

# Software Requirement Specification Document for Complete blood count mobile application

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January 19, 2022

Table 1: Document version history

Version	Date	Reason for Change
1.0	7-Oct-2021	Initial version for SRS

**Github:** <https://github.com/YoussifAssem/Complete-Blood-Count.git>

# Contents

<b>1</b>	<b>Introduction</b>	<b>3</b>
1.1	Purpose of this document . . . . .	3
1.2	Scope of this document . . . . .	3
<b>2</b>	<b>Similar Systems</b>	<b>3</b>
<b>3</b>	<b>System Description</b>	<b>5</b>
3.1	Problem Statement . . . . .	5
3.2	System Overview . . . . .	6
3.3	System Scope . . . . .	6
3.4	System Context . . . . .	6
3.5	Objectives . . . . .	7
3.6	User Characteristics . . . . .	7
<b>4</b>	<b>Functional Requirements</b>	<b>7</b>
4.1	System Functions . . . . .	7
<b>5</b>	<b>Interface Requirements</b>	<b>10</b>
5.1	User Interfaces . . . . .	10
5.1.1	External APIs . . . . .	18
<b>6</b>	<b>Non-functional Requirements</b>	<b>18</b>
6.1	Safety . . . . .	18
6.2	Availability . . . . .	18
6.3	Scalability . . . . .	18
<b>7</b>	<b>Data Design</b>	<b>18</b>
7.1	Data Description . . . . .	18
7.2	Database design description . . . . .	20
<b>8</b>	<b>Preliminary Object-Oriented Domain Analysis</b>	<b>30</b>
8.1	Class descriptions . . . . .	32
<b>9</b>	<b>Operational Scenarios</b>	<b>33</b>
9.1	Patient . . . . .	33
9.2	Doctor . . . . .	33
9.3	Complete Blood Cells (CBC) mobile application . . . . .	33
<b>10</b>	<b>Project Plan</b>	<b>33</b>

## **Abstract**

The complete blood count (CBC) with differential is one of the most essential common laboratory tests performed today to know the problems we suffer from before it expands. If we don't address the problem early on, the human body is one of the most vulnerable to a number of disorders. We want to make a smartphone application that can read the results of a complete blood count (CBC). Furthermore, the application will inform the user whether there is a possibility that the CBC contains corona or not. Otherwise, the application will advise the user on the most specific specialized area of expertise for the user. An enhanced understanding of this laboratory test is essential to providing quality care.[1]

# **1 Introduction**

## **1.1 Purpose of this document**

The aim of this document is to provide a full description of Complete blood count(CBC) mobile application. The usage of blood analytics is required due to the nature of the subject. Therefore It will outline the system's objectives and characteristics, as well as the system's interfaces. It will also cover what the system will preform, the constraints under which It will operate, and, most importantly, how the system will react to external stimulation.

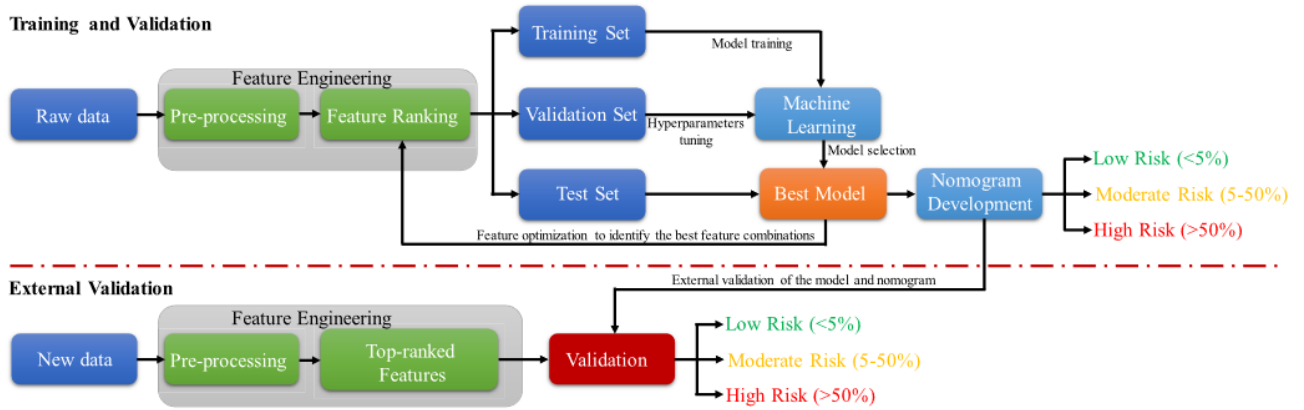
## **1.2 Scope of this document**

This Software Requirements Specification is to create a fully functional mobile application for displaying blood analytics results and indicate which area of expertise the user should consult. This shall target users like patients with minimal experience in reading blood analytics (determining whether the patient has corona virus or not)

# **2 Similar Systems**

[2]Following an epidemic in Wuhan, the coronavirus illness 2019 (COVID-19) has become increasingly widespread over the world. A quick, accurate, and easily accessible clinical assessment of the disease's severity can aid in resource allocation and prioritisation in order to prevent mortality. The study's goal was to create and evaluate an early scoring tool that used widely available complete blood count (CBC) biomarkers to stratify the risk of death. From January 10 to February 18, 2020, 375 COVID-19 patients were hospitalised to Tongji Hospital in China, and a retrospective study was done on twenty-three CBC blood indicators for predicting disease mortality. Machine learning-based core biomarkers among CBC values have been identified as mortality predictions. For forecasting the mortality risk among COVID-19 patients, a multivariate logistic regression-based nomogram and scoring system were created to categorise the patients into three risk groups (low, moderate, and high). The random forest feature selection technique was used to identify lymphocyte count, neutrophil count, age, white blood cell count, monocytes (percent), platelet count, and red blood cell distribution width parameters gathered at hospital admission as key indicators for death prediction. A CBC score was developed to calculate the patients' death probability and was used to divide them into three sub-risk groups: low "(=5 percentage, moderate

(>5 and =50 percentage), and high (>50 percentage), respectively".[3] For the development and internal validation cohorts, the model's area under the curve (AUC) was 0.961 and 0.88, respectively. An external cohort of 103 patients from Dhaka Medical College in Bangladesh was used to validate the proposed model, yielding an AUC of 0.963. The proposed CBC parameter-based prognostic model and related web-application can assist medical physicians in improving the care of COVID-19 patients in low-resource countries by predicting mortality risk early.



[4] The workflow that can be used to construct COVID-19 machine learning diagnosis systems based on multimodal data is investigated in this thesis. Medical records are now maintained in an unorganised manner, making analysis difficult. Prequalifying for Real Time PCR tests, which can take up to a day, are expensive, often limited, and require specialist laboratory equipment, can benefit from such study.

they provide a strategy for establishing a user-friendly website that allows anyone to acquire a prediction based on their input and outline possible data processing approaches, particularly for huge medical datasets. they also show three models that can be used as stand-alone solutions or stages in the COVID-19 machine diagnosis. The first model uses natural language analysis to extract COVID-19 infection-related variables from doctor-written reports, particularly those detailing heart and lung issues. For COVID-19 diagnosis based on X-ray scans, the second model employs convolutional neural networks. they also look into data balancing approaches such as undersampling and oversampling, as well as a classification model for analysing whole blood count results.

Log Out

COVID-19 machine diagnosis based on CBC & X-Ray

RBC [ $10^{12}/l$ ]:

RDW [%]:

WBC [ $10^9/l$ ]:

% EO [%]:

MCH [pg]:

PLTC [ $10^9/l$ ]:

% LYMPH [%]:

% BASO [%]:

% NRBC [%]:

MCHC [g/dl]:

MPV [fl]:

% MONO [%]:


IG [ $10^9/l$ ]:

Submit

Predict from image

Log Out

COVID-19 machine diagnosis based on CBC & X-Ray



Upload another image

Submit

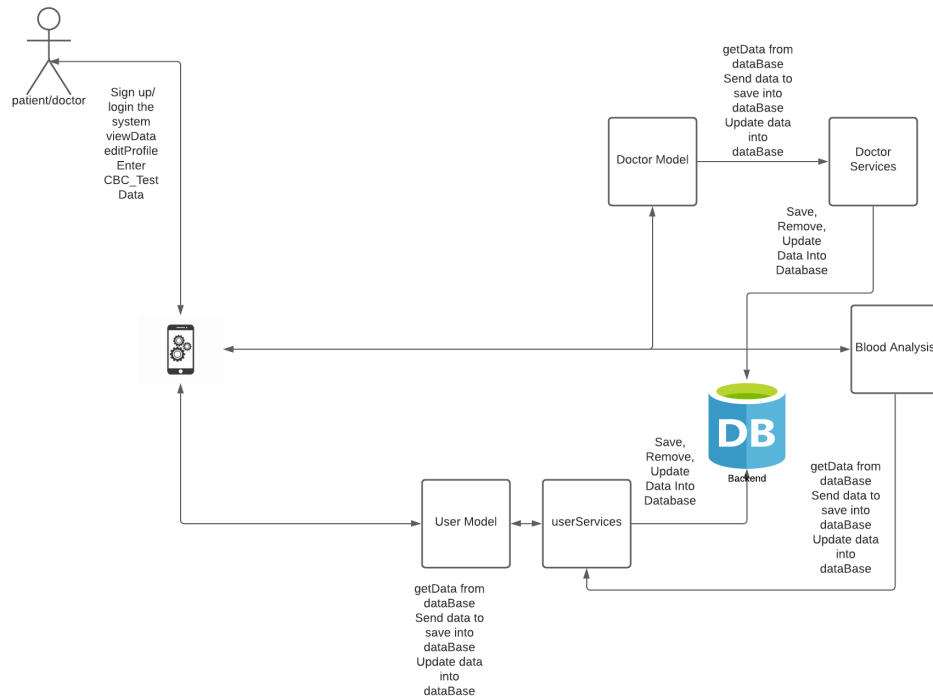
Predict from blood count

## 3 System Description

### 3.1 Problem Statement

Patients are having and suffering from a lot of issues(corona virus now days)because they can't understand the blood test data and aren't sure what to do or which doctor to see. The results of the blood tests do not reveal the specific nature of the problem to the patient.

