Stable MMPI-2 Scoring: Introduction to Kernel Extension Techniques

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Abstract

The current study introduces a new technique called Geometric Harmonics for scoring the MMPI-2 test. Like Factor Analysis (PCA), the technique is a spectral method in which each person's response is characterized by a small number of values derived from eigenvectors of a matrix. However, instead of calculating correlations between items, similarities between people's responses are measured. Using these similarities a map, which assigns a position for each person according to their response, is created. Namely, people with similar responses are located close to one another. The subjects coordinates on the map (GH scores) can be viewed as new interm scales (GH scales). It can be demonstrated how the use of 15 GH scales is sufficient to characterize an MMPI-2 response set. The GH scales are unique in many ways. a) They are constructed in a purely computational automatic way which makes this method applicable to other tests as well. b) They can be evaluated even under conditions of a large number of missing data (In the case of MMPI-2, there can be over 250 missing items) c) Finally, MMPI-2 scale scores can be derived on the basis of GH scales using a simple conversion formula. These derived scales scores are closely, with correlations ranging from 0.85 to 0.98, to for the basic clinical and RC scales. Being able to demonstrate the efficacy of this approach using large MMPI-2 non-normative data bases, we can offer the new techniques as an alternative means for scale development and imputation of missing data.

KEYWORDS

Dimensionality Reduction, Spectral Graph Theory, Geometric Harmonics, Diffusion Processes, Machine Learning, Out-of-sample Function Extension, Learning on Manifolds, Personality Assessment, MMPI-2, Personality Testing.

INTRODUCTION

The Geometric Harmonic approach can be viewed as organizing people on a map. The map we build is called the Diffusion Map. On the Diffusion Map, examinees with similar responses are put close to one another. The degree of similarity between two people is measured by a Markov process. The Markov matrix K contains at entree $K(i,j)$ a value which is proportional to the similarity between i's and j's responses. The idea is that similar responses should be scored somewhat similarly. And so, a person's score can be deduced from his/her region on the map. We therefor define the GH scale scores for a given individual as their position (coordinates) on the map.

We claim Diffusion Maps are the most appropriate choice for this application. Yet, there are other methods in which one can attain data organizing maps such as IsoMaps [10] Laplacian Eigenmaps [1], Kernel PCA [9], Hessian Eigenmaps [7], and others.

In section I we show how one goes about building the aforementioned Diffusion Map using a base data set of a few hundred records. We show that indeed different regions of the map receive different MMPI-2 scores.

Once the map in built, evaluating a new person's GH scores amounts to finding their appropriate position on the map. This is done using a method called the Nyström extension[6], which is explained in section II. In section III, we claim that the scoring method used in section II

allows us to deal with large numbers of missing items without the need to fill-in the missing answers.

Finally we show in section IV that there is a simple conversion formula from the GH scores to MMPI-2 scores. By that we conclude our description of the GH scoring method for the MMPI-2 test.

Section VI will deal with data Analisys. We show that evaluating MMPI-2 scores using the GH scales incurs many advantages. For example one can evaluate all the scales equally accurately even with a large number of missing items. without performing data imputation. An extreme case of this phenomenon is shown where each scale is evaluated with all it's items missing.

Detailed explanations of both Diffusion Maps and Geometric Harmonics can be found in [8], [5], [6]. More explanations of similar methods and applications can be found in [3], [4], [2]

I. Building Personality Diffusion Maps

In order to build a map we need an initial set of responses. Assume we are given a set of n sample cases. We denote as x_i the sequence of answers of person i, where $x_i(k)$ is person i's response to item k. $x_i(k) = \{1, -1\}$ for responses "True" and "False" respectively [1]. We further define a distance measure between pairs of people.

$$D(i,j) = \frac{1}{Q}\frac{\sum_{k=1}^{Q}|x_i(k) - x_j(k)|}{2}$$

$D(i,j)$ is the fraction of items that person i and person j answered differently, and Q is the overall number of items in the questioner.

[1] We deal with the case of missing answers in a later section. We assume that the sampled n cases are complete records.

