

Coefficient α (Part II)

```
library(psych)
library(tidyverse)
library(modelsummary) # for summarizing data
```

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Warning in attr(.knitEnv$meta, "knit_meta_id"): 'xfun::attr()' is deprecated.
Use 'xfun::attr2()' instead.
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We'll once again use the bfi data set, this time with the Openness items

```
data(bfi, package = "psych")
head(bfi[c("01", "02", "03", "04", "05")])
```

```
      01 02 03 04 05
61617  3  6  3  4  3
61618  4  2  4  3  3
61620  4  2  5  5  2
61621  3  3  4  3  5
61622  3  3  4  3  3
61623  4  3  5  6  1
```

Descriptive Statistics

```
# Get means and variances
mv <- datasummary(O1 + O2 + O3 + O4 + O5 ~ Mean + Var, data = bfi,
  output = "data.frame")
# Correlation, adding means and variances
datasummary_correlation(bfi[c("01", "02", "03", "04", "05")],
  add_columns = mv[-1])
```

```
Warning in attr(.knitEnv$meta, "knit_meta_id"): 'xfun::attr()' is deprecated.
```


	O1	O2	O3	O4	O5	Mean	Var
O1	1	4.82	1.28
O2	-0.21	1	.	.	.	2.71	2.45
O3	0.40	-0.26	1	.	.	4.44	1.49
O4	0.18	-0.07	0.19	1	.	4.89	1.49
O5	-0.24	0.32	-0.31	-0.18	1	2.49	1.76

See `help("Deprecated")`

Warning in `attr(.knitEnv$meta, "knit_meta_id")`: 'xfun::attr()' is deprecated.
Use 'xfun::attr2()' instead.

See `help("Deprecated")`

Warning in `attr(x, "align")`: 'xfun::attr()' is deprecated.

Use 'xfun::attr2()' instead.

See `help("Deprecated")`

Warning in `attr(x, "format")`: 'xfun::attr()' is deprecated.

Use 'xfun::attr2()' instead.

See `help("Deprecated")`

You can find that O2 and O5 have negative correlations with other items

α Without Recoding

```
cov1 <- cov(bfi[c("O1", "O2", "O3", "O4", "O5")], use = "complete")
# Compute alpha by hand using formula
5 / (5 - 1) * (1 - sum(diag(cov1)) / sum(cov1))
```

```
[1] -0.1568749
```

```
# Using `psych::alpha()`; the estimate is labelled "raw_alpha"
psych::alpha(bfi[c("O1", "O2", "O3", "O4", "O5")])
```

Warning in `psych::alpha(bfi[c("O1", "O2", "O3", "O4", "O5")])`: Some items were negatively correlated. Items should be reversed.

To do this, run the function again with the 'check.keys=TRUE' option

Some items (02 05) were negatively correlated with the first principal component and probably should be reversed.

To do this, run the function again with the 'check.keys=TRUE' option

Reliability analysis

Call: psych::alpha(x = bfi[c("01", "02", "03", "04", "05")])

raw_alpha	std.alpha	G6(smc)	average_r	S/N	ase	mean	sd	median_r
-0.13	-0.097	0.096	-0.018	-0.088	0.035	3.9	0.56	-0.12

95% confidence boundaries

	lower	alpha	upper
Feldt	-0.2	-0.13	-0.07
Duhachek	-0.2	-0.13	-0.06

Reliability if an item is dropped:

	raw_alpha	std.alpha	G6(smc)	average_r	S/N	alpha	se	var.r	med.r
01	-0.194	-0.235	-0.0276	-0.0500	-0.191	0.037	0.066	-0.12369	
02	-0.031	0.026	0.1617	0.0066	0.027	0.032	0.082	-0.00034	
03	-0.096	-0.146	0.0089	-0.0328	-0.127	0.033	0.054	-0.12369	
04	-0.232	-0.240	0.0297	-0.0508	-0.193	0.039	0.103	-0.22636	
05	0.028	0.135	0.2170	0.0374	0.156	0.031	0.067	0.05503	

