Stat Project

Arka

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Contents

Chapter 1

Abstract of the Data paper

The novel coronavirus disease 2019 (COVID-19) continues its rampage. Hence, there is been an effort to mitigate this virus and its effects with several means including vaccination which is one of the most effective ways of controlling the virus. However, efforts at getting people to vaccinate have met several challenges. To help with understanding the reasons underlying an individual's willingness to take COVID-19 vaccine or not, a scale called Motors of COVID- 19 Vaccination Acceptance Scale (MoVac-COVID19S) was developed.

To expand its usability worldwide (as it has currently been limited to only China and Taiwan), data were collected in other countries (regions) too. Therefore, this MoVac-COVID19S data is from five countries (that is, India, Ghana, Afghanistan, Taiwan, and mainland China) which cut across five regions. A total of 6053 participants across the stated countries completed the survey between January and March 2021 using a cross-sectional survey design. The different sections of the survey solicited sociodemographic information (e.g., country, age, gender, educational level, and profession) and the MoVac-COVID19S data from the participants.

Chapter 2

Utility of the Data

This data is useful as it comprises data from a largescale survey across five regions/countries worldwide on COVID-19 vaccination acceptance. Hence, the data can always be used to verify the psychometric properties of the MoVac-COVID19S (COVID-19 vaccination acceptance scale; also named as DrVac-COVID19S) and its suitability for use worldwide.

The data can be beneficial to the following group of persons: Researchers who are interested in communicable disease, psychometrics, health promotion, health psychology, public health, epidemiology, and health behavior as the findings from this dataset will serve as the basis for assessing citizens' willingness to take COVID-19 vaccination.

The data may be useful for researchers who want to replicate or extend the psychometric properties (especially, measurement invariance) of the MoVac-COVID19S by adding their country's data to this data.

Chapter 3

Data Description

The Motors of COVID-19 Vaccination Acceptance Scale (MoVac-COVID19S; also named as Drivers of COVID-19 Vaccination Acceptance Scale [DrVac-COVID19S]) was, therefore, developed to help with understanding the reasons underlying an individual's willingness to take COVID-19 vaccine or not.

A total of 6053 participants across the above- stated countries completed the survey between January and March 2021 using a cross-sectional survey design. The sections of the survey solicited sociodemographic information (e.g., country, age, gender, educational level, and profession) and the MoVac-COVID19S data from the participants.

For the demographic characteristics, the codes used were 0 and 1 for gender (females and males respectively), 1, 2, and 3 for educational levels (oth- ers, undergraduate, and postgraduate respectively), and 0 and 1 for profession (not health related and health related respectively). For the MoVac-COVID19S, the codes 1, 2, 3, 4, 5, 6, 7 were used to represent Strongly Disagree, Disagree, Slightly Disagree, Neither Disagree nor Agree, Slightly Agree, Agree, and Strongly Agree respectively. For group (countries), 1, 2, 3, 4, and 5 were used as codes for Taiwan, mainland China, India, Ghana, and Afghanistan respectively.

Chapter 4

Responses of Sociodemographic variables

The following table demonstrates the distribution of responses in relation to sociodemographic variables, from the data collected :–

Socio-demographics	Taiwan (n=932; 15.4%)	China (n=3145; 52%)	India (n=508; 8.4%)	Ghana (n=1244; 20.6%)	Afghanistan (n=224; 3.7%)	Total (n=6053; 100%)
Age; Mean±SD	25.39±6.46	20.84±2.67	24.46±7.34	20.34±1.75	26.82±4.76	22.00±4.56
<30 years	805 (14.1%)	2935 (51.3%)	385 (6.7%)	1132 (19.8%)	168 (2.9%)	5425 (94.7%)
≥30 years	125 (2.2%)	45 (0.8%)	83 (1.4%)	1 (0%)	47 (0.8%)	301 (5.3%)
Gender						
Male	354 (5.9%)	1567 (26.2%)	176 (2.9%)	789 (13.2%)	144 (2.4%)	3030 (50.6%)
Female	578 (9.7%)	1578 (26.4%)	328 (5.5%)	393 (6.6%)	80 (1.3%)	2957 (49.4%)
Educational Level						
Others	0 (0%)	31 (0.5%)	67 (1.2%)	147 (2.6%)	NA	245 (4.3%)
Undergraduate	595 (10.3%)	3026 (52.6%)	215 (3.7%)	988 (17.2%)	NA	4824 (83.9%)
Postgraduate	337 (5.9%)	88 (1.5%)	226 (3.9%)	32 (0.6%)	NA	683 (11.9%)
Profession						
Not Health related	468 (7.9%)	2904 (49.1%)	432 (7.3%)	1043 (17.6%)	0 (0%)	4847 (82.0%)
Health related	403 (6.8%)	241 (4.1%)	76 (1.3%)	121 (2.%)	224 (3.8%)	1065 (18.0%)

Chapter 5

Questionnaire

The items of the questionnaire, along with the frequency of responses, are summarized in the table below :–

Items		Frequency	Percentages
1. Vaccination is a very effective way to protect me against the COVID-19.	Strongly Disagree	143	2.4
	Disagree	88	1.5
	Slightly disagree	249	4.1
	Neither disagree nor agree	826	13.6
	Slightly agree	1291	21.3
	Agree	1753	29.0
	Strongly Agree	1703	28.1
2. I know very well how vaccination protects me from the COVID-19.	Strongly Disagree	182	3.0
	Disagree	132	2.2
	Slightly disagree	303	5.0
	Neither disagree nor agree	890	14.7
	Slightly agree	1313	21.7
	Agree	1538	25.4
	Strongly Agree	1695	28.0
3. It is important that I get the COVID-19 jab.	Strongly Disagree	190	3.1
	Disagree	110	1.8
	Slightly disagree	210	3.5
	Neither disagree nor agree	899	14.9
	Slightly agree	1018	16.8
	Agree	1613	26.6
	Strongly Agree	2013	33.3

