Evidence-Based Design and Evaluation of a Whole Genome Sequencing Clinical Report for the Reference Microbiology Laboratory

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Mycobacterium Whole Genome Sequencing Report from MGIT Positive Samples

Not for diagnostic use 01/02/1915

Sample Details

Sequencing Location	Oxford	**Date received in Lab**	
Local Lims Specimen ID	123456789	**Run date**	01/01/19150115
Guuid	123456-79aab-910abr-15243hg		

Organism Identification

Predicted/closest match	
TBCOMP/microti	100%
TBCOMP	100%
TBCOMP/TB	96.77%
TBCOMP/tuberculosis-canettii	35.71%
MACCOMP	21.21%

Sample/Sequencing Quality

Total reads (~millions)	**Mapped %**	**No reads mapped (~millions)**	**Coverage %**
4.73	99.47	4.7	91.99

Resistance Summary

INH	**RIF**	**EMB**	**PZA**	**QUI**	**SM**	**AG**
U	S	S	S	S	S	S

Resistotype

Drug	**Mutation**	**Nucleotides**	**Support (ACGT)**	**Source – (R/Total)**	**Prediction**
INH	katG_A727T	GCC->ACC	(160/0/1/0) (0/164/0/0) (0/167/0/0)	Unclassified	UNK

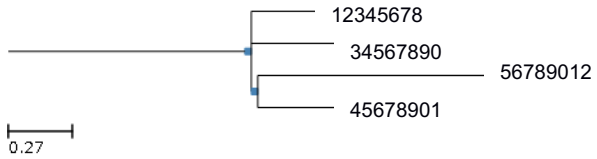
Relatedness

NB: This data may be added or updated at a later date

Nearest neighbour(s)

Sample -Plate Name	**Date received in Lab**	**Centre**	**No. of SNPs apart**
123456789		Oxford	0
34567890	1900-01-01		10
45678901	1015-01-31	Oxford	15
56789012		London	8

The alignment width is 285. Multiply this number by the tree metrics.

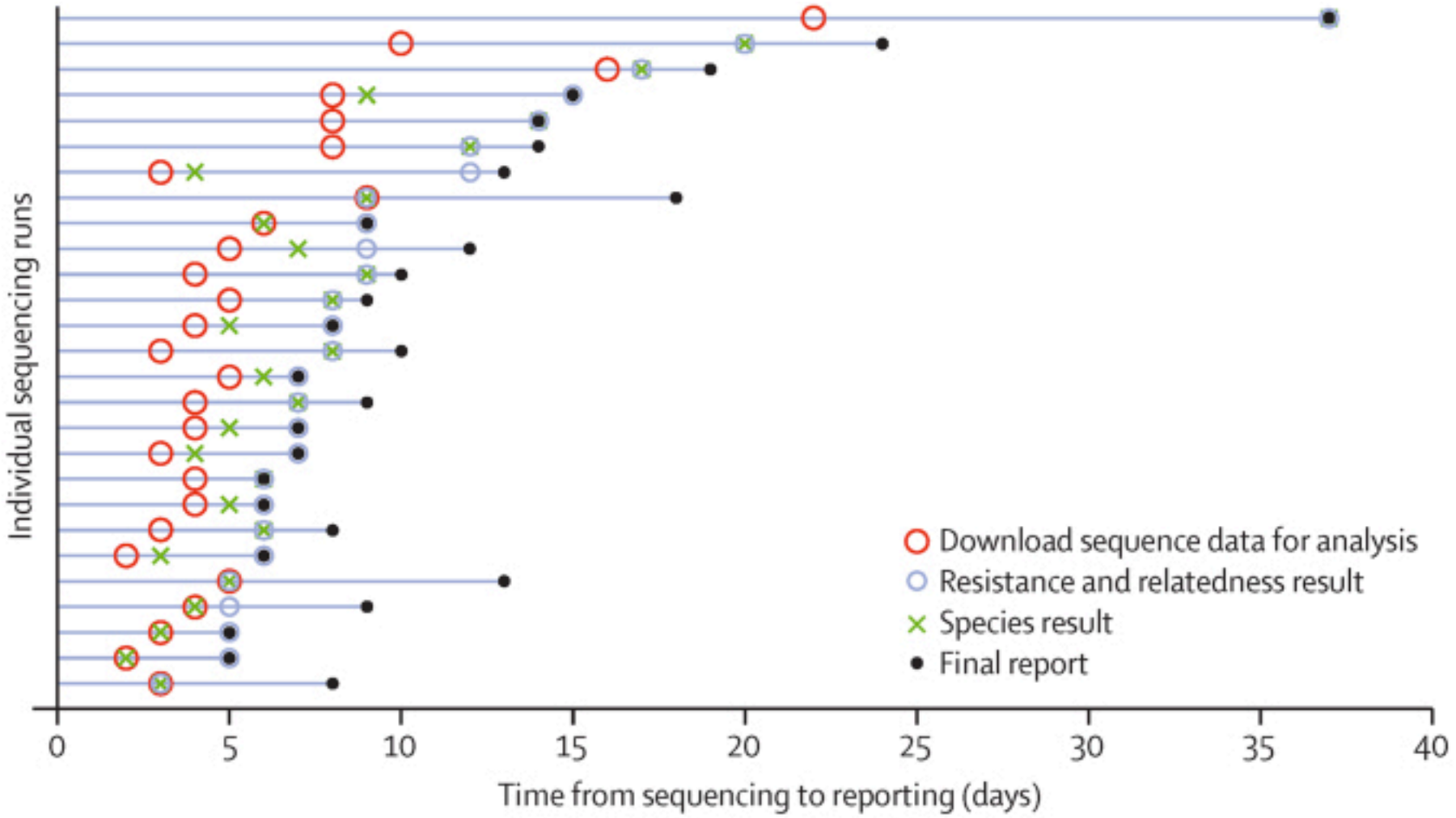


Comments

Authorised

Signature:	**Print name:**
Position:	**Date:**

COMPASS-TB : Clinical WGS for Mycobacteria



Pankhurst (2016) Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study

COLLABORATION

THE UNIVERSITY OF BRITISH COLUMBIA

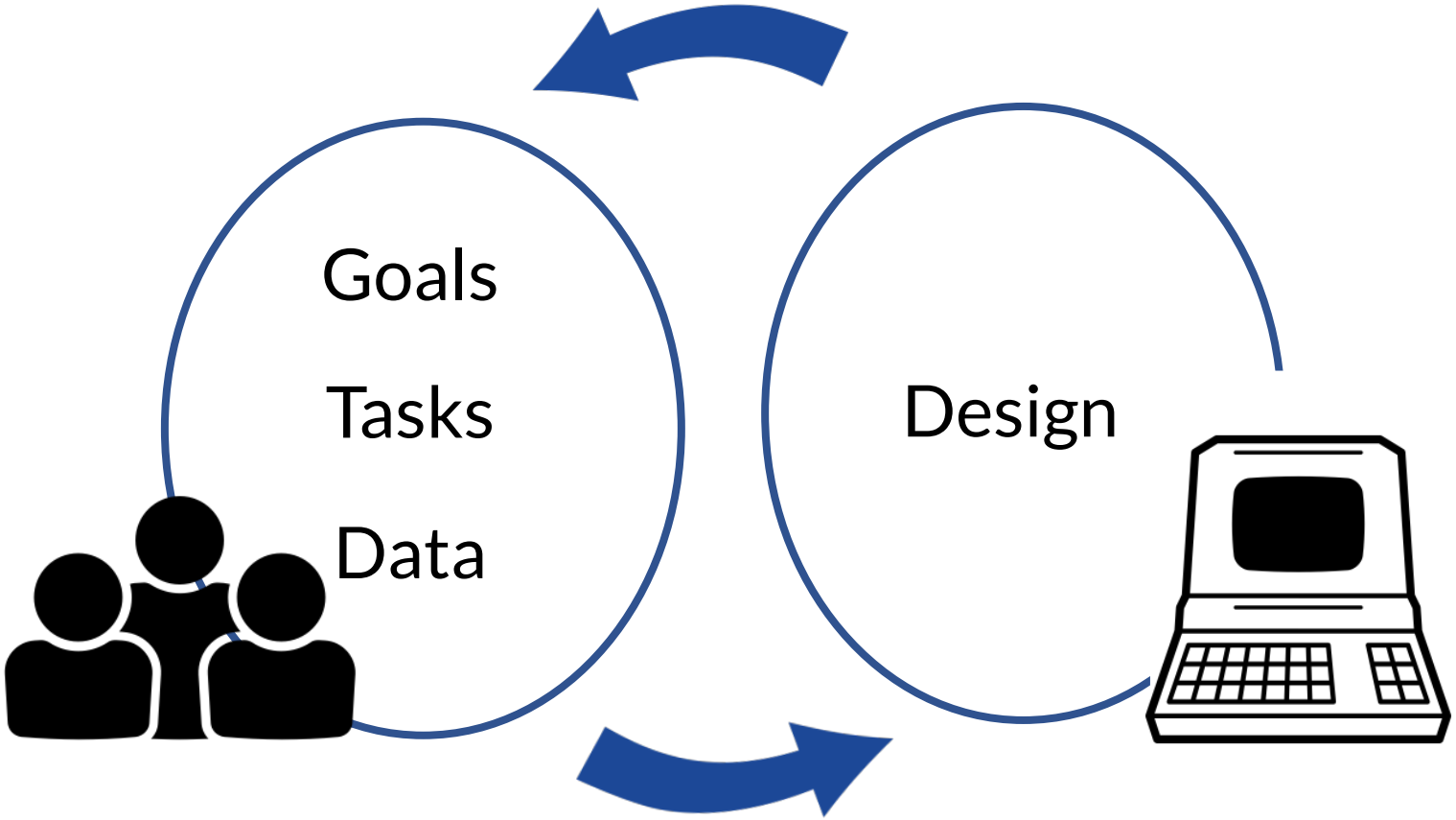
BC Centre for Disease Control

Public Health England

Our Approach: a Human Centered Design Process

"Design is not just what it looks like and feels like – design is how it works"

Steve Jobs



Using a Design Study Methodology + Mixed Methods Approaches

Discovery

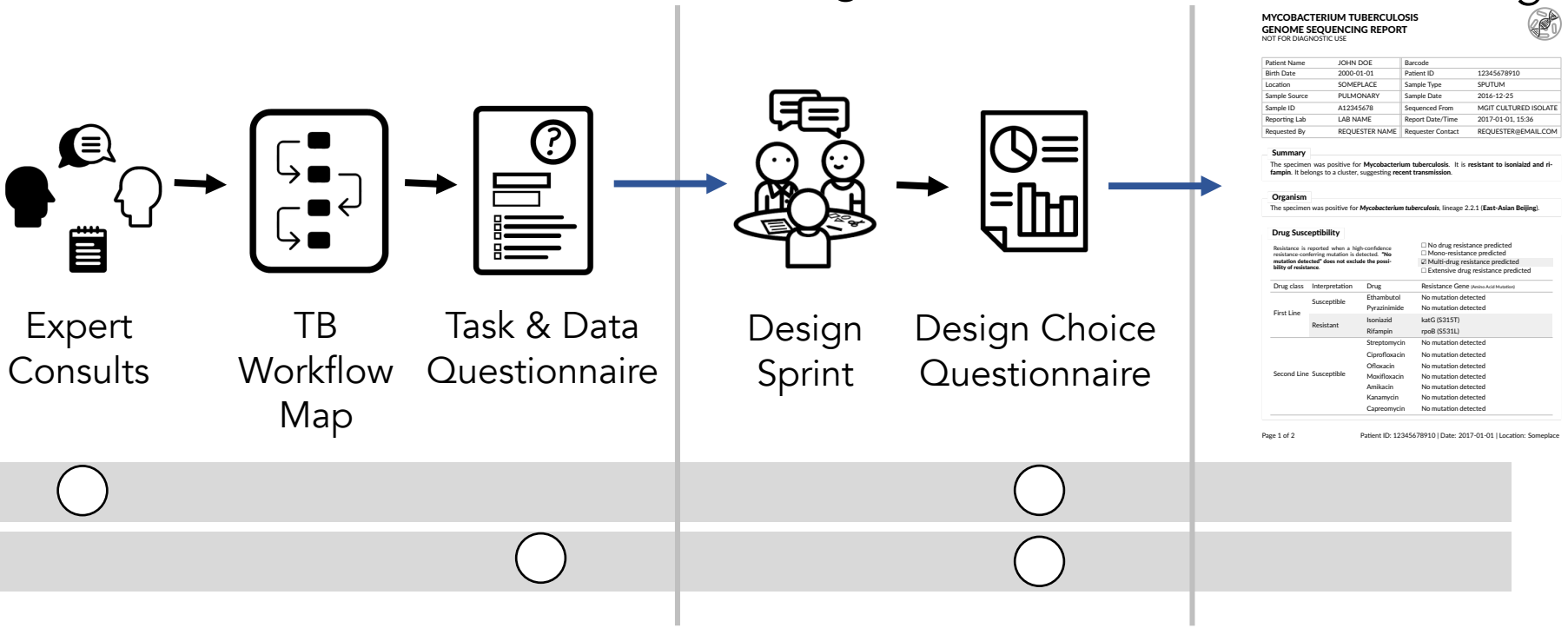
Information Gathering

Design

Design & Evaluation

Implement

Finalize Design



Data Gathered

Qualitative

Quantitative

Study Design

Exploratory Sequential Model

Embedded Model

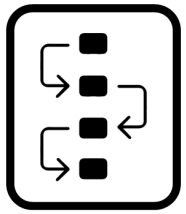
Sedlmair (2013). Design Study Methodology: Reflections from the Trenches and the Stacks


DISCOVERY

Discovery Stage Components

Expert Consults

- Map out TB diagnosis, treatment, and surveillance steps
- Assess role of WGS and identify major barriers



TB workflow

- Formalize tasks (what people do) & data used for those tasks
- Not further elaborated on here

Task & Data Questionnaire

- Assess generality of expert findings, workflow tasks & data

Expert Consultations : Participants & Methods

Public Health Role	Total
Clinician	2
Nurse	1
Laboratorian	2
Researcher	0
Surveillance	1
Other	1
Total	7

- Semi-structured interviews
  - *Sampling:* Experts known to us
  - *Data Collected:* Qualitative (interviewer notes)
- Analyzed for common themes
- Used to establish TB workflow
  - Steps from diagnosis to treatment to surveillance
  - Intended to link tasks to data
  - Identify genomic actionable steps

Common Themes from Expert Consults

Procedural Insights

- Limited time to digest content
- Many documents arriving at different times
- Reporting formats varied considerably : PDF, EHR, Fax
  - Black & white essential

"10 seconds [to review content] is likely, one minute is luxurious"

Data Insights

- Different data needs (clinicians, non-clinicians)
- Different expectations about level of detail
- Emphasis on clinically actionable results

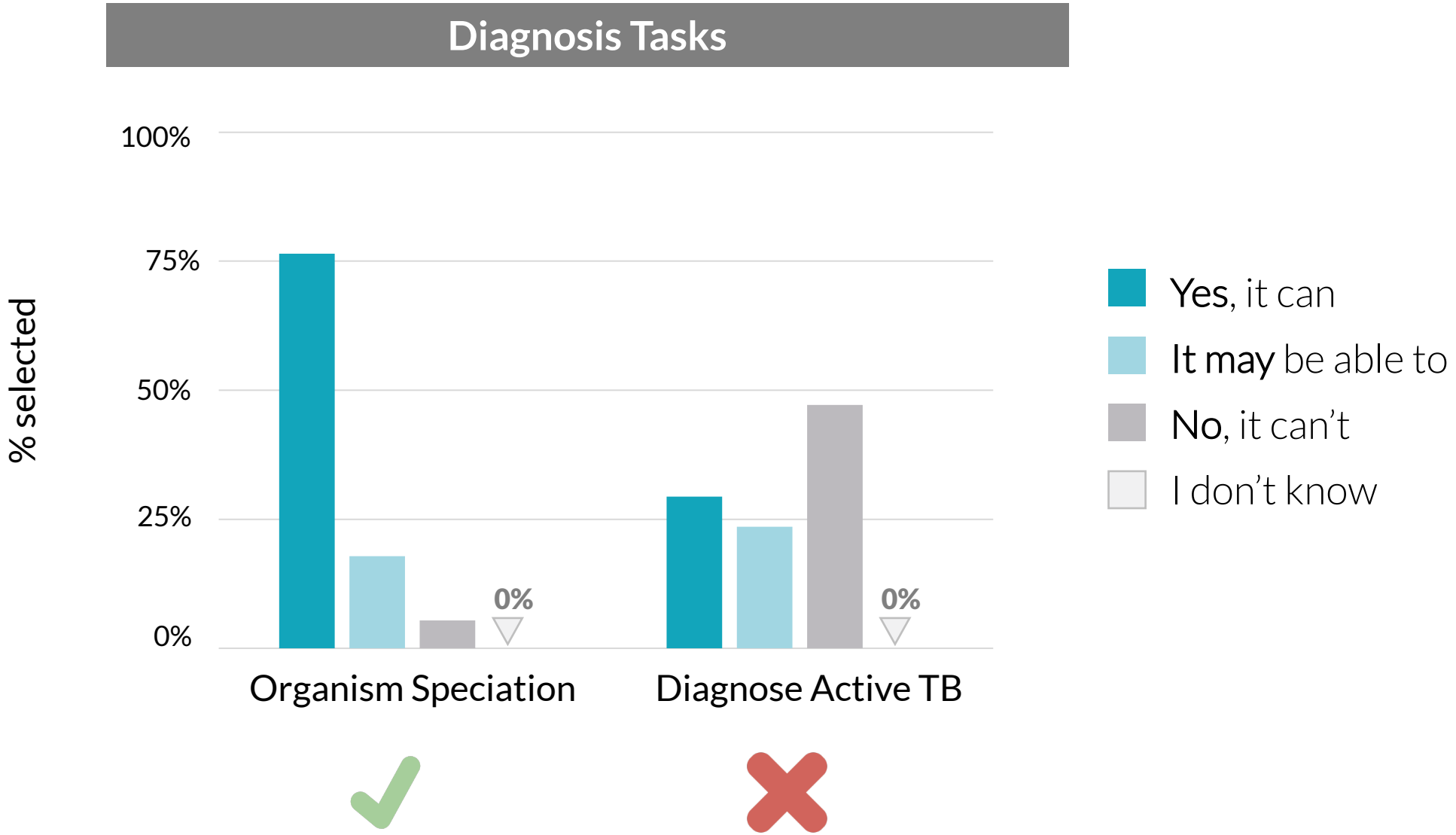
"my patient's isolate is 6 SNPs from someone diagnosed 3 years ago. What is the clinical action?"

