Chad's Infectious Disease Surveillance In Context: An Analysis Of 2014-2023 Case Report Data

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CHAD'S INFECTIOUS DISEASE SURVEILLANCE IN CONTEXT: AN ANALYSIS OF 2014-2023 CASE REPORT DATA

by

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A Master’s Thesis
Submitted to the Department of Epidemiology of Microbial Diseases
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Primary Advisor: Sten H. Vermund, MD, PhD
Secondary Advisor: Virginia Pitzer, ScD
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**Research in context**

**Evidence before this study**
There is a paucity of literature available on Chad. To evaluate the availability of evidence, we conducted a review of published literature in PubMed for relevant reports published in English or French up to April 18, 2024, with no start date restriction. Search terms included “(Chad[MeSH Terms]) AND (surveillance[Title/Abstract] OR vaccine[Title/Abstract] OR infectious[Title/Abstract] OR infection[Title/Abstract] OR "disease trend"[Title/Abstract]),” “(Chad[MeSH Terms]) AND ("meningitis"[Title/Abstract]) OR ("yellow fever"[Title/Abstract]) OR ("neonatal tetanus"[Title/Abstract]) OR ("COVID-19"[Title/Abstract]) OR ("acute flaccid paralysis"[Title/Abstract]) OR ("measles"[Title/Abstract]) OR ("malaria"[Title/Abstract]) OR ("Guinea worm"[Title/Abstract]),” and “("Sub-Saharan Africa"[Title/Abstract]) AND ("surveillance"[Title/Abstract]) AND ("yellow fever"[Title/Abstract]) OR ("neonatal tetanus"[Title/Abstract]) OR ("acute flaccid paralysis"[Title/Abstract]) OR ("measles"[Title/Abstract]) OR ("meningitis"[Title/Abstract]) OR ("malaria"[Title/Abstract])).” French search terms included “Tchad AND ("ménigite" OR "fièvre jaune" OR "tétanos néonatal" OR "COVID-19" OR "paralysie flasque aiguë" OR "rougeole" OR "paludisme" OR "ver de Guinée").” We identified multiple publications specific to Chad for measles, meningitis, malaria, and Guinea worm, but very limited evidence for yellow fever, neonatal tetanus, and acute flaccid paralysis. There were no trend analyses of multi-disease surveillance data from Chad.

**Added value of this study**
This is the first study of ten-year trends in national infectious disease patterns using Chad’s surveillance data. It describes ten-year and seasonal trends across several infectious diseases and changes in spatial distribution at the province-level to characterize shifts in the disease burden throughout the past decade. It additionally seeks to evaluate the extent to which the impacts of immunization campaigns and COVID-19 are represented in the surveillance data, overall to determine the baseline capacity of Chad’s surveillance reporting. Our findings highlight the increasing burden of infectious diseases linked to climate change, such as yellow fever, as well as the significant impacts of eradication and immunization campaigns.

**Implications of all the available evidence**
This effort will improve evaluation of ongoing public health interventions and facilitate more accurate analyses of surveillance data, particularly after further INSAPT efforts to improve public health infrastructure have been implemented. The scope of the study was narrowed to diseases of particular public health interest, such as the subjects of eradication campaigns (e.g., meningitis and Guinea worm) or indicators of health infrastructure (e.g., neonatal tetanus and measles), helping identify potential priority areas for future surveillance efforts. By 2025, INSAPT hopes to use its surveillance data for aberration detection and to further integrate surveillance work with other public health units, resulting in overall improved capacity and more immediate infectious disease outbreak responses; the analysis presented in this report reflects the current capabilities of the Chadian surveillance system and will serve as a historical baseline for any future analysis of surveillance data.
Abstract

Background
Infectious diseases remain a leading cause of mortality and morbidity in Chad. We aimed to assess trends in the most recent ten years of surveillance data collected by the Ministry of Public Health in Chad to characterize the country’s current disease burden.

Methods
In this analysis of Chadian surveillance data, we analyzed reports of suspected cases across seven diseases from 2014-2023. Data included weekly aggregated case counts by district. We used the data to describe temporal and spatial trends, particularly from 2014-2019 compared to 2020-2023.

Findings
Measles case counts showed seasonal peaks of varying intensity throughout most of 2014-2023. Province-level incidence decreased throughout most of the country between the pre-pandemic and post-pandemic periods, but increased most in Mandoul (356·6%) and Moyen-Chari (493·3%). Meningitis cases declined in the past four years, reaching their lowest level in ten years. Yellow fever cases significantly increased in the past three years. Six provinces had increases of over 100% between the two periods: Guéra (129·6%), Mandoul (505·5%), Mayo-Kebbi Ouest (164·4%), Ouaddaï (113·4%), Tandjilé (281·7%), and Tibesti (137·9%), five of which are in the southern half of the country. Neonatal tetanus experienced a slight upward trend throughout the ten-year period, with a similar distribution across nearly all provinces between the two periods under examination. Malaria had a similar steady increase throughout the ten-year period, with most provinces reporting slightly higher incidences during the post-pandemic period (2·6 to 68·1%). Acute flaccid paralysis experienced larger increases in the past four years, with the largest increases in incidence in the south, in Mandoul (185·6%) and Tandjilé (188·5%). The number of Guinea worm cases was abnormally high in 2019, then declined to pre-2019 levels. Fewer provinces reported cases of Guinea worm in the post-pandemic period compared to the pre-pandemic period.

Interpretation
Trends in the seven diseases included in this report varied throughout the time period, highlighting the importance of a shift in future priorities to best respond to infectious disease challenges in Chad.

Funding
The U.S. Agency for International Development.
Introduction

Chad is a low-income country in the Sahel region of east-central Africa, ranked 189 of 193 nations in the 2023-2024 Human Development Index report.1 The nation is experiencing significant population flux from neighboring countries’ displaced populations, high rates of malnutrition and food insecurity, and extreme weather events exacerbated by climate change, all of which increase the stress on its healthcare system and the incidence of infectious diseases.2,3 The country has been burdened recently by the COVID-19 pandemic, declared an emergency by the Ministry of Public Health on March 19, 2020.4 Beyond the immediate disease burden of COVID-19, the pandemic disrupted health systems by delaying immunization efforts and training already under-resourced health infrastructure.5

In preparation for the impact of COVID-19 in Chad, the Chadian government conceptualized the Institut National de Santé Publique du Tchad (INSAPT) and established a partnership with the Yale School of Public Health (YSPH) to support efforts in COVID-19 contact tracing and surveillance, beginning in 2021.6 In 2022, funding was renewed to focus on the development of INSAPT via the establishment of essential public health functions, such as surveillance; laboratory capacity; leadership and mentoring; community engagement for vaccine promotion; epidemiology and biostatistics training; and initiatives in critical care, surgery, and anesthesiology.

