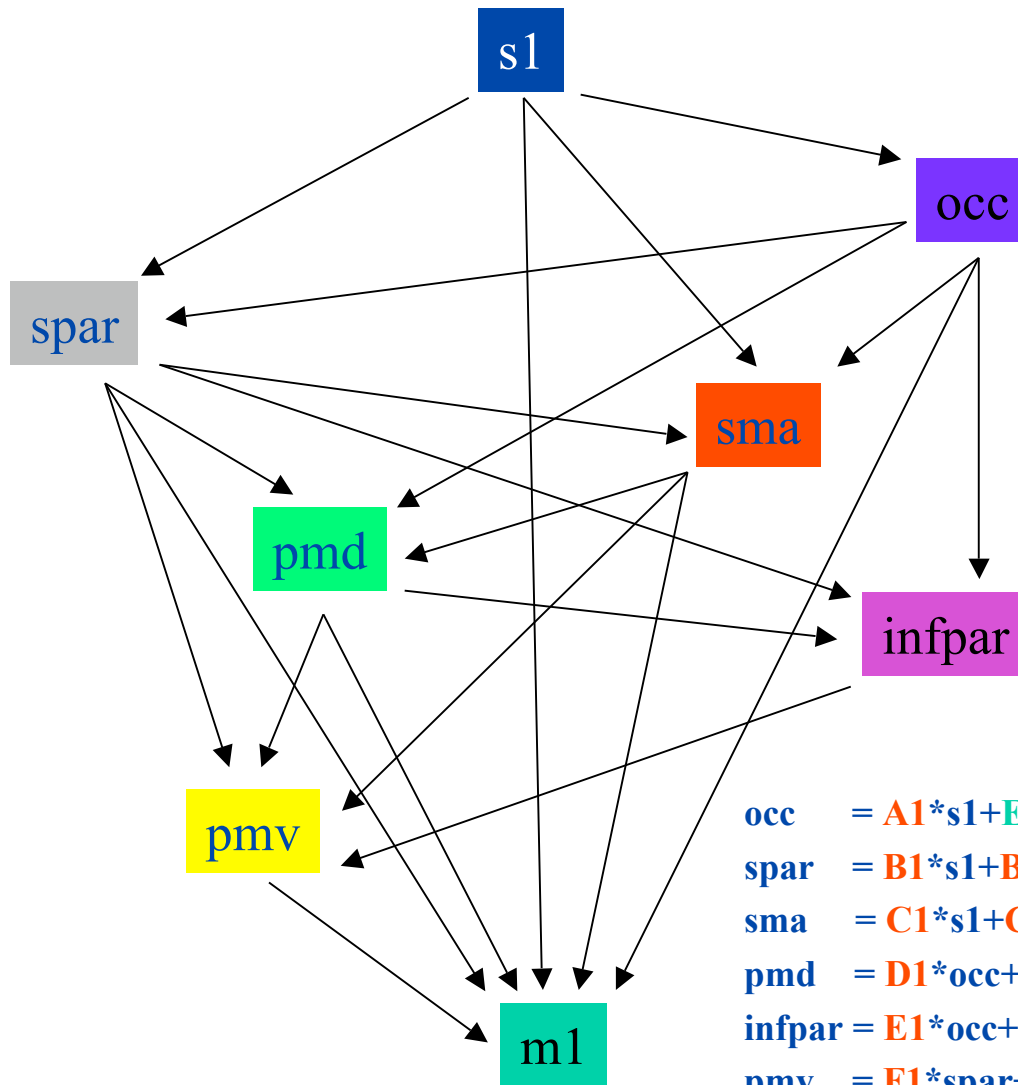


Networks in fMRI Brain Data using Structural Equation Models

03/06/09

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An SEM Model



Built from Natasha' xml files but with a small difference - there is a missing connection.

