

# Assessing Personality with Massively Missing Completely at Random data: An information Theoretic Approach

Part of an Experts Meeting on Personality Measurement:  
Edinburgh, Scotland, September 6-8

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Slides at <http://personality-project.org/sapa>



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## Outline

### Introduction

Measuring individual differences: the tradeoff between breadth versus depth

SAPA techniques for everyone: It does not require large samples

### SAPA theory

Synthetic Aperture Astronomy as an analogy

Sample items as well as people

### Simulating SAPA with real data

2000 subjects 15 items

400 subjects: How low can we go?

### What about ESM?

### Conclusions

### Appendices

## Overview

1. Using big data techniques has changed the way we study personality. The increase in power due to very large samples allows the detection of small but meaningful effects – structural measures can have finer resolution than previously available and cross-validated predictive accuracy can be substantially enhanced.
2. But these techniques are not limited to big data. We discuss one such approach that can be used for both large ( $N > 10^5$ ), medium ( $N \approx 10^3 - 10^4$ ) as well as smallish ( $N=100-400$ ) size samples.
3. We show how SAPA procedures improve scale reliability and validity over using short scales when giving random subsets of items selected from larger scales.
4. We encourage the use of item sampling (SAPA) techniques in many typical research applications, including ESM.

## SAPA overview

1. At the [sapa-project.org](https://sapa-project.org) we use Synthetic Aperture Personality Assessment (SAPA) methods to assess 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](#), assess temperament, cognitive ability, interests and attitudes as well as self reported behaviors.
2. Conventional psychometric techniques are used to identify homogeneous scales; empirical item selection procedures are use to develop optimal item composites to predict a wide range of criteria. Data analysis code is done using the *psych* package (Revelle, 2018) in R (R Core Team, 2018).

## The basic problem: Fidelity versus bandwidth

1. Many personality traits, interests and cognitive abilities are multidimensional and have complex structure.
  - To measure these, we need to have the precision that comes with many participants.
  - But we also need the bandwidth that comes with many items.
  - But participants are reluctant to answer very many items.
2. This has led to the quandary of should you give many people a few items or a few people, many items?
3. Our answer is to do both, but with a *Massively Missing Completely At Random* (MMCAR) data structure.
4. We refer to this technique as *Synthetic Aperture Personality Assessment* (SAPA) to recognize the analogy to synthetic aperture radio astronomy (Revelle, Wilt & Rosenthal, 2010; Revelle, Condon, Wilt, French, Brown & Elleman, 2016)
5. This is functionally what Frederic Lord (1955, 1977) suggested 63 years ago. It is time to take him seriously.

## Lord (1955) and matrix sampling

1. Given an  $N$  (subjects) by  $n$  (item) matrix, we can sample:
2. Type 1: Subjects – basic statistical theory
  - $\bar{x}$  and its standard error  $\sqrt{\frac{\sigma^2}{N-1}}$
  - $r_{xy}$  and its standard error  $\sqrt{\frac{1-r^2}{N-2}}$
3. Type 2: Items – this is the basis of classical reliability theory especially domain sampling (Tryon, 1957, 1959)
  - $KR_{20} = \alpha = \lambda_3$  represent the correlation of a test with a test just like it sampled from a larger population of items
  - $\omega_h$  and  $\omega_t$  similarly are estimates of what the general factor,  $\omega_h$ , or total,  $\omega_t$ , correlation would be with another representation in the domain
4. Type 12: Matrix sampling of subjects and items
  - Special case is balanced incomplete blocks (BIB).
  - General case is Missing Completely at Random (MCAR).

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### 3 Methods of collecting 256 subject \* items data

- 1) 8 x 32 complete      2) 32 x 8 complete      12) 32 x 32 MCAR p=.25

46213634521143453443645331212414  
21243623166421516154432261516513  
51661351155165463622224435623344  
11141343362332215612152135614522  
25353121264561433433232246526411  
61335154566424114612641225353516  
24634342151536242425413513435116  
11554654453123111162423325516334

Type 1 = sample subjects

Type 2 = sample items

Type 12 sample items and subjects

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

..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.....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..32..