Given the significant infectious disease burden in Chad, improved surveillance is an essential component of INSAPT support efforts. As the country improves its laboratory capacity and achieves centralization of its data collection infrastructure, it is expected that its surveillance reports will increasingly accurately reflect Chad’s actual disease burden. Some of this work has already been accomplished—in 2023, Chadian laboratory workers successfully processed two pathogens (Plasmodium falciparum and dengue virus) from sample collection to full sequence analysis for the first time. To evaluate the success of improved surveillance capabilities, however, it is essential to analyze Chad’s historical surveillance data. The diseases and conditions of interest included in its reports are dictated by World Health Organization (WHO) guidance and local needs and priorities.6

As part of its surveillance objectives, the INSAPT-YSPH partnership sought to assist the Ministry of Public Health in the consolidation of the past ten years of data collected by the National Unit for Epidemiological Surveillance into a centralized database, providing historical context and facilitating more advanced analysis in the future. The establishment of a historical baseline is essential in building the country’s public health infrastructure. In this Article, we describe the trends of seven diseases of high intervention priority and global health interest: measles, meningitis, yellow fever, neonatal tetanus, malaria, acute flaccid paralysis, and Guinea worm.

Methods

Data sourcing and preprocessing

We accessed surveillance records from 2014-2023 provided by the Chadian Ministry of Health. Chad collects data in all 23 of its provinces. Surveillance records included reported cases of acute flaccid paralysis, chikungunya, cholera, COVID-19, dog bites, gastroenteritis, Guinea worm, hepatitis E, influenza, malaria, maternal deaths, measles, meningitis, moderate and severe malnutrition, neonatal tetanus, neonatal and perinatal deaths, scorpion stings, snakebites, and yellow fever. The records included disease/condition, number of cases, number of deaths, province, district, year, and epidemiological week. Cases were considered suspected cases unless otherwise indicated, because they were not verified via laboratory diagnostic testing. All diseases included in this analysis were suspected cases. Initial records were formatted in Excel, and all data were consolidated into a centralized Excel database. This step included standardization of district names due to observed variations in spelling across years. The original records included a numerical value for all regions and weeks, with a value of zero for both missing reports and no reported cases. The centralized database included only non-zero values and was restricted to measles, meningitis, yellow fever, neonatal tetanus, malaria, acute flaccid paralysis, and Guinea worm.
District level population data were obtained from the national census, and a shapefile for the heat maps was downloaded from the Massachusetts Institute of Technology library database. The data were imported into the open-source R statistical software, where all further processing was performed.

Temporal trends
We used the centralized and standardized data to visualize ten-year time series. Because the weekly reporting day varied and there were no available dating records, we standardized epidemiological weeks to the first Sunday of each week. To create a continuous plot, all weeks with missing values were filled in with zero cases. To improve visualization of trends for neonatal tetanus, a 15-week moving average was calculated and plotted on top of the count data.

Spatial trends by province
We compared the distribution of cases across provinces before and after the onset of the COVID-19 pandemic, which coincided with the beginning of the current INSAPT-YPSP partnership. The pre-pandemic period was defined as 2014-2019, and the post-pandemic period was defined as 2020-2023. The sum of cases in each province for the entire subperiod was calculated and then divided by the number of years in the subperiod (i.e., six years for 2014-2019 and four years for 2020-2023) to obtain the average number of annual cases. Because data from 2019 were not available for acute flaccid paralysis, the pre-pandemic case data were divided by five years. The average number of annual cases of Guinea worm was plotted directly because of low case counts. The average annual case values for the other diseases were divided by the mean population in each time period to obtain the crude incidence, which was reported per 100 000 population. The average annual incidence by province was visualized as a heat map. The percentage change in incidence between the two periods was calculated.

Role of the funding source
The funder of the study had no role in study design, data collection, data analysis, data interpretation, or writing of the report.

Results
The time series for measles showed a decrease in cases at the beginning of 2014, which persisted until early 2018, and then seasonal peaks of varied intensity; the highest peak was in 2019 (1374 weekly cases), which occurred at the end of the lull period, and then the peak intensity decreased until 2022, when it began to increase again (figure 1a). The incidence decreased throughout most of the country, but it increased in three adjacent provinces: Tandjilé (2·1%), Mandoul (356·6%), and Moyen-Chari (493·3%) (figure 2a; table 2).

Meningitis also exhibited a peak of high intensity in 2019. Prior to 2019, mild annual seasonal peaks occurred, which continued after the 2019 peak but with decreasing intensity. By the end of the ten-year period, meningitis’s seasonal peak appeared significantly flattened, and cases had reached the lowest level in the ten years of data (figure 1b; table 1). During both periods, the highest incidence was in Mandoul (figure 2b). No province experienced a percent change greater than 81%, and only four provinces had increases in cases: Barh el Ghazel (28·2%), Ennedi Est (61·2%), Tandjilé (21·4%), and Ville de N’Djamena (17·0%) (table 2).

Yellow fever exhibited a reasonably stationary pattern until 2021, when cases significantly increased. There was a high intensity peak in 2021, followed by peaks in 2022 and 2023 (Figure 1c). As a result, the number of annual cases of yellow fever more than doubled in the last three years of data compared to the period from 2014-2020 (table 1). While nine provinces experienced increases ranging from 9·4 to 92·4%, and eight provinces experienced decreases from -9·0 to -71·0%, six provinces had increases of over 100%. These included Guéra (129·6%), Mandoul (505·5%), Mayo-Kebeit Ouest (164·4%), Ouaddaï
(113·4%), Tandjilé (281·7%), and Tibesti (137·9%) (table 2). With the exception of Tibesti, these provinces are all in the southern half of the country (figure 2c).

The 15-week moving average of neonatal tetanus cases showed an upward trend in total cases throughout the ten-year period (figure 1d). The relative change in incidence was below 30% for thirteen provinces, and only one province had a change above 100% (table 2). Beyond this large increase in Mandoul (292·0%), neonatal tetanus did not seem to have any significant changes in distribution (figure 2d).

The time series for malaria also indicated an increase in cases throughout the period under examination, with peaks of increasing intensity and an increasing off-peak baseline (Figure 1e). Seven provinces experienced decreases (from -3·6 to -10%); this group was composed of Chari-Baguirmi, Logone Occidental, Logone Oriental, Mayo-Kebbi Ouest, and Salamat in the south and Ennedi Ouest and Tibesti in the north (figure 2e; table 1). Most provinces reported slightly higher incidences during the post-pandemic period, ranging from 2·6 to 68·1% (table 2).

Acute flaccid paralysis displayed an increase in the mean number of cases over time, with several weeks with significantly elevated case counts—particularly from the end of 2021 onward. Data were not available for 2019 (figure 1f). Only three provinces experienced relative decreases in cases across the two time periods, while the remaining twenty provinces experienced increases, primarily in the eastern half of the country (figure 2f). The highest increases in incidence occurred in Mandoul (185·6%) and Tandjilé (188·5%) (table 2).