## 3.2 System Overview



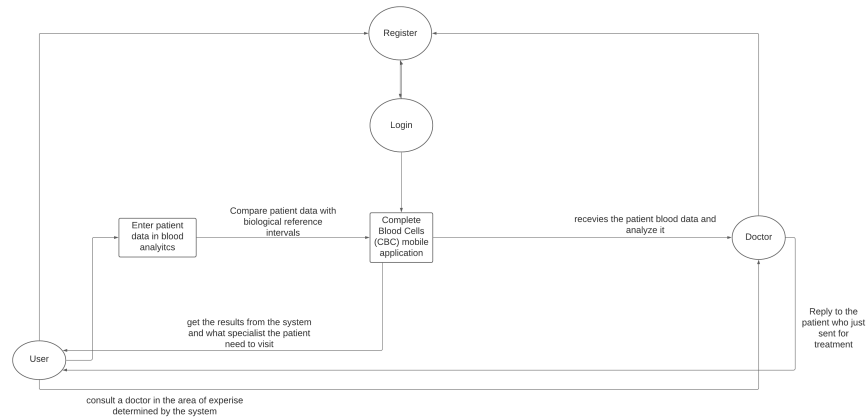
The user can quickly determine whether the patient has corona virus or not, where the system analyze the blood data entered by The patient and sends back a report whether he/she positive .if the patient is diagnosed with COVID-19 , the application will ask the one to see a doctor or provide a communication with any doctor in the application’s chat system.

## 3.3 System Scope

In the proposed application, the user (patient) enters his blood numbers, and the application analyses the data and gives the user feedback whether the user has corona or not and which type of doctor he/she should see, or the user can use the application’s chat system to exchange messages with a doctor who is also using the app to help patients with their specific illness.

## 3.4 System Context

**Context Diagram:** [https://lucid.app/lucidchart/33492a5b-ab8f-4fc5-801e-f1bc8d02328c/edit?viewport\\_loc=-1522%2C84%2C4992%2C2253%2C0\\_0&invitationId=inv\\_963edc47-f0b0-467e-90df-e99e434384c2](https://lucid.app/lucidchart/33492a5b-ab8f-4fc5-801e-f1bc8d02328c/edit?viewport_loc=-1522%2C84%2C4992%2C2253%2C0_0&invitationId=inv_963edc47-f0b0-467e-90df-e99e434384c2)



### 3.5 Objectives

#### USER OBJECTIVES:

- If the user is signing up for the first time, he must create an account
- Users may enter and submit their blood analytics data , system starts to analyze data and sends back a report whether the one has a corona virus or not
- The user can communicate with the doctor and send him messages.
- In addition, the user can provide feedback and rate the app in the play store

### 3.6 User Characteristics

- Patient: Shall have a basic understanding of how to use a mobile device and navigate through the mobile application.
- Doctor: Shall have a basic understanding of the the mobile application's interface and how to navigate through it.

## 4 Functional Requirements

### 4.1 System Functions

Table 2: Add User into database Description

<b>Name</b>	addUserIntoDatabase
<b>Code</b>	FR01
<b>Priority</b>	Extreme
<b>Critical</b>	It's extremely important.
<b>Description</b>	Add a new user into the system and the firebase.
<b>Input</b>	strings from the user's form
<b>Output</b>	No outputs for this function
<b>Pre-condition</b>	The user will enter the system and free to use all other functions
<b>Post-condition</b>	Redirect to the login page
<b>Dependency</b>	This function depends on the user being registered into the system
<b>Risk</b>	Without it we can't proceed into the system without users

Table 3: Edit Profile Description

<b>Name</b>	editProfile
<b>Code</b>	FR02
<b>Priority</b>	Important
<b>Critical</b>	It's a normal function.
<b>Description</b>	The user can edit his/her profile including firstname , lastname, email, birthdate, phone, password
<b>Input</b>	firstname, lastname, email, birthdate, phone, password
<b>Output</b>	Updates the user info
<b>Pre-condition</b>	After user input something in the system
<b>Post-condition</b>	Redirect to the home page after giving a message to the user that his/her info has been updated.
<b>Dependency</b>	This function depends on the user input when the user is added into the system
<b>Risk</b>	The users can't update their update if they written their information wrong

Table 4: View results

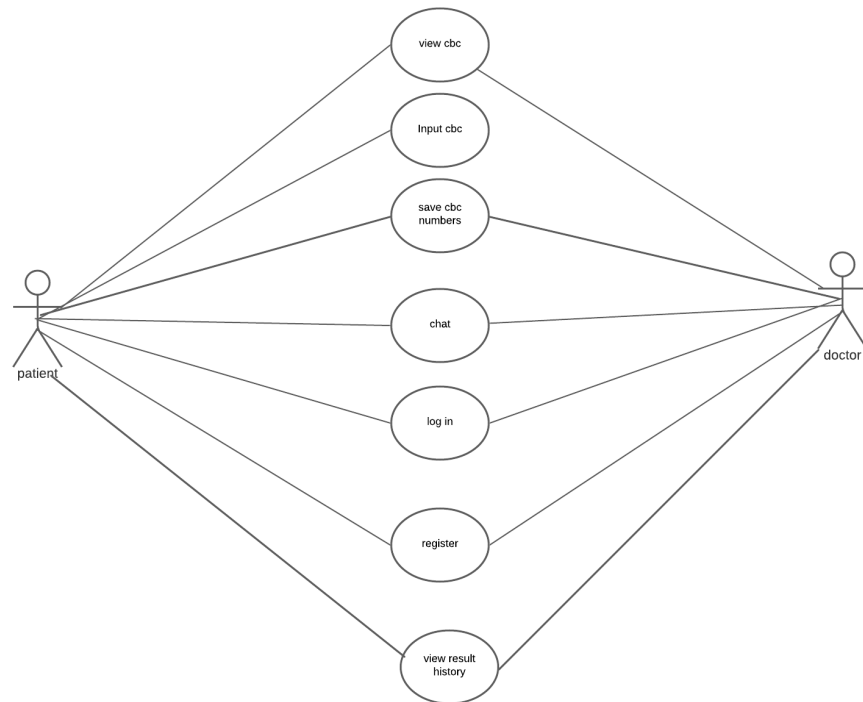
<b>Name</b>	viewHistory
<b>Code</b>	FR02
<b>Priority</b>	Important
<b>Critical</b>	It's a normal function.
<b>Description</b>	The users can see their results history from previous CBC tests
<b>Input</b>	No inputs for this function
<b>Output</b>	It will view the history from the firestore
<b>Pre-condition</b>	After user input something in the system
<b>Post-condition</b>	View the information for every CBC test that the user has made before
<b>Dependency</b>	This function depends on the user and whether or not has made a test before or not
<b>Risk</b>	Not having the option to see previous results is not efficient and can be client demanding



Table 5: getResults

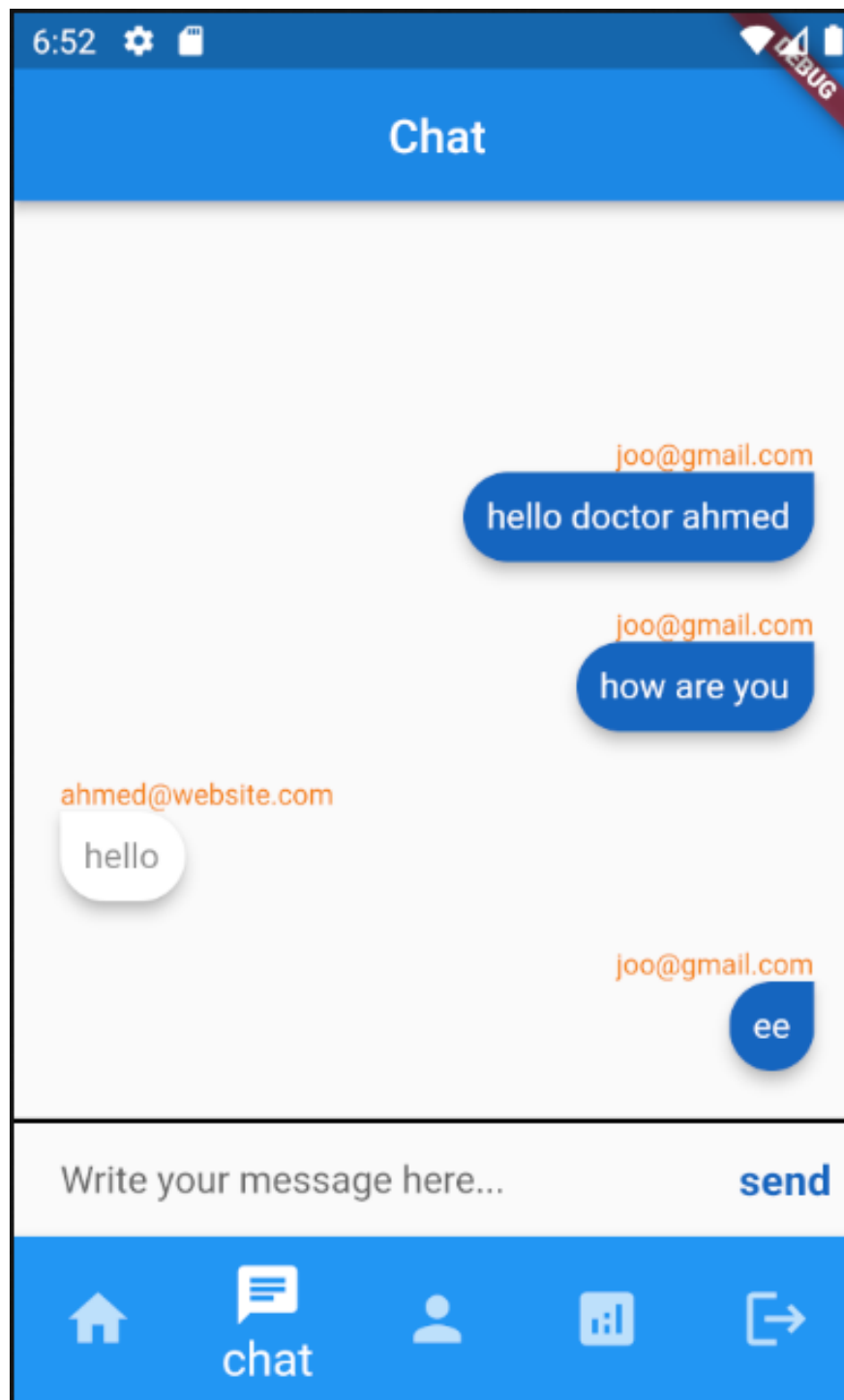
<b>Name</b>	getResults
<b>Code</b>	FR03
<b>Priority</b>	Important
<b>Critical</b>	It's a normal function.
<b>Description</b>	The users can see what is problem in the test
<b>Input</b>	No inputs for this function
<b>Output</b>	It will view the problems in the test
<b>Pre-condition</b>	After user input data of CBC test
<b>Post-condition</b>	View the information results of CBC test that the user entered it
<b>Dependency</b>	This function depends on the data that the user entered
<b>Risk</b>	if the user don't enter the data of CBC this function will not run

