

symptoms were rash (67%), fever (42%), and arthritis/arthralgia (24%). In two cases, ZIKV was reported in the father. Mean gestational age at birth was 37.8 weeks (± 1.95 weeks), and 13% were born ≤ 36 weeks. The mean HC was 28.1 cm (SD ± 2.1 cm). Severe microcephaly was detected in 67 (84%) cases, and 41% had an HC on the zero percentile for gestational age. Having insurance was associated with higher mean HC ($P = 0.01$) while preterm birth was associated with lower mean HC ($P = 0.004$). None of the variables were found to be significant predictors of HC z-score or severe microcephaly.

Conclusion. There was substantial infant morbidity during the 2016–2017 epidemic. Most infants were born to asymptomatic women or women not reported to the Ministry during acute illness. More cases of microcephaly have been reported beyond the observation period which highlights the need for continued surveillance.

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448. Can Electronic Clinical Notes Identify Travelers with Zika?

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Background. Travel history can help differentiate a public health emergency from a travel-related infection by providing information on exposure but such information is often available only in unstructured clinical documents. We explored the feasibility extracting these mentions from the electronic health record in an automated fashion.

Methods. As a collaboration with the National Biosurveillance Integration Center (NBIC), clinical notes were extracted from patient encounters with Zika, dengue and chikungunya virus testing in the Department of Veterans Affairs (VA; a large healthcare system providing care in its facilities from Puerto Rico to the Philippines) between January 1, 2015 and February 28, 2016. From a corpus of 250,133 notes, we gathered a collection of 4,584 unique snippets by an automated bootstrapping process to identify documents containing potentially relevant information using phrases and travel locations. After establishing a guideline, snippets were manually annotated for travel affirmation and locations visited (see Figure 1). Using machine learning including a neural language model, snippets were used to train a Conditional Random Field (CRF) model to extract affirmed travel locations outside of the continental United States. We did not extract the time of travel.

Results. Of annotated snippets, 2,659 (58%) contained an affirmed mention of travel history whereas 347 (7.6%) were negated. An inter-rater reliability (IRR) analysis resulted in an agreement of 89% and an associated kappa-coefficient of 0.65. Analysis of annotated snippets resulted in 551 unique location strings identified (see Figure 2). On a held out test set of 459 snippets (10%), the machine learning model achieved performance metrics of 85.6% positive predictive value and 76.7% sensitivity. The algorithm now runs daily and is being evaluated for prospective use (see Figure 3).

Conclusion. Targeted travel history extraction is feasible in a large medical system with acceptable accuracy. Our approach was able to extract novel places that would not necessarily be found in a curated list (e.g., Mexican Riviera). Further research could improve accuracy and could incorporate this into models improving the early detection of autochthonous transmission.

Example snippets	Negated?
... she returned from <u>Trinidad</u> and not feeling well ...	No
... denies bug bites and also traveled to <u>Dibouti</u> on the trip ...	No
... Any recent Travel? <u>Jakarta</u> ...	No
... Pt did not travel to <u>Laos</u> or the <u>South of Bali</u> ...	Yes
...In the past 21 days, have you traveled to <u>West Africa</u> ? [] Y [X] N...	Yes

Figure 1: Synthetic examples similar to annotated candidate snippets. Example location annotation text spans are underlined. Besides identifying travel locations, status of negation was also captured.

Positive Locations	Negated Locations
Iraq	Liberia
Mexico	Guinea
Dominican Republic	Sierra Leone
Costa Rica	Democratic Republic of Congo
Vietnam	West Africa
Afghanistan	Mali
Puerto Rico	Nigeria
Jamaica	Western Africa

Figure 2: Human annotated location mentions ranked by descending frequency which were positively affirmed or negated. Some mentions vary by geographic specificity (e.g. regions, countries, territories) since annotators were guided to annotate any location type. Many positive locations include likely military deployments and many negated locations are likely due to template questions about potential exposure to the Ebola virus.

Extracted Location	Count
Vietnam	571
Iraq	569
Mexico	392
Costa Rica	301
Dominican Republic	259
Afghanistan	254
Jamaica	160
Honduras	134
Kuwait	109
Brazil	94

Figure 3: Location strings extracted using the CRF model from the full set of 250,133 notes. Locations filtered to gazetteer entries of country names from geonames.org.

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449. Post-Hurricane Maria Surveillance for Infectious Diseases in the Veterans Affairs San Juan Medical Center, Puerto Rico

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Background. On September 20, 2017 Category 4 Hurricane Maria made landfall in Puerto Rico (PR), causing widespread flooding, power outages, and lack of water service. Given the potential for infectious disease outbreaks, the Department of Veterans Affairs (VA) and Centers for Disease Control and Prevention established enhanced surveillance to actively monitor priority infections at VA facilities.