Finally the Gaussian Kernel $\widetilde{K}$ is defined.

$$\begin{aligned}\widetilde{K}(i,j) &= e^{-D(i,j)^2/\sigma^2} \\ \sigma &= \max_i \min_{j,j\neq i} D(i,j).\end{aligned}$$

Notice that $\widetilde{K}$ is an $n \times n$ Symmetric Positive Semidefinite matrix. Moreover the entrees $K(i,j)$ equal roughly 1 if person i and j answered similarly, and roughly 0 if the responses are dissimilar.

We continue by normalizing $\widetilde{K}$ to be bi-stochastic. by computing a vector w.

$$\begin{aligned}K(i,j) &= \frac{\widetilde{K}(i,j)}{w(i)w(j)} \\ \sum_i K(i,j) &= 1 \\ \sum_j K(i,j) &= 1\end{aligned}$$

A further explanation as to how such a vector can be computed can be found in [**?**]

At this point, the eigenvectors and eigenvalues of K, $K\varphi_l = \lambda_l \varphi_l$, are examined. Since K is Positive Semidefinite, Bi-stochastic, and symmetric all of it's eigenvalues are between zero and one $1 = \lambda_0 \geq \lambda_l \geq 0$. The set of eigenvectors is orthogonal, $\varphi_l \cdot \varphi_m^T = \delta(l,m)$[2]. If only the eigenvectors that correspond to the largest 15 eigenvalues are considered, x_i's position on the map (and his/her GH scores) can be defined as the values $(\varphi_0(i), \varphi_1(i), \ldots, \varphi_{14}(i))$. For example, the score of person 108 in the base data set on scale GH4 is $\varphi_4(108)$.

Whereas in PCA the number of eigenvectors used is decided according to the size of the eigenvalues[3], Here the choice to keep only the first[4] 15 eigenvectors does not arise from consid-

[2] $\delta(l,m)$ is the kronecker delta. $\delta(l,m) = 1$ if $l = m$ and 0 if $l \neq m$.

[3] Small eigenvalues are dimmed insignificant and ignored

[4] Corresponding to the largest 15 eigenvalues

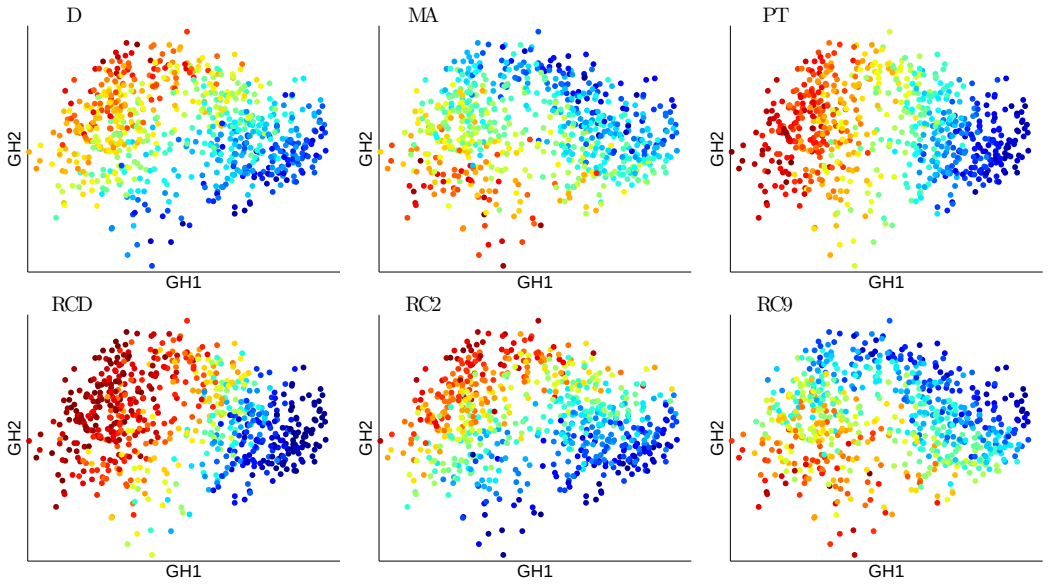

Fig. 1. Six copies of the same map created for 500 people, each point corresponds to a position assigned to one person. The x and y axis are the scores on GH1 and GH2 respectively. The color of each point is the scale score the specific person received on the scales (left-to-right and up-down) D, MA, PT, RCD, RC2, and RC7.

eration of eigenvalue decay. Yet, since our choice relays on the accuracy of the GH to MMPI-2 score conversion this point will be further discussed later.