**Inheritance Relationships:** [https://lucid.app/lucidchart/48345e3a-c507-4b03-9faf-68bfcc699b24/edit?page=0\\_0&invitationId=inv\\_b25ba821-350a-44fc-ac79-4b279512782d#](https://lucid.app/lucidchart/48345e3a-c507-4b03-9faf-68bfcc699b24/edit?page=0_0&invitationId=inv_b25ba821-350a-44fc-ac79-4b279512782d#)



## 5 Interface Requirements

### 5.1 User Interfaces



6:55

DEBUG

Login

WELCOME

new to this app?

sign up


Email


Password

[forget password](#)

Log In

or log in with:







Sign Up

## Sign up

Name

Email

Phone Number

0/11

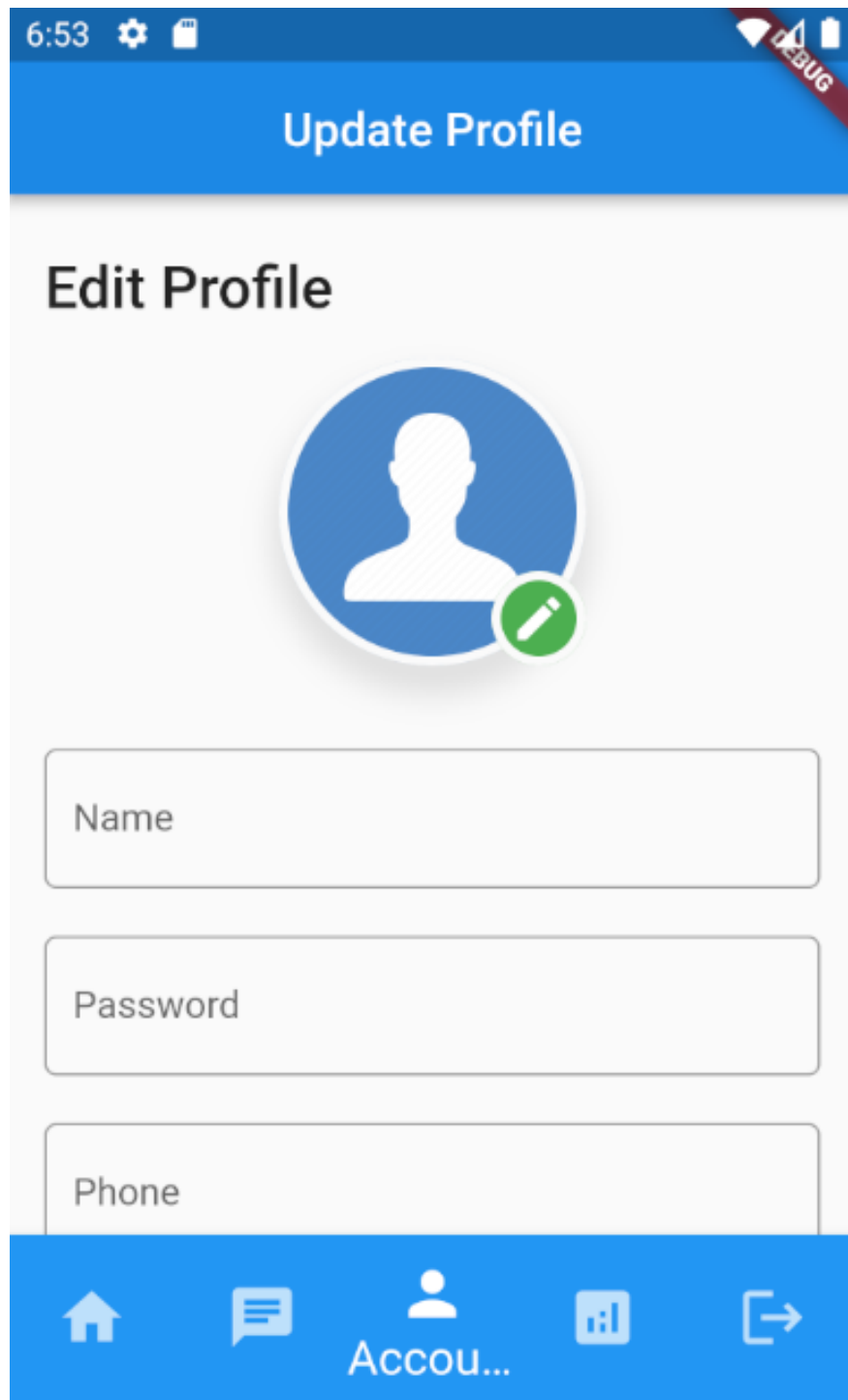
Password





Confirm Password

**Gender** Male ▼






**Type** Patient ▼








Sign Up

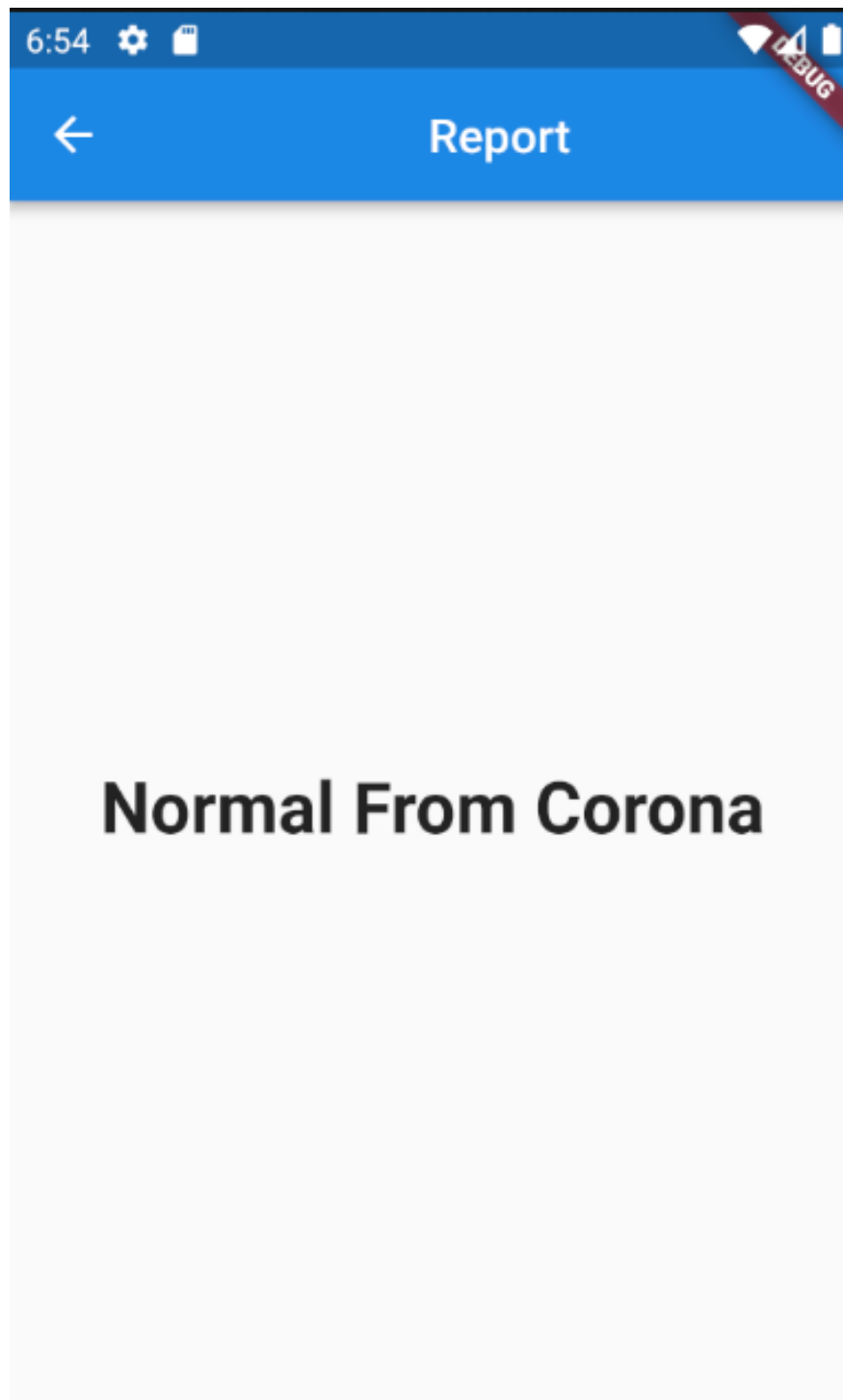


6:53    

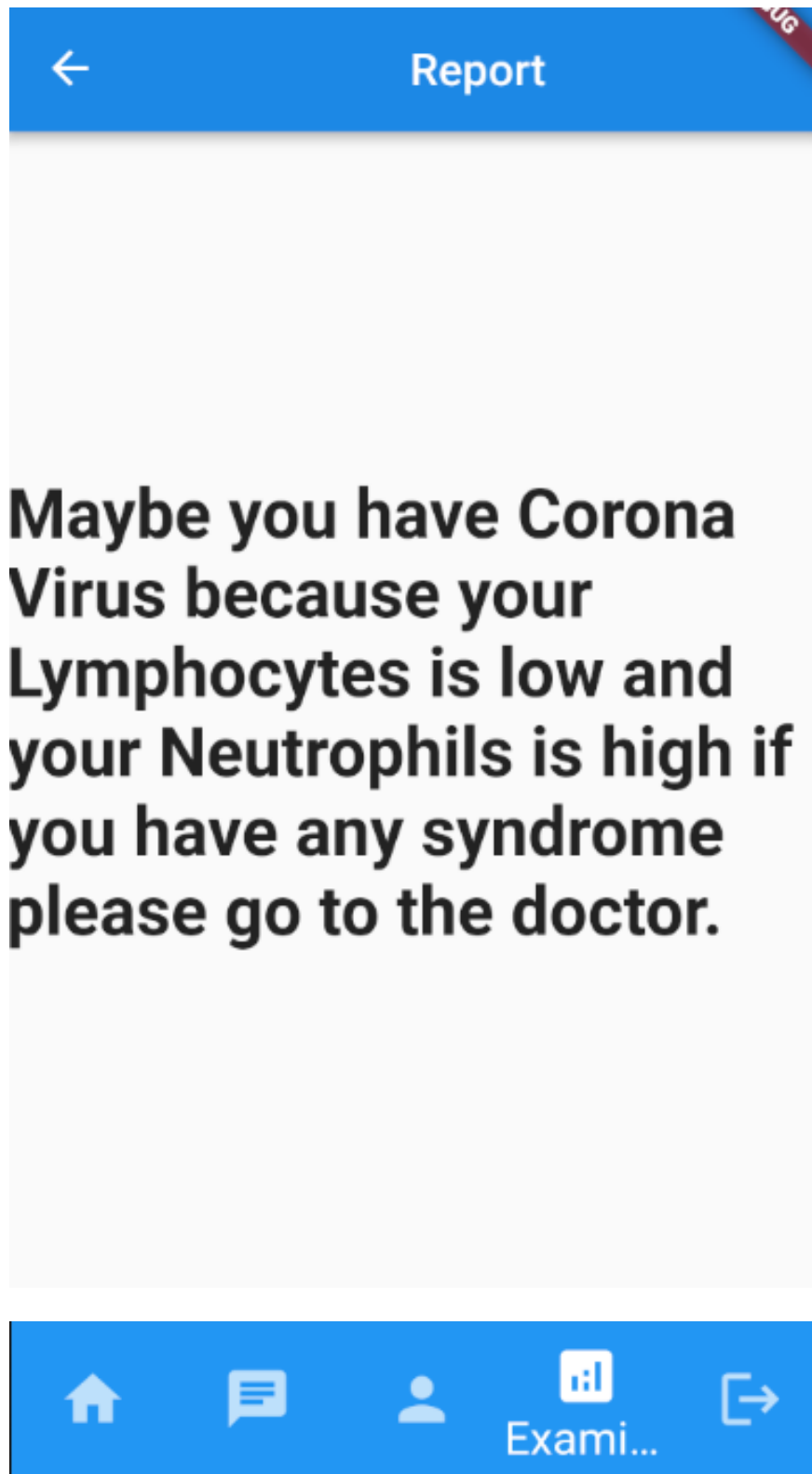
Examine me			
Test Name	Results	Unit	Biolog refere interv
Haemoglobin	Result	g/dl	11.5-1
Haematocrit (PCV)	Result	%	36-4
RBCs Count	Result	millions/cmm	4-5.
MCV	Result	fl	80-1
MCH	Result	pg	27-3
MCHC	Result	g/dl	31-3






Exami...

6:54      			
<div>  <div>Examine me</div> </div>			
Test Name	Results	Absolute Value	Biolog refere intern
Neutrophils	Result	% <b>1.60</b> x10 <sup>9</sup> /L	2-7
Lymphocytes	Result	% <b>2.25</b> x10 <sup>9</sup> /L	1-4.
Monocytes	Result	% <b>0.40</b> x10 <sup>9</sup> /L	0.2-
Eosinophils	Result	% <b>0.07</b> x10 <sup>9</sup> /L	0.1-0
Basophils	Result	% <b>0.04</b> x10 <sup>9</sup> /L	0-0.
<div>View Report</div>			







### **5.1.1 External APIs**

[5] Smart Blood Analytics Swiss (SBAS) is an API that uses advanced machine learning algorithms to provide different AI models for predicting the most probable diagnoses, based solely on an individual's blood test results.

Gather patient's blood test results: Complete blood count with differential and common parameters from biochemistry, hemostatic, enzyme, lipid, protein amino acids, vitamins and hormone panels are usually sufficient for our models to predict the right disease, confirm a human made diagnosis or expand the differential diagnosis.

Decode blood test results: Using machine learning algorithms built revolutionary models to predict hundreds of groups of diseases and medical conditions in the field of internal medicine. Our models can recognize disease-related blood laboratory patterns that are beyond medical knowledge, resulting in a higher diagnostic accuracy compared to traditional quantitative interpretations based on reference ranges or physician's decision-based reference intervals.

Take diagnostics to a higher level Smart Blood Analytics report includes a list of most likely diseases and includes an intuitive multilevel pie chart, which helps physicians to speed up and improve diagnostics, or help patients to be better informed about the outcome of their blood tests and therefore increase their participation during the treatment decision-making process.

## **6 Non-functional Requirements**

### **6.1 Safety**

The system will detect any attacks and it should be secure

### **6.2 Availability**

The system should be available at any time without any failure.

### **6.3 Scalability**

our system is able to increase its capacity and functionalities based on the users demand. it can remain stable while adapting to changes and upgrades