Task & Data Questionnaire: Participants & Methods

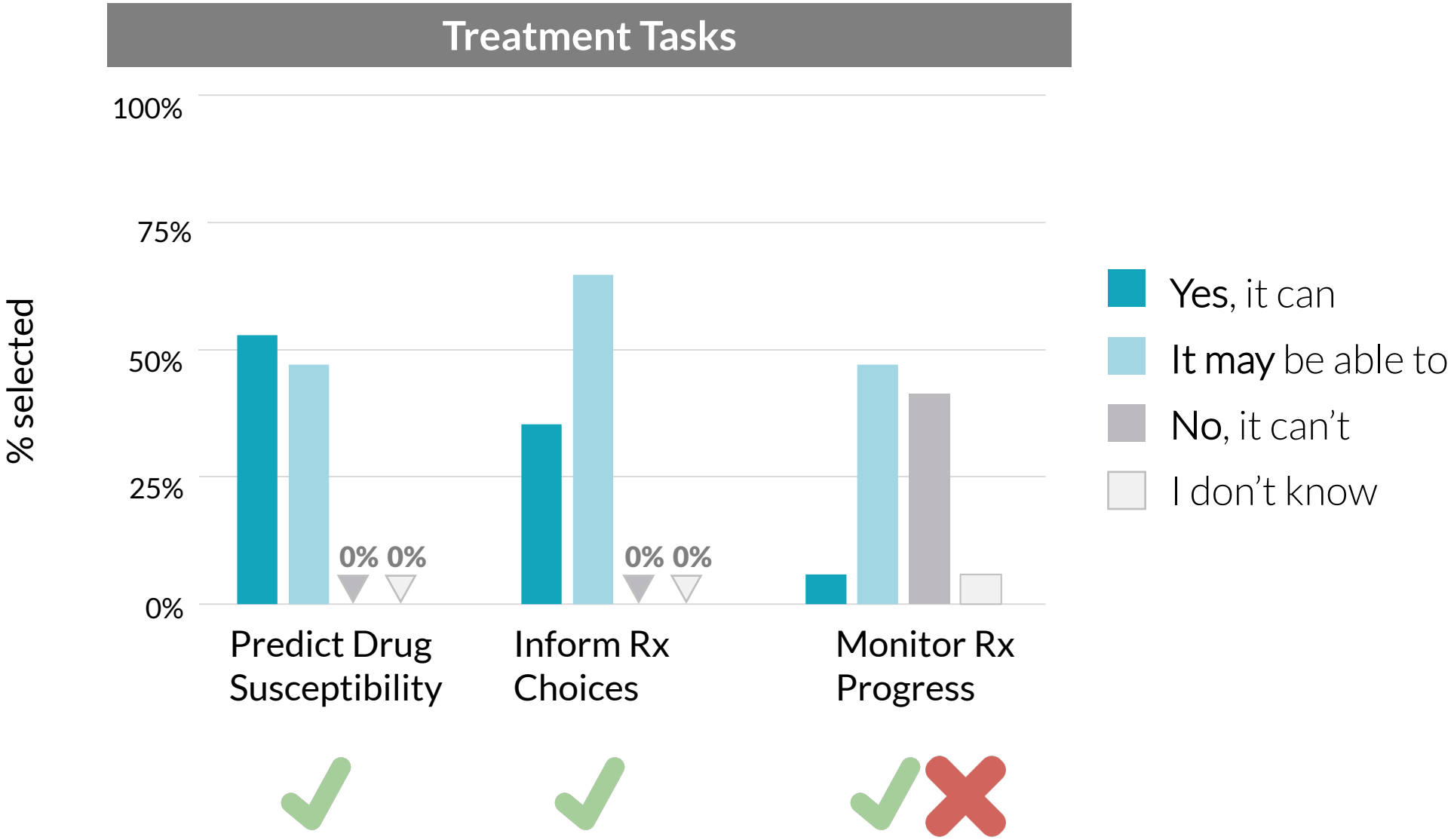
Public Health Role	Total
Clinician	7
Nurse	3
Laboratorian	3
Researcher	1
Surveillance	3
Other	0
Total	17

- Online survey
  - *Sampling* : Convenience & Snowball
  - *Data collected:* Quantitative, some qualitative
- Questions about task & data
  - Emphasized genomic results
  - Utility of data types
  - Interpretation confidence

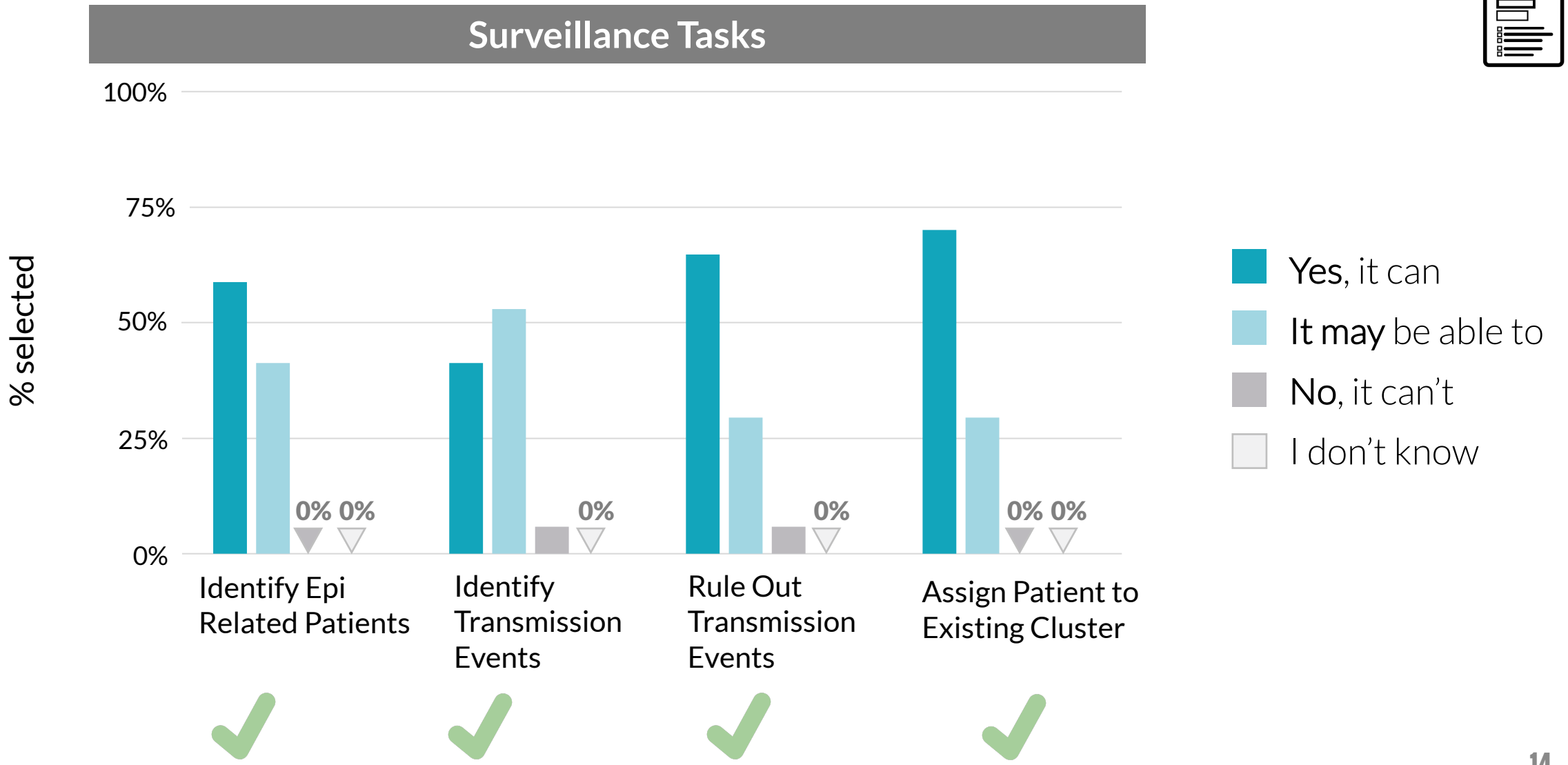
Can Genomic Data be used for this Task (now or eventually)?



Can Genomic Data be used for this Task (now or eventually)?



Can Genomic Data be used for this Task (now or eventually)?



But… Variable Consensus for Data used across Tasks

		DIAGNOSIS TASKS				TREATMENT TASKS			SURVEILLANCE TASKS					
	WGS equivalent	*Diagnose Latent TB*	*Diagnose Active TB*	*Reactive vs New Infection*	*Characterize Transmission Risk*	*Choose Meds*	*Choose Tx Duration*	*Assess Response to Tx*	*Guide Contact Tracing*	*Report to Public Health*	*Define a Cluster*	*Connect Case to Existing Cluster*	*Guide Public Health Response*	**TOTAL SCORE**
Patient Identifier	Same	3	3	3	3	3	3	3	2	1	1	1	1	26
Sample Collection Date	Same	3	3	2	3	3	3	3	1	1	1	1	1	24
Patient Prior TB Results	Same	3	2	3	3	3	3	3	1	1	1	0	1	23
Speciation	Speciation	1	3	2	3	3	3	3	2	1	1	1	1	23
Sample Type (sputum, fine needle aspirate etc.)	Same	2	3	2	3	3	3	3	1	1	1	0	1	22
Culture results	NA	1	3	2	3	3	3	3	2	1	1	0	1	22
Sample Collection Site (lymph node, lung etc..)	Same	2	3	2	3	3	3	3	1	1	0	0	1	21
Acid Fast Bacilli Smear	Speciation	2	3	2	3	2	3	3	1	1	1	0	1	21
Resistotype	Predicted DST	0	2	3	1	3	3	2	2	1	1	1	1	19
Phenotypic DST	Predicted DST	0	2	3	2	3	3	2	1	1	1	0	1	18
Chest x-ray	NA	3	3	2	3	0	2	3	1	0	0	0	0	17
Report Release Date	Same	2	2	1	2	2	2	2	1	0	1	0	1	15
Requester IDs	Same	2	2	2	2	2	2	2	1	0	0	0	0	15
Interpretation or comments from reviewer	Same	2	2	1	2	2	2	3	1	0	0	0	0	15
Predicted DST	Predicted DST	0	2	2	1	3	3	2	1	0	1	0	0	15
MIRU-VNTR	SNPs	0	2	3	1	1	1	1	1	1	1	1	1	13
Cluster Assignment	Same	0	2	2	1	1	1	0	1	1	1	1	1	11
SNP/variant distance	SNPs	0	1	2	1	1	1	0	1	1	1	1	1	10
Phylogenetic Tree	Same	0	2	1	1	1	1	0	1	0	1	1	1	9
Reviewer ID	Same	1	1	1	1	1	1	1	1	0	0	0	0	8
TST results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
IGRA results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
Lab QC	WGS Specific	0	1	2	1	1	1	0	1	0	0	0	0	7
Spoligotype	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3
RFLP	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3

Degree of Consensus: High (3) | Some (2) | Low (1) | Very low (0)

But… Variable Consensus for Data used across Tasks

		DIAGNOSIS TASKS				TREATMENT TASKS			SURVEILLANCE TASKS					
	WGS equivalent	*Diagnose Latent TB*	*Diagnose Active TB*	*Reactive vs New Infection*	*Characterize Transmission Risk*	*Choose Meds*	*Choose Tx Duration*	*Assess Response to Tx*	*Guide Contact Tracing*	*Report to Public Health*	*Define a Cluster*	*Connect Case to Existing Cluster*	*Guide Public Health Response*	TOTAL SCORE
Patient Identifier	Same	3	3	3	3	3	3	3	2	1	1	0	1	24
Sample Collection Date	Same	3	3	2	3	3	3	3	1	1	1	0	1	24
Patient Prior TB Results	Same	3	2	3	3	3	3	3	1	1	1	0	1	23
Speciation	Speciation	1	3	2	3	3	3	3	2	1	1	0	1	22
Sample Type (sputum, fine needle aspirate etc.)	Same	2	3	2	3	3	3	3	1	1	1	0	1	22
Culture results	NA	1	3	2	3	3	3	3	2	1	1	0	1	22
Sample Collection Site (lymph node, lung etc..)	Same	2	3	2	3	3	3	3	1	1	0	0	1	21
Acid Fast Bacilli Smear	Speciation	2	3	2	3	2	3	3	1	1	1	0	1	21
Resistotype	Predicted DST	0	2	3	1	3	3	2	2	1	1	1	1	19
Phenotypic DST	Predicted DST	0	2	3	2	3	3	2	1	1	1	0	1	18
Chest x-ray	NA	3	3	2	3	0	2	3	1	0	0	0	0	17
Report Release Date	Same	2	2	1	2	2	2	2	1	0	1	0	1	15
Requester IDs	Same	2	2	2	2	2	2	2	1	0	0	0	0	15
Interpretation or comments from reviewer	Same	2	2	1	2	2	2	3	1	0	0	0	0	15
Predicted DST	Predicted DST	0	2	2	1	3	3	2	1	0	1	0	0	15
MIRU-VNTR	SNPs	0	2	3	1	1	1	1	1	1	1	1	1	13
Cluster Assignment	Same	0	2	2	1	1	1	0	1	1	1	1	1	11
SNP/variant distance	SNPs	0	1	2	1	1	1	0	1	1	1	1	1	10
Phylogenetic Tree	Same	0	2	1	1	1	1	0	1	0	1	1	1	9
Reviewer ID	Same	1	1	1	1	1	1	1	1	0	0	0	0	8
TST results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
IGRA results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
Lab QC	WGS Specific	0	1	2	1	1	1	0	1	0	0	0	0	7
Spoligotype	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3
RFLP	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3

- Administrative data is most commonly used data type

Degree of Consensus: High (3) | Some (2) | Low (1) | Very low (0)

But… Variable Consensus for Data used across Tasks

		DIAGNOSIS TASKS				TREATMENT TASKS			SURVEILLANCE TASKS					
	WGS equivalent	*Diagnose Latent TB*	*Diagnose Active TB*	*Reactive vs New Infection*	*Characterize Transmission Risk*	*Choose Meds*	*Choose Tx Duration*	*Assess Response to Tx*	*Guide Contact Tracing*	*Report to Public Health*	*Define a Cluster*	*Connect Case to Existing Cluster*	*Guide Public Health Response*	TOTAL SCORE
Patient Identifier	Same	3	3	3	3	3	3	3	2	1	1	1	1	16
Sample Collection Date	Same	3	3	2	3	3	3	3	1	1	1	1	1	14
Patient Prior TB Results	Same	3	2	3	3	3	3	3	1	1	1	0	1	23
Speciation	Speciation	1	3	2	3	3	3	3	2	1	1	1	1	21
Sample Type (sputum, fine needle aspirate etc.)	Same	2	3	2	3	3	3	3	1	1	1	0	1	22
Culture results	NA	1	3	2	3	3	3	3	2	1	1	1	1	22
Sample Collection Site (lymph node, lung etc..)	Same	2	3	2	3	3	3	3	1	1	0	0	1	21
Acid Fast Bacilli Smear	Speciation	2	3	2	3	2	3	3	1	1	1	1	1	20
Resistotype	Predicted DST	0	2	3	1	3	3	2	2	1	1	1	1	19
Phenotypic DST	Predicted DST	0	2	3	2	3	3	2	1	1	1	0	1	18
Chest x-ray	NA	3	3	2	3	0	2	3	1	1	0	0	0	17
Report Release Date	Same	2	2	1	2	2	2	2	1	0	1	0	1	15
Requester IDs	Same	2	2	2	2	2	2	2	1	0	0	0	0	15
Interpretation or comments from reviewer	Same	2	2	1	2	2	2	3	1	0	0	0	0	15
Predicted DST	Predicted DST	0	2	2	1	3	3	2	1	0	1	0	0	15
MIRU-VNTR	SNPs	0	2	3	1	1	1	1	1	1	1	1	1	13
Cluster Assignment	Same	0	2	2	1	1	1	0	1	1	1	1	1	11
SNP/variant distance	SNPs	0	1	2	1	1	1	0	1	1	1	1	1	10
Phylogenetic Tree	Same	0	2	1	1	1	1	0	1	0	1	1	1	9
Reviewer ID	Same	1	1	1	1	1	1	1	1	0	0	0	0	8
TST results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
IGRA results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
Lab QC	WGS Specific	0	1	2	1	1	1	0	1	0	0	0	0	7
Spoligotype	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3
RFLP	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3

- Administrative data is most commonly used data type
- Speciation & DST are the most useful WGS derived data

Degree of Consensus: High (3) | Some (2) | Low (1) | Very low (0)

But… Variable Consensus for Data used across Tasks

	WGS equivalent	DIAGNOSIS TASKS: Diagnose Latent TB	Diagnose Active TB	Reactive vs New Infection	Characterize Transmission Risk	TREATMENT TASKS: Choose Meds	Choose Tx Duration	Assess Response to Tx
Patient Identifier	Same	3	3	3	3	3	3	3
Sample Collection Date	Same	3	3	2	3	3	3	3
Patient Prior TB Results	Same	3	2	3	3	3	3	3
Speciation	Speciation	1	3	2	3	3	3	3
Sample Type (sputum, fine needle aspirate etc.)	Same	2	3	2	3	3	3	3
Culture results	NA	1	3	2	3	3	3	3
Sample Collection Site (lymph node, lung etc..)	Same	2	3	2	3	3	3	3
Acid Fast Bacilli Smear	Speciation	2	3	2	3	2	3	3
Resistotype	Predicted DST	0	2	3	1	3	3	2
Phenotypic DST	Predicted DST	0	2	3	2	3	3	2
Chest x-ray	NA	3	3	2	3	0	2	3
Report Release Date	Same	2	2	1	2	2	2	2
Requester IDs	Same	2	2	2	2	2	2	2
Interpretation or comments from reviewer	Same	2	2	1	2	2	2	3
Predicted DST	Predicted DST	0	2	2	1	3	3	2
MIRU-VNTR	SNPs	0	2	3	1	1	1	1
Cluster Assignment	Same	0	2	2	1	1	1	0
SNP/variant distance	SNPs	0	1	2	1	1	1	0
Phylogenetic Tree	Same	0	2	1	1	1	1	0
Reviewer ID	Same	1	1	1	1	1	1	1
TST results	Speciation*	3	1	1	1	0	0	0
IGRA results	Speciation*	3	1	1	1	0	0	0
Lab QC	WGS Specific	0	1	2	1	1	1	0
Spoligotype	SNPs	0	1	1	1	0	0	0
RFLP	SNPs	0	1	1	1	0	0	0

- Administrative data is most commonly used data type
- Speciation & DST are the most useful WGS derived data
- Strong consensus for data used in diagnosis and treatment tasks

Degree of Consensus: High (3) | Some (2) | Low (1) | Very low (0)

