Map Methodology

Loa loa

Estimated prevalence of Eye Worm:

Surveys informing this layer were conducted using the RAPLOA methodology[1]. ArcGIS 10.0 was used for spatial analysis of the data. The prevalence of history of eye worm for each village was submitted to a logit transformation. The transformed prevalence data were then analyzed through a geostatistical method called kriging. The kriging analysis involved variography to determine the spatial correlation pattern in the survey data and a process of weighted spatial smoothing to predict the distribution of the logit prevalence throughout the surveyed area. This layer corresponds to figure 4 of the article by Zoure´ et al.[2], and was provided by the [Expanded Programme for the Elimination of NTDs](#).

Lymphatic Filariasis (LF)

LF Average Prevalence (points):

Relevant data on the prevalence of LF were identified through a combination of (i) structured searches of electronic bibliographic databases (mostly PubMed and MEDLINE), (ii) additional searches of the 'grey' literature, including unpublished surveys and government and international archives, and (iii) direct contact with researchers and control programme managers. Studies were included if they provided: (i) the number of people surveyed, (ii) the number of LF positive cases, (iii) details about the methodology of diagnosis and (iv) details of the specific site where they were conducted, regardless of the administrative level. This layer was provided by the [Global Atlas of Helminth Infection](#).

LF transmission boundaries:

Boosted regression trees (BRT) modelling was used for mapping the spatial limits of LF transmission[3]. Six environmental variables (precipitation in the wettest quarter, annual minimum temperature, population density 1990-2015, elevation, enhanced vegetation index and regions) were used to build the final risk map. The resulting predictive map quantifies the environmental suitability for LF transmission. In order to convert this continuous metric into a binary map outlining the limits of transmission, a threshold value of environmental suitability was chosen which maximized the trade-off between sensitivity, specificity and proportion correctly classified. Finally, we masked the environmental distribution map to remove areas which are known to be currently non-endemic according to WHO and other sources. Non-endemicity was considered when no cases had been reported for the last 10 years and transmission assessment surveys confirmed the interruption of LF transmission. This layer was provided by the [Global Atlas of Helminth Infection](#).

LF Prevalence (ICT)

Using a suite of environmental and demographic data and prevalence surveys, spatiotemporal multivariate models were fitted separately for microfilaraemia (mf) prevalence and antigenaemia prevalence within a Bayesian framework and used to make predictions for non-sampled areas[4]. This layer shows predicted prevalence based on ICT, as the primary diagnostic used to guide control interventions. This layer was provided by the [Global Atlas of Helminth Infection](#).

Onchocerciasis (oncho)

Pre-control onchocerciasis

A model-based geostatistical analysis of Rapid Epidemiological Mapping of Onchocerciasis (REMO) data was undertaken to generate high-resolution maps of the predicted pre-

(Prevalence of nodules):	control prevalence of nodules in the 20 African Programme for Onchocerciasis Control (APOC) countries[5]. The geostatistical analysis included the nodule palpation data for 14,473 surveyed villages. Data was provided by the [Expanded Programme for the Elimination of NTDs](#).
Pre-control onchocerciasis (Prevalence of microfilaraemia):	A model-based geostatistical analysis of pre-control microfilarial prevalence data from 737 villages across the 11 constituent countries in the Onchocerciasis Control Programme (OCP) epidemiological database. This was used to generate a continuous surface (at pixel resolution of 5 km x 5km) of microfilarial prevalence in West Africa prior to the commencement of the OCP[6]. Data was provided by [Imperial College London](#).

Schistosomiasis

Schisto prevalence (points); Blood in urine	Survey data were identified through structured searches of electronic bibliographic databases (PubMed, EMBASE, MEDLINE) using specified queries (*Schistosomiasis OR bilharzia OR Schistosoma mansoni OR Schistosoma haematobium OR Schistosoma intercalatum AND country name).* This was complemented with manual searches of local archives and libraries and direct contact with researchers. Estimates of infection prevalence were included according to pre-defined criteria: only cross-sectional prevalence surveys; data were excluded if based on hospital or clinic surveys, post-intervention surveys, or surveys among sub-populations, such as among refugees, prisoners or nomads. No restrictions were placed on sample size or diagnostic method. The longitude and latitude of each survey were determined using a combination of resources including national school's databases, village databases digitised from topographical maps, a range of electronic gazetteers (Geonames, Fuzzy Gazetteer, Google Earth) and contact with authors who used GPS. This methodology is a continuation of work done by Brooker et al[7]. This layer was provided by the [Global Atlas of Helminth Infection](#).
Schisto average prevalence (district classification):	The average prevalence of schistosomiasis was calculated for districts where **at least 5 surveys with a minimum of 250 individuals** (in total) were conducted **within a 2-year period** in the past decade. Districts that did not fulfil these criteria but where any survey reported infection in the past decade were classified as having evidence for transmission. This layer was provided by the [Global Atlas of Helminth Infection](#).

Soil transmitted helminths (STH)

STH Prevalence (points)	Survey data were identified through structured searches of electronic bibliographic databases (PubMed, EMBASE, MEDLINE) using specified queries (*hookworm OR ascariasis OR trichuriasis OR Necator americanus OR Ancyclostoma duodenale OR Ascaris lumbricoides OR Trichuris trichiura OR intestinal parasites OR geohelminths OR soil-transmitted helminths AND country name).* This was complemented with manual searches of local archives and libraries and direct contact with researchers. Estimates of infection prevalence were included according to pre-defined criteria: only cross-sectional prevalence surveys; data were excluded if based on hospital or clinic surveys, post-intervention surveys, or surveys among sub-populations, such as among refugees, prisoners or nomads. No restrictions were placed on sample size or diagnostic method. The longitude and latitude of each survey were determined using a combination of

resources including national schools' databases, village databases digitised from topographical maps, a range of electronic gazetteers (Geonames, Fuzzy Gazetteer, Google Earth) and contact with authors who used GPS. This methodology is a continuation of work done by Brooker et al[7].