The model is very hierarchical with higher nodes not depending on lower nodes i.e., higher nodes have no input from lower nodes.

$$\text{occ} = A1*s1 + \text{Err1}$$

$$\text{spar} = B1*s1 + B2*occ + \text{Err2}$$

$$\text{sma} = C1*s1 + C2*occ + C3*spar + \text{Err3}$$

$$\text{pmd} = D1*occ + D2*spar + D3*sma + \text{Err4}$$

$$\text{infpar} = E1*occ + E2*spar + E3*pmd + \text{Err5}$$

$$\text{pmv} = F1*spar + F2*sma + F3*pmd + F4*infpar + \text{Err6}$$

$$\text{m1} = G1*s1 + G2*occ + G3*spar + G4*sma + G5*pmd + G6*pmv + \text{Err7}$$

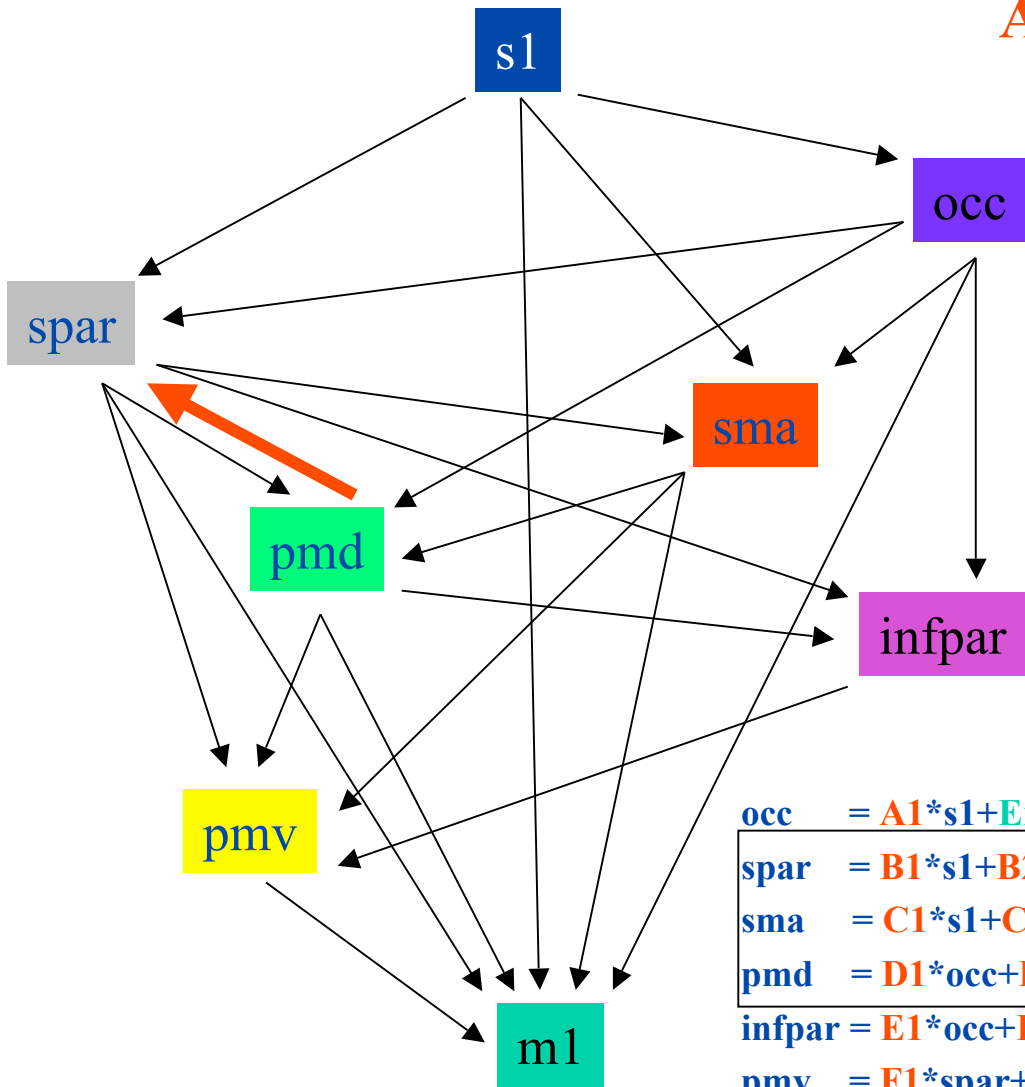
Solution with R (Standardized Time Series)

