prevalence (post-crosswalk) versus mean out-of-sample predictions for individual data points in Southeast Asia, by year and country, from the spatiotemporal model. Vertical bars represent 95% UI, and red lines indicate equivalence.



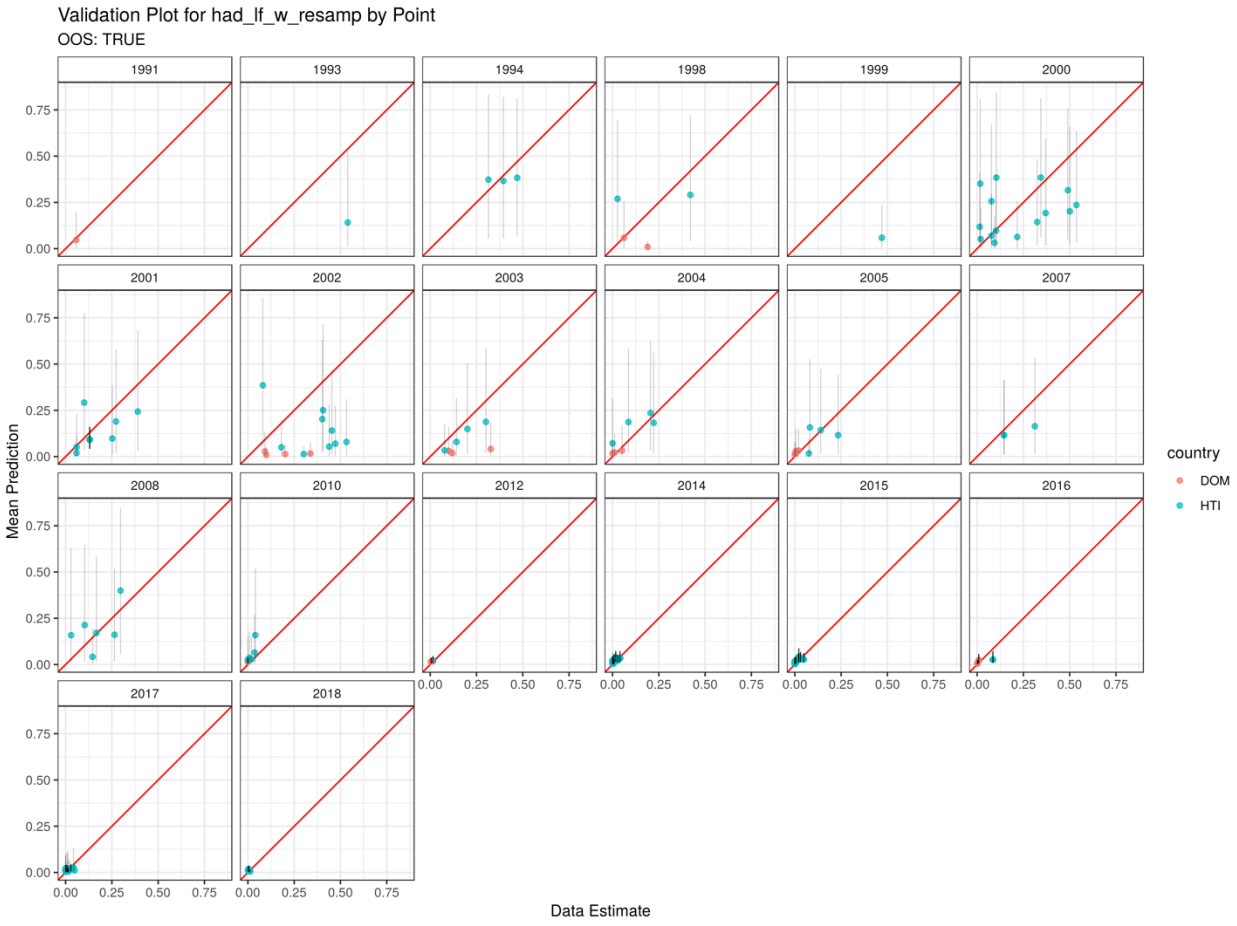
Supplementary Figure 18. Time-stationary model validation scatterplots for Southeast Asia

Reported prevalence (post-crosswalk) versus mean out-of-sample predictions for individual datapoints in Southeast Asia, by year and country, from the time-stationary model. Vertical bars represent 95% UI, and red lines indicate equivalence.



Supplementary Figure 42. Spatiotemporal model validation scatterplots for Hispaniola

Reported prevalence (post-crosswalk) versus mean out-of-sample predictions for individual datapoints in Hispaniola, by year and country, from the spatiotemporal model. Vertical bars represent 95% UI, and red lines indicate equivalence.



Supplementary Figure 43. Time-stationary model validation scatterplots for Hispaniola

Reported prevalence (post-crosswalk) versus mean out-of-sample predictions for individual datapoints in Hispaniola, by year and country, from the time-stationary model. Vertical bars represent 95% UI, and red lines indicate equivalence.

