

Estimating the Prevalence of Hepatitis Delta in the UK: A Migration Model Approach Applied in Practice

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Introduction:

Hepatitis delta (HDV) is a rare condition, affecting a subset of HBV+ patients. HDV is recognised as the most severe form of viral hepatitis-induced liver disease, with the most rapid progression to cirrhosis and hepatocellular carcinoma¹⁻².

Until recently there have been no licenced treatments for HDV. The EMA recently approved the first treatment for this condition³.

Despite its severity, the prevalence of HDV is largely unknown⁴. There are several factors which contribute to this:

- 1. It is a sub-set of patients that are chronic HBV infection, and it is likely that a considerable number of these patients remain undiagnosed⁵
- 2. HDV diagnostics are not widely available and there is no standardization for HDV RNA assays, which are used for monitoring response to antiviral therapy⁶
- 3. Impact of HBV paediatric vaccination changes chronic HBV prevalence and thus will impact HDV prevalence⁶
- 4. Within the UK, HBV (and therefore HDV) risk factors are associated with migratory populations from countries where HBV is considered endemic by the WHO⁷⁻⁹

Key factors influencing the likely prevalence of HDV within the UK include country of birth, HBV status and HDV co-infection rate according to the country where the infection was likely to have occurred. The objective of this research was to estimate prevalence of HDV+ in England, Scotland & Wales in preparation for local and national budget discussions with clinicians and payers.

Methods:

Using a multivariate model framework (poster MSR36), prevalence of HDV+ was calculated for: England, Scotland and Wales, based on previously collated prevalence estimates of both HBV and HDV by country of birth.

Population data:

Overall population data were obtained for each country from specific government sources¹⁰⁻¹⁴, by age and gender.

Migration data & estimates:

Data regarding demographic country composition according to country of birth were obtained to estimate the most robust view of the in-country population at the time of analysis (2021/2022). Data from the Annual Population survey and EU settlement statistics were combined to produce a single representative estimate of the populations in England, Scotland & Wales by country of birth.

Sub-national estimates:

Data at sub-national level were sought to better support local access discussions, including data at individual health board level for Scotland and Wales¹³⁻¹⁴.

Population data were fed into the model to estimate HDV prevalence based on prior HBV and HDV prevalence by country of origin.

Sensitivity analysis was conducted to estimate variance in model outputs. In addition, data regarding likely diagnosis of HBV (reported HBV diagnoses in the past 10 years) and testing for HDV were combined with the estimated total disease burden prevalence to better reflect the likely caseload of HDV patients accessing care.