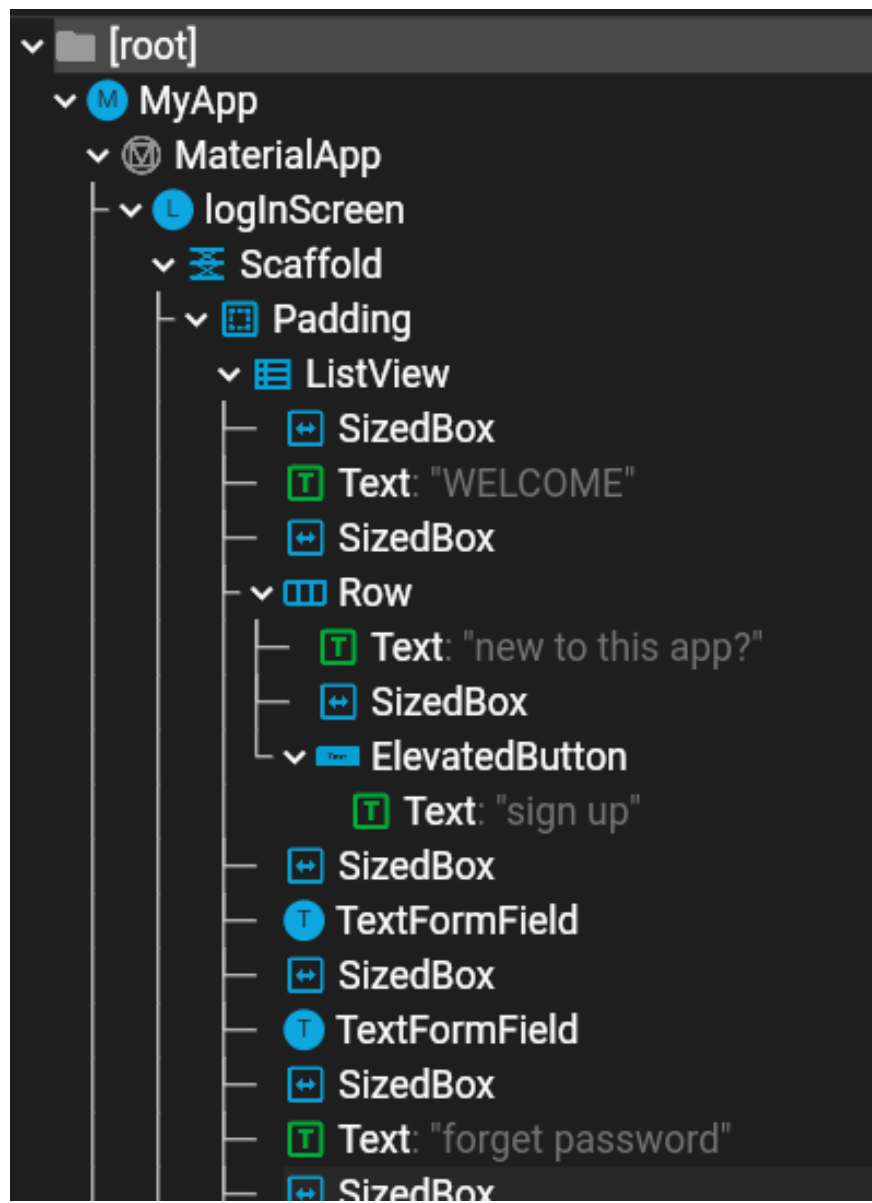
## **7 Data Design**

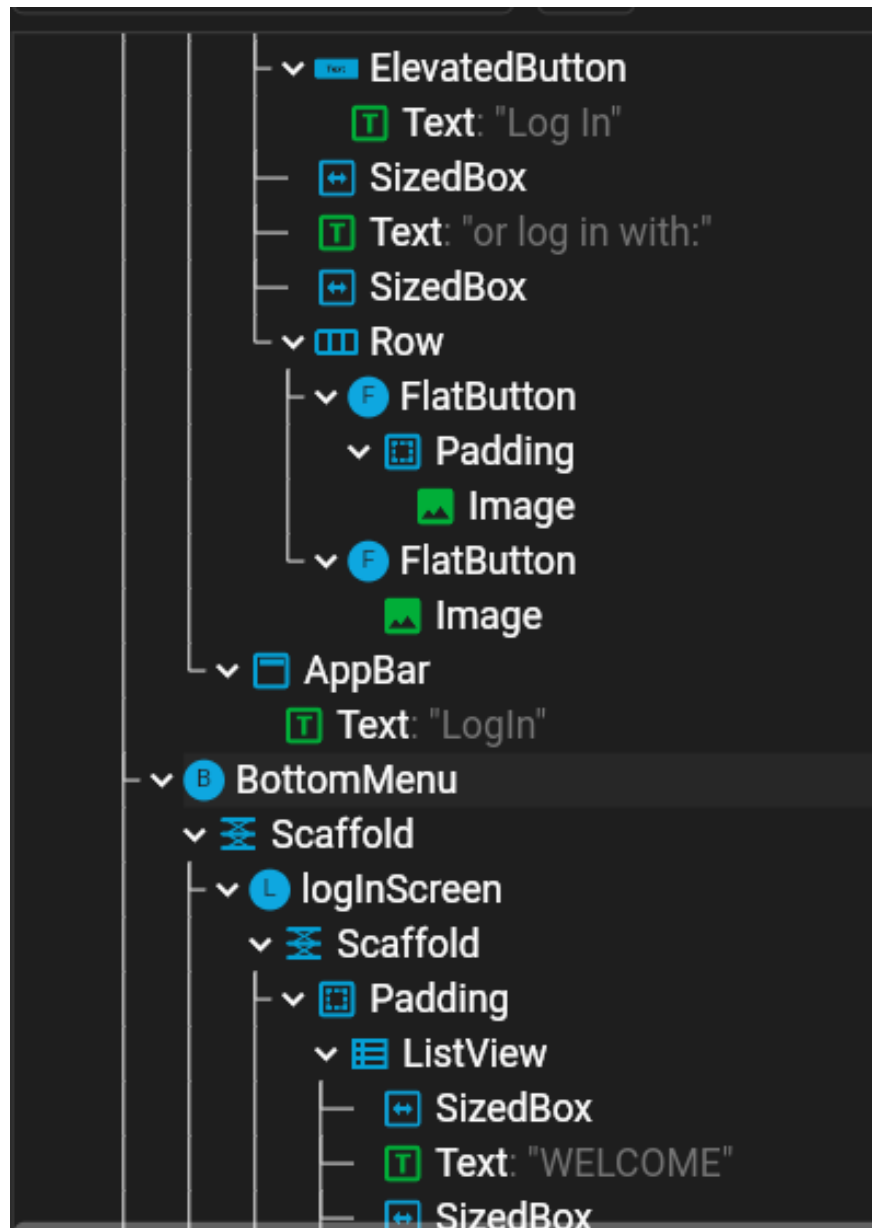
### **7.1 Data Description**

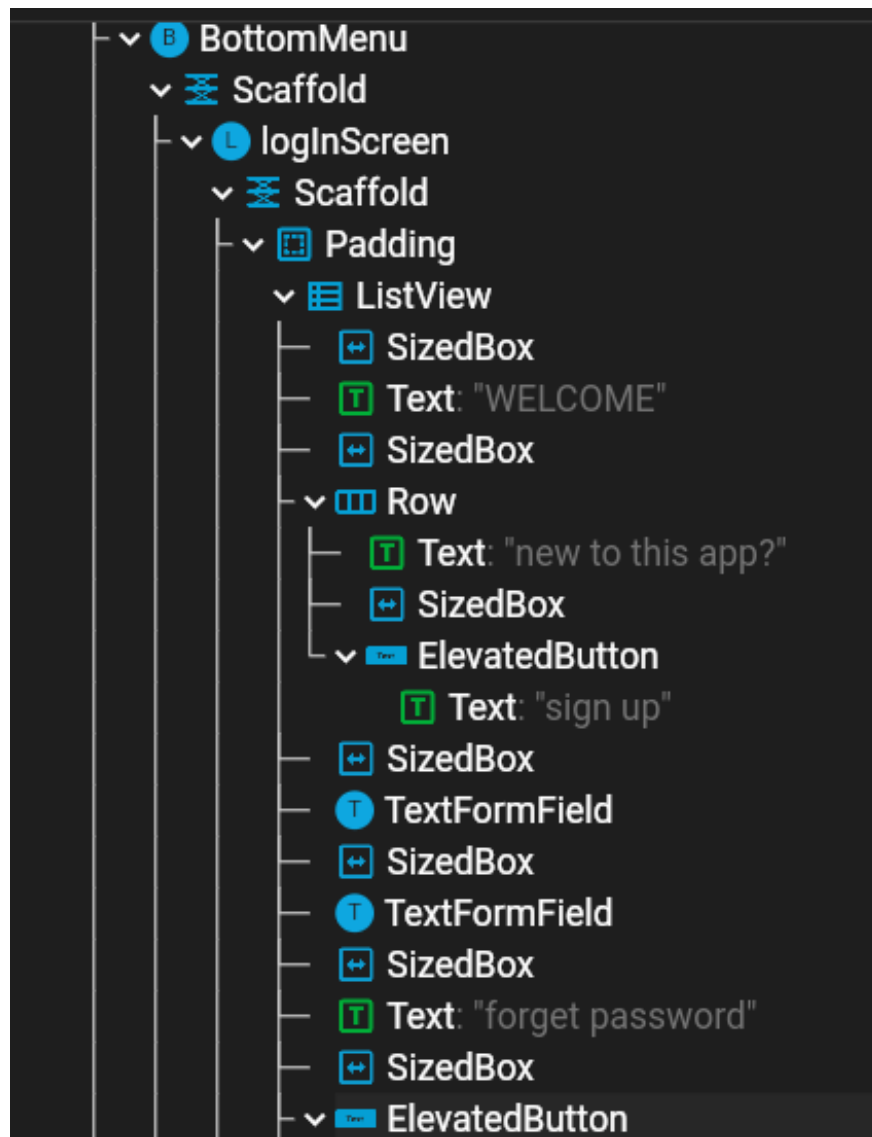
- The data was originally stored in a paper-based format.
- Forms and API are the methods we use to collect data in our system.
- The database size will be determined by the number of people that register and log in to the system.

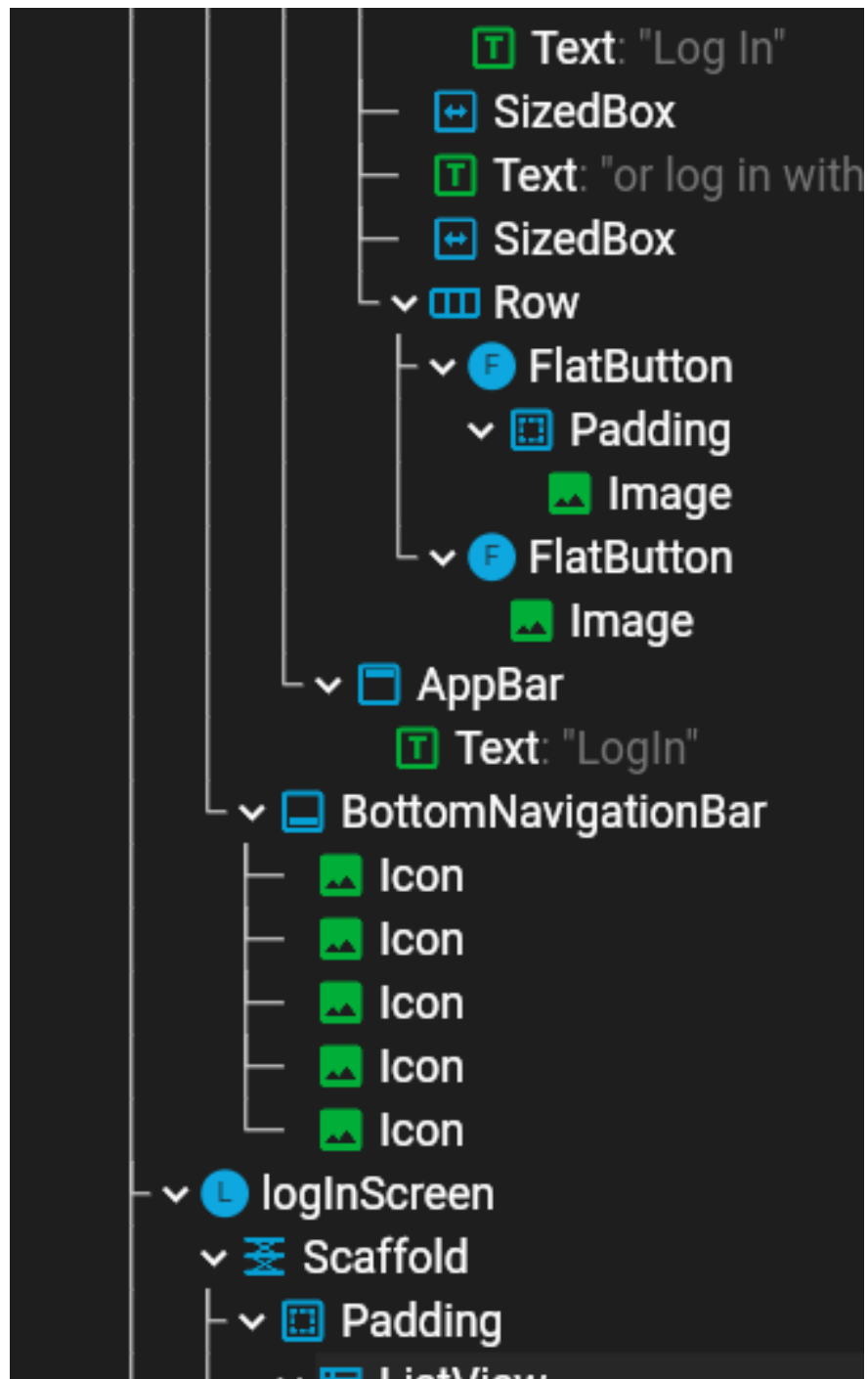
- We expect a small percentage of individuals to use the app, with the majority of them being patients and doctors, and we expect the number of users to expand over time as the service continues to perform properly with no issues.
- How is your entity keys(ids) constructed (is there a specific code or format for ID definition)
- In the chat section, where patients and doctors exchange messages, the data will include the date and time of the text sent, as well as the time and day of the text sent.
- we are using Fire base .
- The insert, delete, and edit, queries are the most significant queries that we will employ in our data.