Item statistics

	n	raw.r	std.r	r.cor	r.drop	mean	sd
01	2778	0.42	0.52	0.46	0.020	4.8	1.1
02	2800	0.49	0.36	-0.11	-0.088	2.7	1.6
03	2772	0.39	0.47	0.37	-0.054	4.4	1.2
04	2786	0.48	0.52	0.28	0.039	4.9	1.2
05	2780	0.36	0.28	-0.33	-0.136	2.5	1.3

Non missing response frequency for each item

	1	2	3	4	5	6	miss
01	0.01	0.04	0.08	0.22	0.33	0.33	0.01
02	0.29	0.26	0.14	0.16	0.10	0.06	0.00
03	0.03	0.05	0.11	0.28	0.34	0.20	0.01
04	0.02	0.04	0.06	0.17	0.32	0.39	0.01
05	0.27	0.32	0.19	0.13	0.07	0.03	0.01

You can see that α is negative.

Recode

```
bfi$02r <- 7 - bfi$02  
bfi$05r <- 7 - bfi$05
```

α After Recoding

```
cov2 <- cov(bfi[c("01", "02r", "03", "04", "05r")], use = "complete")  
# Compute alpha by hand using formula  
5 / (5 - 1) * (1 - sum(diag(cov2)) / sum(cov2))
```

```
[1] 0.6025464
```

```
# Using `psych::alpha()`; the estimate is labelled "raw_alpha"  
psych::alpha(bfi[c("01", "02r", "03", "04", "05r")])
```

Reliability analysis

```
Call: psych::alpha(x = bfi[c("01", "02r", "03", "04", "05r")])
```

raw_alpha	std.alpha	G6(smc)	average_r	S/N	ase	mean	sd	median_r
0.6	0.61	0.57	0.24	1.5	0.012	4.6	0.81	0.23

95% confidence boundaries

	lower	alpha	upper
Feldt	0.58	0.6	0.62
Duhachek	0.58	0.6	0.62

Reliability if an item is dropped:

	raw_alpha	std.alpha	G6(smc)	average_r	S/N	alpha	se	var.r	med.r
01	0.53	0.53	0.48	0.22	1.1	0.014	0.0092	0.23	
02r	0.57	0.57	0.51	0.25	1.3	0.013	0.0076	0.22	
03	0.50	0.50	0.44	0.20	1.0	0.015	0.0071	0.20	
04	0.61	0.62	0.56	0.29	1.6	0.012	0.0044	0.29	
05r	0.51	0.53	0.47	0.22	1.1	0.015	0.0116	0.20	

Item statistics

	n	raw.r	std.r	r.cor	r.drop	mean	sd
--	---	-------	-------	-------	--------	------	----

01	2778	0.62	0.65	0.52	0.39	4.8	1.1
02r	2800	0.65	0.60	0.43	0.33	4.3	1.6
03	2772	0.67	0.69	0.59	0.45	4.4	1.2
04	2786	0.50	0.52	0.29	0.22	4.9	1.2
05r	2780	0.67	0.66	0.52	0.42	4.5	1.3

Non missing response frequency for each item

	1	2	3	4	5	6	miss
01	0.01	0.04	0.08	0.22	0.33	0.33	0.01
02r	0.06	0.10	0.16	0.14	0.26	0.29	0.00
03	0.03	0.05	0.11	0.28	0.34	0.20	0.01
04	0.02	0.04	0.06	0.17	0.32	0.39	0.01
05r	0.03	0.07	0.13	0.19	0.32	0.27	0.01

Here is an example for reporting α in a manuscript:

 Tip

The reliability coefficient of the composite scores of the five Openness items for our sample was .60, 95% CI [.58, .62].