But… Variable Consensus for Data used across Tasks

- Very little consensus for data used in surveillance tasks

	WGS equivalent	DIAGNOISIS TASKS: Diagnose Latent TB	Diagnose Active TB	Reactive vs New Acquisition	Characterize Transmission Risk	TREATMENT TASKS: Choose Meds	Choose Rx Duration	Assess Response to Rx	SURVEILLENCE TASKS: Guide Contact Tracing	Report to Public Health	Define a Cluster	Connect case to Existing Cluster	Guide Public Health Response	TOTAL SCORE
Patient Identifier	Same	3	3	3	3	3	3	3	2	1	1	1	1	26
Sample Collection Date	Same	3	3	2	3	3	3	3	1	1	1	1	1	24
Patient Prior TB Results	Same	3	2	3	3	3	3	3	1	1	1	0	1	23
Speciation	Speciation	1	3	2	3	3	3	3	2	1	1	1	1	23
Sample Type (sputum, fine needle aspirate etc.)	Same	2	3	2	3	3	3	3	1	1	1	0	1	22
Culture results	NA	1	3	2	3	3	3	3	2	1	1	0	1	22
Sample Collection Site (lymph node, blood draw etc.)	Same	2	3	2	3	3	3	3	1	1	0	0	1	21
Acid Fast Bacilli Smear	Speciation	2	3	2	3	2	3	3	1	1	1	0	1	21
Resistotype	Predicted DST	0	2	3	1	3	3	2	2	1	1	1	1	19
Phenotype DST	Predicted DST	0	2	3	2	3	3	2	1	1	1	0	1	18
Chest x-ray	Same	2	2	1	2	0	2	3	1	0	0	0	0	17
Report Release Date	Same	2	2	1	2	2	2	2	1	0	1	0	1	15
Requester IDs	Same	2	2	2	2	2	2	2	1	0	0	0	0	15
Interpretation or comments from reviewer	Same	2	2	1	2	2	2	3	1	0	0	0	0	15
Predicted DST	Predicted DST	0	2	2	1	3	3	2	1	0	1	0	0	15
MIRU-VNTR	SNPs	0	2	3	1	1	1	1	1	1	1	1	1	13
Cluster Assignment	Same	0	2	2	1	1	1	0	1	1	1	1	1	11
SNP/variant distance	SNPs	0	1	2	1	1	1	0	1	1	1	1	1	10
Phylogenetic Tree	Same	0	2	1	1	1	1	0	1	0	1	1	1	9
Reviewer ID	Same	1	1	1	1	1	1	1	1	0	0	0	0	8
TST results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
IGRA results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
Lab QC	WGS Specific	0	1	2	1	1	1	0	1	0	0	0	0	7
Spoligotype	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3
RFLP	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3

Degree of Consensus: High (3) | Some (2) | Low (1) | Very low (0)

But… Variable Consensus for Data used across Tasks

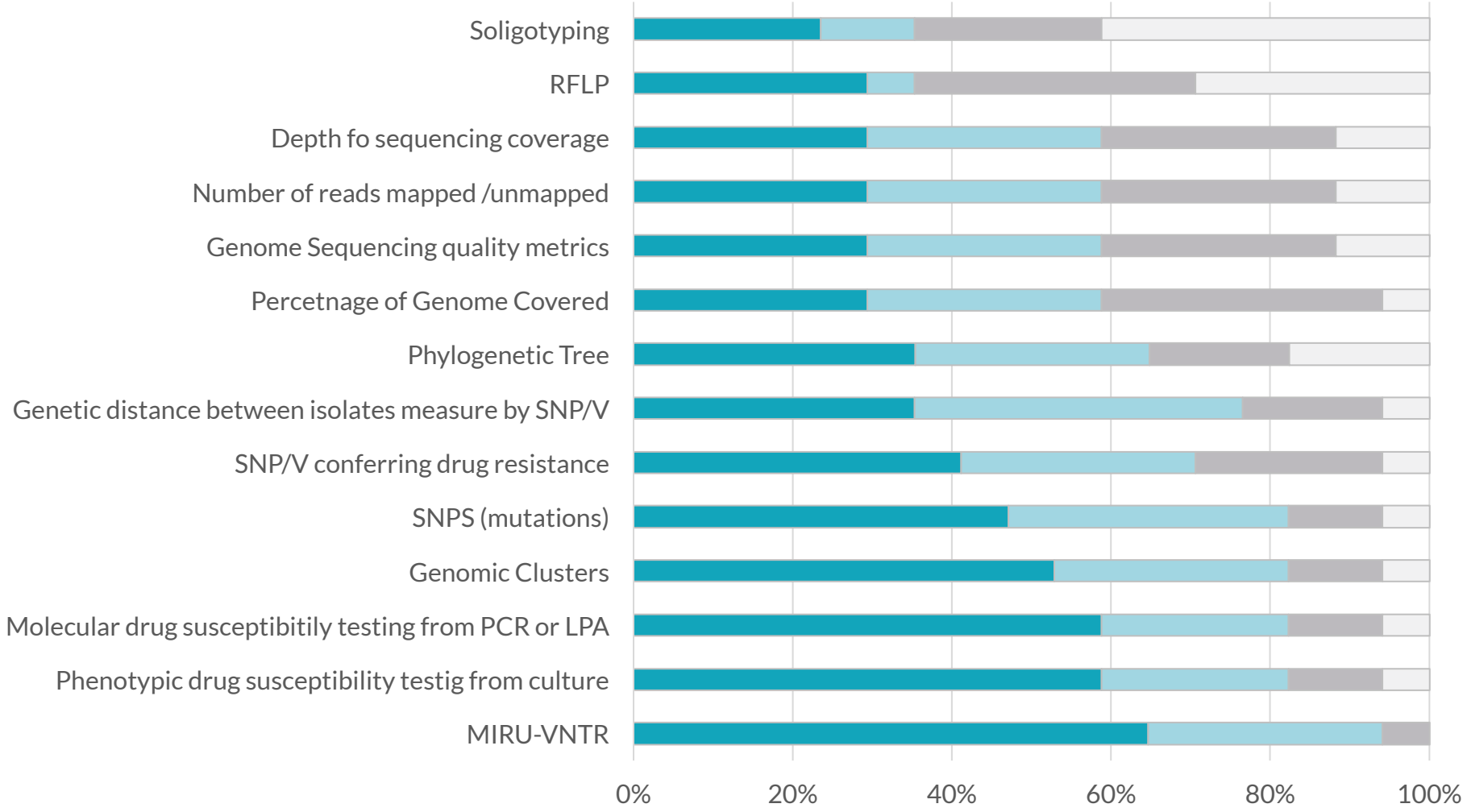
- Cluster assignments & phylogenetic trees also not frequently used

		DIAGNOISIS TASKS				TREATMENT TASKS			SURVEILLENCE TASKS					
	WGS equivalent	Diagnose Latent TB	Diagnose Active TB	Reactive vs New Acquisition	Characterize Transmission Risk	Choose Meds	Choose Rx Duration	Assess Response to Rx	Guide Contact Tracing	Report to Public Health	Define a Cluster	Connect case to Existing Cluster	Guide Public Health Response	TOTAL SCORE
Patient Identifier	Same	3	3	3	3	3	3	3	2	1	1	1	1	26
Sample Collection Date	Same	3	3	2	3	3	3	3	1	1	1	1	1	24
Patient Prior TB Results	Same	3	2	3	3	3	3	3	1	1	1	0	1	23
Speciation	Speciation	1	3	2	3	3	3	3	2	1	1	1	1	23
Sample Type (sputum, fine needle aspirate etc.)	Same	2	3	2	3	3	3	3	1	1	1	0	1	22
Culture results	NA	1	3	2	3	3	3	3	2	1	1	0	1	22
Sample Collection Site (lymph node, blood draw etc.)	Same	2	3	2	3	3	3	3	1	1	0	0	1	21
Acid Fast Bacilli Smear	Speciation	2	3	2	3	2	3	3	1	1	1	0	1	21
Resistotype	Predicted DST	0	2	3	1	3	3	2	2	1	1	1	1	19
Phenotype DST	Predicted DST	0	2	3	2	3	3	2	1	1	1	0	1	18
Chest x-ray	NA	3	3	2	3	0	2	3	1	0	0	0	0	17
Report Release Date	Same	2	2	1	2	2	2	2	1	0	1	0	1	15
Requester IDs	Same	2	2	2	2	2	2	2	1	0	0	0	0	15
Interpretation or comments from reviewer	Same	2	2	1	2	2	2	3	1	0	0	0	0	15
Predicted DST	Predicted DST	0	2	2	1	3	3	2	1	0	1	0	0	15
MIRU-VNTR	SNPs	0	2	3	1	1	1	1	1	1	1	1	1	13
Cluster Assignment	Same	0	2	2	1	1	1	0	1	1	1	1	1	11
SNP/variant distance	SNPs	0	1	2	1	1	1	0	1	1	1	1	1	10
Phylogenetic Tree	Same	0	2	1	1	1	1	0	1	0	1	1	1	9
Reviewer ID	Same	1	1	1	1	1	1	1	1	0	0	0	0	8
TST results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
IGRA results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	0	7
Lab QC	WGS Specific	0	1	2	1	1	1	0	1	0	0	0	0	7
Spoligotype	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3
RFLP	SNPs	0	1	1	1	0	0	0	0	0	0	0	0	3

Degree of Consensus: High (3) | Some (2) | Low (1) | Very low (0)

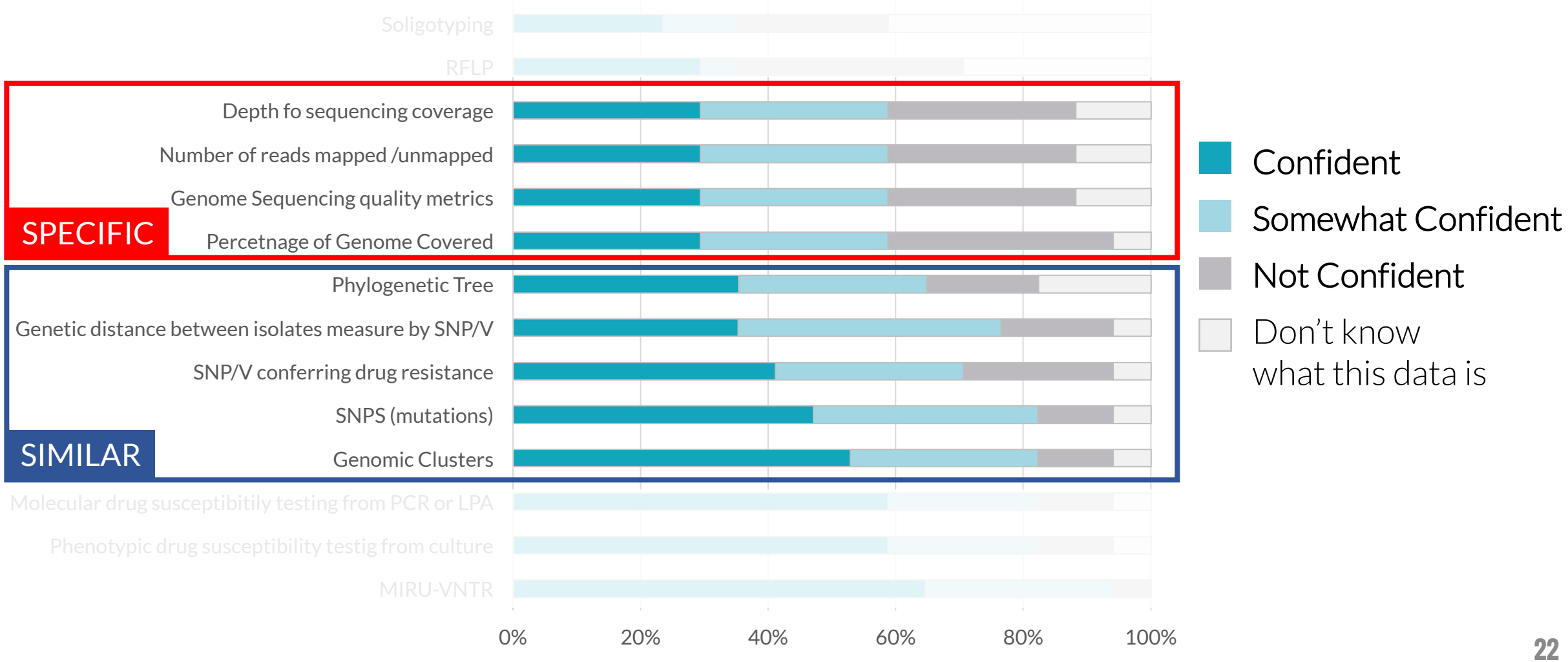
… and Variable Confidence to Interpret Data

Results are ordered from least confident (top) to most confident (bottom)



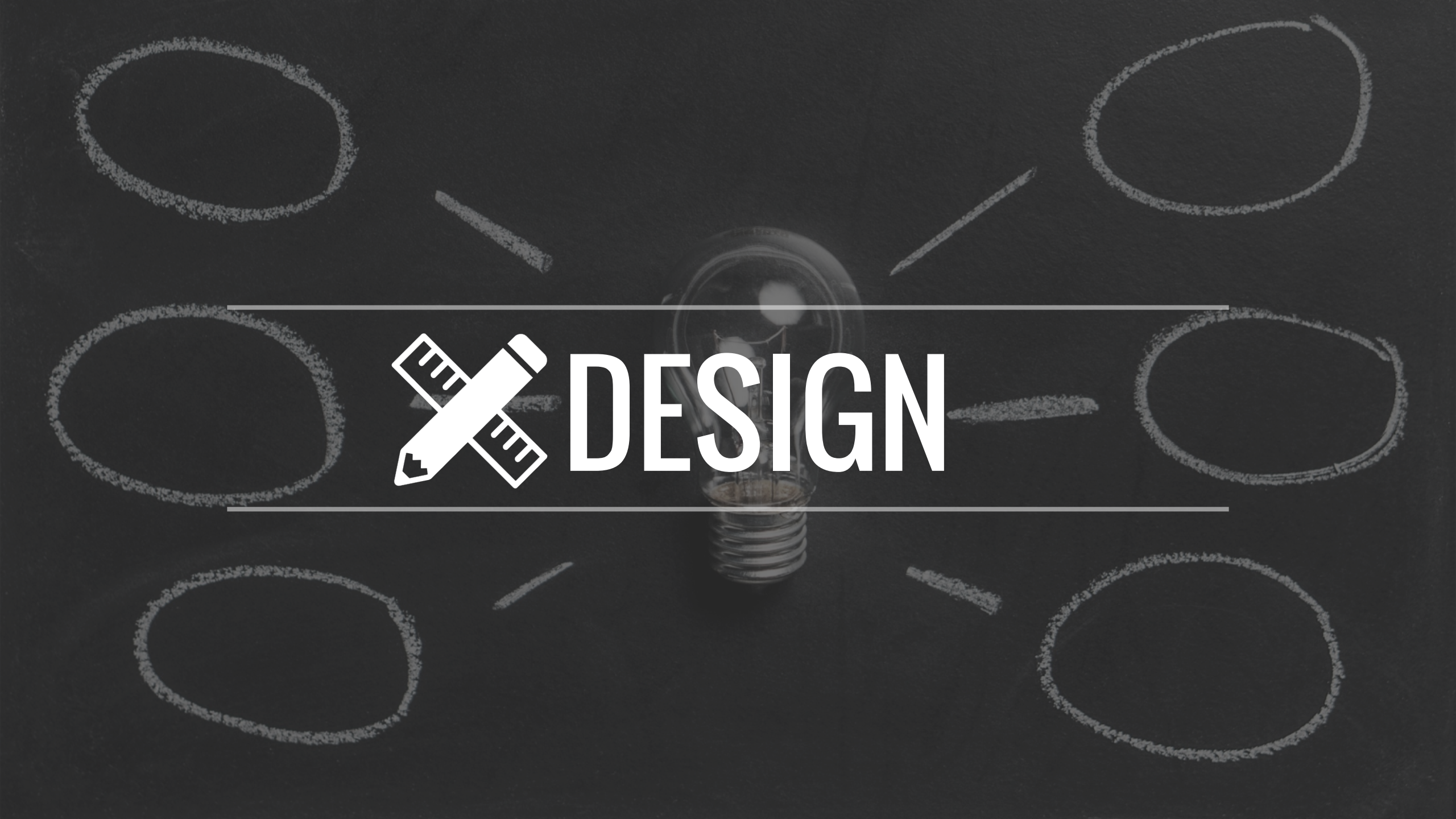
… and Variable Confidence to Interpret Data

Emphasis: data specific to WGS or similar with older genotyping technology



Take away messages

- Prioritizing relevant information is important
- There are variable perceptions on value of different data types
- There's little consensus on data that is useful for surveillance tasks
- WGS data is useful, but some lack confidence to interpret it