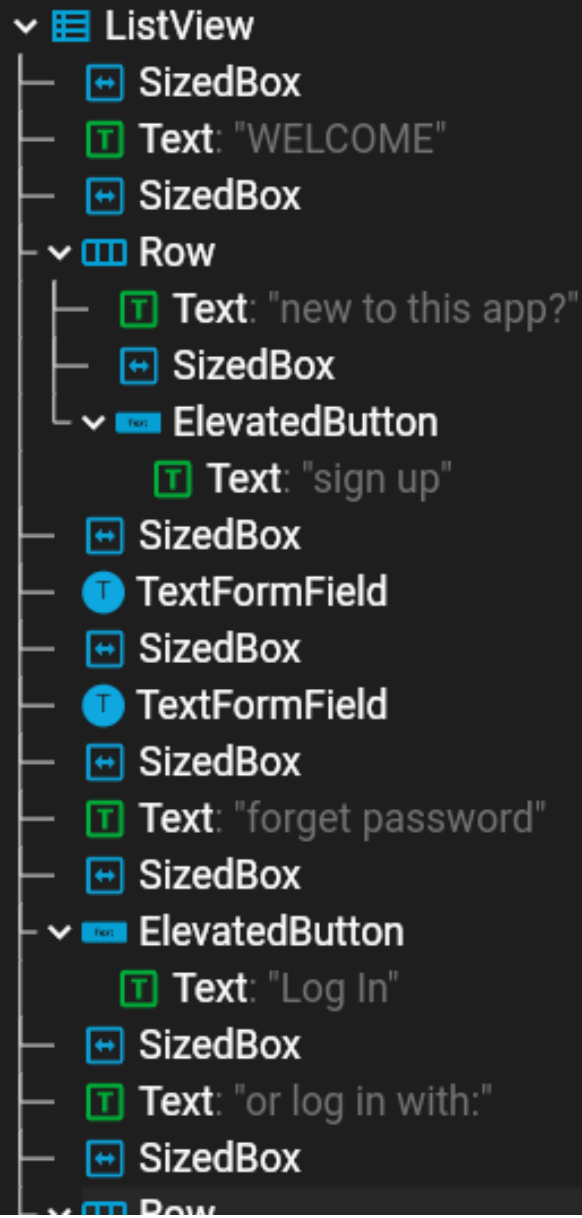
## 7.2 Database design description



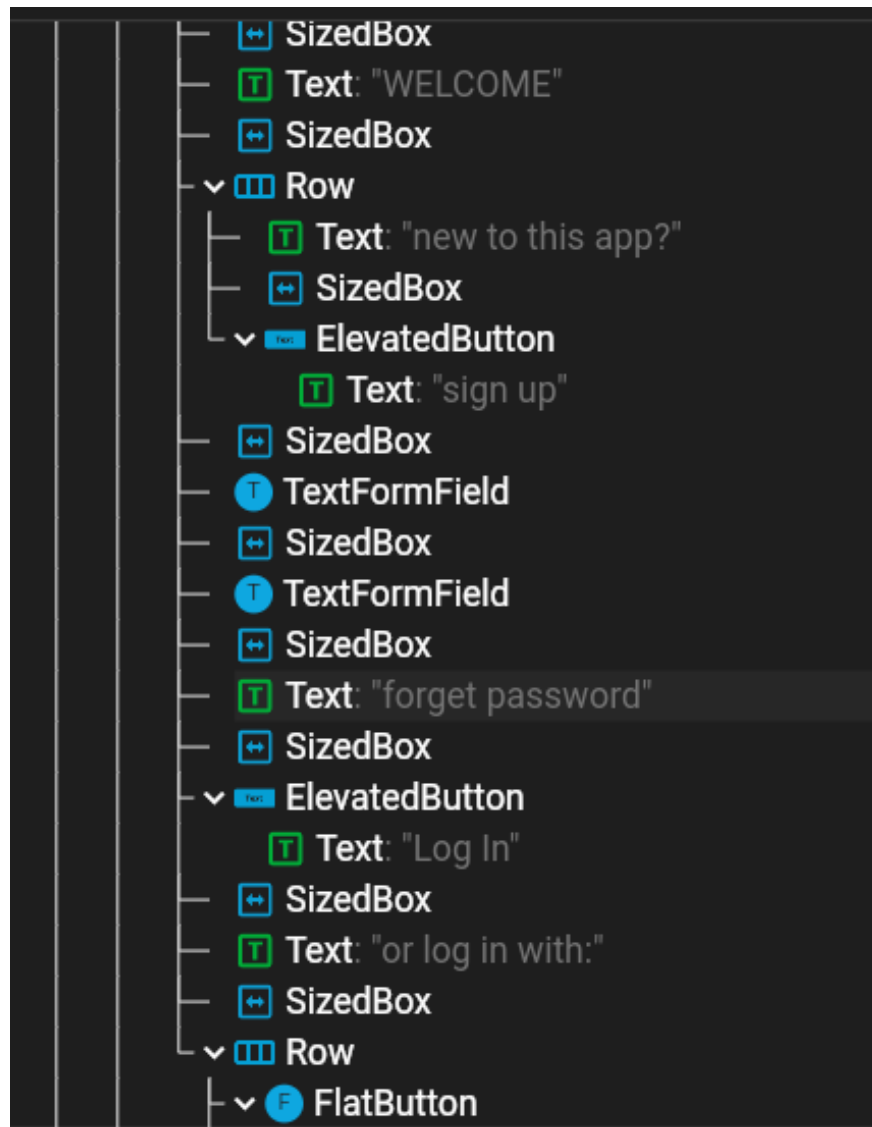


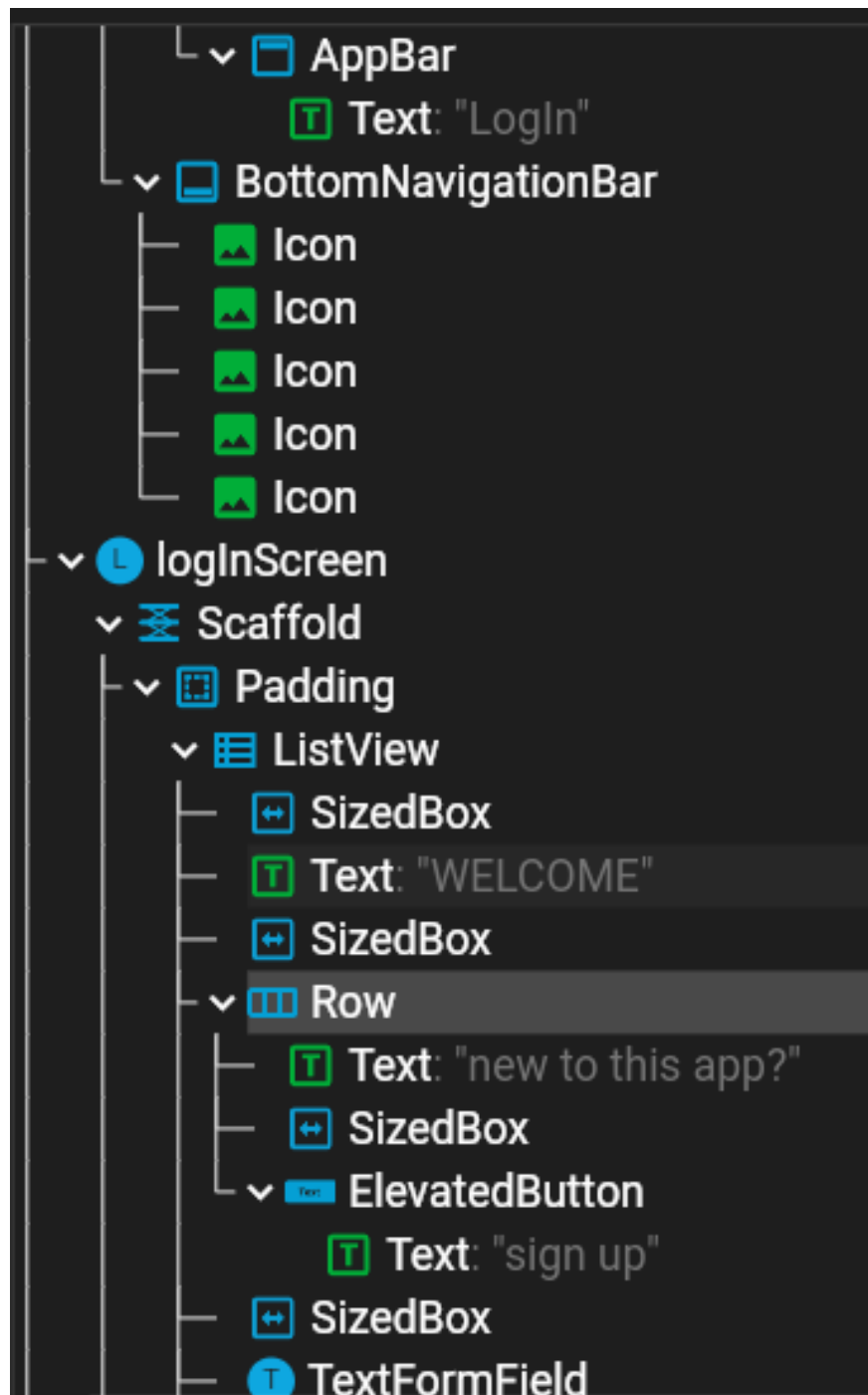


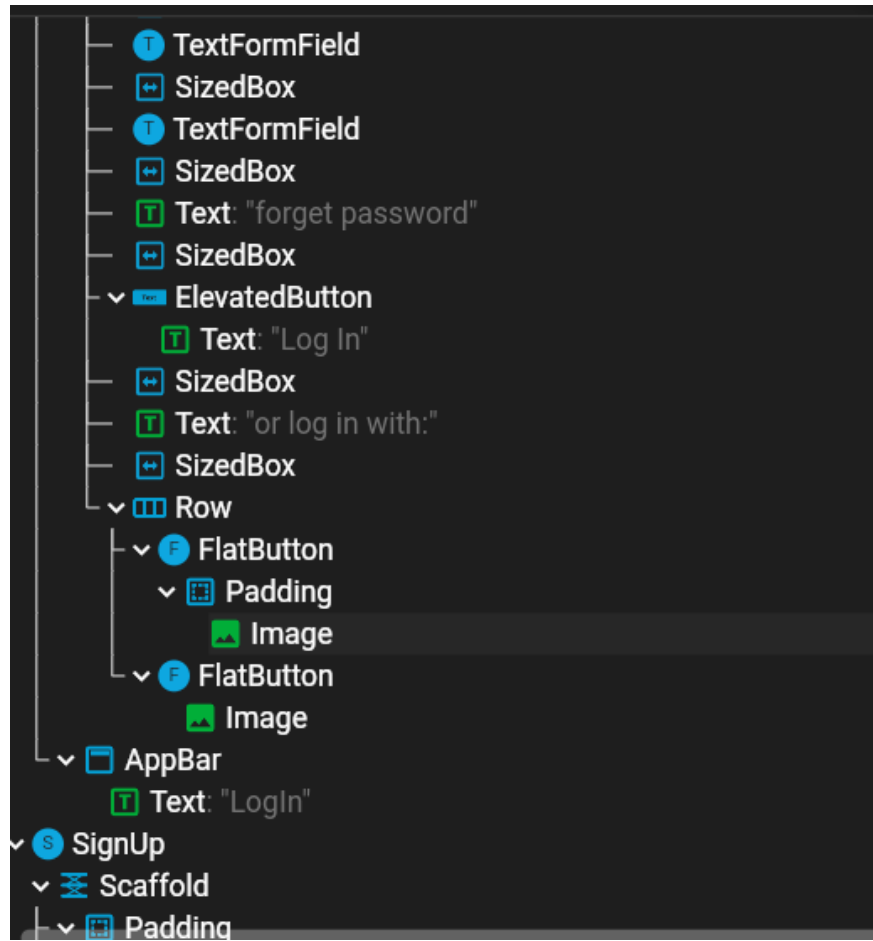


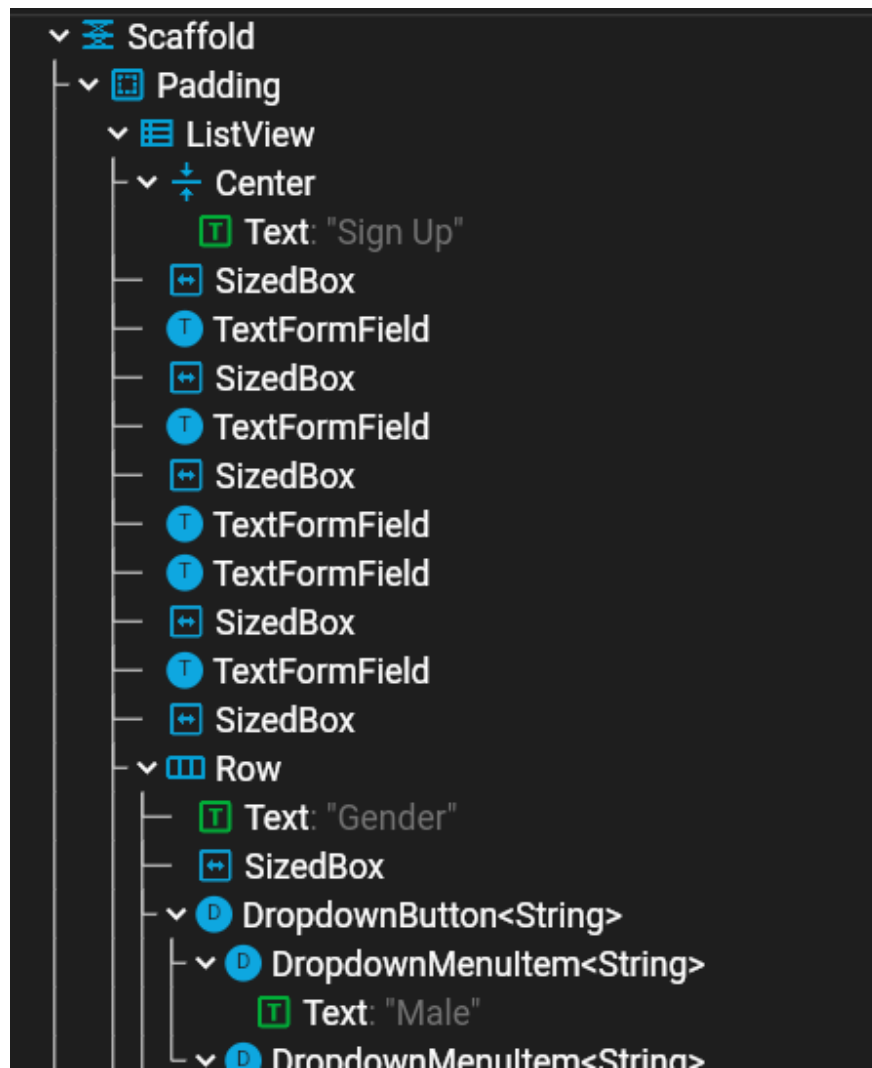


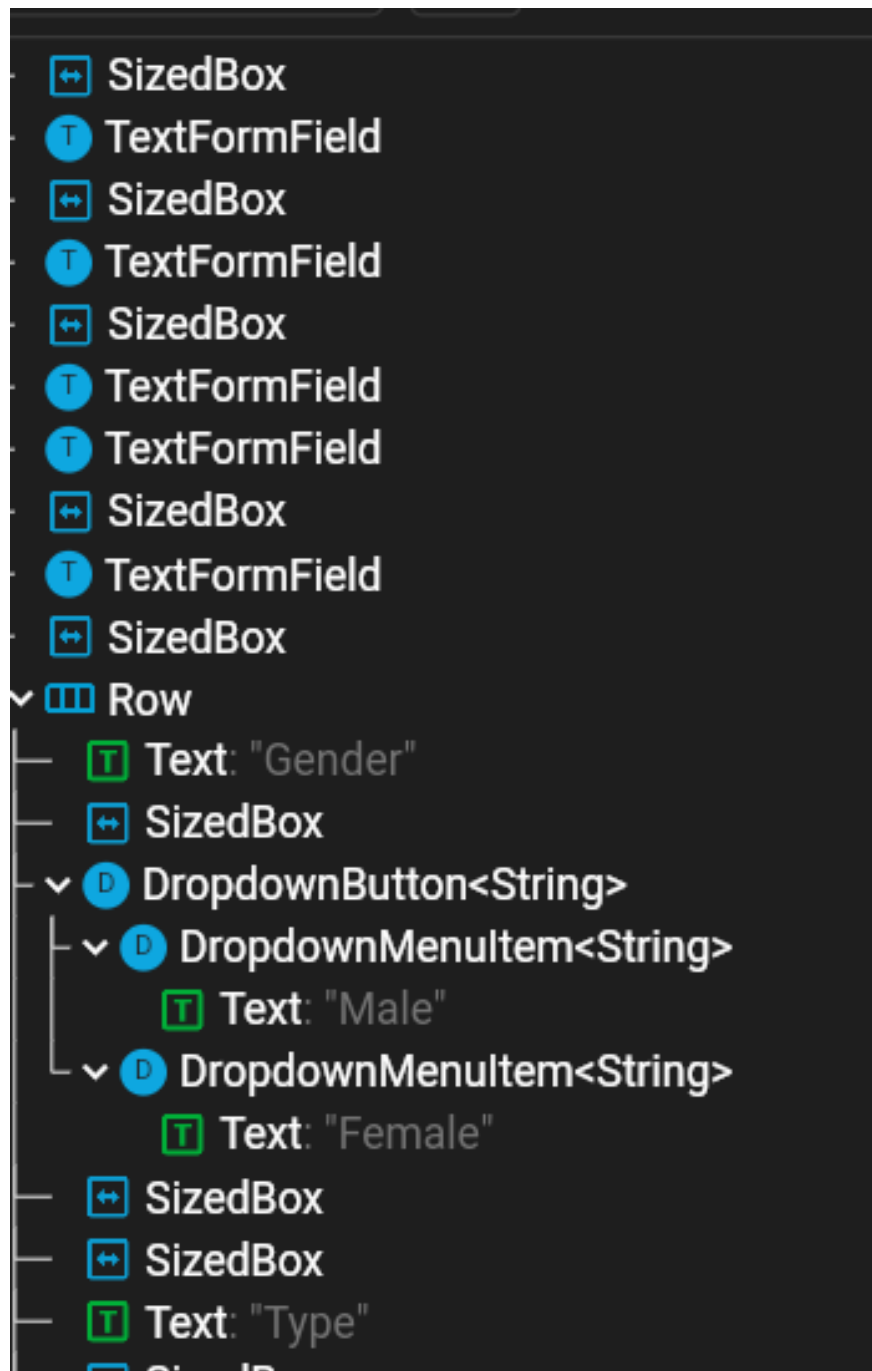


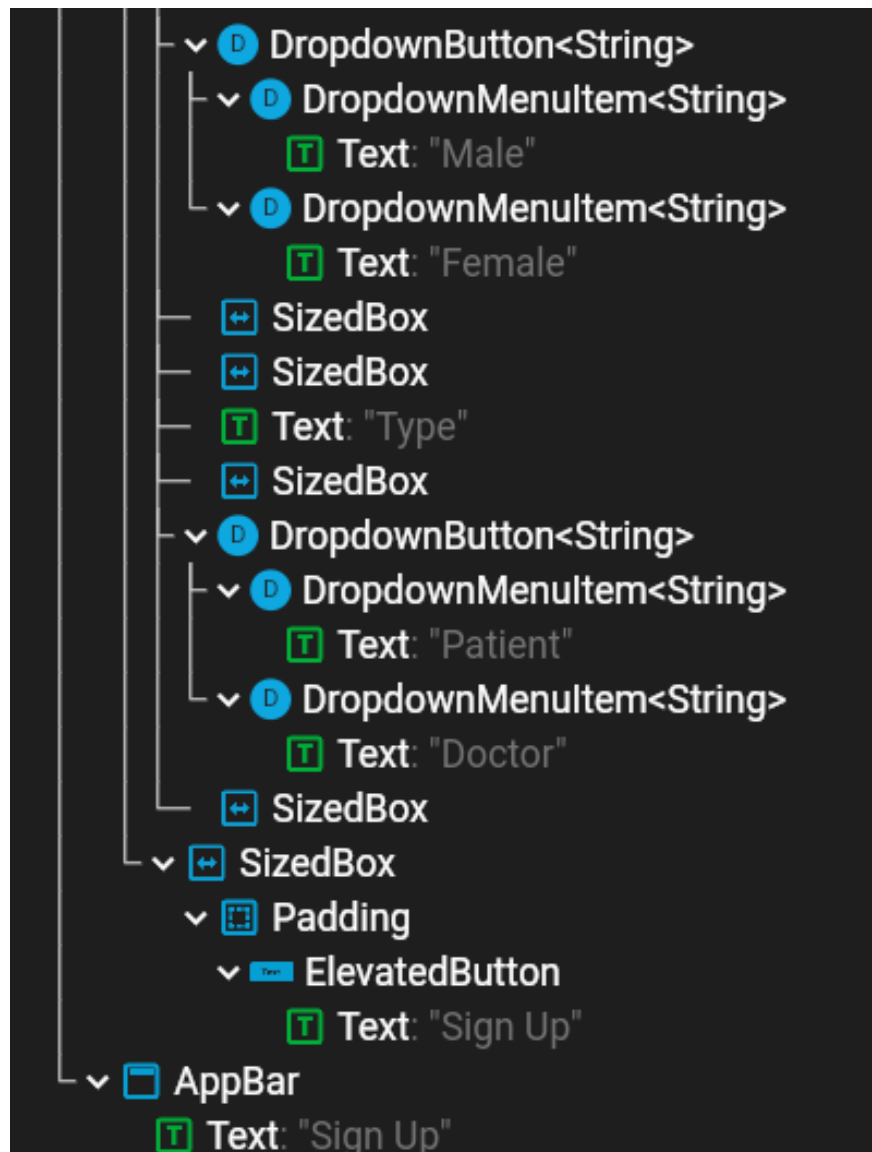






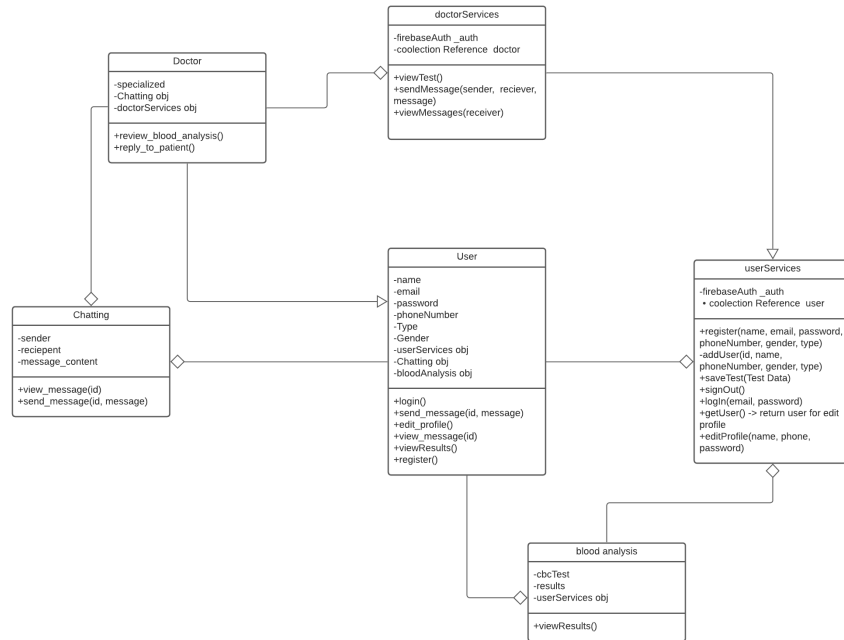




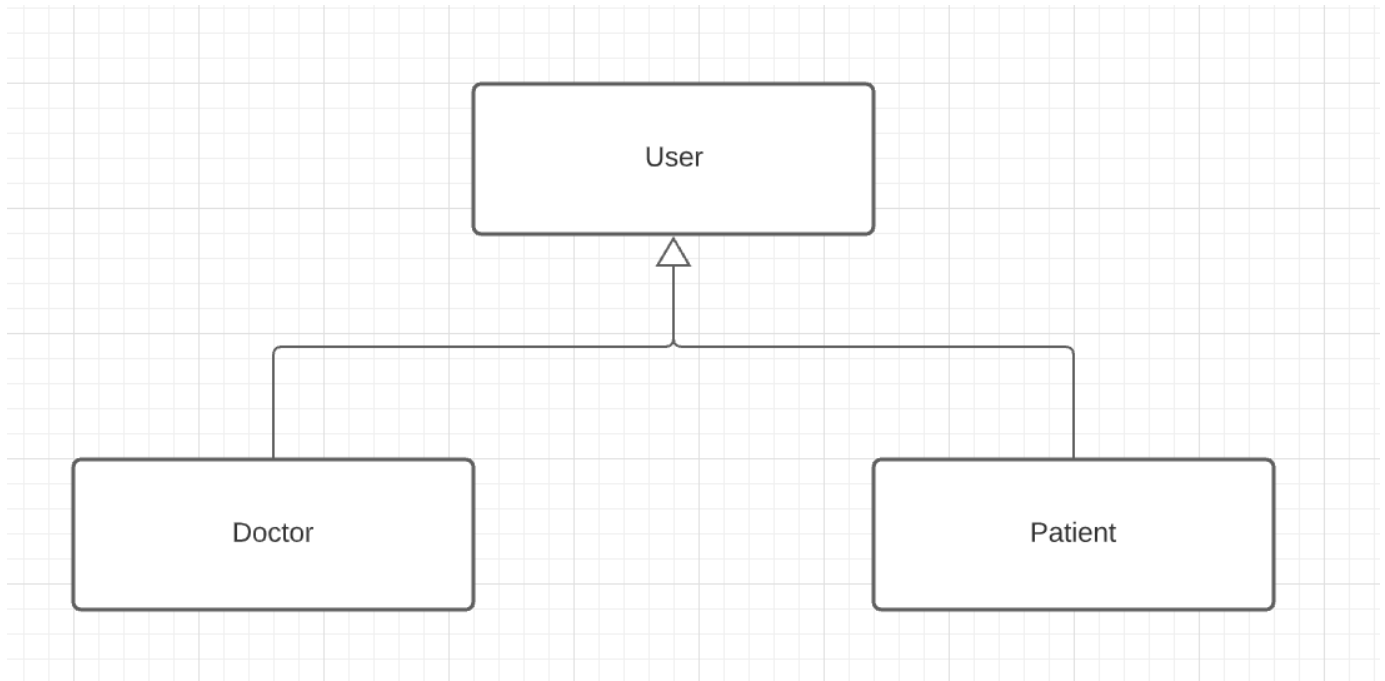


## 8 Preliminary Object-Oriented Domain Analysis

**Class Diagram:** [https://lucid.app/lucidchart/4552dc0c-9328-4188-a4cd-3c290f0092d8/edit?viewport\\_loc=-618%2C-302%2C3328%2C1502%2C0\\_0&invitationId=inv\\_2f7ff5fb-6351-470e-b0c9-6a1257a12dd6](https://lucid.app/lucidchart/4552dc0c-9328-4188-a4cd-3c290f0092d8/edit?viewport_loc=-618%2C-302%2C3328%2C1502%2C0_0&invitationId=inv_2f7ff5fb-6351-470e-b0c9-6a1257a12dd6)



**Inheritance Relationships:** [https://lucid.app/lucidchart/2a772a96-7d90-4ce7-bcf8-d79ce92a3554/edit?viewport\\_loc=90%2C78%2C1664%2C751%2C0\\_0&invitationId=inv\\_42581e07-7aaa-412d-bd64-caa80ef6e304](https://lucid.app/lucidchart/2a772a96-7d90-4ce7-bcf8-d79ce92a3554/edit?viewport_loc=90%2C78%2C1664%2C751%2C0_0&invitationId=inv_42581e07-7aaa-412d-bd64-caa80ef6e304)



## 8.1 Class descriptions

Table 6: User

<b>Abstract or Concrete:</b>	concrete
<b>List of Superclasses</b>	null
<b>List of Subclasses</b>	doctor
<b>Purpose</b>	Make a general class that will contain all data of doctors and patients.
<b>Collaborations</b>	This class will interact with patient and doctor because it contains all data of doctors and patients.
<b>Attributes</b>	-name -email -password -gender -type
<b>Operations</b>	+login(email, password) +sendMessage(receiver, message) -addUserInDB() -checkUser() +viewResults() +editProfile(name, phone, password) +signUp(name, email, password, phoneNumber, gender, type) +signOut()
<b>Constraints</b>	enter wrong name or password

Table 7: Doctor

<b>Abstract or Concrete:</b>	concrete
<b>List of Superclasses</b>	User
<b>Purpose</b>	Receives the patient blood data and analyze it and Reply to the patient who just sent for treatment.
<b>Collaborations</b>	Doctor will interact with patients and view blood analysis.
<b>Attributes</b>	-specialized
