Fitting the Common Factor Model

PSY544 – Introduction to Factor Analysis

Week 5

- In the past two weeks, we introduced the Common Factor Model in multiple forms.
- First, we introduced the data model:

- After making some assumptions, we derived a covariance structure model
- For correlated factors:

• For uncorrelated factors:

• And we have seen how the covariance structure model can be transformed into a correlation structure model.

• For correlated factors:

• For uncorrelated factors:

- You learned a LOT already!
- More than a majority of factor analysis practitioners know about the model ^(c) (pretty sad, huh?)

Fitting the model

- One important thing to note is that these models are intended for a population they are population models, describing how stuff works in a population.
- Anyway, at the beginning we learned that there are two sides to factor analysis theory and methodology.
- What we have covered so far was the **theory** (the model itself)
- Now, we will focus on the methodology (how to fit the model on data / how to estimate the unknowns in the model)

Fitting the model

- More specifically, we will focus on the **theoretical basis** for fitting the model. Later on in the course, we will cover the actual thing in practice (software and examples).
- A model represents some hypothesized structure of data. Different **methods** are available for fitting the model to data and obtaining estimates of model parameters (the elements in model matrices) and providing us with information on how well the model **fits** the data.

Fitting the model

- For the sake of argument, we will consider the hypothetical scenario where the population correlation matrix **P** is known, and the model holds exactly in the population (i.e., the model explains **P** perfectly)
- This will never ever be the case in practice, but it's a better starting point to begin understanding the principles.
- Later, we will drop these assumptions, no worries.

The population correlation matrix

 Last time we talked about the case where the model holds exactly and the common factors are uncorrelated (orthogonal). In such a case, the population correlation matrix P has the structure:

...or, alternatively:

• Strictly speaking, we should use and , but let's omit the stars now for convenience.

- We have a bit of a "problem".
- If we can find a single p x m factor loading matrix such that , and if m > 2 (i.e., we have two or more factors), then there are infinitely many other p x m factor loading matrices such that

• Am I kidding? Nope. Let me show you.

• Suppose I'm not wrong and it indeed holds that:

(we're just considering two solutions now, but there are infinitely many)

In that case, one solution () has to be linked in some way with the other solution (). To be precise, = where T is a m x m orthogonal matrix ()

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• See? and are equally fine solutions.

- In other words, if we can find one solution, we can find other alternative solutions. We simply choose any matrix T such that TT' = I and we define =
- We've just seen that and are equally good solutions, since

• This is called rotational indeterminacy. Later, when we learn about rotation, we will see that this describes a procedure used to produce alternative (and equally good) solutions to .

- However, we must resolve this problem somehow if we want to find a single, unique solution for every time we perform a factor analysis.
- In other words, we need to find a criterion for defining this unique solution.
- Luckily, we can arrive at a solution with the help of Eigenvalues and Eigenvectors.

- Recall what we have learned about eigenvalues and eigenvectors.
- The eigenstructure of a symmetric matrix **S** is the following:

...where the columns of **U** are eigen**vectors** and the diagonal elements of are eigen**values** (this is a diagonal matrix).

- So, a symmetric matrix S may be expressed as the product of some matrix () which has some vectors for columns (these are the eigenvectors) and some diagonal matrix () which has some values on its diagonal (these are the eigenvalues)
- Thus, we can basically decompose a symmetric matrix S into two other matrices (one of them is a diagonal matrix) that, when multiplied in some way, give you back your S matrix.
- We're not trying to understand *why* that is or *what exactly* do the two matrices (and) represent. We don't care at the moment. All we need to know is that this is possible and (as you will see) useful for FA.

- Alright. For now, we will take the matrix
- Remember, this is the population correlation matrix with unique variances (in) subtracted from the diagonal (because is diagonal)
- This matrix is also square and symmetric, just like **S** from the previous slide.