DESIGN

Design Stage Components

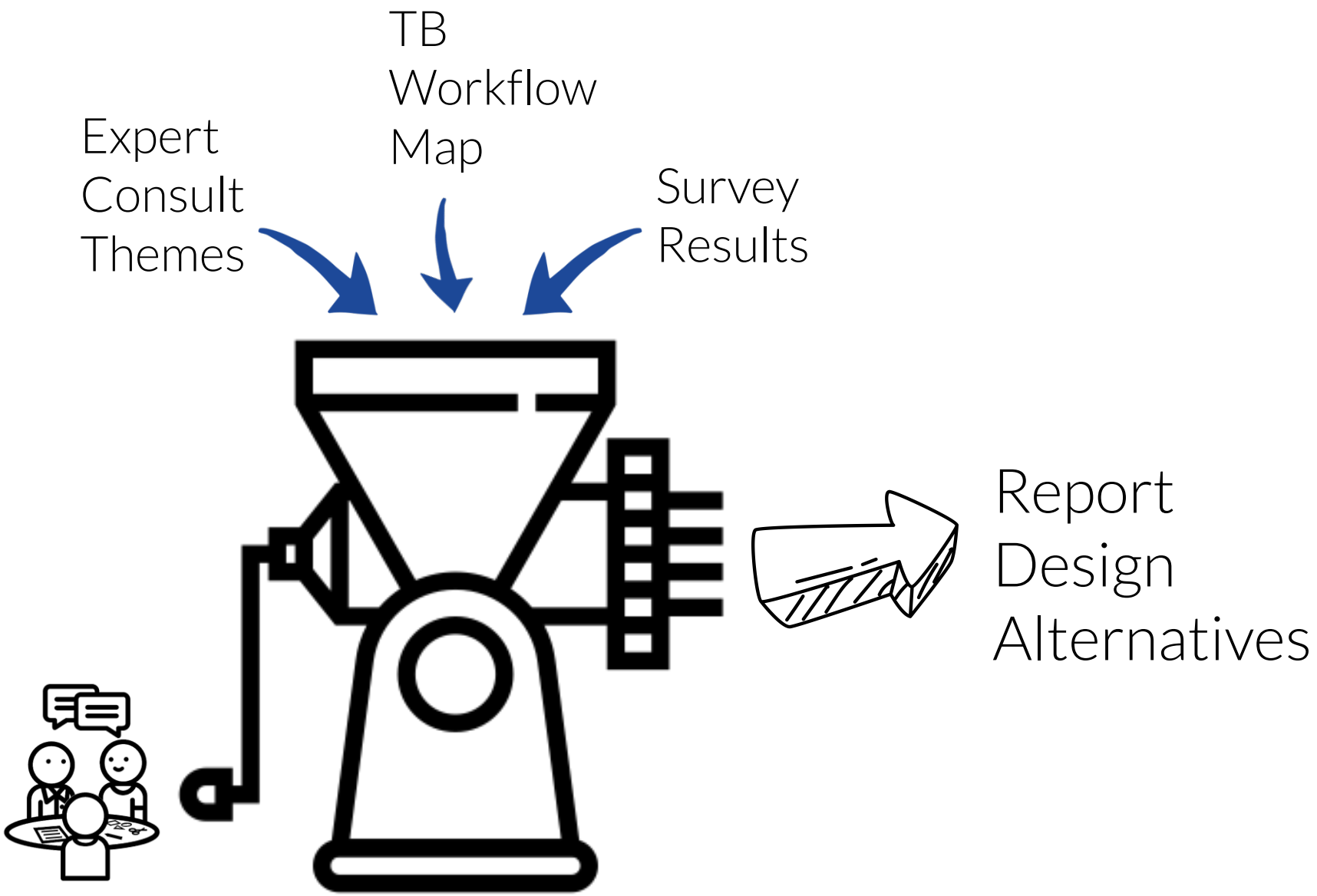
Design Sprint

- Using **Discovery** findings and designing alternative reports

Design Choice Questionnaire

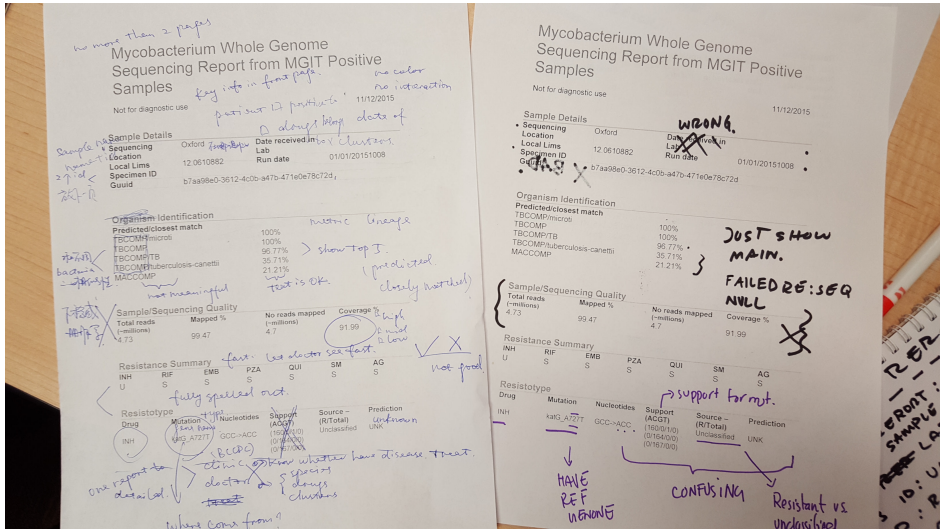
- Test designs from sprint with stakeholders
- Assess preferences for wording, information design, & data visualization
- Assess consistency between clinicians and non-clinicians

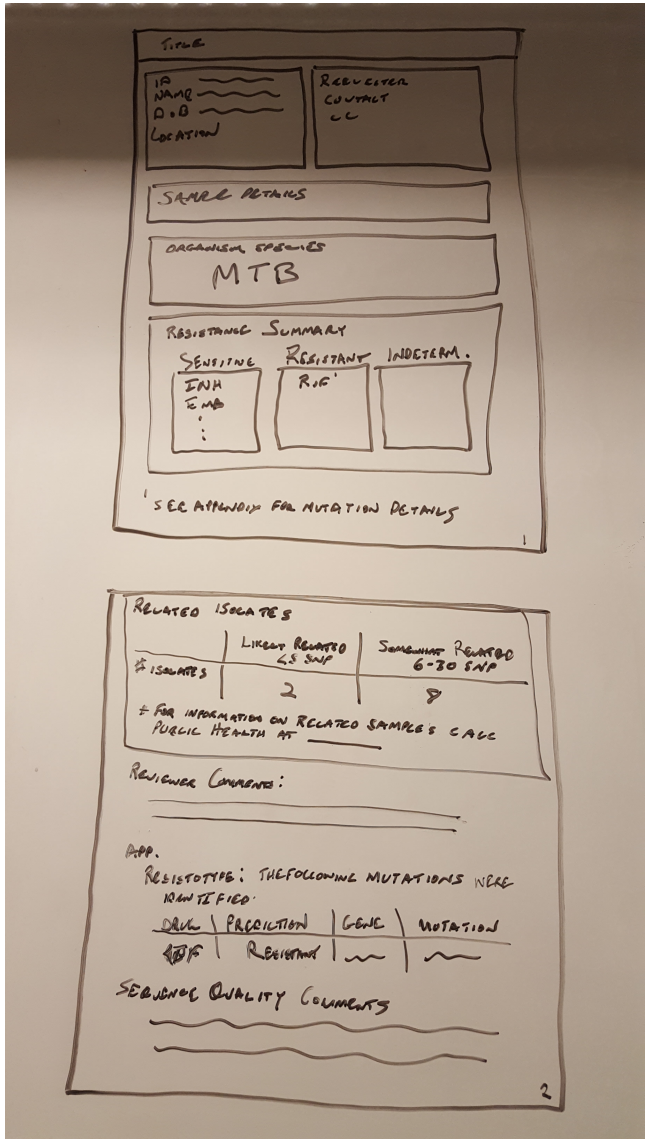
Design Sprint: Half Day Interactive Design Session



Design Sprint: Half Day Interactive Design Session

- Participants
  - *4 UBC infovis group students + us*
- Built paper prototypes
- Discussed design choices
- Developed digital mock-ups afterwards

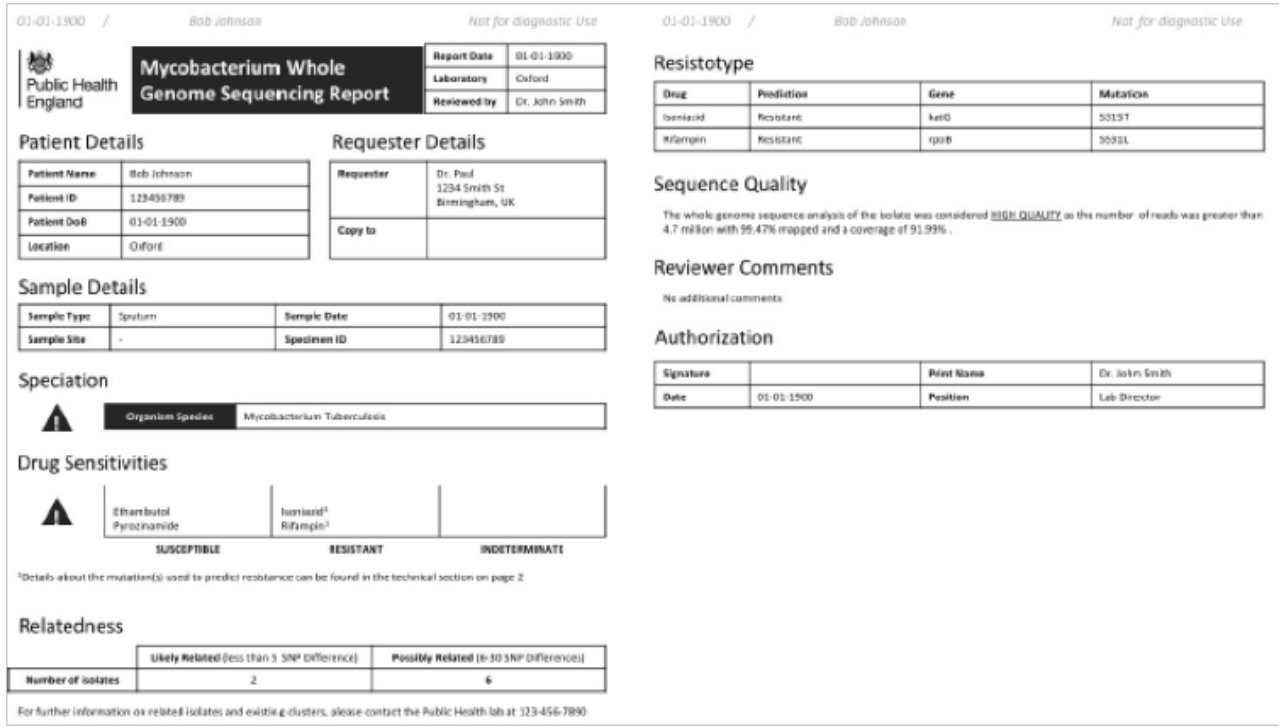




Digital Mock-ups of Paper Prototypes

Example of digital mock-ups for 2 out of 4 whole report prototypes

Example 1



01-01-1900 / Bob Johnson Not for diagnostic Use

Public Health England

Mycobacterium Whole Genome Sequencing Report

Report Date	01-01-1900
Laboratory	Oxford
Reviewed by	Dr. John Smith

Patient Details

Patient Name	Bob Johnson
Patient ID	123456789
Patient DoB	01-01-1900
Location	Oxford

Requester Details

Requester	Dr. Paul 1234 Smith St Birmingham, UK
Copy to	

Sample Details

Sample Type	Sputum	Sample Date	01-01-1900
Sample Site	-	Specimen ID	123456789

Speciation

Organism Species	Mycobacterium Tuberculosis

Drug Sensitivities

SUSCEPTIBLE	RESISTANT	INDETERMINATE
Ethambutol Pyrazinamide	Isoniazid[1] Rifampin[1]	

[1]Details about the mutation(s) used to predict resistance can be found in the technical section on page 2

Relatedness

	Likely Related (less than 5 SNP Difference)	Possibly Related (5-30 SNP Differences)
Number of isolates	2	6

For further information on related isolates and existing clusters, please contact the Public Health lab at 123-456-7890

01-01-1900 / Bob Johnson Not for diagnostic Use

Resistotype

Drug	Prediction	Gene	Mutation
Isoniazid	Resistant	katG	S315T
Rifampin	Resistant	rpoB	S531L

Sequence Quality

The whole genome sequence analysis of the isolate was considered HIGH QUALITY as the number of reads was greater than 4.7 million with 99.47% mapped and a coverage of 91.99% .

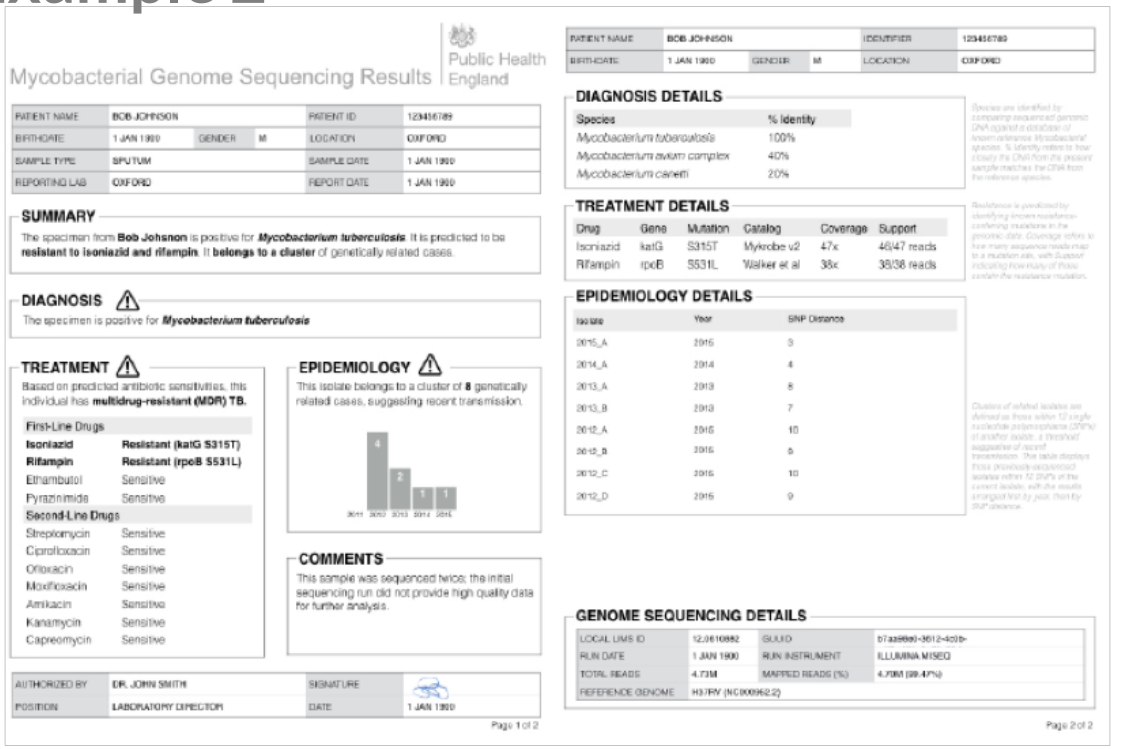
Reviewer Comments

No additional comments

Authorization

Signature		Print Name	Dr. John Smith
Date	01-01-1900	Position	Lab Director

Example 2



Mycobacterial Genome Sequencing Results

Public Health England

PATIENT NAME	BOB JOHNSON			PATIENT ID	123456789
BIRTHDATE	1 JAN 1900	GENDER	M	LOCATION	OXFORD
SAMPLE TYPE	SPUTUM			SAMPLE DATE	1 JAN 1900
REPORTING LAB	OXFORD			REPORT DATE	1 JAN 1900

SUMMARY

The specimen from **Bob Johnson** is positive for ***Mycobacterium tuberculosis***. It is predicted to be **resistant to isoniazid and rifampin**. It **belongs to a cluster** of genetically related cases.

DIAGNOSIS

The specimen is positive for ***Mycobacterium tuberculosis***

TREATMENT

Based on predicted antibiotic sensitivities, this individual has **multidrug-resistant (MDR) TB.**

First-Line Drugs	
Isoniazid	**Resistant (katG S315T)**
Rifampin	**Resistant (rpoB S531L)**
Ethambutol	Sensitive
Pyrazinimide	Sensitive
Second-Line Drugs	
Streptomycin	Sensitive
Ciprofloxacin	Sensitive
Ofloxacin	Sensitive
Moxifloxacin	Sensitive
Amikacin	Sensitive
Kanamycin	Sensitive
Capreomycin	Sensitive

EPIDEMIOLOGY

This isolate belongs to a cluster of **8** genetically related cases, suggesting recent transmission.

COMMENTS

This sample was sequenced twice; the initial sequencing run did not provide high quality data for further analysis.

AUTHORIZED BY	DR. JOHN SMITH	SIGNATURE	
POSITION	LABORATORY DIRECTOR	DATE	1 JAN 1900

Page 1 of 2

PATIENT NAME	BOB JOHNSON			IDENTIFIER	123456789
BIRTHDATE	1 JAN 1900	GENDER	M	LOCATION	OXFORD

DIAGNOSIS DETAILS

Species	% Identity
Mycobacterium tuberculosis	100%
Mycobacterium avium complex	40%
Mycobacterium canetti	20%

TREATMENT DETAILS

Drug	Gene	Mutation	Catalog	Coverage	Support
Isoniazid	katG	S315T	Mykrobe v2	47x	46/47 reads
Rifampin	rpoB	S531L	Walker et al	38x	38/38 reads

EPIDEMIOLOGY DETAILS

Isolate	Year	SNP Distance
2015_A	2015	3
2014_A	2014	4
2013_A	2013	5
2013_B	2013	7
2012_A	2015	10
2015_B	2015	5
2012_C	2015	10
2012_D	2015	9

GENOME SEQUENCING DETAILS

LOCAL LIMS ID	12-0610882	GUID	b7aa88e0-3612-4c0b-
RUN DATE	1 JAN 1900	RUN INSTRUMENT	ILLUMINA MISEQ
TOTAL READS	4.73M	MAPPED READS (%)	4.70M (99.47%)
REFERENCE GENOME	H37RV (NC000962.2)		

Page 2 of 2

Isolated Components Derived from Design Sprint

Original Report Element

1

Resistance Summary

INH	RIF	EMB	PZA	QUI	SM	AG
U	S	S	S	S	S	S

2 4 5

3

Tested Design Element

1. Alternative titles

A - Drug Resistance

B - Drug Sensitivity

C - Drug Susceptibility

D - Treatment

2. Drug name format

A - 3 letter abbreviation (Ex. INH)

B - Full Name (Ex. Isoniazid)

C - Show me everything (Ex. Isonizaid (INH,H))

D - The are equally informative

3. Susceptibility status format

A - 1 letter abbreviation (Ex. S,R,U)

B - Full Name (Ex. Susceptible, Resistant, Unknown)

C - They are equally informative

Isolated Components Derived from Design Sprint

Original Report Element

1

Resistance Summary

INH	RIF	EMB	PZA	QUI	SM	AG
U	S	S	S	S	S	S

2 4 5

3

Tested Design Element

4. Presentation order or categorization of drugs

A – Drugs by category

Drug Susceptibility

Drug	Prediction
Sensitive	Ethambutol, Pyrazinamide
Resistant	Isoniazid, Rifampin
Indeterminate	-

B – Listed by drug

Drug Susceptibility

Drug	Prediction
Isonazid	Resistant
Rifampin	Resistant
Ethambutol	Sensitive
Pyrazinimde	Sensitive

C – Summary Sentence

Drug Susceptibility

The specimen was resistant to isoniazid and rifampin, and sensitive to ethambutol and pyrazinamide

D – Drugs by category bin

Drug Susceptibility

Resistant	Sensitive	Indeterminate
Isoniazid Rifampin	Ethambutol Pyrazinamide	

E – Abbreviation listed by drug

Drug Susceptibility

INH	RIF	EMB	PZE
R	R	S	S

Isolated Components Derived from Design Sprint

Original Report Element

1

Resistance Summary

INH	RIF	EMB	PZA	QUI	SM	AG
U	S	S	S	S	S	S

2 4 5

3

Tested Design Element

5. Summary Statement

A - None

Drug Susceptibility

Drug	Prediction
Isoniazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinamide	Resistant

B - Summary sentence

Drug Susceptibility

Based on predicted antibiotic mutations, the individual has **multidrug resistant TB**

Drug	Prediction
Isoniazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinamide	Resistant

C – Tick boxes

Drug Susceptibility

Mono-resistant ☐
Multidrug-resistant (MDR) ☐
Extremely Drug Resistant (XDR) ☒

Drug	Prediction
Isoniazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinamide	Resistant

