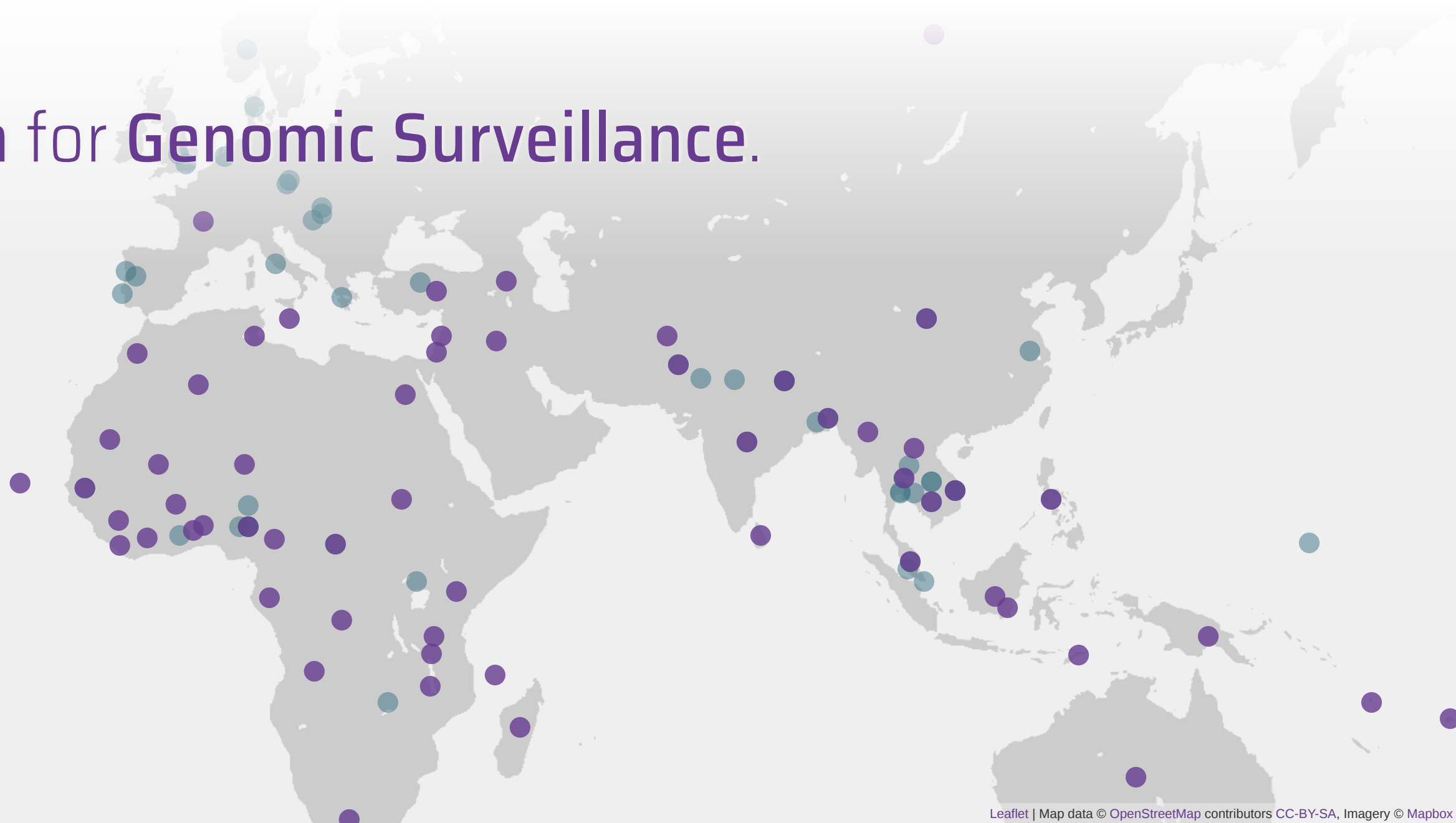




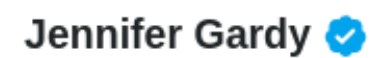
A Global Platform for Genomic Surveillance.