4. Vaccination greatly reduces my risk of catching COVID-19.	Strongly Disagree	186	3.1
	Disagree	93	1.5
	Slightly disagree	216	3.6
	Neither disagree nor agree	769	12.7
	Slightly agree	1117	18.5
	Agree	1742	28.8
	Strongly Agree	1930	31.9
5. I understand how the COVID-19 jab helps my body fight the COVID-19 virus.	Strongly Disagree	190	3.1
	Disagree	154	2.5
	Slightly disagree	303	5.0
	Neither disagree nor agree	940	15.5
	Slightly agree	1273	21.0
	Agree	1557	25.7
	Strongly Agree	1636	27.0
6. The COVID-19 jab plays an important role in protecting my life and that of others.	Strongly Disagree	157	2.6
	Disagree	98	1.6
	Slightly disagree	188	3.1
	Neither disagree nor agree	773	12.8
	Slightly agree	1016	16.8
	Agree	1820	30.1
	Strongly Agree	2001	33.1
7. I feel under pressure to get the COVID-19 jab.	Strongly Disagree	526	8.7
	Disagree	333	5.5
	Slightly disagree	506	8.4
	Neither disagree nor agree	1331	22.0
	Slightly agree	1322	21.8
	Agree	1048	17.3
	Strongly Agree	987	16.3
8. The contribution of the COVID-19 jab to my health and well-being is very important.	Strongly Disagree	165	2.7
	Disagree	88	1.5
	Slightly disagree	175	2.9
	Neither disagree nor agree	898	14.8
	Slightly agree	1110	18.3
	Agree	1761	29.1
	Strongly Agree	1856	30.7

Items		Frequency	Percentages
9. I can choose whether to get a COVID-19 jab or not.	Strongly Disagree	201	3.3
	Disagree	101	1.7
	Slightly disagree	158	2.6
	Neither disagree nor agree	891	14.7
	Slightly agree	973	16.1
	Agree	1662	27.5
	Strongly Agree	2067	34.1
10. How the COVID-19 jab works to protect my health is a mystery to me.	Strongly Disagree	503	8.3
	Disagree	414	6.8
	Slightly disagree	482	8.0
	Neither disagree nor agree	1204	19.9
	Slightly agree	1306	21.6
	Agree	1041	17.2
	Strongly Agree	1103	18.2
11. I get the COVID-19 jab only because I am required to do so.	Strongly Disagree	590	9.7
	Disagree	481	7.9
	Slightly disagree	657	10.9
	Neither disagree nor agree	1389	22.9
	Slightly agree	1117	18.5
	Agree	847	14.0
	Strongly Agree	972	16.1
12. Getting the COVID-19 jab has a positive influence on my health.	Strongly Disagree	222	3.7
	Disagree	130	2.1
	Slightly disagree	254	4.2
	Neither disagree nor agree	1336	22.1
	Slightly agree	1289	21.3
	Agree	1415	23.4
	Strongly Agree	1407	23.2

Chapter 6

Cross-Sectional Survey Design

Cross-sectional study design is a type of observational study design. As discussed in the earlier articles, we have highlighted that in an observational study, the investigator does not alter the exposure status. The investigator measures the outcome and the exposure(s) in the population, and may study their association.

In a cross-sectional study, the investigator measures the outcome and the exposures in the study participants at the same time. Unlike in case - control studies (participants selected based on the outcome status) or cohort studies (participants selected based on the exposure status), the participants in a cross-sectional study are just selected based on the inclusion and exclusion criteria set for the study. Once the participants have been selected for the study, the investigator follows the study to assess the exposure and the outcomes.

Suppose we are interested to know the prevalence of vitiligo in a village. We design a population-based survey to assess the prevalence of this condition. We go to all the houses that were supposed to be included in the study and examine the population. The total sample surveyed is 5686. Of these, we found that 98 individuals have vitiligo. Thus, the prevalence of vitiligo in this community is:

$$Prevalence = \frac{98}{5686} = \frac{17.23}{1000} population$$

This is an example of a cross sectional study used for population – based survey.

Advantages of cross – sectional study :
Cross-sectional studies can usually be conducted relatively faster and are inexpensive These study designs may be useful for public health planning, monitoring, and evaluation.

Chapter 7

Snowball Sampling

In sociology and statistics research, snowball sampling (or chain sampling, chain-referral sampling, referral sampling) is a non – probability technique where existing study subjects recruit future subjects from among their acquaintances. Thus the sample group is said to grow like a rolling snowball. As the sample builds up, enough data are gathered to be useful for research. This sampling technique is often used in hidden populations (such as drug users), which are difficult for researchers to access.

As sample members are not selected from a sampling frame, snowball samples are subject to numerous biases. For example, people who have many friends are more likely to be recruited into the sample. Advantages –

- Locating hidden populations – It is possible for the surveyors to include people in the survey that they would not have known but, through the use of social network.
- Methodology – As subjects are used to locate the hidden population, the researcher invests less money and time in sampling. Snowball sampling method does not require complex planning and the staffing required is considerably smaller in comparison to other sampling methods.

Disadvantages –

- Community bias – The first participants will have a strong impact on the sample. Snowball sampling is inexact and can produce varied and inaccurate results. The method is heavily reliant on the skill of the individual conducting the actual sampling, and that individual's ability to vertically network and find an appropriate sample.
- Unknown population sampling size – There is no way to know the total size of the overall population.

- Lack of control over sampling method – As the subjects locate the hidden population, the research has very little control over the sampling method, which becomes mainly dependent on the original and subsequent subjects, who may add to the known sampling pool using a method outside of the researcher's control.

Chapter 8

Psychometrics

Psychometrics is a scientific discipline concerned with the construction of assessment tools, measurement instruments, and formalized models that may serve to connect observable phenomena (e.g., responses to items in an IQ-test) to theoretical attributes (e.g., intelligence).

Psychometrics generally refers to specialized fields within psychology and education devoted to testing, measurement, assessment, and related activities.

Psychometrics is concerned with the objective measurement of latent constructs that cannot be directly observed, examples of which include intelligence, introversion, mental disorders and educational achievement.

The levels of individuals on non - observable latent variables are inferred through mathematical modelling based on what is observed from individuals' responses to items on tests and scales.

Chapter 9

Cognitive Model of Empowerment

Cognitive modeling is an area of computer science that deals with simulating human problem-solving and mental processing in a computerized model.