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## 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..
```

## Type 12 sampling (matrix sampling)

1. Balanced incomplete blocks works but is hard if giving less than 50% coverage
  - 50% requires 6 blocks to be fully balanced (divide into 4ths and then present all pairs of the fourths)
  - AB, AC, AD, BC, BD, CD where A, B, C, and D are 1/4 of the total
  - Even then, items within blocks co-occur more than items between blocks
  - 33% samples require 15 blocks, 25% 28 blocks
2. SAPA sampling (Massively Missing Completely at Random) allows any sampling rate.
3. BIB can be done with printed forms, MMCAR requires computer administration.
4. Possible to do FIML with BIB design, need to do pairwise complete for SAPA.

## Why we care: Breadth vs. depth of measurement

1. Factor structure of domains needs multiple constructs to define structure.
2. Each construct needs multiple items to be measured reliably.
3. This leads to an explosion of potential items.
4. But, people are willing to answer only a limited number of items.
5. This leads to the use of short and shorter forms (the NEO-PI-R (Costa & McCrae, 1992) with 300, the IPIP (Goldberg, 1999) Big 5 with 100, the BFI (John, Donahue & Kentle, 1991) with 44 items, the BFI2 (Soto & John, 2017) with 60, the 30 item 'Short Five' (Konstabel, Lönnqvist, Leikas, Velázquez, H, Verkasalo, & et al., 2017), the TIPI (Gosling, Rentfrow & Swann, 2003) with 10 and the 10 item BFI (Rammstedt & John, 2007) ) to include as part of other surveys.
6. Unfortunately, with this reduction of items, breadth of substantive content is lost. We offer an alternative procedure.

## Example studies with subject/item tradeoffs

1. The Potter-Gosling internet project ([outofservice.com](http://outofservice.com)) has given over 10,000,000 tests since 1997. Originally the 44 items of the Big Five Inventory (BFI) (John et al., 1991) although they are now giving the BFI2 (Soto & John, 2017).
2. The Stillwell-Kosinski ([mypersonality.org](http://mypersonality.org)) Facebook application (no longer in service) gave 7,765 people the IPIP version of the NEO-PI-R with facets (300 items), 1,108,472 the IPIP NEO-PI R domains (100 items), and 3,646,237 brief (20 item) surveys. Cross linked to likes and Facebook pages (Kosinski, Matz, Gosling, Popov & Stillwell, 2015; Youyou, Kosinski & Stillwell, 2015).
3. Johnson reports [two data sets](#): 300 IPIP-NEO items for 145,388 participants and 120 IPIP-NEO items for 410,376 participants (Johnson, 2014).
4. Smaller scale studies include the [BBC data set](#) of the 44 items of the BFI on 386,375 and the initial report on the BFI-2 (Soto & John, 2017) with several thousand subjects with 60 items.

## Exceptions to the shorter and shorter inventory trend

1. Lew Goldberg and his colleagues at the University of Oregon developed the Eugene-Springfield sample (Goldberg & Saucier, 2016) which has given several thousand items to  $\approx 1,000$  predominantly white middle class participants over 10 years. This sample has been the basis of the development and validation of the International Personality Item Pool (see [ipip.ori.org](http://ipip.ori.org)).
2. In fact, many of the subsequent attempts at personality scale development have used the Eugene-Springfield sample, e.g., the BFI (John et al., 1991), and the Big Five Aspect Scales (BFAS) of DeYoung, Quilty & Peterson (2007).

## The Eugene Springfield sample and the International Personality Item Pool

1. Unfortunately, many of the items that have come out of the E-S sample were prematurely selected to represent the Big 5. That is, even though meant to capture the many dimensions of the lexicon, the adjectival descriptors used had been trimmed to those matching the 5 factors that have been known since the 1950's (Kelly & Fiske, 1950, 1951; Tupes & Christal, 1961; Norman, 1963).
2. Because of the ease of use and the openness of the IPIP, most of the short forms followed the Big Five structure that came out of the E-S sample.

## SAPA techniques can work for you

1. At the [Personality Project](https://sapa-project.org) (Revelle et al., 2010, 2016) (now at [sapa-project.org](https://sapa-project.org)) we have taken the opposite direction and have given more and more items including measures of temperament, ability, and interests and we are now developing item statistics on more than 6,600 items (Condon & Revelle, 2017) for almost 500,000 participants (but using SAPA procedures).
2. We have reported computer simulations of our procedures but now we want to demonstrate with real data the amazing power of massively missing data.
3. In particular, we want to show that the techniques can work on relatively small samples (as small as  $\approx 100 - 400$  as well as the the larger ones we have been working with.
4. We reported some of this before at ECP-19 (Revelle & Condon, 2018) and are now pushing even further,

## Trading items for people: Studies, Items, People, Items x People

**Table:** Data sets vary in their sampling strategy and the Potter-Gosling and Stillwell/Kosinski data sets seem to have more data than the others

Study	N	Items (n)	Items/ Person (k)	Items* People
Potter-Gosling	$10^7$	44	44	$4.4 * 10^8$
Stillwell-Kosinski	$4.5 * 10^6$	20-300	20-300	$1.7 * 10^8$
Johnson	$4.1 * 10^5$	120	120	$4.9 * 10^7$
Johnson	$1.4 * 10^5$	300	300	$4.3 * 10^7$