Leaflet | Map data © OpenStreetMap contributors CC-BY-SA, Imagery © Mapbox

Richard Goater





10:24 PM - Oct 9, 2017

60



10:34 PM - Oct 9, 2017

8



Upload your own genomes and metadata

Speciation, MLST, AMR genes/SNPs, assembly quality

Interactive trees for *S. aureus*, *S. Typhi*, and *N. gonorrhoeae*



<https://pathogen.watch>

Use cases for Public Health 

wgsa.net available until 2019, now read-only

What's new? ✨

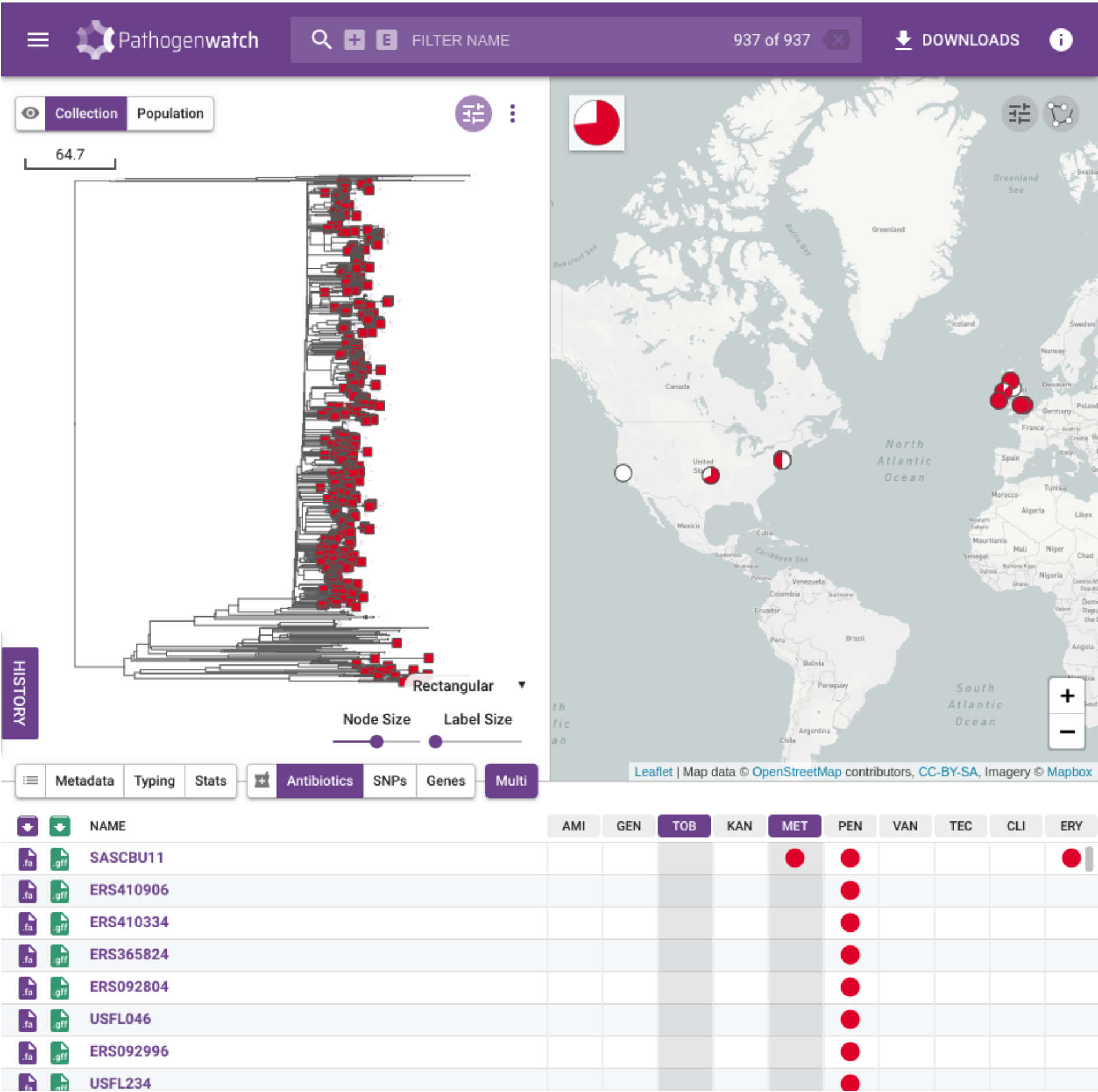
(apart from branding)


Improved Tree Pipeline



Up to 1000 genomes 💪

Quicker! ⌚

Interactive while building
👉



935 of 935 


 DOWNLOADS 


ST8 Demo

(no description)

Organism	Created
<i>Staphylococcus aureus</i>	13/09/2018

SHARING

 **Private**
Available to you only.

 **Shared**
Available to anyone with the link, no sign-in required.

SAVE FOR OFFLINE USE

Page will refresh once saved.