- The factor model says that
- So, what we want is to find a unique matrix that satisfies this model.
- Given our rotational indeterminacy problem, we really want to find a **unique** solution in some way, so that we would get this same solution every time we would run a factor analysis.

- Okay, so how do we use the eigen-stuff to find this unique solution?
- Some smart folks have invented the following:
- The eigen-decomposition of yields some and some
- If and satisfy the common factor model for *m* factors, then a loading matrix can be constructed from the *m* largest eigenvalues of and the corresponding *m* standardized eigenvectors of (remember, each eigenvalue is associated with some eigenvector, hence the word "corresponding")

- The eigen-decomposition of yields some and some
- If and satisfy the common factor model for *m* factors, then a loading matrix can be constructed from the *m* largest eigenvalues of and the corresponding *m* standardized eigenvectors of
- Actually, the rest of the eigenvalues in (p m largest eigenvalues) are all zero.
- Anyway, if we take the eigenvalues in , take their square roots and put them back again into a matrix we will call , then

- Magic.
- Remember, we don't care about why this works or how it works. All we care about now is that this procedure allows us to come up with a unique solution to
- For the procedure to work, we need to know , or the unique factor variances.

- Let's look at an example, using the example data we have seen before.
- The matrix **P** is given as follows:

	РС	VO	AR	MPS
PC	1			
VO	.49	1		
AR	.14	.07	1	
MPS	.48	.42	.48	1

• Assume the unique variances are known:

• So the matrix **P** with communalities in the diagonal is given by:

- We can obtain the eigenvalues and eigenvectors of (
- The non-zero eigenvalues are:

• And the corresponding eigenvectors:

• The factor loading matrix can be obtained:

• Wait...that's not the loading matrix I have shown you last time for the example data, is it?

It's a transformation of the matrix I have shown you earlier, in the rotational indeterminacy sense,



• Both matrices provide an exact solution to the model. The procedure involving eigen-stuff allowed us to identify the unique solution, though.

- Okay, so, I have just shown you how to obtain the solution () if:
 - You know the population correlation matrix, P
 - You know the contents of *,* so you know the unique variances or (conversely) the communalities
 - The model holds exactly in the population

- Huh. Putting the "model holds exactly" thing aside, you will never know
 P and you will never know , so this is a theoretical scenario.
- That's true, but this serves as a basis for things to come.

- As I said, the solution obtained by doing the eigen-decomposition of () requires that you know either the unique variances or the communalities (once you know one, you know the other one, right?)
- But we don't know these, since finding out what they are is a part of the problem we face.
- When factor analysis was young, this was called the "Communality problem"

- Many solutions were suggested to the communality problem.
- The one that "won" (was and is the most widely used) was suggested by Louis Guttman in 1940.
- Guttman suggested *squared multiple correlations* (SMCs) as the initial approximations to communalities.

- Just what is a *squared multiple correlation* (SMC)?
- Imagine you have p manifest variables. You can try to predict the j-th manifest variable from the other (p - 1) manifest variables, linear regression-style.
- This prediction will be imperfect. You can correlate these predicted values of the *j*-th manifest variable with the actual values of the variable. What you will get is a correlation coefficient, the multiple correlation coefficient. Square it and you get the SMC.

- Guttman has shown that if the factor model applies to the population correlation matrix P, then the squared multiple correlation of the *j*-th manifest variable on the other (*p* 1) manifest variables is the *lower bound* for the communality of the *j*-th manifest variable.
- So, not knowing the contents of , one might approximate the manifest variable communalities with manifest variable SMCs, computed from P. These approximations can then be substituted into the diagonal of P and one can, again, use the eigenvalue-eigenvector approach on this modified P matrix to obtain .

- However, in order to obtain the population SMCs, we need to know **P** in the first place. Most often, we don't.
- In practice, we can apply the same procedure to a sample correlation matrix, R, in order to obtain sample SMCs. Since, in reality, we usually work with sample correlation matrices, let's slowly shift the gear towards thinking more about a sample correlation matrix R and less about the population correlation matrix, P.