SAPA* (2010-2017)	$2.5 * 10^5$	2000	100-150	$2.5 * 10^7$
SAPA+ (2017-2018)	$2 * 10^5$	6,600	100-150	$2 * 10^7$
SAPA- (pre 2010)	$6.3 * 10^4$	500	100-150	$9.4 * 10^6$
Eugene-Springfield	$10^3$	3,000	3,000	$3 * 10^6$

But given basic statistical theory, is it worth while to increase the sample size so much? What is the effect of giving more items at the cost of reducing the sample size?

Consider the amount of *information* which varies by number of correlations  $\frac{n*(n-1)}{2}$  and  $1/(\text{standard error of the } r) \approx \sqrt{N}$ .



## Trading items for people: Studies: Items, People, Items x People and Information

Information varies by the number of correlations ( $n * (n - 1) / 2$ ) weighted by their standard errors which vary by  $\sqrt{N}$

**Table:** Data sets vary in their sampling strategy and the seemingly smaller sets, by giving many more items actually have more total information

Study	N	Items (n)	Items/ Person (k)	Items* People	Information
SAPA+	$2 * 10^5$	6,600	100-150	$2 * 10^7$	$2.2 * 10^8$
E-S	$10^3$	3,000?	3,000	$3 * 10^6$	$1.4 * 10^8$
S-Ki	$4.5 * 10^6$	20-300	20-300	$1.7 * 10^8$	$9.5 * 10^7$
SAPA*	$2.5 * 10^5$	1-2,000	100-150	$2.5 * 10^7$	$7.5 * 10^7$
Johnson	$1.4 * 10^5$	300	300	$4.3 * 10^7$	$1.7 * 10^7$
SAPA (pre 2010)	$4.3 * 10^3$	500	100-150	$2.5 * 10^7$	$9.3 * 10^6$
Johnson	$4.1 * 10^5$	120	120	$4.9 * 10^7$	$4.6 * 10^6$
P-G	$10^7$	44	44	$4.4 * 10^8$	$3.0 * 10^6$

SAPA pairwise:

+SAPA 2017-2018 (100)    \* SAPA 2013-2017 (1,400)    -SAPA 2010-2013 (1100)

## Many items versus many people

1. Not only do want many people, we also want many items.
2. Resolution (fidelity) goes up with sample size, N, (standard errors are a function of  $\sqrt{N}$ )

$$\sigma_{\bar{x}} = \frac{\sigma_x}{\sqrt{N-1}} \quad \sigma_r = \sqrt{\frac{1-r^2}{N-2}}$$

3. Also increases as number of items, n, measuring each construct (reliability as well as signal/noise ratio varies as number of items and average correlation of the items)

$$\lambda_3 = \alpha = \frac{n\bar{r}}{1 + (n-1)\bar{r}} \quad s/n = \frac{n\bar{r}}{(1 - n\bar{r})}$$

4. Breadth of constructs (band width) measured goes up by number of items (n).
5. Thus, we need to increase N as well as n. But how?

## A short diversion: the history of optical telescopes

Resolution varies by aperture diameter (bigger is better)

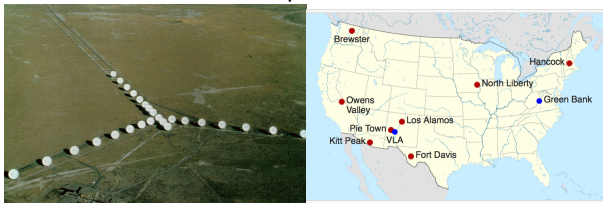


## A short diversion: history of radio telescopes

Resolution varies by aperture diameter (bigger is still better)



Aperture can be synthetically increased across multiple telescopes  
or even multiple observatories





## Can we increase $N$ (subjects) and $n$ (items) at the same time?

1. Frederic Lord (1955) introduced the concept of sampling people as well as items.
2. Apply basic sampling theory to include not just people (well known) but also to sample items within a domain (less well known).
3. Basic principle of Item Response Theory and tailored tests.
4. Used by Educational Testing Service (ETS) to pilot items.
5. Used by Programme for International Student Assessment (PISA) in incomplete block design (Anderson, Lin, Treagust, Ross & Yore, 2007).
6. Discussed at IMPS (2017) meeting by Rutkowski and Matta in the missing data symposium.
7. Can we use this procedure for the study of individual differences without being a large company?
8. Yes, apply the techniques of radio astronomy to combine measures synthetically and take advantage of the web.

## Subjects are expensive, so are items

1. In a survey such as Amazon's Mechanical Turk (MTURK), we would need to pay by the person and by the item.
2. Volunteer subjects are not very willing to answer many items.
3. Why give each person the same items? Sample items, as we sample people.
4. Synthetically combine data across subjects and across items. This will imply a missing data structure which is
  - Missing Completely At Random (MCAR), or even more descriptively:
  - Massively Missing Completely at Random (MMCAR) (we sometimes have 99% missing data although our median is only 93% missing!)
5. This is the essence of Synthetic Aperture Personality Assessment (SAPA) (Condon & Revelle, 2014; Condon, 2014; Revelle et al., 2016, 2010).
6. This is a much higher rate of missingness than discussed in the balanced incomplete block design of NAEPS or PISA.



### 3 Methods of collecting 256 subject \* items data

a) 8 x 32 complete

b) 32 x 8 complete

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

46213634521143453443645331212414  
21243623166421516154432261516513  
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25353121264561433433232246526411  
61335154566424114612641225353516  
24634342151536242425413513435116  
11554654453123111162423325516334

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13514321  
66365663  
12264546  
31466135  
32645514  
66151251  
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5.....243..5...41.....1..  
..5..3..4...4.4..5..1.....4..  
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...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..32..

## Synthetic Aperture Personality Assessment

1. Give each participant a random sample of  $p_n$  items taken from a larger pool of  $n$  items.  $p_i$  might be anywhere from .01 to 1.
2. Find covariances based upon “pairwise complete data”. Each pair appears with probability  $p_i p_j$  with a median of .01.