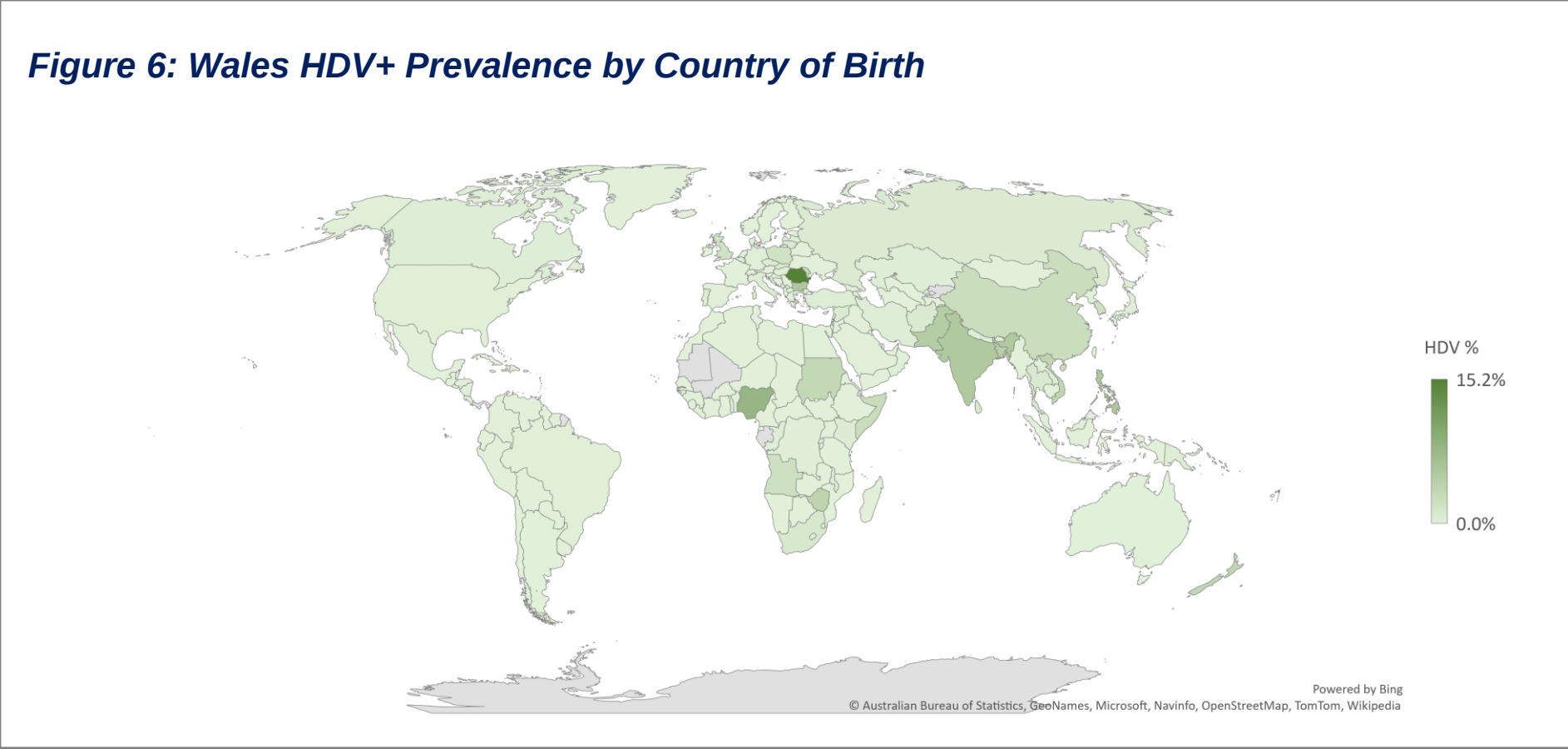
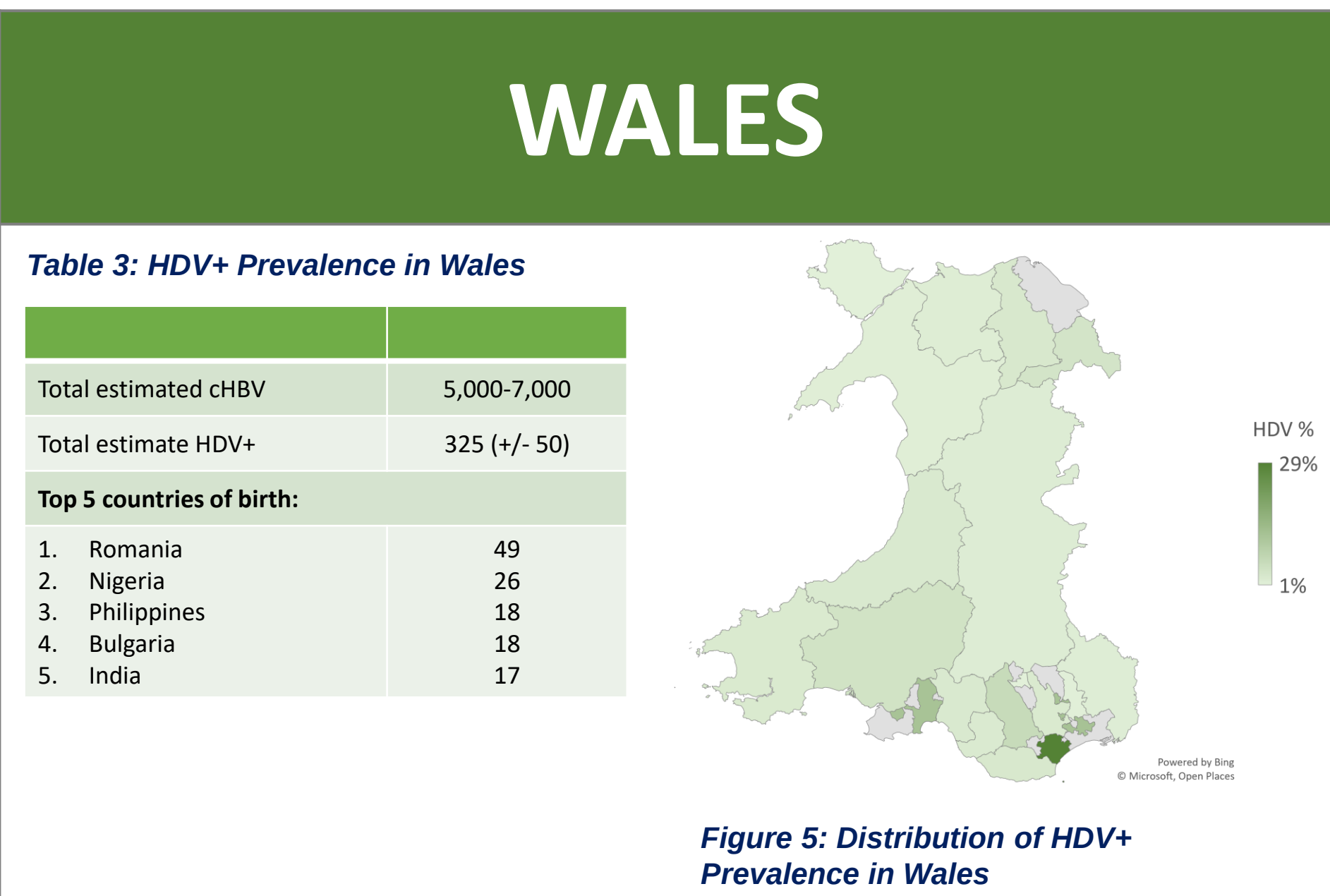