Design Choice Questionnaire : Participants & Methods

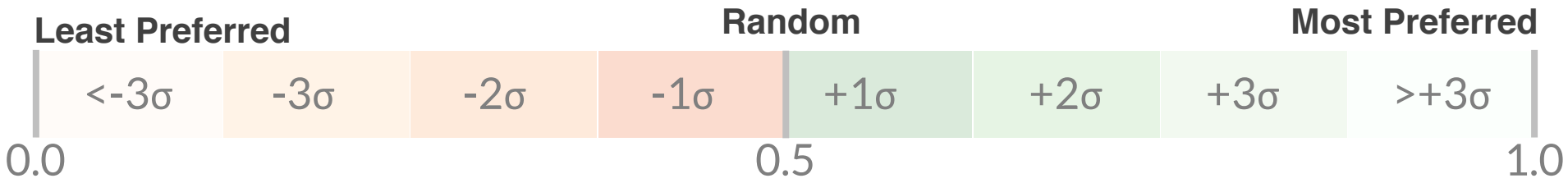
Public Health Role	Total
Clinician	13
Nurse	5
Laboratorian	3
Researcher	8
Surveillance	8
Other*	12
Total	54

- Online survey
  - *Sampling* : Convenience & Snowball
  - *Data collected*: Quantitative and qualitative
- Questions about design preferences
  - Wording, information design, and data visualization preferences
  - Consensus between clinicians and non-clinicians
- Analytic approach varied by question type

*Others were individuals that were involved in communicable disease research, but not tuberculosis specifically

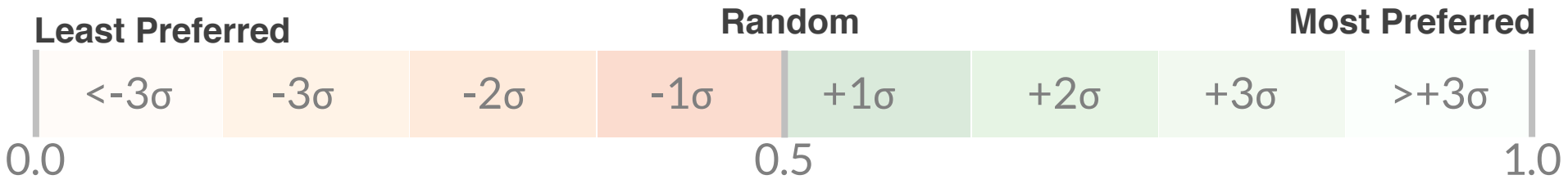
Design Choice Questionnaire : Analytic Approaches

- Reference distribution for all quantitative responses
  - Random distribution, with mean and standard deviation informed by questionnaire results



Design Choice Questionnaire : Analytic Approaches

- Reference distribution for all quantitative responses
  - Random distribution, with mean and standard deviation informed by questionnaire results



- Some "mathy" details
  - *Multiple choice questions*: report proportion of participants selecting option
  - *Rank score:* rescale the rank scores

$$= \frac{\left(\sum_{p=1}^{P} R_{i,p}\right) - P}{P \times (N-1)}$$

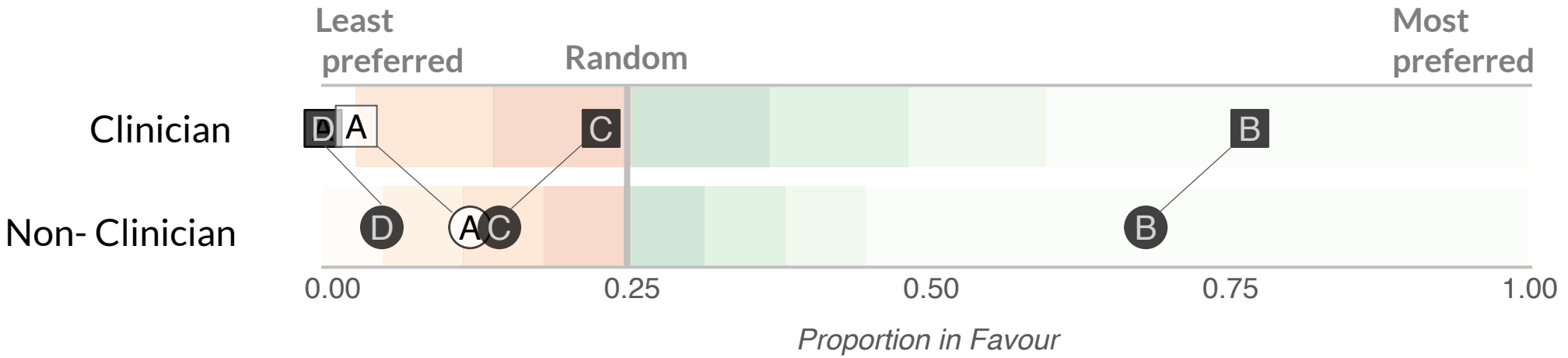
Where for each design choice (D_i)

$i = \{1..N\}$, where N is the total number of design choices

$R = \{1..N\}$, and is the chosen rank

P= is the total number of participants

[Wording] Report Drug Names as Abbreviations, or Not?



LEGEND

Public Health Role

Clinician

Non-clinician

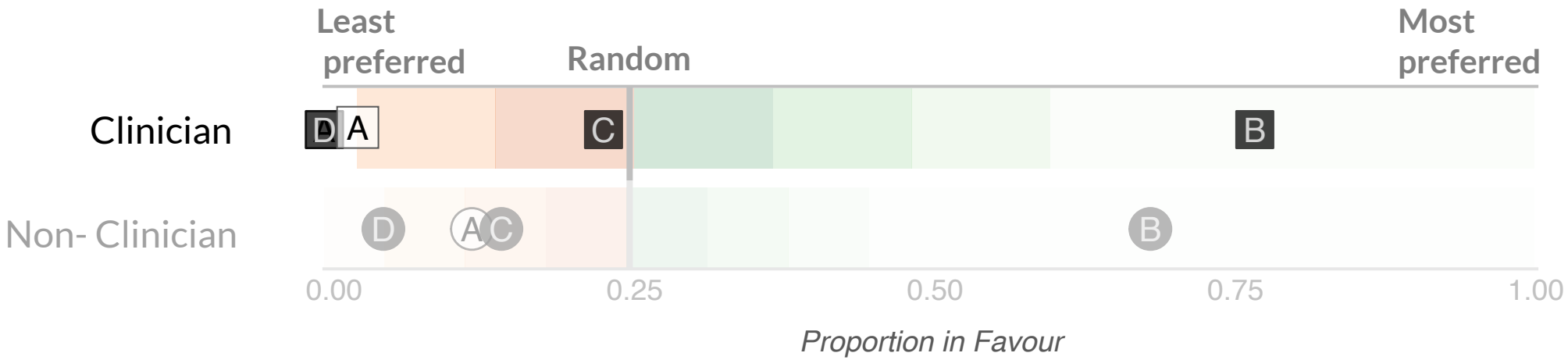
Design Option

Control

Alternative

A, B,.. *Option Indicator*

[Wording] Report Drug Names as Abbreviations, or Not?



LEGEND

Public Health Role

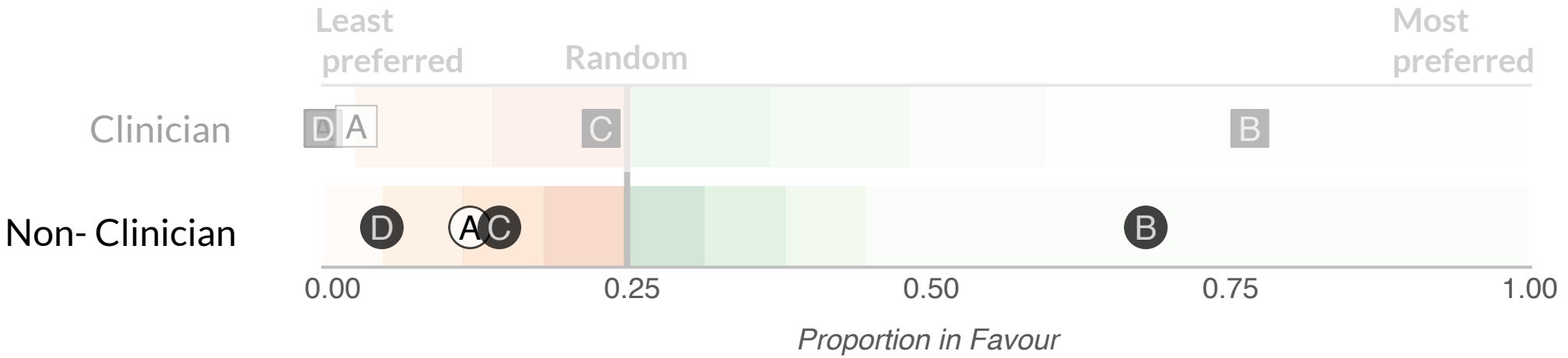
- *Clinician*
- *Non-clinician*

Design Option

- *Control*
- *Alternative*
- *A, B,..* *Option Indicator*

Top row (*square shape*) : Selections made by clinicians

[Wording] Report Drug Names as Abbreviations, or Not?



LEGEND

Public Health Role

- *Clinician*
- *Non-clinician*

Design Option

- *Control*
- *Alternative*
- *A, B,..* *Option Indicator*

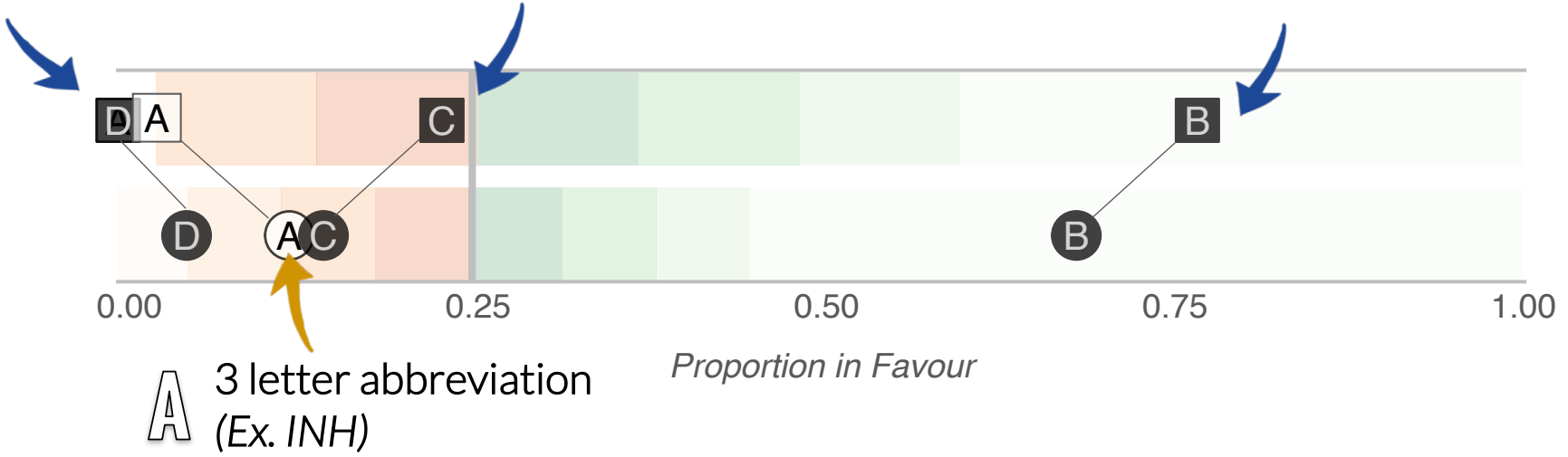
Bottom row (*circle shape*) : Selections made by non-clinicians

[Wording] Report Drug Names as Abbreviations, or Not?

D They are equally informative

C Show me everything *(Ex. Isoniazid (INH,H))*

B Full Name *(Ex. Isoniazid)*



A 3 letter abbreviation *(Ex. INH)*

LEGEND

Public Health Role

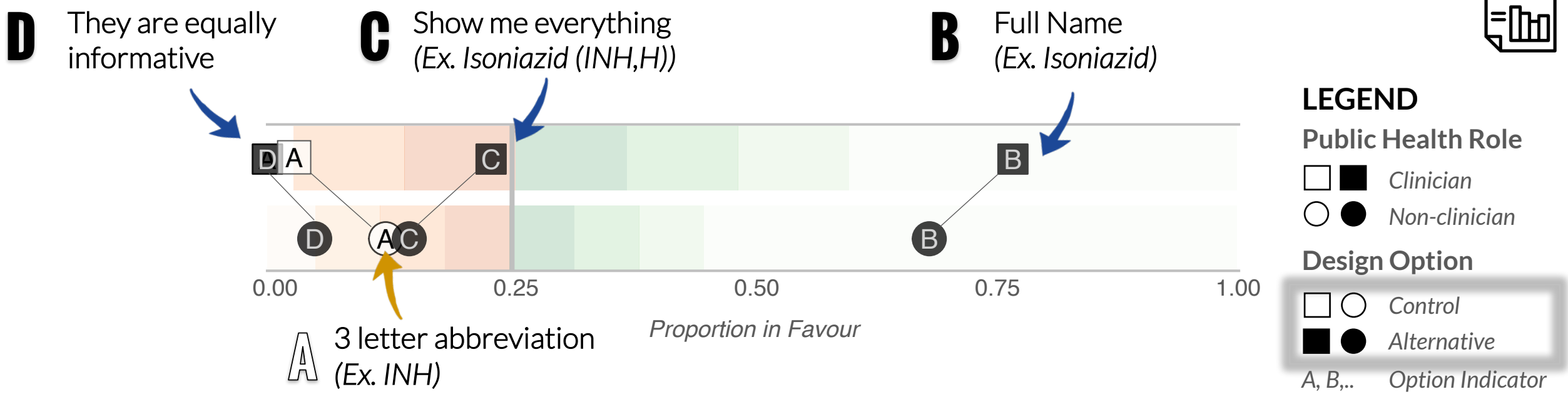
- *Clinician*
- *Non-clinician*

Design Option

- *Control*
- *Alternative*
- *A, B,..* *Option Indicator*

Letters within shapes link to options on survey

[Wording] Report Drug Names as Abbreviations, or Not?

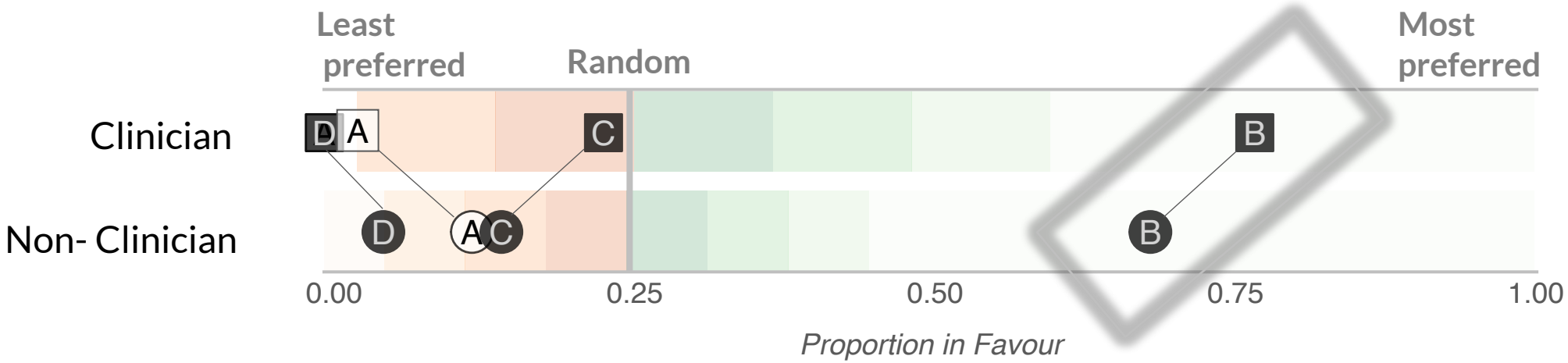


The *fill* of the shape indicates alternative (black) and control (white) designs

Control: Option A (3 letter abbreviation)

Alternative: Options B,C,D

[Wording] Report Drug Names as Abbreviations, or Not?



LEGEND

Public Health Role

Clinician

Non-clinician

Design Option

Control

Alternative

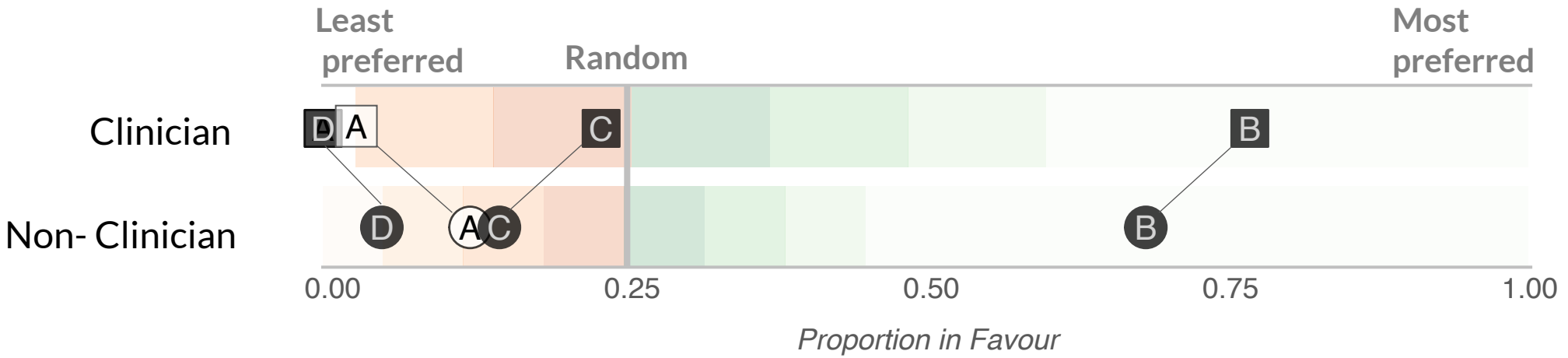
A, B,.. *Option Indicator*

Lines connect design options between clinicians and non clinicians

Non-crossing lines : consensus between clinicians and non-clinicians

Crossing lines : discordance between clinicians and non-clinicians

[Wording] Report Drug Names as Abbreviations, or Not?