3. Find scales based upon basic covariance algebra.
  - Let the raw data be the matrix  ${}_N\mathbf{X}_n$  with  $N$  observations converted to deviation scores.
  - Then the item variance covariance matrix is  ${}_n\mathbf{C}_n = \mathbf{X}'\mathbf{X}N^{-1}$
  - and scale scores,  ${}_N\mathbf{S}_s$  are found by  $\mathbf{S} = {}_N\mathbf{X}_p\mathbf{K}_s$ .
  - ${}_n\mathbf{K}_s$  is a keying matrix, with  $k_{ij} = 1$  if *item*<sub>*i*</sub> is to be scored in the positive direction for scale *j*, 0 if it is not to be scored, and -1 if it is to be scored in the negative direction.
  - In this case, the covariance between scales,
 
$${}_s\mathbf{C}_s = {}_s\mathbf{S}'{}_N\mathbf{S}_sN^{-1} =$$

$${}_s\mathbf{C}_s = (\mathbf{X}\mathbf{K})'(\mathbf{X}\mathbf{K})N^{-1} = \mathbf{K}'\mathbf{X}'\mathbf{X}\mathbf{K}N^{-1} = \mathbf{K}'{}_n\mathbf{C}_n\mathbf{K}. \quad (1)$$
4. That is, we can find the correlations/covariances between scales from the item covariances, not the raw items.





## Total information

1. The information in a correlation varies by its standard error

$$\sigma_r = \sqrt{\frac{1-r^2}{N-2}}$$

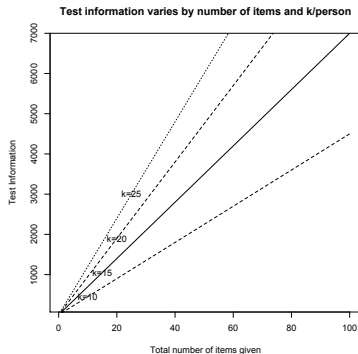
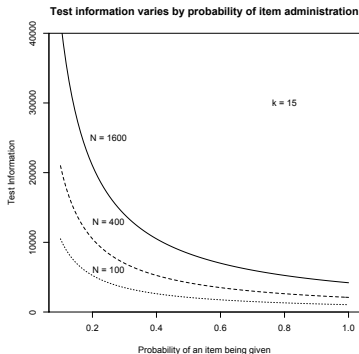
2. In SAPA, k items/person are randomly selected with probability p from a larger number, n ( $k = pn$ ).
3. Thus, the number of subjects per item is  $pN$ .
4. The total number of correlations is just  $\frac{n*(n-1)}{2}$  and the number of subjects per correlation is  $p^2N$ .
5. Total information is number of correlations \*  $\sqrt{p^2N} = \frac{n*(n-1)}{2} \sqrt{p^2N} = \frac{(k/p)((k/p)-1)}{2} * \sqrt{p^2N} = \frac{k*(k-1)\sqrt{N}}{2*p}$ .
6. For the "normal case" where  $p = 1$ , the information is just what we expect—a quadratic function of k:  $I_{kN} = \frac{k*(k-1)\sqrt{N}}{2}$ .
7. But the more interesting case (the SAPA case) is for  $p < 1$  the information is a hyperbolic function of p:  
 $I_{pkN} = \frac{k*(k-1)\sqrt{N}}{2*p}$  but a linear function of the total number of items given ( $n = k/p$ )  $I_{pkN} = \frac{n*(k-1)}{2} * \sqrt{N}$



## Total information varies by the number of items (n) and the probability of sampling (p) and total sample size (N)

For k items/subject and N subjects, if every item is given with probability p, the information in the test is

$$I_{pkN} = \frac{k*(k-1)\sqrt{N}}{2*p} = \frac{n*(k-1)}{2} * \sqrt{N}$$

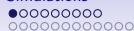


## Demonstrations of SAPA with real data

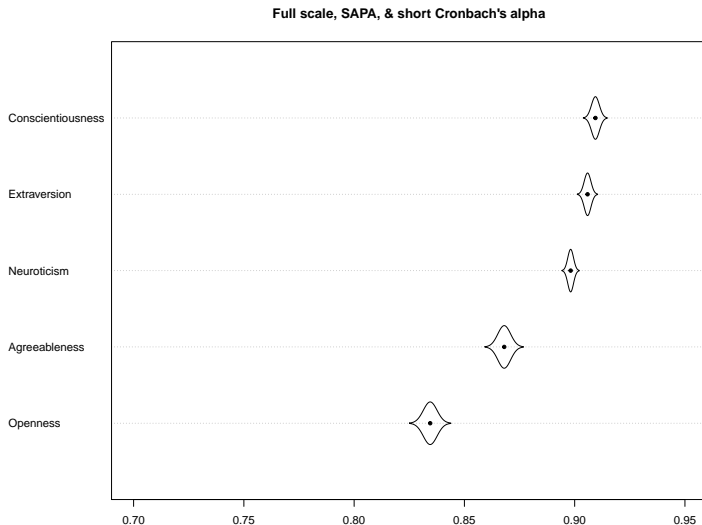
1. At ECP (Revelle & Condon, 2018) we showed simulations of SAPA techniques using 70 items from the SPI-135 (Condon, 2017)
  - We demonstrated full recovery of structure for short (15 item) “sapaized” scales sampled from the SPI-70.
  - Reported success at 2,000 subjects, hinted at it working for 1,000
  - The question was: “how low can we go?”
2. Now we show simulations of SAPA technique using John Johnson’s NEO-IPIP-300 data (145,388 complete participants) from Johnson (2014) from which we derived the 120-item IPIP-NEO
3. We show results for 15 item “sapaized” scales from the full 120 for 2,000 subjects and for 30 item “sapaized” scales for 400 subjects.

## Simulation technique

1. From a complete data set do 20 non-overlapping samples (“K-fold”) of size  $N=2000$  or 400 for  $n=120$  items
2. Compare 3 types of models
3. The structure of all items (i.e.,  $k = 120$ )
4. The structure of sapaized items ( $k = 15/30$ )
  - For each of  $N$  subjects, make all except  $k=15/30$  missing completely at random
  - Thus  $p = k/n = 15/120 = .125$  or  $p = 30/120 = .25$
5. The structure of short scales (Big 5 from 15/30 items)
6. We now compare the full data, “sapaized” data, and the short scales.
7. For each graph we show cats eyes for the complete data, error bars for sapaized and short scales.



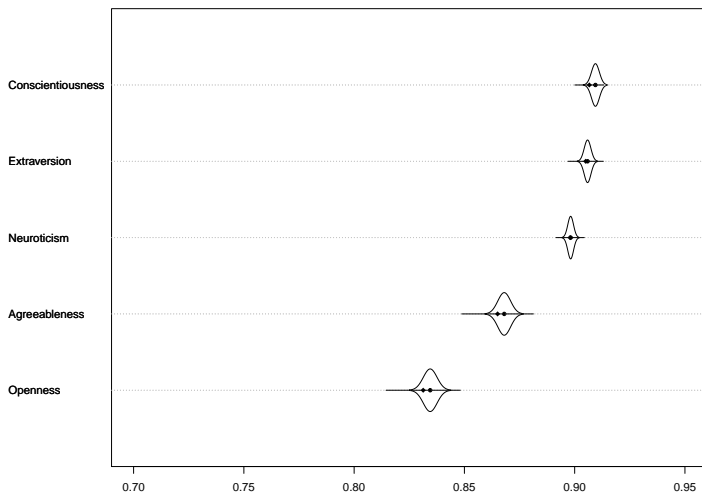
## $\alpha$ for 2000 subjects sample from Johnson 120 item IPIP, full scales





## $\alpha$ for 2000 from Johnson 120 item IPIP, sapa sampling 15 items

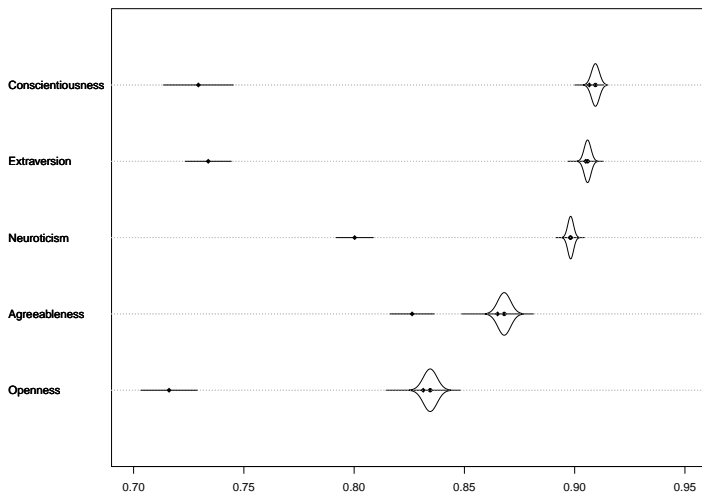
Full scale, SAPA, & short Cronbach's alpha



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$\alpha$  N=2000 from Johnson 120 item IPIP, 15 item sapo + short scales

Full scale, SAPA, & short Cronbach's alpha



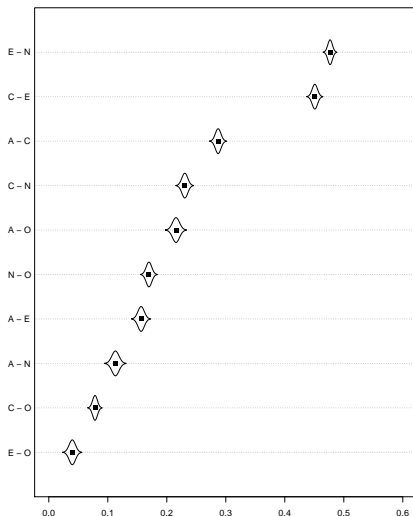
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# N = 2000 subjects Johnson 120 item IPIP, full scales

Full scale, SAPA, & short scale (absolute) correlations  $\pm 1$  SD

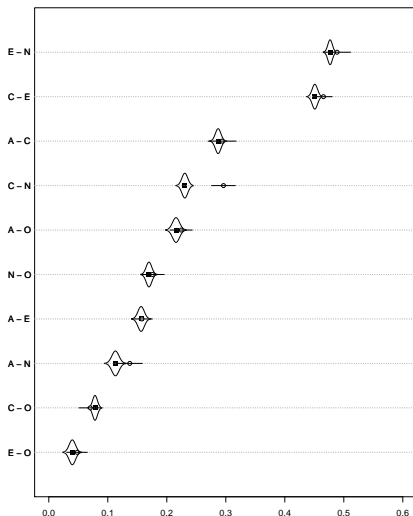




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# N=2000 Johnson 120 item IPIP, sapa sampling 15 items

Full scale, SAPA, & short scale (absolute) correlations  $\pm 1$  SD



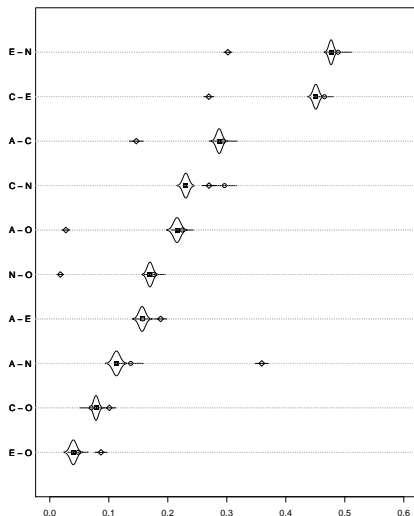
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# N=2000 120 item IPIP, 15 item sapa and short scales

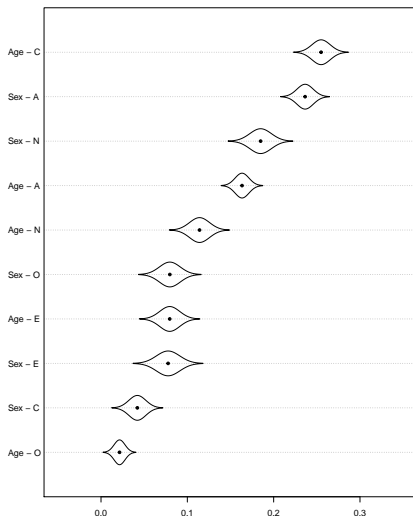
Full scale, SAPA, & short scale (absolute) correlations  $\pm 1$  SD



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# N=2000 from Johnson 120 item IPIP, full scales: Validity

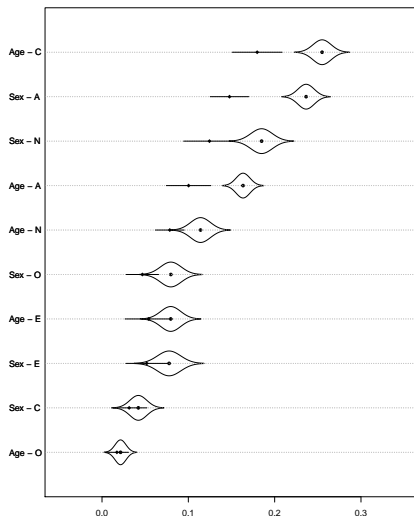
Full scale, SAPA, & short scale (absolute) validity coefficients



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# N=2000 Johnson 120 item IPIP, sapa sampling 15 items: Validity

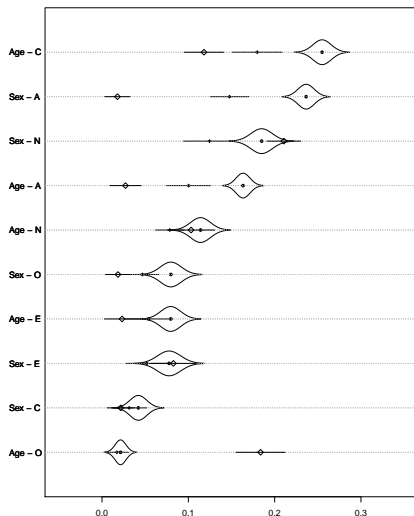
Full scale, SAPA, & short scale (absolute) validity coefficients