Such a model can be used to simulate or predict human behavior or performance on tasks similar to the ones modeled and improve human-computer interaction.

Empowerment can be thought of as "increased intrinsic task motivation". CME identifies four cognitions (task assessments) as the basis for worker empowerment: sense of impact, competence, meaningfulness, and choice. Adopting an interpretive perspective, we have used the model also to describe cognitive processes through which workers reach these conclusions.

Chapter 10

Measurement Invariance

Measurement invariance or measurement equivalence is an important property that identifies whether the score difference of an instrument (e.g., the DrVac-COVID19S in the present study) detects the true differences between subsamples or whether the differences are due to various interpretations of the item descriptions in the instrument.

It is a statistical property of measurement that indicates that the same construct is being measured across some specified groups. For example, measurement invariance can be used to study whether a given measure is interpreted in a conceptually similar manner by respondents representing different genders or cultural backgrounds. Violations of measurement invariance may preclude meaningful interpretation of measurement data.

Chapter 11

Levels of Measurement Invariance

1. Configural Invariance
   Configural invariance, also referred to as pattern invariance, means that the number of factors and pattern of loadings is the same for both groups. In other words, the specific items that load on each of the respective factors are the same for both groups.

2. Metric Invariance
   Metric invariance (also referred to as weak invariance), means that not only are the same items loading on the same factors for both groups, but the actual magnitude of the loadings are the same across groups for each respective item.

3. Scalar Invariance
   Scalar invariance (also referred to as strong invariance) imposes the same constraints as configural and metric invariance, but with the added constraint that the thresholds (τ) are equated across groups.

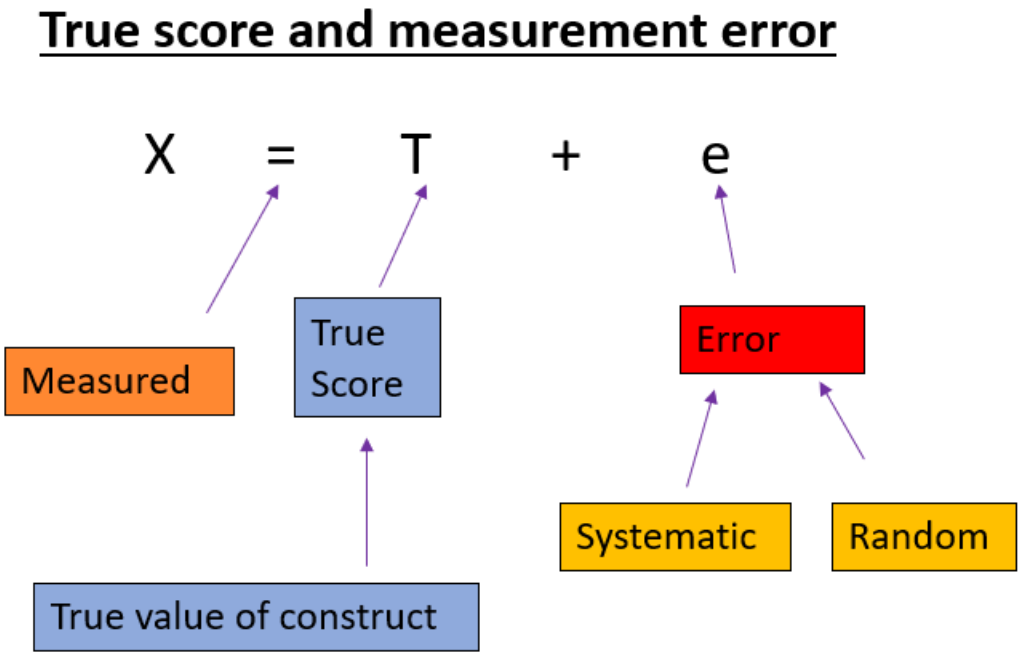
4. Residual Invariance
   Residual invariance means that the sum of specific variance (variance of the item that is not shared with the factor) and error variance (measurement error) is similar across groups.

Chapter 12

Structural Equation Modelling

Structural equation modeling (SEM) is a label for a diverse set of methods used by scientists in both experimental and observational research across the sciences, business, and other fields. It is used mostly in the social and behavioral sciences. SEM is not one statistical 'technique', rather, it integrates a number of different multivariate techniques into one model fitting framework. It is useful for research questions that –

- Involve complex, multifaceted constructs that are measured with error
- That specify systems of relationships rather than a dependent variable and a set of predictors (which is basically the theme of regression)
- Focus on indirect (mediated) as well as direct effects of variables on other variables



- Most social scientific concepts are not directly observable, e.g., intelligence, social capital etc.
- This makes them hypothetical or 'latent' constructs
- We can measure latent variables using observable indicators
- We can think of the variance of a questionnaire item as being caused by:
- The latent construct we want to measure
- Other factors (error/unique variance)
- It is the diagrammatic representation of a theoretical model using standardized notation.
- Regression equations specified between measured variables
- Effects of predictor variables on criterion / dependent variables can be:
- Direct
- Indirect
- Total