LEGEND

Public Health Role

Clinician

Non-clinician

Design Option

Control

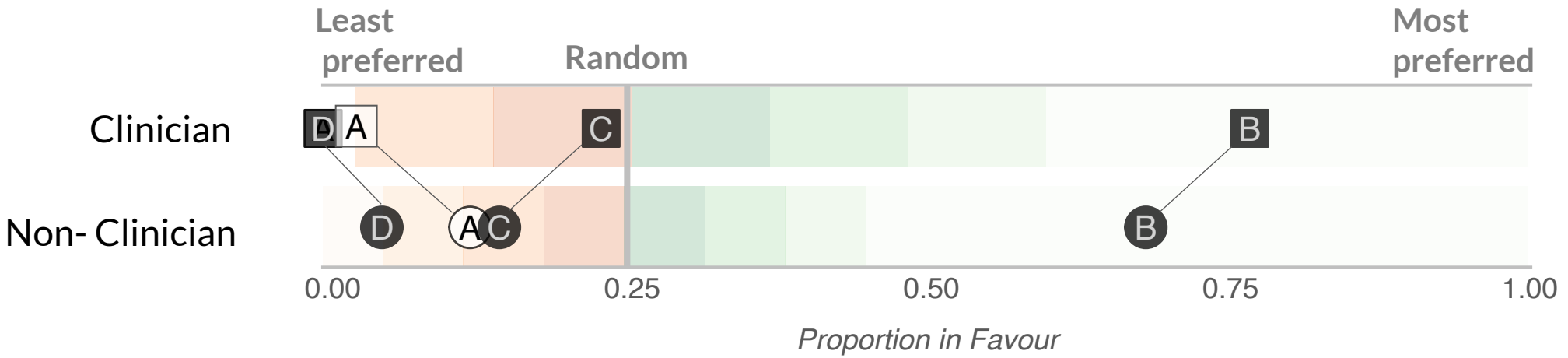
Alternative

A, B,.. *Option Indicator*

Interpretation:

- Clinicians & non-clinicians preferred option *B (provide full drug name)*
- Option B was an alternative suggestion
- There is general consensus between clinicians and non-clinicians

[Wording] Report Drug Names as Abbreviations, or Not?



LEGEND

Public Health Role

Clinician

Non-clinician

Design Option

Control

Alternative

A, B,.. *Option Indicator*

Comments from respondents:

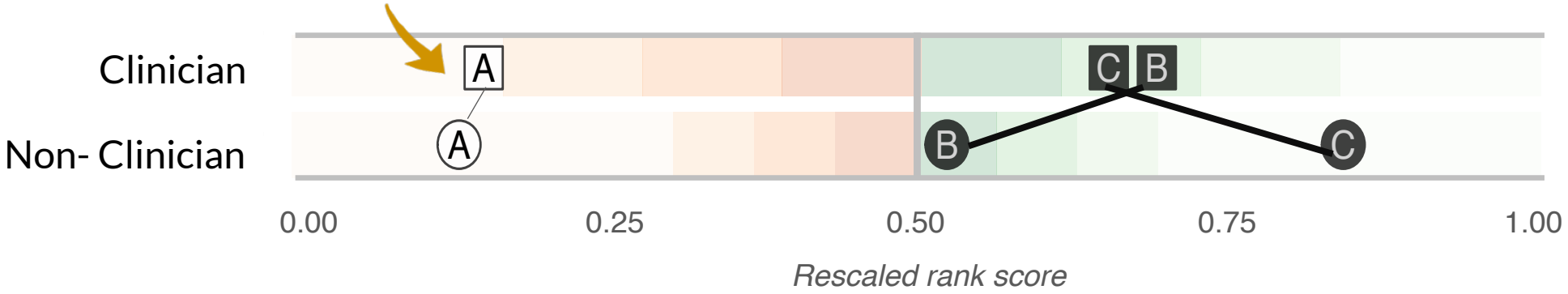
"not all clinicians [are] likely to recognize the abbreviations"

"[using the full name] reduces the risk of errors, especially if new to TB"

[Design] Show Summary of Resistance Results ?

Drug Susceptibility

Drug	Prediction
Isonazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimde	Resistant



Control design : no summary information, just table

[Design] Show Summary of Resistance Results ?

Alternative designs :

Tick-boxes

Drug Susceptibility

Mono-resistant ☐
Multidrug-resistant (MDR) ☐
Extremely Drug Resistant (XDR) ☒

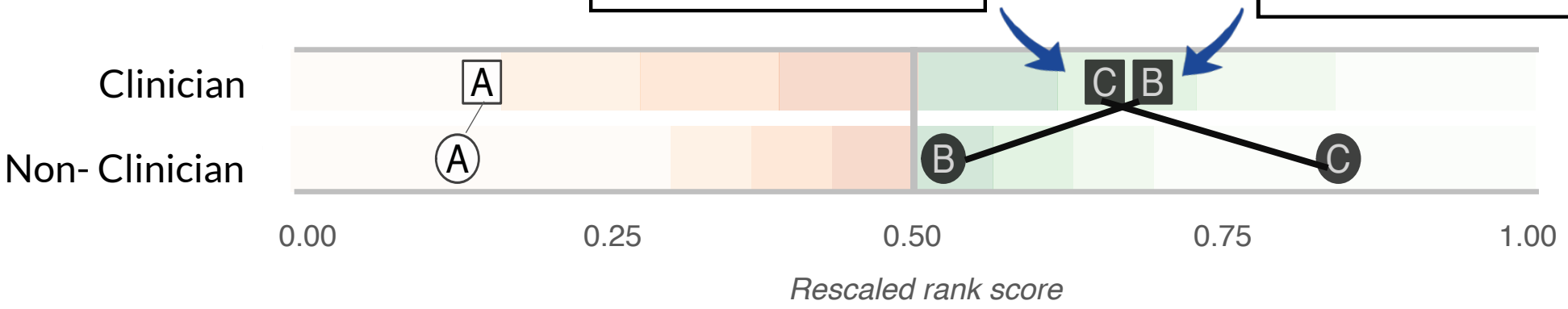
Drug	Prediction
Isonazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimde	Resistant

Summary Sentence

Drug Susceptibility

Based on predicted antibiotic mutations, the individual has **multidrug resistant TB**

Drug	Prediction
Isonazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimde	Resistant



[Design] Show Summary of Resistance Results ?

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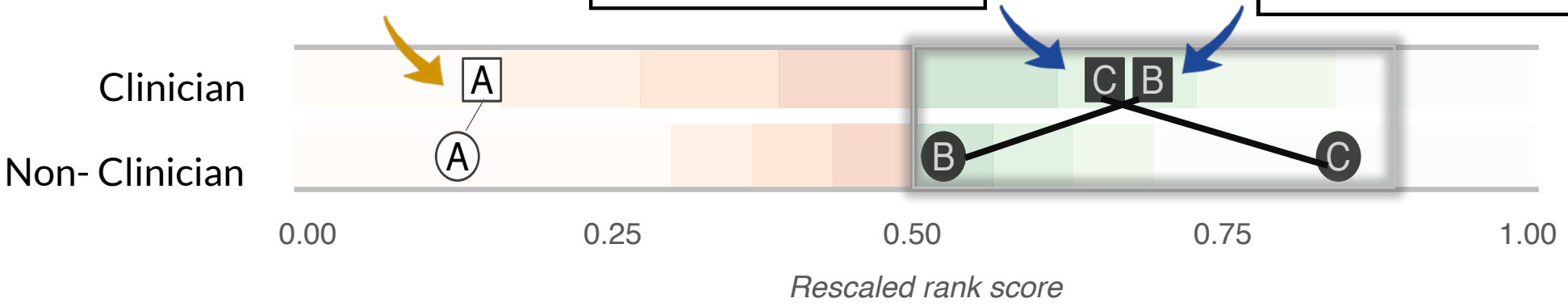

Interpretation:

- Alternative design preferred (C or B)
- Some difference between clinicians & non-clinicians preferences

[Design] Show Summary of Resistance Results ?

Drug Susceptibility

Drug	Prediction
Isonazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimde	Resistant

Drug Susceptibility

Mono-resistant ☐
Multidrug-resistant (MDR) ☐
Extremely Drug Resistant (XDR) ☒

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Drug Susceptibility

Based on predicted antibiotic mutations, the individual has **multidrug resistant TB**

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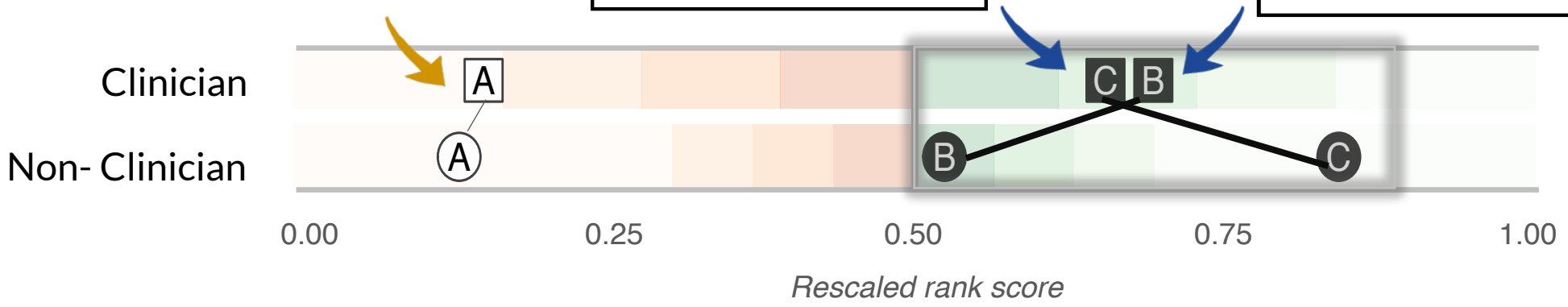
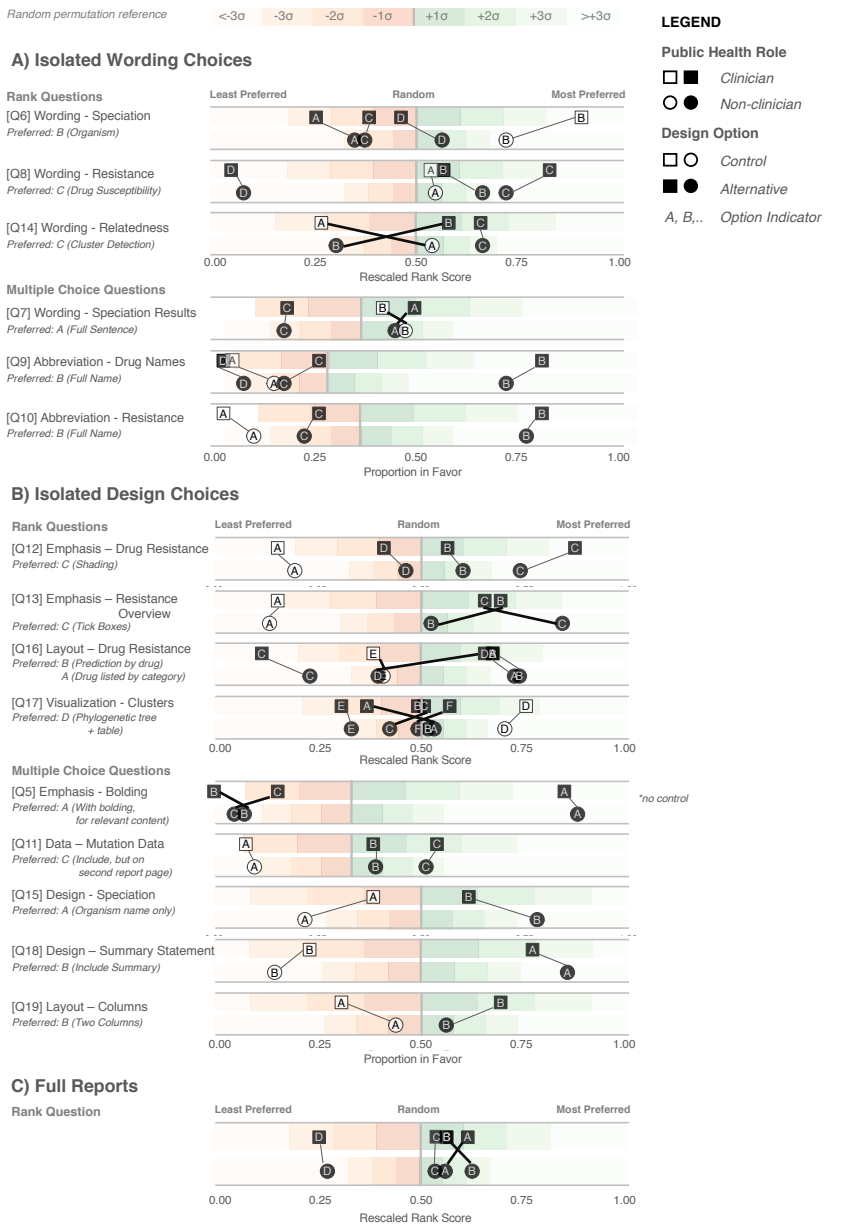


Comments from respondents:

"the check boxes provide an at-a-glance result"

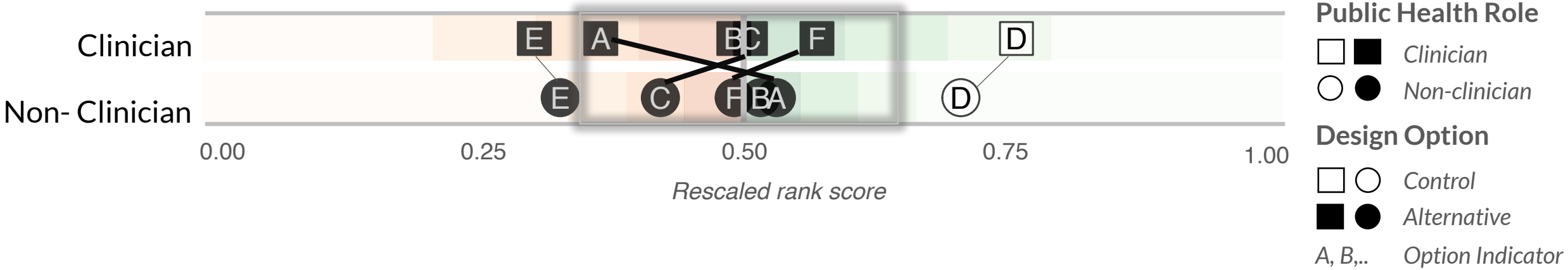
*"tick boxes may cause confusion when clinicians read XDR without realizing that option is **not** selected."*

Full Results : Summary of Findings



- Generally, alternative designs preferred
  - in 12 out of 14 comparisons to control
- Designs should promote patient safety & precise interpretability
  - Abbreviations should be avoided
  - Debate about prioritizing susceptible vs. resistant drugs
- Clinically actionable data to be given priority
  - Surveillance tasks aren't clinically actionable
- Sometimes we didn't provide good alternatives
  - Example: visualizing cluster results
- Isolated components showed clearer preferences than comparing full reports

Interesting Finding : Uncertainty over Data Visualization

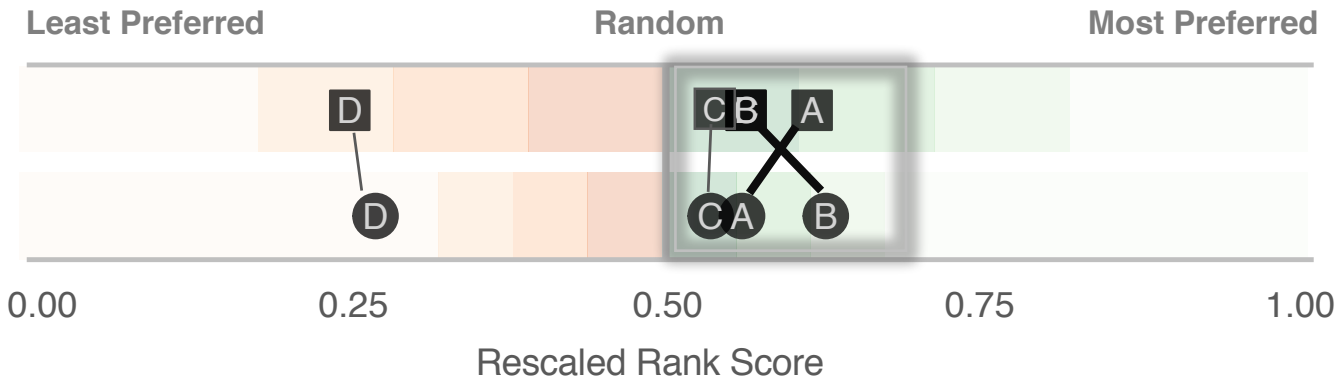


Few good alternatives were suggested

"If you can combine the phylogenetic tree with some kind of graph showing temporal spread that would be perfect. Adding geographical data would be a really helpful bonus too."