The number of Guinea worm cases was abnormally high in 2019 compared to all other years, with a weekly maximum of 8 cases (figure 1g; table 1). The frequency of case reports also decreased after 2019 (figure 1g). No cases were reported in the surveillance data from 2023 (table 1). While seven provinces reported cases of Guinea worm during the pre-pandemic period, only five provinces reported cases in the post-pandemic period, all of which were included in the pre-pandemic group (figure 3).

**Discussion**

To our knowledge, this constitutes the first comprehensive presentation of Chad’s most recent ten-year surveillance data. Furthermore, publications specific to Chad on these diseases are very limited—for several of the diseases included in this analysis, no relevant studies were identified in the literature search. The findings of this study are an important step in the generation of directions for future exploration, particularly as INSAPT increases its capacity to study and respond to the epidemiological profile of the country.

Vaccine preventable diseases (VPDs) are of especially high priority, as changes in their incidences and spatial distributions reflect the effectiveness of vaccination efforts. Declines in vaccination coverage were documented on a global scale and in Chad as a result of the COVID-19 pandemic, making an assessment of recent trends in surveillance data especially prescient. Measles, meningitis, yellow fever, and neonatal tetanus have all been the targets of immunization campaigns in Chad throughout the past decade, with varied results seemingly reflected in the data.

Immunization efforts against measles were launched in 2014, in collaboration with Médecins sans Frontières (MSF) and the United Nations Children’s Fund (UNICEF), and a complete national campaign was undertaken in 2015. These campaigns coincided with significant decreases in the incidence of measles cases in the first half of 2014, which were maintained until 2018. In spite of immunization efforts, vaccination coverage as estimated by the World Health Organization (WHO) remained below 50% from 2015-2020 and below 60% through 2022. Because this rate has not significantly changed throughout the period represented by the data, it seems that measles outbreaks have not been adequately prevented by vaccination efforts; the country remains at risk of measles outbreaks. While crude incidence
did decrease in most provinces in the post-pandemic period compared to pre-pandemic levels, district-specific outbreaks in regions of N’Djamena and Moyen-Chari during 2023 underscore the significant risk posed by measles, as it still has the potential to cause large outbreaks.

In comparison, meningitis has been the focus of a targeted multinational campaign using the meningococcal type A conjugate vaccine (MACV) to reduce Neisseria meningitidis serogroup A (NmA) bacterial meningitis. This bacteria has caused 90% of epidemic cases in the meningitis belt, a geographic region that experiences an extremely high burden of meningitis and in which Chad is located. MACV’s introduction in 2011-2012 substantially reduced the incidence of NmA meningitis in Chad; an analysis of surveillance data from 2006-2015 found a 91% reduction in incidence following introduction of the vaccine. The reduced meningitis burden was reflected in the time series from 2014-2018, as the number of suspected cases remained close to levels identified in the study.

In spite of quantifiable reductions in the meningitis burden as a result of MACV, Chad remained challenged by the disease. Chad was integrated into the MenAfriNet program, a case-based surveillance (CBS) network intended to monitor MACV effectiveness and shifts in the meningitis burden, in 2016. Analysis of CBS data has found that as NmA meningitis decreased, the relative and absolute incidences of other meningitis diseases have increased. These shifts in the meningitis burden likely drove the increase in cases observed particularly from 2018-2020, during which the annual number of cases was often twice as high as the period immediately following MACV rollout. Recently, however, cases have reached their lowest levels in ten years, and these decreases in annual cases have occurred in nearly all provinces. Because Mandoul experienced the highest burden in both the pre- and post-pandemic periods, as well as the highest number of cases in 2023, meningitis efforts seem to have reduced the disease burden from a national priority to a province-level issue. While the increased diversity in meningitis pathogens may make it more difficult to implement macro-scale interventions, such a degree of specificity may be possible in this localized context.

Yellow fever seemed relatively stable throughout the first six years of data, however, increases in Chad from 2021 onward reflect the growing burden of the disease in Sub-Saharan Africa. Recent outbreaks have been reported in other Sub-Saharan African countries, including Nigeria (2017-2019) and Senegal (2020-2021). These trends have been attributed to factors such as increased mosquito vector ranges due to climate change, misdiagnoses stemming from poor laboratory capacity, and decreased immunization coverage—particularly following the COVID-19 pandemic. The data observed in Chad potentially support these hypotheses; the south of the country features tropical savannas and a wet season from May to October, which shortens towards the center of the country, while the north of Chad is arid and experiences little rainfall. As average temperatures increase and rainfall decreases in much of Sub-Saharan Africa, the southern region of Chad in particular may become more suitable to the Aedes aegypti vector, contributing to the increases in yellow fever transmission. This hypothesis is corroborated by the increase in incidence observed between the pre- and post-pandemic periods in many southern states, especially in Mandoul. As a result, immunization efforts against yellow fever are of even greater importance. A recent report of a fatal case of yellow fever in Laï (located in Tandjilé province) highlighted immunization coverage below the 80% target as a factor facilitating re-emergence of the virus. Yellow fever vaccination should be more heavily prioritized in national public health planning alongside other climate resilience efforts.

Neonatal tetanus is unique amongst the VPDs included in this analysis because it is specifically indicative of Chad’s maternal and neonatal care capacity. The global Maternal and Neonatal Tetanus Elimination Initiative was launched in 2000 to address neonatal tetanus. Until 2019, Chad was one of fourteen countries yet to be verified. It is slightly worrisome that annual reported cases of neonatal tetanus were higher on average in the period following this verification. It is necessary to obtain national birth data to determine if Chad remains below the elimination threshold of 1 case per 1,000 live births, particularly
because the annual number of cases has increased since 2019, and the incidence in the province of Mandoul has increased by 292.0%. The fact that Chad’s surveillance has captured this increase, however, means that the reporting system is generating actionable data for the country’s public health priorities. Chad should emphasize the importance of vaccination of women of childbearing age to prevent any further increases.

Overall, the trends observed in the VPDs included in this analysis seem indicative of successes in immunization efforts for diseases with stable contextual factors. Yellow fever, however, is becoming a more prominent issue because of its interactions with climate change; it is necessary to establish a more targeted public health response to determine the key drivers of this trend and promote better immunization coverage. Beyond VPDs, other targets of widespread prevention campaigns are also of high priority as measures of success and identification of areas for further research. These diseases and conditions include malaria, acute flaccid paralysis, and Guinea worm.

As observed with yellow fever, the increases observed in malaria potentially reflect the effects of climate change in the region. The steady increase in transmission regardless of seasonal timing and across nearly all provinces has resulted in an annual burden of twice as many suspected cases in 2023 compared to 2014. The heat maps show that the disease is particularly prominent in the south of the country, where the malaria season is longest, and tapers off towards the north; this finding is consistent with previously published studies. The steady increase seems indicative of a true increase in the disease burden, rather than the influence of a sudden shift in surveillance accuracy. Ultimately, it is imperative that Chad receive increased investment in its malaria programs, as it is concerning that the leading cause of mortality and morbidity in the country is increasing.

