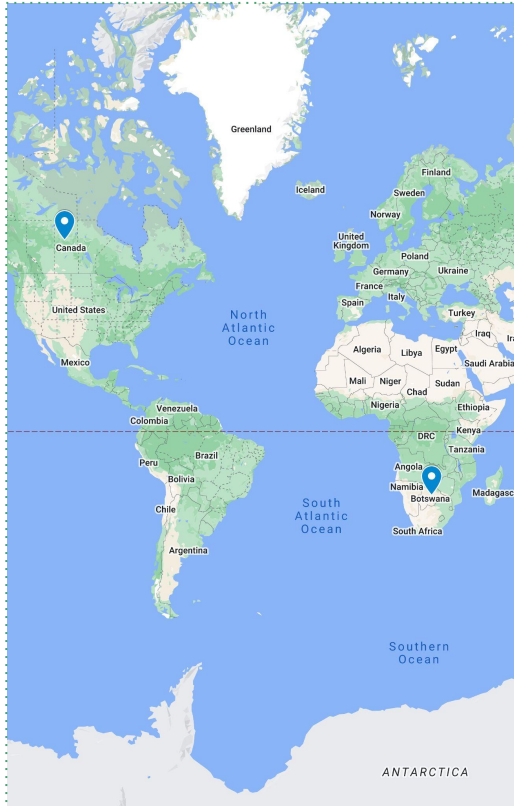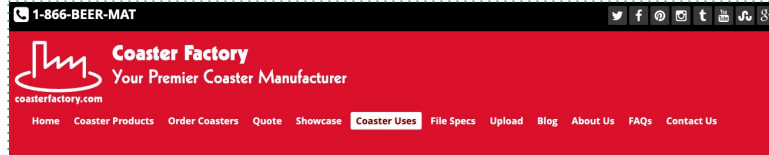# Introduction of Software Engineering & RGI

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

About Me

- Born in Botswana

- Studied Computer Engineering (2004-2008)@McMasterU

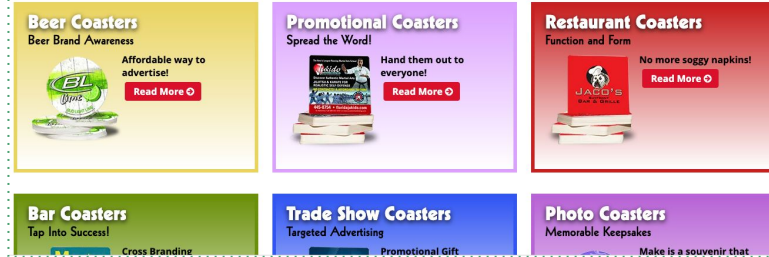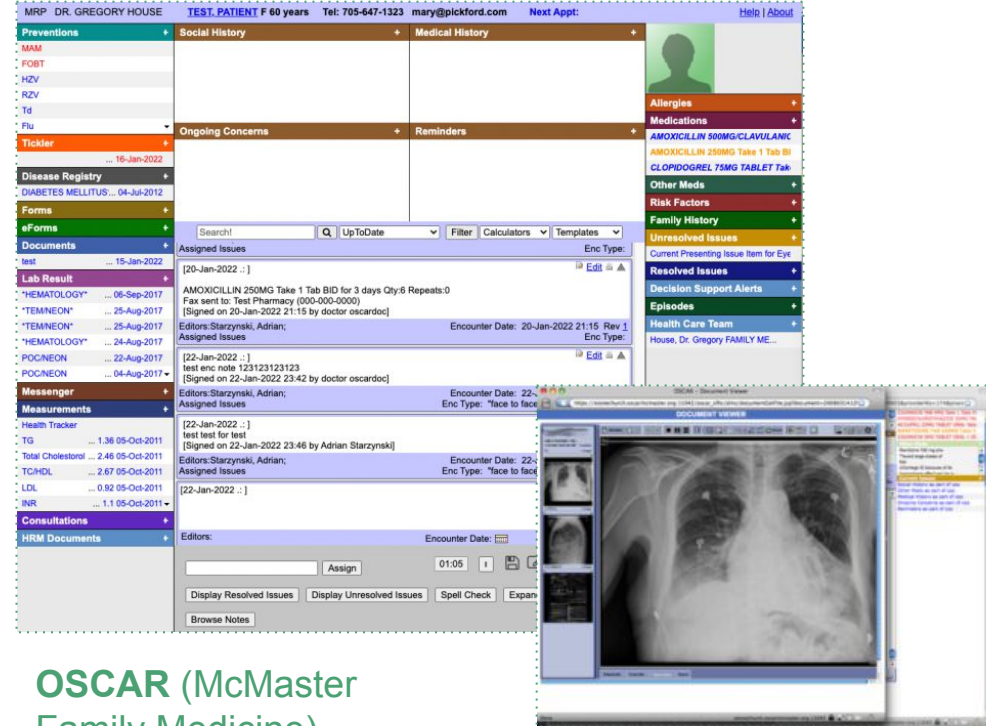- Currently M.Sc. Biochemistry (2021-present)

About Me

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

Amos' Lab notebook 2015

Task at Hand

How do we obtain genomes?