"Not useful for clinician. you need to refer this question to public health officials who do contact tracing"

Full Report Comparison : No Real Preference Consensus



LEGEND

Public Health Role

Clinician

Non-clinician

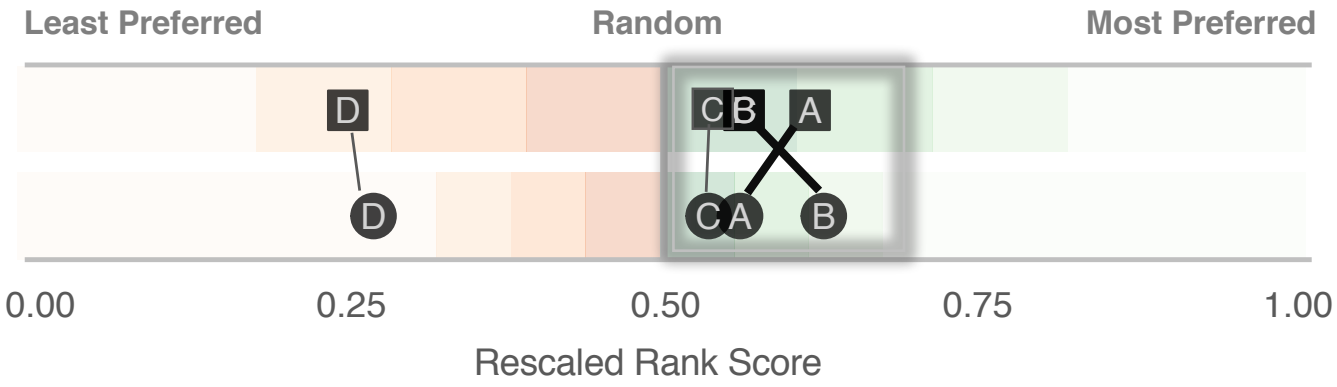
Design Option

Control

Alternative

A, B,.. *Option Indicator*

Full Report Comparison : No Real Preference Consensus



LEGEND

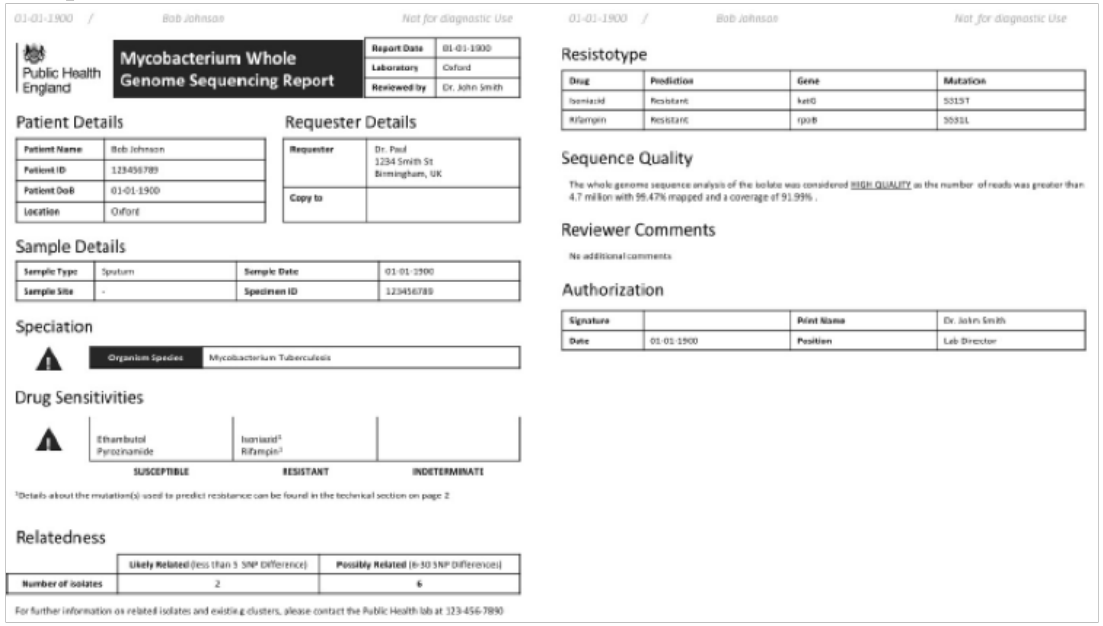
Public Health Role

- *Clinician*
- *Non-clinician*

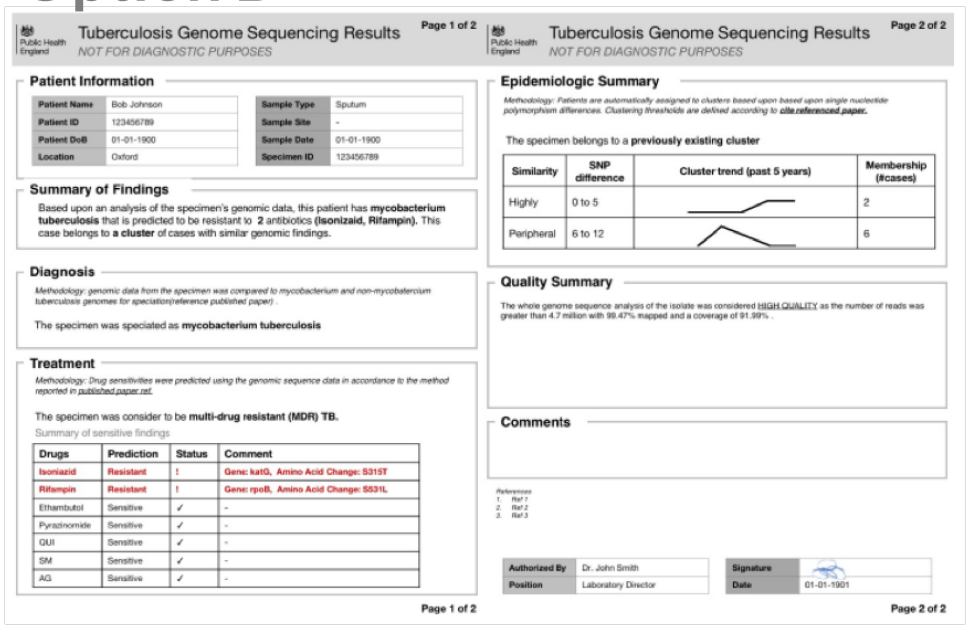
Design Option

- *Control*
- *Alternative*

Option A



Option B

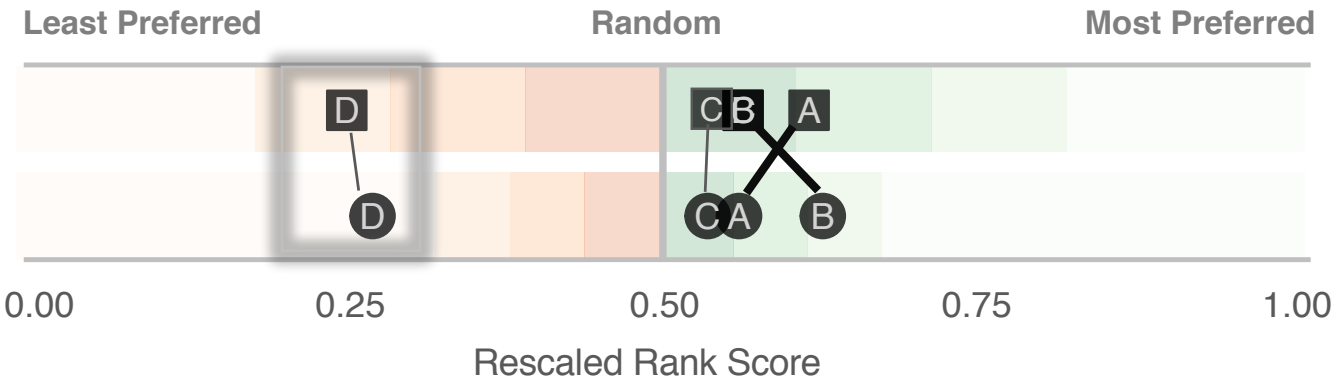


Full Report Comparison : No Real Preference Consensus

"None are especially good (see previous comments on individual parts)"

- Participant Comment

Full Report Comparison : No Real Preference Consensus



LEGEND

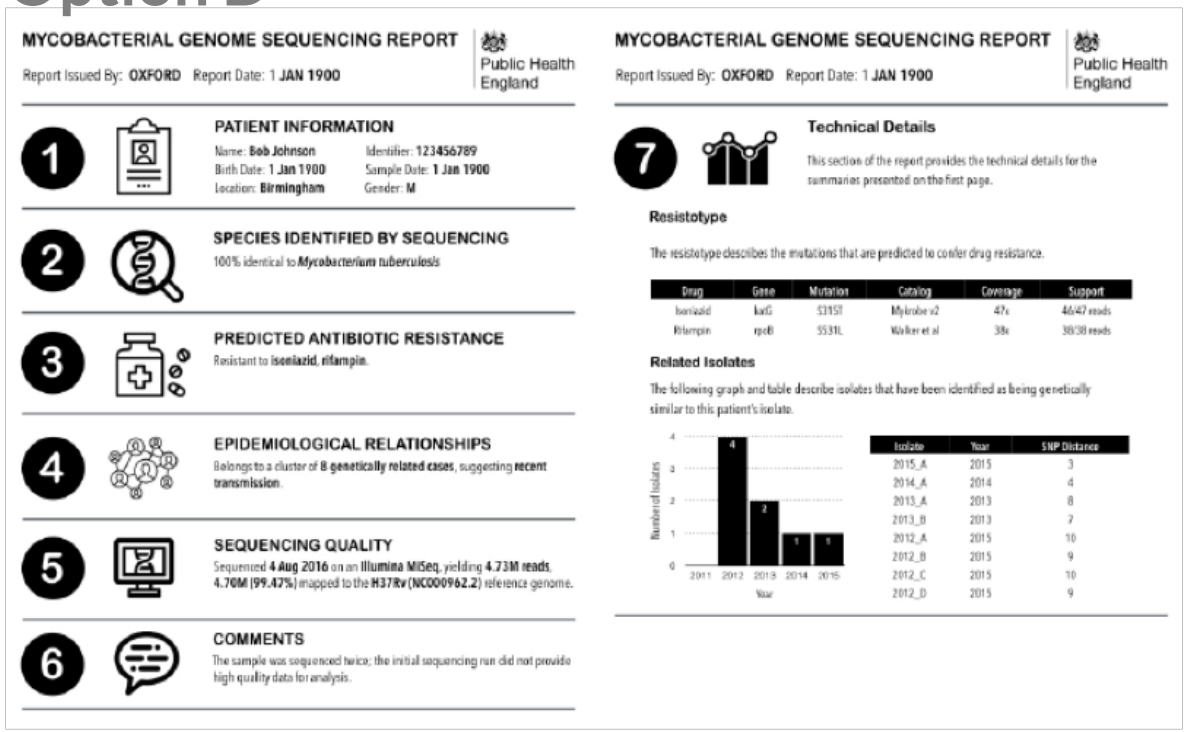
Public Health Role

- □ ■ *Clinician*
- ○ ● *Non-clinician*

Design Option

- □ ○ *Control*
- ■ ● *Alternative*
- *A, B,..* *Option Indicator*

Option D



MYCOBACTERIAL GENOME SEQUENCING REPORT

Report Issued By: **OXFORD** Report Date: 1 **JAN 1900**

Public Health England

1 PATIENT INFORMATION

Name: **Bob Johnson** Identifier: **123456789**
Birth Date: **1 Jan 1900** Sample Date: **1 Jan 1900**
Location: **Birmingham** Gender: **M**

2 SPECIES IDENTIFIED BY SEQUENCING

100% identical to ***Mycobacterium tuberculosis***

3 PREDICTED ANTIBIOTIC RESISTANCE

Resistant to **isoniazid, rifampin.**

4 EPIDEMIOLOGICAL RELATIONSHIPS

Belongs to a cluster of **8 genetically related cases**, suggesting **recent transmission**.

5 SEQUENCING QUALITY

Sequenced **4 Aug 2016** on an **Illumina MiSeq**, yielding **4.73M reads**. **4.70M (99.47%)** mapped to the **H37Rv (NC000962.2)** reference genome.

6 COMMENTS

The sample was sequenced twice; the initial sequencing run did not provide high quality data for analysis.

MYCOBACTERIAL GENOME SEQUENCING REPORT

Report Issued By: **OXFORD** Report Date: 1 **JAN 1900**

Public Health England

7 Technical Details

This section of the report provides the technical details for the summaries presented on the first page.

Resistotype

The resistotype describes the mutations that are predicted to confer drug resistance.

Drug	Gene	Mutation	Catalog	Coverage	Support
Isoniazid	katG	S315T	Mykrobe v2	47x	46/47 reads
Rifampin	rpoB	S531L	Walker et al	38x	38/38 reads

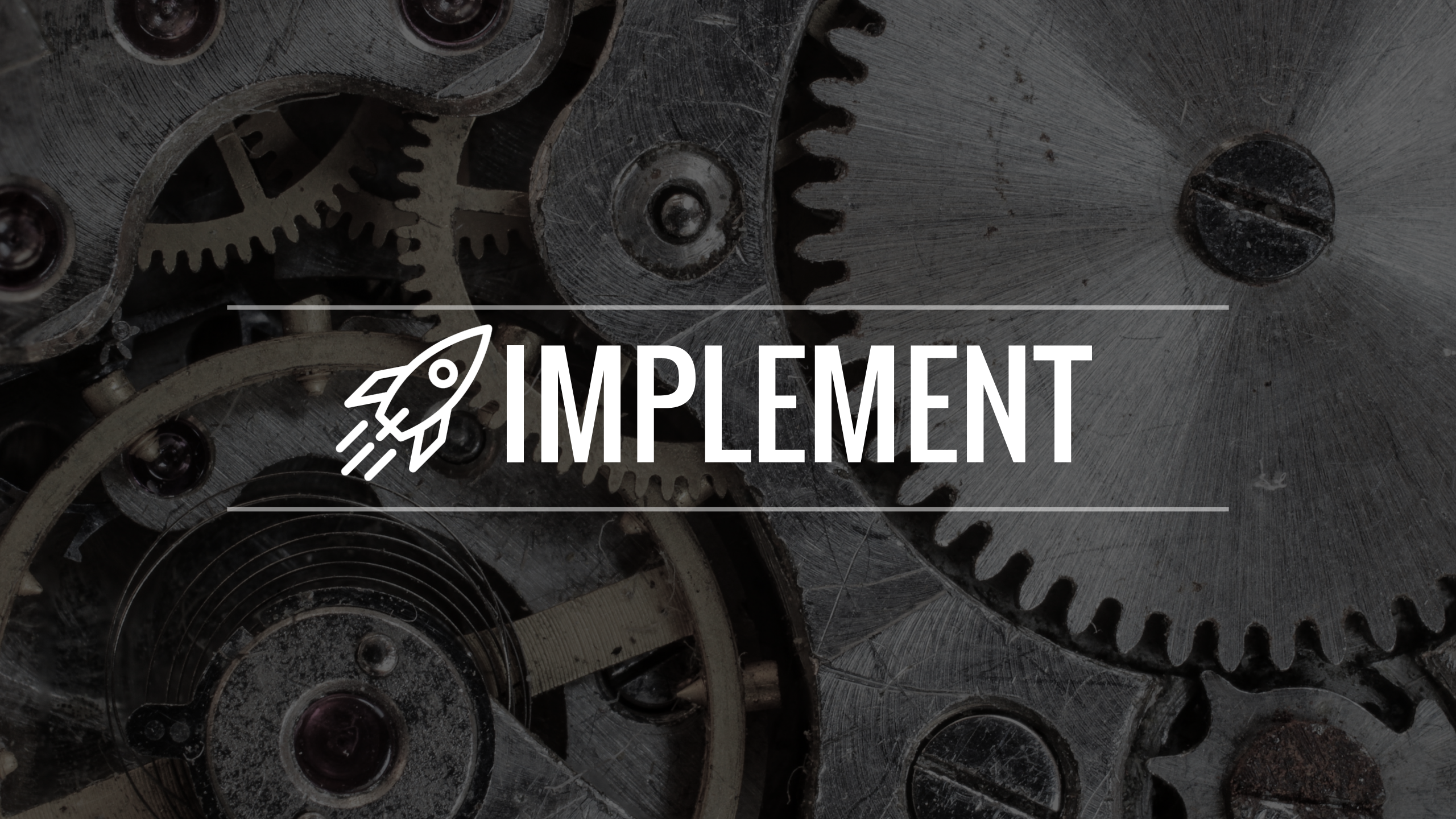
Related Isolates

The following graph and table describe isolates that have been identified as being genetically similar to this patient's isolate.

Isolate	Year	SNP Distance
2015_A	2015	3
2014_A	2014	4
2013_A	2013	8
2013_B	2013	7
2012_A	2015	10
2012_B	2015	9
2012_C	2015	10
2012_D	2015	9

Take Away Messages

- General consensus in clinician & non-clinician preferences
- Alternative elements were preferred when compared against controls
- Some reporting areas need more work (surveillance)
- Isolated components showed clearer preferences than full reports


IMPLEMENT

Input from Stakeholders on Report Design

- Draft of report presented to a global TB working group
- Revised report was approved with minor changes
  - Revising some language (chiefly, sensitive -> susceptible)
  - Adding place for lineage details
  - Adding summary of assay + pipeline details
  - Adding a standard disclaimer

Mycobacterium Whole Genome Sequencing Report from MGIT Positive Samples

Not for diagnostic use 01/02/1915

Sample Details

Sequencing Location	Oxford	**Date received in Lab**	
Local Lims Specimen ID	123456789	**Run date**	01/01/19150115
Guuid	123456-79aab-910abr-15243hg		

Organism Identification

Predicted species	match
TBCOMP/[illegible]croti	100%
TBCOMP [illegible]	10[illegible]%
TBCOMP/[illegible]	96[illegible]7%
TBCOMP/[illegible]bercu[illegible]sis-[illegible]netti	35[illegible]1%
MACCOMP [illegible]	21[illegible]1%

Original

Sample/Sequencing Quality

Total reads (~millions)	Mapped %	No reads mapped (~millions)	Coverage %
4.73	99.47	4.7	91.99

Resistance Summary

INH	RIF	EMB	PZA	QUI	SM	AG
U	S	S	S	S	S	S

Resistotype

Drug	Mutation	Nucleotides	Support (ACGT)	Source – (R/Total)	Prediction
INH	katG_A727T	GCC->ACC	(160/0/1/0) (0/164/0/0) (0/167/0/0)	Unclassified	UNK

MYCOBACTERIUM TUBERCULOSIS GENOME SEQUENCING REPORT

NOT FOR DIAGNOSTIC USE

Patient Name	JOHN DOE	Barcode	
Birth Date	2000-01-01	Patient ID	12345678910
Location	SOMEPLACE	Sample Type	SPUTUM
Sample Source	PULMONARY	Sample Date	2016-12-25
Sample ID	A12345678	Sequenced From	MGIT CULTURED ISOLATE
Reporting Lab	LAB NAME	Report Date/Time	2017-01-01, 15:36
Requested By	REQUESTER NAME	Requester Contact	REQUESTER@EMAIL.COM

Redesigned

Summary

The specimen was positive for **Mycobacterium tuberculosis**. It is **resistant to isoniaizd and rifampin**. It belongs to a cluster, suggesting **recent transmission**.

Organism

The sp[illegible] wa[illegible] for *[illegible]acte[illegible]ber[illegible]osis* [illegible] 2[illegible] Asia[illegible]g).

Drug Susceptibility

[illegible]sistan[illegible] reporte[illegible] when a high confidence resistance-conferring mutation is detected. **"No mutation detected" does not exclude the possibility of resistance.**

☐ No [illegible]ta[illegible] pr[illegible]cted
☐ Mo[illegible]-resis[illegible]ce predicted
☑ Multi-drug resistance predicted
☐ Extensive drug resistance predicted

Drug class	Interpretation	Drug	Resistance Gene (Amino Acid Mutation)
First Line	Susceptible	Ethambutol	No mutation detected
		Pyrazinimide	No mutation detected
	Resistant	Isoniazid	katG (S315T)
		Rifampin	rpoB (S531L)
Second Line	Susceptible	Streptomycin	No mutation detected
		Ciprofloxacin	No mutation detected
		Ofloxacin	No mutation detected
		Moxifloxacin	No mutation detected
		Amikacin	No mutation detected
		Kanamycin	No mutation detected
		Capreomycin	No mutation detected

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Local Lims Specimen ID	123456789	**Run date**	01/01/19150115
Guuid	123456-79aab-910abr-15243hg		

Organism Identification

Predicted/closest match	
TBCOMP/microti	100%
TBCOMP	100%
TBCOMP/TB	96.77%
TBCOMP/tuberculosis-canettii	35.71%
MACCOMP	21.21%

Sample/Sequencing Quality

Total reads (~millions)	**Mapped %**	**No reads mapped (~millions)**	**Coverage %**
4.73	99.47	4.7	91.99

Resistance Summary

INH	**RIF**	**EMB**	**PZA**	**QUI**	**SM**	**AG**
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Drug	**Mutation**	**Nucleotides**	**Support (ACGT)**	**Source – (R/Total)**	**Prediction**
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The specimen was positive for **Mycobacterium tuberculosis**. It is **resistant to isoniaizd and rifampin**. It belongs to a cluster, suggesting **recent transmission**.

