YF Weekly Epidemiological Surveillance (WES) data and malaria RDT-positivity monthly averages for acute febrile illnesses (AFI) for the two sub-counties in the same period.

Results: Nationally, 1,882 and 710 suspected cases of YF were reported monthly and WES respectively, representing a respective average monthly and weekly notification of 18 and 13 cases. Average malaria positivity rate for health facilities in Kebisomi among AFI patients ranged between 3.6 – 27.0% while in Buwunga, malaria positivity rate ranged between 40.0 – 60.0%.

Conclusion: The high number of uninvestigated suspected YF cases in Uganda and the reporting of the cases as aggregate data demonstrate a missed opportunity to detect YF outbreaks as this reporting makes retrospective suspect case follow up impossible. Additionally, case-based YF surveillance among YF suspect cases and the malaria negative acute febrile illness pool could increase the detection of YF cases.

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20.060

A real-time surveillance dashboard for monitoring viral phenotype from sequence

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Purpose: Genome sequencing has become routine in outbreak surveillance. Apart from its utility in tracking evolutionary trajectories, genome sequences also contain information necessary for predicting biochemical phenotypes of outbreak pathogens, such as drug resistance and antigenic distance from vaccine strains. Having the capability to predict and visualize a pathogen's phenotype from its genome, in real-tiem, and at a location near the source of the outbreak, would provide epidemiologists with additional useful data that could help tailor outbreak responses and appropriately mobilize limited resources.

Methods & Materials: We provide a design for an extensible digital dashboard for infectious disease genomic surveillance. This open-source dashboard is written in the Python programming language. The application back-end is written using the Flask web framework. Automated machine learning model and parameter selection is enabled using the 'numpy' and 'scikit-learn' packages. Data visualization is provided by the 'bokeh' package. Data are stored in SQLite databases. Automated tests using 'py.test' are used to test for data and application integrity. The dashboard's backend is modularly designed, with separate "microservices" for the web interface, data ingestion and preprocessing, machine learning, and visualization. This design enables the addition of new pathogens, phenotypes, machine learning models, and visualization types as needed.

Results: We have developed a proof-of-concept dashboard, using sequence-phenotype data from the HIV drug resistance database and the Los Alamos HIV Sequence Database.The dashboard takes in a new virus' sequence, and returns a visualization of its predicted drug resistance profile. We show how research groups can programmatically submit standardized phenotype data to update the database and machine learning models. We demonstrate the portability of the data and models. We also provide examples on how to extend the dashboard.

Conclusion: New "gold-standard" genotype-phenotype data and integrated prediction systems are required to fully realize the utility of genomic sequencing data by connecting genotype to phenotype. We have designed this dashboard, and implemented a proof-of-concept, as part of our efforts to realize this vision.

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20.061

A surveillance system of diseases of small companion animals in the Veneto Region (Italy)

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Purpose: Experts and international public health organizations stress the lack of surveillance systems of diseases of companion animals and the necessity of implementing it as a priority of the One Health perspective. This paper proposes a project addressing this public health challenge. It presents the features of a system for collection, analysis, interpretation and dissemination of data about the health status of pets in the Veneto Region, Italy.

Methods & Materials: The system provides the construction of a web-based database containing the diagnoses of transmissible and non-transmissible diseases of dogs and cats made by veterinary practitioners joining the initiative voluntarily and without profit. Each diagnosis constitutes a single record, also containing data on the identification of the individual animal and on several characteristics of epidemiological relevance. The WHO International Classification of Diseases of humans has been adapted to canine and feline diseases to standardize the diagnostic nomenclature. A software for on-line data entry and data management has been specifically created.

Results: Up to now about the 12% (n=80) of the overall veterinary practices of the Veneto Region have joined the project and about 1000 (∥750 dogs and ∥250 cats) records have been entered the database. Three basic epidemiological reports have been distributed among the network and other stakeholders (veterinary associations, people responsible for human and animal health public services, academic experts). Reports and other interactive resources are freely obtainable from the website of the project.

Conclusion: Expected outcomes are to monitor disease frequencies and their behaviour in time and space, to identify associated risk factors and to produce disease and risk maps, thus providing epidemiological knowledge supporting the everyday clinical practice. Further expected outcomes are to assess the risk of transmission to humans and to set off the possible role of pets as early sentinels of emerging health threats and as models for the study of the effects of the exposure to environmental risk factors. The perspective is to stimulate networking within the veterinary profession and between human and animal health professionals, to promote general awareness of the public health relevance of pets and to provide a useful tool to scientists and health policy makers.

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