Multilevel Reliability

```
# Example data from Bolger & Laurenceau (2013) chapter 7
dat <- read.csv(
  "https://raw.githubusercontent.com/The-Change-Lab/collaborations/refs/heads/main/Bolger_1
  header = TRUE
)
# Reshape the data to have items in multiple columns, which is more common
dat2 <- dat |>
  pivot_wider(names_from = "item", names_prefix = "x",
              values_from = "y")
head(dat2, 20)
```

```
# A tibble: 20 x 6
  person time    x1    x2    x3    x4
  <int> <int> <int> <int> <int> <int>
1     301     1     2     2     3     4
2     301     2     2     3     3     2
3     301     3     3     3     2     2
```

4	301	4	4	3	3	3
5	301	5	2	2	2	2
6	301	6	2	2	1	2
7	301	7	2	2	1	2
8	301	8	2	2	2	2
9	301	9	2	3	2	2
10	301	10	3	3	3	3
11	309	1	3	3	NA	1
12	309	2	3	3	3	3
13	309	3	3	3	3	1
14	309	4	3	1	3	1
15	309	5	1	1	1	1
16	309	6	3	1	1	1
17	309	7	1	1	3	1
18	309	8	1	1	1	1
19	309	9	1	1	1	1
20	309	10	1	1	1	1

As can be seen, each person has 10 time points, each time with 4 items. We can get three types of composites:

```
# Raw composite
xsum <- rowSums(dat2[c("x1", "x2", "x3", "x4")])
var(xsum, na.rm = TRUE) # total variance
```

```
[1] 11.88269
```

```
# Between composite (one for each person)
xsumb <- tapply(xsum, INDEX = dat2$person, FUN = mean)
var(xsumb, na.rm = TRUE) # between variance
```

```
[1] 7.962253
```

```
# Within composite
xsumw <- xsum - ave(xsum, dat2$person)
var(xsumw, na.rm = TRUE) # within variance
```

```
[1] 3.91179
```

And you can compute reliability for each composite using the following code:

```
source("https://github.com/marklhc/mcfa_reliability_supp/raw/master/multilevel_alpha.R")
multilevel_alpha(dat2[c("x1", "x2", "x3", "x4")],
                 id = dat2$person)
```

Loading required package: lavaan

This is lavaan 0.6-19
lavaan is FREE software! Please report any bugs.

Attaching package: 'lavaan'

The following object is masked from 'package:psych':

cor2cov

Warning: lavaan->lav_data_full():

Level-1 variable "y2" has no variance within some clusters . The cluster
ids with zero within variance are: 409, 431, 501.

Warning: lavaan->lav_data_full():

Level-1 variable "y3" has no variance within some clusters . The cluster
ids with zero within variance are: 351, 451, 463.

Warning: lavaan->lav_data_full():

Level-1 variable "y4" has no variance within some clusters . The cluster
ids with zero within variance are: 351, 423, 447, 451, 471.

Warning: lavaan->lav_data_full():

Level-1 variable "y2" has no variance within some clusters . The cluster
ids with zero within variance are: 409, 431, 501.

Warning: lavaan->lav_data_full():

Level-1 variable "y3" has no variance within some clusters . The cluster
ids with zero within variance are: 351, 451, 463.

Warning: lavaan->lav_data_full():

Level-1 variable "y4" has no variance within some clusters . The cluster
ids with zero within variance are: 351, 423, 447, 451, 471.

Parallel analysis suggests that the number of factors = NA and the number of components =
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```
$alpha
  alpha2l   alphab   alphaw
0.8342556 0.8218115 0.7679396
```

```
$alpha_ci
           2.5%    97.5%
alpha2l 0.7655752 0.8834255
alphab  0.7013840 0.8877646
alphaw  0.7117038 0.8122969
```

```
$omega
  omega2l   omegab   omegaw
0.8326827 0.8158880 0.7717208
```

```
$omega_ci
           2.5%    97.5%
omega2l 0.7566153 0.8828240
omegab  0.6723170 0.8870760
omegaw  0.7150554 0.8116054
```

```
$ncomp
  within between
      1       1
```

The values are labelled “alpha2l”, “alphab”, and “alphaw”, followed by the corresponding 95% CIs.