

Exploring the Persome:

A presentation from the PMC-SAPA lab for the Personality, Development and Health “zoom in”

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Based on a talk given at UCB:

<https://personality-project.org/revelle/presentations/ucb.20.pdf> and

Revelle, Dworak and Condon (2020)

<https://doi.org/10.1016/j.paid.2020.109905>



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Outline

Open Science

SAPA

Persomonics

Genome Wide Association Studies: GWAS ::
Persome Wide
Association Studies: PWAS
Profiles

Big Data

Open Science: A new idea or a long term tradition?

1. Science is a process for asking questions that have answers
 - Our questions and our answers need to be open and shared.
 - Our way of addressing these questions should be open to others.
 - Our results are for everyone, not just those who can afford to pay for journals.
 - Our results need to be trusted and trustworthy.
2. This is not a new idea, sharing ideas, methods and results is as old as the Royal Society from 1660.
 - It was an 'invisible college' of natural philosophers and physicians.
 - Royal Society's motto 'Nullius in verba' is taken to mean 'take nobody's word for it'. (We might now say, does it replicate?)
3. Personality research is an example of open science.
 - Tends to be well powered and replicable.
 - Tends to involve multiple studies over multiple years.
 - Growing tendency to use open and shared materials.

Questions we ask in personality

1. Kluckholm and Murray's (Kluckhohn & Murray, 1948) basic trichotomy remains active today
 - All people are the same (human nature)
 - Some people are the same (individual differences)
 - No person is the same (unique life stories of the individual)
2. Much of personality research is at this middle level of how some people are the same and differ from other people.
 - Description of individual differences
 - Dimensional models include Block's 2 (Block, 1971, 2002), Eysenck's Giant 3 (Eysenck, 1994), Big 5 (Digman & Takemoto-Chock, 1981; Digman, 1990; Goldberg, 1990), 8-9 (Comrey, 1995), Cattell's 16 (Cattell & Stice, 1957), and even Condon's "little 27" (Condon, 2018)
 - Different theoretical explanations of individual differences
 - SocioAnalytic (Hogan, 1982)
 - Biological (Eysenck, 1967; Gray, 1991; Corr, 2002; DeYoung, 2010, 2015)
 - Practical use of individual differences
 - Prediction of leadership effectiveness (Hogan, 2007), academic performance (Sackett & Kuncel, 2018) mortality, marital status, occupational choice, and mental health (Ozer & Benet-Martinez, 2006).

Traditional latent trait approach to measurement of personality

1. Known since [Spearman \(1904\)](#) that measures are befuddled with error.
2. Can reduce befuddlement (increase reliability) by aggregating items ([Brown, 1910](#); [Spearman, 1910](#)).
3. Structure of scales can be analyzed by latent trait (factor analytic) or components (not latent trait models, but frequently confused with them).
4. Factor analytic approaches led to convergence on a “consensual structure” of 5 factors ([Digman, 1990](#); [Goldberg, 1990](#))
5. Then, a race to bottom in developing shorter and shorter measures of the Big 5.
 - Goldberg’s original set of 100 adjectives ([Goldberg, 1992](#))
 - Gerard Saucier and the 40 mini markers [Saucier \(1994\)](#) and Oliver John et al ([John, Donahue & Kentle, 1991](#)) 44 phrased items.
 - Beatrice Rammstedt and Oliver John’s 10 items ([Rammstedt & John, 2007](#)) and the Gosling et al TIPI ([Gosling, Rentfrow & Swann, 2003](#)).
 - The lower bound: the 5 items of Ken Konstabel ([Konstabel, Lönnqvist, Leikas, Velázquez, H, Verkasalo, & et al., 2017](#))

A different approach: the power of the item

1. But personality \neq Big 5.
2. An alternative approach to giving fewer and fewer items to measure just the Big 5 is to give more and more items to measure as much of personality as possible.
3. In the PMC lab we are now examining the structure of more than 6,000 items and are on the way to 10,000 ([Condon, 2018](#); [Revelle, Wilt & Rosenthal, 2010](#); [Revelle, Condon, Wilt, French, Brown & Elleman, 2016](#))
4. We do this because we think that although only about 20% of any item measures a single higher order trait, at least 80-90% of an item is reliable variance.
5. We need ways to give more items and to examine the total reliable variance of the item.
6. But how to do this?
7. By apply techniques analogous to those of radio astronomy but already known to psychologists ([Lord, 1955](#)) as sampling of people and items.