<b>Operations</b>	+reviewbloodanalysis() +replytopatient()
<b>Constraints</b>	chat system isn't working , doctor sends wrong messages to wrong patients

Table 8: userServices

<b>Abstract or Concrete:</b>	concrete
<b>List of Superclasses</b>	null
<b>Purpose</b>	Connection and save, remove and update data into database
<b>Collaborations</b>	Enter data that will saved and updated into dataBase
<b>Attributes</b>	-FirebaseAuth <i>auth</i> – <i>CollectionReference</i> <i>user</i>
<b>Operations</b>	+register(name, email, password, phoneNumber, gender, type) + <i>addUser</i> (id, name, phoneNumber, gender, type) + <i>saveTest</i> (TestData) + <i>signOut</i> () + <i>logIn</i> (email, password) + <i>getUser</i> () – <i>&gt;</i> <i>returnuserdatatouploadprofile</i> + <i>editProfile</i> (name, phone, password)
<b>Constraints</b>	Send data to user not true or update data in wrong user and so on



Table 9: Chatting

<b>Abstract or Concrete:</b>	concerte
<b>Purpose</b>	patients and doctors interacts and sends messages with each other
<b>Collaborations</b>	patients and doctors interact and send messages with each other
<b>Attributes</b>	-sender -reciepent -messagecontent
<b>Operations</b>	+viewmessage(id) +sendmessage(id, message)
<b>Constraints</b>	chat system isn't working

Table 10: Blood Analysis

<b>Abstract or Concrete:</b>	concerte
<b>Purpose</b>	Compare patient data with biological reference intervals
<b>Collaborations</b>	patients and doctors interact and send messages with each other
<b>Attributes</b>	-TestData -userServices obj
<b>Operations</b>	+BloodAnalysis(Test Data) +saveTest() +getResults() All of these functions return low or high or normal data -getHaemoglobin() -getHaematocrit() -getRbcs() -getMcv() -getMch() -getMchc() -getRdwCv() -getPlateletCount() -getNeutrophils() -getLymphocytes() -getMonoCytes() -getEosinophils() -getBasophils()
<b>Constraints</b>	whole system shut or breaks down

## 9 Operational Scenarios

### 9.1 Patient

The patient can login or create account if he is using application for the first time ,then he enters his data in blood analytic and get the results from the system to show whether of not the patient/user may have corona or not from the complete blood count data that will be enter by him/her.