# N=2000 120 item IPIP, sapa 15 items + Short scales: Validity

Full scale, SAPA, & short scale (absolute) validity coefficients

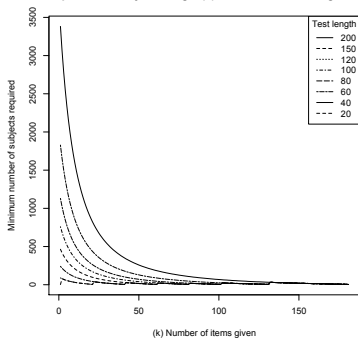


## Can we apply SAPA to smaller samples: e.g. How low can we go?

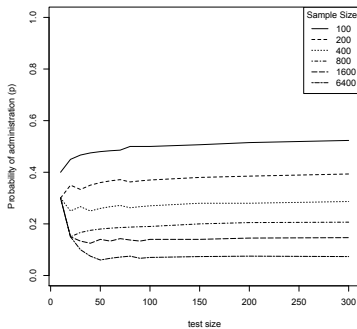
1. It seems as if the limit of the procedure is based upon the likelihood of random samples not producing empty correlation cells.
2. If we sample items with probability  $p$ , then the expected number of observations per pairwise correlation is  $p^2 N$ .
3. But the standard deviation of a binomial with probability  $P = \sqrt{\frac{PQ}{N}}$  where  $Q = 1-P$ .
4. We need to make sure that  $p^2 N - 3 * \sqrt{\frac{p^2 * (1-p^2)}{N}} > 2$
5. Functionally, this means that  $p^2 N > 25$ .
6. Thus, we can calculate the number of items ( $k$ ) we can sample from the total number of items ( $n$ ) for sample size ( $N$ ).
7. We show this graphically

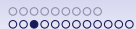
## Probability of sampling is limited by sample size

N required varies by test length (n) and number of items given (k)



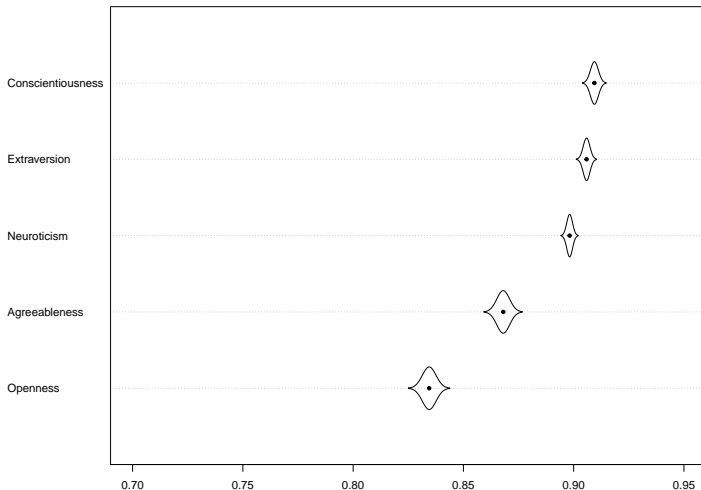
Minimum Probability for SAPA





## $\alpha$ N=400 Johnson 120 item IPIP, full scales

Full scale, SAPA, & short Cronbach's alpha

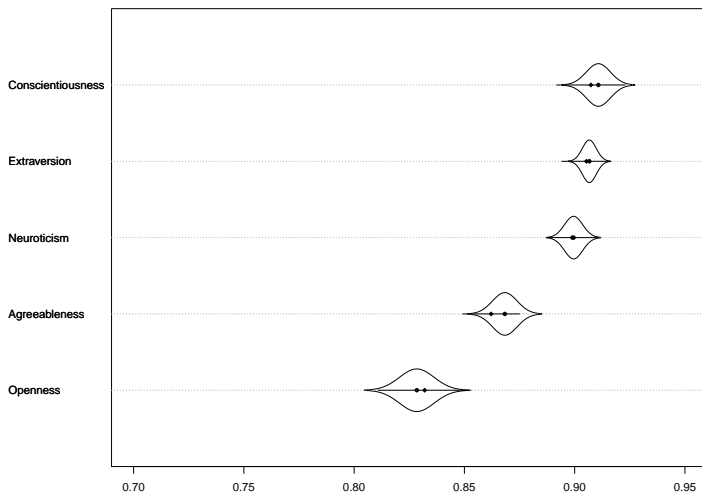






## $\alpha$ N=400 Johnson 120 item IPIP, sapa sampling 30 items at a time

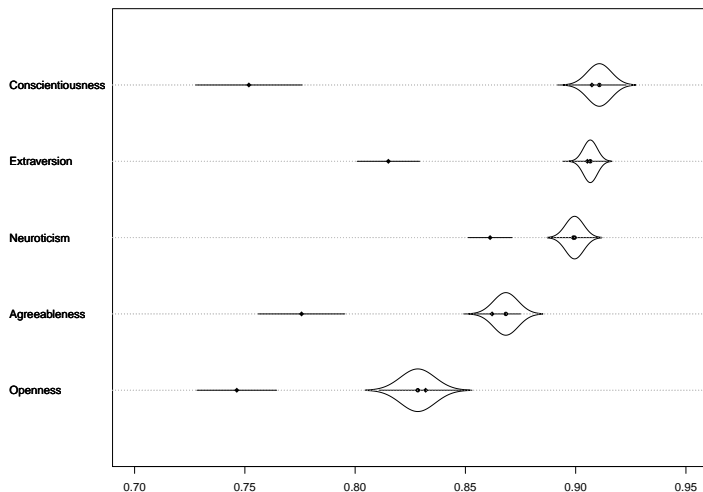
Full scale, SAPA, & short Cronbach's alpha





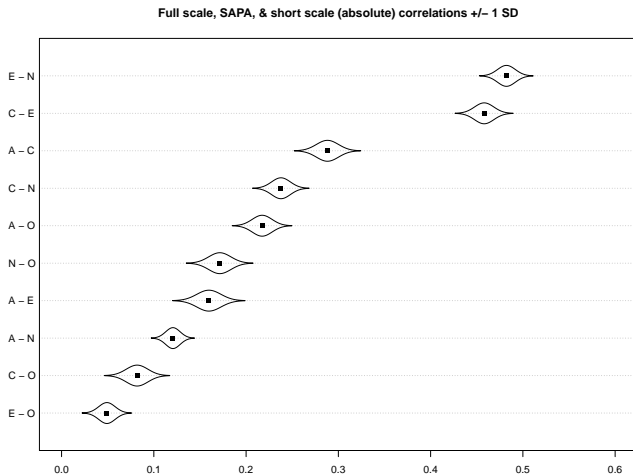
# $\alpha$ N = 400 Johnson 120 item IPIP, 30 item sapo and short scales

Full scale, SAPA, & short Cronbach's alpha

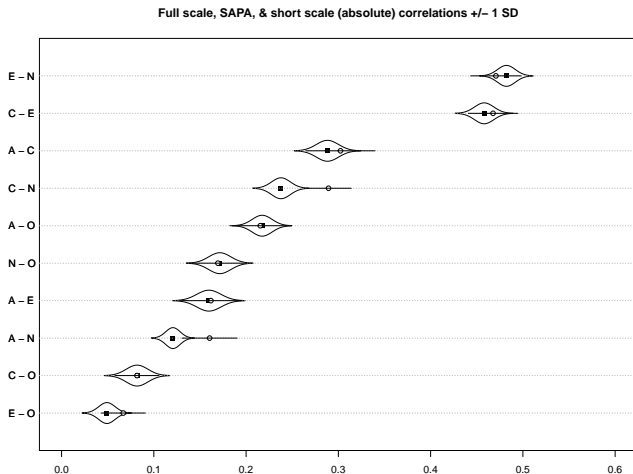




# N=400 subjects Johnson 120 item IPIP, full scales: correlations

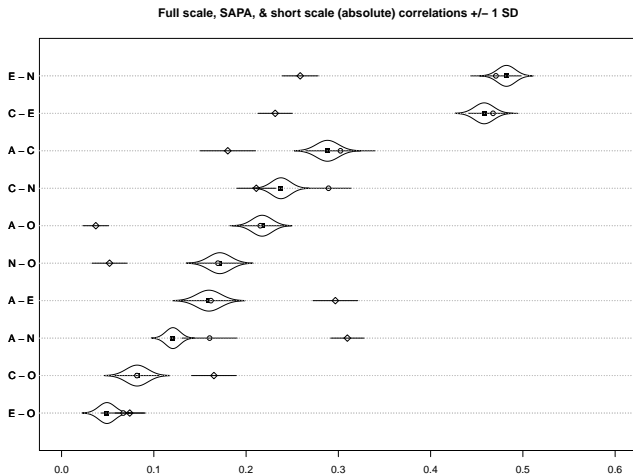


# N=400 Johnson 120 item IPIP, sapa sampling 30 items: correlations





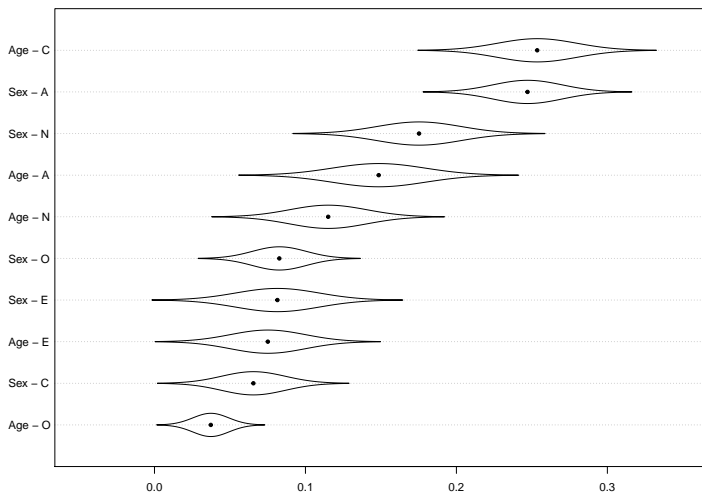
# N=400 120 item IPIP, sapa sampling 30 at +short scales





## N=400 from Johnson 120 item IPIP, full scales: Validity

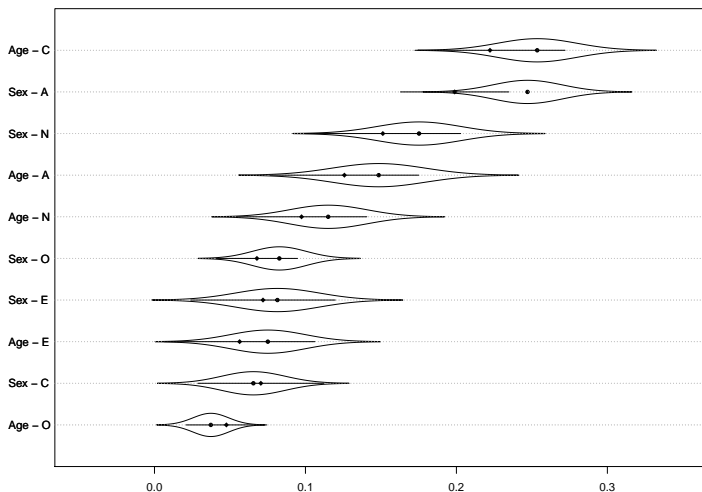
Full scale, SAPA, & short scale (absolute) validity coefficients





## N=400 Johnson 120 item IPIP, sapa sampling 30 items: Validity

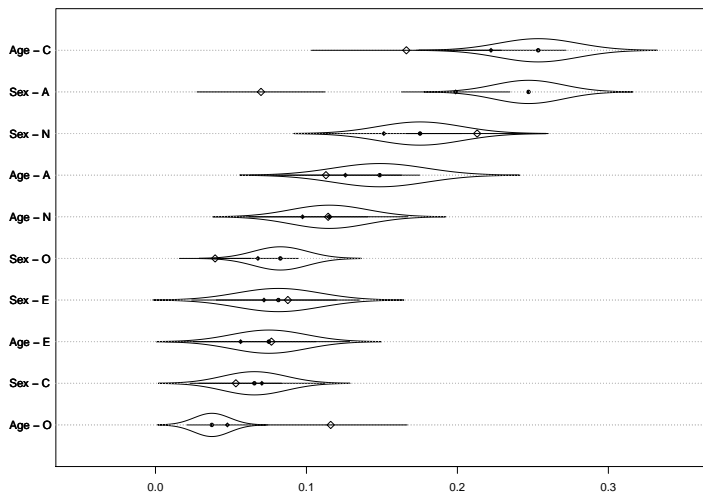
Full scale, SAPA, & short scale (absolute) validity coefficients





# N=400 120 item IPIP, sapa 30 items + Short scales: Validity

Full scale, SAPA, & short scale (absolute) validity coefficients





## Some comments

1. These simulations were done with 400-2,000 simulated (but real) subjects
2. With  $p=.25$ , the number of pairwise correlations was  $p^2N = .04 * 400 \approx 25/pair$  and yet the results are very stable!
3. With such missingness, the correlation matrices are improper, but the `fa` function will give a minres solution anyway.
4. Even better is to use *minchi* fitting to take into account the variation of sample sizes.

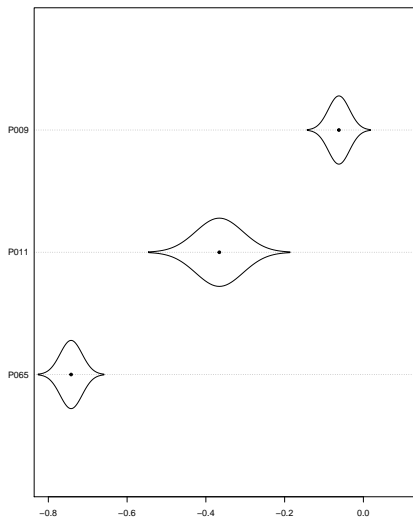
## Experience Sampling Methods

1. We can also apply this technique to ESM data
2. Two data sets were examined: Fisher (2015) and Wilt, Funkhouser & Revelle (2011)
3. We were particularly interested in the correlation within subjects between Positive and Negative Affect
4. Rather than do k-fold sampling, we did boot strap resampling of the entire data or with 50% sapaized samples

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## Aaron Fisher data - as reported

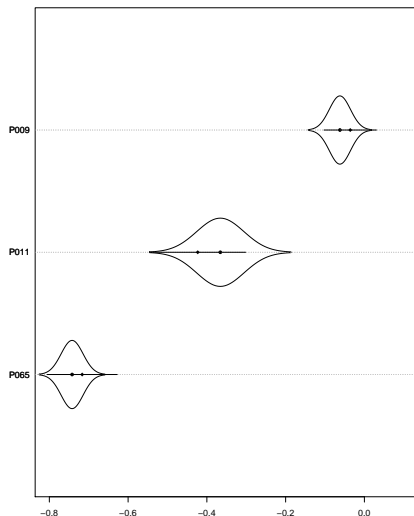
Full scale, SAPA, and short correlations between  
PA and NA  $\pm$  1 SD (Fisher's data)



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## Aaron Fisher data – comparing full versus sapaized 50%

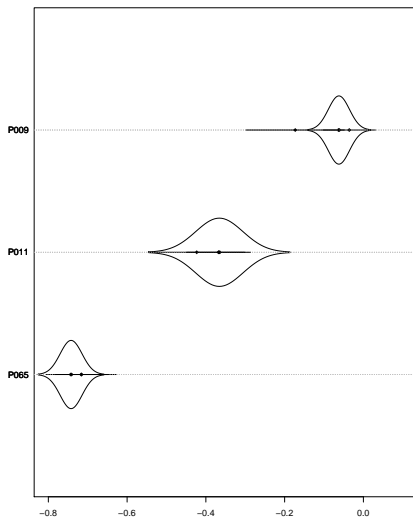
Full scale, SAPA, and short correlations between  
PA and NA  $\pm$  1 SD (Fisher's data)



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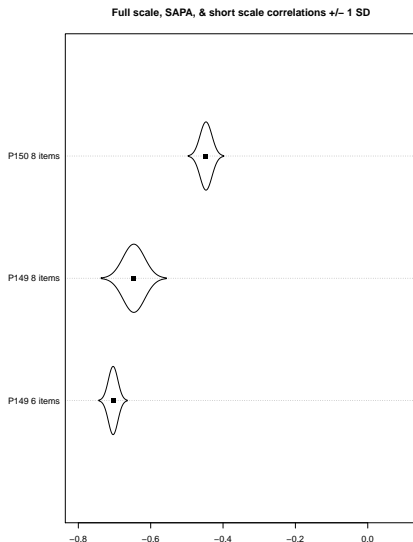
## Aaron Fisher data – comparing full versus sapaized 50%

Full scale, SAPA, and short correlations between  
PA and NA  $\pm$  1 SD (Fisher's data)



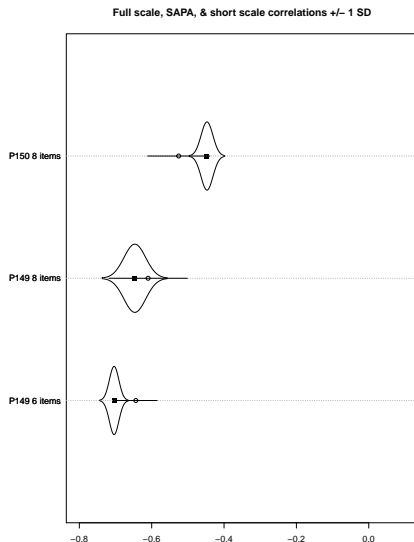
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## Wilt-Revelle data - as reported



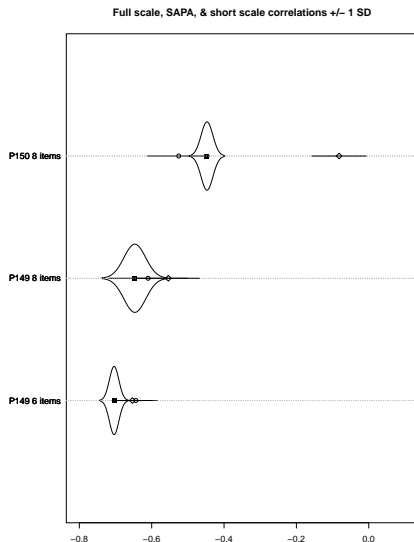
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## Wilt-Revelle data – comparing full versus sapaized 50%



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## Wilt-Revelle data – comparing full versus sapaized 50%





## SAPA or MMCAR procedures are very powerful

1. At the SAPA-project we estimate difficulty parameters and covariance structures for 1,000s of items even though only 100-150 items are answered per subject.
2. More importantly, the same procedures can be used for people with smaller sample sizes with fewer items (e.g. MTurk research).
3. Structure of ability measures using the open source ability test from the International Cognitive Ability Resource (ICAR)  
<http://icar-project.com>
4. Data sharing: <https://dataverse.harvard.edu/dataverse/SAPA-ProjectCode/manuscript/>
5. SPI development (Condon, 2017): <https://sapa-project.org/research/SPI/SPIdevelopment.pdf>
6. SPI scales, norms, IRT parameters:  
<https://sapa-project.org/research/SPI>
7. Today's slides at <http://personality-project.org/sapa>
8. Join the ICAR and SAPA projects.

## R code

The next few slides show the R code used for these analyses

### R code