It is important to note that since K is bi-stochastic the eigenvector φ_0, and therefore GH0, is constant[5]. In other words the GH0 score for all subjects is $\frac{1}{\sqrt{n}}$ regardless of their responses. GH0 is therefore not a scale at all since it provides no information on the subjects. It will become clear later why it is convenient to keep GH0 as a "scale" but for now we will ignore it. The two dimensional Diffusion Map created by GH1 and GH2 scores for 500 subjects is presented in figure 1, the colors are their scores on the indicated MMPI-2 scales.

Notice that for each of the scales shown in figure 1 it seams possible to infer each person's score (color) according to his/her position on the map. Indeed this inference is possible and even

[5]The largest eigenvalue of a stochastic matrix is 1, $\lambda_0 = 1$, corresponding to the constant vector $\frac{1}{\sqrt{n}}(1, 1, \ldots, 1)^T$.

simple. Before showing that, scoring new cases will first be demonstrated.

II. SCORING NEW CASES

So far, it was demonstrated how GH sores are calculated for a fixed number of examinees, namely n. Furthermore, saw that that the GH scores can be viewed as coordinates on the diffusion map. We now address the issue of finding the appropriate position on the map for a new person, who's answer sequence is not one of the n given in the base data set. Since a subjects GH scores are taken to be his/her coordinates on the map, by finding the subjects position we also obtain his/her GH scores.

The GH scores for the base n cases are derived from eigenvectors of a the kernel K. These values are defined only for answer sequences $x_1, \ldots, x_n$.

$$\begin{aligned} \lambda_l \varphi_l &= K\varphi_l \\ \lambda_l \varphi_l(x_i) &= \sum_{j=1}^{n} k(x_i, x_j)\varphi_l(x_j) \\ \varphi_l(x_i) &= \frac{1}{\lambda_l}\sum_{j=1}^{n} \frac{e^{-\frac{\|x_i - x_j\|^2}{\sigma^2}}}{w(x_i)w(x_j)}\varphi_l(x_j) \end{aligned}$$

Yet, using the Nysrtöm Extension one can evaluate the GH scores for a new response x, if the kernel $K(x, x_i)$ can be evaluated for every i.

In the equation above x_i is replaced by a new answer sequence, x, in order to calculate $\varphi_l(x)$. There is no difficulty calculating $\|x - x_j\|$ for any x since that is the distance of the new point to the points in the data set. Since the value $w(x)$ is not known it is approximated by

$$w(x) \approx \sqrt{\sum_{j=1}^{n} e^{-\frac{\|x - x_j\|^2}{\sigma^2}}} \equiv \widetilde{w}(x)$$

Replacing $w(x)$ with it's approximation leads to:

$$\varphi_l(x) \;=\; \frac{1}{\lambda_l}\sum_{j=1}^{n}\frac{e^{-\frac{\|x-x_j\|^2}{\sigma^2}}}{\widetilde{w}(x)w(x_j)}\varphi_l(x_j)$$

Now $\varphi_l(x)$ can be evaluated for every x. Since $\varphi_0(x),\ldots,\varphi_{14}(x)$ are the appropriate coordinates for x on the diffusion map they are also x's GH scores. This concludes the scoring process for the a answer string x.

It is now clear that the GH scales depend on all items equally since the only way in which a person's response can be examined is by distance calculations of the form $\|x-x_i\|$ which do not depend on the items' content or order. This property gives the GH scales both flexibility and stability. In particular it enables dealing with heavily corrupted response sets, without the need to "fill-in" missing answers.

III. Dealing with Missing Values

It should be noted that the only measure of a person's response evaluated, in order to evaluate his/her GH scores, is it's distances from other people's responses[6]. Using the same approach a case is considered where $x(k)\in\{1,0,-1\}$ and $x(k)=0$ if the new case x did not respond to item k. In this case the distance calculation is revised.

$$\begin{aligned} D(x,x_i) &= \frac{1}{Q-q}\frac{\sum_{k=1}^{Q}|x(k)-x_i(k)|-q}{2} \\ q &= \sum_{k=1}^{Q}1-|x(k)| \quad = \text{Number of missing items} \end{aligned}$$

[6]The probability that they answer differently.