Chapter 13

Maximum Likelihood Estimation

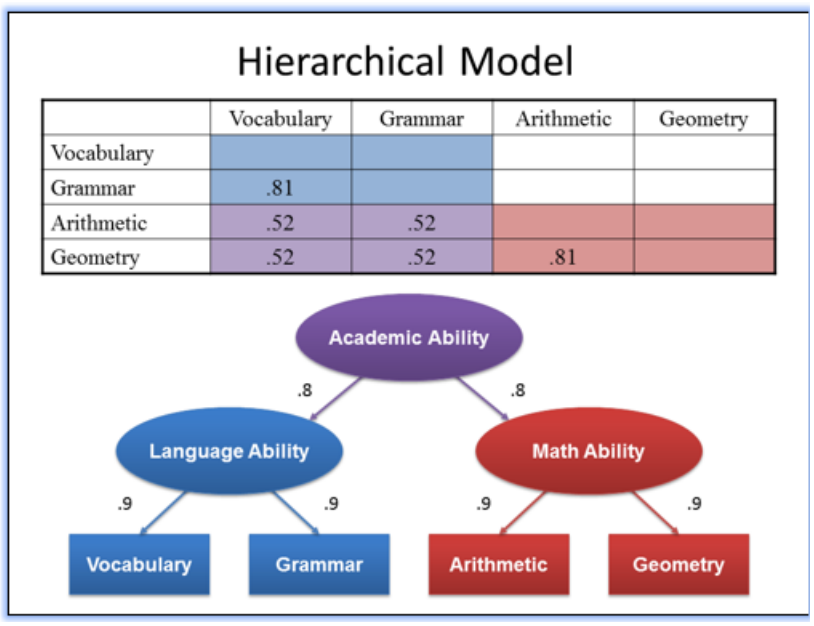
In statistics, maximum likelihood estimation (MLE) is a method of estimating the parameters of an assumed probability distribution, given some observed data. This is achieved by maximizing a likelihood function so that, under the assumed statistical model, the observed data is most probable.]The likelihood function (often simply called the likelihood) is the joint probability of the observed data viewed as a function of the parameters of a statistical model.
In statistics, maximum likelihood estimation (MLE) is a method of estimating the parameters of an assumed probability distribution, given some observed data. This is achieved by maximizing a likelihood function so that, under the assumed statistical model, the observed data is most probable.
The logic of maximum likelihood is both intuitive and flexible, and as such the method has become a dominant means of statistical inference.]The point in the parameter space that maximizes the likelihood function is called the maximum likelihood estimate.
The logic of maximum likelihood is both intuitive and flexible, and as such the method has become a dominant means of statistical inference.

Chapter 14

Factor Analysis

Factor analysis is a statistical method used to describe variability among observed, correlated variables in terms of a potentially lower number of unobserved variables called factors. For example, it is possible that variations in six observed variables mainly reflect the variations in two unobserved (underlying) variables Factor analysis searches for such joint variations in response to unobserved latent variables.

The observed variables are modelled as linear combinations of



Chapter 15

Exploratory Factor Analysis

EFA is a technique within factor analysis, whose overarching goal is to identify the underlying relationships between measured variables It is commonly used by researchers when developing a scale (questionnaire) and serves to identify a set of latent constructs underlying a battery of measured variables. It should be used when the researcher has no a priori hypothesis about factors or patterns of measured variables

Measured variables are any one of several attributes of people that may be observed and measured Examples of measured variables could be the physical height, weight, and pulse rate of a human being. Usually, researchers would have a large number of measured variables, which are assumed to be related to a smaller number of "unobserved" factors.

Chapter 16

Limitations of EFA

It is inductive and atheoretical, in the sense that we have the data dictating us what the theory should be, whereas we generally want to have it the other way around. It relies on a subjective judgement, and heuristic rules about what a large amount of variability to explain, and hence there is a lot of room for subjectivity in determining what our model should be.

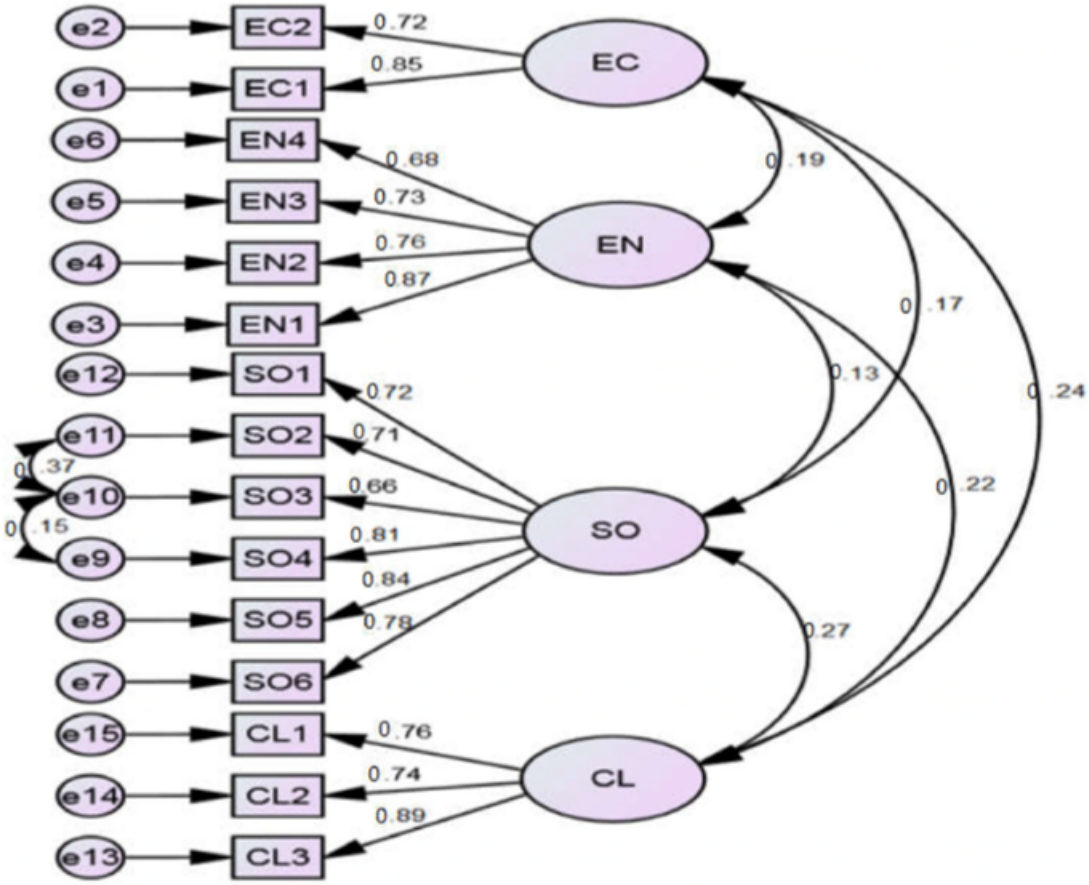
Chapter 17

Confirmatory Factor Analysis

It is a special form of factor analysis (also known as the restricted factor model), most commonly used in social science research. It is used to test whether measures of a construct are consistent with a researcher's understanding of the nature of that construct (or factor). As such, the objective of confirmatory factor analysis is to test whether the data fit a hypothesized measurement model. This hypothesized model is based on theory and/or previous analytic research.