```
sapa <- read.file() #this searched for and loaded the master data file
icar.dictionary <- read.file() #this searches for and loads a dictionary file

sapa <- SAPAdata18aug2010thru7feb2017 #change the name to make the following analyses clear
#the raw sapa has alphanumeric codes for some fields. Convert to numeric
sapa <- char2numeric(sapa)
icar <- sapa[rownames(icar.dictionary)] #Identify the ICAR items
icar.keys <- ItemLists[417:421] #the keys are loaded as part of the sapa read.file line
icar #show the item numbers of ICAR

icar.16 <- c("q_12007","q_12033" ,"q_12034","q_12058","q_12045", "q_12046","q_12047",
"q_12055", "q_11003", "q_11004","q_11006" ,"q_11008","q_12004","q_12016", "
q_12017", "q_12019")

#now do random resamples, 100 times each of various fractions of the icar.16 data
icar.16.sapa.05 <-fa.sapa(sapa[icar.16],4,n.iter=100,frac=.05)
icar.16.sapa.1 <-fa.sapa(sapa[icar.16],4,n.iter=100,frac=.1)
icar.16.sapa.2 <-fa.sapa(sapa[icar.16],4,n.iter=100,frac=.2)
icar.16.sapa.4 <-fa.sapa(sapa[icar.16],4,n.iter=100,frac=.4)
```

## More R

### R code