Using the new distance definition, the distance between x and x_i can be evaluated even when x contains many missing answers. It can be seen that instead of trying to predict how x would have answered the missing items, They are simply ignored. There is another way of looking at it; the new distance is actually identical to the old one but on a partial MMPI-2 questionnaire that contains only the questions x answers[7]. For example if x answered the first 200 questions, out of $Q = 567$ items, then $q = 367$ and we have:

$$\begin{aligned} D(x, x_i) &= \frac{1}{567 - 367} \frac{\sum_{k=1}^{200} |x(k) - x_i(k)|}{2} \\ &+ \frac{1}{567 - 367} \frac{\sum_{k=201}^{567} |0 - x_i(k)| - 367}{2} \\ &= \frac{1}{200} \frac{\sum_{k=1}^{200} |x(k) - x_i(k)|}{2} \end{aligned}$$

as a consequence the GH scoring method can be used to score corrupted records without the need to "fill-in" missing values.

In a different experiment that will not be described here, on a different questionnaire (not MMPI-2), the subjects were given the option to rate the relevance of each item to them or ignore questions as they see fit. The result was an improvement in prediction accuracy. It is assumed that the increase in accuracy results from the fact that the subjects answered only items they dimmed relevant or felt strongly about. Unfortunately, since we did not have similar data for the MMPI-2, no quantitative comparison could be made.

IV. Converting GH scores to MMPI-2 scores

The issue of converting GH scores to MMPI-2 scores will be addressed in this section. In order to convert GH scores to MMPI-2 scores we use that fact that the GH scales orthogonal

[7]Notice that a) We still use the original map built from complete records b) If $q = 0$, corresponding to no missing items, the new distance is identical to the old one.

which results from the scales being as a set of eigenvectors of a symmetric matrix, and the fact that we can score the initial set accurately using an automated system[8]. Based on these, the original MMPI-2 scale scores can be readily approximated using a linear combination of the GH scales. Let f be the values of an MMPI-2 scale for the base n cases.

$$\begin{aligned} f(i) &\approx \sum_{l=0}^{14} a_l \varphi_l(i) \\ a_l &= \langle f, \varphi_l \rangle \\ &= \sum_{i=1}^{n} f(i)\varphi_l(i) \end{aligned}$$

These a_l conversion factors are constant for each scale and can be precalculated. Moreover they constitute the optimal least squares solution $min_{a_l} \sum_i (f(i) - \sum_l a_l \varphi_l(i))^2$. For example, the RCD score for a new record x will be approximated by

$$RCD(x) \approx (GH0(x), GH1(x), \ldots, GH14(x))^T (a_0, a_1, \ldots, a_{14})$$

where the a_l's were calculated for the RCD scale and the GH scores where calculated according to the previous section.

Why do we need GHO?

It was mentioned before that GH0 is a constant vector and therefore has no predictive power whatsoever. However, keeping it makes the conversion simple. Since GH0 is normalized, $GH0(i) = 1/\sqrt{n}$. Therefore $a_0 = \sqrt{n}\overline{f}$ and $a_0\varphi_0(i) = \overline{f}$. Here $\overline{f}$ denotes the mean value of f.

[8]That is possible in the case where the base data set contains complete records.

Keeping GH0 automatically adds, to each scale, it's average and enables us to have a simple conversion vector from GH scores to MMPI-2 scores, while keeping all the variance in scales GH1-GH14.

Estimating smoothness of MMPI-2 scales

The φ_l's are a set of smooth functions on the data set. If one sets out to construct a noisy "jagged" function using them, there is bound to be some reconstruction error. In other words the smoother a function is the better it can be predicted by the GH scales. Therefore, a measure of smoothness S is devised. S is the percentage in which the function f is projected on the first 15 eigenvectors (i.e the GH scales). Any part of f which is not projected on the GH scales will be unrecoverable by the reconstruction procedure and therefor lost.

The smoothness measure S is set to be:

$$S = \sqrt{\frac{\sum_{i=1}^{14} a_i^2}{\sum_{j=1}^{n} (f(j) - \overline{f})^2}}$$

The measure S ranges between $S = 1$ indicating perfect estimation and $s = 0$ corresponding to no predictive power, and gives an a priori knowledge as to how well the score f is predicted by the GH scales.

