A Bayesian Approach to Measurement Bias in Networking Studies
Statistical Appendix

Contents

1 Supplementary Statistics for the Empirical Bayes IRT Model

Table 1: Summary of Coefficients based on the Generalized Partial Credit Model

Networking Node	Cat.1	Cat. 2	Cat.3	Cat.4	Cat.5	*Discrimination*
Local Public Officials	-2.523	-1.570	1.575	2.781	4.168	0.763
State Public Officials	-2.317	0.298	2.476	2.433	3.278	1.056
State Regulatory Agencies	-2.142	0.680	2.450	2.261	3.476	1.483
State Medicaid	-0.399	1.316	2.581	2.005	1.914	1.067
State Medicare	-0.109	1.620	2.371	2.816	1.805	0.755
Accrediting Agencies	-2.597	2.659	3.536	1.676	5.822	0.756
Social Service Agencies	-0.078	0.538	3.259	3.926	1.951	0.470
Civic Groups	-2.178	-2.347	1.305	3.947	5.059	0.470
Insurance Companies	-0.500	0.700	3.304	2.593	1.315	0.463
State Hospital Associations	-2.571	-2.332	1.576	2.978	3.944	0.515
National Hospital Associations	-1.515	0.708	2.336	2.401	3.338	0.737
Other Professional Associations	-1.370	-0.235	2.676	2.950	3.974	0.633

Table 2: Summary of Coefficients based on the Graded Response Model

Networking Node	Cat.1	Cat. 2	Cat.3	Cat.4	Cat.5	*Discrimination*
Local Public Officials	-2.817	-1.146	1.172	2.933	4.869	1.231
State Public Officials	-2.059	0.198	2.138	3.212	4.357	1.526
State Regulatory Agencies	-1.898	0.534	2.244	3.056	4.258	1.922
State Medicaid	-0.508	1.089	2.346	2.871	3.390	1.667
State Medicare	-0.392	1.226	2.427	3.336	3.964	1.330
Accrediting Agencies	-2.196	1.928	3.853	4.665	7.539	1.013
Social Service Agencies	-0.864	0.692	2.647	4.166	5.137	0.953
Civic Groups	-3.171	-1.500	1.004	3.531	6.037	0.867
Insurance Companies	-1.043	0.627	2.366	3.367	4.211	0.970
State Hospital Associations	-3.329	-1.581	1.016	3.023	5.037	0.919
National Hospital Associations	-1.449	0.443	2.032	3.174	4.525	1.268
Other Professional Associations	-1.583	-0.048	1.983	3.438	5.039	1.196

Figure 1: Item Category Characteristic Curves based on the Non-Bayesian Generalized Partial Credit Model (*Category 1= Never, Category 2=Yearly, Category 3=Monthly, Category 4= Weekly, Category 5=More than Weekly, Category 6=Daily*)

