Analysis Report

This report is structured as follow.

Contents

Sample Characterization

The report starts with the characterization of the sample, which is consisted by 619 subjects (N = 619). The table below shows the sample characteristics. 66.1% of the sample is female.

		Count	Column N %
Race	American Indian	15	2.6%
	AAPI	73	12.7%
	Black	58	10.1%
	Hispanics	83	14.4%
	White	348	60.3%
Age	18-24	72	11.6%
	25-40	199	32.1%
	41-55	206	33.3%
	55-70	113	18.3%
	> 70	29	4.7%
Gender	Man	194	31.5%
	Non-binary or Transgender	15	2.4%
	Woman	407	66.1%

General Descriptive Statistics

The table below shows the mean scores, standard deviations, skewness and kurtosis of each scale under study.

Descriptive Statistics

	N	Mean	Std. Deviation	Skewness		Kurtosis	
	Statistic	Statistic	Statistic	Statistic	Std. Error	Statistic	Std. Error
TOTAL GMRI	619	105.44	12.189	-.311	.098	.793	.196
Total AAG	619	30.89	4.579	.090	.098	2.048	.196
TotalGQ6	619	33.83	6.348	-.529	.098	-.673	.196
TotalTGS	619	74.53	12.837	-.654	.098	.428	.196
TotNADA	619	37.27	11.463	.373	.098	-.273	.196
Valid N (listwise)	619						

Skewness and Kurtosis are almost all within the ±1.5 range, which indicates they are approximately normally distributed. The only value outside this range is kurtosis of Total AAG. A slight depart from normality is not an issue since ANOVA is robust to violations of normality (Pallant, 2010).

Analysis of Variance

The tables below show mean scores of all the five scales, along with the results of ANOVAs. These are appropriate tests to test if there are significant differences among mean scores. A large F-statistic indicates that there is more variability between the groups (caused by the independent variable) than there is within each group. A significant test ($p < 0.05$) indicates that we can reject the null hypothesis, which states that the population means are equal. In other words, one may conclude that the mean scores are different among the groups being compared (with 95% confidence). The test does not, however, tell us which of the groups differ. For this we need to conduct post-hoc tests (Pallant, 2010). Post-hoc tests were conducted in the form of pairwise tests of equality of means. APA-subscript letters are used to denote which groups are statistically different at the 95% confidence level. If two values are significantly different within a single column, those values display different subscript letters. For example, for TOTAL GMRI scores, American Indians show a significantly lower score compared to all other races, which are not different (American Indian shows a different subscript letter compared to all other races, who share the same letter 'b'). The ANOVA test for Race was highly significant ($p < 0.001$).

		TOTAL GMRI	F	p	Total AAG	F	p	TotalGQ 6	F	p
Race	American Indian	91.600a	6.250	0.000	30.800a	1.943	0.102	31.667a.b	6.423	0.000
	AAPI	104.233b			32.041a			30.726a		
	Black	105.034b			31.362a			33.155a.b		
	Hispanics	105.084b			31.530a			34.265b		
	White	106.655b			30.612a			34.560b.c		
Age	18-24	99.639a	4.948	0.001	30.556a	1.191	0.314	30.125a	12.738	0.000
	25-40	105.648b			31.146a			32.889b		
	41-55	106.291b			31.112a			34.607c		
	55-70	106.965b			30.619a			35.858c		
	> 70	106.345a.b			29.448a			36.138b.c		
Gender	Man	106.428a	0.920	0.399	32.119a	10.293	0.000	31.907a	16.925	0.000
	Non-binary or Transgender	103.333a			30.667a.b			31.600a.b		
	Woman	105.211a			30.332b			34.926b		

Note: Values in the same column and subtable not sharing the same subscript are significantly different at $p < .05$ in the two-sided test of equality for column means. Cells with no subscript are not included in the test. Tests assume equal variances.[1]

1. Tests are adjusted for all pairwise comparisons within a row of each innermost subtable using the Bonferroni correction.