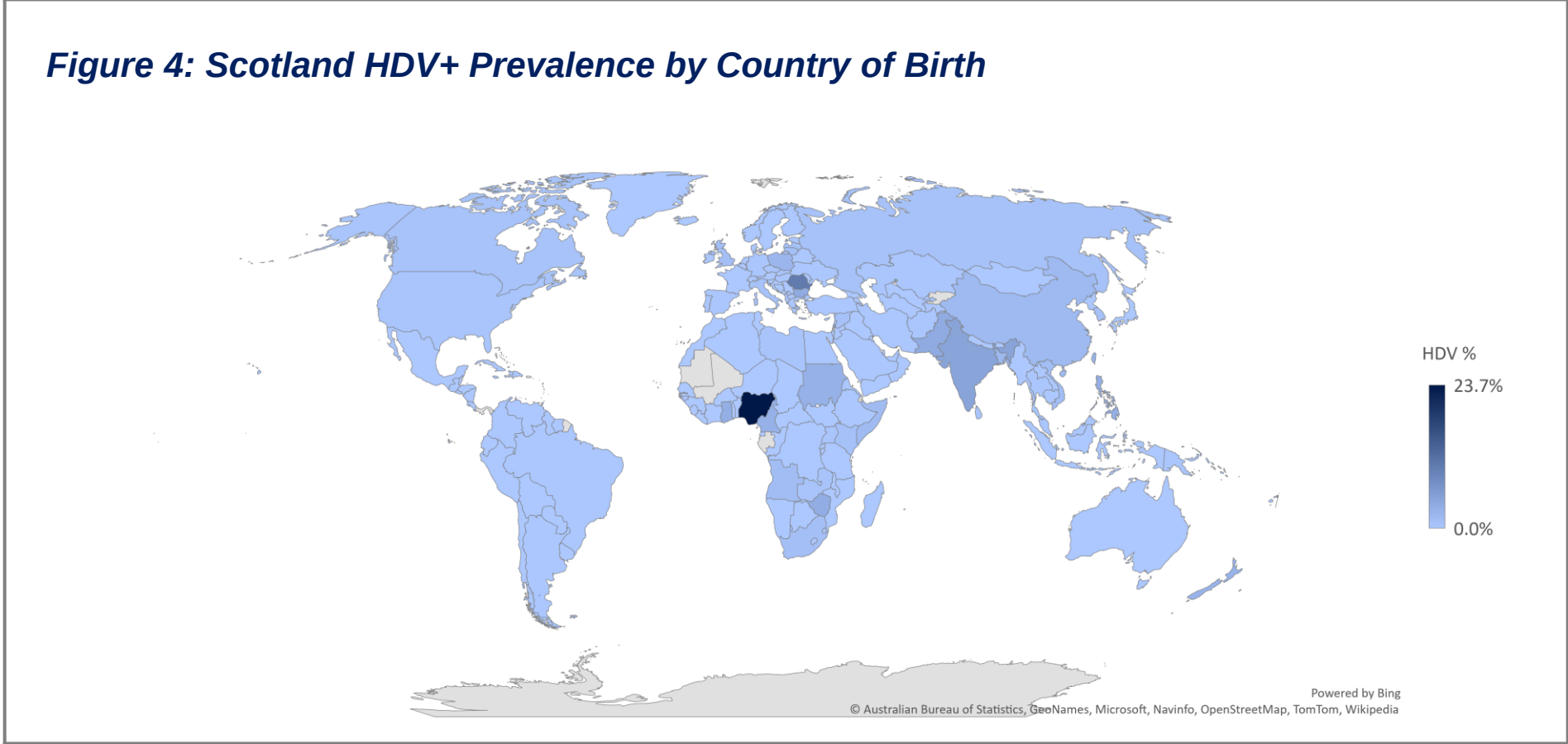