Privacy

Sign-in required to upload

Data is private by default 

Explicit sharing 

ERS068556

Streptococcus pneumoniae

Country **United States of America** Date **2006**



Metadata

Mlst 8487	Project_accession PRJEB2255	Region Maryland
Country USA	Date 2006	Scientific_name Streptococcus_pneumoniae
Taxa_id 1313	Sanger_sample_number LMG87	Sample_accession ERS068556

Multilocus Sequence Typing (MLST)

<https://pubmlst.org/data/profiles/spneumoniae.txt>

Sequence Type 8487	Profile						
	aroE	ddl	gdh	gki	recP	spi	xpt
	15	546	16	19	15	6	20

Antimicrobial Resistance (AMR)

Agent	Full Name	Genotype	SNPs/Genes
KAN	Kanamycin	Not Found	
MAC	Macrolides	Resistant	mefA_10_AF376746, msrD_2_AF274302
CHL	Chloramphenicol	Not Found	
TCY	Tetracycline	Resistant	tetM_2_X90939
TMP	Trimethoprim	Resistant	folA_AE007317_I100L
SSS	Sulfamethoxazole	Not Found	
FLQ	Fluoroquinolones	Not Found	

GENOMES

- TOP
- METADATA
- MLST
- AMR
- ASSEMBLY
- ORGANISM

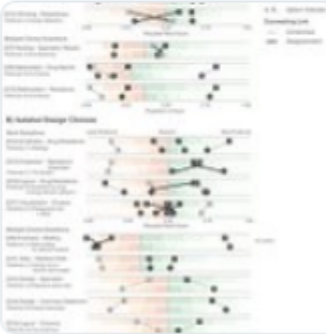


Ana Crisan
@amcrisan



Our @PeerJ paper is out today: peerj.com/articles/4218/
learn more about reporting for #genomics data using
methodologies from #infovis #design

8:38 PM - Jan 10, 2018



Evidence-based design and evaluatio...

Background Microbial genome sequencing
is now being routinely used in many clinical
and public health laboratories.
peerj.com

♡ 34 💬 17 people are talking about this



WHO PRIORITY PATHOGENS LIST FOR R&D OF NEW ANTIBIOTICS

Priority 1: CRITICAL[#]

Acinetobacter baumannii, carbapenem-resistant

Pseudomonas aeruginosa, carbapenem-resistant

*Enterobacteriaceae**, carbapenem-resistant, 3rd generation cephalosporin-resistant

Priority 2: HIGH

Enterococcus faecium, vancomycin-resistant

Staphylococcus aureus, methicillin-resistant, vancomycin intermediate and resistant

Helicobacter pylori, clarithromycin-resistant

Campylobacter, fluoroquinolone-resistant

Salmonella spp., fluoroquinolone-resistant

Neisseria gonorrhoeae, 3rd generation cephalosporin-resistant, fluoroquinolone-resistant