SAPA overview

1. At the sapa-project.org we use Synthetic Aperture Personality Assessment (SAPA) methods to assess $\approx 20K$ participants per month. This is just a technique of Massively Missing Completely at Random (MMCAR) data presentation. Each participant is given a random subset of items chosen from an item pool of more than 6600 items. These items, extended from the [International Personality Item Pool](#) (Goldberg, 1999) and the [International Cognitive Ability Resource](#) (Condon & Revelle, 2014; Revelle, Dworak & Condon, 2020; Dworak, Revelle, Doebler & Condon, 2020), assess temperament, cognitive ability, interests and attitudes as well as self reported behaviors and demographic information.
2. Conventional psychometric techniques (both classical and IRT) are used to identify homogeneous scales; empirical item selection procedures are used to develop optimal item composites to predict a wide range of criteria. Data analysis code is done using the *psych* package (Revelle, 2020) in R (R Core Team,

3 Methods of collecting 256 subject * items data

1) 8 x 32 complete

46213634521143453443645331212414
21243623166421516154432261516513
51661351155165463622224435623344
11141343362332215612152135614522
25353121264561433433232246526411
61335154566424114612641225353516
24634342151536242425413513435116
11554654453123111162423325516334

Type 1 = sample subjects

Type 2 = sample items

Type 12 sample items and subjects

2) 32 x 8 complete

46323114
25443314
43315423
26314145
41435614
42236153
62421344
35234443
34514166
63415154
44441342
13514321
66365663
12264546
31466135
32645514
66151251
14411441
62443636
33316236
63325425
11531126
61155546
33245361
52241654
63212356
24414663
63661414
45555223
14364433
21461416
33232365

12) 32 x 32 MCAR $p=.25$

..3..2..6....4.55.....44.....
.....4..6..45..3.4..6...1
6..3.....6.1.....6.2.....5.6
...3522.....5.3...3.....5...
...3.2.2.....3..2.....65..5..
...51....324.....23.....5
...552.....25...54.5...
...44.4.5...3..6...6.....3..
...61.523.2...2.....3..
5.....42.4..6.5.....61..
...3...3.6..1.4...1..5.....5..
1...54.....2.4.33..6.....
4...52..6....44.3.....2
..44...1.....1..42...5..1..
..1..3.....2..3.521.....6..
.....3.142.....22.....12..
..4...2.....3..162...4....4
..4..6..3.4...1...5.33.....
5.....243..5...41.....1..
..5..3..4...4.4..5..1.....4..
...4.....3..5.2.....64.4..4..
...1.1.2...6....4.....55...2..
...3..2..53.....2..2.3.3.....
.....1...2..43...3.13.....5..
..2.....4..54...2.3..62...
22.....332..1...5.....6...
...5..3.4.....3...5.241.....
.....63.1.....6..5..4..2...5
..2.4..5.....52.4...44...
2.55...2...6.....6.....55...
..5.....4...6341.4..2...
55...5...45...3...2...

3 Methods of collecting 256 subject * items data

1) complete (Ideal)

22552141414336514122645166143244
32144265454235634562343524256611
43553143152141541641526114551151
52654223445614444431162645313124
62222255242315442652355414213325
22125412454242154221456444214564
65113311244511226522615346451412
54436452425245244554632246526466
55223643555215245514633426121226
35522554332664265346655451531612
6326124134146631124322223323541
32224431433144451645255464435552
11564655513111334341463561655541
24532624664444656366642463322555
255163622465232655665245644125611
322556354223423531523143414221354
23244456631411361161615126144214
34526633236542563633625123624421
13451522616451531355135621451536
31625444241623135123121345134162
4425252636555663352252162313453
54361436651313615433261662235132
46635454552135645224352362433436
26511624245416441145655363265265
635123312355426445524352562623235
1152366543365644645252332216333
56436532623253433145633663651242
15136366233651513351113353151452
46321152211446344326554442255226
62156523111352364233551656146433
65342552265235623363226156136333
553252123411346661654143661563535

2) Sample people

[illegible]

3) Items

22552141
32144265
43553143
52654223
62222255
22125412
65113311
54436452
55223643
35522554
63261241
32224431
11564655
24532624
25516362
32255635
23244456
34526633
13451522
31625444
44252526
54361436
46635454
26511624
63512331
11523665
56436532
15136366
46321152
62156523
65342552
55325212

