



# Antimicrobial Resistance Characterization in Metagenomes

NastyBugs

Bug\_And\_Drugs

Nasty\_Metagenomes

## The goal:

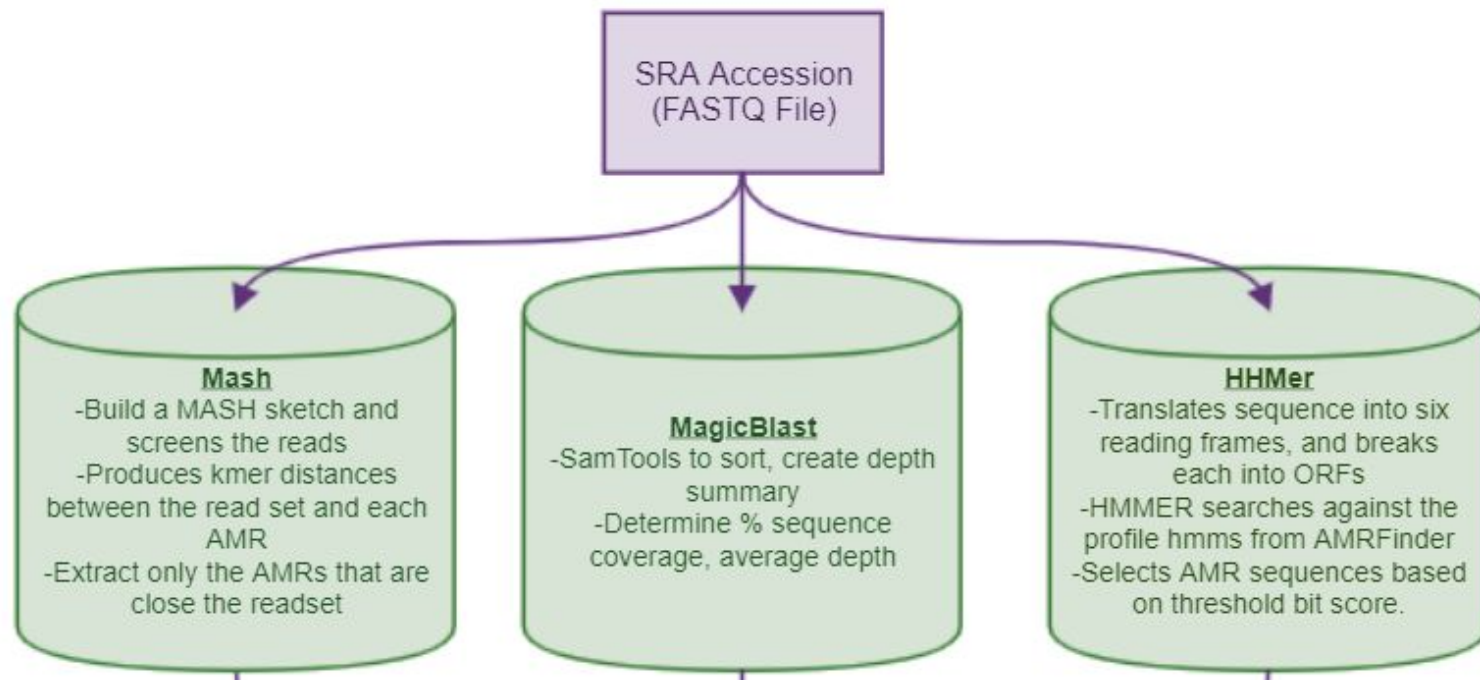
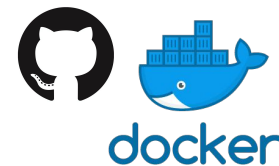
- Comparison of MagicBlast to HMM-er
- Local assembly for AMR “hits”
- Species identification and plasmid detection

## The tools:

- AMR Finder: includes CARD, resFinder, Lahey, Pasteur Institute Beta Lactamases, NIH
- Workflow: Nextflow
- Container: Docker

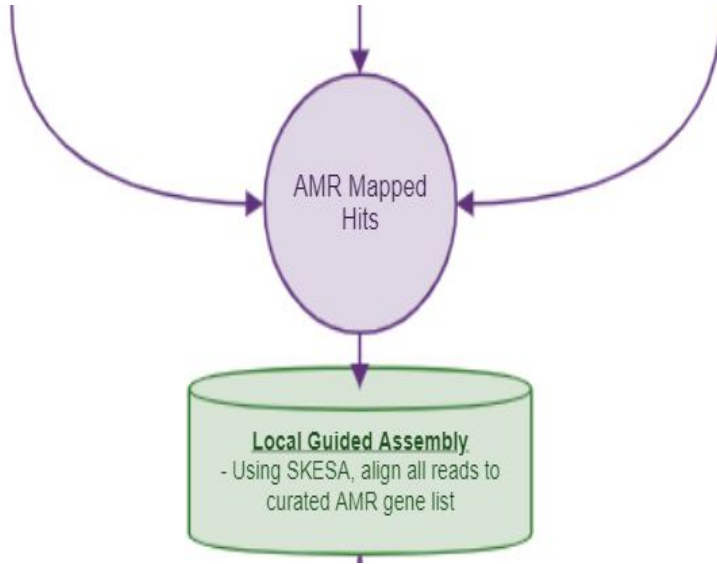
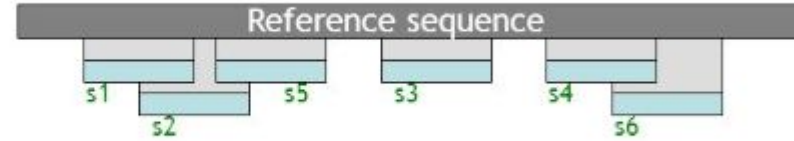
# Workflow