Culture and Isolate a single microbe

DNA extraction and fragmentation

Sequencing and Assembly

.....ATGGAATTGCCCAATATTATGCAC...
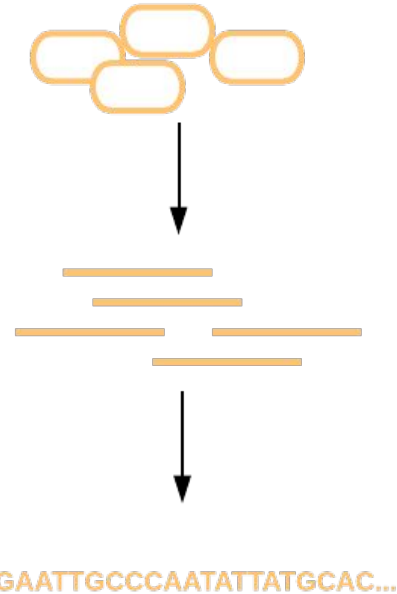
How do we obtain Metagenomes?

multiple microbes (mainly unculturable)

DNA extraction and fragmentation

Sequencing and Assembly

.....ATGGAATTGCCCAATATTATGCAC...

....ATGGAATTGCCCAATATTATGCAC...

....ATGGAATTGCCCAATATTATGCAC...

....ATGGAATTGCCCAATATTATGCAC...

Metagenomes Vs Genomes

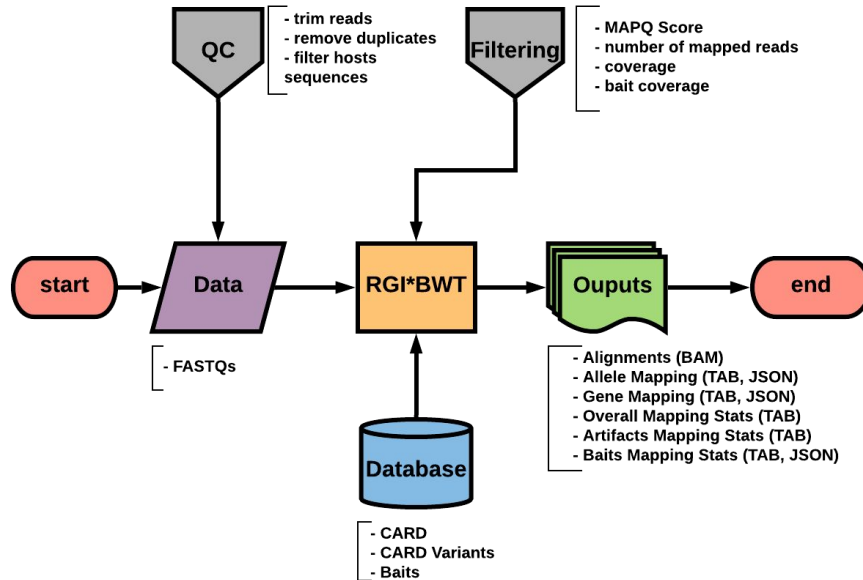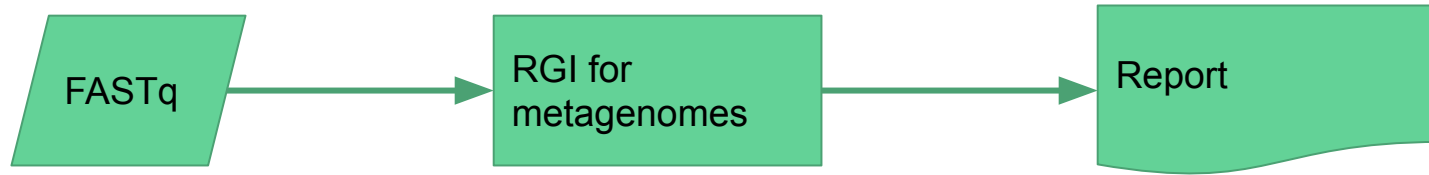|	**Genomes**	**Metagenomes**
Assembly	Easy	Difficult
Gene prediction	Easy	Difficult
Microbes captured	Culturable only	All