V. Choosing 15 scales

Being able to score new cases and convert their GH scores to MMPI-2 scores, the claim that 15 GH scales are sufficient can be revisited. Usually in spectral methods one looks at the eigenvalue decay to decide on the proper truncation. Yet, in this case the decay is very slow due to high dimensional noise. Figure 2 Shows the eigenvalue decay of the Diffusion Kernel compared to that of the Factor Analysis kernel. Figure 3 shows that the 15'th eigenvalue is not

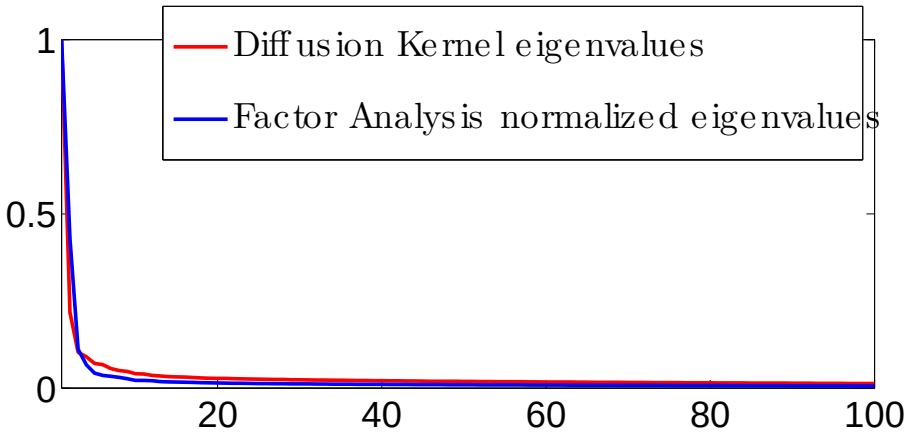

Fig. 2. Eigenvalue decay for the Diffusion kernel and Factor Analysis kernel. It is evident that the decays show no significant difference. For example, the 20'th eigenvalues are 0.02 and 0.03, and the the 50'th eigenvalues are 0.012 and 0.019 for the diffusion and Factor Analysis kernels respectively.

significantly bigger or smaller then the 10'th or the 20'th for example. Yet when one thinks about it, the eigenvalue decay is not relevant to us in this case since we are not trying to reconstruct the input vectors but to predict scores. We turn to measure the prediction accuracy of the current method while taking different numbers of eigenvectors. Figures 3 and 4 compare the predictive quality of the current method that of Factor Analysis while using the same number eigenvectors.

It can be seen that after the 15'th eigenfunction there is no significant improvement in prediction accuracy. However, even though it may seem that either 10 or 20 GH scales can be chosen, using less then 10 eigenfunctions may result in loss of prediction accuracy, whereas choosing more then 20 hold no additional predictive information for MMPI-2 scores. Nonetheless, figures 3 and 4 suggest that even with only 5 eigenvectors The GH scores achieve better predictions then PCA does for any number of eigenvalues.

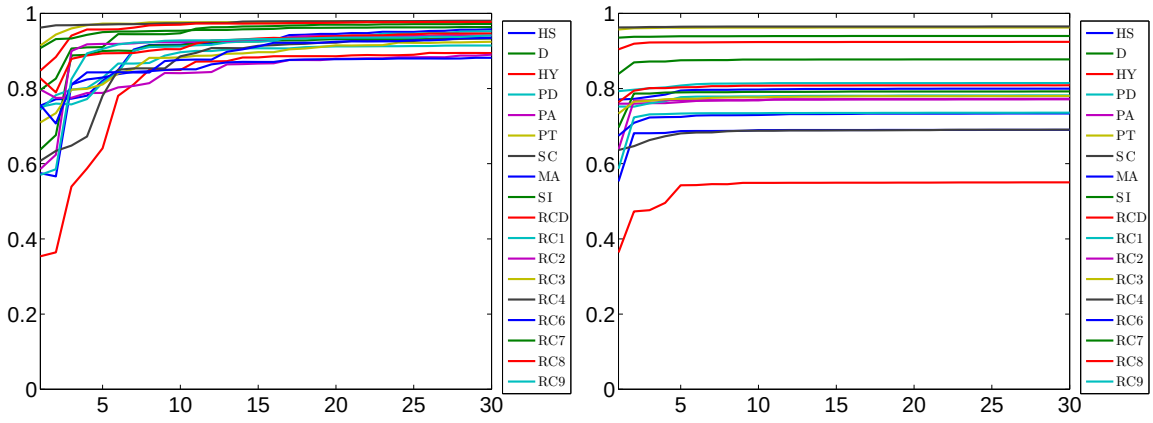

Fig. 3. LEFT: On the Y axis, the Pearson Correlation between two scoring methods. a) Conversion from the k GH scales. b) The accepted method of summation over keyed entries. k , the number of eigenvectors used, is indicated on the X axis.

