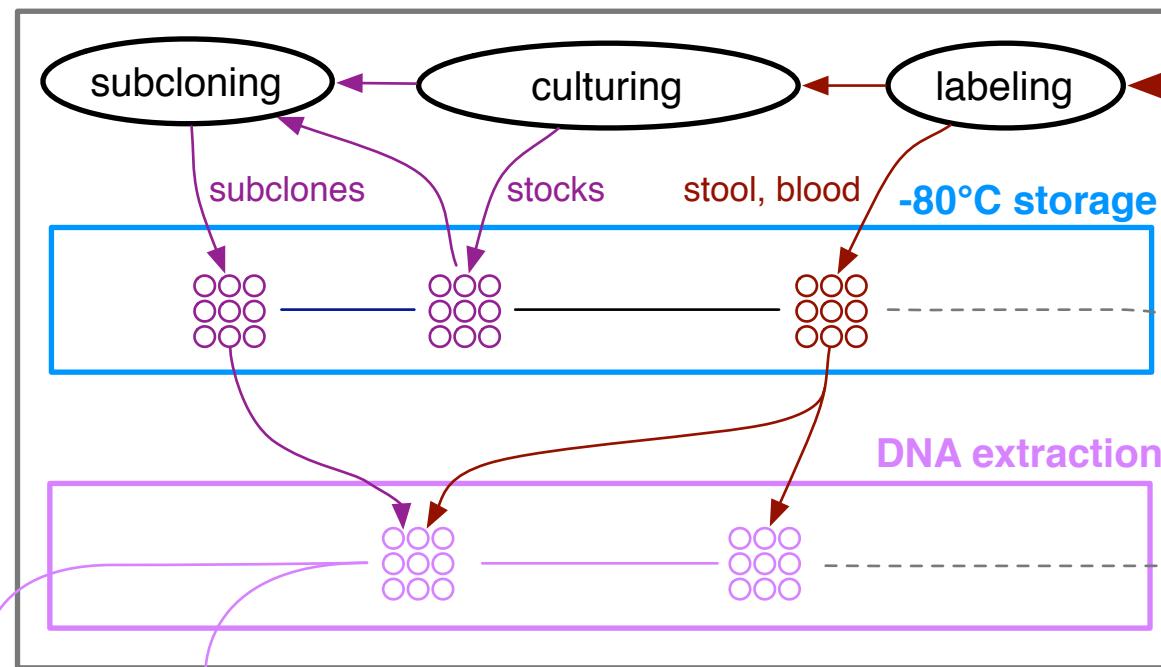


# Pathogen Surveillance Program @



Bakel Lab



daily specimen delivery  
specimens

Clinical Micro Lab



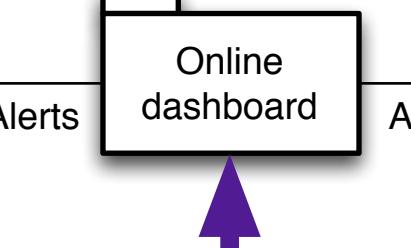
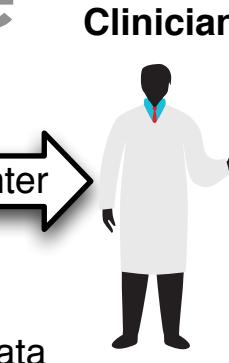
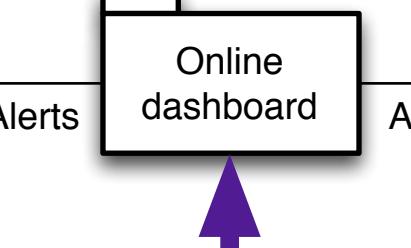
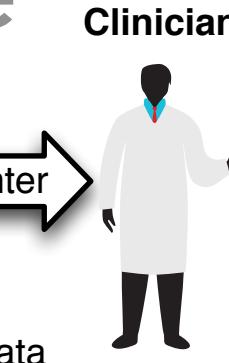
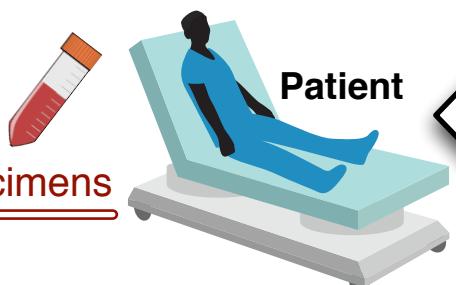
VITEK 2™