### 9.2 Doctor

If the doctor is using the application for the first time, he can also login or establish an account. The doctor will get the patient's blood data and study it before responding to the patient who has been sent for treatment.

### 9.3 Complete Blood Cells (CBC) mobile application

The application compares patient data to biological reference intervals, obtains the results, and gives them to the patient, along with information on which doctor they should see.

## 10 Project Plan

Planyway: <https://planyway.com/app?boardId=61699ca0043a605bca2a068a>



## References

- [1] Jingyuan Liu, Yao Liu, Pan Xiang, et al. “Neutrophil-to-Lymphocyte Ratio Predicts Severe Illness Patients with 2019 Novel Coronavirus in the Early Stage”. In: *medRxiv* (2020). DOI: [10.1101/2020.02.10.20021584](https://doi.org/10.1101/2020.02.10.20021584). eprint: <https://www.medrxiv.org/content/early/2020/02/12/2020.02.10.20021584.full.pdf>. URL: <https://www.medrxiv.org/content/early/2020/02/12/2020.02.10.20021584>.
- [2] Tawsifur Rahman, Amith Khandakar, Md Enamul Hoque, et al. “Development and Validation of an Early Scoring System for Prediction of Disease Severity in COVID-19 Using Complete Blood Count Parameters”. In: *IEEE Access* 9 (2021), pp. 120422–120441. DOI: [10.1109/ACCESS.2021.3105321](https://doi.org/10.1109/ACCESS.2021.3105321).
- [3] Zachary Illg, Gregory Muller, Matthew Mueller, et al. “Analysis of absolute lymphocyte count in patients with COVID-19”. In: *The American Journal of Emergency Medicine* 46 (Mar. 2021). DOI: [10.1016/j.ajem.2021.02.054](https://doi.org/10.1016/j.ajem.2021.02.054).
- [4] Aleksander Obuchowski and Bartosz Rydziński. *Analysis of X-ray scans with reports and complete blood count (CBC) tests and their applications in COVID-19 machine diagnosis based on artificial neural network*. Mar. 2021. DOI: [10.13140/RG.2.2.16411.18725](https://doi.org/10.13140/RG.2.2.16411.18725).
- [5] Yeliz Enderle, Kathrin Foerster, and Jürgen Burhenne. “Clinical feasibility of dried blood spots: Analytics, validation, and applications”. In: *Journal of Pharmaceutical and Biomedical Analysis* 130 (2016), pp. 231–243.