In contrast to the previously discussed diseases, cases of acute flaccid paralysis (AFP) stem from elimination efforts. In 2016, Chad was certified polio-free; however, there have been increases in AFP in many provinces. These increases may reflect improved vaccination coverage, but they may also pose challenges to maintaining immunization efforts both against polio and other VPDs by promoting mistrust of vaccination services. In many other certified countries, however, a decrease in AFP sensitivity and quality reporting has been observed as polio surveillance becomes deprioritized; while it is concerning that AFP seems to be increasing in Chad, these findings mean that the country has retained its capacity to detect potential outbreaks of polio from imported cases.

Guinea worm in Chad has been a target of the Guinea Worm Eradication Program (GWEP), particularly since an outbreak in 2010 ended a decade-long period of elimination in the country. The number of cases has remained low, beyond an abnormally high number reported in 2019, and localized to a few provinces in the south. The data provided by the Chadian surveillance team, however, reported zero cases in 2023, which is inconsistent with the nine cases reported by the Carter Center. Though this inconsistency is concerning, records from other years report case numbers aligned with data released by the Carter Center; 2023 seems to represent an abnormality in reporting accuracy for Guinea worm. While the total number of cases remains low, the role of zoonotic transmission, particularly via dogs, has made it difficult to achieve eradication. Chad’s surveillance data has been presented in this study as a matter of global health interest.

Our study had a few limitations, including its use of reported cases, which are not verified by laboratory diagnostic testing. While clinical signs of Guinea worm are easily diagnosed from observation, the symptoms of diseases such as malaria or yellow fever may be nonspecific and more frequently misdiagnosed. Because the period under examination spanned only ten years, it is possible that any inaccuracies in diagnoses or reporting occurred systematically, making it feasible to evaluate relative changes. Given the historical resource limitations of Chad’s public health infrastructure, however, it is essential to consider the extent to which case trends may reflect variations in reporting accuracy, rather
than actual shifts in disease burdens. Generally, because the INSAPT-YSPH partnership sought to increase surveillance capacity, it is expected that reporting accuracy increased from 2020 onward; the decrease observed for meningitis in particular more likely represents a true decrease in the disease burden. As future data becomes available alongside records of reporting completion, it will be more feasible to assess recent trends.

Additionally, it was difficult to analyze the net effect of the COVID-19 pandemic (which likely resulted in under-reporting) and the work of the INSAPT-YSPH partnership (which likely improved reporting) on surveillance accuracy, as these two events coincided chronologically. Broadly, however, the onset of the COVID-19 pandemic in 2020 offered the opportunity to examine Chad’s public health infrastructure resilience in the context of an acute global health crisis; comparing multiple disease burdens during the pre-pandemic (2014-2019) and post-pandemic (2020-2023) periods revealed that COVID-19 did not seem to universally disrupt Chadian surveillance, as there was no systematic decrease in case counts.

The data presented in this report underscore the importance of long-term trend analyses of the data produced by resource-limited nations, as these data can provide significant insight into both local capacity and priorities. INSAPT’s surveillance capabilities have promoted in-country ownership of data and increased Chad’s ability to participate in the many disease campaigns active within its borders. As it becomes increasingly well equipped to conduct surveillance activities, such as contact tracing and diagnostic laboratory testing, the trends assessed here will serve as an important baseline for the evaluation of future progress in surveillance.
Figure 1: Time series of reported cases, 2014-2023.


Table 1: Total reported cases per year, 2014-2023.

<table>
<thead>
<tr>
<th>Year</th>
<th>Measles (n)</th>
<th>Meningitis (n)</th>
<th>Yellow Fever (n)</th>
<th>Neonatal Tetanus (n)</th>
<th>Malaria (n)</th>
<th>Acute Flaccid Paralysis (n)</th>
<th>Guinea Worm (n)</th>
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<td>337</td>
<td>154</td>
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<td>2015</td>
<td>1 828</td>
<td>227</td>
<td>428</td>
<td>195</td>
<td>1 230 145</td>
<td>465</td>
<td>9</td>
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<td>2016</td>
<td>803</td>
<td>206</td>
<td>420</td>
<td>172</td>
<td>1 281 583</td>
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<td>2017</td>
<td>349</td>
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<td>607</td>
<td>177</td>
<td>1 485 562</td>
<td>634</td>
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<td>400</td>
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<td>191</td>
<td>1 473 436</td>
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<td>528</td>
<td>237</td>
<td>1 932 215</td>
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<td>251</td>
<td>1 882 123</td>
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<td>269</td>
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<td>1195</td>
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<td>2023</td>
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<td>197</td>
<td>1110</td>
<td>315</td>
<td>2 470 739</td>
<td>1294</td>
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Figure 2: Heat maps of average annual incidence by province, 2014-2019 vs. 2020-2023.

(a) Measles, 2014-2019 vs. 2020-2023
(b) Meningitis, 2014-2019 vs. 2020-2023
(c) Yellow Fever, 2014-2019 vs. 2020-2023
Figure 2 continued below.¹

¹Five-year annual average for acute flaccid paralysis due to missing 2019 data.
Table 2: Incidence and percentage change in incidence by province, 2014-2019 to 2020-2023.

<table>
<thead>
<tr>
<th>Province</th>
<th>Measles (2014-2019 per 100,000)</th>
<th>Measles (2020-2023 per 100,000)</th>
<th>Change (%)</th>
<th>Meningitis (2014-2019 per 100,000)</th>
<th>Meningitis (2020-2023 per 100,000)</th>
<th>Change (%)</th>
<th>Yellow Fever (2014-2019 per 100,000)</th>
<th>Yellow Fever (2020-2023 per 100,000)</th>
<th>Change (%)</th>
<th>Neontal Tetanus (2014-2019 per 100,000)</th>
<th>Neontal Tetanus (2020-2023 per 100,000)</th>
<th>Change (%)</th>
<th>Malaria (2014-2019 per 100,000)</th>
<th>Malaria (2020-2023 per 100,000)</th>
<th>Change (%)</th>
<th>Acute Flaccid Paralysis (2014-2019 per 100,000)</th>
<th>Acute Flaccid Paralysis (2020-2023 per 100,000)</th>
<th>Change (%)</th>
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<td>Barh el Ghazel</td>
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<td>0.05</td>
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Figure 3: Average number of annual Guinea worm cases in 2014-2019 vs. 2020-2023.
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Appendix 1

Supplementary tables

Table S1: Annual case counts by province for measles, 2014-2023.

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Table S6: Annual case counts by province for acute flaccid paralysis, 2014-2023.