5.5 Sensitivity analyses

5.5.1 Urbanicity and LF case estimates

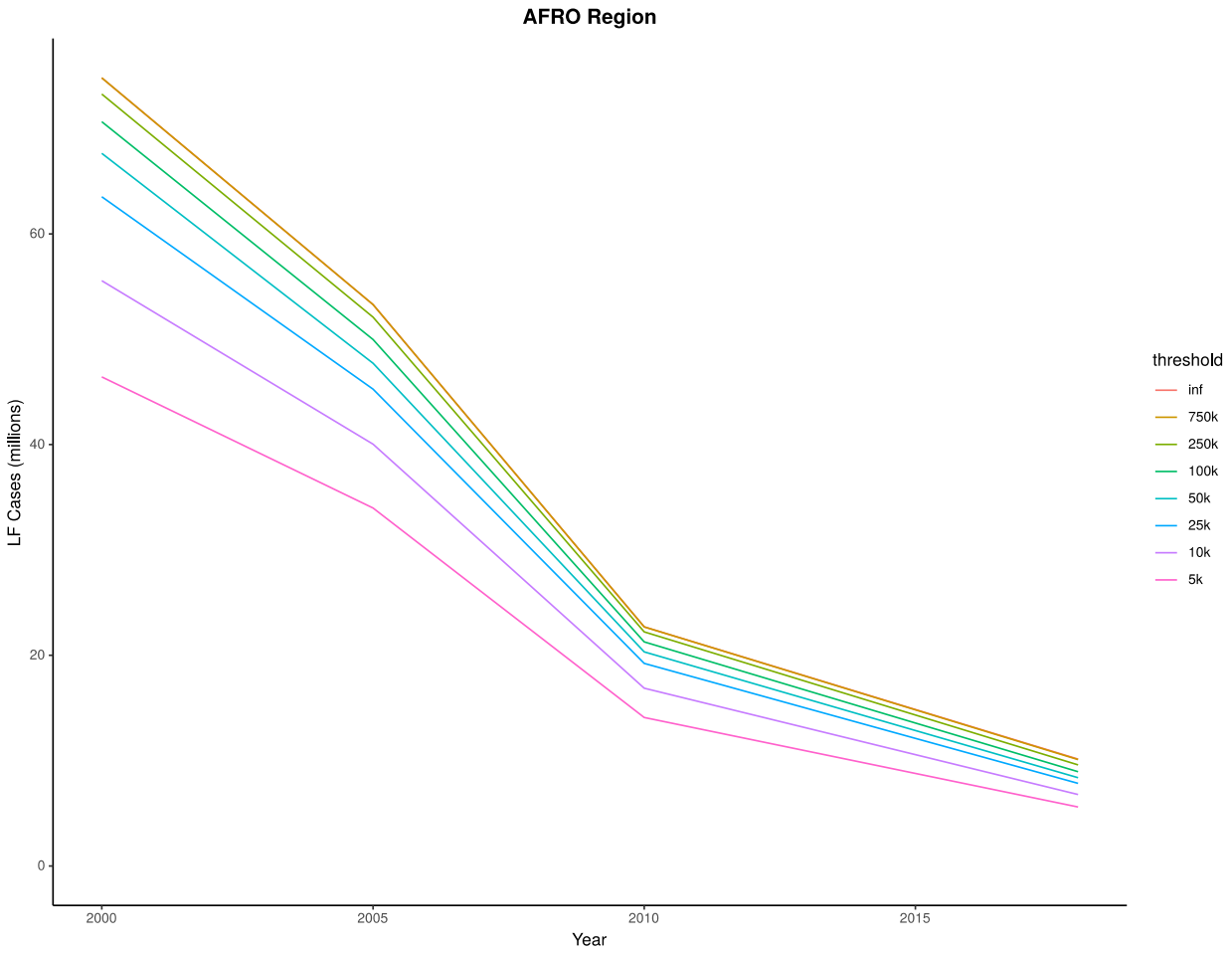
Core estimates of LF cases by region and year were derived from our model under the assumption that associations between human population density and LF prevalence are adequately captured by inclusion of population density as a covariate in the stacker submodels. However, there are limited LF prevalence data from urban areas[150] and urbanicity has typically been considered to be negatively correlated with LF prevalence. The application of spatially smoothed prevalence estimates derived largely from rural data sources could therefore potentially bias the estimates of regional and global LF cases upward when calculations include high population areas. We performed sensitivity analyses in which a series of progressively smaller population thresholds were applied during the calculation of estimated LF cases (ranging from 10,000 to 750,000 per 5 × 5-km grid cell). Any 5 × 5-km grid cell whose population count exceeded a given threshold was considered to have an LF prevalence of 0, thus removing its contribution to case estimates.

Results from this sensitivity analysis are displayed in Supplementary Figures 44–49. Population thresholds ranging from 750,000 down to 25,000 people per 5 × 5-km grid cell had only a minor impact on regional and global case estimates. In contrast, removal of grid cells with between 10,000 and 25,000 people per 5 × 5-km grid cell had a pronounced impact on case estimates for the SEARO region and globally.