All Nodes	Remove m1	Remove m1, pmv	Remove m1, pmv, infpar	Remove m1, pmv, infpar, pmd	Remove m1, pmv, infpar, pmd, sma.	Remove m1, pmv, infpar, pmd, sma, spar
par01 0.823	par01 0.823	par01 0.823	par01 0.823	par01 0.823	par01 0.8230	par01 0.8230
par02 0.847	par02 0.847	par02 0.847	par02 0.847	par02 0.847	par02 0.8471	err01 0.3226
par03 0.157	par03 0.157	par03 0.157	par03 0.157	par03 0.157	par03 0.1578	err02 1.0000
par04 0.936	par04 0.936	par04 0.936	par04 0.936	par04 0.936	err01 0.3226	err03 1.0000
par05 -0.114	par05 -0.114	par05 -0.114	par05 -0.114	par05 -0.114	err02 0.0374	err04 1.0000
par06 0.139	par06 0.139	par06 0.139	par06 0.139	par06 0.139	err03 1.0000	err05 1.0000
par07 0.172	par07 0.172	par07 0.172	par07 0.172	err01 0.322	err04 1.0000	err06 1.0000
par08 0.044	par08 0.044	par08 0.044	par08 0.044	err02 0.037	err05 1.0000	err07 1.0000
par09 0.804	par09 0.804	par09 0.804	par09 0.804	err03 0.038	err06 1.0000	err08 1.0000
par10 -0.113	par10 -0.113	par10 -0.113	err01 0.322	err04 1.000	err07 1.0000	
par11 0.843	par11 0.843	par11 0.843	err02 0.037	err05 1.000	err08 1.0000	
par12 0.230	par12 0.230	par12 0.230	err03 0.038	err06 1.000		
par13 0.222	par13 0.222	err01 0.322	err04 0.023	err07 1.000		
par14 0.191	par14 0.191	err02 0.037	err05 1.000	err08 1.000		
par15 0.245	par15 0.245	err03 0.038	err06 1.000			
par16 0.308	par16 0.308	err04 0.023	err07 1.000			
par17 0.830	err01 0.322	err05 0.056	err08 1.000			
par18 0.116	err02 0.037	err06 1.000				
par19 -0.465	err03 0.038	err07 1.000				
par20 0.179	err04 0.023	err08 1.000				
par21 0.274	err05 0.056					
par22 0.071	err06 0.091					
err01 0.322	err07 1.000					
err02 0.037	err08 1.000					
err03 0.038						
err04 0.023						
err05 0.056						
err06 0.091						
err07 0.012						
err08 1.000						

Number of Iterations = 0!

- > Removing lower nodes does not change the coefficients of higher nodes.
- > In-fact for this network, removing any node has not change coefficient of any other node i.e., the equations are independent.

Adding Connection pmd→spar



Introducing this term in SEM creates a feedback between the three equations during likelihood minimization.

$$\begin{aligned}
 \text{occ} &= A1*s1 + \text{Err1} \\
 \text{spar} &= B1*s1 + B2*occ + \text{Err2} + B3*pmd \\
 \text{sma} &= C1*s1 + C2*occ + C3*spar + \text{Err3} \\
 \text{pmd} &= D1*occ + D2*spar + D3*sma + \text{Err4} \\
 \text{infpar} &= E1*occ + E2*spar + E3*pmd + \text{Err5} \\
 \text{pmv} &= F1*spar + F2*sma + F3*pmd + F4*infpar + \text{Err6} \\
 \text{m1} &= G1*s1 + G2*occ + G3*spar + G4*sma + G5*pmd + G6*pmv + \text{Err7}
 \end{aligned}$$

