

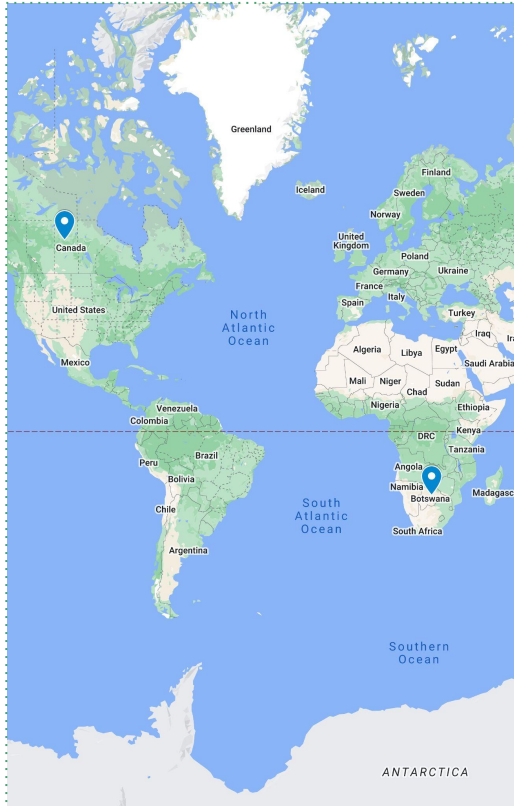
# Introduction of Software Engineering & RGI

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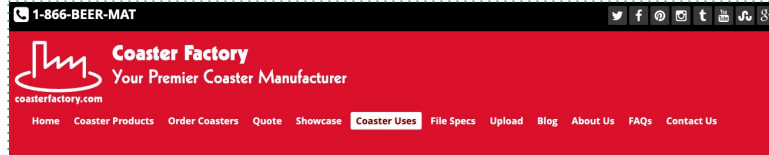
Amogelang R. Raphenya, B.Eng, M.Sc Candidate  
McArthur Lab  
26 May 2022

# About Me

- Born in Botswana
- Studied Computer Engineering (2004-2008)@McMasterU
- Currently M.Sc. Biochemistry (2021-present)