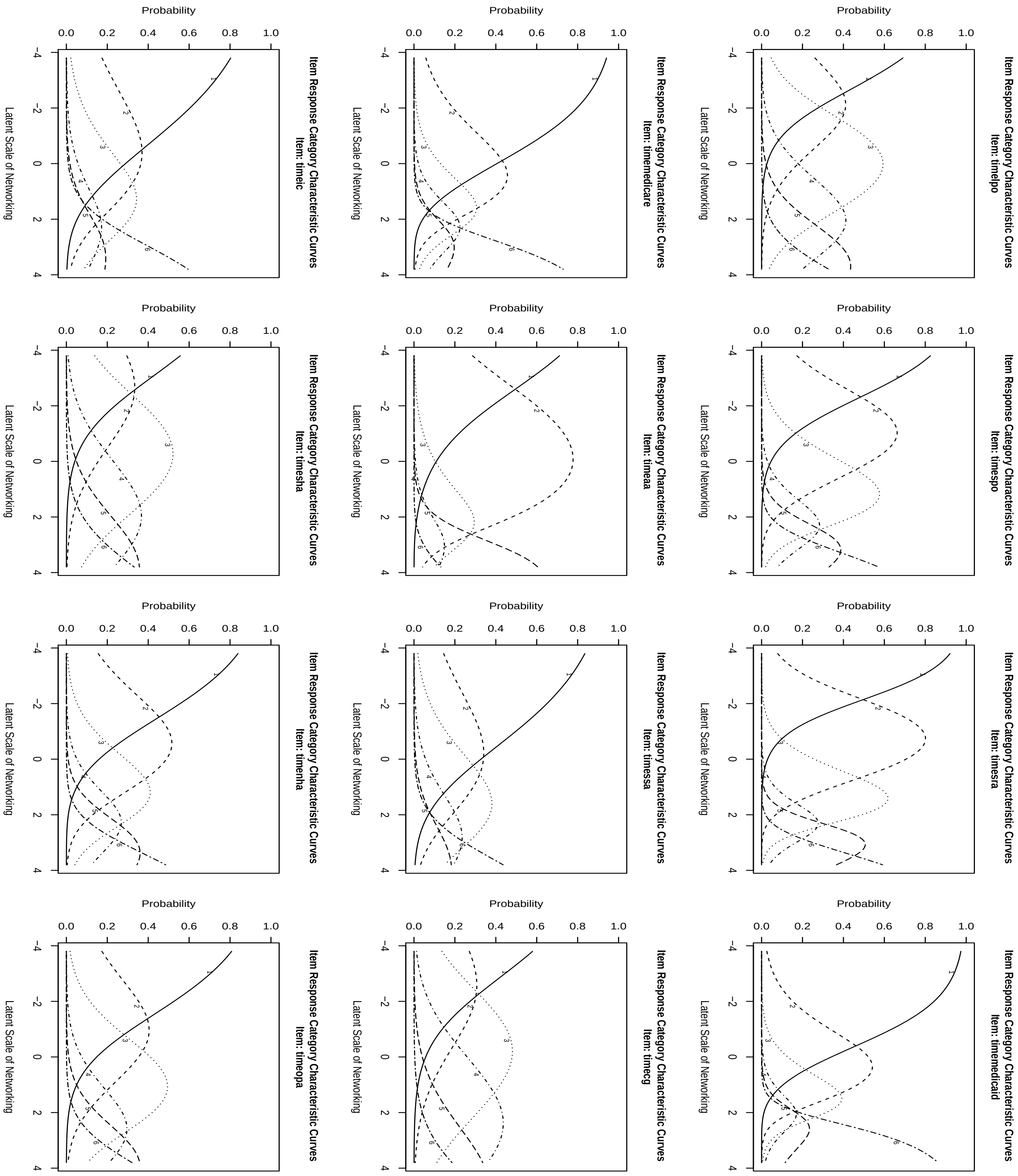


Figure 2: Item Information Characteristic Curves Based on the Non-Bayesian Generalized Partial Credit Model