The researcher first develops a hypothesis about what factors they believe are underlying the measures used, and may impose constraints on the model based on these a priori hypotheses. It gives us an idea of which indicators measure which factors in a construct, and which factors are unrelated to which ones. It also specifies which factors are correlated / uncorrelated amongst each other.

An Example of a Four factor, Fifteen Item CFA



Chapter 18

Fit Indices

An index of fit is a catch-all term for a variety of methods to tell us how well observed data fits a particular probability distribution. An index of fit is typically normalized (i.e. units of measurement are removed), and the values will usually be between 0 and 1. What these values mean depends on which index of fit you are using; but it tells us, numerically, how well the data matches a particular distribution.

They can be classified into two types as follows :

- Absolute Fit Indices – They are computed using formulas based on the discrepancies in a data set, as well as sample size. Absolute fit indices do not compare the model with a particular distribution; they use the data to generate a model. Specifically, the obtained and implied covariance matrices and the ML (Maximum Likelihood) minimization function.
- Relative Fit Indices – Also called the incremental fit, they include a factor that represents deviations from a null model, so these are sometimes called comparative indices. The null model, also called the baseline model, should always have a poor fit.

Chapter 19

Comparative Fit Index

Comparative fit index (CFI) analyzes the model fit by examining the discrepancy between the data and the proposed model while adjusting for the issues of sample size intrinsic in the chi-squared test, and the normed fit index. It is considered very good if it is equal to or greater than 0.95, good between 0.9 and 0.95, suffering between 0.8 and 0.9 and bad if it is less than 0.8. The computational formula is given as follows:

$$CFI = 1 - \frac{\max\left[X^2_{proposed\ model} - df_{proposed\ model}, 0\right]}{\max\left[X^2_{null\ model} - df_{null\ model}, 0\right]}$$

Chapter 20

Normed Fit Index

Normed fit index (NFI) is also called Bentler-Bonett Normed Fit Index. It analyzes the discrepancy between the chi-squared value of the proposed model and the chi-squared value of the null model. NFI tends to be negatively biased. It is considered very good if it is equal to or greater than 0.95, good between 0.9 and 0.95, suffering between 0.8 and 0.9 and bad if it is less than 0.8. The computational formula is given as follows:

$$NFI = 1 - \frac{X^2\ (proposed\ model)}{X^2\ (null\ model)}$$

Chapter 21

Root Mean Square Error of Approximation

Root Mean Square Error of Approximation (RMSEA) is a measure that attempts to correct the tendency of chi-square statistics to reject models with large samples. It avoids issues of sample size by analyzing the discrepancy between the proposed model, with optimally chosen parameter estimates, and the population covariance matrix. RMSEA is considered very good if it is equal to or less than 0.05, good between 0.05 and 0.08, mediocre between 0.08 and 0.10 and unacceptable if it is higher than 0.10

The computational formula is given as follows :-

$$RMSEA = \sqrt{max\left(\frac{X^2_{proposed\ model} - df_{proposed\ model}}{df_{proposed\ model} \times (N-1)}, 0\right)}$$

Where N is the sample size and *df* the degrees of freedom. Additionally, RMSEA provides a one-sided test with the following hypotheses:
H_0: the RMSEA equals 0.05 (what is called a close-fitting model)
H_1 : the RMSEA is higher than 0.05

Chapter 22

Tucker – Lewis Index

Tucker-Lewis index (TLI) is also known as a non-normed fit index (NNFI). It is a combination of a measure of parsimony with a comparative index between the proposed model and the null model. It is considered very good if it is equal to or greater than 0.95, good between 0.9 and 0.95, suffering between 0.8 and 0.9 and bad if it is less than 0.8. The computational formula is given as follows –

$$TLI = \frac{\frac{X^2_{null\ model}}{df_{null\ model}} - \frac{X^2_{proposed\ model}}{df_{proposed\ model}}}{\frac{X^2_{null\ model}}{df_{null\ model}} - 1}$$

Chapter 23

Standardized Root Mean Squared Residual

The SRMR is defined as the difference between the observed correlation and the model implied correlation matrix. Thus, it allows assessing the average magnitude of the discrepancies between observed and expected correlations as an absolute measure of (model) fit criterion. A value less than 0.10 or of 0.08 are considered a good fit.

$$\widehat{\mathrm{SRMSR}} = \sqrt{\frac{1}{t}\sum_{i\leq j}\widehat{\varepsilon}_{ij}^{2}} = \sqrt{\frac{1}{t}\widehat{\varepsilon}'\widehat{\varepsilon}},$$

where the standardized residual variances and covariances are

$$\widehat{\varepsilon}_{ij} = \frac{s_{ij} - \widehat{\sigma}_{ij}}{\sqrt{s_{ii}s_{jj}}}$$

Chapter 24

Summary of reference values

The following table gives a summary of reference values for the adjustment indices

