Projects and Organization of the Minor Application Design

Year 2017-2018

Introduction

This document describes both the organization and projects of the Minor Application Design. In Theme 11 you will gather specifications and create a design. You will also start learning the technologies required to carry out the chosen project successfully. Of course, you will also start creating functional aspects of the application, together with a JUnit test suite. In Theme 12, you will finish the development of your product and deploy it as a working application.

Organization and Assessment

In principle, you will work together with one or two other students of the same minor. You will work using the Scrum methodology, in Sprints of approximately two weeks, with tickets/issues being managed using Trello. The Sprint milestones are in the timeline below.

Each class session will start with a **Daily Scrum** meeting in which you will have to pitch your work in a few minutes; what you have been doing since the last Scrum, what was successful and what wasn't, and if you are blocked on some issue. If you need help/assistance with issues, you should say so during the daily Scrum.

At the **End of Sprint** meetings, your group will have to present the status of your project (maximum 10 minutes per project). It always has this structure:

1. Start with a (single-sentence) description of your work and your principals (*opdrachtgevers*)
2. List the goals that were set for this Sprint, and indicate which were met and which weren't. Try to explain your failed goals.
3. List the goals for the upcoming Sprint
4. Finish with a demonstration of your –working!- application.

First quarter: Theme 11

At the end of Theme 11, you will create and present a poster at the ILST poster day where you will publish the progress on your project.

The products you will have to submit at the end of theme 11 are

- Your poster, in pdf format
- An application (or research) design document, according to the provided template (see course website). There should be a final chapter describing the current status of development.
- A link to your Bitbucket repo containing all code and JUnit tests. The individual commits will be studied and taken into account in the grading process.

You will be assessed and graded both on your product and your professional attitude and participation in Scrum meetings.

Second quarter: Theme 12

During Theme 12 you will continue the implementation of your product.

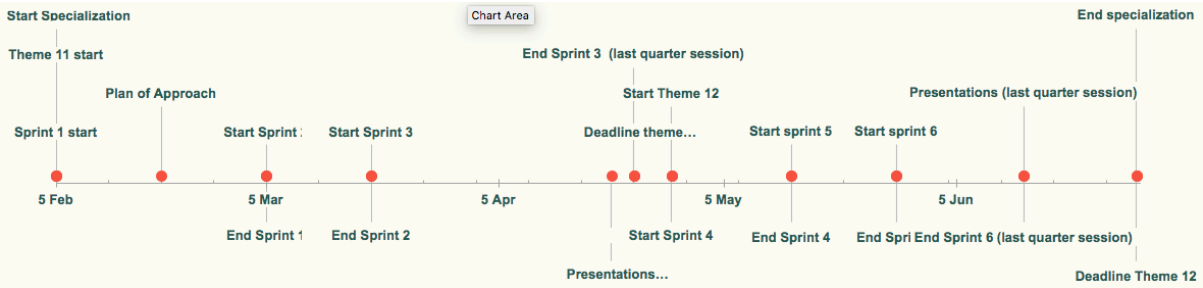
The graded products (aspects) of theme 12 are

- A final presentation

- A working deployed application, demonstrated at the final presentation. Only minor bugs and errors are acceptable here (experimental/alpha versions of features should be excluded from this release)
- A short report describing design and features of the final product, including
    - Feedback from your client on the product you delivered
    - A JUnit test report. If any test fails, try to explain the cause of this test failure.
- A link to your Bitbucket repo containing all code and JUnit tests. Again, the individual commits will be studied and taken into account in the grading process.

Specialization timeline

Below you find the specialization timeline.
The dates are mainly based on week starts (Mondays), so if there is no project lesson on your roster for that Monday, it will be on the first project lesson of that week.



DATE	MILESTONE
05/02/2018	Start Specialization
05/02/2018	Theme 11 start
05/02/2018	Sprint 1 start
19/02/2018	Plan of Approach
05/03/2018	End Sprint 1
05/03/2018	Start Sprint 2
19/03/2018	End Sprint 2
19/03/2018	Start Sprint 3
28/04/2018	Presentations (last quarter session)
28/04/2018	End Sprint 3 (last quarter session)
20/04/2018	Deadline theme 11 (last Friday of quarter)
23/04/2018	Start Theme 12
23/04/2018	Start Sprint 4
14/05/2018	End Sprint 4
14/05/2018	Start sprint 5
28/05/2018	End Sprint 5
28/05/2018	Start sprint 6
14/06/2018	End Sprint 6 (last quarter session)
14/06/2018	Presentations (last quarter session)
29/06/2018	Deadline Theme 12
29/06/2018	End specialization

The projects

1. **iEAR: Inner Ear Antibody Resource**
2. **iDatabase: immune database for systems genetic analysis**
3. **Pedigree visualization and demographics analysis**
4. **User-friendly microbiome data**

