# Requirements Document

Team Name: **ViewCrobe Software**

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# Requirements

## Sample Subset

The project should allow users to select a subset of at most 9 samples to compare. This is to improve user-friendliness. Restricting the number of models shown may reduce distractions, allowing users to better compare certain samples.

## Organism Subset

The project should allow users to select a subset of organism appearing in the samples. This subset is limited by the number of model parameters which we can support, which should be at least 150.

## Model Parameter Assignment

The project should allow users to specify certain model parameters to correspond to certain measurements in the data file, such as the population of a certain microbe corresponding to eye shape. This is to improve user-friendliness by allowing users to match parameters used in an existing result, or to allow certain features to be made more obvious.

## BIOM Format Support

Initially, the project should support the BIOM format for data files. It is relatively human readable as it is essentially JSON, which makes it a good choice for a proof of concept. Expanding file format support is a stretch goal.

## Transforming Data

The project should transform the data from the data file into a format that can be used to generate the models. This allows us to produce a standard format for model generation, which allows us to expand supported file formats.

## Producing a Model

The project should produce a 3d human model based on the parameters from each selected sample. For each model generated in the batch, the same data parameter corresponds to the same model parameter. For example, if the population of a certain microbe in a certain sample corresponded to the straightness of the produced model’s nose for that sample, then the population of the same microbe in a second sample would correspond to the straightness of its model’s nose.

## Drawing Models

The project should draw the produced models to the screen such that each of the models are viewable at the same time. This is to facilitate the comparison.

## User Controls

The project should allow users to rotate, pan, and zoom around the models in order to better compare them. All models should rotate, pan, and zoom in unison, and there will be a default camera location, as well as buttons that allow the user to easily jump to common viewing angles, such as a front view or a profile view.

# User Stories

|  |  |  |
| --- | --- | --- |
| **As a** | **I want to** | **In order to** |
| User | Select sample microbial data files to use through a user interface | Focus attention on a given subset of samples |
| User | Generate facial images and models based on my chosen samples | Compare sample data |
| User | Export images of the models | Reference features of the data later |
| User | Manipulate the models | Better inspect different aspects of the models |
| User | Recognize which features of the model correspond to which features of the data | Recognize the significance of the similarities and differences |

# Stretch Goals

These goals may be achieved later on if time allows.

## Expand File Type Support

In addition to BIOM file type, our project may support:

* mothur
* QIIME OUT table tab separated format
* MG-RAST organism abundance table (tab separated value)
* MEGAN (csv)
* STAMP profile
* Phoenix 2

## Provide a web version

In addition to the local version, this would provide a web UI which would invoke the component that generates models on the server. These models would then be sent to the client browser to be presented to the user.

## Export Images for Later Comparison

This feature would allow users to not only compare samples in the same file, but also to compare to files compared earlier. However, this would allow the user the opportunity to associate different data parameters with different model parameters between the two results, which could lead to misleading results.