

Artefact Agreement

Webscape Team

1. Introduction

The Webscape team has been assigned a Capstone Project titled “Staphopia User Portal”. This project worked with The Read Lab at Emory University which is based in Atlanta, USA to build upon the existing work from a previous capstone team. The Read Lab based at Emory University works on sequencing and computational analysis of infectious pathogens. The main domain of this project is in the health and research sector, focusing on bacterial pathogen *Staphylococcus Aureus* (S. Aureus) and its antimicrobial resistance (AMR) genes, with our clients being Professor Timothy Read in Emory University and Professor Jim Hogan in the Queensland University of Technology. The clients want to have a user- friendly, readily usable system that allows scientists and clinicians to find strains of a pathogen bacterial and its relationship to others, especially S. Aureus.

2. The Artefact

Scope:

After discussing with the clients, the goals for the current state of this project are to add new features of finding and predicting AMR genes in S. Aureus samples; and to improve features from a previous Capstone Project. The clients have provided to our team a Staphopia API and we have been tasked to work with the data provided in the API to extend new features for the website.

Below are the objectives for the project:

- Display and visualize the relationship of AMR genes of every sample of S. Aureus with 2 visualizations.
- Allow user interaction with the visualizations.
- Enhance the system with search, filter, and showing metadata functions.

The Medium Fidelity Prototype for the Website can be seen in [Figure 3].

To be delivered:

Basic Features:

A user-friendly user portal for exploring the AMR relationship among all samples. The system should include 2 AMR visualizations:

1. AMR Bubble Graph

The graph above does not represent the final design that the project intends to do [Figure 1]. The idea of this prototype the size of the circles represents the percentage of samples in Staphopia API resist to which antibiotics, whereas the circles representing the antibiotics.

The Medium Fidelity Prototype for the Bubble Graph can be seen in [Figure 4].

2. AMR Node Network

The nodes would represent the samples and the edges connect two nodes when the nodes have the same antibiotic resistance. The weight of the edges could be calculated by the number of the same antibiotics found between the two nodes [Figure 2].

The Medium Fidelity Prototype for the Node Graph can be seen in [Figure 5].

Advanced Features:

1. User interactions with visualizations

User should be able to drag, select, add, and remove samples from the visualizations. Hovering, click actions will clearly highlight the sample.

2. Showing sample metadata and AMR information

In the AMR visualizations page, there are panels that show AMR information of the sample and the antibiotics when user select the sample.

3. Handover Details:

The deliverables will be provided to the project supervisor Jim Hogan via a Github repository and a deployed User Acceptance Testing server deployed on Heroku.

User stories will be presented along with the artefacts showing the system, how to integrate with the previous projects in terms of UI system as well as the data storage.

A user guide outlining how to access the resources and use the Staphobia User portal will be provided upon handover. The handover will be conducted during the final week of the semester as negotiated with the client.