		TotalTGS	F	p	TotNADA	F	p
Race	American Indian	72.667a.c.e	5.831	0.000	37.000a	1.128	0.342
	AAPI	71.685a.b			39.068a		
	Black	78.431c.e			39.172a		
	Hispanics	79.482c.d			38.060a		
	White	73.853b.e			36.678a		
Age	18-24	67.083a	8.413	0.000	34.431a	4.732	0.001
	25-40	74.256b			38.518a.b		
	41-55	76.631b			38.864b		
	55-70	76.230b			34.912a		
	> 70	73.241a.b			33.621a.b		
Gender	Man	72.139a	11.111	0.000	37.366a	0.193	0.825
	Non-binary or Transgender	65.133a			38.933a		
	Woman	76.165b			37.130a		

Note: Values in the same column and subtable not sharing the same subscript are significantly different at p< .05 in the two-sided test of equality for column means. Cells with no subscript are not included in the test. Tests assume equal variances.[1]

1. Tests are adjusted for all pairwise comparisons within a row of each innermost subtable using the Bonferroni correction.

Correlation Analysis

A correlation analysis was performed to examine the degree of association between the psychographic scales under study. The table below shows a correlation matrix with Pearson's correlation coefficients and p-values (Sig.). P-values lower than 0.05 indicate the association is statistically significant at the 95% confidence level. Total GMRI correlates positively with TotalGQ6 (r = 0.497) and TotalTGS (r = 0.582). It also correlates positively with all the subscales (p < 0.05).

Correlations

		(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
TotalGQ6 (1)	Pearson Correlation	1	.607**	.497**	.361**	.239**	.070	.423**	.393**
	Sig. (2-tailed)		.000	.000	.000	.000	.080	.000	.000
	N	619	619	619	619	619	619	619	619
TotalTGS (2)	Pearson Correlation	.607**	1	.582**	.500**	.521**	.166**	.063	.584**
	Sig. (2-tailed)	.000		.000	.000	.000	.000	.118	.000
	N	619	619	619	619	619	619	619	619
TOTAL GMRI (3)	Pearson Correlation	.497**	.582**	1	.705**	.684**	.611**	.333**	.676**
	Sig. (2-tailed)	.000	.000		.000	.000	.000	.000	.000
	N	619	619	619	619	619	619	619	619
GMCBonds (4)	Pearson Correlation	.361**	.500**	.705**	1	.467**	.271**	-.084*	.519**
	Sig. (2-tailed)	.000	.000	.000		.000	.000	.037	.000
	N	619	619	619	619	619	619	619	619
GMGrowth (5)	Pearson Correlation	.239**	.521**	.684**	.467**	1	.189**	-.173**	.675**
	Sig. (2-tailed)	.000	.000	.000	.000		.000	.000	.000

	N	619	619	619	619	619	619	619	619
GMPeace (6)	Pearson Correlation	.070	.166**	.611**	.271**	.189**	1	.141**	.182**
	Sig. (2-tailed)	.080	.000	.000	.000	.000		.000	.000
	N	619	619	619	619	619	619	619	619
GMEmptiness (7)	Pearson Correlation	.423**	.063	.333**	-.084*	-.173**	.141**	1	-.099*
	Sig. (2-tailed)	.000	.118	.000	.037	.000	.000		.014
	N	619	619	619	619	619	619	619	619
GMValuing	Pearson Correlation	.393**	.584**	.676**	.519**	.675**	.182**	-.099*	1
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000	.014	
	N	619	619	619	619	619	619	619	619

**. Correlation is significant at the 0.01 level (2-tailed).
*. Correlation is significant at the 0.05 level (2-tailed).

The matrix below shows the coefficients for all the total subscales.

Correlations

		TotalGQ6	TotalTGS	TOTAL GMRI	Total AAG	TotNADA
TotalGQ6	Pearson Correlation	1	.607**	.497**	-.098*	.047
	Sig. (2-tailed)		.000	.000	.015	.240
	N	619	619	619	619	619
TotalTGS	Pearson Correlation	.607**	1	.582**	.242**	.405**
	Sig. (2-tailed)	.000		.000	.000	.000
	N	619	619	619	619	619
TOTAL GMRI	Pearson Correlation	.497**	.582**	1	.255**	.309**
	Sig. (2-tailed)	.000	.000		.000	.000
	N	619	619	619	619	619
Total AAG	Pearson Correlation	-.098*	.242**	.255**	1	.315**
	Sig. (2-tailed)	.015	.000	.000		.000
	N	619	619	619	619	619
TotNADA	Pearson Correlation	.047	.405**	.309**	.315**	1
	Sig. (2-tailed)	.240	.000	.000	.000	
	N	619	619	619	619	619

**. Correlation is significant at the 0.01 level (2-tailed).
*. Correlation is significant at the 0.05 level (2-tailed).

The only pair of scales that don't correlate significantly ($p > 0.05$) is TotNADA and TotalGQ6, indicating these concepts are not associated.