12 (Matrix) Sampling Methods of collecting 256 subject * items data

a) 32 x 16 balanced incomplete

```

.....4122645166143244
.....4562343524256611
.....1641526114551151
.....4431162645313124
.....2652355414213325
.....45424215.....44214564
.....24451122.....46451412
.....42524524.....46526466
.....55521524.....26121226
.....33266426.....51531612
.....3414663112432222
.....4331444516452554
.....5131113343414635
.....6644446563666424
.....2645232556652456
32255635.....14221354
23244456.....26144214
34526633.....23624421
13451522.....21451536
31625444.....45134162
44252526.....35225241
54361436.....54332616
46635454.....52243523
26511624.....11456553
63512331.....55243525
1152366543365644
5643653262325343
1513636623365151
4632115221144634
6215652311135236
.....

```

b) 32 x 8 SAPA $p = .25$

```

..55.....1.....4...6...16.....4.
..2...4...45.....3.....2.2...1
..5.....1.....4...1...6...551...
..6...2.....4.....64...3.24
..22...5.....4.2...2...4...2...
..2.2...1.4.....1...2.....4.....6.
.....1124.....65...1...6.....
..44...4.2.....2.....2...52...
..5...3...5.....4...1.6.....1...6
...25.....2.....6...65.....61.
...1...3.....311.4...22.....
...244.....44...45.....2
..1.....1.11...4.4...5.....4.
...6.4.....3.66.2...2...5.
25...3.2.....6.....4.12...
...3...22...3...1...42...3.
..2...5...31...1.....2...21.
...2.6...3...2.6.....12...2...
...5...1...1.3135.1.....
...2...4.....35.....13.16.
..2...6...5.....2...1...3.53
543.....5.....2...2.51...
4...54...2...6.....3...36
...1...424...4...6.....5.6.
...235...6.....262...5
..15...5...3...4.4.....2...3.
...6.3.....1.5.3...63...2.
..1...66.....35...1.35.....
...5221.....4.....42...5...
..21.....3.....1.5.1.6...3
...4...2.523...3...2.....3...
55...2...4...3...1...6...5

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Reported in a recent article



Personality and Individual Differences

Available online 6 March 2020, 109905

In Press, Corrected Proof



Exploring the persome: The power of the item in understanding personality structure

William Revelle , Elizabeth M. Dworak, David M. Condon

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Characteristics of SAPA reported recently

1. Total number in shared data sets discussed today 126,884. Roughly 1,000,000 total have been collected.
2. Age 14-90 (mean = 26, median= 22)
3. Gender 63% Female (have switched to non-binary scale for more recent participants)
4. Education 15% less than 12 years, 9% HS grad, 41% in college, 6% some college 15% BA, 5% in grad school, 10% Grad or prof degree
5. 68% US, 4.3% Can, 3.7% UK, 2.1% AUS, ...

More items, alternative structures

1. Of about 2,084 item in the IPIP, representing 200 different scales, David Condon found that 696 items were actually unique and had no dominant factor structure (Condon, 2018) . However, he found that 135 of the items could be well organized in terms of 5 broad factors (the Big 5) and 27 narrower factors (the little 27).