Appendix

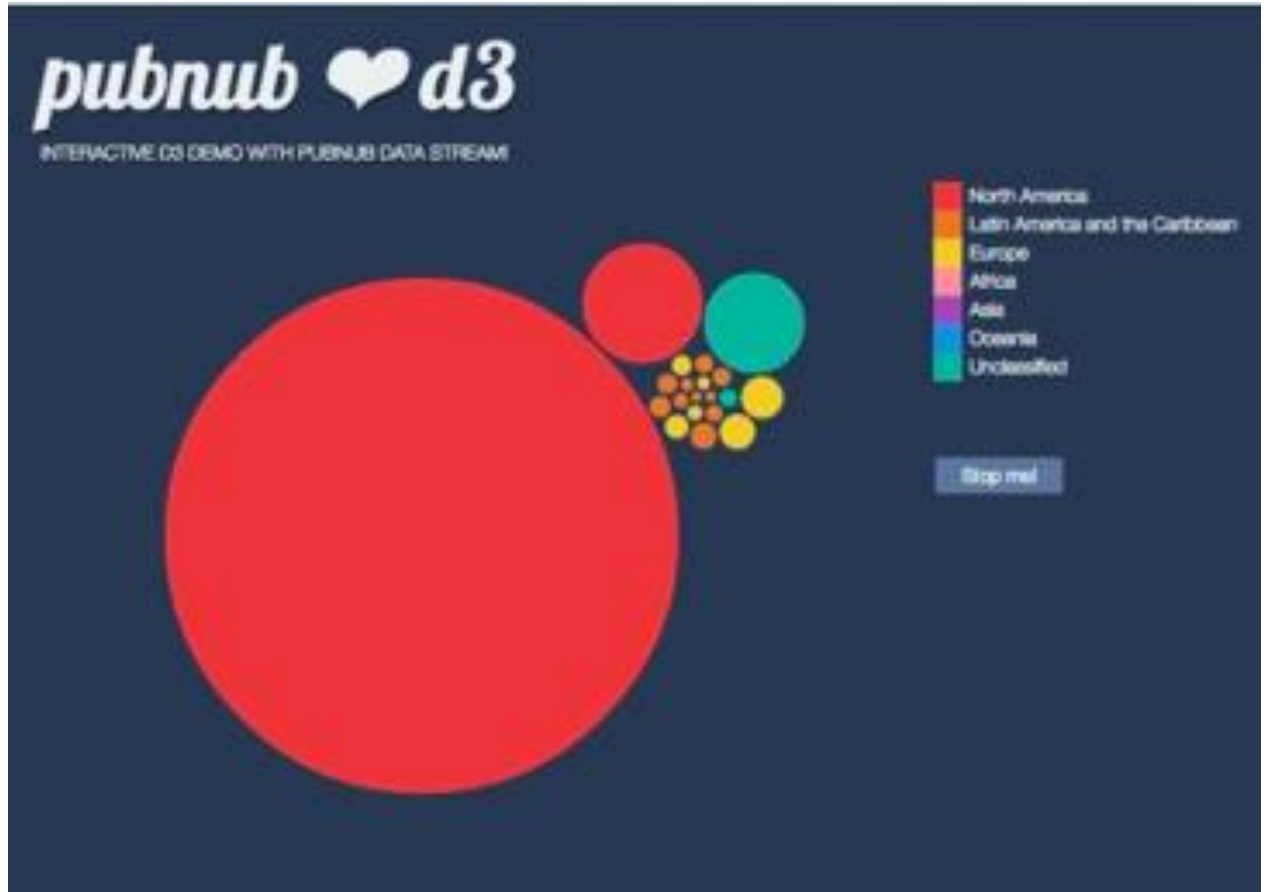


Figure 1

◀ ▶ In Flourish you can easily make a network chart by uploading data in spreadsheet format.

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1840s and earlier 1870s 1890s 1990s 2000s 2010s