```

error.dots(icar.16.sapa.05,head=40,tail=40,sort=FALSE,main="ICAR 16 4 Factors pairwise = 12
error.dots(icar.16.sapa.1,head=40,tail=40,sort=FALSE,main="ICAR 16 4 Factors pairwise = 2479
error.dots(icar.16.sapa.2,head=40,tail=40,sort=FALSE,main="ICAR 16 4 Factors pairwise = 4950
error.dots(icar.16.sapa.4,head=40,tail=40,sort=FALSE,main="ICAR 16 4 Factors 4 pairwise = 9

#now show the factor intercorrelations
names(icar.16.sapa.05$cis$means.rot) <- label.icar.rot
names(icar.16.sapa.1$cis$means.rot) <- label.icar.rot
names(icar.16.sapa.2$cis$means.rot) <- label.icar.rot
names(icar.16.sapa.4$cis$means.rot) <- label.icar.rot

error.dots(icar.16.sapa.05$cis$means.rot,se=icar.16.sapa.05$cis$sds.rot,sort=FALSE,xlim=c(0,2
error.dots(icar.16.sapa.1$cis$means.rot,se=icar.16.sapa.1$cis$sds.rot,sort=FALSE,xlim=c(0,2
error.dots(icar.16.sapa.2$cis$means.rot,se=icar.16.sapa.2$cis$sds.rot,sort=FALSE,xlim=c(0,2
error.dots(icar.16.sapa.4$cis$means.rot,se=icar.16.sapa.4$cis$sds.rot,sort=FALSE,xlim=c(0,2

op <- par(mfrow=c(2,2))
error.dots(icar.16.sapa.05$cis$means.rot,se=icar.16.sapa.05$cis$sds.rot,sort=FALSE,xlim=c(0,2
error.dots(icar.16.sapa.1$cis$means.rot,se=icar.16.sapa.1$cis$sds.rot,sort=FALSE,xlim=c(0,2
error.dots(icar.16.sapa.2$cis$means.rot,se=icar.16.sapa.2$cis$sds.rot,sort=FALSE,xlim=c(0,2
error.dots(icar.16.sapa.4$cis$means.rot,se=icar.16.sapa.4$cis$sds.rot,sort=FALSE,xlim=c(0,2

```

## More R

R code