The prevalence of infection with any STH species (i.e. cumulative prevalence of STH) was calculated using a simple probabilistic model of combined infection, incorporating a small correction factor to allow for non-independence between species, following the approach of de Silva and Hall[8]. The cumulative prevalence of STH was estimated as $PHAT \div 1.06$ where $PHAT$ is the uncorrected cumulative STH prevalence calculated as $PHAT = H + A + T - (HA) - (AT) - (HT) + (HAT)$. H is the prevalence of hookworm infection, A the prevalence of *A. lumbricoides* and T the prevalence of *T. trichiura*. This layer was provided by the Global Atlas of Helminth Infection.

STH Average prevalence (district classification)	The average prevalence of STH was calculated for districts where **at least 5 surveys with a minimum of 250 individuals** (in total) were conducted **within a 2-year period** in the past decade. Districts that did not fulfil these criteria but where any survey reported infection in the past decade were classified as having evidence for transmission. This layer was provided by the Global Atlas of Helminth Infection.
STH transmission boundaries	This layer describes the suitability of the environment for STH transmission. Limits were established as described in Pullan & Brooker[9] based on high and low land surface temperature and the aridity of environment. This layer was provided by the Global Atlas of Helminth Infection.

Trachoma

Trachoma prevalence:	The data represented in the trachoma layer is trachomatous follicular (TF) derived from population-based prevalence surveys (PBPS). The 10% threshold illustrates the WHO recommended guideline for district level mass drug administration (MDA) of antibiotic[10]. Data were collected through structured searches of published and unpublished literature to identify cross-sectional epidemiological data on the burden of trachoma since 1980, as a continuation of works done by Smith et al[11]. This data was provided by the Global Atlas of Trachoma.
Trachoma treatments:	Azithromycin is the recommended antibiotic used in mass drug administration for trachoma. Pfizer generously donates Zithromax® to treat and prevent active infection each year. These layers illustrate where Pfizer donated Zithromax® has been reported as distributed annually since 2012. This data was provided by the Global Atlas of Trachoma.

Water Supply and Sanitation[12]

Data sources for WSS:	Data on household access to drinking-water supply, sanitation and open defecation were abstracted from national Demographic and Health surveys (DHS), multiple indicator cluster surveys (MICS), national malaria and AIDS indicator surveys (MIS/AIS) and living standard measurement studies (LSMS). Extracted data are based upon criteria set down for monitoring the Millennium Development Goal 7C.

Safe drinking water:	Maps show the predicted proportion of households with access to an improved drinking-water source. This is defined as one that is protected from outside faecal contamination: piped water, standpipes, tubewells, borewells, protected dug wells, protected springs and rainwater. This layer was provided by the Global Atlas of Helminth Infection.
Adequate sanitation	Maps show the predicted proportion of households with access to an improved sanitation facility. This is defined as one that hygienically separates excreta from human contact: flush toilets, piped sewer systems, septic tanks, ventilated improved pit latrines, pit latrines with a slab and composting toilets. This metric includes households that share access to an improved facility. This layer was provided by the Global Atlas of Helminth Infection.
Open defecation	Maps show the predicted proportion of households who report habitually defecating in the open, and have no access to an improved or unimproved sanitation facility. This layer was provided by the Global Atlas of Helminth Infection.
Estimating access at district level:	Spatially-explicit statistical models were developed and used to predict household access at high spatial resolution (district-level or equivalent) for 2010. These models consider the hierarchical structure of the whole dataset; this allows 'borrowing' of information from neighbouring districts to supplement available date, thus creating sufficient statistical power to generate reliable estimates for comparison of district estimates for evaluation purposes. The model also allows different time trends for urban and rural populations by country, but assumes an overall linear change over time. In practice, this means that countries (and districts within countries) are assumed to follow the region (and national) average in cases where trend (or coverage) information is sparse or absent. Further details are provided in Pullan *et al* (2013).

Yaws

Yaws (cases recorded):	Number of people with active disease at the first administrative level (eg, province, region, and prefecture) between Jan 1, 2010, and Dec 31, 2013 were identified from country estimates of yaws cases, whenever possible[13]. For countries for which no recent data were available, yaws control programme managers were contacted to obtain official national routine surveillance data. This layer was provided by the Barcelona Institute for Global Health.

Boundaries and Population

Admin0, Admin1, Admin2, Admin3	These layers depict administrative boundaries including country (admin0), first-order administrative regions, (admin1), second-order administrative regions (admin2) and third-order administrative regions (admin3) sourced from Geoconnect[14]. The names assigned to these (e.g. districts, provinces, regions, counties) vary by country.
Population Density:	A gridded map of estimated population density (individuals/km^2) for 2010 has been provided by the WorldPop project (www.worldpop.org.uk/), with national totals adjusted to match UN population division estimates. This project aims to provide high spatial resolution and contemporary data on human population distribution for the accurate measurement of the impact of population growth, for monitoring changes and for planning interventions.

Urbanization: WorldPop gridded population density maps were used to identify urban and peri-urban areas, which may experience different levels of risk to rural areas for many NTDs[15]. Urban areas are defined as those with population density ≥1,000 persons/km^2 and peri-urban areas as having >250 persons/km^2 within 15 km of an urban area.

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