5.5.2 Loiasis endemicity

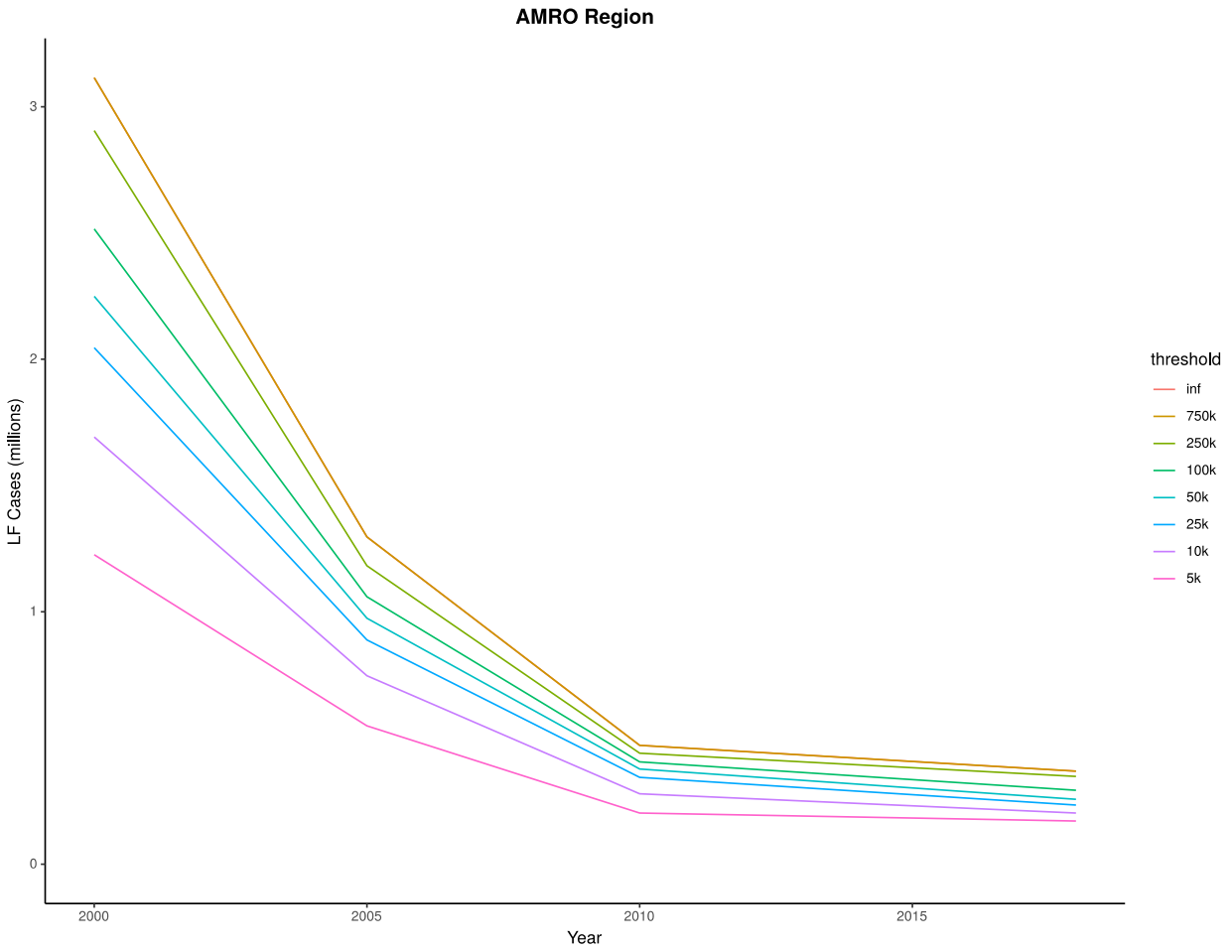
Previous studies have demonstrated cross-reactivity of circulating filarial antigen tests (ICT and FTS) for *W. bancrofti* with *Loa loa*, the filarial nematode responsible for loiasis[151]. In *Loa*-endemic areas (restricted to parts of central Africa), this cross-reactivity may lead to false positives for *W. bancrofti* and produce inflated estimates of LF prevalence. Work by Wanji and colleagues and others (reviewed by Kelly-Hope and colleagues[152]) have suggested low or zero endemicity of *W. bancrofti* in at least some areas of high *L. loa* endemicity, implying that MDA for LF may not be needed in some locations otherwise suggested as LF-endemic by surveys that have utilised antigen tests.

While we did not adjust for the possible cross-reactivity of LF antigen tests with *Loa loa* in our geospatial models of LF prevalence, we examined the possible impact of this cross-reactivity on our estimates. We first retrieved data on IU-level loiasis endemicity classification from ESPEN[153] for 2015 and identified the data in our LF dataset that hailed from those districts. In total, our dataset contains 1411 FTS or ICT survey observations (including both point- and polygon-level data) from IUs considered to be hyper- or meso-endemic for loiasis, from Central African Republic, Cameroon, Republic of Congo, Democratic Republic of Congo, Gabon, Equatorial Guinea, Nigeria, South Sudan, and Chad. By overlaying the districts that are hyper- or meso-endemic for loiasis on the WorldPop population raster and our LF mean prevalence raster for 2018, we calculated that these districts had a total estimated population of 104 877 440 individuals and contributed 1 524 163 cases (or 15.0% of the AFRO total) to our 2018 LF mean case estimates. These results suggest that our estimates of LF burden in Central Africa could be inflated if false positivity rates have been high in the available LF antigen survey data for this region. Additional surveys are needed to understand the true distribution and prevalence of LF in areas endemic for *L. loa*.