Regression Model

To evaluate effects of TotalGQ6, TotalTGS and TotNADA on GMRI, a multiple regression model was used.

Multiple Regression analysis is a technique used to explore the relationships between a continuous dependent variable and two or more independent (or predictor) variables (Pallant, 2010). The objective of multiple regression analysis is to use the independent variables whose values are known to predict the single dependent value selected by the researcher. Each independent variable is weighted by the regression analysis procedure to ensure maximal prediction from the set of independent variables. The weights denote the relative contribution of the independent variables to the overall prediction and facilitate interpretation as to the influence of each variable in making the prediction, although correlation among the independent variables complicates the interpretative process. The set of weighted independent variables forms the regression variate, a linear combination of the independent variables that best predicts the dependent variable (Hair et al., 2014).

The model showed good fit ($F = 130.873$, $p < 0.001$, $R^2 = 0.390$). There was no multicollinearity in the model since Variance Inflation Factors for all variables were below 10.000.

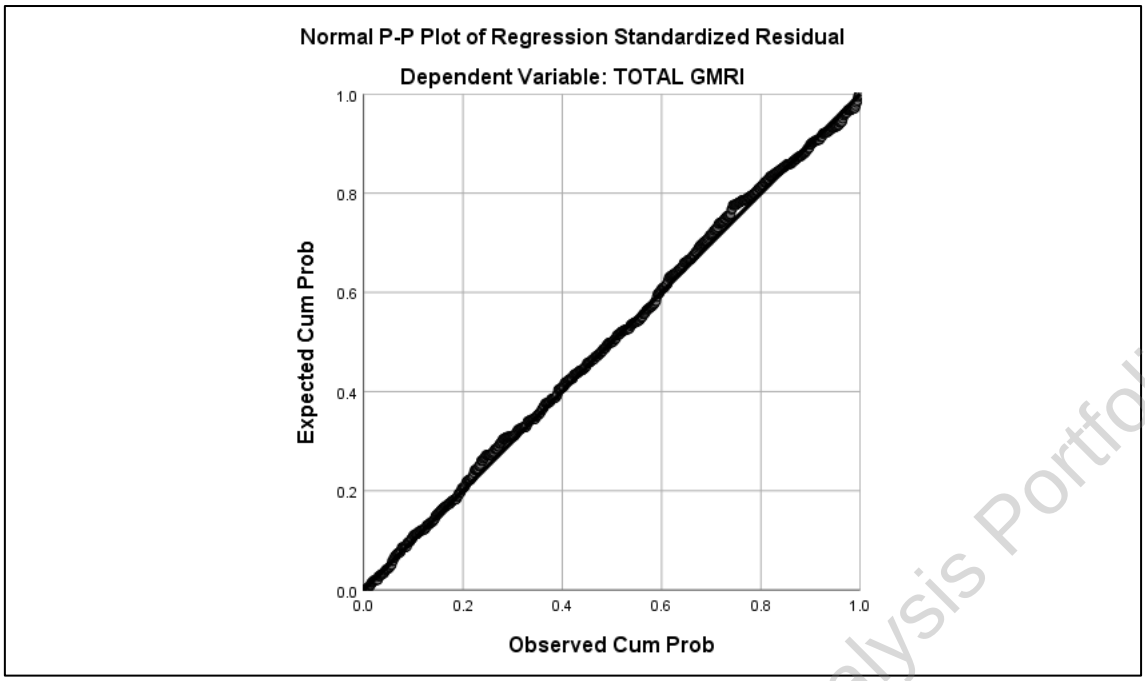
The table below shows the model coefficients. TotalGQ6 has a positive effect on GMRI ($\beta = 0.275$, $p < 0.001$). TotalTGS also has a significant positive effect on GMRI ($\beta = 0.354$, $p < 0.001$). The same result was observed for TotNADA ($\beta = 0.153$, $p < 0.001$). When these scales increase, a significant increase is also expected on TotalGMRI.