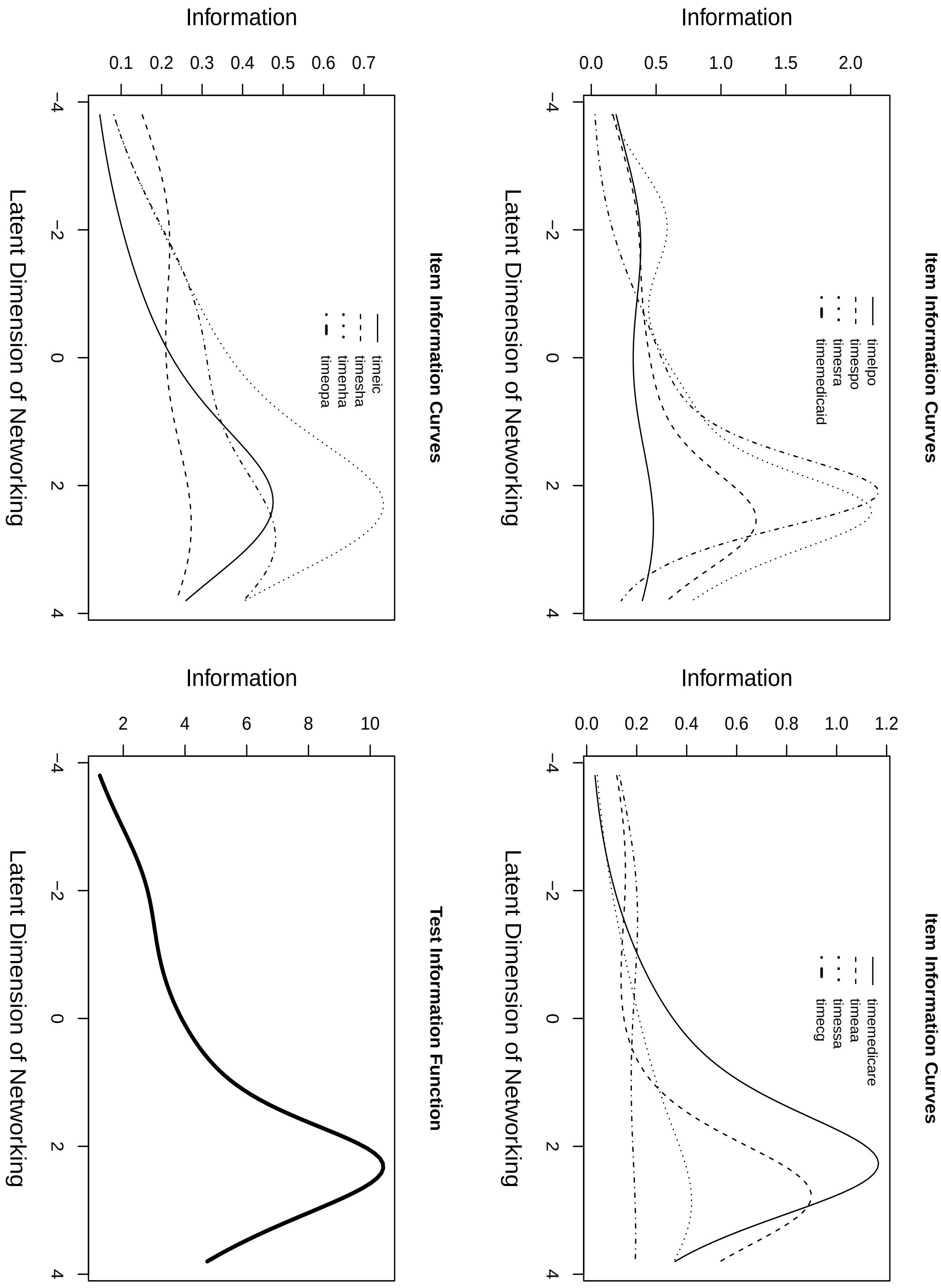


Figure 3: Item Category Characteristic Curves based on the Non-Bayesian Graded Response Model (*Category 1= Never, Category 2=Yearly, Category 3=Monthly, Category 4= Weekly, Category 5=More than Weekly, Category 6=Daily*)