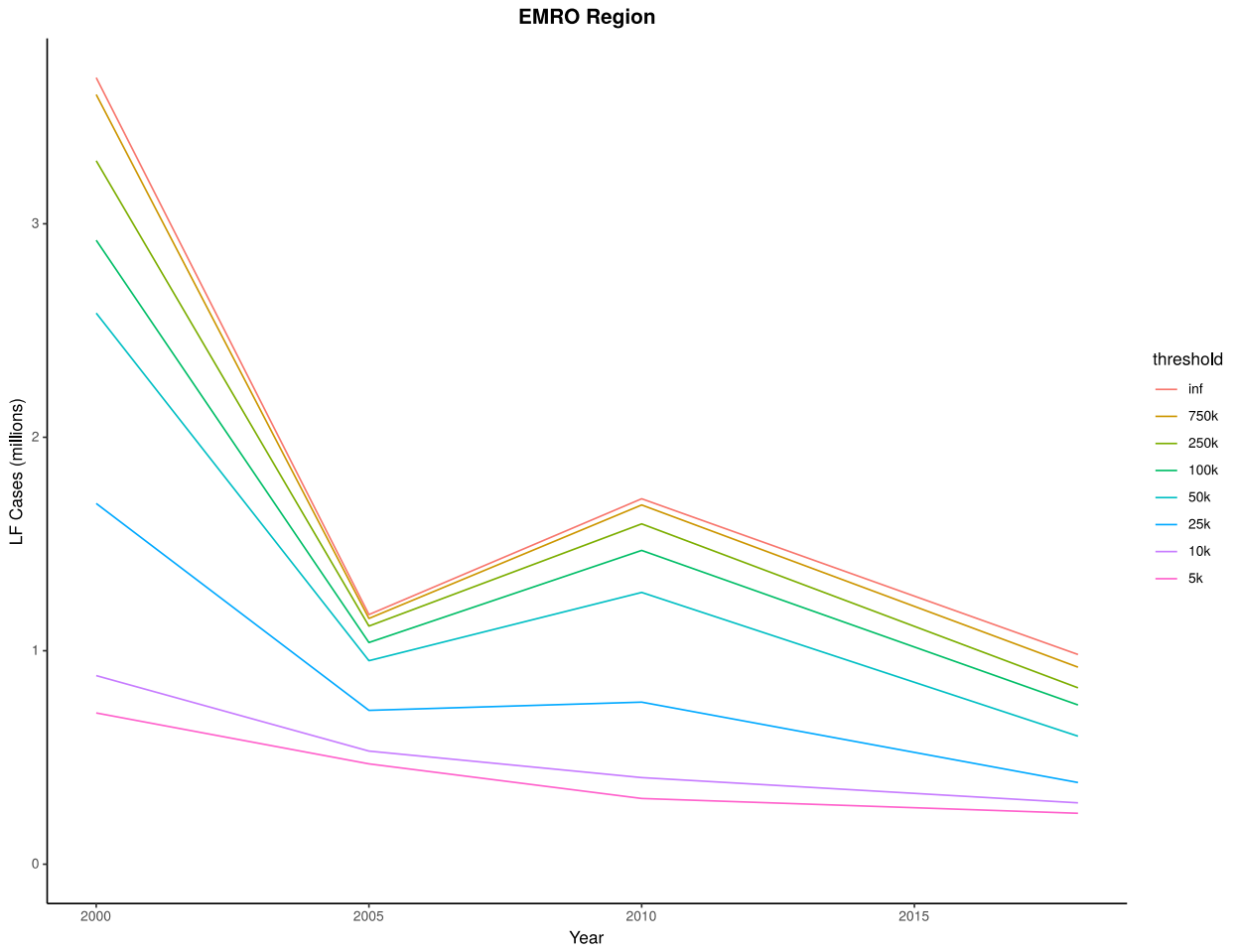
Supplementary Figure 44. Sensitivity of LF case estimates to varying population thresholds in the AFRO WHO region

Estimates of LF cases are displayed by model year (2000, 2005, 2010, 2018), using various population thresholds to remove the contributions of locations with high population density.



