

Showcasing design study methodology through simpler design challenges: An application to a microbial genomics clinical report design

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Challenge

- ### Introducing infovis to domain specialists
- Needed: simple vehicle to convey infovis methods to specialists in other domains
 - Solution: use less complex design problem, like a static report

- ### Application & collaboration context
- Collaborate with COMPASS-TB project team to redesign a clinical report for tuberculosis (TB) whole genome sequencing (WGS)
 - Show a design study methodology in action

Discovery

Expert Consults

Experts

Tuberculosis clinicians, nurses, epidemiologists, and researchers

- ### Expert consult themes
- Procedural considerations
 - Current issue: multiple documents with different results
 - Limited time to read content

"10 seconds [to review content] is likely, one minute is luxurious"
 - Design considerations
 - Emphasize: clinically actionable results

"my patient's isolate is 6 SNPs from someone diagnosed 3 years ago. What is the clinical action?"
 - Design Constraints
 - Limit to available data
 - Conform to ISO15189:2012 requirements
 - No interactivity, no colour (must be deliverable by PDF, Fax,)

Relationship between data and tasks

Limited consensus of data used for surveillance tasks

	DIAGNOSIS TASKS				TREATMENT TASKS			SURVEILLANCE TASKS				TOTAL SCORE	
	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
WGS equivalent													
Patient Identifier	Same	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	24
Patient Prior TB Results	Same	3	2	3	3	3	3	3	1	1	1	0	23
Speciation	Speciation	1	3	2	3	3	3	3	2	1	1	1	23
Sample Type (sputum, fine needle aspirate etc.)	Same	2	3	2	3	3	3	3	1	1	1	0	22
Culture results	NA	1	3	2	3	3	3	3	2	1	1	0	22
Sample Collection Site (lymph node, blood draw etc.)	Same	2	3	2	3	3	3	3	1	1	0	0	21
Acid Fast Bacilli Smear	Speciation	2	3	2	3	2	3	3	1	1	1	0	21
Resistotype	Predicted DST	0	2	3	3	3	3	2	2	1	1	1	19
Phenotype DST	Predicted DST	0	2	3	2	3	3	2	1	1	1	0	18
Chest x-ray	NA	3	3	2	3	0	2	3	1	0	0	0	17
Report Release Date	Same	2	2	1	2	2	2	2	1	0	1	0	15
Requester IDs	Same	2	2	2	2	2	2	2	1	0	0	0	15
Interpretation or comments from reviewer	Same	2	2	1	2	2	2	3	1	0	0	0	15
Predicted DST	Predicted DST	0	2	2	1	3	3	2	1	0	1	0	15
MIRU-VNTR	SNPs	0	2	3	1	1	1	1	1	1	1	1	13
Cluster Assignment	Same	0	2	2	1	1	1	0	1	1	1	1	11
SNP/variant distance	SNPs	0	1	2	1	1	1	0	1	1	1	1	10
Phylogenetic Tree	Same	0	2	1	1	1	1	0	1	0	1	1	9
Reviewer ID	Same	1	1	1	1	1	1	1	1	0	0	0	8
TST results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	7
IGRA results	Speciation*	3	1	1	1	0	0	0	1	0	0	0	7
Lab QC	WGS Specific	0	1	2	1	1	1	0	1	0	0	0	7
Spoligotype	SNPs	0	1	1	1	0	0	0	0	0	0	0	3
RFLP	SNPs	0	1	1	1	0	0	0	0	0	0	0	3