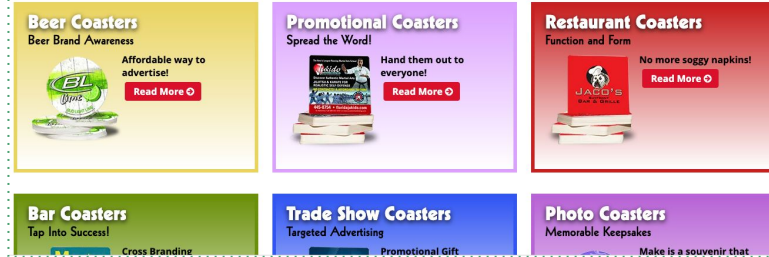
# About Me



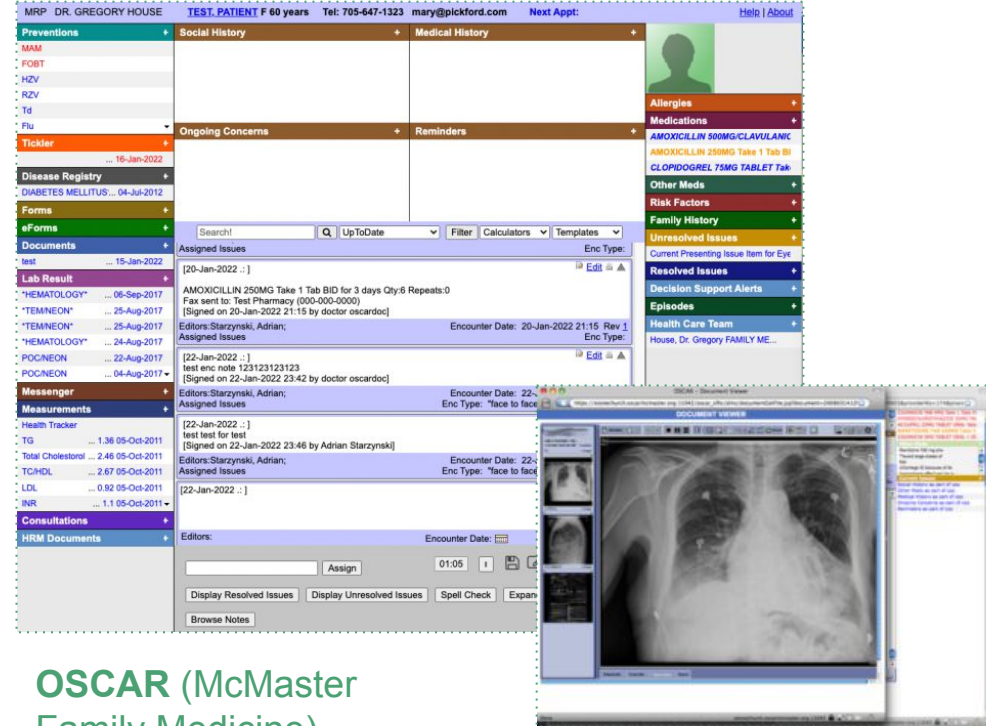
## Ways to use Custom Coasters

### Coasters can be Versatile.

Coasters can come in many different shapes, sizes, and weights, but how they are used can make a huge difference. While their obvious strength in promoting beverage brands is well-known, they are also an excellent platform for any kind of promotion, including promoting bars, restaurants, trade shows, advertising campaigns, weddings, sponsorship events, and even used for scrapbooking!



coasterfactory.com



OSCAR (McMaster Family Medicine)

# About Me

- Joined McArthur Lab in 2015
- I didn't know much about Biology
- I haven't worked with Ontologies

Wifi McArthur-Net : greenismyctlov  
Gite: 130.113.155.177  
Git URL: [http://130.113.155.177/users/sign\\_in](http://130.113.155.177/users/sign_in)  
username: anaphenga

- plasmid?
  - cvterm\_crossref tables?
  - how is the results updated and precalculated?
  - populating cvterm\_crossref table
    - load cvterm\_crossref.
  - GFF3 file?
  - sequence ontology (SO) vs Gene Ontology (GO)
  - Chado CV module??
  - CARD custom ontologies?
    - ARO (Antibiotic Resistance Ontology)
    - NCBITaxon (Taxonomy Ontology).
    - PUBO (Publication Ontology)
  - cvtermpath?
  - main modules?
  - kurz gesagt - In a nutshell
  - State of Gmod - Scott Cain.
- 
- Skype: Justin - justin\_jia2006  
Andrew - agmcarthur

<http://so.genomics.net/>

# Task at Hand

Organism	Source	Count	Notes
E. coli	NML	426	peptide <sup>S</sup> /contigs <sup>421</sup> 16S
Salmonella	USDA	247	peptide
Pseudomonas	GC/CF	390	contigs 16S
TB microbaine	India/UDelhi	24	peptides
Acinetobacter	France	X	
GW Salmonella	Wright	1	contigs

*Handwritten diagram:*

contigs → RGI  
~~ARO~~ → info

\* genomes | ARO + models | RGI

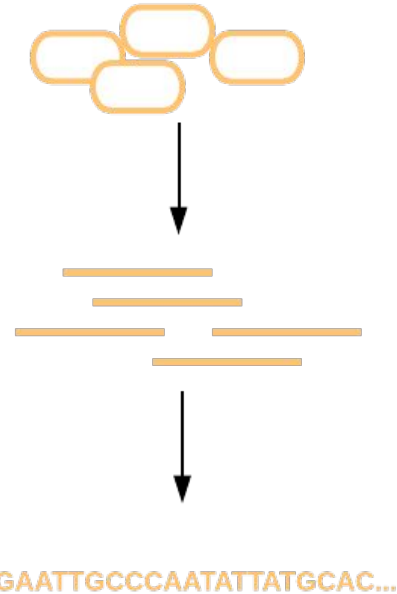
Curation

# How do we obtain genomes?

Culture and Isolate a single microbe

DNA extraction and fragmentation

Sequencing and Assembly



# How do we obtain Metagenomes?

multiple microbes (mainly unculturable)