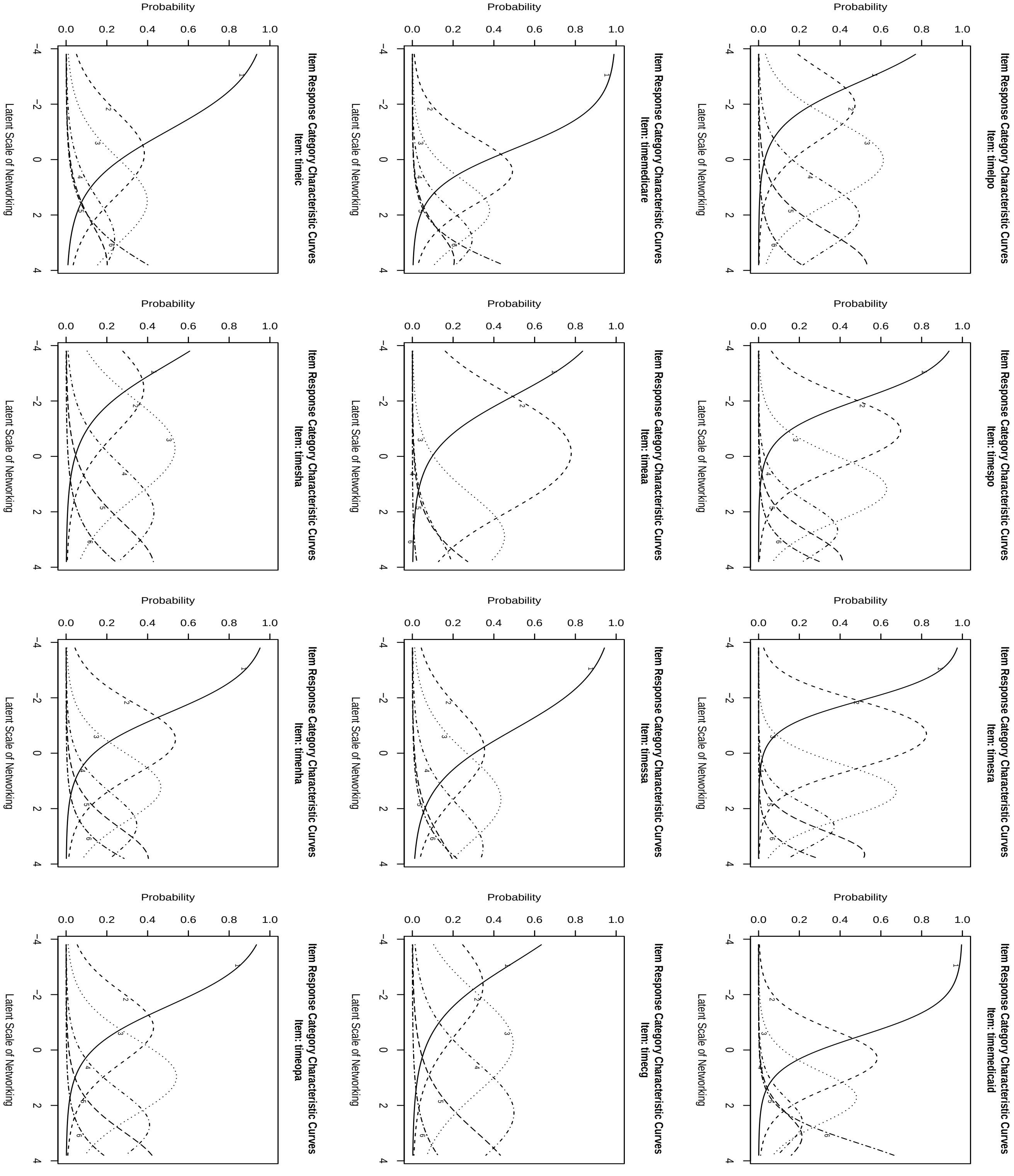


Figure 4: Item Information Characteristic Curves Based on the Non-Bayesian Graded Response Model