Fig. 4. RIGHT: For comparison we show the prediction correlations of the same number of eigenfunction that arise from Factor Analysis (PCA).

VI. MMPI-2 Data Analysis

The last step in the introduction of the GH technique is empirical examination of its utility and efficacy. In order to do that we used two large MMPI-2 data sets. One data set contained 2400 records (Ben-Porat, Graham and McNulty, 1997) and the other 4300 records (Almagor, 2005) of outpatient subjects. The examination was repeated separately for each of the two data sets.

One thousand subjects were randomly selected. These records were scored twice. First, by using the standard scoring software (Almagor, 2003), and second by using the GH conversion method. In order to evaluate the GH scale scores a diffusion map was required. Five hundred subjects were randomly selected ($m = 500$) for this purpose[9]. The distances $D(i,j)$ was calculated using $Q = 567$, and $\sigma = 0.35$.

[9]No records were used for both purposes simultaneously

For the purpose of simplifying the presentation we chose to present the basic and reconstructed clinical scales, namely HS, D, HY, PD, PA, PT, SC, MA, SI, RCD, RC1, RC2, RC3, RC4, RC6, RC7, RC8 and RC9.

Correlation between Scoring Methods

In order to assess the correspondence between the methods, we correlated the results of the standard scoring and the GH scoring for 1000 subjects. The results are depicted in Table I.

Table I shows, in addition to the Pearson correlation coefficients, the scale smoothness parameter S (the upper bound of the expected correlations) in order to corroborate the quality of the estimation.

Table I includes two histograms describing the frequency of cases where there was a difference between the scores produced by the two methods of d. The histogram labeled Err shoes the difference between the GH scores and the MMPI-2 standard scores. Err_{PCA} shows the difference while using PCA (15 eigenvectors) instead of the GH scales.

Treatment of missing items

As claimed earlier, the GH technique is quite effective in dealing with missing data. In order to test this claim we used the same data set that included 1000 subjects. This time q items were randomly deleted. Pearson correlation coefficients were calculated between the full record scale scores and the scores calculated by the GH technique using the corrupted records. Figure 5 shows the correlation decay as a function of q, the number of missing values. We see that even with up to 300 missing items most scales can be scored almost as well as they can be on complete records.

