

Supporting Information

Supplementary material

This appendix was part of the submitted manuscript and has been peer reviewed. It is posted as supplied by the authors.

Appendix to: Skinner T, Brown A, Teixeira-Pinto A, et al. Sensitivity and specificity of Aboriginal-developed items to supplement the adapted PHQ-9 screening measure for depression: results from the Getting it Right study. *Med J Aust* 2024; doi: 10.5694/mja2.52406.

Appendix 1

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Table 1. STARD 2015 Checklist

Section & topic	No	Item	Reported on page no.
TITLE OR ABSTRACT			
	1	Identification as a study of diagnostic accuracy using at least one measure of accuracy (such as sensitivity, specificity, predictive values, or AUC)	Sensitivity and Specificity in Title
ABSTRACT			
	2	Structured summary of study design, methods, results, and conclusions (for specific guidance, see STARD for Abstracts)	Abstract follows <i>MJA</i> requirements, contains, Objective, Design, Setting, Main Outcome Measure, Results, Conclusion
INTRODUCTION			
	3	Scientific and clinical background, including the intended use and clinical role of the index test	Pages 2 & 3
	4	Study objectives and hypotheses	Page 3
METHODS			
Study design	5	Whether data collection was planned before the index test and reference standard were performed (prospective study) or after (retrospective study)	Prospective Study, pages 3 & 4
Participants	6	Eligibility criteria	Page 4
	7	On what basis potentially eligible participants were identified (such as symptoms, results from previous tests, inclusion in registry)	Procedure page 4
	8	Where and when potentially eligible participants were identified (setting, location and dates)	Procedures page 4 & Appendix 2
	9	Whether participants formed a consecutive, random or convenience series	Consecutive page 4
Test methods	10a	Index test, in sufficient detail to allow replication	Questionnaire, described in Introduction, page 2, Results Table 1 and in previous papers
	10b	Reference standard, in sufficient detail to allow replication	MINI page 4

	11	Rationale for choosing the reference standard (if alternatives exist)	Procedures page 4	
12a			Statistical Method pag 5, Results pages 5 and 6 and Table 2	
	12b	Definition of and rationale for test positivity cut-offs or result categories of the reference standard, distinguishing pre-specified from exploratory	Statistical Method page 5, Results pages 5 and 6 and Table 2	
	13 a	Whether clinical information and reference standard results were available to the performers/readers of the index test	Not Available, Procedures page 4	
	13b	Whether clinical information and index test results were available to the assessors of the reference standard	Not Available, Procedures page 4	
Analysis	14	Methods for estimating or comparing measures of diagnostic accuracy	Statistical Method page 5	
	15	How indeterminate index test or reference standard results were handled	N/A	
	16	How missing data on the index test and reference standard were handled	Statistical Method page 5	
	17	Any analyses of variability in diagnostic accuracy, distinguishing pre-specified from exploratory	N/A	
	18	Intended sample size and how it was determined	This is reported in the protocol and baseline papers	
RESULTS			* A A	
Participants	19	Flow of participants, using a diagram	Flow Diagram published in main paper	
	20	Baseline demographic and clinical characteristics of participants	Appendix 1, and main paper	
	21a	Distribution of severity of disease in those with the target condition	Results page 5 and 6	
	21b	Distribution of alternative diagnoses in those without the target condition	Results page 5 and 6	
	22	Time interval and any clinical interventions between index test and reference standard	Time interval specified in Procedures page 4 No Clinical Interventions	
Test results	23	Cross tabulation of the index test results (or their distribution) by the results of the reference standard	Results Table 2	

	24	Estimates of diagnostic accuracy and their precision (such as 95% confidence intervals)	Results, Table 2
	25	Any adverse events from performing the index test or the reference standard	None
DISCUSSION			
	26	Study limitations, including sources of potential bias, statistical uncertainty, and generalisability	Pages 7 and 8
	27	Implications for practice, including the intended use and clinical role of the index test	Pages 7 and 8
OTHER INFORMATION			
	28	Registration number and name of registry	Ethics details page 3
	29	Where the full study protocol can be accessed	Reference 10
	30	Sources of funding and other support; role of funders	Acknowledgements

Table 2. Demographic characteristics of participants (n = 500) in the Getting it Right study*