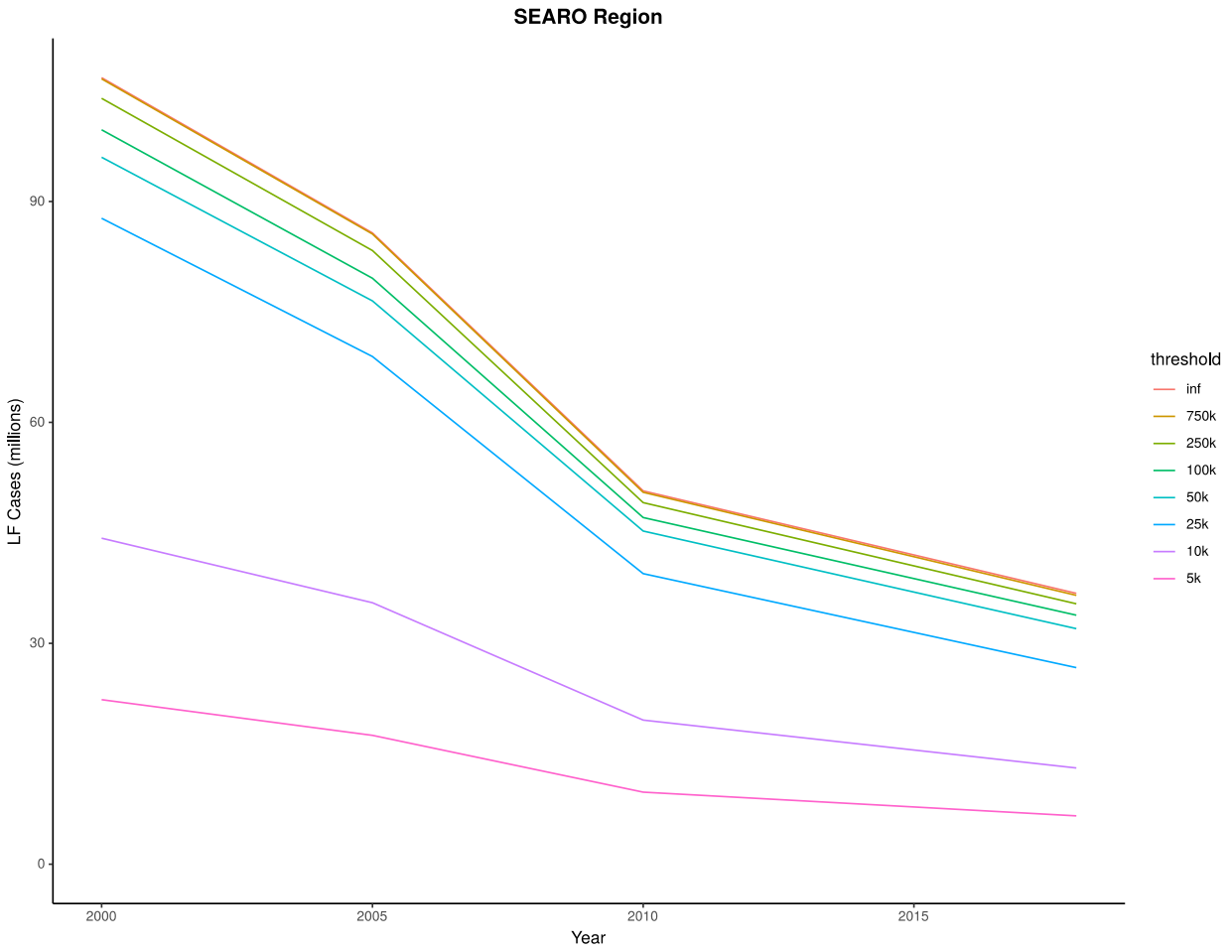
Supplementary Figure 45. Sensitivity of LF case estimates to varying population thresholds in the AMRO WHO region

Estimates of LF cases are displayed by model year (2000, 2005, 2010, 2018), using various population thresholds to remove the contributions of locations with high population density.



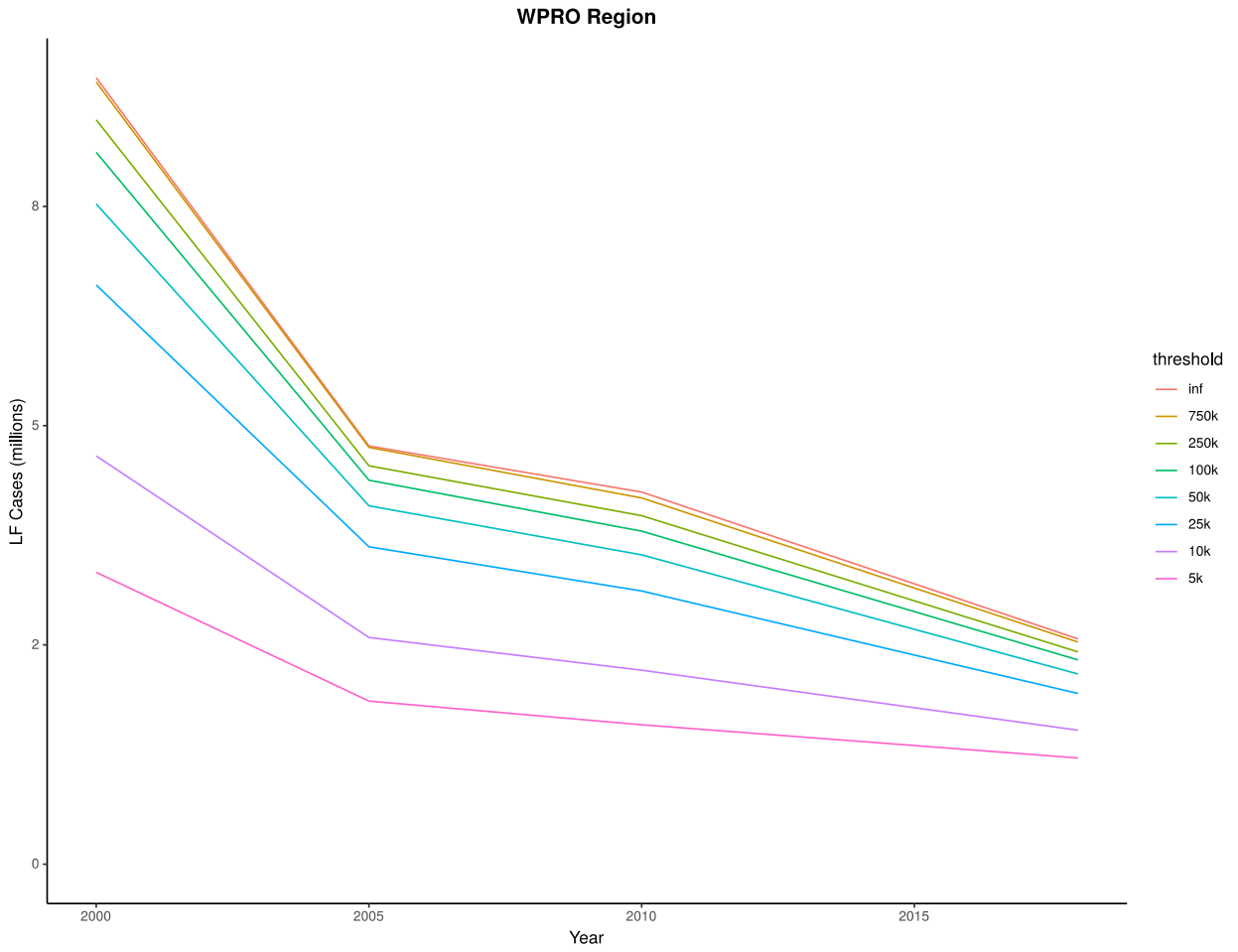
Supplementary Figure 46. Sensitivity of LF case estimates to varying population thresholds in the EMRO WHO region