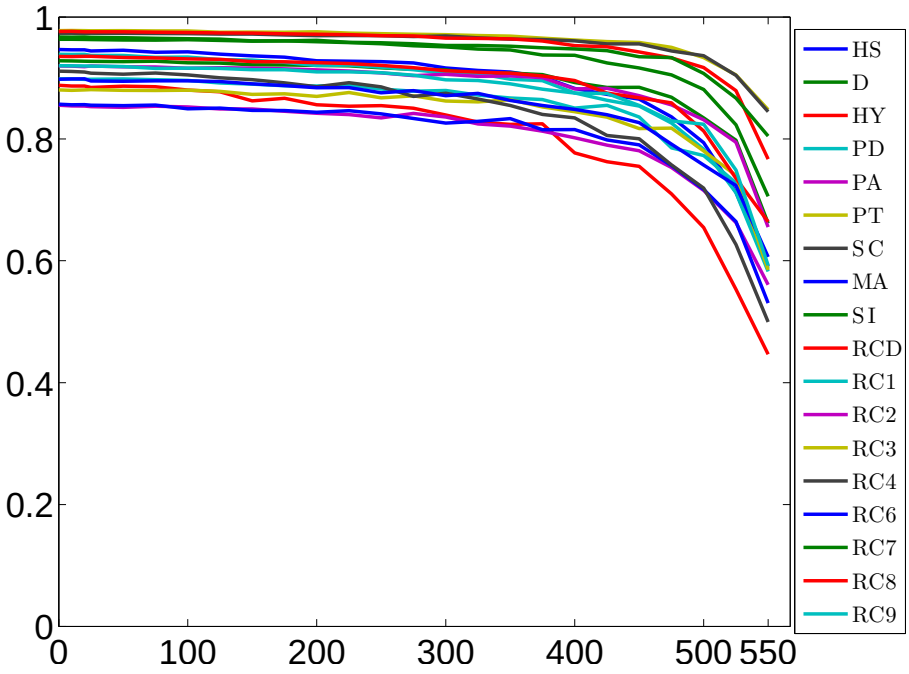

Fig. 5. The Y axis represents the Pearson correlation between MMPI-2 scores on complete records and GH converted scores on records with q missing items. The X axis indicates the number of missing items q in each record. the different lines correspond to different scales HS, D, HY, PD, PA, PT, SC, MA, SI, RCD, RC1, RC2, RC3, RC4, RC6, RC7, RC8 and RC9.

Table II depicts the results of the analysis similar to those presented in Table I. Challengingly, the scale scores are calculated under the condition that all the relevant scale items are missing!! This is an extreme case where all the common imputation methods are not indicated Table 2II strongly indicates that even in such a condition scoring via the GH conversion scheme leads to a pretty good estimation of the original, non-corrupted scores.

For comparison we also try to deal with the missing scale problem using Monte Carlo Markov Chains (MCMC) [**?**]. In the MCMC approach one constructs a stochastic probability matrix that is used to predict each missing answer. Then the completed record is scored by item summation. Table II also includes ρ_{MC}, which is the correlation between scoring in this fashion and the real

scores (summation over the uncorrupted records). We see that the correlations obtained by our method are higher. That is due to the fact that the MCMC method builds on simple correlations between items which are much less meaningful across different scales. Similarly to table I we show in table II histograms of the actual scoring errors using both methods.

VII. Conclusion and future work

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TABLE I

CORRELATION ρ, FOR EACH SCALE, BETWEEN SCORES ATTAINED IN TWO DIFFERENT METHODS. A) MMPI-2 SCORES ATTAINED BY SUMMATION OVER THE KEYED ITEMS. B) MMPI-2 SCORES APPROXIMATED BY CONVERTING 15 GH SCORES. THE TABLE ALSO INCLUDES THE SMOOTHNESS MEASURE S FOR EACH SCALE. THE FIRST HISTOGRAM, LABELED Err, COUNTS HOW MANY PEOPLE WERE SCORED WITH ERROR OF d. d IS THE DIFFERENCE BETWEEN SCORING METHODS. THE DIFFERENT COLUMNS CORRESPOND TO $d < -15$, $-15 < d < -10$, $-10 < d < -5$, $-5 < d < -2$, $-2 < d < 2$, $2 < d < 5$, $5 < d < 10$, $10 < d < 15$ AND $15 < d$. THE HISTOGRAM LABELED Err_{PCA} SHOWS THE SAME PLOT FOR THE BEST ACHIEVABLE SCORING POSSIBLE WITH 15 PCA VECTORS

