

Load EFA/CFA:

```
load("01B_out_efacfa_2021-03-03-1824-31.RData")
library(psych)

## Warning: package 'psych' was built under R version 3.6.3
library(lavaan)

## Warning: package 'lavaan' was built under R version 3.6.3
## This is lavaan 0.6-7
## lavaan is BETA software! Please report any bugs.
##
## Attaching package: 'lavaan'
## The following object is masked from 'package:psych':
##
##      cor2cov
get_lims <- function(icol){
  c(min(icol), max(icol))
}
```

Open relevant tab:

```
itab = "TPFQ" # Change Me!
iresults = results[[itab]]
idata = data_tabs[[itab]]
ilookup = lookups_all[[itab]]
q_legacy = ncol(ilookup)-2
```

Get Goodness of fit (gof):

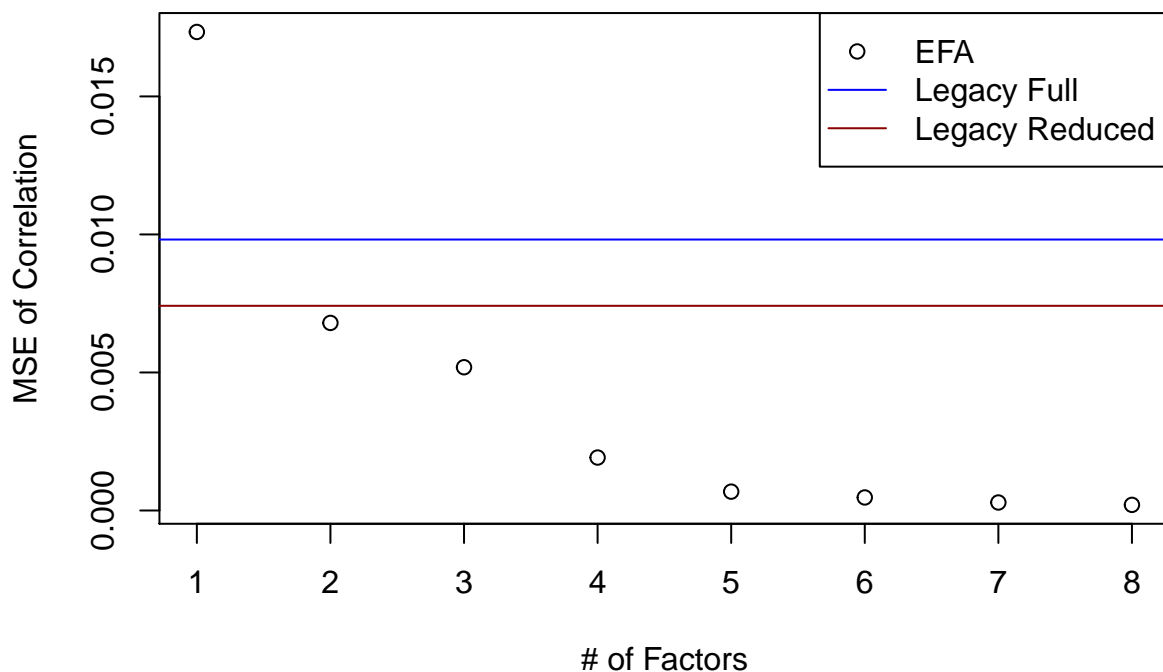
```
efa_gof = sapply(iresults$efa, get_efa_gof)
legacy_gof = c(
  "full"=get_cfa_gof(iresults$cfa$full$legacy)
  , "reduced"=get_cfa_gof(iresults$cfa$reduced$legacy)
)
rand_gof = data.frame(cbind(
  "full"=sapply(iresults$cfa$full$rand, get_cfa_gof)
  , "reduced"=sapply(iresults$cfa$reduced$rand, get_cfa_gof)
))
legacy_less_gof = data.frame(cbind(
  "full"=sapply(iresults$cfa$full$legacy_less, get_cfa_gof)
  , "reduced"=sapply(iresults$cfa$reduced$legacy_less, get_cfa_gof)
))
rownames(legacy_less_gof) = colnames(ilookup)[-c(1,2)]
legacy_one_gof = data.frame(cbind(
  "full"=sapply(iresults$cfa$full$legacy_one, get_cfa_gof)
  , "reduced"=sapply(iresults$cfa$reduced$legacy_one, get_cfa_gof)
))
rownames(legacy_one_gof) = colnames(ilookup)[-c(1,2)]
```

{Reduced vs Full:} When doing CFA we consider two models. The first is a reduced (sparse) model where  $\Lambda$  is 0/1. The second is a full model where certain  $\lambda_{ij} = 0$  but the rest are unrestricted. In both cases we allow for an unrestricted  $\Phi$ . Done in Lavaan.