Predicting AMR genes from genomes
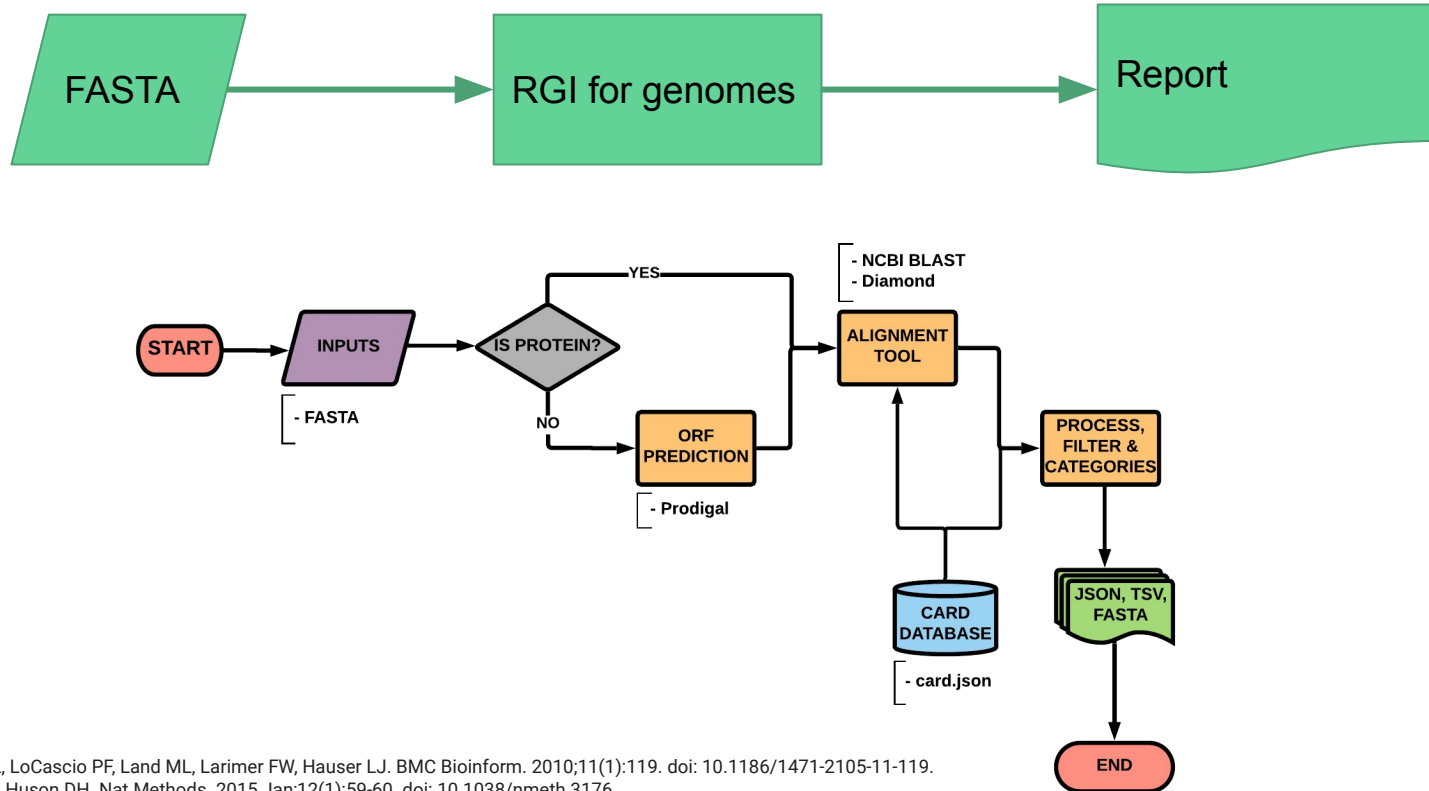
Hyatt D, Chen G-L, LoCascio PF, Land ML, Larimer FW, Hauser LJ. BMC Bioinform. 2010;11(1):119. doi: 10.1186/1471-2105-11-119.
Buchfink B, Xie C, Huson DH. Nat Methods. 2015 Jan;12(1):59-60. doi: 10.1038/nmeth.3176.
Camacho C, et al. BLAST+: architecture and applications. BMC Bioinformatics. 2009 Dec 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.