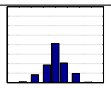
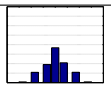
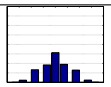
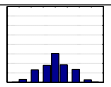
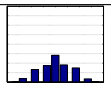
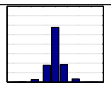
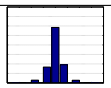
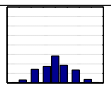
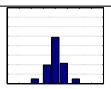
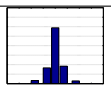
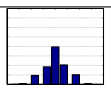
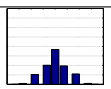
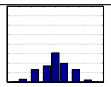
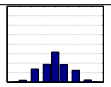
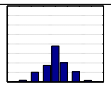
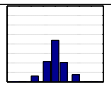
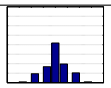
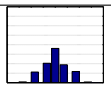
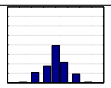
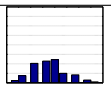
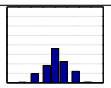
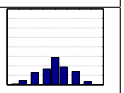
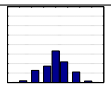
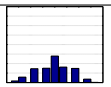
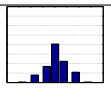
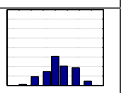
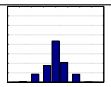
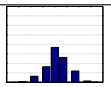
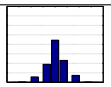
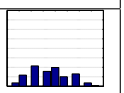
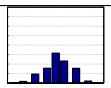
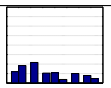
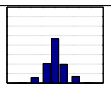
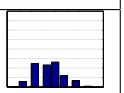
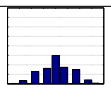
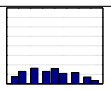
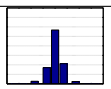
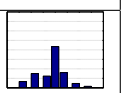
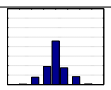
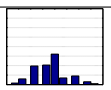
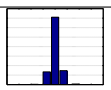
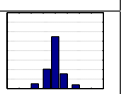
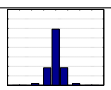
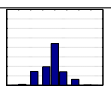
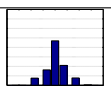
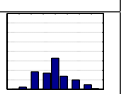
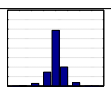
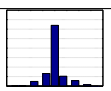
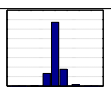
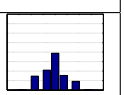
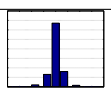
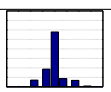
Scale Name	ρ	σ_ρ	S	Err	Err_{PCA}	Scale name	ρ	σ_ρ	S	Err	Err_{PCA}
HS	0.92	0.008	0.94			D	0.91	0.002	0.92		
HY	0.87	0.006	0.88			PD	0.86	0.008	0.88		
PA	0.84	0.009	0.85			PT	0.97	0.002	0.97		
SC	0.97	0.002	0.97			MA	0.84	0.009	0.86		
SI	0.95	0.003	0.96			RCD	0.97	0.002	0.97		
RC1	0.92	0.010	0.93			RC2	0.91	0.004	0.91		
RC3	0.87	0.010	0.89			RC4	0.88	0.012	0.89		
RC6	0.90	0.012	0.91			RC7	0.94	0.003	0.95		
RC8	0.91	0.007	0.92			RC9	0.91	0.004	0.92		

TABLE II

THE TABLE SHOWS HOW ONE CAN RECOVER A PERSON'S MMPI-2 SCORE ON A SCALE THAT ALL OF IT'S ITEMS ARE MISSING. ρ IS THE CORRELATION BETWEEN THE ORIGINAL SCORES AND THE GH CONVERTED SCORES WHILE NOT USING ANY OF THE MISSING ITEMS. ρ_{MC} IS ATTAINED BY IMPUTING THE MISSING ITEMS USING A MONTE CARLO MARKOV CHAIN (MCMC) PROCESS, AND SCORING THE COMPLETED RECORD USING THE MMPI-2 SCALES. THE FIRST HISTOGRAM, LABELED Err, COUNTS HOW MANY PEOPLE WERE SCORED WITH ERROR OF d. d IS THE DIFFERENCE BETWEEN MMPI-2 SCORES AND THE GH SCORES ON THE CORRUPTED RECORDS. THE DIFFERENT COLUMNS CORRESPOND TO $d < -15$, $-15 < d < -10$, $-10 < d < -5$, $-5 < d < -2$, $-2 < d < 2$, $2 < d < 5$, $5 < d < 10$, $10 < d < 15$ AND $15 < d$. IN THE SECOND HISTOGRAM d IS THE DIFFERENCE BETWEEN THE MMPI-2 SCORES ON THE COMPLETE RECORD AND THOSE COMPUTED AFTER IMPUTING THE MISSING SCALE USING THE MCMC METHOD.

Scale Name	ρ	ρ_{MC}	Err	Err_{MC}	Scale name	ρ	ρ_{MC}	Err	Err_{MC}
HS	0.85	0.74			D	0.89	0.82		
HY	0.77	0.54			PD	0.86	0.77		
PA	0.79	0.76			PT	0.96	0.92		
SC	0.96	0.93			MA	0.83	0.72		
SI	0.91	0.84			RCD	0.95	0.86		
RC1	0.85	0.69			RC2	0.91	0.82		
RC3	0.85	0.75			RC4	0.78	0.61		
RC6	0.82	0.81			RC7	0.95	0.91		
RC8	0.90	0.84			RC9	0.89	0.74