Degree of Consensus: High Some Low Very low

Task and Data Questionnaire

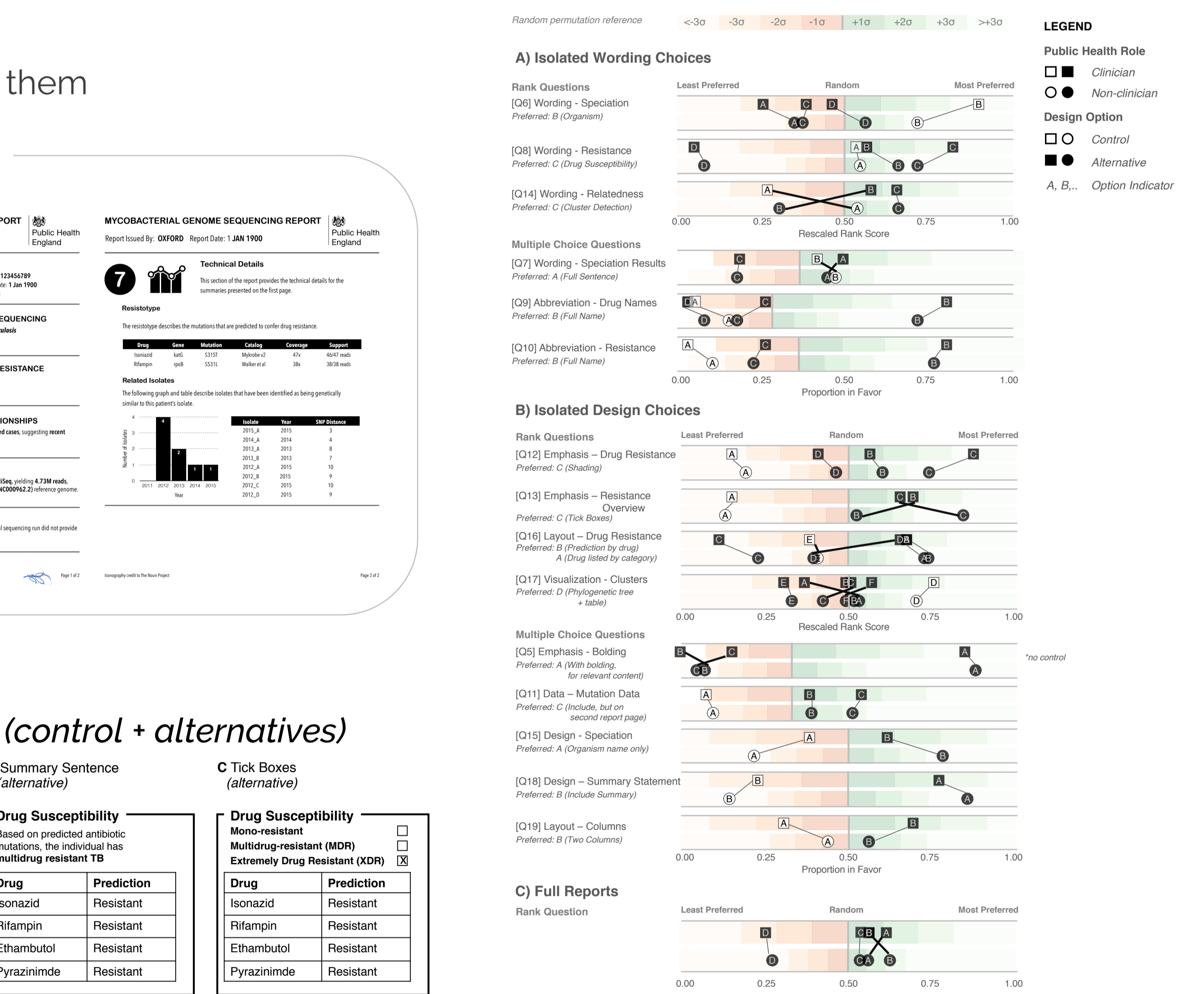
Design sprint outcomes

- 1) Example of whole reports
- Four alternative options generated, below are two of them

Option A

Option D

Participant design preferences



- 2) Example of isolated components

Original report element

Drug	Prediction
Isoniazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimide	Resistant

Tested elements (control + alternatives)

A Current COMPASS-TB Report (control)

Drug	Prediction
Isoniazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimide	Resistant

B Summary Sentence (alternative)

Based on predicted antibiotic resistances, the individual has multidrug resistant TB

Drug	Prediction
Isoniazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimide	Resistant

C Tick Boxes (alternative)

Drug	Prediction
Isoniazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimide	Resistant

Tested wording, abbreviations, adding a summary (right), and grouping drugs

Implement

Original Report

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: 01/01/19150115

Local Lims Specimen ID: 123456789 Run date: 01/01/19150115

Guid: 123456789ab-910abr-15243hg

Executive summary wanted

Organism Identification

Predicted/closest match: 100%

TBCOMP: 96.77% Only show top match

TBCOMP/TB: 35.71%

TBCOMP/tuberculosis-canetti: 21.21%

MACCCOMP: 21.21%

Sample/Sequencing Quality

Total reads: 4.73 Mapped %: 99.47 No reads mapped: 4.7 Confusing data

Resistance Summary

Drug	Prediction
Isoniazid	Resistant
Rifampin	Resistant
Ethambutol	Resistant
Pyrazinimide	Resistant

"Drug Susceptibility" preferred title

Relatedness

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

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

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

Redesigned Report

MYCOBACTERIUM TUBERCULOSIS WHOLE GENOME SEQUENCING REPORT NOT FOR DIAGNOSTIC USE

Patient Name: DOUGLAS JONES Patient ID: 12345678910

Birth Date: 1800-01-01 Location: OXFORD

Sample Type: SPUTUM Sample Date: 1916-12-25

Reporting Lab: OXFORD Report Date: 1917-01-01

Summary

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

Organism

The specimen was positive for Mycobacterium tuberculosis

Drug Susceptibility

Drug class	Prediction	Drug	Resistance Gene (known/acid fastness)
Sensitive		Ethambutol	No resistance mutation detected
		Pyrazinimide	No resistance mutation detected
		Isoniazid	katG (S315T)
Resistant		Rifampin	rpoB (S531L)
		Streptomycin	No resistance mutation detected
Second Line: Sensitive		Ciprofloxacin	No resistance mutation detected
		Ofloxacin	No resistance mutation detected
		Moxifloxacin	No resistance mutation detected
		Amikacin	No resistance mutation detected
		Kanamycin	No resistance mutation detected
		Capreomycin	No resistance mutation detected

Cluster Detection

Current specimen was found to be closely clustered with previous specimens suggesting recent transmission

Relatedness: Likely Related (< 5 SNPs apart) 2 isolates

Possibly Related (6 to 30 SNPs apart) 6 isolates

More details

Reflection

- ### Experimental Guidelines
1. Design around tasks
 2. Compare components not just whole designs
 3. Compared against a control

- ### Design Guidelines
1. Exploit visual hierarchy
 2. Use emphasis carefully
 3. Use words precisely
 4. Use images judiciously
 5. Information density OK, with caution