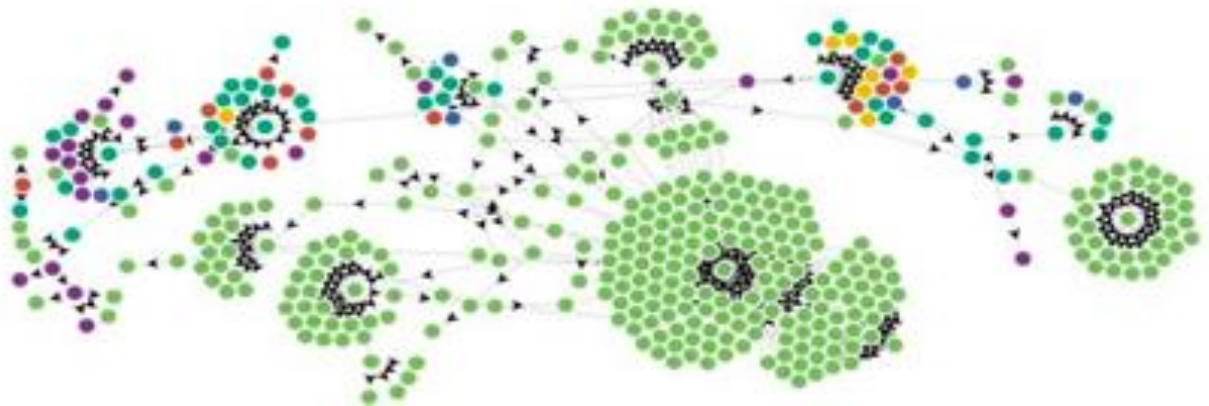


Figure 2

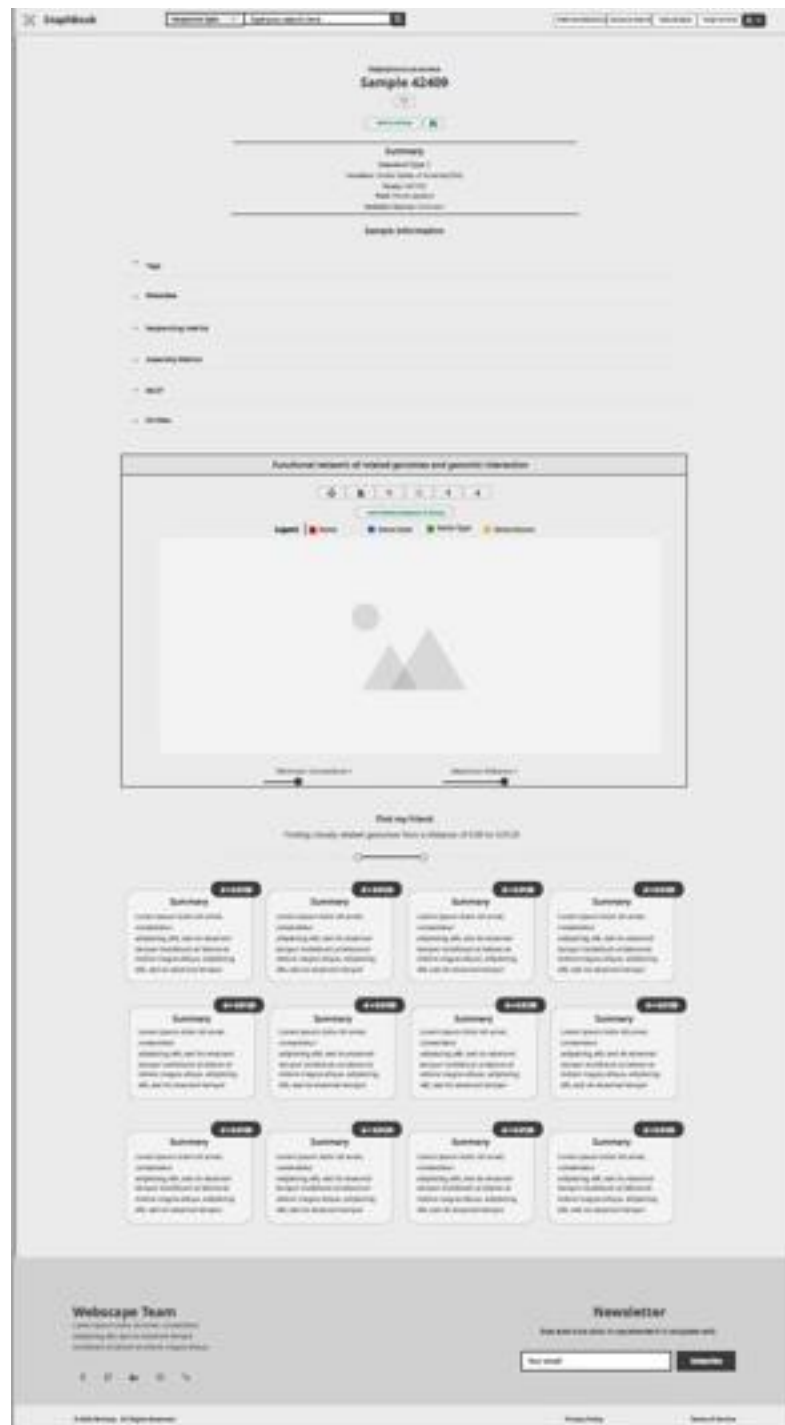


Figure 3

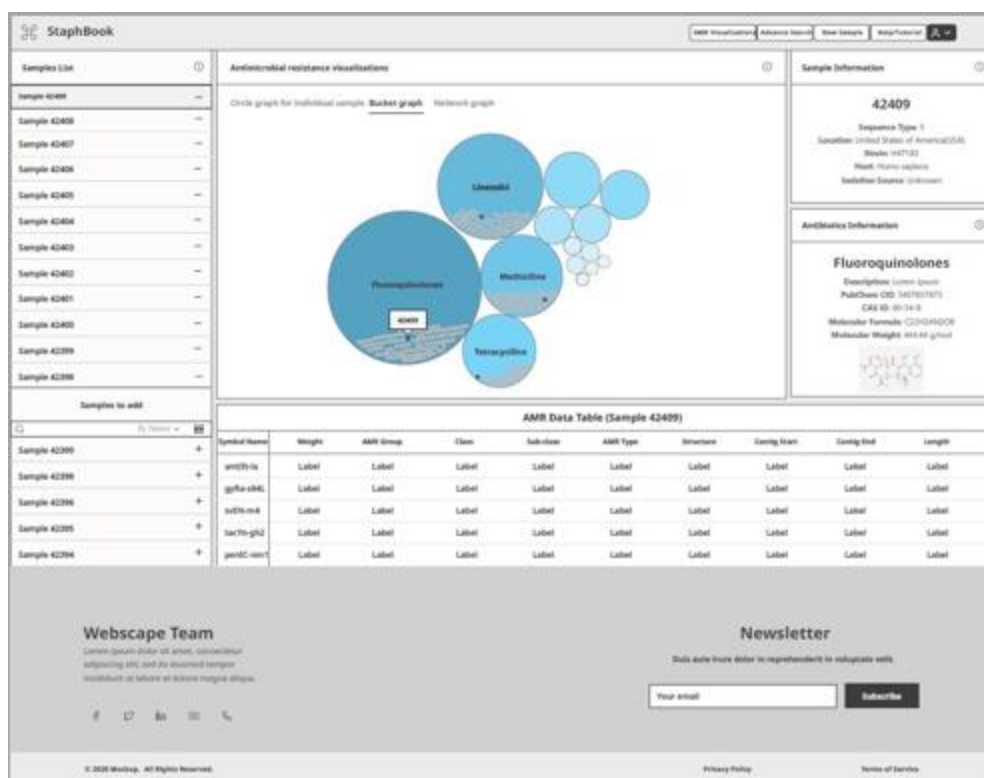


Figure 4



Figure 5