1. iEAR: Inner Ear Antibody Resource

Client:
Sonja Pyott, Ph.D.
Assistant Professor and Rosalind Franklin Fellow
University Medical Center Groningen
Department of Otorhinolaryngology

Goal
Create an online, searchable database of antibodies used in the investigation the inner ear

Background
Antibodies are small molecules normally made by the body as part of the immune system. They bind very specifically to the target molecule (called antigen). Today antibodies can be produced in a variety of ways and are essential for a variety of laboratory applications, including western blot assays, flow cytometry, immunohistochemistry (IHC), and enzyme-linked immunosorbent assays (ELISAs). Importantly, antibodies allow detection and localization of molecules that cannot otherwise be seen. Antibodies are still quite expensive to make and purchase and (for reasons that are not always clear) do not always detect the antigen of interest in a particular application and/or tissue. Thus, careful characterization of antibodies for specific research applications is essential. Unfortunately, this information is not carefully documented or made available to other researchers, wasting time and money.

My laboratory uses various antibodies to investigate molecules important for our sense of hearing an balance. We have tested hundreds of antibodies for their ability to detect antigens in sensory and supporting cells of the inner ear, the structure responsible for hearing and balance. This information is invaluable to investigating the molecular and cellular mechanisms underlying normal function of the inner ear and also loss of function associated with deafness and vertigo (dizziness). We share this information with other researchers when requested.

To further extend the accessibility of this information, the goal of this research project is to create an online, searchable database, called "iEAR", in which researchers can identify antibodies by antigen, cell structure identified, as well as vendor and class. When available, supporting images will also be included. Antibodies that do not work in tested applications will also be indicated (since this information can save unnecessary wasteful duplication of efforts).

Tasks
- Compile relevant information about antibodies into a single searchable database with interactive visual interface
- Create an interface that allows researchers within my laboratory and also from other laboratories to upload supporting information about antibodies already included in the database as well as upload information about antibodies not already included in the database.

2. iDatabase: immune database for systems genetic analysis (UMCG)

Client: Dr. Yang Li, y.li01@umcg.nl (UMCG Genetics department)

The human immune system is represented by a complex network of organs, tissues, cells and molecules that evolved primarily to protect the host against infections. Individuals exhibit significantly increased inter-individual variability in the levels of different immune parameters. We have recently observed a strong impact of genetic heritability on cytokine production capacity and cell frequency using 500- Human Functional Genomics (500FG) cohort [Aguirre-Gamboa et al, Cell Report 2016; Li et al, Cell 2016]. In this project, we are going to build a web interface for visualizing and integrating the existing data and results from systems genetic analysis using 500FG cohort. This web-based tool will enable the biologists to explore the multi-scale data sets and facilitate the interpretation of the complex genetic data in a systematic way.

This project is a continuation of a project of last year (https://github.com/veerdonk/idatabase). Some thoughts on goals for this project:
1. add new QTL datasets to the database: eQTL, mQTL, interactionQTL etc
2. Add more "search" options: in addition to "from SNP to QTL", add "Gene to QTL", "genomic region to QTL" etc.
3. Add plotting function for visualisation
…

3. Pedigree visualization (UMCG)

Client: Sipko van Dam; sipkovandam@gmail.com (UMCG)

Dit project is een vervolg op en uitbreiding van een succesvol project van vorig jaar. Zie https://bitbucket.org/riharman/genealogyapplication