specimens

Clinical Micro Lab

VITEK 2™

# Patient Care



EMR data  
Culture results  
Antimicrobial susceptibilities

Data Warehouse  
Epic

nightly import  
barcoded links

de-identification  
PHI

de-identified specimen metadata

Isolate times & locations

XMFA alignment

Pairwise SNP distances

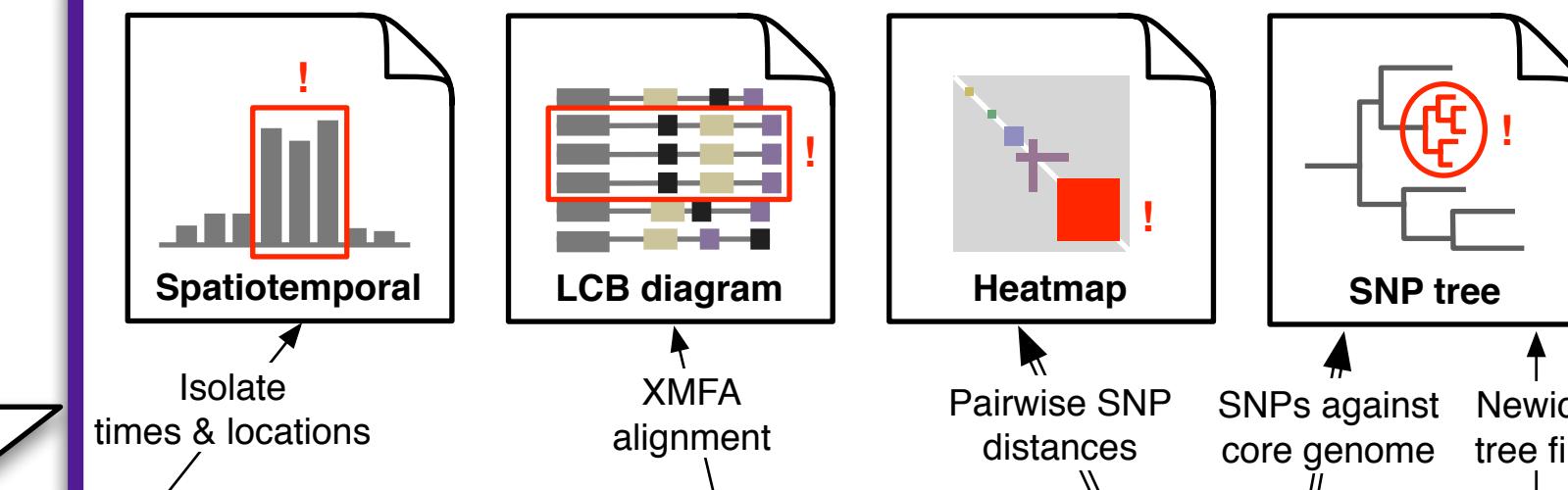
SNPs against core genome

Newick tree file

Targeted intervention  
Surveillance sampling  
Isolation  
Unit cleaning

Goal: ↓ HAI

# pathogenDB-viz



# pathogenDB-pipeline



PacBio RS II instrument

H5 Files

BLASR + quiver resequencing

FASTA assembly

BLAST reorientation

FASTA assembly

circlator circularization

FASTA assembly

prokka annotation

FASTA assembly

QC analyses + deposition

GRIMM rearrangement distance

Mauve multiple genome alignment

show-snps find SNPs in unique mappings

HGAP de novo assembly

FASTA assembly

FASTQ error-corrected reads

bwa mem alignment

samtools mpileup consensus calling

Corrected FASTA assembly

rake fetch dependencies

IGB Quickload repository

MUMmer pairwise genome alignment

RAXML max-likelihood phylogeny

Illumina instrument

FASTQ reads

bwa mem alignment

BAM alignment

GenBank annotated assembly

FASTA assemblies

FASTA assemblies

FASTA assemblies

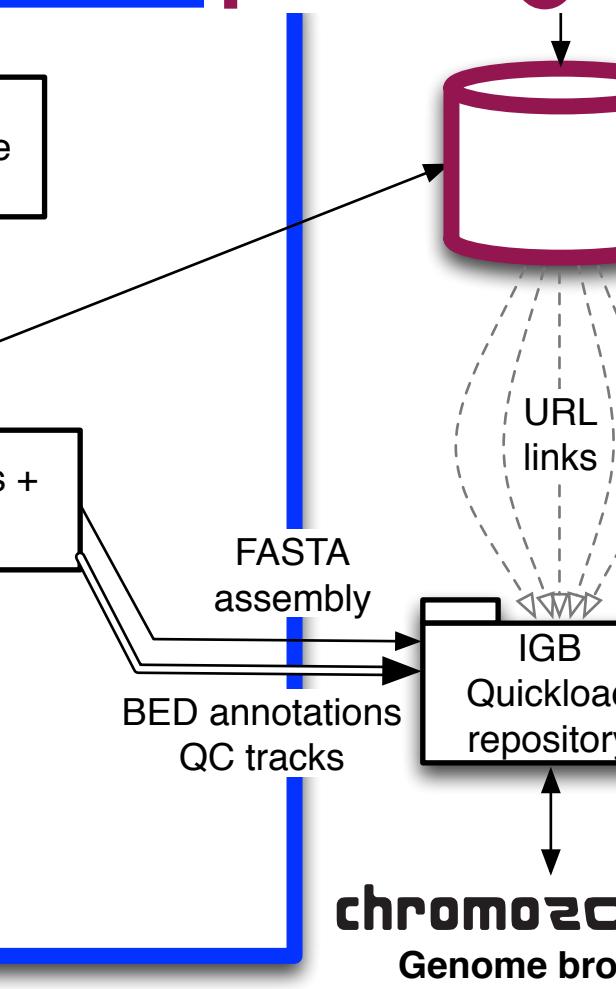
FASTA assemblies

FASTA assemblies

FASTA assemblies

MGSeq

# pathogenDB



# pathogenDB-comparison

XMFA alignment

Mauve multiple genome alignment

show-snps find SNPs in unique mappings

GRIMM rearrangement distance

IGB Quickload repository

MUMmer pairwise genome alignment

FASTA assemblies

FASTA assemblies