Comparing Solutions from R

Without pmd→spar	With pmd→spar
par01 0.823000	par01 0.823000
par02 0.847101	par02 1.558634
par03 0.157836	par03 0.220357
----	par04 -0.776183
par04 0.936952	par05 0.540872
par05 -0.114054	par06 -0.187853
par06 0.139114	par07 0.606686
par07 0.172685	par08 0.118168
par08 0.044904	par09 0.183013
par09 0.804023	par10 0.722109
par10 -0.113474	par11 -0.113474
par11 0.843071	par12 0.843071
par12 0.230716	par13 0.230716
par13 0.222588	par14 0.222588
par14 0.191396	par15 0.191396
par15 0.245908	par16 0.245908
par16 0.308556	par17 0.308556
par17 0.830969	par18 0.830969
par18 0.116996	par19 0.116996
par19 -0.465222	par20 -0.465222
par20 0.179366	par21 0.179366
par21 0.274801	par22 0.274801
par22 0.071542	par23 0.071542
err01 0.322671	err01 0.322671
err02 0.037433	err02 0.052610
err03 0.038098	err03 0.046281
err04 0.023864	err04 0.025022
err05 0.056198	err05 0.056198
err06 0.091127	err06 0.091127
err07 0.012968	err07 0.012968
err08 1.000000	err08 1.000000

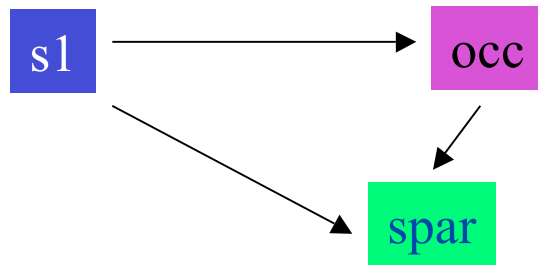
Coupled equations'
coefficients change

Coefficients
unchanged

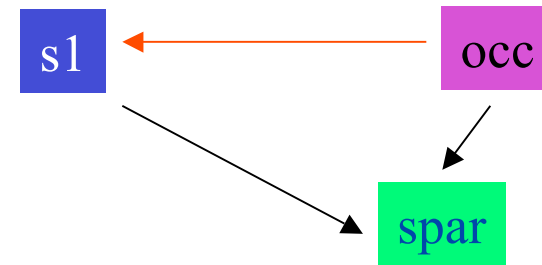
Number of Iterations = 70
for model with pmd→spar

- > The hierarchical model has fit coefficients in range (-1,+1).
- > Model with pmd→spar link has coefficients outside (-1,+1) range.
- > R does not have methods to find solutions with bounded coefficients. AMOS may have this facility. I know Minimizers in ROOT do have this.

Direction in the Network is Imposed by Anatomy



par01=0.823 occ <--- s1
par02=0.847 spar <--- s1
par03=0.157 spar <--- occ

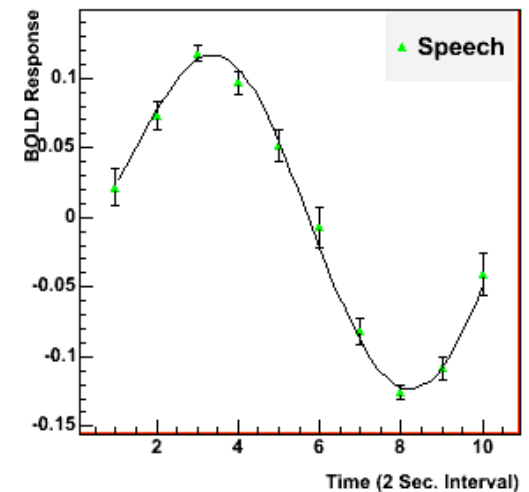


par01=0.823 s1 <--- occ
par02=0.847 spar <--- s1
par03=0.157 spar <--- occ

Same coefficient for $s1 \rightarrow occ$ and $occ \rightarrow s1$, while other connections are left as is.