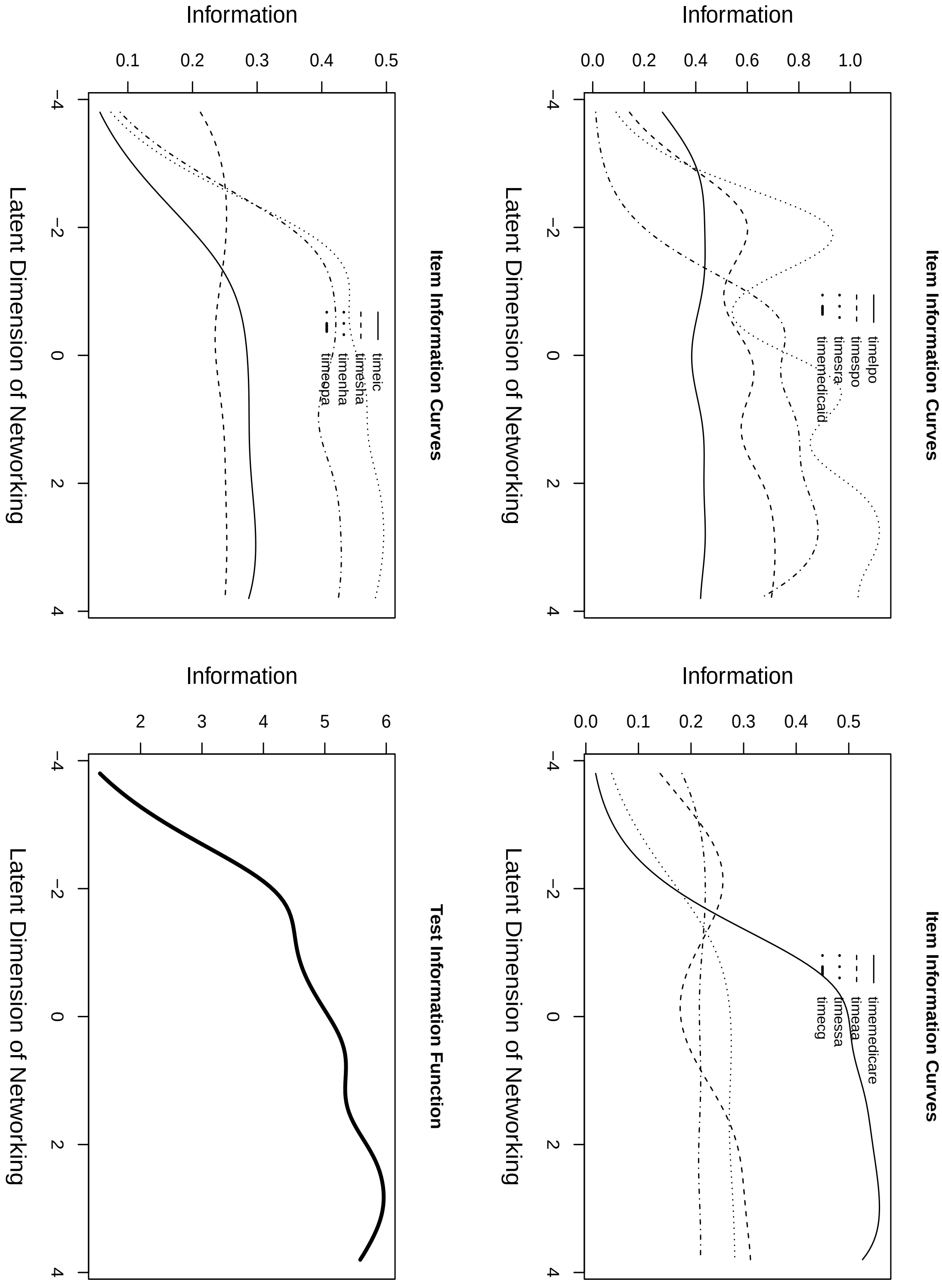
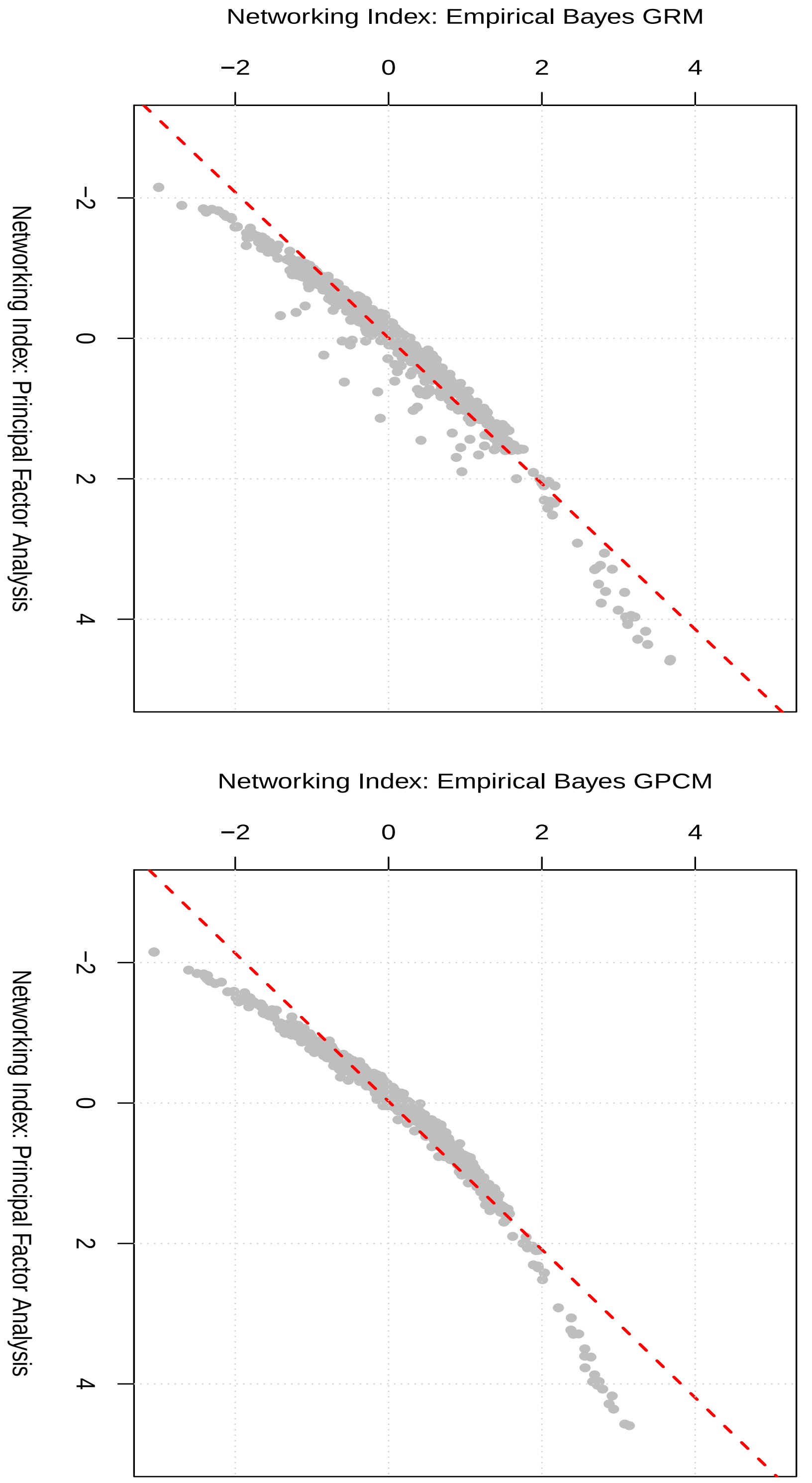


