INTRODUCTION
Invasive Meningococcal Disease (IMD) is caused by the human-associated bacterium Neisseria meningitidis when it invades the blood, causing septicemia, and/or the meninges, causing meningitis. IMD affects most nations and age groups, though age distribution is not uniform, with the highest rates in infants, children and teenagers. Epidemiological information is crucial for the public health response.

CHALLENGES
There are reference databases of genomic data, including PubMLST.org, which have been developed to facilitate open access. PubMLST contains extensive curated databases of over 100 different microbial species and genera. The large size and complexity of these rich genomic databases mean that it is very difficult to gain insight into, and understanding of, the information they contain.

INTERACTIVE WEB-BASED IMD STORYBOARD
We have developed an interactive web-based ‘Storyboard’, using data from PubMLST, that provides information on IMD occurrence in England. The Storyboard is directed at both public engagement and disease surveillance applications. It supports user exploration and analysis of the time-evolution of, and detail about, the changes in, and distribution of, IMD. Users can interactively explore the epidemiological years, serogroup, clonal complex, geographical region and age group, and thus, for instance, discern patterns and trends of disease, Figures 1 - 3.

CONCLUSIONS
The Storyboard enables users to explore and understand the complex information in an easy manner, and without the need for training or a user manual.

This system is applicable to all types of users: the general public, policy makers and decision makers, epidemiologists, researchers, genomics specialists and others.

FUNDING
Meningitis Research Foundation (MRF) and Biomedical Resource Grant from the Wellcome Trust.