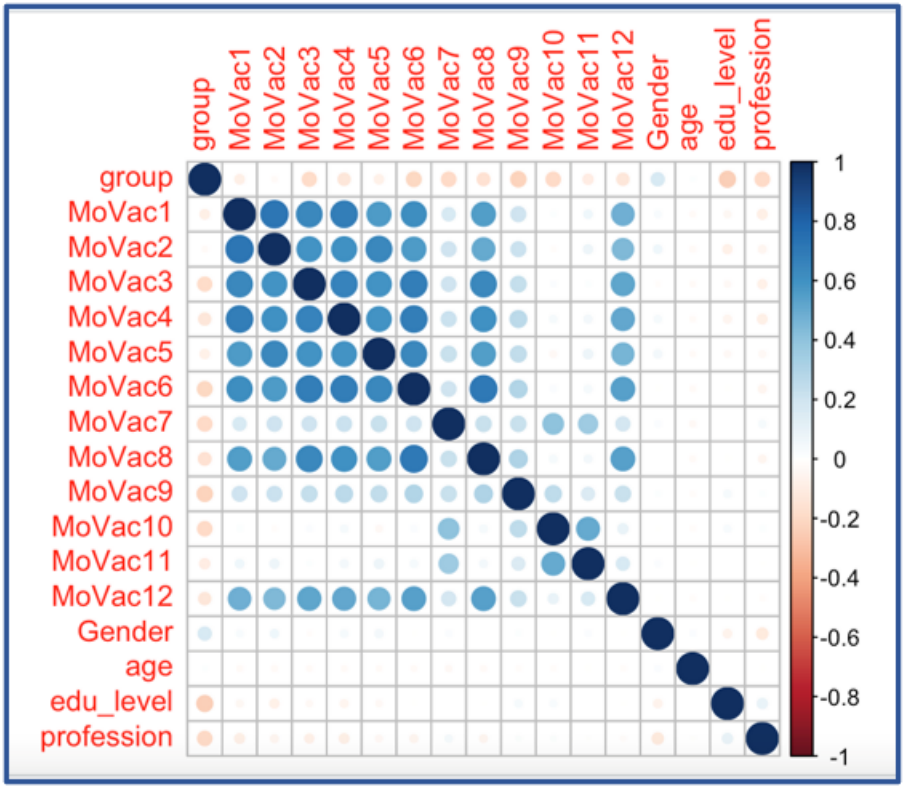
	Very Good	Good	Suffering	Bad
X^2/df	≤ 1	]1,2]	]2,5]	> 5
NFI	≥ 0.95	[0.9; 0.95[	[0.8; 0.9[	< 0.8
CFI	≥ 0.95	[0.9; 0.95[	[0.8; 0.9[	< 0.8
RFI	the better the closer to 1			
TLI	≥ 0.95	[0.9; 0.95[	[0.8; 0.9[	< 0.8
RMSEA ($p - value \geq 0.05$)	≤ 0.05	]0.05, 0.08]	]0.08,0.10]	> 0.10

Chapter 25

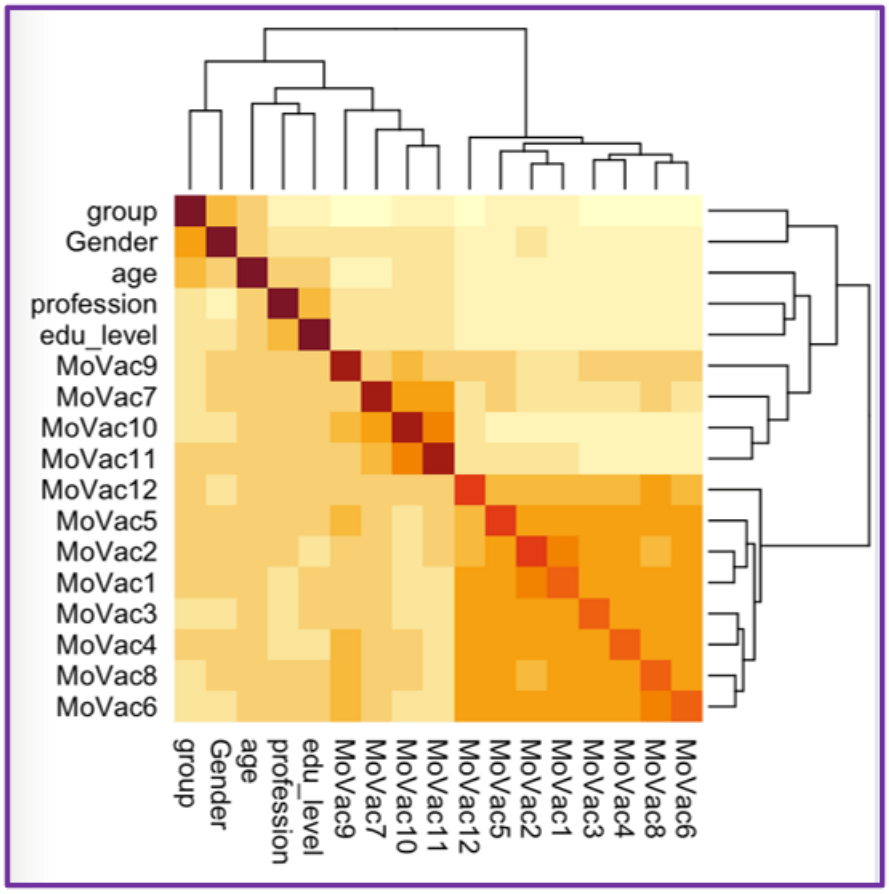
The four CFA models for the DrVac – COVID19S

In our project we have recreated the four CFA models described in the data paper, and drawn the necessary conclusions

