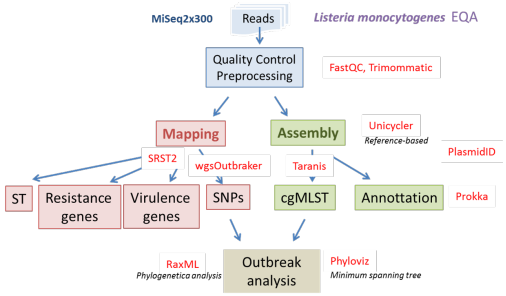
Bacterial WGS training : Exercise 5

Title	**Chromosome, plasmid, resistance and virulence annotation**
Training dataset:	
Questions:	• How many genes there are in my sample? • Are there virulence and/or antibiotic resistance genes? • Where are the genes located? • Which plasmids are present in the sample? • How do I visualize the results?
Objectives:	• Annotate virulence and ABR genes • Determine gene variants • Determine plasmidome • Locate annotated genes • Results interpretation
Time estimation:	1 h
Key points:	• Comparing annotation using mapping vs assembly • Plasmid, virulence and resistance determination

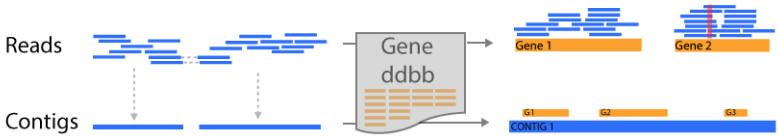
Introduction

Training summary



Training dataset description

This dataset is an *in silico* dataset obtained with wg-sim usint a sample from *Klebsiella pneumoniae subsp. pneumoniae HS11286*.



Exercise

Mapping based annotation

```
cd
cd Documents/wgs
nextflow run BU-ISCIII/bacterial_wgs_training \
-profile singularity \
--reads '/home/pjsola/Documents/wgs/training_dataset/plasmidid_test/KPN_TEST_R{1,2}.fastq.gz' \
--fasta training_dataset/listeria_NC_021827.1_NoPhagues.fna \
--gtf training_dataset/listeria_NC_021827.1_NoPhagues.gff \
--srst2_resistance training_dataset/ARGannot.r1.fasta \
--srst2_virulence training_dataset/EcOH.fasta \
--step mapAnnotation
```

Results

Sample	DB	gene	allele	coverage	depth	diffs	uncertainty	divergence	length	maxMAF	clusterid	seqid	annotation
KPN_TEST_R	ARGannot.r1	RmtB_AGly	RmtB_1580	100.0	12.09	1snp		0.132	756	0.125	309	1580	no;no;RmtB;AGly;AB263754;2843-3598;756
KPN_TEST_R	ARGannot.r1	TEM-1D_Bla	TEM-117_968	100.0	33.386	2snp		0.262	764	0.382	205	968	no;no;TEM-117;Bla;AY130282;1-764;764
KPN_TEST_R	ARGannot.r1	KPC-1_Bla	KPC-14_809	100.0	5.412	1indel		0.0	876	0.333	184	809	no;no;KPC-14;Bla;JX524191;396-1271;876
KPN_TEST_R	ARGannot.r1	AmpH_Bla	AmpH_634	100.0	11.373	14snp		1.206	1161	0.143	86	634	no;no;AmpH;Bla;CP003785;4208384-4209544;1161
KPN_TEST_R	ARGannot.r1	CTX-M-9_Bla	CTX-M-14_102	100.0	26.676	1snp		0.114	876	0.412	190	102	no;yes;CTX-M-14;Bla;AF252622;1741-2616;876

Sample	DB	gene	allele	coverage	depth	diffs	uncertainty	divergence	length	maxMAF	clusterid	seqid	annotation
KPN_TEST_R	ARGannot.r1	StrA_AGly	StrA_1501	100.0	12.502	2snp		0.249	804	0.167	263	1501	no;no;StrA;AGly;AJ627643;3725-4528;804
KPN_TEST_R	ARGannot.r1	StrB_AGly	StrB_1614	100.0	9.545	1snp		0.119	837	0.167	227	1614	no;no;StrB;AGly;KR091911;169145-169981;837
KPN_TEST_R	ARGannot.r1	AadA_AGly	AadA2_1605	100.0	9.306	2snp		0.256	780	0.167	229	1605	yes;no;AadA2;AGly;X68227;166-945;780
KPN_TEST_R	ARGannot.r1	SHV-OKP-LEN_Bla	SHV-11_1287	100.0	9.401			0.0	861	0.143	164	1287	yes;no;SHV-11;Bla;HM751098;1-861;861
KPN_TEST_R	ARGannot.r1	TetRG_Tet	TetRG_605	96.209	6.48	10snp24holes	edge0.0	1.642	633	0.5	373	605	no;no;TetRG;Tet;S52438;113-745;633
KPN_TEST_R	ARGannot.r1	DfrA_Tmt	DfrA12_1089	99.799	8.389	1indel		0.0	498	0.143	418	1089	yes;no;DfrA12;Tmt;Z21672;310-807;498
KPN_TEST_R	ARGannot.r1	TetG_Tet	TetG_632	100.0	9.963			0.0	1176	0.25	80	632	no;no;TetG;Tet;NC_010410;3672607-3671432;1176
KPN_TEST_R	ARGannot.r1	SulII_Sul	SulII_1219	100.0	11.094	1snp		0.123	816	0.2	256	1219	no;no;SulII;Sul;KR091911;167466-168281;816