- So far, we have studied factor analysis limiting ourselves to the ideal scenario in which we know the population correlation matrix, P. Moreover, we only considered the case where the model holds exactly in the population.
- Now, let's consider the real world in which we do not have access to P but we do have access to R. In this real world scenario, we are not even sure the sample correlation matrix R is drawn from a population with a correlation matrix P for which the model holds.
- As before, let's just consider the uncorrelated / orthogonal model for now.

• First of all, we should tone down the optimism. In our hypothetical scenarios, we could select and to reconstruct **P** perfectly:

• In reality, our *estimates* of and , and , will generally not be able to exactly reproduce our sample correlation matrix **R**:

- So, what we want is a parsimonious model (m << p) that provides a relatively good approximation to the data we have observed.
- This degree of approximation (how well the model fits the data) is reflected in the **residual matrix**, defined as
- The residual matrix tells us how far away the correlation matrix **R** we have observed is from the correlation matrix the model predicts. In other words, how far is the observed correlation matrix from the model-implied correlation matrix (which is simply)

- Every element in the residual matrix tells us how far is the model-implied (predicted) value of this element from its observed value.
- Alright, so again, we don't have a population correlation matrix P which we used for all the computations and methods covered before. What are we going to do?
- Of course, we're going to pretend like the problem isn't there and we'll start by doing things in the exact same way.

- First, we will obtain some initial communality estimates and plug them into the diagonal of **R**. We can use the SMCs.
- This way, we will arrive at our () matrix just as we did arrive previously at the () matrix. [Oh, by the way, did I ever call this a *reduced* correlation matrix? I didn't? Well, now I do.]
- We get the eigenvalues and eigenvectors for this reduced [see?] sample correlation matrix.

- Again, we will obtain some eigenvalues and some eigenvectors. However, in this case (**not** having a population correlation matrix, **not** being sure the model holds exactly in the population), we will generally not obtain an eigen-solution where the (p - m) smallest eigenvalues are zero.
- Thus, we cannot rely on the number of non-zero eigenvalues to show us the "true" number of factors (*m*). Thus, we will have to choose *m* ourselves beforehand, based on our best judgement (more on that later)

- Thus, having chosen the number *m* beforehand, we will take the *m* largest eigenvalues and their corresponding *m* eigenvectors.
- Just like before, we will take the square root of the eigenvalues, sort them by size and place them in a diagonal matrix
- And, just like before, we will create a matrix with the corresponding eigenvectors as columns.

• Then, we can use the eigenvalues and eigenvector matrices to compute our estimate of factor loadings:

• The obtained in this way minimizes the residual sum of squares (RSS):

- ()

- This results in minimum sum of squared residuals, **conditional** on the given set of prior communality estimates.
- This method is known as the *principal factor method using prior communality estimates* (whoa, that's a LONG name)
- Let's look at an example.

 Previously, we used the population correlation matrix for the four-tests-data for examples. Assume we have a sample correlation matrix **R** from the same data, different from the population matrix **P**:



• We would like to estimate the model, but we do not know the true communalities. Also, we do not know if the model holds in the population.

- We can, however, compute the SMCs as approximations to the true communalities.
- In this case, we would get the following SMCs: .29, .377, .156 and .39 (respectively). We will replace the diagonal elements in **R** with the communality estimates to get our reduced sample correlation matrix:

• Choosing *m* = 2, we get the following *m* eigenvalues and *m* eigenvectors:

• ...and we compute :



• Interesting point: the sums of squares of each column correspond to the eigenvalues.

• Then, we can compute the model-implied **reduced** correlation matrix:



- On the diagonal of this matrix are the communalities for this solution. These values are the sums of squares of factor loading in each row of
- Off the diagonal are the correlations between the MVs as reconstructed by this particular model solution.

• Compare the model-implied reduced correlation matrix to the observed reduced correlation matrix:



• They don't match – the model does not fit the data perfectly.