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### R code

```r
# packages and source code
```

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```

library(readxl)
library(surveillance)
library(tidyr)
library(dplyr)
library(lubridate)
library(ggplot2)
library(table1)
library(MMWRweek)
library(shiny)
library(zoo)
library(ciTools)
library(MASS)
library(gridExtra)
library(raster)
library(mapdata)
library(sf)
library(reshape2)
```

source('./Rsetup/Farrington_setup.R')
source('./Rsetup/surv.ds.convert.R')
source('./Rsetup/glrpoisApp.R')
```

...  

```{r}
a1 <- read_excel("SL_Chad_database_vF.xlsx")
MMWRyear = a1$Année
MMWRweek = a1$Semaine

a2 <- a1 %>%
mutate(MMWRweek2Date(MMWRyear, MMWRweek))

a2 <- a2 %>%
  rename(year_week = 'MMWRweek2Date(MMWRyear, MMWRweek)') %>%
  rename(attack_rate = "Taux d'attaque")

a2 <- a2 %>%
  rename(cases = "Cas Suspects") %>%
  rename(disease = "Maladie/Condition") %>%
  rename(deaths = "Décès")

a2$year_week <- as.Date(a2$year_week, "%d%b%Y")

a2$disease[a2$disease == "Suspicion Fièvre Jaune"] <- "Fièvre Jaune"
a2$disease[a2$disease == "Suspicion Paludisme"] <- "Paludisme"

# rename provinces for shapefile merge

a2$Province[a2$Province == "BARH EL GAZAL"] <- "Barh el Ghazel"
a2$Province[a2$Province == "BATHA"] <- "Batha"
a2$Province[a2$Province == "BORKOU"] <- "Borkou"
```
a2$Province["CHARI BAGIRMI"] <- "Chari-Baguirmi"
a2$Province["ENNEDI EST"] <- "Ennedi Est"
a2$Province["ENNEDI OUEST"] <- "Ennedi Ouest"
a2$Province["GUERA"] <- "Guéra"
a2$Province["HADJER LAMIS"] <- "Hadjer-Lamis"
a2$Province["KANEM"] <- "Kanem"
a2$Province["LAC"] <- "Lac"
a2$Province["LOGONE OCCIDENTAL"] <- "Logone Occidental"
a2$Province["LOGONE ORIENTAL"] <- "Logone Oriental"
a2$Province["MANSOUR"] <- "Mandoul"
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a2$Province["MOYEN CHARI"] <- "Moyen-Chari"
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a2$Province["TANDJILE"] <- "Tandjilé"
a2$Province["TIBESTI"] <- "Tibesti"
a2$Province["N’DJAMENA"] <- "Ville de N’Djamena"
a2$Province["WADI FIRA"] <- "Wadi Fira"

# population vectors
```
# manual input of population total for Hadjer-Lamis due to "missing" for Mani district
pop1419 <- a2 %>%
  mutate(Population = ifelse(Province == "Hadjer-Lamis" & Année == 2015, 673249 , Population)) %>%
  distinct(Province, Population, Année) %>%
  group_by(Province) %>%
  summarise(pop17 = sum(Population)/6)
```

pop2023 <- a2 %>%
  filter(Année == 2020 | Année == 2021 | Année == 2022 | Année == 2023) %>%
  distinct(Province, Population, Année) %>%
  group_by(Province) %>%
  summarise(pop22 = sum(Population)/4)

a3 <- merge(a2, pop1419, by="Province", all.y= TRUE)
a4 <- merge(a3, pop2023, by="Province", all.y=TRUE)

# disease specific df
```
# [r]
a4 <- a4 %>%
  filter (disease == "Rougeole" | disease == "Meningite" | disease == "PFA" | disease == "TNN" | disease == "Ver de Guinée" | disease == "Fièvre Jaune" | disease == "Paludisme")
```
meas1 <- a4 %>%
  filter(disease == "Rougeole")
men1 <- a4 %>%
  filter(disease == "Meningite")
pfa1 <- a4 %>%
  filter(disease == "PFA")
tnn1 <- a4 %>%
  filter(disease == "TNN")
gworm1 <- a4 %>%
  filter(disease == "Ver de Guinée")
yfev1 <- a4 %>%
  filter(disease == "Fièvre Jaune")
mal1 <- a4 %>%
  filter(disease == "Paludisme")

# correct malaria input error
```
# week33 <- subset(mal1, year_week == "2023-08-13", select = c("cases", "year_week", "District"))
# df_total = sum(week33$cases)
# ppt_total = 51830
# diff_mal = df_total - ppt_total
# error1 = 326326
# error1 - diff_mal
```
mal1 <- mal1 %>%
  mutate(cases = ifelse(District == "Guelendeng" & year_week == "2023-08-13", 326, cases))

```
# annual counts
# [r]
a5 <- a4 %>%
  group_by(Année) %>%
  summarise(meas_cases = sum(cases[disease == "Rougeole"]),
            men_cases = sum(cases[disease == "Meningite"]),
            yfev_cases = sum(cases[disease == "Fièvre Jaune"]),
            tnn_cases = sum(cases[disease == "TNN"]),
            mal_cases = sum(cases[disease == "Paludisme"]),
            pfa_cases = sum(cases[disease == "PFA"]),
            gworm_cases = sum(cases[disease == "Ver de Guinée"]))
```

```
# TNN by distrct
# [r]
tnn2 <- tnn1 %>%
  filter(Année == 2023) %>%
```
group_by(District) %>%
summarise(case_tot = sum(cases), inc1 = case_tot / Population, inc2 = inc1 * 1000)

tnn3 <- tnn1 %>%
group_by(District) %>%
summarise(cases14 = sum(cases[Année == "2014"]),
cases15 = sum(cases[Année == "2015"]),
cases16 = sum(cases[Année == "2016"]),
cases17 = sum(cases[Année == "2017"]),
cases18 = sum(cases[Année == "2018"]),
cases19 = sum(cases[Année == "2019"]),
cases20 = sum(cases[Année == "2020"]),
cases21 = sum(cases[Année == "2021"]),
cases22 = sum(cases[Année == "2022"]),
cases23 = sum(cases[Année == "2023"]))

tnn4 <- tnn1 %>%
group_by(District) %>%
summarise(cases14 = (sum(cases[Année == "2014"]) / Population) * 1000,
cases15 = (sum(cases[Année == "2015"]) / Population) * 1000,
cases16 = (sum(cases[Année == "2016"]) / Population) * 1000,
cases17 = (sum(cases[Année == "2017"]) / Population) * 1000,
cases18 = (sum(cases[Année == "2018"]) / Population) * 1000,
cases19 = (sum(cases[Année == "2019"]) / Population) * 1000,
cases20 = (sum(cases[Année == "2020"]) / Population) * 1000,
cases21 = (sum(cases[Année == "2021"]) / Population) * 1000,
cases22 = (sum(cases[Année == "2022"]) / Population) * 1000,
cases23 = (sum(cases[Année == "2023"]) / Population) * 1000)