Priority 3: MEDIUM

Streptococcus pneumoniae, penicillin-non-susceptible

Haemophilus influenzae, ampicillin-resistant

Shigella spp., fluoroquinolone-resistant

cgMLST calling for 18 schemes

Acinetobacter baumannii

Campylobacter coli

Campylobacter jejuni

Enterococcus faecium

Escherichia

Klebsiella pneumoniae

Klebsiella quasipneumoniae

Klebsiella variicola

Listeria

Mycobacterium africanum

Mycobacterium bovis

Mycobacterium canettii

Mycobacterium tuberculosis

Neisseria gonorrhoeae

Neisseria meningitidis

Salmonella enterica

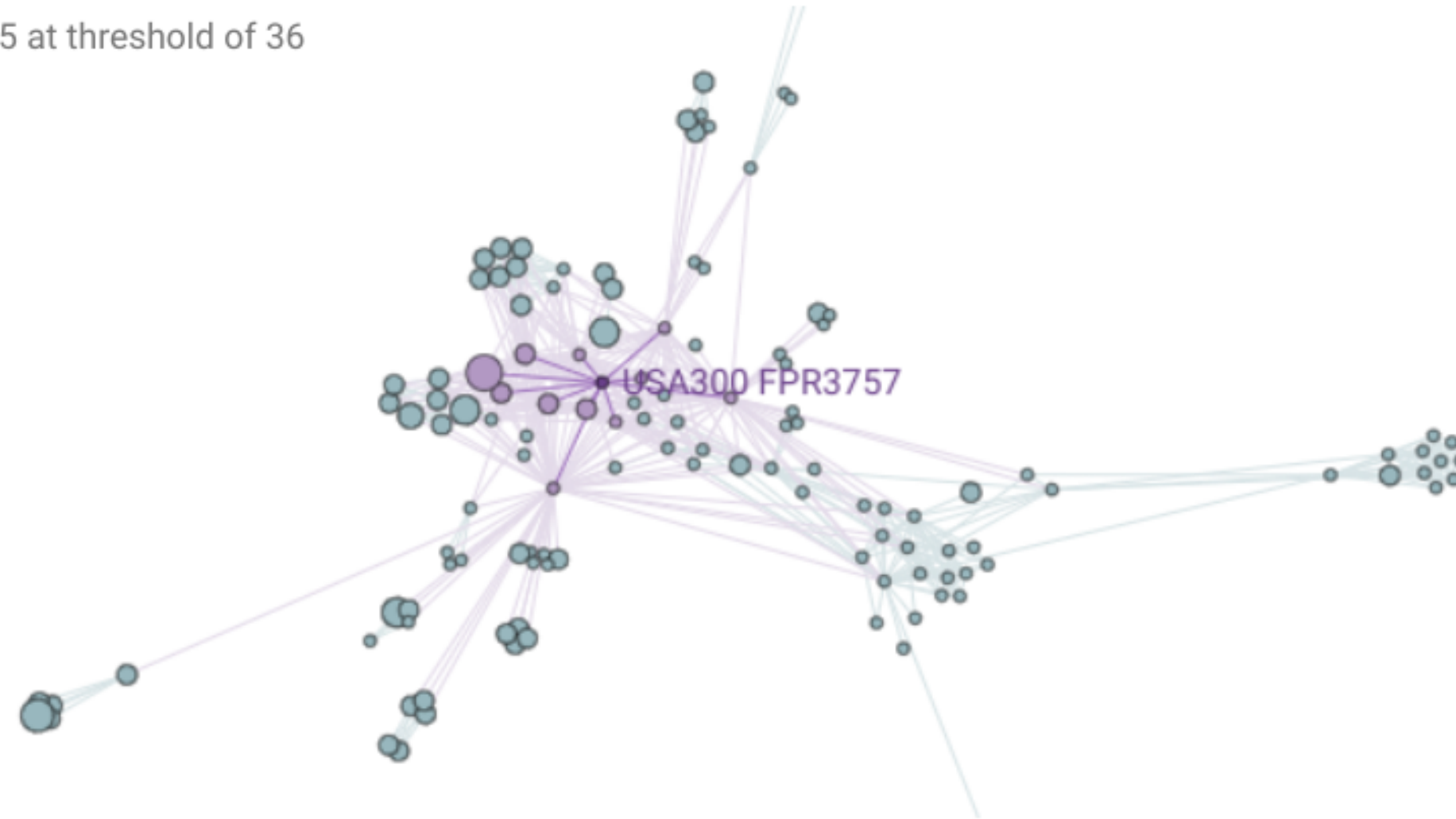
Shigella

Staphylococcus aureus

Core Genome Clustering

http://rest.pubmlst.org/db/pubmlst_saureus_seqdef/schemes/2

Cluster of 225 at threshold of 36



Pick a threshold by clicking on the chart below



Clustering

Single-linkage, allele differences

Test with 24,000 *Salmonella enterica* :