2. Scores for 4,000 visitors to the SAPA-project for these 135 items and 10 criteria are included in the *psychTools* package which accompanies the *psych* package (Revelle, 2020) for R (R Core Team, 2019).
3. I am going to use this example set for a series of demonstrations. To encourage you to do these analyses yourself, we included the R code in the appendix to (Revelle et al., 2020)
4. I will also discuss another public data set for 126,884 participants with scores on the 696 items and 22 distinct criteria (Condon & Revelle, 2015; Condon, Roney & Revelle, 2017b a).

Yet another analogy – genetics

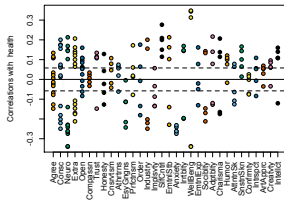
1. Most target gene studies have been dreadfully underpowered and produce too many type I errors.
2. With the exception of a few genes (color blindness, PKU), most genetic effects are very small.
3. Each Single Nucleotide Polymorphism (SNP) accounts for very little variance.
4. But with the ability to do Genome Wide studies aggregated across 100,000s to 1,000,000s of people, it is now possible to reliably identify SNPS associated with phenotypic traits.
5. It is also possible to find genetic propensity scores (basically just linear sums) of 1,000s SNPs at a time.
6. GWAS also introduces the concept of a genetic correlation, which is the correlation across the genome of effect sizes.
7. These genetic correlation assess the amount that the genetic variance in any two phenotypes is similar.

Analogous to GWAS is Persome Wide Association Studies (PWAS)

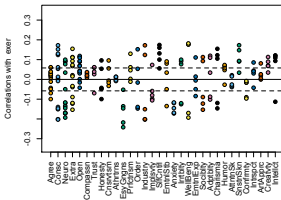
1. “Manhattan” plots are just ways of displaying GWAS or PWAS correlations.
2. In GWAS the plots are SNPS by chromosome.
3. in PWAS we organize the items by the scale they are associated with.
4. We do this for the spi data on three criteria: health, exercise and smoking.

Manhattan plots can show the raw correlations or $-\log p$ values

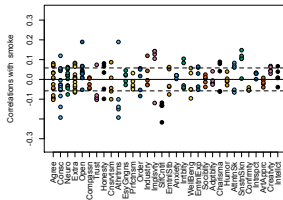
Manhattan Plot of health



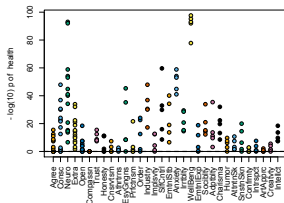
Manhattan Plot of exer



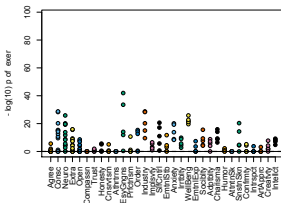
Manhattan Plot of smoke



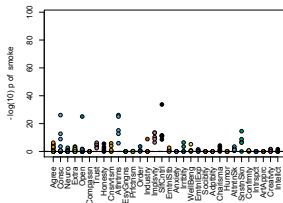
health



exer



smoke

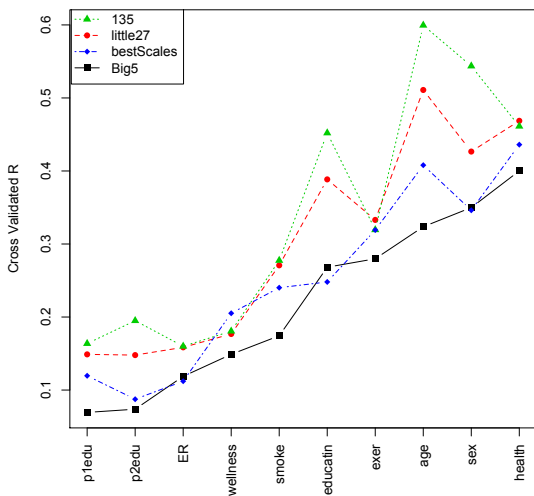


An alternative to regression: `bestScales`

1. An alternative to multiple regression is to choose the best unit weighted items. (see the Manhattan plots)
2. We described a new algorithm based upon very old ideas (Elleman, McDougald, Revelle & Condon, 2020).
3. Choose items most correlated with a criterion. Cross validate these multiple times (using k-folds or bagging) and then form the unit weighted composites.
4. Based upon the “Robust beauty of improper linear models” (Dawes, 1979) and the idea that regression weights are fungible (Waller, 2008).