# by province
```{r}
meas_byyr <- meas1 %>%
group_by(Province, Année) %>%
summarise(prov_case = sum(cases))
meas_all <- dcast(meas_byyr, Province ~ Année)
men_byyr <- men1 %>%
group_by(Province, Année) %>%
summarise(prov_case = sum(cases))
men_all <- dcast(men_byyr, Province ~ Année)
yfev_byyr <- yfev1 %>%
group_by(Province, Année) %>%
summarise(prov_case = sum(cases))
yfev_all <- dcast(yfev_byyr, Province ~ Année)

tnn_byyr <- tnn1 %>%
group_by(Province, Année) %>%
summarise(prov_case = sum(cases))
tnn_all <- dcast(tnn_byyr, Province ~ Année)
mal_byyr <- mal1 %>%
group_by(Province, Année) %>%
summarise(prov_case = sum(cases))
mal_all <- dcast(mal_byyr, Province ~ Année)
```
pfa_byyr <- pfa1 %>%
group_by(Province, Année) %>%
summarise(prov_case = sum(cases))

pfa_all <- dcast(pfa_byyr,Province~Année)

```{r}
read_shape_URL <- function(URL){
  temp <- tempfile()
  download.file(url = URL, destfile = temp)
  temp2 <- tempfile()
  unzip(temp, exdir = temp2)
  st_read(dsn = temp2)
}

chad_map <- read_shape_URL("https://stacks.stanford.edu/file/druid:fm167kn7344/data.zip")

```{r}
meas_prov1 <- meas1 %>%
    Année == 2017 | Année == 2018 | Année == 2019) %>%
  rename(NAME_1 = "Province") %>%
  group_by(NAME_1) %>%
  summarise(incidence17 = (((sum(cases)/6)/pop17)*100000))

meas_prov2 <- meas1 %>%
  filter(Année == 2020 | Année == 2021 | Année == 2022 |
    Année == 2023) %>%
  rename(NAME_1 = "Province") %>%
  group_by(NAME_1) %>%
  summarise(incidence22 = (((sum(cases)/4)/pop22)*100000))
```

```{r}
meas_map2014 <- left_join(chad_map, meas_prov1, by = "NAME_1")
meas_map2020 <- left_join(chad_map, meas_prov2, by = "NAME_1")

meas_map1 <- ggplot(data = meas_map2014) +
  geom_sf(aes(fill = incidence17)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2014-2019") +
  coord_sf()

meas_map2 <- ggplot(data = meas_map2020) +
  geom_sf(aes(fill = incidence22)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2020-2023") +
  coord_sf()
```

```{r}
meas_map1 <- ggplot(data = meas_map2014) +
  geom_sf(aes(fill = incidence17)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2014-2019") +
  coord_sf()

meas_map2 <- ggplot(data = meas_map2020) +
  geom_sf(aes(fill = incidence22)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2020-2023") +
  coord_sf()
```

```{r}
meas_map1 <- ggplot(data = meas_map2014) +
  geom_sf(aes(fill = incidence17)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2014-2019") +
  coord_sf()

meas_map2 <- ggplot(data = meas_map2020) +
  geom_sf(aes(fill = incidence22)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2020-2023") +
  coord_sf()
```

```{r}
meas_map1 <- ggplot(data = meas_map2014) +
  geom_sf(aes(fill = incidence17)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2014-2019") +
  coord_sf()

meas_map2 <- ggplot(data = meas_map2020) +
  geom_sf(aes(fill = incidence22)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2020-2023") +
  coord_sf()
```

```{r}
meas_map1 <- ggplot(data = meas_map2014) +
  geom_sf(aes(fill = incidence17)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2014-2019") +
  coord_sf()

meas_map2 <- ggplot(data = meas_map2020) +
  geom_sf(aes(fill = incidence22)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2020-2023") +
  coord_sf()
```

```{r}
meas_map1 <- ggplot(data = meas_map2014) +
  geom_sf(aes(fill = incidence17)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2014-2019") +
  coord_sf()

meas_map2 <- ggplot(data = meas_map2020) +
  geom_sf(aes(fill = incidence22)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2020-2023") +
  coord_sf()
```

```{r}
meas_map1 <- ggplot(data = meas_map2014) +
  geom_sf(aes(fill = incidence17)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2014-2019") +
  coord_sf()

meas_map2 <- ggplot(data = meas_map2020) +
  geom_sf(aes(fill = incidence22)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2020-2023") +
  coord_sf()
```

```{r}
meas_map1 <- ggplot(data = meas_map2014) +
  geom_sf(aes(fill = incidence17)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2014-2019") +
  coord_sf()

meas_map2 <- ggplot(data = meas_map2020) +
  geom_sf(aes(fill = incidence22)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(5,170)) +
  ggtitle("Measles, 2020-2023") +
  coord_sf()
```
rename(NAME_1 = "Province") %>%
group_by(NAME_1) %>%
summarize(incidence17 = (((sum(cases)/6)/pop17)*100000))

men_prov2 <- men1 %>%
filter(Année == 2020 | Année == 2021 | Année == 2022 | Année == 2023) %>%
rename(NAME_1 = "Province") %>%
group_by(NAME_1) %>%
summarize(incidence22 = (((sum(cases)/4)/pop22)*100000))

men_map1 <- ggplot(data = men_map2014) +
 geom_sf(aes(fill = incidence17)) +
 scale_fill_continuous(high = "#132B43", low = "#56B1F7",
 name = "Cases per 100,000",
 limits = c(0, 30)) +
 ggtitle("Meningitis, 2014-2019") +
 coord_sf()

men_map2 <- ggplot(data = men_map2020) +
 geom_sf(aes(fill = incidence22)) +
 scale_fill_continuous(high = "#132B43", low = "#56B1F7",
 name = "Cases per 100,000",
 limits = c(0, 30)) +
 ggtitle("Meningitis, 2020-2023") +
 coord_sf()

# heat map malaria
mal_prov1 <- mal1 %>%
rename(NAME_1 = "Province") %>%
group_by(NAME_1) %>%
summarize(incidence17 = (((sum(cases)/6)/pop17)*100000))

mal_prov2 <- mal1 %>%
filter(Année == 2020 | Année == 2021 | Année == 2022 | Année == 2023) %>%
rename(NAME_1 = "Province") %>%
group_by(NAME_1) %>%
summarize(incidence22 = (((sum(cases)/4)/pop22)*100000))

mal_map1 <- ggplot(data = mal_map2014) +
 geom_sf(aes(fill = incidence17)) +
 scale_fill_continuous(high = "#132B43", low = "#56B1F7",
 name = "Cases per 100,000",
 limits = c(2000, 23500)) +
 ggtitle("Malaria, 2014-2019") +
 coord_sf()

mal_map2 <- ggplot(data = mal_map2020) +
geom_sf(aes(fill = incidence22)) +
scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(2000, 23500)) +
ggtitle("Malaria, 2020-2023") +
coord_sf() ... 

# heat map yellow fever
```r```
yfev_prov1 <- yfev1 %>%
        Année == 2017 | Année == 2018 | Année == 2019) %>%
    rename(NAME_1 = "Province") %>%
    group_by(NAME_1) %>%
    summarize(incidence17 = ((sum(cases)/6)/pop17)*100000)
yfev_map1 <- ggplot(data = yfev_map2014) +
geom_sf(aes(fill = incidence17)) +
scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(0, 20)) +
ggtitle("Yellow Fever, 2014-2019") +
coord_sf() ... 

```r```
yfev_map2014 <- left_join(chad_map, yfev_prov1, by = "NAME_1")
yfev_map2020 <- left_join(chad_map, yfev_prov2, by = "NAME_1")
```r```
yfev_map1 <- ggplot(data = yfev_map1) +
geom_sf(aes(fill = incidence17)) +
scale_fill_continuous(high = "#132B43", low = "#56B1F7",
    name = "Cases per 100,000",
    limits = c(0, 20)) +
ggtitle("Yellow Fever, 2014-2019") +
coord_sf() ... 

