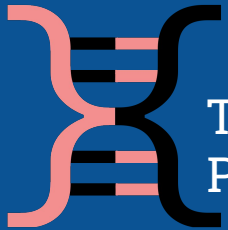


GUI for Massively Multiplexed Pathogen Detection

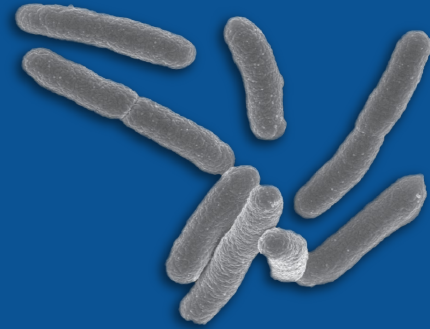
By Turan Naimey, Austin Kelly, Alex Lacy and Chance Nelson
Mentor: Isaac Shaffer



Team
PathLab

Introduction

- E. Coli Outbreak Germany 2011
- 3500 cases of infection
- 51 deaths
- Spanish Cucumbers
- Failure to detect the right strain



Multiplexed Genomics Testing

- Pathogen screening panel
- Diagnostic Tests
- Optimization of Tests
- Efficient Detection of Pathogens



The Client: Fofanov Lab

- Bioinformatics
- Epidemiology
 - Detection
 - Tracking
- **Primacy** - Pathogen tracking optimisation tool

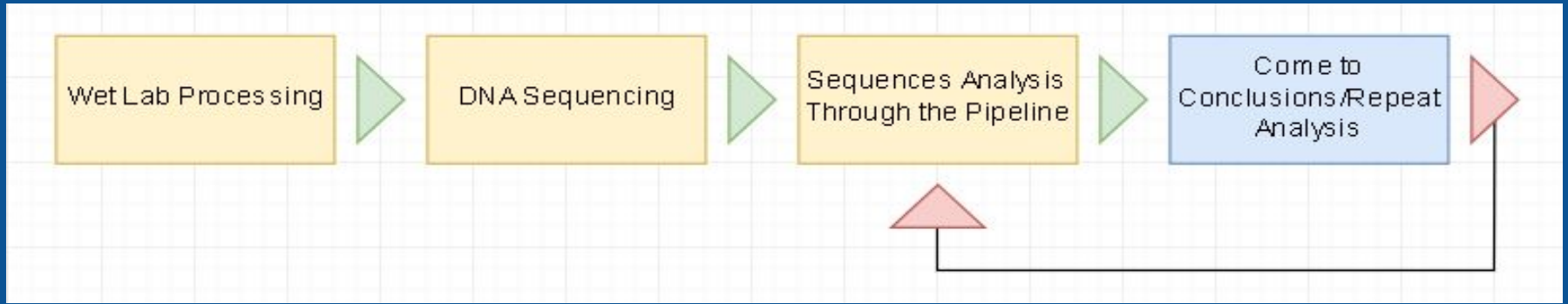


Viacheslav Fofanov,
Ph.D.



Tara Furstenau,
Ph.D.

Client's Business Model and Workflow



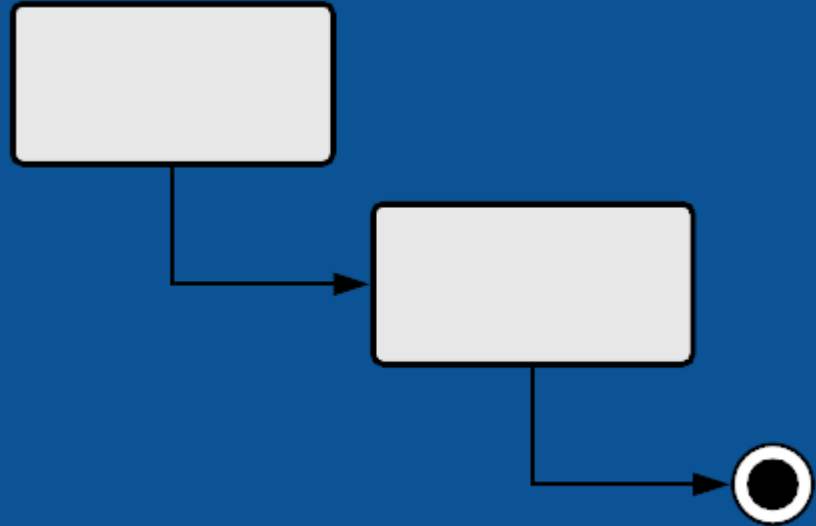
Problem Overview

- Learning Curve
- CLI can be intimidating for non technical individuals
- Lack of appeal
- Unforgiving

```
~/Qiime2-Tutorials/Atacama-Sample qiime dada2 denoise-paired \  
--i-demultiplexed-seqs demux.qza \  
--p-trim-left-f 13 \  
--p-trim-left-r 13 \  
--p-trunc-len-f 150 \  
--p-trunc-len-r 150 \  
--o-table table.qza \  
--o-representative-sequences rep-seqs.qza \  
--o-denoising-stats denoising-stats.qza  
Saved FeatureTable[Frequency] to: table.qza  
Saved FeatureData[Sequence] to: rep-seqs.qza  
Saved SampleData[DADA2Stats] to: denoising-stats.qza
```

Solution: GUI

- Easy to use | Easy to read
- Sectioned
 - Independant
 - Re-runnable
 - Intuitive inputs
- Data Parsing
 - Statistics
 - Usefully displayed
 - Graphs
 - Most useful results



Development Plan

- Research Suitable Technologies
- Implement Empty Prototype
- Tailor to Client Desires
- Write Requirements Document