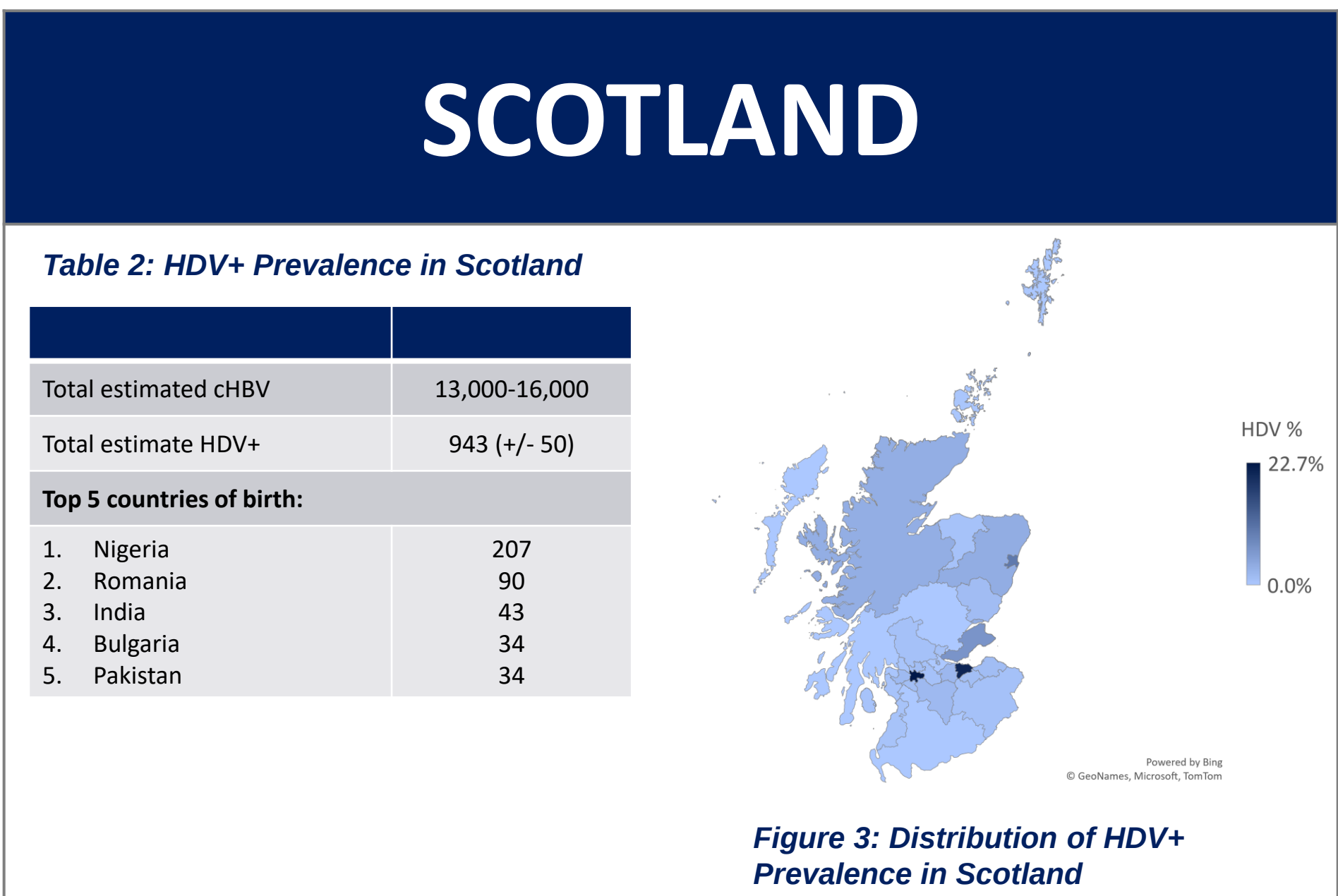
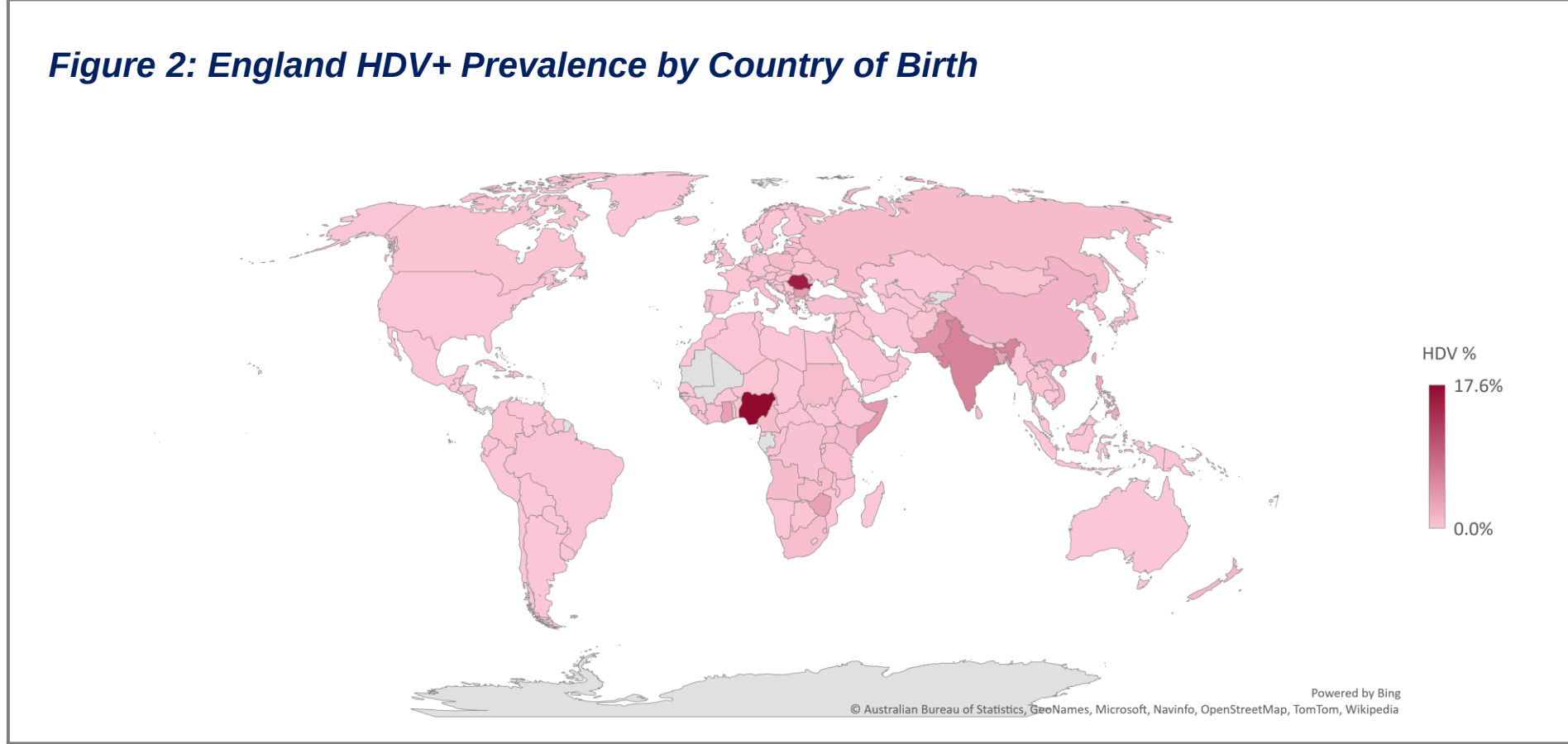