# heat map neonatal tetanus
```r```
tnn_prov1 <- tnn1 %>%
        Année == 2017 | Année == 2018 | Année == 2019) %>%
    rename(NAME_1 = "Province") %>%
    group_by(NAME_1) %>%
    summarize(incidence17 = ((sum(cases)/6)/pop17)*100000)
tnn_prov2 <- tnn1 %>%
    filter(Année == 2020 | Année == 2021 | Année == 2022 |
        Année == 2023) %>%
    rename(NAME_1 = "Province") %>%
    group_by(NAME_1) %>%
    summarize(incidence22 = ((sum(cases)/4)/pop22)*100000) ... 
```
```r```
tnn_map2014 <- left_join(chad_map, tnn_prov1, by = "NAME_1")

tnn_map2020 <- left_join(chad_map, tnn_prov2, by = "NAME_1")

# heat map pfa
```{r}
pfa_map2014 <- ggplot(data = pfa_map2014) + geom_sf(aes(fill = incidence17)) +
scale_fill_continuous(high = "#132B43", low = "#56B1F7", 
    name = "Cases per 100,000", 
    limits = c(0, 12)) +
ggtitle("Acute Flaccid Paralysis, 2014-2019") +
coord_sf()
```

# heat map guinea worm
```{r}
gworm_map2014 <- ggplot(data = gworm_map2014) + geom_sf(aes(fill = incidence22)) +
scale_fill_continuous(high = "#132B43", low = "#56B1F7", 
    name = "Cases per 100,000", 
    limits = c(0, 12)) +
ggtitle("Guinea Worm, 2014-2019") +
coord_sf()
```
rename(NAME_1 = "Province") %>%
group_by(NAME_1) %>%
summarize(case_tot = sum(cases)/6)

gworm_prov2 <- gworm1 %>%
filter(Année == 2020 | Année == 2021 | Année == 2022 |
Année == 2023) %>%
rename(NAME_1 = "Province") %>%
group_by(NAME_1) %>%
summarize(case_tot = sum(cases)/4)

```{r}
gworm_map2014 <- left_join(chad_map, gworm_prov1, by = "NAME_1")
gworm_map2020 <- left_join(chad_map, gworm_prov2, by = "NAME_1")
gworm_map1 <- ggplot(data = gworm_map2014) +
  geom_sf(aes(fill = case_tot)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7", 
                        name = "Cases", 
                        limits = c(0, 10)) +
  ggtitle("Guinea Worm, 2014-2019") +
  coord_sf()
gworm_map2 <- ggplot(data = gworm_map2020) +
  geom_sf(aes(fill = case_tot)) +
  scale_fill_continuous(high = "#132B43", low = "#56B1F7", 
                        name = "Cases", 
                        limits = c(0, 10)) +
  ggtitle("Guinea Worm, 2020-2023") +
  coord_sf()
```

# view heat maps
```{r}
ggridExtra::grid.arrange(meas_map1, meas_map2, ncol=2)
ggridExtra::grid.arrange(men_map1, men_map2, ncol=2)
ggridExtra::grid.arrange(yfev_map1, yfev_map2, ncol=2)
ggridExtra::grid.arrange(tnn_map1, tnn_map2, ncol=2)
ggridExtra::grid.arrange(pfa_map1, pfa_map2, ncol=2)
ggridExtra::grid.arrange(mal_map1, mal_map2, ncol=2)
ggridExtra::grid.arrange(gworm_map1, gworm_map2, ncol=2)
```

# incidence change
```{r}
meas_incdn <- merge(meas_prov1, meas_prov2, by="NAME_1", all = TRUE) %>%
distinct(NAME_1, incidence17, incidence22) %>%
mutate(incd_change = ((incidence22 - incidence17)/incidence17)*100)

men_incdn <- merge(men_prov1, men_prov2, by="NAME_1", all = TRUE) %>%
distinct(NAME_1, incidence17, incidence22) %>%
mutate(incd_change = ((incidence22 - incidence17)/incidence17)*100)

yfev_incdn <- merge(yfev_prov1, yfev_prov2, by="NAME_1", all = TRUE) %>%
distinct(NAME_1, incidence17, incidence22) %>%
mutate(incd_change = ((incidence22 - incidence17)/incidence17)*100)

tnn_incdn <- merge(tnn_prov1, tnn_prov2, by="NAME_1", all = TRUE) %>%
distinct(NAME_1, incidence17, incidence22) %>%
mutate(incd_change = ((incidence22 - incidence17)/incidence17)*100)
```
pfa_incdn <- merge(pfa_prov1, pfa_prov2, by="NAME_1", all = TRUE) %>%
distinct(NAME_1, incidence17, incidence22) %>%
mutate(incd_change = ((incidence22 - incidence17)/incidence17)*100)

mal_incdn <- merge(mal_prov1, mal_prov2, by="NAME_1", all = TRUE) %>%
distinct(NAME_1, incidence17, incidence22) %>%
mutate(incd_change = ((incidence22 - incidence17)/incidence17)*100)

# time series of case counts
```
# measles
meas_count_ts <- meas1 %>%
  group_by(year_week) %>%
  summarize(meas1 = sum(cases)) %>%
  tidyr::complete(year_week=seq.Date(min(year_week, na.rm=T),
  max(year_week, na.rm=T), 'week'),
  fill=list(meas1=0))

p1_meas_count = ggplot(meas_count_ts,
  aes(x=year_week, y=meas1)) +
  geom_line() +
  theme_classic() +
  ylim(0,NA) +
  ylab('Cases') +
  xlab('Date') +
  ggtitle('Measles, 2014-2023')