Figure 5: Measurement Agreement Between the Factor Index and the Two Empirical Bayes IRT Indices



2 Identification and Estimation of the Bayesian Generalized Partial Credit Model

We specify noninformative priors for α_j, and $\beta_{j,k}$. Because the latent dimension of managerial networking (θ_i), the discrimination parameter (α_j), and the difficulty parameter ($\beta_{j,k}$) are simultaneously estimated, we set $\beta_{j,k}$ to be 0. In other words, choice 1 ("Never") in all 12 networking nodes are constrained to be 0 for the purpose of identification. Adding this restriction does not come at the cost of altering the possible outcomes (Bafumi et al., 2005; Curtis, 2010; Fox, 2010).

Following Gelman (2006) and Li and Baser (2012), we specify prior distributions as the following:

$$\begin{aligned} \alpha &\sim N(0, 0.001)I(0,) \\ \beta &\sim N(0, 0.001)I(-3.5, 3.5) \\ \theta &\sim N(\mu, \sigma) \end{aligned} \tag{1}$$

We specify α as a normal distribution with mean 0 and precision 0.001. We also set α to take positive values. The truncation is chosen because α is often positive and near 1 in IRT applications. The diffuse prior specifies a large-size variance and a zero mean, as such, it does not inform the model about the specific mean value of α. Similarly, we specify a noninformative prior for β, with mean 0 and precision 0.001. Based on the results of the empirical Bayes GPCM, we place most parameter values in the range (-3.5, 3.5). We did not set θ to be a standard normal distribution. Instead, we adopt the strategy of prior specification in Li and Baser (2012), and set the hyper-prior, μ (underlying mean for the latent networking dimension, θ) to be a normal distribution with mean 0 and precision 0.001. The hyper-prior, σ is defined as a uniform distribution. Similar to the identification strategy used in Treier and Jackman (2008), we center each estimated θ_i to have mean zero and scale them based on the estimated σ. In other words, we impose the rescaling to the MCMC outputs by each iteration. Accordingly, we rescale α_j and $\beta_{j,k}$ using the same strategy.

$$\begin{aligned} \mu &\sim N(0, 0.001) \\ \sigma &\sim dunif(0, 10) \end{aligned} \tag{2}$$

To initialize the model, we use `JAGS` to randomly generate starting values for all the parameters. The Bayesian GPCM is estimated by running 200,000 iterations of Markov Chain Monte Carlo (MCMC) simulations. We specify the burn-in period equals to the first 20,000 (10%)iterations, and restore every 60th sampled value for rescaled α_j, $\beta_{j,k}$, θ_i. To optimize the time for model convergence, we set an initial sampling phase, during which the sampler adapts to improve computation efficiency. The 5,000 samples generated during this adaptive phase is not based on Markov Chain and are not used in inference.

Post estimation diagnostic analysis does not find evidence for non-convergence and non-stationary posterior means (see Section 5). The specific `BUGS` code used in our Bayesian analysis are adapted from prior works by Curtis (2010) and Li and Baser (2012).

BUGS Code

```
model
{
for (i in 1:n){
for (j in 1:p){
numer[i,j,1] <- 0
enume[i,j,1] <- 1
denom[i,j,1] <- 1
}
}
for (i in 1:n){
theta[i] ~ dnorm(mu, tau)
for (j in 1:p){
for (k in 2:K[j]){
numer[i,j,k] <- alpha[j]*(theta[i]-b[j,k])+numer[i,j,k-1]
enume[i,j,k] <- exp(numer[i,j,k])
denom[i,j,k] <- enume[i,j,k] + denom[i,j,k-1]
}
Denom[i,j,1] <- denom[i,j,K[j]]}}

for (i in 1:n){
for (j in 1:p){
for (k in 1:K[j]){
prob[i,j,k] <- enume[i,j,k]/Denom[i,j,1]
}
y[i,j] ~ dcat(prob[i,j,1:K[j]])
}
}
# Priors
mu ~ dnorm(0.0, 0.001)  # Hyper-priors
sigma~dunif(0, 10)
tau<-1/(sigma*sigma)
Sigma<-1/sqrt(tau)

for (i in 1:n){
theta.adj[i] <- (theta[i]-mu)/Sigma # Rescale theta[i]
}
for (j in 1:p){
b[j, 1] <- 0.0
b.adj[j, 1] <- 0.0
alpha[j] ~ dnorm(0, 0.001) I(0, 5) #Prior for alpha[j]
alpha.adj[j] <- alpha[j] * Sigma # Rescale alpha[j]
for (k in 2:K[j])   {
b[j, k] ~ dnorm(0, 0.001) I(-3.5, 3.5) # Prior for beta[j,k]
b.adj[j, k] <- (b[j,k]-mu)/Sigma} # Rescale beta[j,k]
}
}
```