Estimates of LF cases are displayed by model year (2000, 2005, 2010, 2018), using various population thresholds to remove the contributions of locations with high population density.



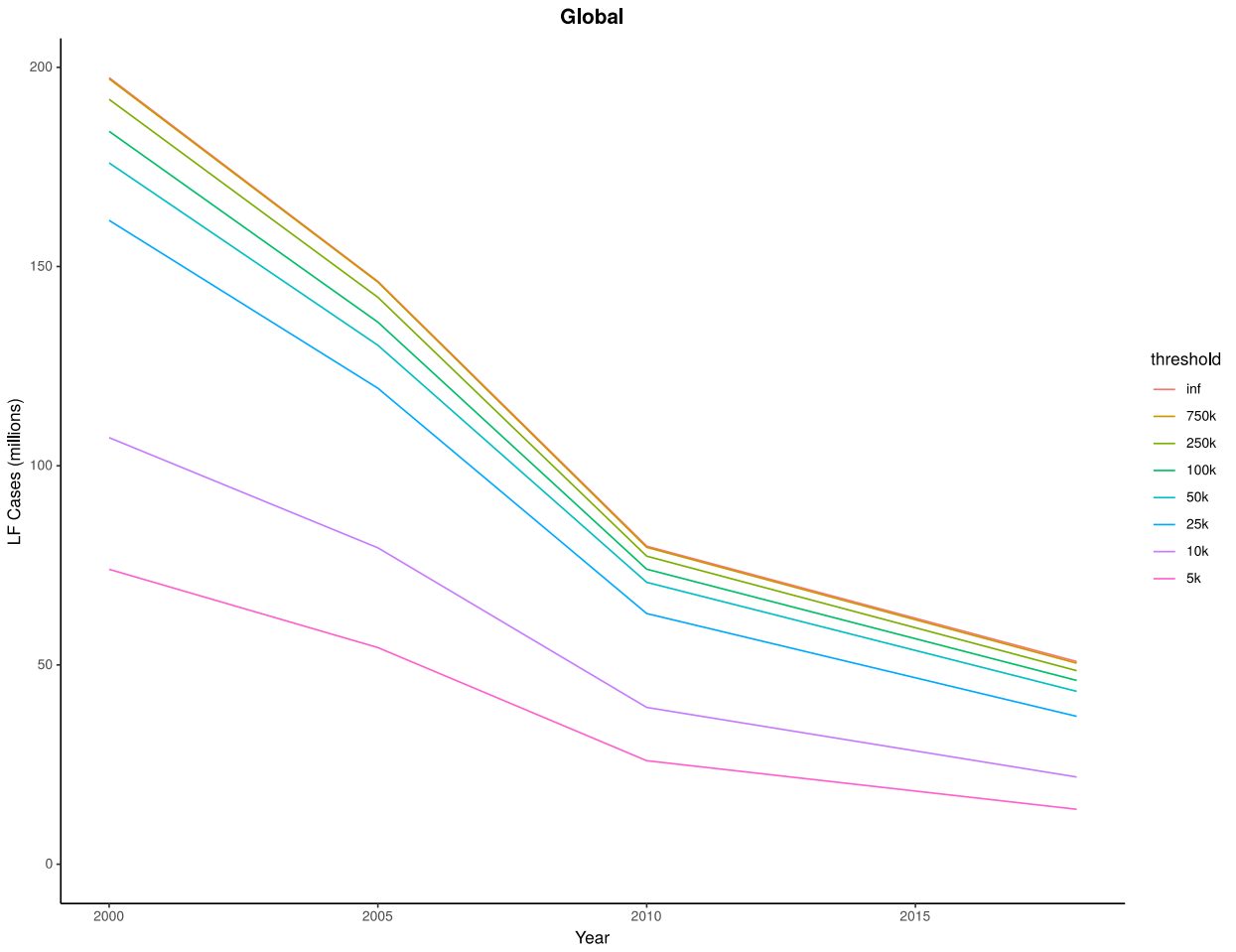
Supplementary Figure 47. Sensitivity of LF case estimates to varying population thresholds in the SEARO WHO region