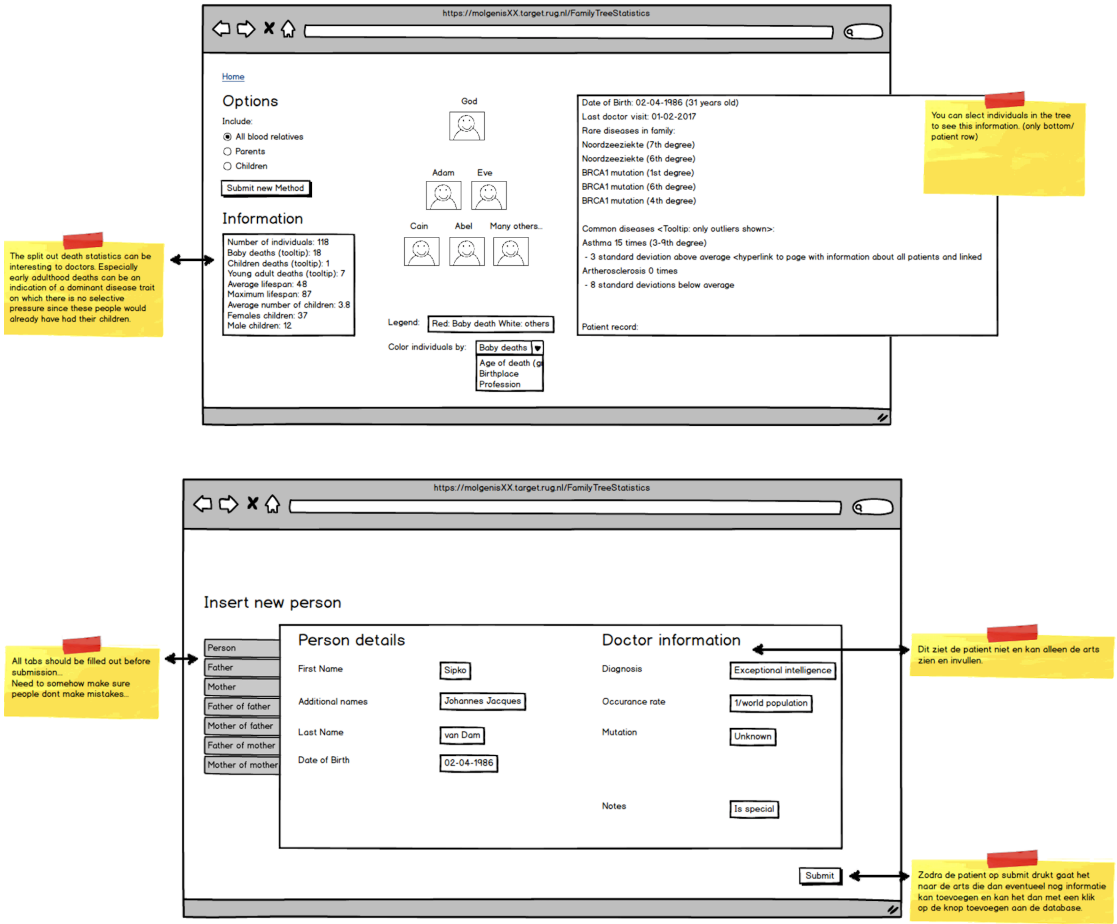
Achtergrond
In het UMCG worden met regelmaat analyses gedaan op patiënten data om te achterhalen welke genetische defecten de gedetecteerde ziektes kunnen verklaren. In ongeveer 2/3 van de patiënten zijn we echter met de huidige technieken niet in staat om een diagnose te kunnen stellen. Het is mogelijk om stamboominformatie te gebruiken om te kijken of er soortgelijke ziektes voorkomen in andere familieleden. Als dit het geval is, lukt het vaak wel om een diagnose te stellen. Helaas is deze informatie vaak maar beschikbaar tot aan opa's en oma's (3 generaties) van de patiënten. Recentelijk hebben wij een methode ontwikkeld waarmee we stambomen kunnen genereren die wel tot 7 generaties teruggaan. Er zijn hoge verwachtingen van deze nieuwe stambomen, maar het gebruik van deze nieuwe informatie wordt bemoeilijkt door het gebrek aan een goede visualisatie interface. De stamboominformatie is beschikbaar in een database of als pedigree (bestand met familierelaties) file.

In dit project gaan jullie een interface (uit)bouwen om over de al bestaande stamboomdatabase te queryen naar verwanten van een patiënt. Vervolgens moet een overzicht van de stamboom aan de gebruiker teruggegeven worden. De database beschrijft de relaties tussen de verschillende familieleden. Normaliter worden stambomen vaak met pen en papier gevisualiseerd, maar voor een stamboom van 7 generaties is dit niet praktisch en dit komt met een aantal extra uitdagingen. Zo kan het mogelijk zijn dat meerdere familieleden in dezelfde boom met elkaar kinderen hebben gekregen, wat duidelijk gevisualiseerd moet worden aangezien dit extra interessant is bij het stellen van diagnoses. Verder is het mogelijk dat een persoon met meerdere personen kinderen krijgt. Ook is het zo dat 2 personen vaak meerdere kinderen hebben, wat betekent dat als je familie data van 1 persoon 7 generaties hoog wilt

visualiseren (inclusief alle achter neefjes en nichtjes) er wel meer dan 1000 personen in voor kunnen komen. Het is de bedoeling om voor deze problemen een oplossing te bedenken en een (web)tool met een overzichtelijke interface te maken die daar mee om kan gaan.