Remark:

At present time resolution in fMRI data cannot be used to establish causal relationship between different regions. fMRI data may not even be suited for this given the nature of BOLD response. Even so, something that may be worth trying is to scan specific ROI layers in a second run. This would give more time points on the HRF and may help establish better timing relation between regions.



It would be interesting to understand this -

In writing SEM, what does it really mean that variance in one ROI can be explained by (co)variances with other ROIs?

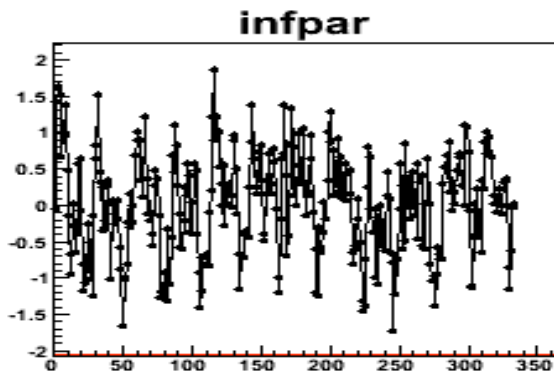
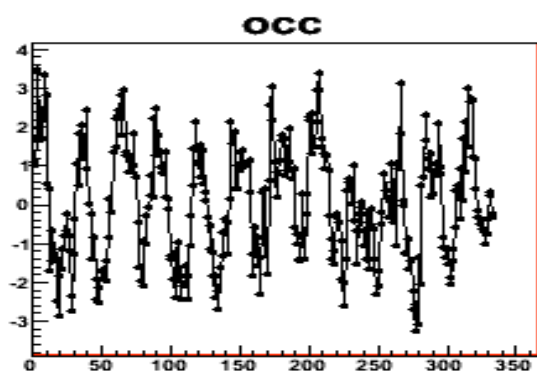
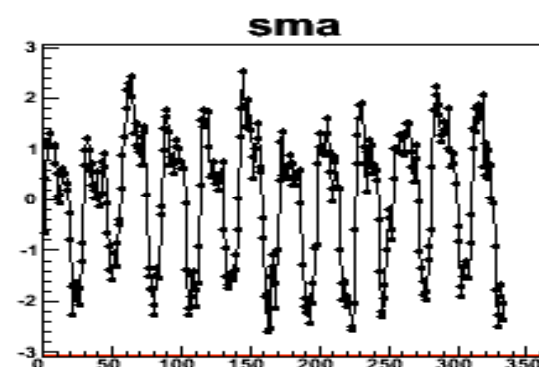
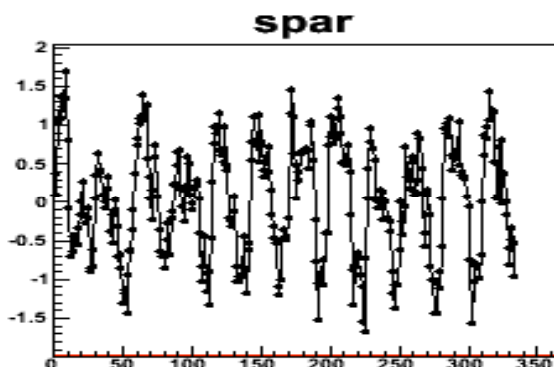
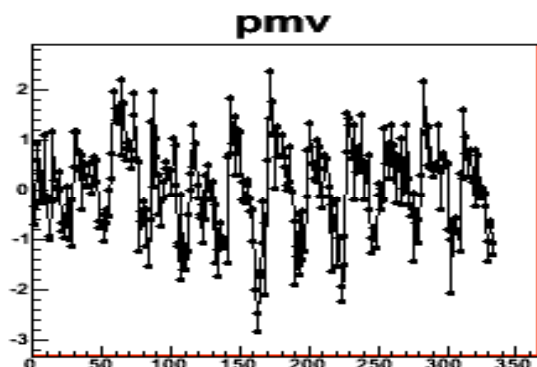
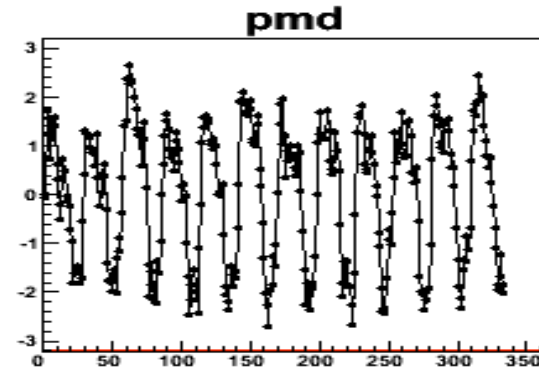
