

COVID RADAR

TEAM ERROR404

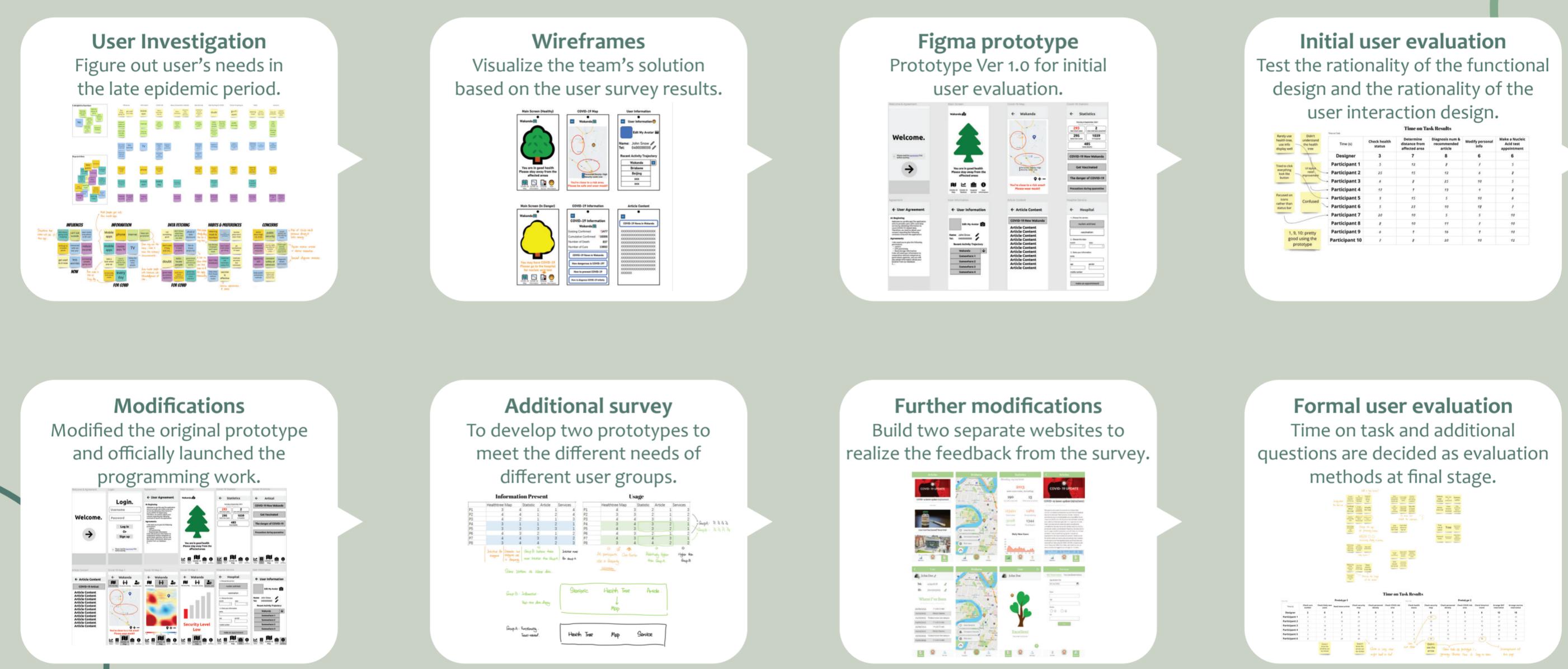
Problem Space

In this project, our domain is to slow and stop the spread of COVID-19 among people by using big data analysis and data visualization. SARS-CoV-2 is spread mainly by coughing, sneezing, inhalation of droplets, and contact. SARS-CoV-2 has been detected in saliva samples. It means saliva is a potential route of transmission for COVID-19 (Li et al., 2020). Because COVID-19 is highly contagious, it is important to find people who are infected with COVID-19 and their close contacts. Moreover, there is no specific treatment for COVID-19 today, and too many drugs currently being tested in COVID-19 patients have an unknown efficacy profile (Scavonev et al., 2020). Therefore, medical isolation of patients and their close contacts is now the most effective way to stop the spread of COVID-19.

Design Concept

How do we find COVID-19 patients around us and how do we know if we are a close contact of COVID-19? Our team focuses on making a mobile application to help the government and citizens avoid the impact of COVID-19 by using big data analysis and data visualization. Our team aims to make COVID-19 data and information available to users all the time. At the same time, the data of COVID-19 are easy for all to understand. The continued spread of COVID-19 has driven the collection of data on this disease and that prompted a desire to track its progress in order to better prepare for the emergence of new areas (Samet et al., 2020). In addition, our team wants to locate and identify close contacts by tracking where patients have been. The most discussed approach is to enable digital contact tracing. Because contact tracing is a traditional epidemiological method used to track and limit the spread of infection in the absence of effective treatment (Redmiles, 2020).

Design Process



Prototype functions

Personal Services Version

After the user agrees, the system will track their itinerary information through positioning, and display the summary to the user for modification. Then, by comparing with the itinerary of the newly diagnosed patient, the tree on the homepage will show different states to show whether the user is likely to be infected. Finally, users can also make appointments for nucleic acid testing and vaccines to the hospital through this version.

Sharing Core Functions

The map function is the common function of the two versions of COVID RADAR, and it is also the core function of the entire system. By selecting different buttons, the map will show the locations where the recently diagnosed patients have been, the population density of different locations, and the locations where special events have occurred. All of them can effectively help users to travel and prevent infection.

Information Center Version

In the version of the information center, users can view the latest and most complete diagnosis information statistics and trends updated daily. They can also view all the information about COVID-19 pushed by the system, including tips for infection prevention and other news that they need to know. Combined with the function of the map, users can learn a lot of useful information.

References

Li, Y., Ren, B., Peng, X., Hu, T., Li, J., Gong, T., Tang, B., Xu, X., & Zhou, X. (2020 May 4). Saliva is a non-negligible factor in the spread of COVID-19. *Molecular oral microbiology*, Volume 35, Issue 4, p141-145.

Redmiles, E. M. (2020 Nov 17). User Concerns & Tradeoffs in Technology-facilitated COVID-19 Response. *Digital Government: Research and Practice*, Volume 2, Issue 1, Article No.6, p1-12.

Samet, H., Han, Y., Kastner, J., & Wei, H. (2020 Nov). Using Animation to Visualize Spatio-Temporal Varying COVID-19 Data. *COVID-19: Proceedings of the 1st ACM SIGSPATIAL International Workshop on Modeling and Understanding the Spread of COVID-19*, p53-62.

Scavone, C., Brusco, S., Bertini, M., Sportiello, L., Rafaniello, C., Zoccoli, A., Berriom, L., Racagni, G., Rossi, F., & Capuano, A. (2020 April 24). Current pharmacological treatments for COVID-19: What's next?. *British Journal of Pharmacology*, Volume 177, Issue 21, p4813-4824.