5. Generally pretty good, if not optimal, and much more understandable in that we can examine what the best items are.
6. We do this for the `spi` data set and compare the cross validated correlations with those of the Big5, little 27 and 135 item multiple Rs.

Cross validation for 5, 27, 135 and bestScales for the spi

Cross validation of multiple regression on spi data



1. Best scales (made up of the top 20 items are not as good as
2. linear regression from all 135 items
3. linear regression from 27 factors (using 135 items)
4. but are better than big 5 (using 70 items)

What are the best items predicting these criteria

Table: Smoking

A table from the psych package in R

Variable	Freq	men.r	sd.r	item
q_1461	10	-0.24	0.01	Never spend more than I can afford.
q_1867	10	-0.20	0.01	Try to follow the rules.
q_1609	10	0.19	0.01	Rebel against authority.
q_1173	10	0.17	0.01	Jump into things without thinking.
q_1624	10	-0.17	0.01	Respect authority.
q_369	10	-0.16	0.01	Believe that laws should be strictly enforced.
q_56	10	-0.16	0.01	Am able to control my cravings.
q_35	10	0.16	0.01	Act without thinking.
q_1462	10	-0.15	0.01	Never splurge.
q_1424	10	0.15	0.01	Make rash decisions.
q_736	10	-0.15	0.01	Easily resist temptations.
q_598	10	0.14	0.01	Do crazy things.
q_1590	10	-0.13	0.01	Rarely overindulge.
q_1452	9	0.13	0.01	Neglect my duties.
q_4276	9	0.12	0.01	Often make decisions on the spur of the moment.

Best items predicting rated health

Table: health

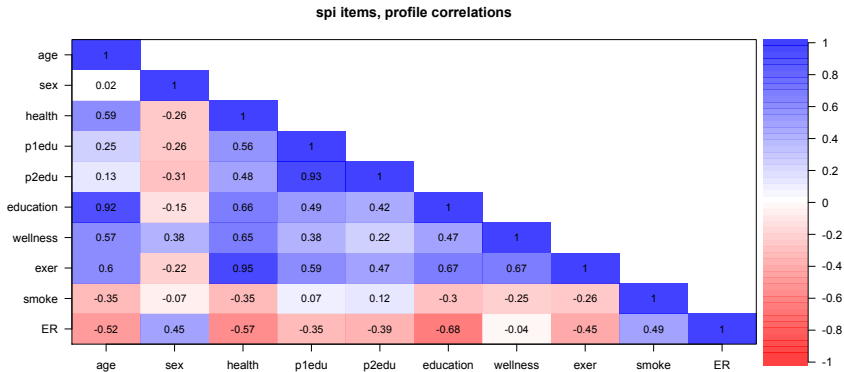
A table from the psych package in R

Variable	Freq	men.r	sd.r	item
q_820	10	0.36	0.01	Feel comfortable with myself.
q_811	10	-0.35	0.01	Feel a sense of worthlessness /hopelessness.
q_2765	10	0.35	0.00	Am happy with my life.
q_578	10	-0.34	0.01	Dislike myself.
q_1371	10	0.31	0.01	Love life.
q_56	10	0.28	0.01	Am able to control my cravings.
q_1505	10	-0.28	0.01	Panic easily.
q_808	10	-0.27	0.01	Fear for the worst.
q_4249	10	-0.27	0.01	Would call myself a nervous person.
q_1452	10	-0.24	0.01	Neglect my duties.
q_979	10	-0.24	0.01	Get overwhelmed by emotions.
q_39	10	0.24	0.01	Adjust easily.
q_4252	10	-0.24	0.01	Am a worrier.
q_1444	10	-0.23	0.01	Need a push to get started.
q_1024	10	-0.23	0.01	Hang around doing nothing.
q_1840	10	0.23	0.01	my moods don't change more than most peoples.
q_1989	10	-0.22	0.01	Worry about things.
q_1052	0	0.21	0.01	Have a slow pace to my life.

PWAS correlations

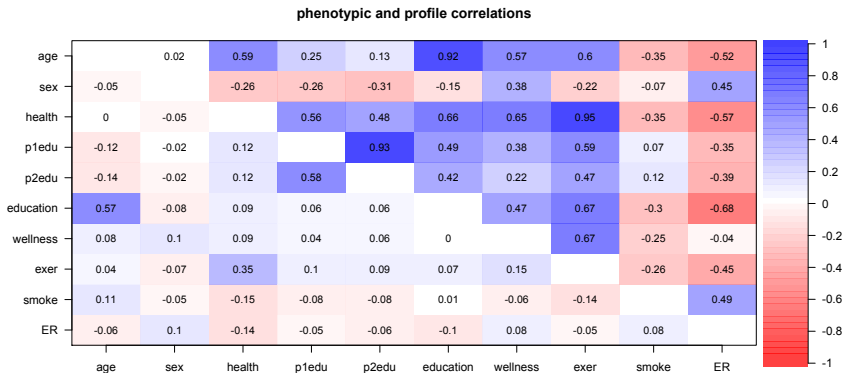
1. Genetic correlations are correlations taken across the genome and reflect the amount of shared genetic variance in two pheontypes.
2. So, we can find the profile correlation across the persome to examine shared predictable variance of phenotypes
3. I show three different correlation plots
 - Phenotypic correlations of our 10 spi crteria
 - Profile correlations of these same 10 criteria where the profile is essentially the Manhattan plot