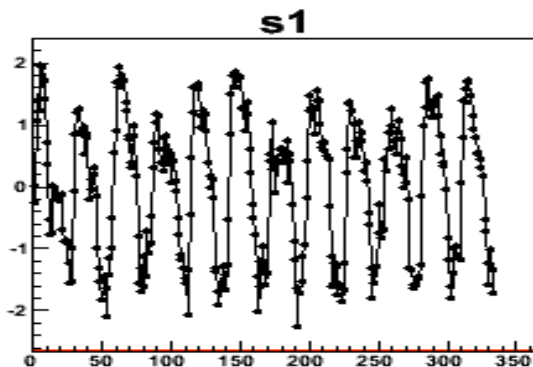
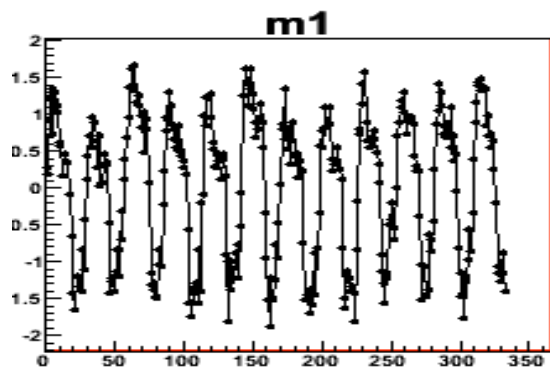
- > Variance in the time series in a given region will have random effects (noise) that are local and are presumably modeled by the error term in the of SEM equation. But depending on the number of input nodes the error term can change.
- > Active voxels will be implicitly correlated to the HRF used by selection algorithms. Building a network from voxels that have very high significance may lead to not so interesting an SEM model. To illustrate, if the correlation matrix used for the model on slide 2 is artificially modified such that each from term is 0.95. The fit result is shown on the right. In this extreme case coefficient in each equation get values equally split between all the coefficients in that equation.