# meningitis
men_count_ts <- men1 %>%
  group_by(year_week) %>%
  summarize(men1 = sum(cases)) %>%
  tidyr::complete(year_week=seq.Date(min(year_week, na.rm=T),
  max(year_week, na.rm=T), 'week'),
  fill=list(men1=0))

p1_men_count = ggplot(men_count_ts,
  aes(x=year_week, y=men1)) +
  geom_line() +
  theme_classic() +
  ylim(0,NA) +
  ylab('Cases') +
  xlab('Date') +
  ggtitle('Meningitis, 2014-2023')

# yellow fever
yfev_count_ts <- yfev1 %>%
  group_by(year_week) %>%
  summarize(yfev1 = sum(cases)) %>%
  tidyr::complete(year_week=seq.Date(min(year_week, na.rm=T),
  max(year_week, na.rm=T), 'week'),
  fill=list(yfev1=0))

p1_yfev_count = ggplot(yfev_count_ts,
  aes(x=year_week, y=yfev1)) +
  geom_line() +
  theme_classic() +
  ylim(0,NA) +
  ylab('Cases') +
  xlab('Date') +
  ggtitle('Yellow Fever, 2014-2023')

# malaria
mal_count_ts <- mal1 %>%
  group_by(year_week) %>%
  summarize(mal1 = sum(cases)) %>%
  tidyr::complete(year_week=seq.Date(min(year_week, na.rm=T),
  max(year_week, na.rm=T), 'week'),
  fill=list(mal1=0))

p1_mal_count = ggplot(mal_count_ts,
  aes(x=year_week, y=mal1)) +
geom_line() +
theme_classic() +
ylim(0, NA) +
ylab('Cases') +
xlab('Date') +
ggtitle('Malaria, 2014-2023')

# polio
pfa_count_ts <- pfa1 %>%
group_by(year_week) %>%
summarize(pfa1 = sum(cases)) %>%
tidy::complete(year_week = seq.Date(min(year_week, na.rm = T), max(year_week, na.rm = T), 'week'), fill = list(pfa1 = 0))

p1_pfa_count = ggplot(pfa_count_ts, aes(x = year_week, y = pfa1)) +
geom_line() +
theme_classic() +
ylim(0, NA) +
ylab('Cases') +
xlab('Date') +
ggtitle('Acute Flaccid Paralysis, 2014-2023')

# tn
tnn_count_ts <- tnn1 %>%
group_by(year_week) %>%
summarize(tnn1 = sum(cases)) %>%
tidy::complete(year_week = seq.Date(min(year_week, na.rm = T), max(year_week, na.rm = T), 'week'), fill = list(tnn1 = 0))

p1_tnn_count = ggplot(tnn_count_ts, aes(x = year_week, y = tnn1)) +
geom_line() +
theme_classic() +
ylim(0, NA) +
ylab('Cases') +
xlab('Date') +
ggtitle('Neonatal Tetanus, 2014-2023')

# guinea worm
gworm_count_ts <- gworm1 %>%
group_by(year_week) %>%
summarize(gworm1 = sum(cases)) %>%
tidy::complete(year_week = seq.Date(min(year_week, na.rm = T), max(year_week, na.rm = T), 'week'), fill = list(gworm1 = 0))

p1_gworm_count = ggplot(gworm_count_ts, aes(x = year_week, y = gworm1)) +
geom_line() +
theme_classic() +
ylim(0, NA) +
ylab('Cases') +
xlab('Date') +
ggtitle('Guinea Worm, 2014-2023')

p2_gworm_count = ggplot(gworm_count_ts, aes(x = year_week, y = gworm1)) +
geom_line() +
theme_classic() +
ylim(0, NA) +
scale_x_date(limits = as.Date(c("2013-12-29","2023-12-24"))) +
ylab('Cases') +
xlab('Date') +
ggtitle('Guinea Worm, 2014-2023')

...
meas_count_ts2 <- meas_count_ts %>%
    mutate(case_03 = zoo::rollmean(meas1, k = 3, fill = NA),
           case_05 = zoo::rollmean(meas1, k = 5, fill = NA),
           case_09 = zoo::rollmean(meas1, k = 15, fill = NA)) %>%
    dplyr::ungroup()

# meningitis
men_count_ts2 <- men_count_ts %>%
    mutate(case_03 = zoo::rollmean(men1, k = 3, fill = NA),
           case_05 = zoo::rollmean(men1, k = 5, fill = NA),
           case_09 = zoo::rollmean(men1, k = 15, fill = NA)) %>%
    dplyr::ungroup()

tnn_count_ts2 <- tnn_count_ts %>%
    mutate(case_03 = zoo::rollmean(tnn1, k = 3, fill = NA),
           case_05 = zoo::rollmean(tnn1, k = 5, fill = NA),
           case_09 = zoo::rollmean(tnn1, k = 15, fill = NA)) %>%
    dplyr::ungroup()

pfa_count_ts2 <- pfa_count_ts %>%
    mutate(case_03 = zoo::rollmean(pfa1, k = 3, fill = NA),
           case_05 = zoo::rollmean(pfa1, k = 5, fill = NA),
           case_09 = zoo::rollmean(pfa1, k = 15, fill = NA)) %>%
    dplyr::ungroup()

# plots
p2_meas = ggplot(meas_count_ts, aes(x=year_week, y=meas1)) +
    geom_line(color='gray') +
    geom_line(data=meas_count_ts2, aes(x=year_week, y=case_05), color='red') +
    geom_line(data=meas_count_ts2, aes(x=year_week, y=case_09), color='blue') +
    theme_classic() +
    ylim(0,NA) +
    ylab('Cas') +
    xlab('Date') +
    ggtitle('Cas de rougeole')

p2_men = ggplot(men_count_ts, aes(x=year_week, y=men1)) +
    geom_line(color='gray') +
    geom_line(data=men_count_ts2, aes(x=year_week, y=case_05), color='red') +
    geom_line(data=men_count_ts2, aes(x=year_week, y=case_09), color='blue') +
    theme_classic() +
    ylim(0,NA) +
    ylab('Cas') +
    xlab('Date') +
    ggtitle('Cas de méningite')

p2_tnn = ggplot(tnn_count_ts, aes(x=year_week, y=tnn1)) +
    geom_line(color='gray') +
    geom_line(data=tnn_count_ts2, aes(x=year_week, y=case_09), color='blue') +
    theme_classic() +
    ylim(0,NA) +
    ylab('Cases') +
    xlab('Date') +
    ggtitle('Neontal Tetanus, 2014-2023')

p2_pfa = ggplot(pfa_count_ts, aes(x=year_week, y=pfa1)) +
    geom_line(color='gray') +
    geom_line(data=pfa_count_ts2, aes(x=year_week, y=case_09), color='blue') +
    theme_classic() +
    ylim(0,NA) +
    ylab('Cases')+ 34
```r
# view plots - counts
gridExtra::grid.arrange(p1_meas_count, p1_men_count, p1_yfev_count, p2_tnn, ncol=2)
gridExtra::grid.arrange(p1_mal_count, p1_pfa_count, p2_gworm_count, ncol=2)
```

```