R/JAGS Code

```
# Define data and parameters
forJags<-list(y=Y,n=nrow(Y),p=ncol(Y),K=apply(Y, 2, max,na.rm=TRUE))
param<-c("alpha","alpha.adj","b","b.adj","theta.adj")
#Define Model Specification
BayesianIRT<-jags.model(file="GPCM2.bug", data=forJags,n.chains=2,n.adapt=5000)
# Run JAGS
arpa.model<-coda.samples(BayesianIRT,n.iter=200000,
n.burnin=20000,thin=60,variable.names=param)
```

3 Diagnostic Graphs of the Full Bayesian GPCM

Figure 6: Autocorrelation Plots of Selected Parameters

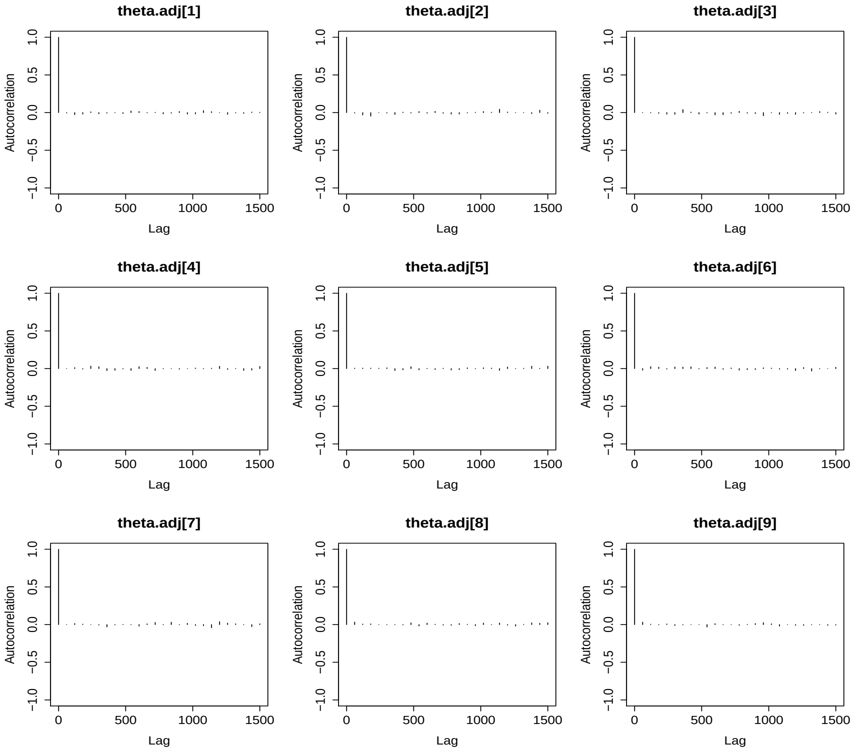


Figure 7: Trace Plots of Selected Discrimination Parameters

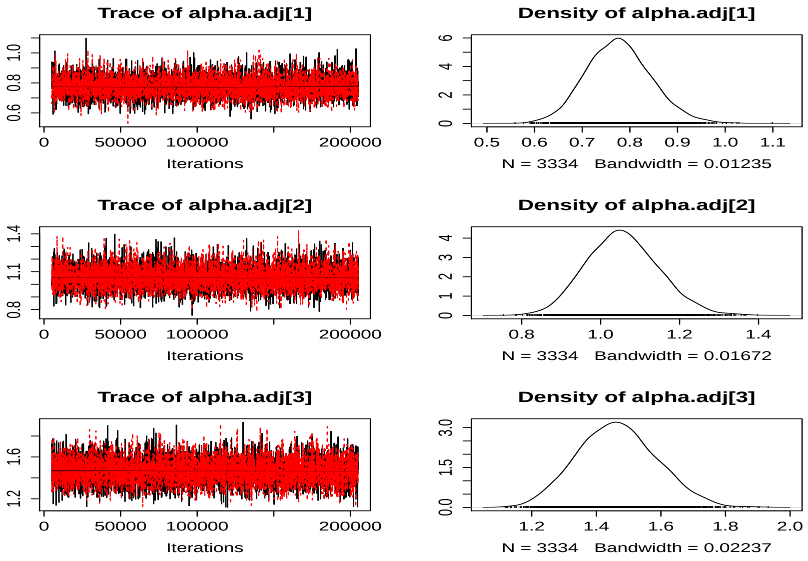
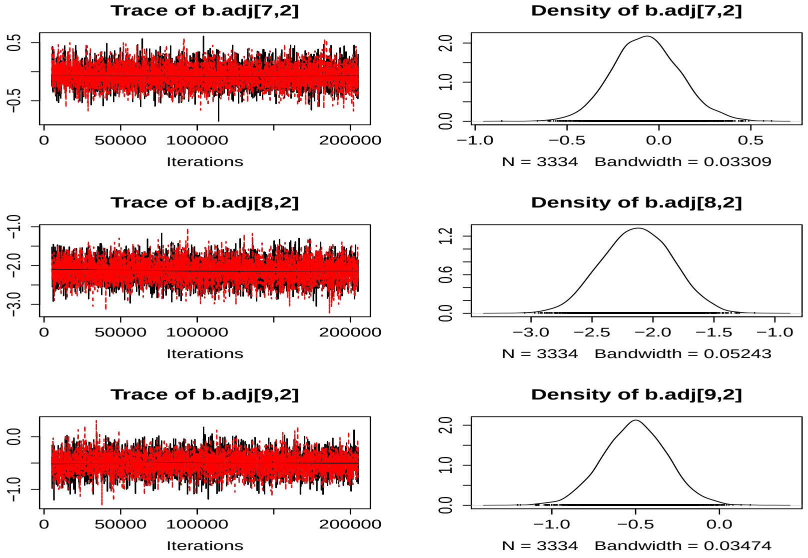


Figure 8: Trace Plots of Selected Difficulty Parameters



4 Supplementary Statistics of the Full Bayesian IRT Model

Table 3: Summary of Posterior Means of the Difficulty and Discrimination Parameters based on the Full Bayesian GPCM

Networking Node	Cat.1	Cat. 2	Cat.3	Cat.4	Cat.5	*Discrimination*
Local Public Officials	-2.455	-1.573	1.563	2.801	3.939	0.777
State Public Officials	-2.327	0.300	2.487	2.449	3.290	1.056
State Regulatory Agencies	-2.165	0.687	2.478	2.254	3.489	1.465
State Medicaid	-0.403	1.355	2.651	2.208	1.846	1.028
State Medicare	-0.100	1.685	2.433	2.890	1.731	0.724
Accrediting Agencies	-2.515	2.606	3.505	1.862	4.110	0.780
Social Service Agencies	-0.070	0.548	3.389	3.805	2.129	0.460
Civic Groups	-2.129	-2.264	1.269	3.905	4.136	0.493
Insurance Companies	-0.504	0.739	3.452	2.706	1.272	0.441
State Hospital Associations	-2.441	-2.319	1.551	2.990	3.783	0.527