0.9500	occ ← s1
0.4870	spar ← s1
0.4870	spar ← occ
0.3270	sma ← s1
0.3270	sma ← occ
0.3270	sma ← spar
0.3270	pmd ← occ
0.3270	pmd ← spar
0.3270	pmd ← sma
0.3270	infpar ← occ
0.3270	infpar ← spar
0.3270	infpar ← pmd
0.2466	pmv ← spar
0.2466	pmv ← sma
0.2466	pmv ← pmd
0.2466	pmv ← infpar
0.1653	m1 ← s1
0.1653	m1 ← occ
0.1653	m1 ← spar
0.1653	m1 ← sma
0.1653	m1 ← pmd
0.1653	m1 ← pmv
0.0970	occ ↔ occ
0.0740	spar ↔ spar
0.0660	sma ↔ sma
0.0660	pmd ↔ pmd
0.0660	infpar ↔ infpar
0.0620	pmv ↔ pmv
0.0580	m1 ↔ m1
1.0000	s1 ↔ s1

It would be interesting. . .

- > Understanding the sources of variation (randomness) in regions will definitely be interesting.
- > Instead of using the time series directly, variables that are more sensitive to time and less sensitive to local fluctuations may be more optimal to use in SEM studies. Using the time series directly, apart from being auto-correlated with other time series, also has small contradiction. Causal relation necessarily implies one event occurs before the other event. But best correlation in the time series will occur when there is no time difference between the two series. If there was sufficient time resolution this apparent contradiction can be fixed in the SEM implementation.

Back to Time Series



334 time points

Average Fit Coefficients from 11 Subjects (Block)

	Without pmd→spar	With pmd→spar
A1	0.698 ± 0.011	0.698 ± 0.011
B1	0.711 ± 0.007	2.037 ± 2.676
B2	0.237 ± 0.009	0.305 ± 0.034
..	---	-1.462 ± 3.058
C1	0.820 ± 0.045	0.539 ± 0.474
C2	0.044 ± 0.016	-0.124 ± 0.050
C3	0.052 ± 0.051	0.518 ± 0.748
D1	0.059 ± 0.007	-0.035 ± 0.011
D2	0.200 ± 0.021	0.250 ± 0.078
D3	0.736 ± 0.013	0.817 ± 0.056
E1	0.018 ± 0.008	0.018 ± 0.008
E2	0.463 ± 0.105	0.463 ± 0.105
E3	0.391 ± 0.129	0.391 ± 0.129
F1	-0.049 ± 0.054	-0.049 ± 0.054
F2	0.079 ± 0.092	0.079 ± 0.092
F3	0.431 ± 0.232	0.431 ± 0.232
F4	0.338 ± 0.033	0.338 ± 0.033
G1	0.487 ± 0.049	0.486 ± 0.049
G2	0.081 ± 0.003	0.081 ± 0.003
G3	-0.209 ± 0.011	-0.209 ± 0.011
G4	0.225 ± 0.021	0.225 ± 0.021
G5	0.430 ± 0.044	0.430 ± 0.044
G6	-0.024 ± 0.012	-0.024 ± 0.012

Out of 11 subjects 9 converged, while 2 did not. Below is the covariance matrix (standardized time series) comparing subject02 that converged and subject12 that did not converge.

	m1	s1	pmd	pmv	spar	sma	occ	infpar
m1	1.000	0.908	0.961	0.733	0.825	0.950	0.715	0.617
s1	0.908	1.000	0.953	0.744	0.921	0.914	0.757	0.680
pmd	0.961	0.953	1.000	0.797	0.898	0.957	0.757	0.684
pmv	0.733	0.744	0.797	1.000	0.708	0.777	0.571	0.669
spar	0.825	0.921	0.898	0.708	1.000	0.844	0.788	0.725
sma	0.950	0.914	0.957	0.777	0.844	1.000	0.661	0.660
occ	0.715	0.757	0.757	0.571	0.788	0.661	1.000	0.585
infpar	0.617	0.680	0.684	0.669	0.725	0.660	0.585	1.000

converged

	m1	s1	pmd	pmv	spar	sma	occ	infpar
m1	1.000	0.950	0.964	0.844	0.851	0.958	0.685	0.550
s1	0.950	1.000	0.958	0.832	0.867	0.935	0.621	0.521
pmd	0.964	0.958	1.000	0.850	0.837	0.967	0.591	0.453
pmv	0.844	0.832	0.850	1.000	0.840	0.861	0.598	0.550
spar	0.851	0.867	0.837	0.840	1.000	0.854	0.736	0.743
sma	0.958	0.935	0.967	0.861	0.854	1.000	0.618	0.545
occ	0.685	0.621	0.591	0.598	0.736	0.618	1.000	0.626
infpar	0.550	0.521	0.453	0.550	0.743	0.545	0.626	1.000

Did not
converge

Why?