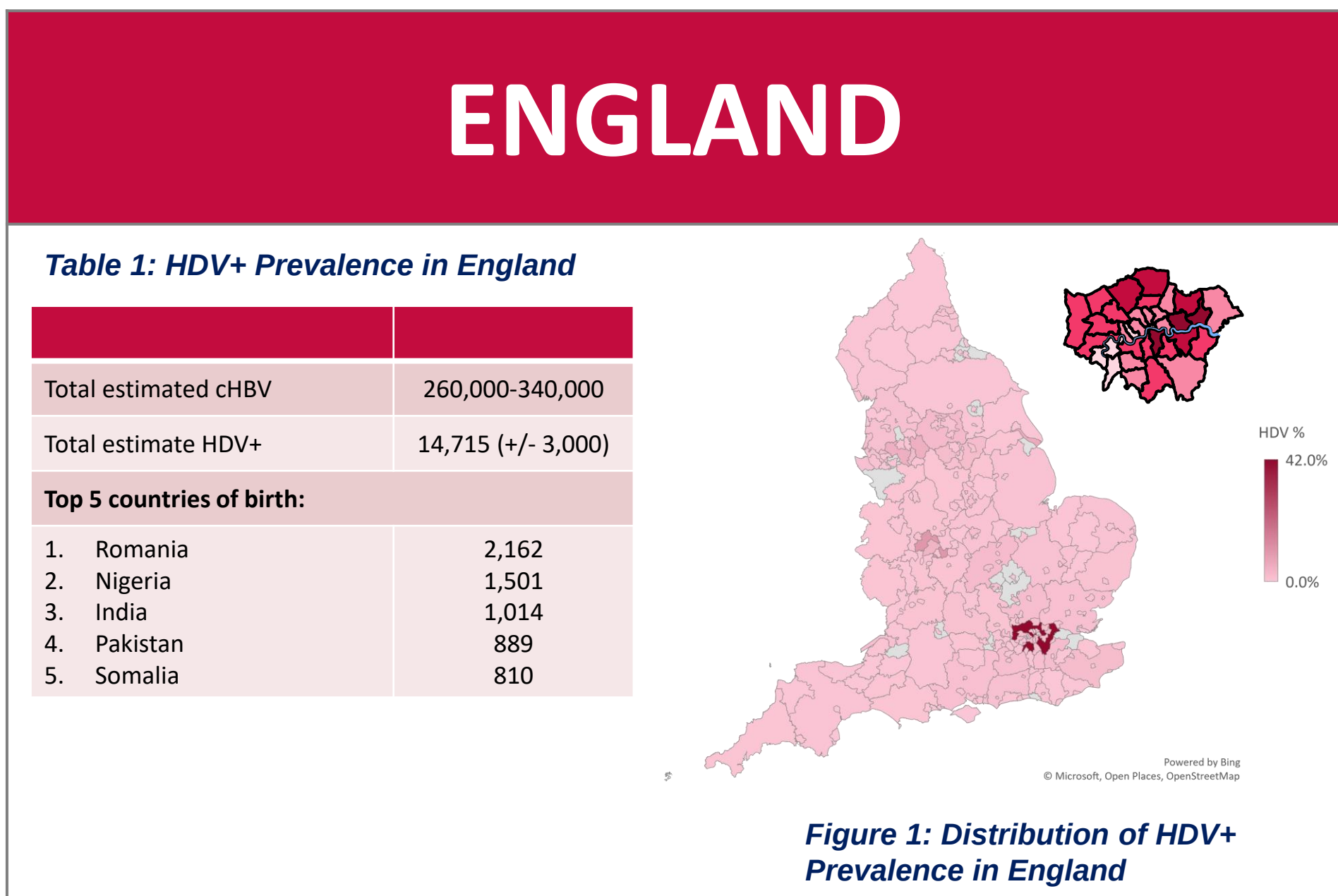
Results:

Total HDV antigen positive prevalence (HDV+) within England, Scotland and Wales was estimated at 12,000-14,000, 900-1,000 and 250-350 patients respectively.

England: The highest regional prevalence for HDV+ in England was found in London (~42% of total England prevalence), with top 5 countries of birth for HDV prevalence identified as Romania, Nigeria, India, Pakistan & Somalia, accounting for ~45% of overall HDV+ prevalence. Key contributing global regions were Sub-Saharan Africa (39%), Eastern Europe (26%) and Asia (25%). Diagnosis rate of HBV was estimated at 40%, suggesting an accessible pool of ~ 4,800-5,600 HDV+ patients.

Scotland: Highest regional prevalence for HDV+ in Scotland was found in Glasgow closely followed by Edinburgh (~ 23% & 21% of total prevalence respectively). Key global regions contributing to HDV prevalence in Scotland included Sub Saharan Africa (44%), Asia (23%) and Eastern Europe (22%). Diagnosis rate for HBV in Scotland estimated to be ~31%, indicating a potentially accessible pool of ~279-310 patients.

Wales: Highest regional prevalence in Wales was found in Cardiff, accounting for ~29% of total HDV+ prevalence in Wales. Top contributing global regions for HDV prevalence included Asia (34%), Eastern Europe (27%) and Sub-Saharan Africa (24%). Diagnosis rate for HBV in Wales estimated to be ~33%, resulting in a potential accessible pool of ~82-115 patients.