Coefficients[a]

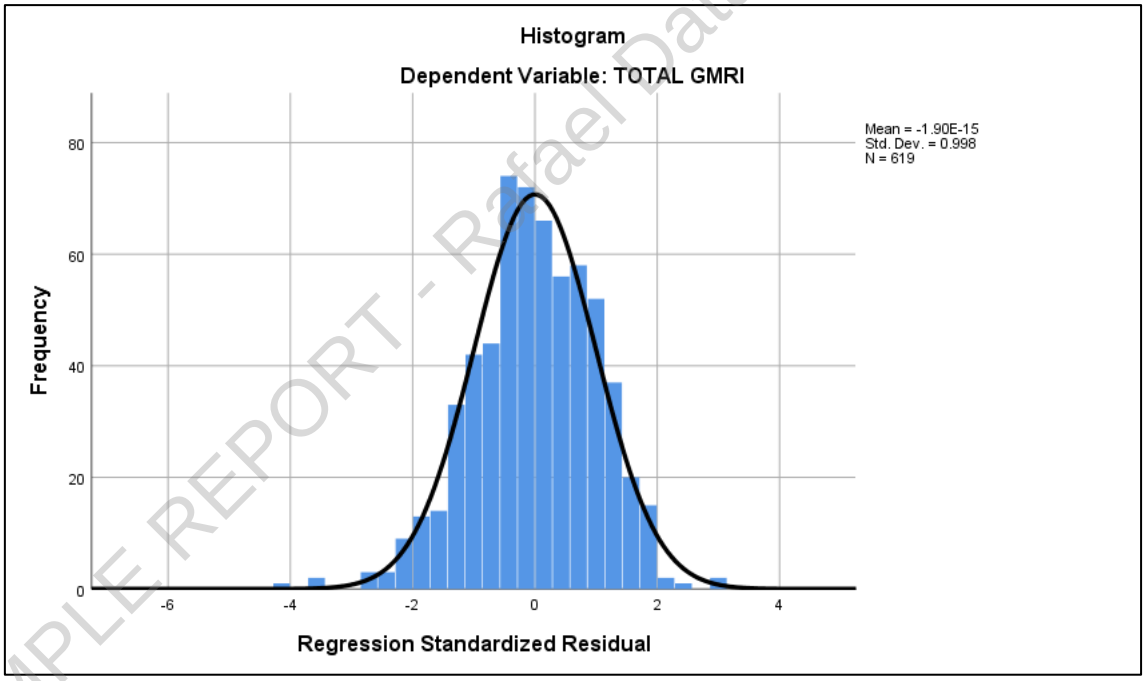
Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.
		B	Std. Error	Beta		
1	(Constant)	56.509	2.507		22.536	.000
	TotalGQ6	.528	.079	.275	6.663	.000
	TotalTGS	.336	.043	.354	7.850	.000
	TotNADA	.162	.038	.153	4.260	.000

a. Dependent Variable: TOTAL GMRI

Lastly, violations of the assumptions of normality, linearity and homoscedasticity of residuals (errors) were examined for the regression model. The next figure shows a P-P plot, which is used to assess the normality of residuals. The observations should follow a diagonal pattern to suggest normality of residuals (Tabachnick & Fidell, 2014).