Methods. We queried VA data sources from August 27, 2017 to February 3, 2018 (pre-storm dates included to establish baselines). Trends in infectious disease ICD-10 syndrome groupings (respiratory illness/pneumonia, influenza-like illness (ILI), gastrointestinal illness, conjunctivitis, rash-like illness, jaundice) as a percent of total emergency department (ED) visits were tracked. The total number of laboratory tests performed, and percent positive per week, for influenza, hepatitis A, dengue (DENV), zika (ZIKV), leptospirosis, and chikungunya (CHIKV) were calculated.

Results. ILI increased from 9.3% to 12.6% during the surveillance period (peak epi week 52: 15.7%) (Figure 1), while other ICD-10–based syndromes remained relatively stable. Weekly influenza testing increased shortly after landfall averaging 105 rapid influenza tests per week (epi weeks 41–4) (Figure 2). Influenza positivity increased in epi weeks 41 and 42 (7%), dropping the following weeks, and peaked at 15% in epi week 2 (Figure 3). Four acute infections were detected: 2 + leptospirosis DNA, 1 + CHIKV RNA, and 1 + Hepatitis A IgM. The remaining 34 positive tests were ZIKV, CHIKV, or DENV IgM positive or equivocal, awaiting confirmation (Figure 3).

Conclusion. We quickly established a simple surveillance system to monitor trends in priority infectious diseases. Increases in ILI, weekly influenza testing volume, and percent positive of influenza tests coincided with onset of influenza season. Diseases of public health importance were identified through laboratory-based surveillance. The impact of Maria on VA healthcare operations, including clinic closures, power outages, and disrupted care seeking patterns limited this system. However, the timeliness and flexibility of this surveillance system provides a model for disease monitoring following future natural disasters.

Figure 1.

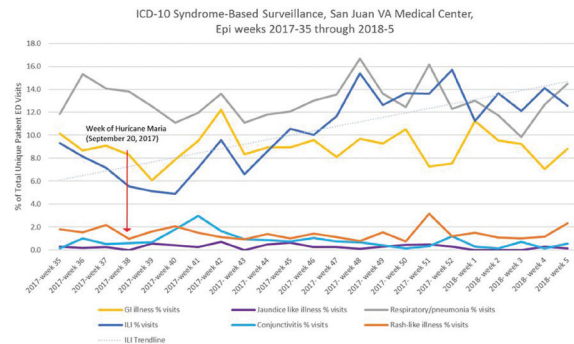


Figure 2.

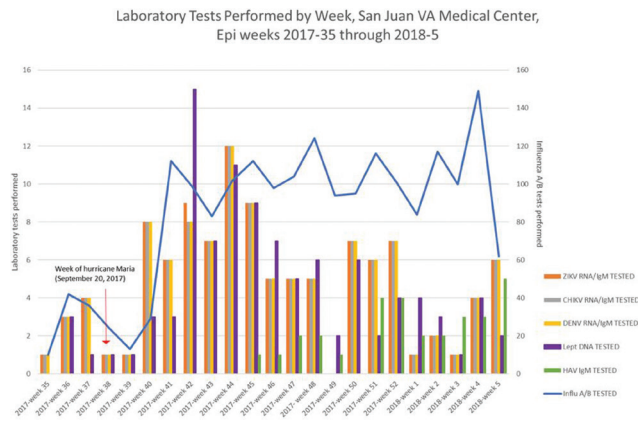
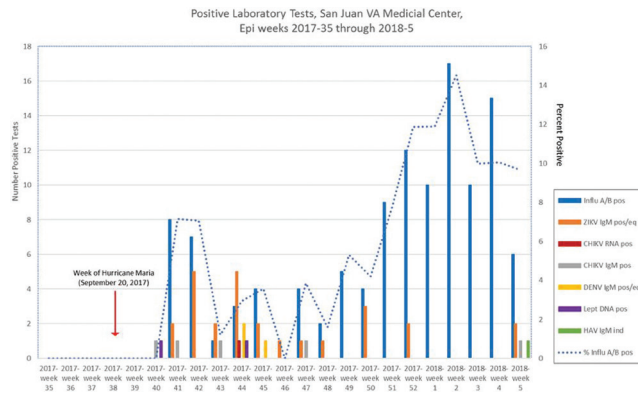


Figure 3.