nextflow



# Workflow

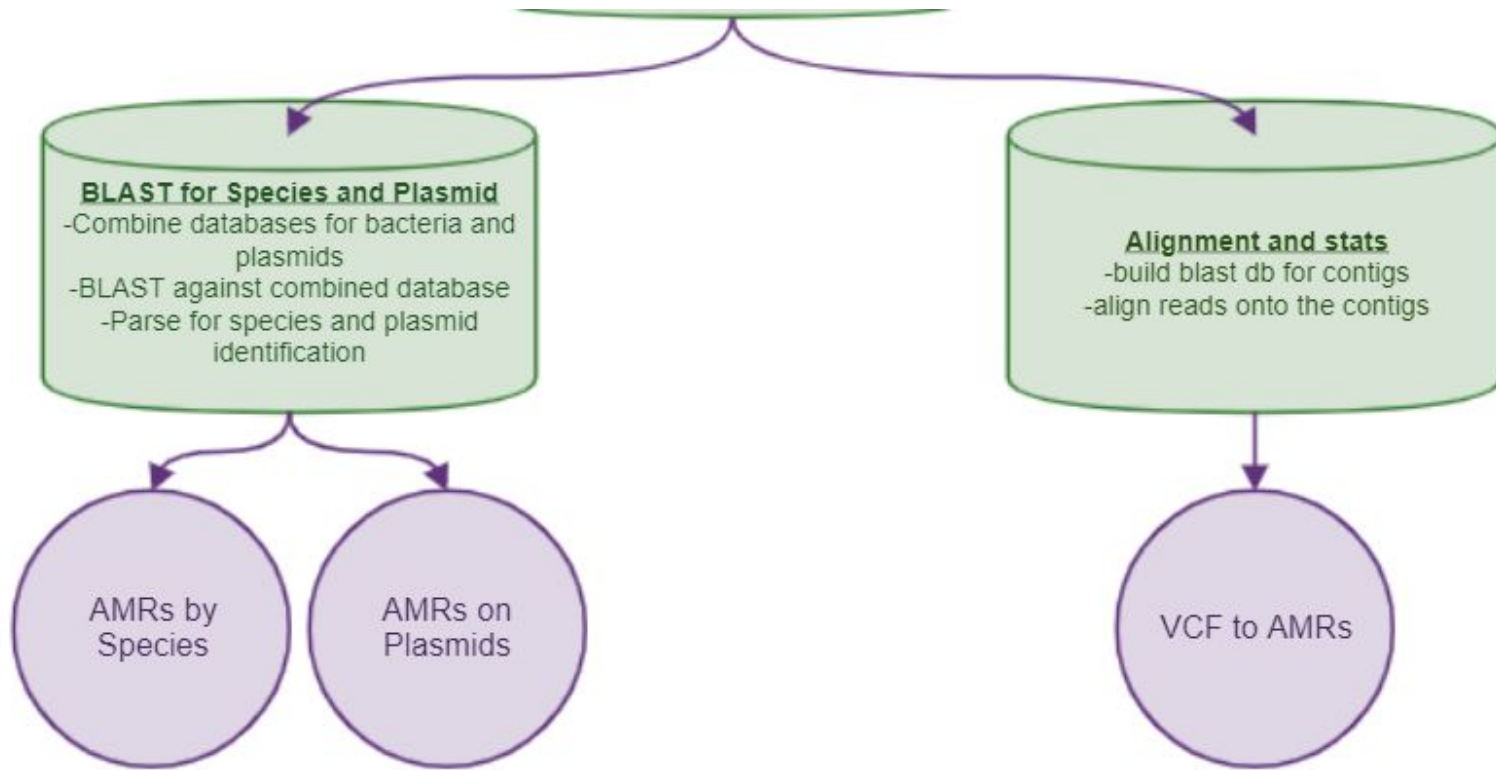
reference-  
guided



**SKESA - Strategic Kmer  
Extension for Scrupulous  
Assemblies**



# Workflow



# Results

Placing contigs in the global context: blast against refseq

Row	run	contig	ref	species	origin	alignment_score	identity
1	ERR1600439	Contig4_kmer41	NZ_BCQC01000002.1	Enterococcus faecalis	Chromosome	21653	100.0
2	ERR1600439	Contig4_kmer41	NZ_KB944590.1	Enterococcus faecalis	Chromosome	21653	100.0
3	ERR1600439	Contig4_kmer41	NZ_UARR01000008.1	Enterococcus faecalis	Chromosome	21653	100.0



## AMR intervals on contigs

Row	run	contig	start	stop	AMR	score	strand
1	ERR1600439	Contig1_kmer41	39921	40189	NG_054942_1	255	+
2	ERR1600439	Contig2_kmer41	13797	14209	NG_047884_1	255	+
3	ERR1600439	Contig2_kmer41	13797	14217	NG_047881_1	255	+
4	ERR1600439	Contig3_kmer41	41661	42522	NG_049989_1	255	+



## Variants called on AMR regions of contigs

Row	run	contig	pos	id	ref	alt	qual
1	ERR1600439	Contig5_kmer41	44600	.	C	T	24.4162
2	ERR1600439	Contig5_kmer41	44600	.	C	T	24.4162



# Work to be done

- Run HHM-er through SKESA
- The workflow in Nextflow