The overall co-infection rate for HBV+ with HDV+ was calculated at 7%, 6% and 5% for England, Scotland & Wales respectively. Results were highly dependent on granularity of population data by country of origin in each country at both the national and local / regional level (+/- 30%) and the methodology used to estimate countries with missing data (+/- 18%). No data were available regarding testing rates for HDV within the HBV diagnosed population.

Conclusions:

HDV prevalence is highly dependant on migration populations and background rates of HBV infection in country of birth. Overall, across the UK, there are an estimated 16k HDV+ patients, however it is unlikely that the majority of these patients are diagnosed or aware of their condition due to low rates of HBV diagnosis and lack of HDV testing within the HBV diagnosed population⁶. Current data on HDV patients in care suggest a disparity between country of origin and representation in the clinical caseload (e.g., patients from sub-Saharan African nations are lower than expected based on prevalence). Due to the diverse background of potential patients, careful consideration will need to be given to how these patient access care and should be supported for their infection.

Additional consideration should be given to coverage, uptake and timing of paediatric HBV vaccinations which will impact the underlying chronic HBV population within which HDV resides. For this analysis, migrant population age cut off of 15 years of age was applied in the absence of detailed vaccination modelling to yield a population remaining at risk.

Since the calculated estimates are highly dependent on the migration populations, better data should be sought to further understand background risk within the migratory cohort as linked to potential exposure to HBV and HDV pathogens (e.g., risk-taking behaviour, socioeconomic factors, clinical history, reason for migration). In addition, data are lacking regarding duration of stay within the UK and potential movement between geographic locations within the UK which could all affect prevalence and location of potential patients.

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