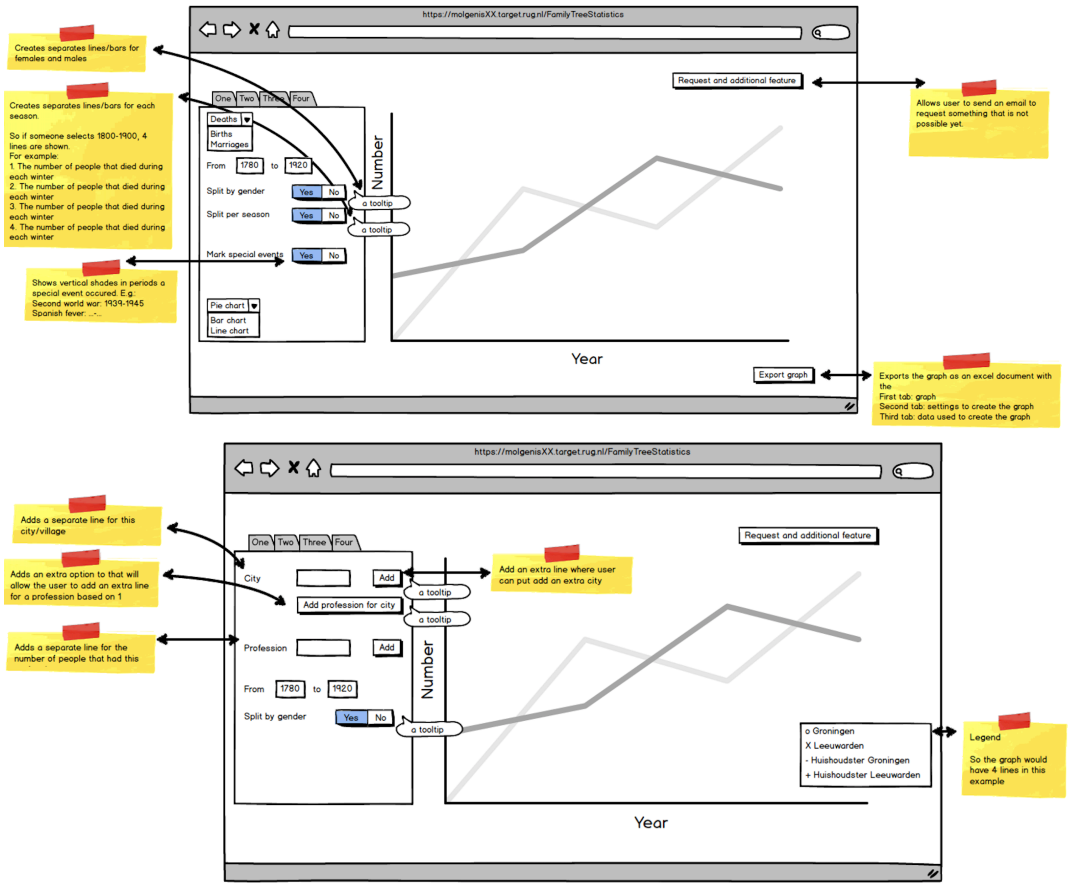
Doelen

1. Het toevoegen van functionaliteiten aan de stamboom visualisaties en het toevoegen van opties om zelf nieuwe individuen toe te voegen. Meer aspecten volgen nog.



Hij gaat binnenkort nog even met wat artsen moeten gaan zitten om hier meer ideeën over te krijgen en voor wat plaatjes van hoe de tool die zij op dit moment gebruiken er uit ziet., met nieuwe aspecten aan stamboomvisualisatie, en verkennen van nieuwe technologie hiervoor.

2. Daarnaast zit er een geheel nieuw deelproject bij: Maken van een interface die gebruikers kunnen gebruiken om zelf grafiekjes te maken van populatie statistieken



4. User-friendly microbiome data: how to report the data to the participants.

Clients
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University Medical Center Groningen
Department of Genetics, CB50

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Курильщиков Александр <alexa.kur@gmail.com>

Background
Lifelines is a population cohort from the North of the Netherlands, that includes extensive collection and analysis of various biological samples in healthy volunteers. For >10,000 of participants, the gut mcirobiome composition has been collected and analyzed using metagenomics sequencing. For these individuals, we have information about the presence and abundance of bacteria and bacterial pathways in their gut.

Participants of Lifelines can request their biological data. However, returning the data in the form of unsupervised tables makes it useless for the participants. The abundance of bacteria is influenced by the methods that have been used for DNA isolation, sequencing and data processing, therefore the individual results should be compared with other samples, processed with the same pipeline. Currently, two different methods have been used for the microbiome analysis in our cohort, so results of each individuals should be compared with the samples processed by the same pipeline.

Goal

The current proposal aims at the development of the user-friendly interface, where every individual can compare his/her results with the pool of the population samples from Lifelines, isolated by the same methods. The example of the interface can be seen in one of the outputs of existing companies, that offer similar service in UK (https://mapmygut.com/tests/16S_Map-My-Gut_V2.5.pdf), USA (https://ubiome.com/) or other countries.