 - To compare these two, I combine them into one plot

Profile correlations of the spi criteria



Show both the phenotypic and profile correlations

Compare the magnitude of the effects



Profile correlations reflect shared predictable variance

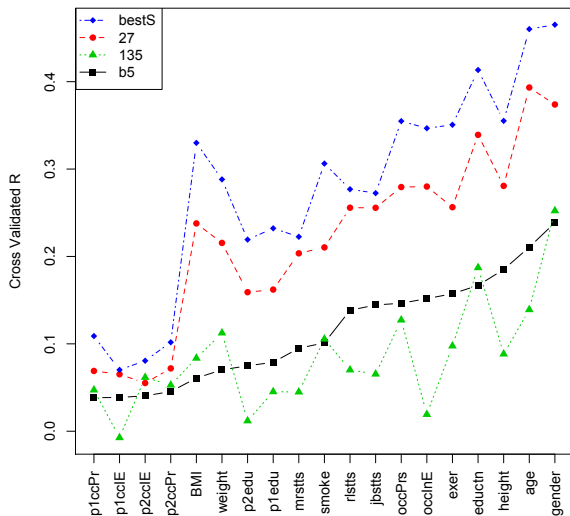
1. Phenotypic correlations reflect all of the variance of the criteria.
2. Profile correlations reflect shared *predictable* variance.
3. Do we achieve a better understanding of the phenomena by examining what they have in common?
4. Consider the correlation between exercise and health (.35 versus .95), Emergency Room visits and smoking (.08 versus .49)
5. Is this an alternative way to adjust correlations for reliability?

We can replicate this with 126,884 cases

1. The data are taken from DataVerse [Condon & Revelle \(2015\)](#); [Condon et al. \(2017a,b\)](#)
2. I show just a few analyses
3. First the cross validated prediction
4. Then the profile results.

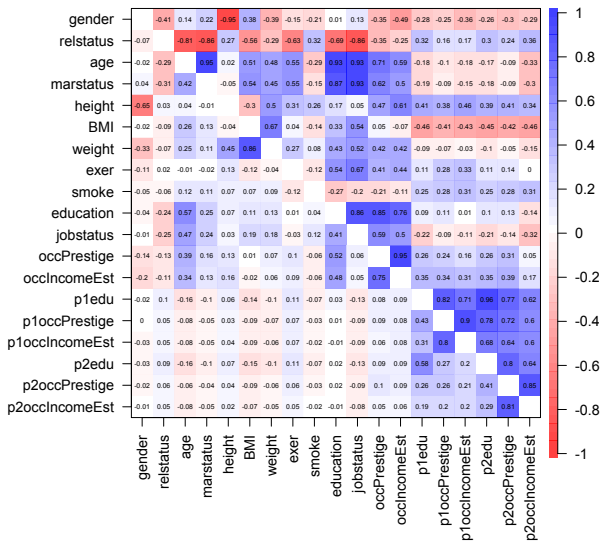
Comparing Big 5, little 27, 135 item regressions with best of 696

Cross validation of multiple regression on sapa data



19 criteria phenotypic versus profile correlations

Phenotypic (lower) and Profile (upper) correlations



Conclusion and an invitation

1. Other sciences have developed techniques that we can share (at least by analogy).
2. Combining techniques similar to those from Radio Astronomy and from genetics allows us to ask different questions than we have been asking.
3. Items have much more information that we think (although the developers of empirical methods such as [Gough \(1957\)](#) or [Hathaway & McKinley \(1943\)](#) knew this years ago).
4. It is time to rethink our reliance on latent variable models., Perhaps we should focus on observables that we care about.
5. This is a direct challenge to those of us who like to think in casual models and the biological basis of personality.
6. Am I advocating personality engineering or personality theory? I am not sure.
7. However, I am sure that it might be time for us to rethink our reliance on latent trait models.

Need for open science

1. These techniques rely on shared materials, shared methods, and open science.
2. Can we use SAPA like techniques to refocus on the power of the item and move beyond the Big 5?
3. We have used a similar approach in the measurement of ability in the International Cognitive Ability Resource (ICAR). By combining traditional temperament measures (e.g. the spi items or the magic 696 with measures of interests and ability, we can go even further.
4. Join us.

Relevant links: A talk given at UCB:

<https://personality-project.org/revelle/presentations/ucb.20.pdf> and Revelle, Dworak and Condon (2020) <https://doi.org/10.1016/j.j.paid.2020.109905>
today: <https://personality-project.org/revelle/presentations/persome.20.pdf>

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