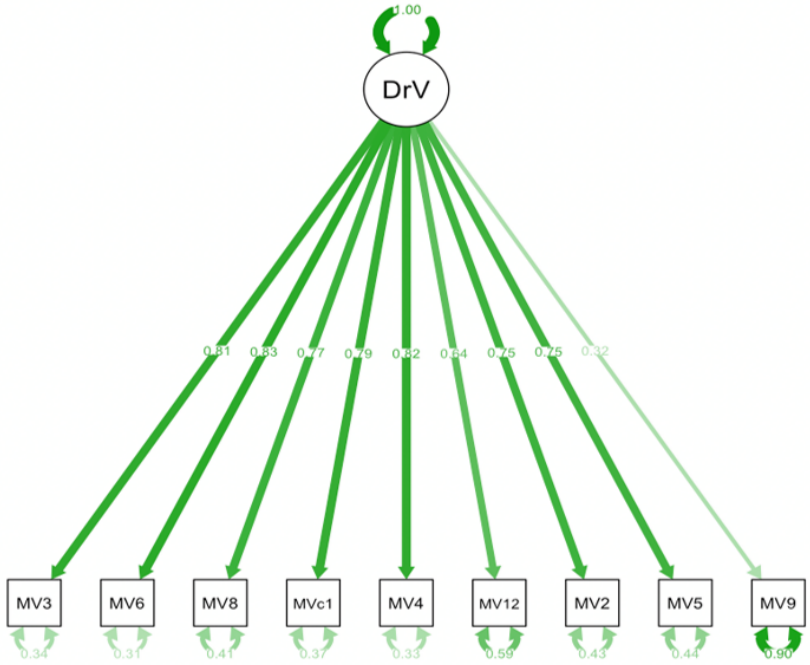
Correlation Plot



Heatmap

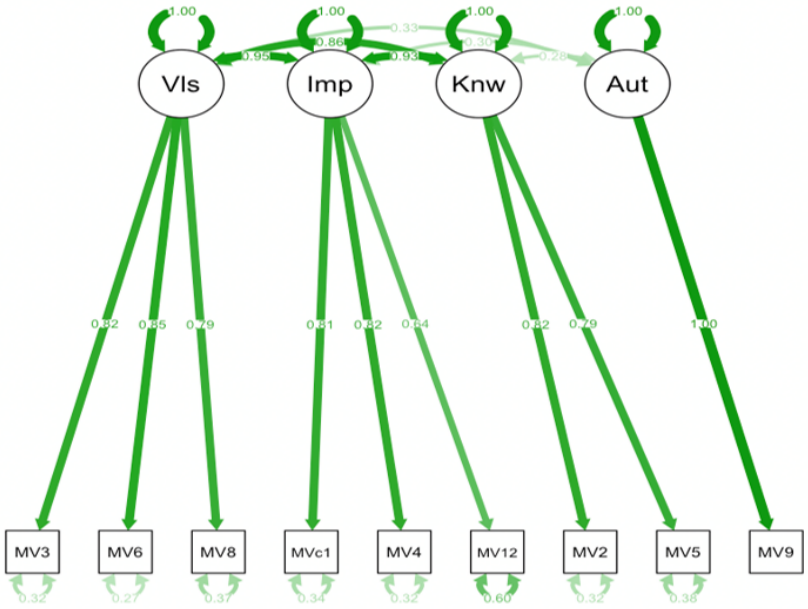

group
Gender
age
profession
edu_level
MoVac9
MoVac7
MoVac10
MoVac11
MoVac12
MoVac5
MoVac2
MoVac1
MoVac3
MoVac4
MoVac8
MoVac6

Model 1: One – trait factor model using 9 positively worded items



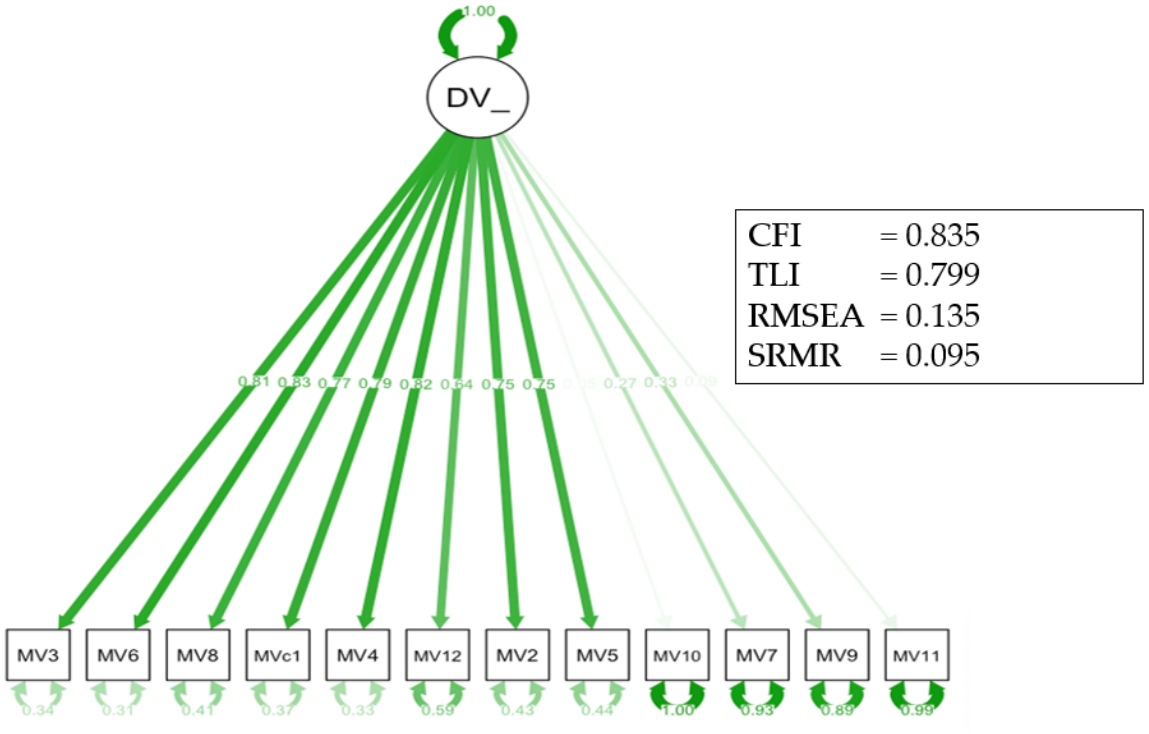
CFI	= 0.936
TLI	= 0.915
RMSEA	= 0.111
SRMR	= 0.037

