

(1) Submission ID#1539777

Interactive Visual Exploration of Neisseria Meningitidis

Author(s)

Margaret J. Varga, PhD

Senior Researcher

Department of Biology, University of Oxford

Holly B. Bratcher, Doctor

Senior researcher and laboratory manager

University of Oxford

Keith A. Jolley, PhD

Senior Researcher

Department of Biology, University of Oxford

James E. Bray, PhD

Senior Researcher

Department of Biology, University of Oxford

Martin C. J. Maiden, PhD

Professor

Department of Biology, University of Oxford

Background

Bacterial meningitis is a widely distributed infectious disease of the human brain that occurs worldwide. A major cause of this often-fatal disease is the bacterium *Neisseria meningitidis* (Nm), also called the meningococcus, which can also grow in the blood causing septicaemia (sepsis). These two diseases can occur separately and are described collectively as invasive meningococcal disease (IMD). Nm causes sporadic, endemic, epidemic outbreaks of IMD worldwide with seasonal variation. Although IMD affects most age groups, age distribution is not uniform, with the highest rates often seen in infants, children and teenagers. However, there are several safe and effective vaccines that can prevent IMD and these have resulted in a dramatic reduction in the global burden of the disease. Decisions, however, always need to be made on which vaccine is appropriate.

Aim/Methods

The Meningococcal Deduced Vaccine Antigen Reactivity (MenDeVAR) Index, which is publicly available on the PubMLST (<https://pubmlst.org>) website, provides an effective metric for analysis of the occurrence and the possible immunological cross-reactivity of the different meningococcal vaccine antigen variants. Genomics specialists and non-specialists can use the MenDeVAR Index to assess the likely reactivity of vaccines for individual cases, for outbreak management and assessment of public health vaccine programs, as well as

retrospective analysis. The availability of IMD isolates, their genomes, and/or non-culture diagnosis provides for the surveillance of the disease and the assessment of the effect of vaccines. However, sheer volume and complexity of the genomic data in its raw form is difficult to understand and exploit. Visual analytics can transform these inherently complex non-visual data into visual forms that enable users easily to exploit the data to gain insights for surveillance and assessment.

Results

An interactive visual analytics dashboard has been developed that provides an effective means for users to explore, analyse and compare the disease and vaccine reactivities in different serogroups in different geographical locations and temporally.

Conclusions

Visual analytics is a powerful enabler in this application where there is a vast volume of complex genomic and its associated provenance data.