20 minutes from cold, 19GB RAM

4 minutes from cache, 25GB RAM



Anthony Underwood

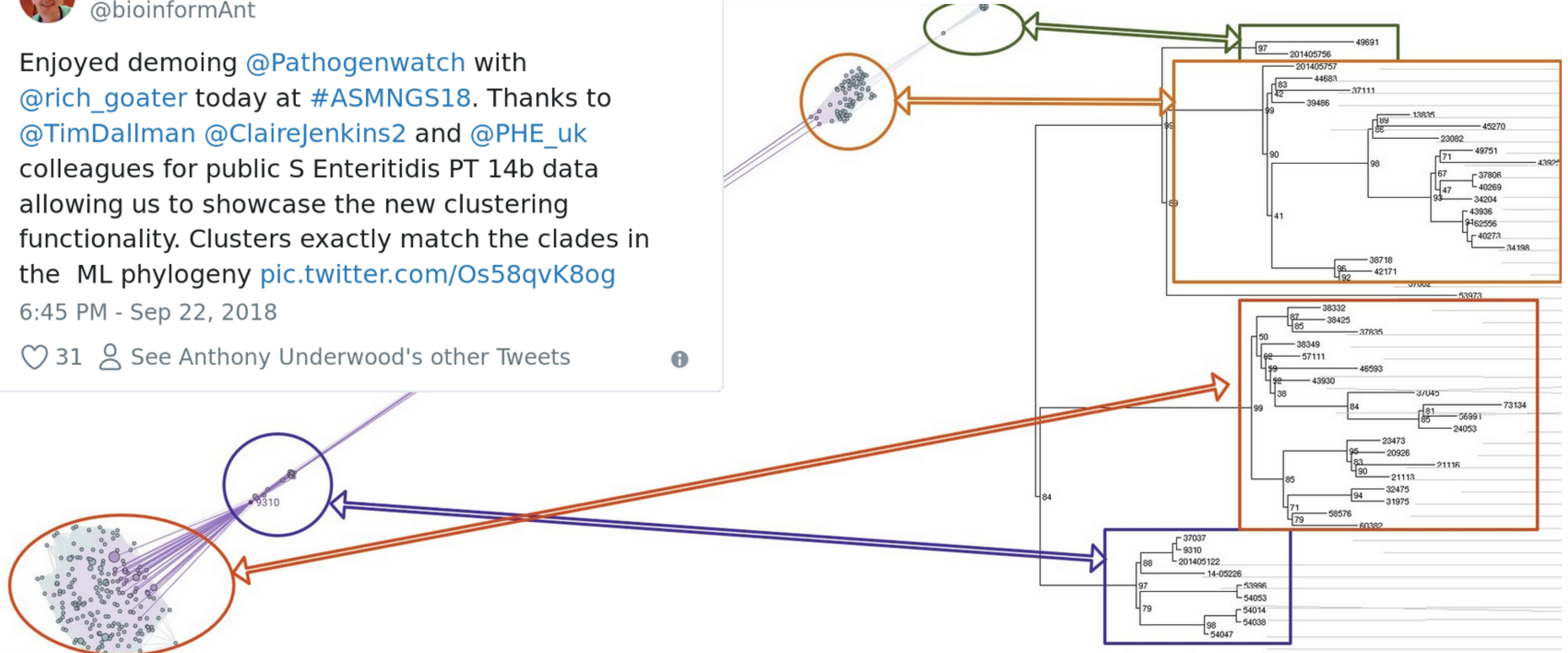
@bioinformAnt



Enjoyed demoing @Pathogenwatch with @rich_goater today at #ASMNGS18. Thanks to @TimDallman @ClaireJenkins2 and @PHE_uk colleagues for public S Enteritidis PT 14b data allowing us to showcase the new clustering functionality. Clusters exactly match the clades in the ML phylogeny pic.twitter.com/Os58qvK8og