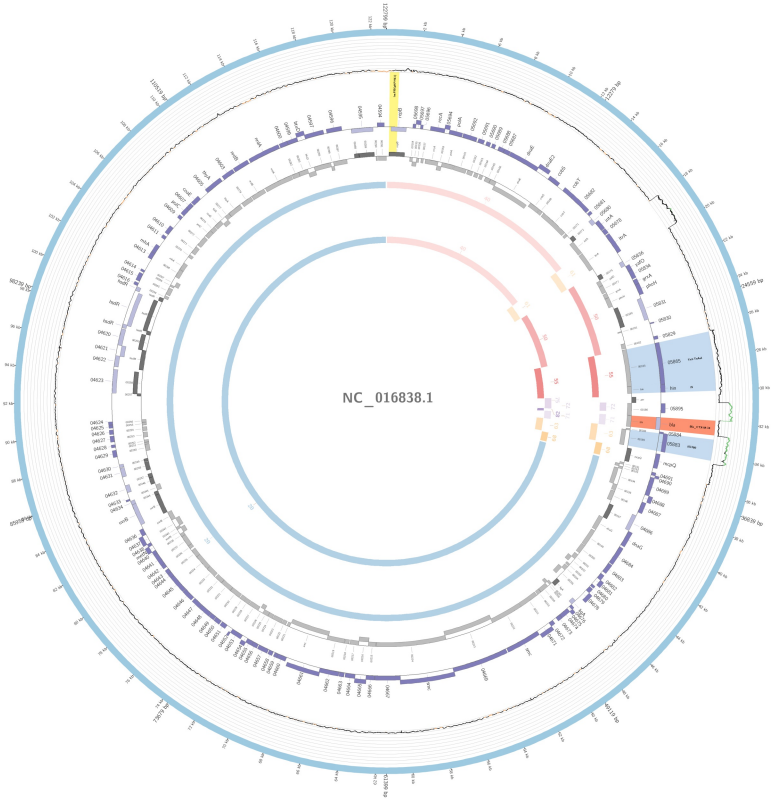
Assembly based annotation

```
cd
cd Documents/wgs
nextflow run BU-ISCIII/bacterial_wgs_training \
-profile singularity \
--reads '/home/pjsola/Documents/wgs/training_dataset/plasmidid_test/KPN_TEST_R{1,2}.fastq.gz' \
--fasta training_dataset/listeria_NC_021827.1_NoPhagues.fna \
--gtf training_dataset/listeria_NC_021827.1_NoPhagues.gff \
--plasmidid_database training_dataset/plasmidid_test/plasmids_TEST_database.fasta \
--plasmidid_config /home/pjsola/Documents/wgs/training_dataset/plasmidid_test/plasmidid_config.txt \
--step plasmidID
```

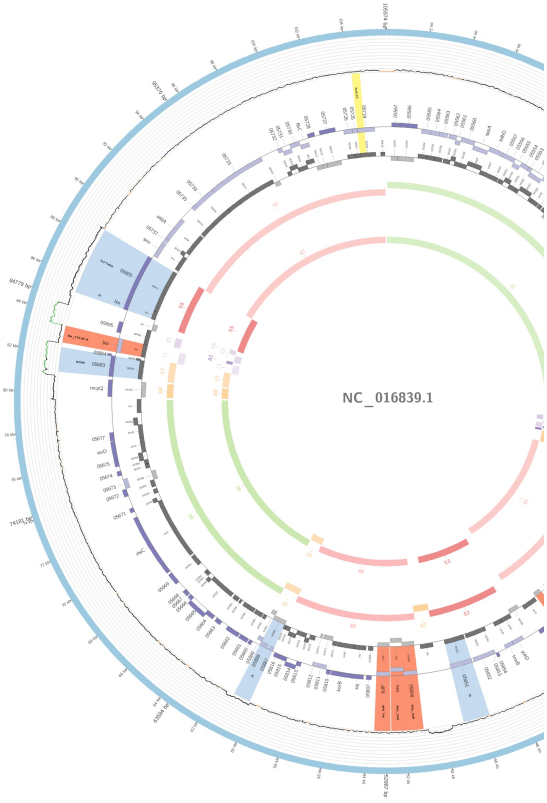
##Results

NC_016838.1	NC_016839.1

NC_016838.1



NC_016839.1



NC_016841.1

NC_016846.1

NC_016838.1	NC_016839.1