```
op <- par(mfrow=c(1,1))
icar.16.sapa.05$ci$mean.pair #1238.375
icar.16.sapa.1$ci$mean.pair # 2478.613
icar.16.sapa.2$ci$mean.pair # 4950.1
icar.16.sapa.4$ci$mean.pair # 9906.598

#now, just take out a general factor
icar.16.sapa.1.05 <-fa.sapa(sapa[icar.16],n.iter=100,frac=.05)
icar.16.sapa.1.1 <-fa.sapa(sapa[icar.16],n.iter=100,frac=.1)
icar.16.sapa.1.2 <-fa.sapa(sapa[icar.16],n.iter=100,frac=.2)
icar.16.sapa.1.4 <-fa.sapa(sapa[icar.16],n.iter=100,frac=.4)

error.dots(icar.16.sapa.1.05,head=40,tail=40,sort=FALSE,main="ICAR 16 1 Factor 5% sample",xlim=c(0,10000))
error.dots(icar.16.sapa.1.1,head=40,tail=40,sort=FALSE,main="ICAR 16 1Factor 10% sample",xlim=c(0,10000))
error.dots(icar.16.sapa.1.2,head=40,tail=40,sort=FALSE,main="ICAR 16 1 Factor 20% sample",xlim=c(0,10000))
error.dots(icar.16.sapa.1.4,head=40,tail=40,sort=FALSE,main="ICAR 16 1 Factor 40% sample",xlim=c(0,10000))

error.dots(icar.16.sapa.1.05,head=40,tail=40,sort=FALSE,main="ICAR 16 1 Factor 5% ",xlim=c(0,10000))
error.dots(icar.16.sapa.1.1,head=40,tail=40,sort=FALSE,main="ICAR 16 1Factor 10% ",xlim=c(0,10000))
error.dots(icar.16.sapa.1.2,head=40,tail=40,sort=FALSE,main="ICAR 16 1 Factor 20% ",xlim=c(0,10000))
error.dots(icar.16.sapa.1.4,head=40,tail=40,sort=FALSE,main="ICAR 16 1 Factor 40% ",xlim=c(0,10000))

icar.keys <- keys.list[398:402]

R3Diq.sapa <-fa.sapa(sapa[icar.keys[[4]]],1,n.iter=100,frac=.05)
R3Diq.sapa.1 <-fa.sapa(sapa[icar.keys[[4]]],1,n.iter=100,frac=.1)
R3Diq.sapa.2 <-fa.sapa(sapa[icar.keys[[4]]],1,n.iter=100,frac=.2)
R3Diq.sapa.4 <-fa.sapa(sapa[icar.keys[[4]]],1,n.iter=100,frac=.4)

R3Diq.sapa$ci$mean.pair
```

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## R code

```

#this next one fails
#R3Diq.sapa.01 <-fa.sapa(sapa[icar.keys[[4]]],1,n.iter=100,frac=.01)
# error.dots(R3Diq.sapa..01,head=40,tail=40,sort=FALSE,main="3D rotation items -- 1% sample
  op <- par(mfrow=c(2,2))
error.dots(R3Diq.sapa,head=40,tail=40,sort=FALSE,main="3D rotation items pairwise = 200",x=
error.dots(R3Diq.sapa.1,head=40,tail=40,sort=FALSE,main="3D rotation items pairwise = 399",x=
error.dots(R3Diq.sapa.2,head=40,tail=40,sort=FALSE,main="3D rotation items pairwise = 798",x=
error.dots(R3Diq.sapa.4,head=40,tail=40,sort=FALSE,main="3D rotation items pairwise=1596",x=

op <- par(mfrow=c(1,1))

samp.size <- data.frame(fraction=fraction,sample = fraction * 255348,icar16=fraction * 74348)

#now, some omega comparisons
om16 <- omega(sapa[icar.16],4) #the complete sample
omega.diagram(om16)

# a 5% sample
sapa.5.samp <- sapa[sample(1:255348,12767,replace=TRUE),icar.16]
om.samp.5 <- omega(sapa.5.samp,4)
omega.diagram(om.samp.5)

mean(count.pairwise(sapa.5.samp,diagonal=FALSE),na.rm=TRUE)
cp <- count.pairwise(sapa.5.samp)
> mean(diag(cp))
[1] 3718.562

corPlot(factor.congruence(om16,om.samp.5),numbers=TRUE,gr=gr,main="Factor Congruence: total sample")

sapa.02.samp <- sapa[sample(1:255348,5000,replace=TRUE),icar.16]
om.02 <- omega(sapa.02.samp,4)
corPlot(factor.congruence(om16,om.02),numbers=TRUE,gr=gr,main="Factor Congruence: total sample")

```

```

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```

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```

# R code

#now some interesting simulations

```
sim.1 <- sim.irt(24,200000,low=-1,high=1,a=3)
```

```
simp <- sim.1$items
```

```
filter <- matrix(NA,nrow=200000,ncol=24)
```

```
filter <- sample(1:24,24*200000,replace=TRUE)
```

```
filter<- matrix(filter,ncol=24)
```

```
simp[filter > 12 ] <- NA. #rhis is a 50% sample
```

```
simp <- matrix(simp,ncol=24)
```

```
sim.fa.008 <- fa.sapa(simp,frac=.008,n.iter=100)
```

```
sim.fa.0016<- fa.sapa(simp,frac=.0016,n.iter=100)
```

```
sim.fa.016<- fa.sapa(simp,frac=.016,n.iter=100)
```

```
sim.fa.032<- fa.sapa(simp,frac=.032,n.iter=100).
```

```
sim.fa.032$ci$mean.pair      #[1] 1600.788
```

#Now, do this again for a 25% sample

```
simp.25 <- sim.1$items
```

```
simp.25[filter > 6 ] <- NA. #rhis is a 50% sample
```

```
simp,25 <- matrix(simp.25,ncol=24)
```

## Error dots for factor loadings

Note that the error bars are smaller for the 25 versus 50 % samples

R code

```
op <- par(mfrow=c(2,2))
error.dots(sim.fa.004,sort=FALSE,xlim=c(0,1),main="200 pairwise, 50
error.dots(sim.fa.008,sort=FALSE,xlim=c(0,1),main="400 pairwise, 50
error.dots(sim.fa.016,sort=FALSE,xlim=c(0,1),main="800 pairwise, 50
error.dots(sim.fa.032,sort=FALSE,xlim=c(0,1),main="1600 pairwise, 5

error.dots(sim.fa.25.016,sort=FALSE,xlim=c(0,1),main="200 pairwise,
error.dots(sim.fa.25.032,sort=FALSE,xlim=c(0,1),main="400 pairwise,
error.dots(sim.fa.25.064,sort=FALSE,xlim=c(0,1),main="800 pairwise,
error.dots(sim.fa.25.128,sort=FALSE,xlim=c(0,1),main="1600 pairwise
op <- par(mfrow=c(1,1))
```

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