DNA extraction and fragmentation

Sequencing and Assembly

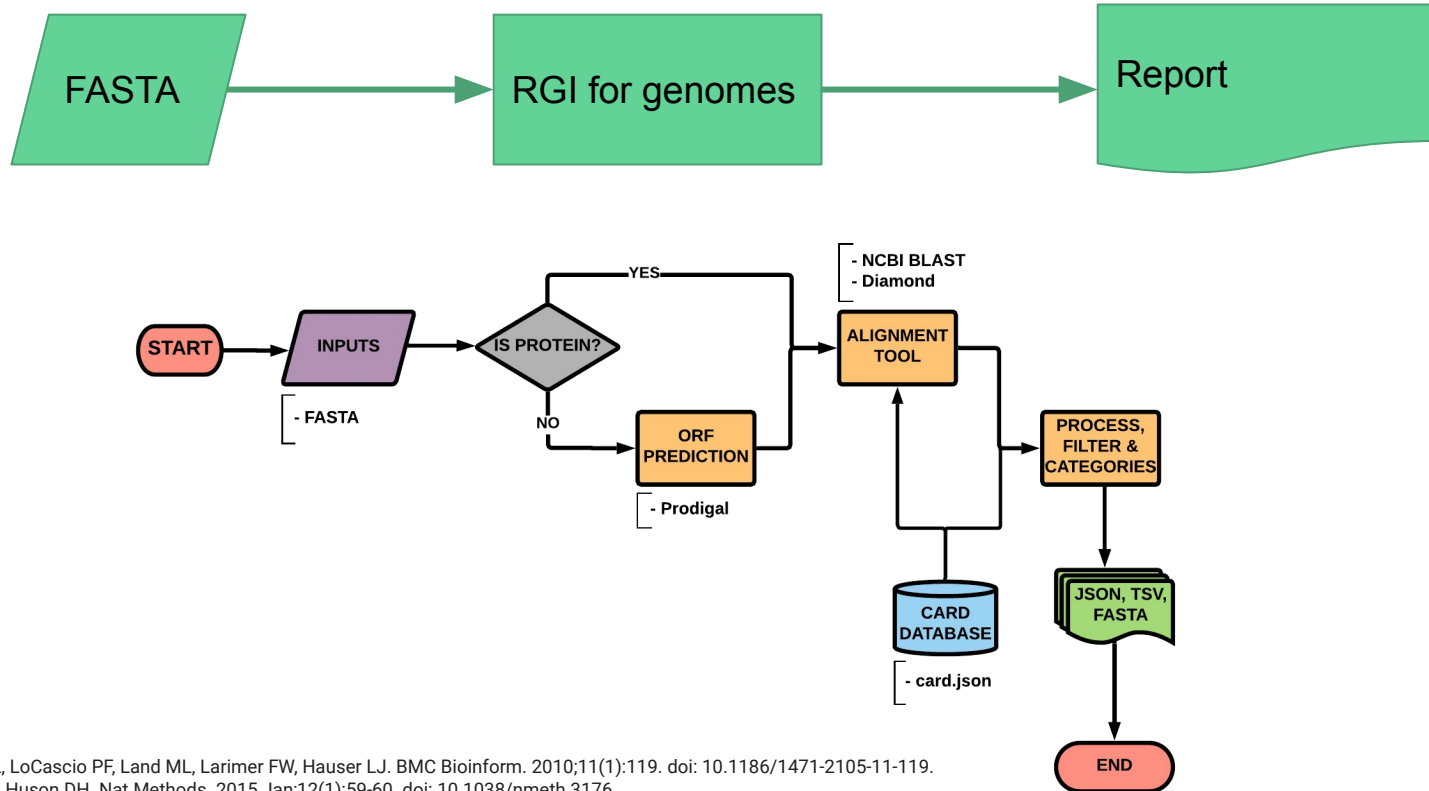


# Metagenomes Vs Genomes

	<b>Genomes</b>	<b>Metagenomes</b>
<b>Assembly</b>	Easy	Difficult
<b>Gene prediction</b>	Easy	Difficult
<b>Microbes captured</b>	Culturable only	All



# Predicting AMR genes from genomes

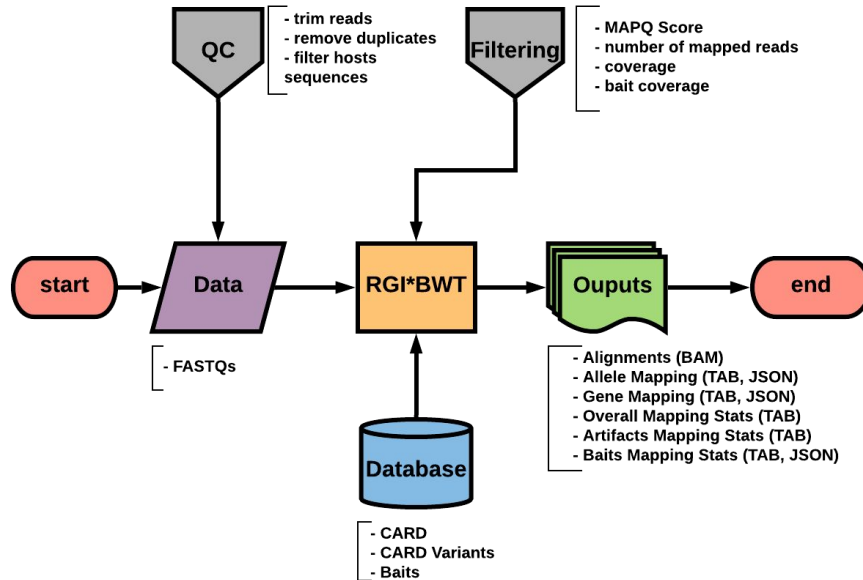
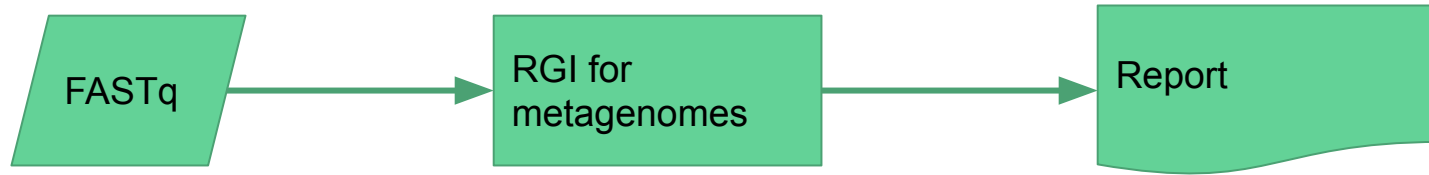


Hyatt D, Chen G-L, LoCascio PF, Land ML, Larimer FW, Hauser LJ. BMC Bioinform. 2010;11(1):119. doi: 10.1186/1471-2105-11-119.

Buchfink B, Xie C, Huson DH. Nat Methods. 2015 Jan;12(1):59-60. doi: 10.1038/nmeth.3176.

Camacho C, et al. BLAST+: architecture and applications. BMC Bioinformatics. 2009 Dec 15;10:421. doi: 10.1186/1471-2105-10-421.

# Predicting AMR genes from metagenomes



# Summary

- RGI predicts AMR genes from genomes and metagenomes
- RGI needs accurate AMR data for good predictions
- RGI is suited for surveillance

Thank you.