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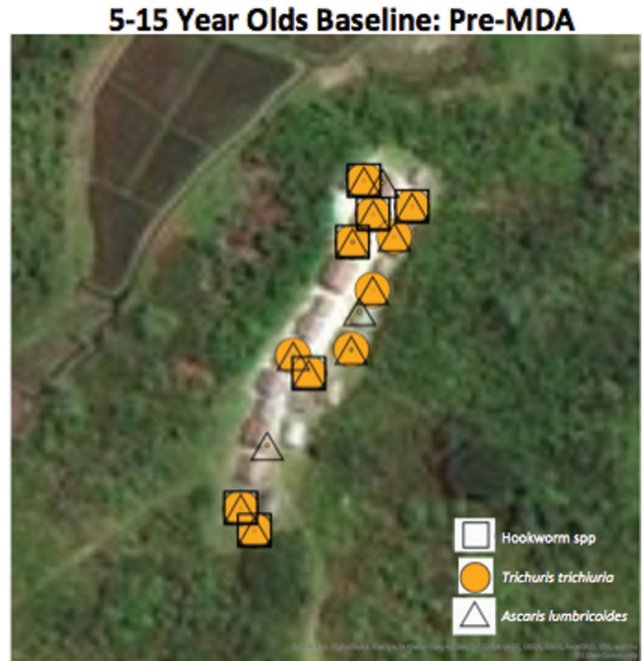
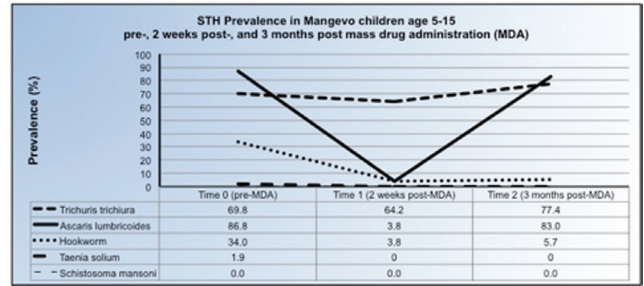
450. Using Geographical Information Systems to Interpret the Efficacy of Mass Drug Administration for Soil-Transmitted Helminthiasis in Rural Madagascar
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Background. In Madagascar, mass drug administration (MDA) of anti-parasitics is administered every 6 months to combat soil-transmitted helminthiasis (STH) in school-aged children, although little information exists as to its efficacy. In recent years, geographical information systems (GIS) have been used for visualization of patterns in disease epidemiology. This inexpensive technology may be leveraged to aid in education of local health workers toward a more integrated approach to control STH.

Methods. Baseline questionnaires and stool/blood samples were collected from participants of Mangevo, a rural village in southeast Madagascar. GPS coordinates and qualitative descriptions were collected from all village homes, common latrines, and animal pens. All children 5–15 years old were given MDA per WHO protocol. Stool was again collected from these children 2 weeks later and 3 months later. Parasitological examination of stool samples for STH eggs was performed using Spontaneous Sedimentation Technique. Results were overlaid onto GIS maps and used to further educate the local mobile health team.

Results. A total of 183 participants were eligible for the study. Analysis found 89% of adults >15 years old were infected with one or more parasite and 100% of children 5–15 were infected with one or more parasite at time 0. *Trichuris trichuria* prevalence fell 8% ($P < 0.5$) in 2 weeks and climbed 17% ($P < 0.05$) by 3 months follow-up. *Ascaris lumbricoides* prevalence fell 96% ($P < 0.0001$) in the 2 weeks and climbed 95% ($P < 0.0001$) by 3 months follow-up. Hookworm prevalence dropped 89% ($P < 0.0001$) in 2 weeks and climbed 5% ($P < 0.5$) by 3 months follow-up. Prevalence data, descriptive results, and GPS coordinates of village homes were integrated into a GIS maps pre- and post-MDA of children, and pre-MDA for adults.



Conclusion. While GIS has been used to yield insights into the ecology of infection, this study examined the efficacy of the current MDA through the lens of small scale GIS mapping. This may be an ideal and inexpensive technology to help in the implementation of future interventions of the government-mandated STH treatment protocol and work toward the strengthening of local health teams.

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451. High-Frequency of Multi-Drug-Resistant Organisms (MDRO) at University Teaching Hospital (UTH), Lusaka, Zambia

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Background. Antibiotic resistance is a worldwide problem. Prior studies on patterns of resistance in Zambia depended on laboratory methods that lacked standardization. UTH is a 1,655-bed quaternary care hospital and the primary teaching hospital of Zambia. Since 2015, the microbiology laboratory has used Vitek 2 Compact (bioMérieux, Inc., France) for standardized detection of resistance.

Methods. We conducted a retrospective cross-sectional study of data collected on bacterial isolates analyzed from July 2015 to April 2017. We entered the data into WHONET 5.6 and aggregated it to develop hospital antibiograms. Due to high levels of resistance, we defined susceptible, intermediate, and resistant as >70%, 40–70%, and <40% of isolates sensitive to a drug, respectively. To improve usability, a version replacing the percent susceptible with these categories was developed.

Results. We analyzed 2,019 isolates to identify susceptibility patterns to commonly used antibiotics at UTH. *Escherichia coli* and *Klebsiella pneumoniae*, the most commonly isolated Gram-negative (GN) organisms, were resistant to most drugs including ceftriaxone, indicating high rates of extended-spectrum β -lactamase production. Methicillin-resistant *Staphylococcus aureus* (MRSA) made up 37% of *S. aureus*