• This lack of fit is represented in the residual matrix:



• The solution produced a residual matrix with minimum sum of squares, conditional on the prior communality estimates. If the prior communality estimates would be different, a different residual matrix would satisfy the RSS criterion.

Short review

- So, what was the principle behind the *principal factor method using prior communality estimates*? Let's do a short recap:
- 1) First, we obtain some communality estimates (like SMCs) and plug them into the diagonal of **R**. Thus, we get our estimate of (
- 2) Then, we obtain the eigen-solution of (
- 3) We use the eigen-solution to obtain
- 4) What we just got is a solution that minimizes the Residual Sum of Squares (RSS) given our initial

- Alternatively, we could try to minimize the RSS criterion by estimating alongside and not sticking only with the initial
- This can be done iteratively, by minimizing RSS with respect to both and
- This technique is called *iterative principal factors* or *ordinary least squares* (OLS) or *unweighted least squares* (ULS) or *minres*

- We will start by doing things the same way we did previously, using the principal factors method:
- 1) First, we obtain some communality estimates (like SMCs) and plug them into the diagonal of **R**. Thus, we get our estimate of (
- 2) Then, we obtain the eigen-solution of (
- 3) We use the eigen-solution to obtain
- ...but we won't end here. We will use the computed to obtain new communality estimates by summing the squared elements in each row of (diagonal elements of)

- We shall take the new communality estimates and plug them into the diagonal of **R**. Thus, we get a new (
- Again, we obtain the eigen-solution of this new () and use it to compute a new
- ...and repeat (use the newly computed to again obtain new communality estimates). We continue this process until the communalities obtained in successive iterations do not significantly differ by some pre-set criterion (convergence criterion).

- That's really all there is (in principle) about OLS.
- By the way, the RSS function (the formula we have seen before) is a discrepancy function – it quantifies the distance between the observed and model-implied correlation matrices. In other words, it expresses the degree of lack of model fit.
- Being a discrepancy function, it is always greater than or equal to zero and is zero **only** when the observed and model-implied correlation matrices are the same.

Heywood cases

- One nasty thing can happen when using OLS estimation
- That is, some communalities can, in the course of the iterations, be greater than one. Conversely, the unique variances can become less than zero (because in a standardized solution, the communality and the unique variance of an MV add up to one)
- But there's no such thing as negative variance. Thus, such a solution would be nonsensical and unacceptable. We call these occurrences *Heywood cases*

Heywood cases

- If you're using smart software, you should be notified whenever a *Heywood case* occurs
- If you're using smart software, it can help you circumvent the problem by placing a constraint on the associated unique variance such that it can only be greater than or equal to zero.

- We considered multiple scenarios of fitting the model to data. Let's do a quick review.
- 1) You know P and you know
 You can obtain the eigen-solution of
 (P) to compute .

....however, this will never be the case in practice.

- We considered multiple scenarios of fitting the model to data. Let's do a quick review.
- 2) You know P but you do not know . You can estimate communalities using SMCs and plug them into the diagonal of P to obtain (P). Afterwards, you obtain the eigen-solution of (P) to obtain .

....however, this will **also** never be the case in practice.

- We considered multiple scenarios of fitting the model to data. Let's do a quick review.
- 3) You do not know P and you do not know . All you have is R. You can estimate communalities using SMCs and plug them into the diagonal of R to obtain (R). Obtain the eigen-solution of (R) to get .

....the solution minimizes RSS given your original . This can happen very often in practice, although we would normally use a better option coming up next.

- We considered multiple scenarios of fitting the model to data. Let's do a quick review.
- 4) You do not know P and you do not know . All you have is R. You can estimate communalities using SMCs and plug them into the diagonal of R to obtain (R). Obtain the eigen-solution of (R) to get . Use the computed to obtain new communality estimates from the diagonal of . Return to the beginning with fresh new communality estimates, repeat until convergence.