{EFA:} We look at the EFA goodness of fit for different number of parameters. Horizontal lines for legacy subscales.

```
# EFA
plot(efa_gof
     , xlab="# of Factors", ylab="MSE of Correlation", main=paste0(itab, ": EFA Goodness of Fit")
     , ylim=get_lims(c(efa_gof, legacy_gof))
)
abline(h=legacy_gof["full"], col="blue")
abline(h=legacy_gof["reduced"], col="darkred")
legend("topright"
      , legend=c("EFA", "Legacy Full", "Legacy Reduced")
      , col=c("black", "blue", "darkred")
      , lty = c(0,1,1)
      , pch = c(1,NA,NA)
)
```

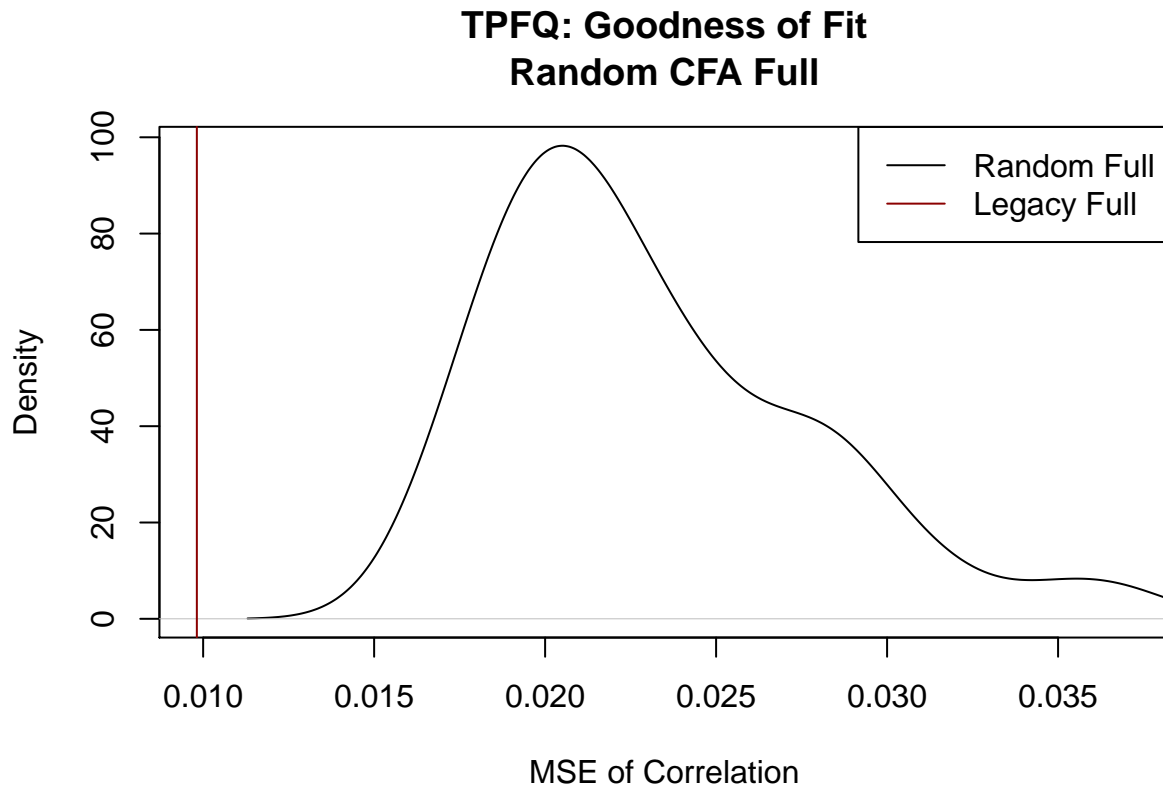
### TPFQ: EFA Goodness of Fit



{CFA Full:} Compared to 100 randomly generated subscales, how well does legacy perform? In both cases we use 'full' model above.

```
# CFA Full
plot(density(rand_gof$full)
     , xlim=get_lims(c(rand_gof$full, legacy_gof["full"]))
     , xlab="MSE of Correlation", main=paste0(itab, ": Goodness of Fit\nRandom CFA Full")
)
abline(v=legacy_gof["full"], col="darkred")
legend("topright"
      , legend=c("Random Full", "Legacy Full")
)
```

```
, col=c("black", "darkred")
, lty = c(1,1))
```



{CFA Reduced:} Compared to 100 randomly generated subscales, how well does legacy perform? In both cases we use 'reduced' model above.

```
# CFA reduced
plot(density(rand_gof$reduced)
, xlim=get_lims(c(rand_gof$reduced, legacy_gof["reduced"])))
, xlab="MSE of Correlation", main=paste0(itab, ": Goodness of Fit\nRandom CFA reduced")
)
abline(v=legacy_gof["reduced"], col="darkred")
legend("topright"
, legend=c("Random reduced", "Legacy reduced")
, col=c("black", "darkred")
, lty = c(1,1))
```

# TPFQ: Goodness of Fit

## Random CFA reduced