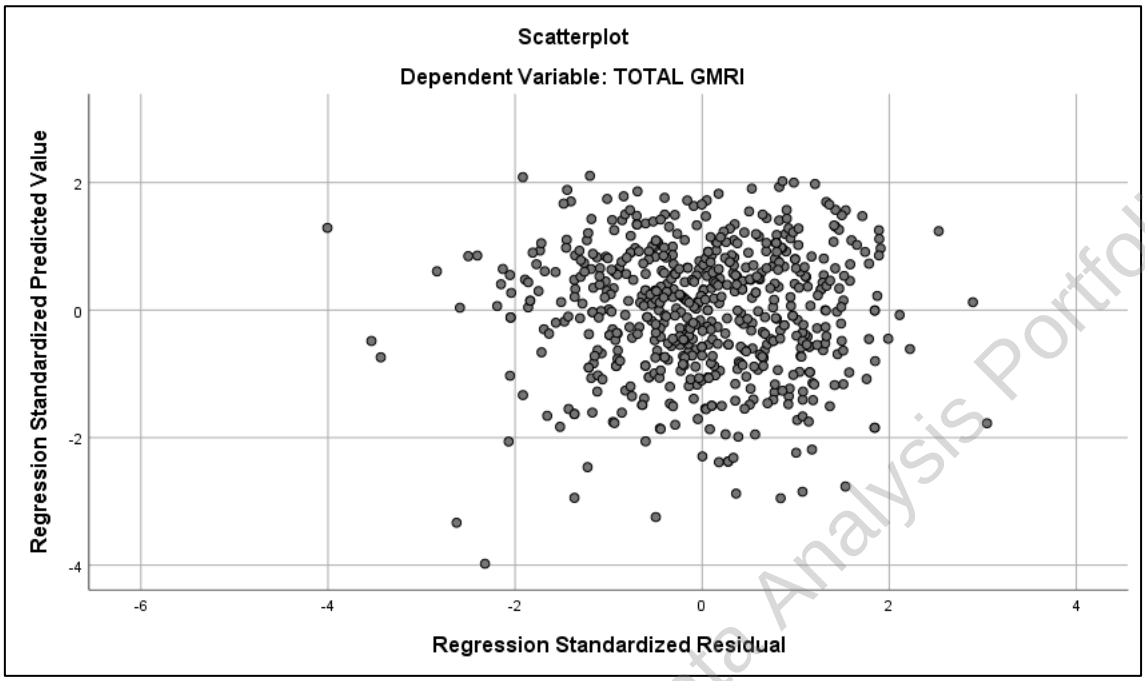


The graph suggests that no substantial violations of normality are present. The histogram below confirms a normal distribution of residuals.



The next figure shows a scatterplot of standardized residuals and standardized predicted values of the dependent variable. If points are well distributed along the X and Y axes, this would suggest homoscedasticity and linearity. Nonlinearity is indicated when most of the residuals are above the zero line on the plot at some predicted values and below the zero line at other predicted values. Lack of homoscedasticity is indicated if values are

more dispersed for a given predicted values than at other values (Tabachnick and Fidell, 2014).



The graph also suggests no violation of assumptions.

References

Pallant, J. (2010). *SPSS Survival Manual* (4th ed.). McGraw-Hill.

Tabachnick, B. G., & Fidell, L. S. (2014). *Using multivariate statistics / Barbara G. Tabachnick, Linda S. Fidell.*

New Regression Model

An additional model was executed which controls for the effect of Age, Race and Gender. These variables were dichotomized and inserted in the model.

The model showed good fit ($F = 39.245$, $p < 0.001$, $R^2 = 0.426$). There was no multicollinearity in the model since Variance Inflation Factors for all variables were below 10.000.

The table below shows the model coefficients. 'Age 18-24', 'Female or other' and 'White' were used as reference categories and are omitted from the table. TotalGQ6 has a positive effect on GMRI ($\beta = 0.287$, $p < 0.001$). TotalTGS also has a significant positive effect on GMRI ($\beta = 0.370$, $p < 0.001$). The same result was observed for TotNADA ($\beta = 0.143$, $p < 0.001$). When these scales increase, a significant increase is also expected on TotalGMRI. Being male has a positive effect on GMRI ($\beta = 0.148$, $p < 0.001$), Being American Indian has a negative effect on GMRI (compared to being White) ($\beta = -0.127$, $p < 0.001$).

Coefficients[a]

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.
		B	Std. Error	Beta		
1	(Constant)	53.736	2.643		20.329	.000
	TotalGQ6	.551	.081	.287	6.814	.000
	TotalTGS	.351	.043	.370	8.260	.000
	TotNADA	.152	.037	.143	4.074	.000
	Age 25-40	1.196	1.296	.046	.923	.356
	Age 41-55	.300	1.323	.012	.227	.821
	Age 56-70	.553	1.461	.018	.379	.705
	Age 70+	1.172	2.096	.020	.559	.576
	Gender - Male	3.874	.826	.148	4.691	.000
	AmInd	-9.487	2.300	-.127	-4.124	.000
	AsianPI	.481	1.163	.013	.414	.679
	Black	-1.273	1.205	-.033	-1.056	.291
	Hispan	-1.614	1.042	-.050	-1.549	.122

a. Dependent Variable: TOTAL GMRI

Power Analysis (a priori)

Use the information below if the intent was to calculate sample size:

Assuming a desired power of 0.80 and an expected R^2 of 0.26 (guidelines of Cohen, 1988), a regression model with 12 predictors (your independent variables + control variables) would need a minimum sample size of 61 for a significance level of 5%.

Power Analysis (post-hoc)

The power of the resulting regression model, with 12 predictors and an F-value of 39.245 is 0.997 for a significance level of 5%.