Estimates of LF cases are displayed by model year (2000, 2005, 2010, 2018), using various population thresholds to remove the contributions of locations with high population density.



Supplementary Figure 48. Sensitivity of LF case estimates to varying population thresholds in the WPRO WHO region

Estimates of LF cases are displayed by model year (2000, 2005, 2010, 2018), using various population thresholds to remove the contributions of locations with high population density.



Supplementary Figure 49. Sensitivity of LF case estimates to varying population thresholds, globally

Estimates of LF cases are displayed by model year (2000, 2005, 2010, 2018), using various population thresholds to remove the contributions of locations with high population density.

5.6 Non-MBG estimation

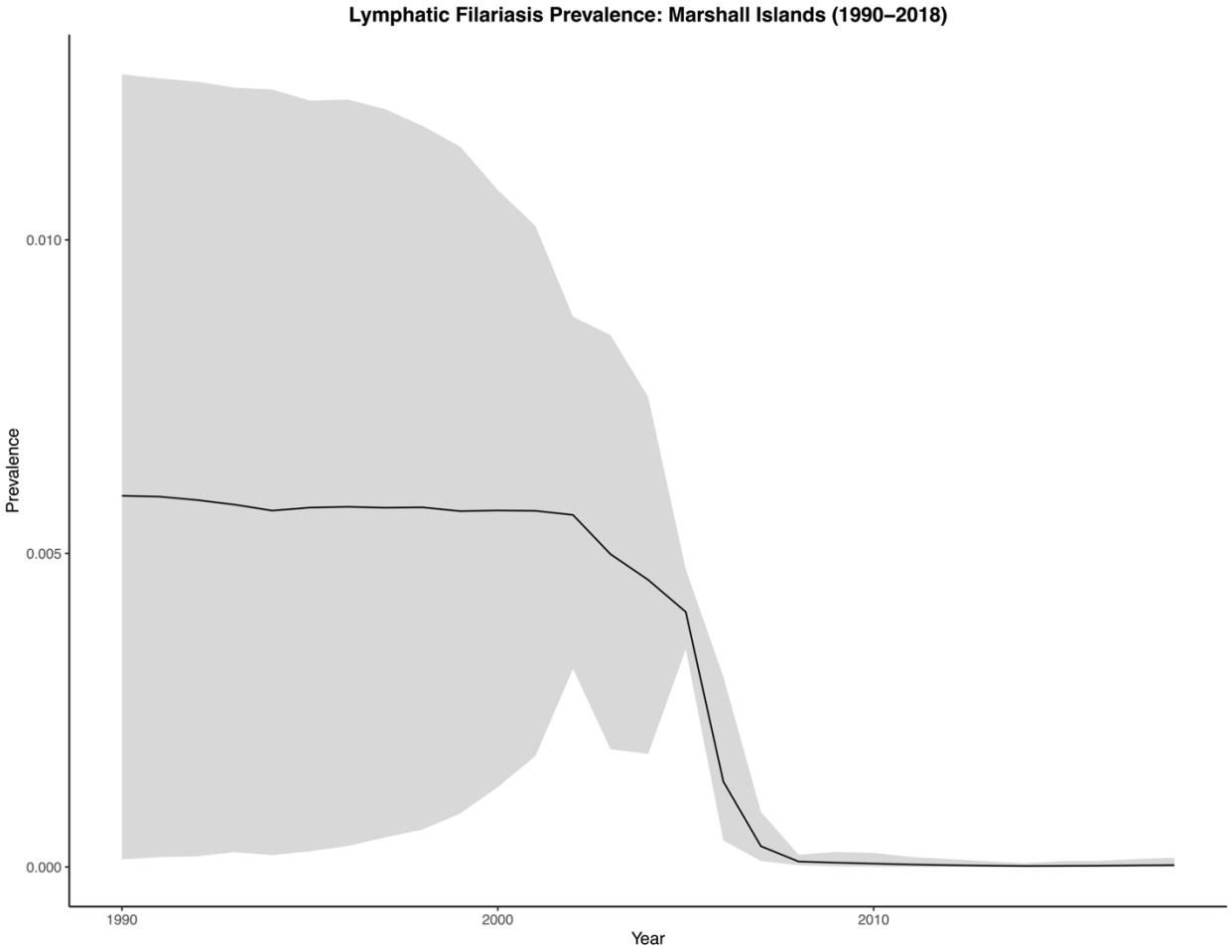
Simple time series prevalence models were constructed for LF-endemic countries outside the core modelling regions of Africa, Asia, and Hispaniola (Supplementary Table 11). These countries represent island nations with small geographical area (several Micronesian and Polynesian nations, plus the Maldives) or South American nations with focal endemicity (Guyana and Brazil). Modelling strategies differed among these countries, depending on the geographical nature of their LF endemicity and available data. For countries in which the entire nation is a single IU, or for which available data are considered nationally representative or could not be reliably geo-referenced to smaller administrative levels, a single national prevalence model was fit. In other nations, prevalence was modelled for subnational administrative units, and national prevalence was calculated as a population-weighted average of subnational prevalence estimates, with zero prevalence assumed for areas considered non-endemic. Due to the small geographic areas of these non-MBG model regions and the absence of highly-resolved gridded population data for many of these countries, population weights were often derived from single-year census data, and population fractions were treated as constant across model years. Where multiple years of census data were available for a given country, the census year closest to 2009 (taken as the approximate midpoint of the model prediction timeframe, 2000–2017) was used.