	Total [†]	No major depressive episode [‡]	Major depressive episode [‡]	P
All participants		392 (78%)	108 (22%)	
Ethnicity				0.597
Aboriginal	485 (97%)	378 (79%)	107 (22%)	
Torres Strait Islander	10 (2%)	9 (90%)	1 (10%)	
Aboriginal and Torres Strait Islander	5 (1%)	5 (100%)	0	
Language used in the interview				0.079
English only	442 (89%)	339 (77%)	103 (23%)	
English and Aboriginal language	19 (4%)	17 (89%)	2 (11%)	
Aboriginal language only	33 (7%)	30 (91%)	3 (9%)	
Age, mean (SD)	43 (15)	44 (44)	42 (12)	0.258
Sex				0.828
Female	267 (53%)	208 (78%)	59 (22%)	
Male	233 (47%)	184 (79%)	49 (21%)	
Marital status				0.271
Never married	200 (40%)	155 (78%)	45 (22%)	
Married or de facto relationship	186 (37%)	150 (81%)	36 (19%)	
Widowed	29 (6%)	26 (90%)	3 (10%)	
Separated but not divorced	53 (11%)	39 (74%)	13 (26%)	
Divorced	29 (6%)	20 (69%)	9 (31%)	
Live alone		, ,		0.899
No	379 (76%)	297 (78%)	82 (22%)	
Yes	118 (24%)	92 (78%)	26 (22%)	
Main income earner		, ,		0.653
No	196 (40%)	157 (80%)	39 (20%)	
Yes	300 (60%)	234 (78%)	66 (22%)	
Anyone close died in the past 2 months				0.170
No	328 (66%)	263 (80%)	65 (20%)	
Yes	170 (34%)	127 (75%)	43 (25%)	
Significant illness that restricted daily		-		0.001
activities in the past 2 months				
No	391 (79%)	319 (82%)	72 (18%)	
Yes	105 (21%)	69 (66%)	36 (34%)	
Chronic disease§				0.034
No	153 (31%)	129 (84%)	24 (16%)	
Yes	347 (69%)	263 (76%)	84 (24%)	

^{*} Data are n (%) unless otherwise indicated. † The proportions in the total column are computed over the valid cases. ‡ Major depressive episode using the MINI International Neuropsychiatric Interview (MINI) 6.0.0 major depressive episode module. § One or more of the following: heart disease, stroke, cancer, diabetes, arthritis, asthma, respiratory disease, chronic kidney disease, obstructive sleep apnoea, high blood pressure.

Appendix 2

Statistical information for decision tree analysis

The Classification and Regression (C&R) Tree node generates a decision tree that allows you to predict or classify future observations. The method uses recursive partitioning to split the training records into segments by minimising the impurity at each step, where a node in the tree is considered "pure" if 100% of cases in the node fall into a specific category of the target field. Target and input fields can be numeric ranges or categorical (nominal, ordinal, or flags); all splits are binary (only two subgroups).

The CHAID node generates decision trees using chi-square statistics to identify optimal splits. Unlike the C&R Tree and QUEST nodes, CHAID can generate non-binary trees, meaning that some splits have more than two branches. Target and input fields can be numeric ranges (continuous) or categorical. Exhaustive CHAID is a modification of CHAID that does a more thorough job of examining all possible splits but takes longer to compute.

The QUEST node provides a binary classification method for building decision trees, designed to reduce the processing time required for large C&R Tree analyses while also reducing the tendency found in classification tree methods to favour inputs that allow more splits. Input fields can be numeric ranges (continuous), but the target field must be categorical. All splits are binary.

The growth limits for the model were specified automatically, with the maximum number of levels of three for CHAID based analyses and five for C&R Tree and QUEST. The minimum number of cases for parent nodes was 100 and for child nodes 50. For C&R Tree, splits are found by maximising the homogeneity of child nodes with respect to the value of the target variable. No tree pruning was specified, and the number of surrogates was one fewer than the number of independent variables. With QUEST, the significance level for the splitting of nodes was 0.05.

In CHAID analyses, the significance level for the splitting of nodes was 0.05 and for the merging of categories 0.05. Model estimation was undertaken with a maximum of 100 iterations, with minimum change in expected cell frequencies 0.001. The significance values were adjusted by Bonferroni method, with re-splitting of merged categories within a node.