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The specimen was positive for ***Mycobacterium tuberculosis***, lineage 2.2.1 (**East-Asian Beijing**).

Drug Susceptibility

Resistance is reported when a high-confidence resistance-conferring mutation is detected. **"No mutation detected" does not exclude the possibility of resistance**.

☐ No drug resistance predicted
☐ Mono-resistance predicted
☑ Multi-drug resistance predicted
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		Moxifloxacin	No mutation detected
		Amikacin	No mutation detected
		Kanamycin	No mutation detected
		Capreomycin	No mutation detected

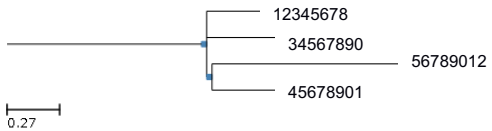
Relatedness

NB: This data may be added or updated at a later date

Nearest neighbour(s)

Sample -Plate Name	Date received in Lab	Centre	No. of SNPs apart
123456789		Oxford	0
34567890	1900-01-01		10
45678901	1015-01-31	Oxford	15
56789012		London	8

The alignment width is 285. Multiply this number by the tree metrics.



Comments

Authorised

Signature:	**Print name:**
Position:	**Date:**

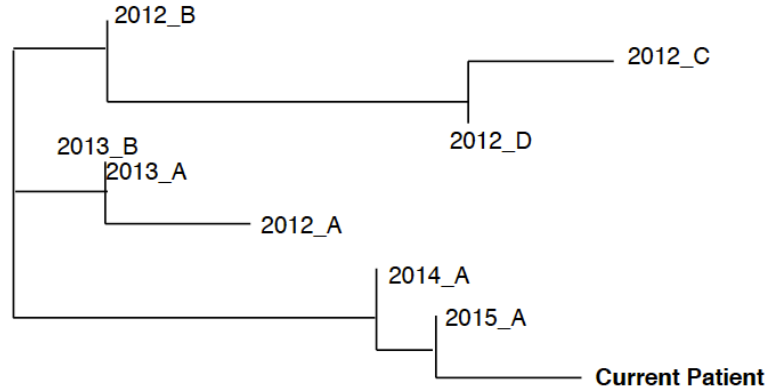
MYCOBACTERIUM TUBERCULOSIS GENOME SEQUENCING REPORT

NOT FOR DIAGNOSTIC USE

Cluster Detection

The current isolate was clustered with previously sequenced isolates, suggesting **recent transmission**.

Relatedness	Number of prior matching isolates
Closely Related (< 5 mutations apart)	**2** isolates
Related (6 to 30 mutations apart)	**6** isolates



Assay Details

Sample ID	A12345678	Barcode	
Sequencer	ILLUMINA HISEQ 2500	Method	WGS
Pipeline	RESEQTB V.3.2C	Reference	H37RV

Comments

No additional comments for this report

Standard Disclaimer: *Low frequency hetero-resistance below the limit of detection by sequencing may affect typing results. The interpretation provided is based on the current understanding of genotype-phenotype relationships.*

Authorised

Signature	Name
Position	Date

Revised Report Designed through Evidence Collected

MYCOBACTERIUM TUBERCULOSIS GENOME SEQUENCING REPORT
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		Amikacin	No mutation detected
		Kanamycin	No mutation detected
		Capreomycin	No mutation detected

- Visual hierarchy that follows a clinical narrative
  - Grouping of common data elements (gestalt)
  - Judicious use of emphasis for "at-a-glance" read
  - Prioritize reading flow for clinical tasks
- Attempts to address timeliness and request for levels of detail

Revised Report Designed Through Evidence Collected

LaTeX Template

https://goo.gl/t4SMdV

https://www.overleaf.com/latex/templates/tb-wgs-report-for-reference-lab/psmnzmcnwrwm

Example with Sweave (R – LaTeX Interface)

https://github.com/amcrisan/TB-WGS-MicroReport

REFLECTION

Why not just hire a Graphic Designer?

"Design is not just what it looks like and feels like – design is how it works"

Steve Jobs

- Form (visual appeal) should follow function
  - Visual appeal is important, but does not guarantee functionality
  - *Example:* report design with pictures was pretty but was also the least preferred
- Functional can also be *beautiful*
  - Report is both functional (*works better)* and also visually appealing
  - Understanding scientific goals, tasks, and data is a scientific problem & linked to function
    - Not necessarily a graphics design issues

Do YOU have to go through all this effort for every report?

It *depends* on what you want to achieve

- Broad data collection can be used for other projects
  - We were also collecting data for future software projects
  - Stayed tuned for more details!

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- At the very least test alternative designs
  - If you can't do a Discovery stage (time, people, budget) at least to the Design stage
  - Check in with stakeholders to avoid *ad hoc* design issues

It *depends* on what you want to achieve

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- At the very least test alternative designs
  - If you can't do a Discovery stage (time, people, budget) at least to the Design stage
  - Check in with stakeholders to avoid *ad hoc* design issues
- Bioinformaticians : you should use human-centered design for your tools!
  - Not command line ≠user friendly
  - If you didn't test it with even one user it's not *"user friendly"* or *"intuitive"*
  - Report design is a very simple example of how to use these methods

THANKS!

UBC

Dr. Jennifer Gardy
Dr. Geoff McKee
Dr. Tamara Munzner

COMPASS TB

Dr. Ana Gibertoni-Cruz
Dr. Grace Smith
Dr. Tim Walker

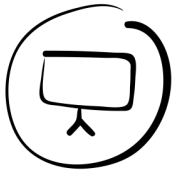
+ UBC infoVis group

Kimberly Dextras-Romagnino, Dylan Dong, Georges Hattab, and Zipeng Liu

+ All of our fantastic study participants

Pre-Print + Other Stuff

https://doi.org/10.1101/199570



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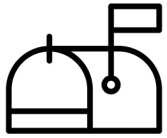
http://www.cs.ubc.ca/labs/imager/tr/2017/MicroReportDesign/

https://goo.gl/6vNqRZ

http://www.cs.ubc.ca/labs/imager/tr/2017/MicroReportDesign/



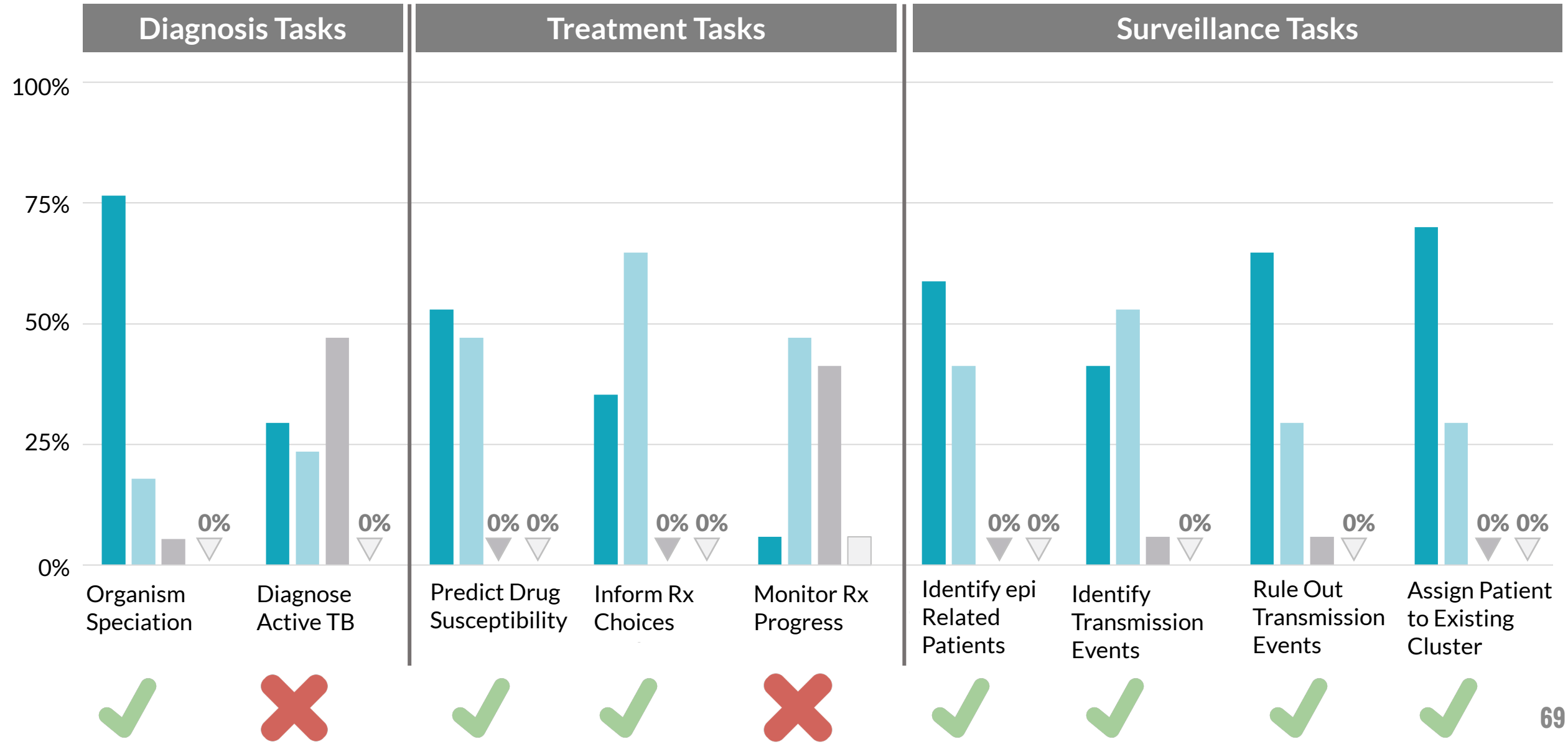
acrisan@cs.ubc.ca

Go forth and analyze!

Icons by noun project and images from pexels

Additional Materials

CAN GENOMIC DATA PERFORM THE FOLLOWING (NOW OR LATER)?



Results: Wording Preferences

Rank Questions

[Q6] Wording - Speciation
Preferred: B (Organism)

[Q8] Wording - Resistance
Preferred: C (Drug Susceptibility)

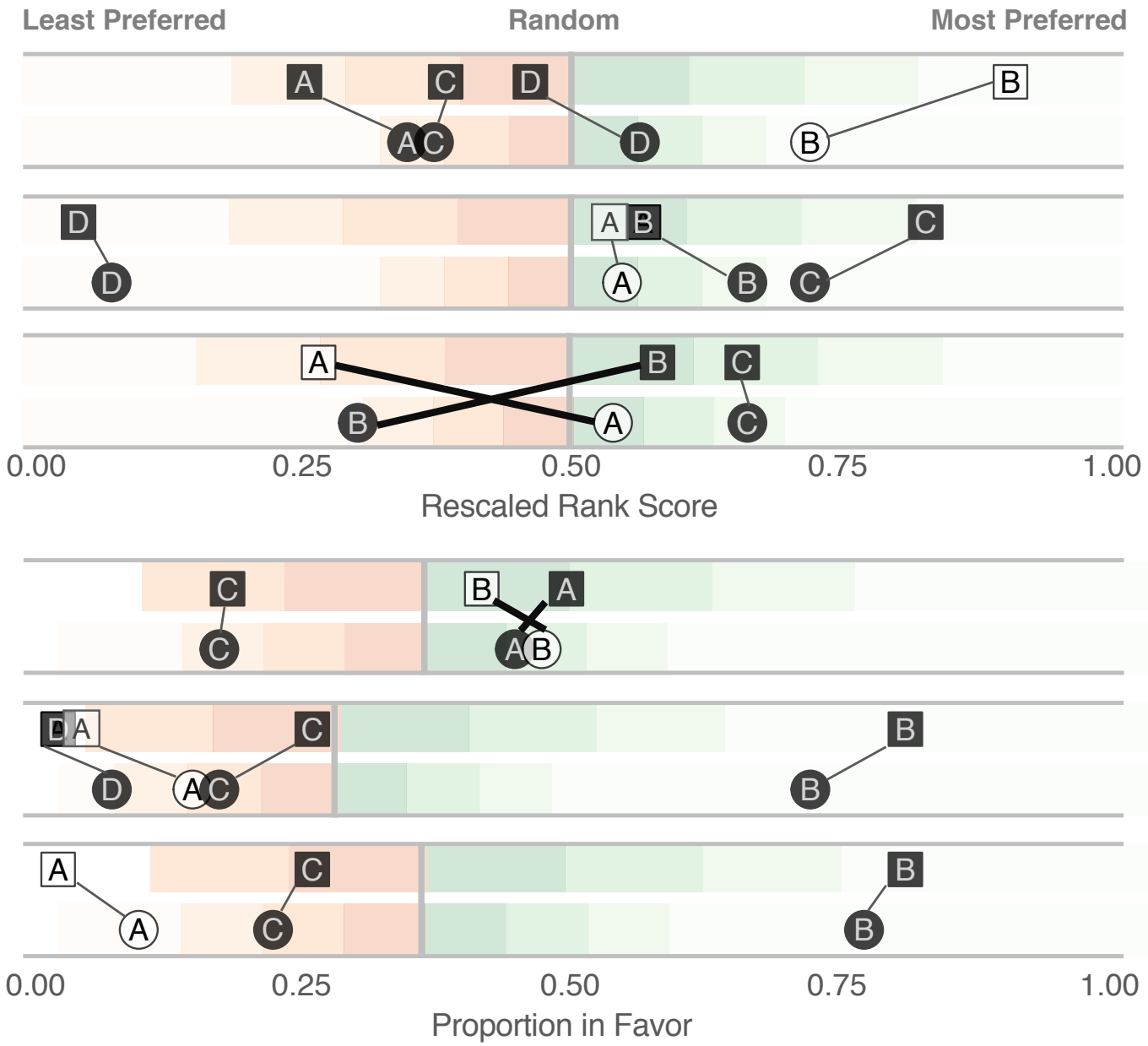
[Q14] Wording - Relatedness
Preferred: C (Cluster Detection)

Multiple Choice Questions

[Q7] Wording - Speciation Results
Preferred: A (Full Sentence)

[Q9] Abbreviation - Drug Names
Preferred: B (Full Name)

[Q10] Abbreviation - Resistance
Preferred: B (Full Name)



LEGEND

Public Health Role

Clinician

Non-clinician

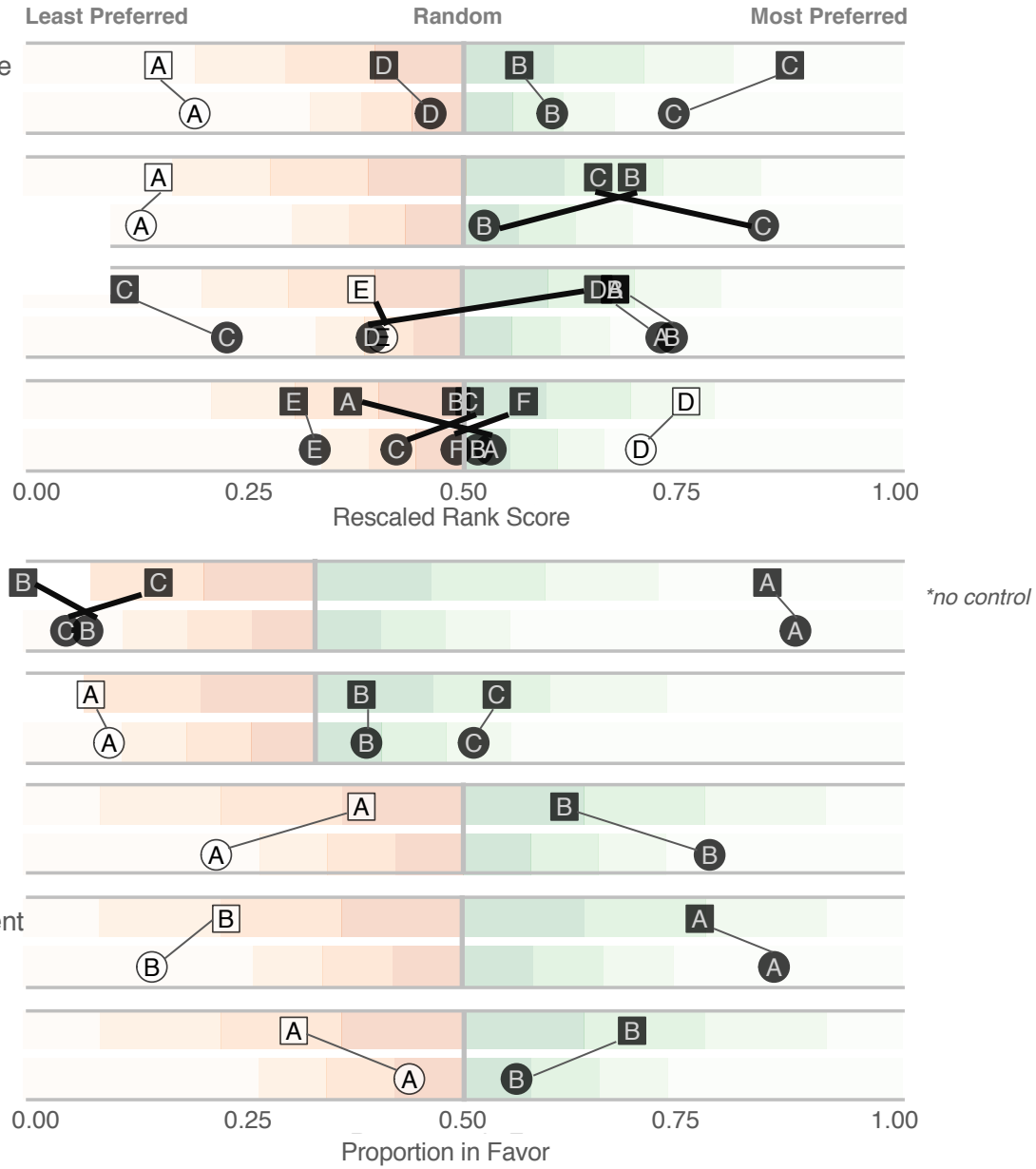
Design Option

Control

Alternative

A, B,.. *Option Indicator*

Results: Information & Visualization Design Preferences



*no control

LEGEND

Public Health Role

- *Clinician*
- *Non-clinician*

Design Option

- *Control*
- *Alternative*
- *A, B,..* *Option Indicator*

Some Helpful Tips on Running these Studies

1. Design around tasks
2. Compared components & whole designs
3. Compare against a control

Some Helpful Tips on using Design Techniques

1. Structure data according to a workflow narrative
2. Use emphasis carefully
3. Use words precisely
4. Use images judiciously
5. Information density OK, with caution