Polygon data were first resampled to point data as in the MBG models. Logistic regression models were then fit with INLA for area i and year t. The following logistic regression model was fit for each country that was treated as a single unit:

$$Y_{i,t} \sim \text{Binomial}\left(p_{i,t}, N_{i,t}\right)$$

$$\text{logit}\left(p_{i,t}\right) = \beta_0 + f_t$$

Notation is as for MBG models in Supplementary Section 5.3.2, with f_t representing a single-order random walk (RW1) model on calendar year. For those countries modelled at a subnational level, two competing models were fit: (1) a single RW1 model with subnational random effects (i.i.d); and (2) independent RW1 models for each subunit. Final models for each country were selected based on comparison of Watanabe-Akaike Information Criterion (WAIC) scores and examination of posterior prediction plots. Brazil was evaluated with an additional model, featuring separate AR(1) temporal models per subunit, as this yielded a more stable time series. Final models selected for each region are listed in Supplementary Table 11. Priors were as in MBG models (Supplementary Section 5.3.3) for hyperparameters common to both model frameworks. RW1 models were specified with a penalized complexity (PC) prior on the log of the precision parameter τ as $\text{loggamma}(0.5, 0.01)$, while the AR(1) model for Brazil was specified with a $\text{loggamma}(1, 0.0005)$ prior on the precision parameter κ and a $\text{N}(\mu = 0, \sigma^2 = 1/0.15)$ prior on the correlation parameter. Predictions of national prevalence were derived from 1000 posterior distribution draws. The estimated model time series for Marshall Islands (1990–2018) is provided in Supplementary Figure 50 as a representative example of the non-MBG country models.



Supplementary Figure 50. Non-MBG example result

Model results from a non-MBG time series model for Marshall Islands (1990–2018), showing mean predicted prevalence (ICT) with 95% UI (gray shading) from 1000 posterior draws.

Supplementary Table 15. Non-MBG geographies, modelling approaches, and sources of subnational population data, where applicable.

Country	Approach	Subnational population data source
American Samoa	Model by district, with independent RW1 models per district	U.S. Census Bureau. 2013. 2010 Census American Samoa.[154]
		Kiribati. 2016. 2015 Population and Housing Census.{Citation}
Brazil	Model by city in Recife Metropolitan Area, with independent AR1 temporal models by city	Brazilian Institute of Geography and Statistics. 2019. Resident population estimates for municipalities and Brazilian federation units with reference date on July 1, 2019.[155]
Cook Islands	National model	N/A
Federated States of Micronesia	Model by state, with independent RW1 models per state	Government of the Federated States of Micronesia. 2012. People.[156]
Fiji	Model by division, with independent RW1 models per division	Fiji Bureau of Statistics. 2017. Fiji Population and Housing Census, 2017.[157]
French Polynesia	Model by administrative subdivision, with independent RW1 models per subdivision	Institute of Statistics of French Polynesia. 2017. Population census 2017.[158]
Guyana	Model by endemic state, with a single RW1 model and random effects by state	WorldPop[159,160]
Kiribati	Model endemic islands, with independent RW1 models per island	Kiribati. 2016. 2015 Population and Housing Census.[161]
Maldives	National model	N/A
Marshall Islands	Model two endemic islands, with independent RW1 models per island	Republic of the Marshall Islands. 2012. The RMI 2011 Census of Population and Housing.[162]Republic of the Marshall Islands. 2012. The RMI 2011 Census of Population and Housing.[162]
New Caledonia	Model for Loyalty Islands vs. remainder of country, with a single RW1 model and random effects by subunit	New Caledonia Institute of Statistics and Economic Studies. 2015. Annual population estimates.[163]
Niue	National model	N/A
Palau	Model the single endemic state (Ngardmau)	Office of Planning and Statistics, Republic of Palau. 2005. Census of Population and Housing.
Samoa	Model by island, with independent RW1 models per island	Samoa Bureau of Statistics. 2011. Population and Housing Census 2011: analytical report.[164]
Tonga	National model	N/A
Tuvalu	National model	N/A
Vanuatu	Model by province, with Ambrym Island treated as a separate province due to its unique programmatic history; single RW1 model with province-level random effects	WorldPop[160,165]
Wallis and Futuna	National model	N/A

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