Model 2: Four – trait factor model using 9 positively worded items

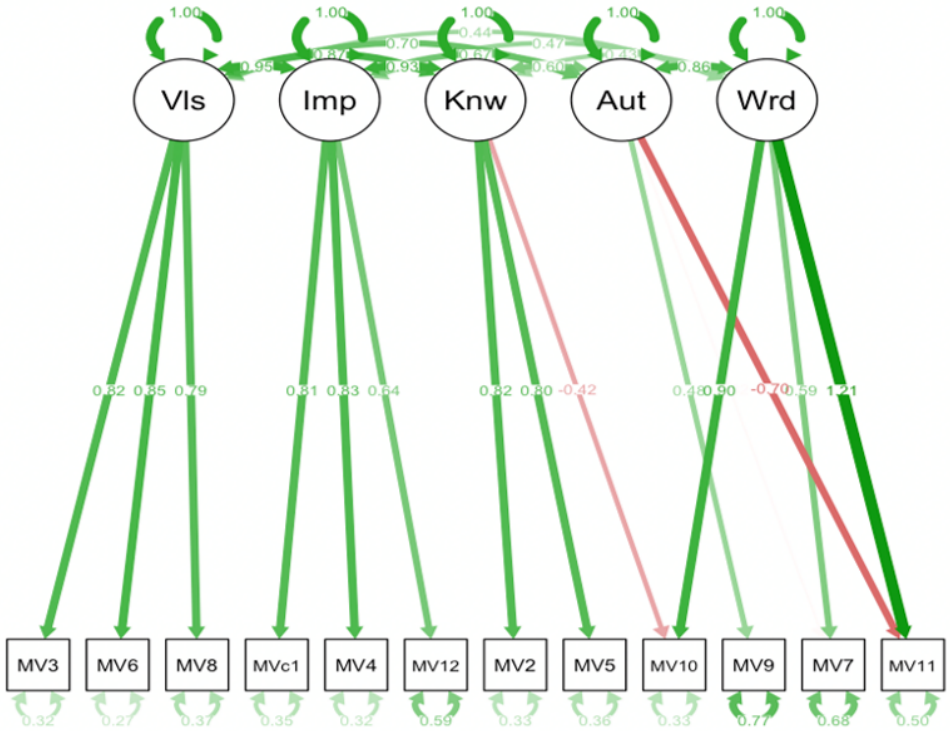


CFI	= 0.955
TLI	= 0.926
RMSEA	= 0.104
SRMR	= 0.032

Model 3: One-trait-factor and two-minus-one-method-factor model using all 12 items



Model 4: Four-trait-factor and two-minus-one-method-factor model using all 12 items



CFI	= 0.954
TLI	= 0.925
RMSEA	= 0.082
SRMR	= 0.029

Measurement Invariance (Taiwan vs. China)

Model (Subsamples)	Nine-Item DrVac-COVID19S		12-Item DrVac-COVID19S	
Fit Indices	**One-Factor**	**Four-Factor**	**One-Factor [a]**	**Four-Factor [a]**
		Configural (Taiwan vs. China)		
χ^2 (df)/p-value	482.57 (50)/<0.001	207.81(40)/<0.001	1171.60 (98)/<0.001	771.18 (86)/<0.001
CFI	**0.993**	**0.997**	**0.984**	**0.990**
RMSEA	**0.067**	**0.046**	**0.075**	**0.064**
SRMR	**0.026**	**0.021**	**0.042**	**0.039**
		Loading constrained (Taiwan vs. China)		
$\Delta\chi^2$ (df)/p-value	153.75 (8)/<0.001	32.55 (5)/<0.001	207.93 (13)/<0.001	182.24 (15)/<0.001
ΔCFI	**−0.002**	**0.000**	**−0.003**	**−0.002**
ΔRMSEA	**0.004**	**0.001**	**0.002**	**0.002**
ΔSRMR	**0.008**	**0.003**	**0.006**	**0.004**
		Loadings and intercepts constrained (Taiwan vs. China)		
$\Delta\chi^2$ (df)/p-value	198.23 (8)/<0.001	500.43 (5)/<0.001	252.63 (10)/<0.001	143.47 (7)/<0.001
ΔCFI	**−0.004**	−0.030	**−0.002**	**−0.002**
ΔRMSEA	**0.006**	0.037	**0.003**	**0.002**
ΔSRMR	**0.009**	**−0.008**	0.011	0.043

Measurement Invariance (Male vs Female)

	Configural (male vs. female)			
χ^2 (*df*)/*p*-value	466.72(50)/<0.001	201.80 (40)/<0.001	1152.51(98)/<0.001	806.23 (86)/<0.001
CFI	**0.994**	**0.997**	**0.986**	**0.991**
RMSEA	**0.065**	**0.046**	**0.074**	**0.066**
SRMR	**0.029**	**0.018**	**0.047**	**0.041**
	Loading constrained (male vs. female)			
$\Delta\chi^2$ (*df*)/*p*-value	55.59 (8)/<0.001	23.07 (5)/<0.001	117.06 (13)/<0.001	109.59 (15)/<0.001
ΔCFI	**−0.001**	**0.000**	**−0.001**	**−0.001**
ΔRMSEA	**−0.001**	**−0.001**	**−0.001**	**−0.002**
ΔSRMR	**0.007**	**0.003**	**0.026**	**0.027**
	Loadings and intercepts constrained (male vs. female)			
$\Delta\chi^2$ (*df*)/*p*-value	236.36 (8)/<0.001	186.10 (5)/<0.001	143.41 (10)/<0.001	63.20 (7)/<0.001
ΔCFI	−0.018	**−0.010**	**−0.003**	**−0.002**
ΔRMSEA	**0.009**	0.016	**0.001**	**0.000**
ΔSRMR	**−0.023**	**−0.015**	**−0.010**	**−0.021**

Measurement Invariance (Health vs Non – health)

	Configural (health vs. non-health)			
χ^2 (*df*)/*p*-value	476.22 (50)/<0.001	186.48 (40)/<0.001	1189.99 (98)/<0.001	803.93 (86)/<0.001
CFI	**0.994**	**0.998**	**0.985**	**0.990**
RMSEA	**0.066**	**0.043**	**0.076**	**0.065**
SRMR	**0.028**	**0.020**	**0.047**	**0.043**
	Loading constrained (health vs. non-health)			
$\Delta\chi^2$ (*df*)/*p*-value	60.75 (8)/<0.001	21.24 (5)/<0.001	97.28 (13)/<0.001	116.93 (15)/<0.001
ΔCFI	**−0.001**	**0.000**	**−0.001**	**−0.001**
ΔRMSEA	**−0.001**	**0.000**	**−0.002**	**−0.001**
ΔSRMR	**0.001**	**0.001**	**0.001**	**0.001**
	Loadings and intercepts constrained (health vs. non-health)			
$\Delta\chi^2$ (*df*)/*p*-value	105.16 (8)/<0.001	388.86 (5)/<0.001	165.84 (10)/<0.001	72.71 (7)/<0.001
ΔCFI	**−0.002**	**−0.026**	**−0.003**	**−0.001**
ΔRMSEA	**0.002**	0.032	**0.001**	**0.001**
ΔSRMR	**0.003**	**−0.013**	**0.005**	0.025