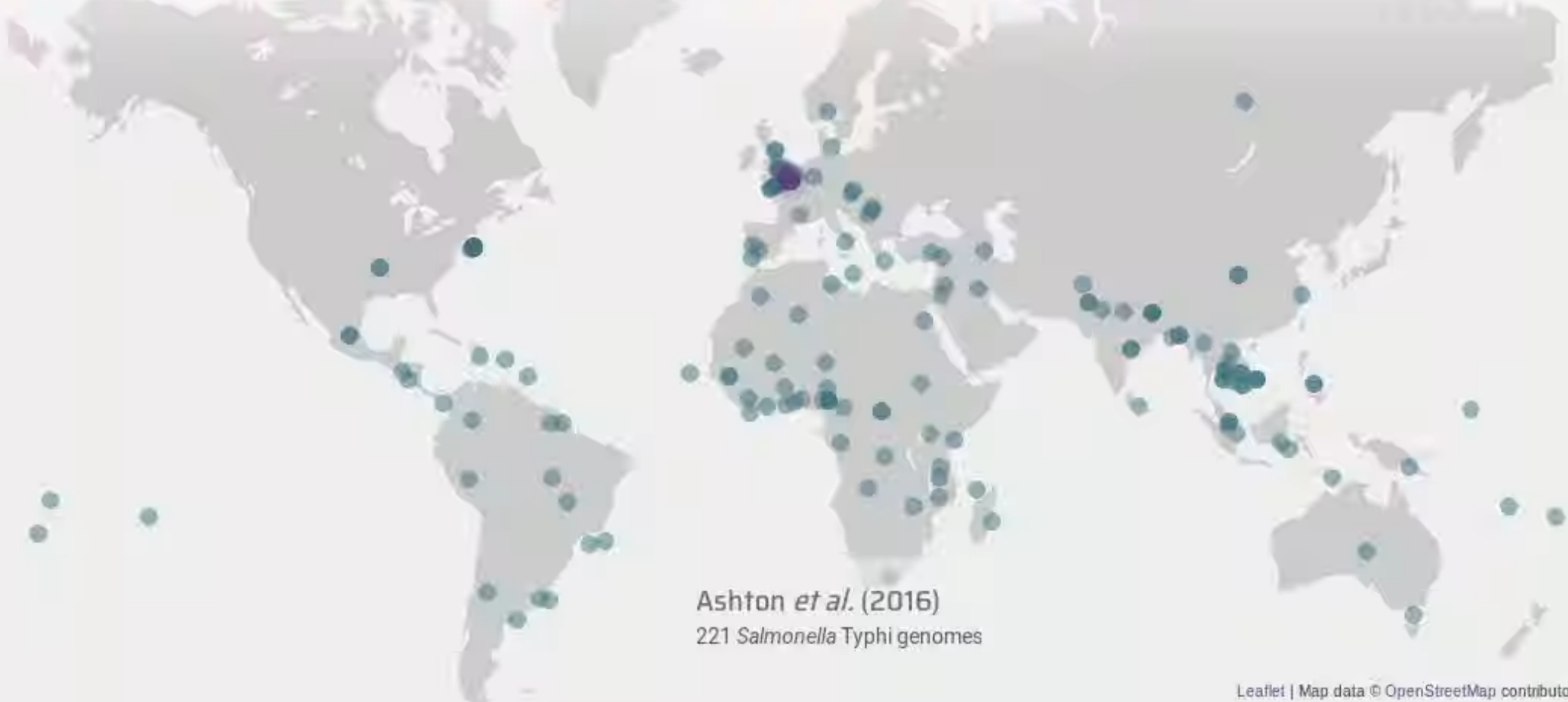
6:45 PM - Sep 22, 2018

♡ 31 👤 See Anthony Underwood's other Tweets





A Global Platform for Genomic Surveillance.



Leaflet | Map data © OpenStreetMap contributors CC-BY-SA, Imagery © Mapbox



Upload



Analyse



Explore

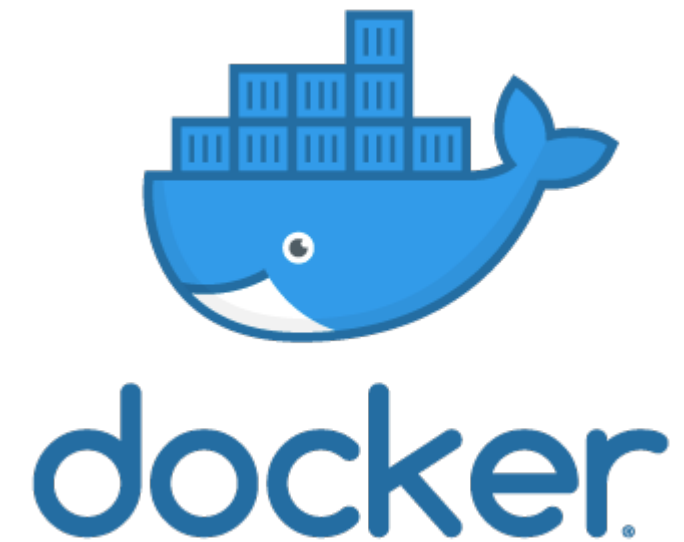
How we've done this 

The “Runner” Architecture

Born in the queue at Atlanta airport 

Reproducibility through Docker 

 Separates scientific programs from system infrastructure 



Runs standardised units of software called “Containers”

“Images” package dependencies, no installation

Reproducible and auditable

Standard Stream Interface

Receive an assembly via stdin 
write JSON results to stdout 

Change the system without modifying scientific programs 

Add new scientific programs without modifying the system 

Adding New Analysis

Package a command line tool in a docker image 

Assign to taxa in a json file 

Add visualisation ✨

There's no such thing as "Done"

- Richard Goater, a lot

cgps@sanger.ac.uk 

@Pathogenwatch on Twitter 

Acknowledgements



Ben Taylor



Khalil Abudahab



Silvia Argimon



Ali Molloy



Corin Yeats



Simon Harris



David Aanensen