National Hospital Associations	-1.532	0.720	2.361	2.429	3.456	0.731
Other Professional Associations	-1.382	-0.242	2.706	3.308	3.741	0.629

5 Specify the Monte Carlo Experiments

As mentioned in the manuscript, we conduct four Monte Carlo experiments with sample sizes to be 50, 100, 600, and 850 to compare parameter estimations for the competing models reported in Table 5 and 6. Given each sample size, we follow the following steps to run the Monte Carlo simulations:

1. Fix the three networking variables $X_i (i = 1, 2, 3)$ in four randomly generated data samples (n=50, 100, 600, 850) from their underlying distributions.To approximate the simulated data sample to the observed values, we use the observed means and standard deviations of the three networking indices as the parameters of the underlying distributions. All simulated data samples are generated from random normal distributions.
2. Fix the baseline parameter values based on the point slope coefficients β_i reported in Model 1-6.
3. Generate baseline values for Y (the dependent variable) as a function of the simulated samples of the three networking variables: $Y_i = \beta X_i + \mu$.
4. Setting the underlying distribution of the stochastic component μ to be a random standardized normal distribution. This specification is the same across all Monte Carlo experiments to make results comparable.
5. Estimate the relationship between Y_i and X_i using an OLS specification.
6. Repeat step 1-5 with 1000 replications and summarize mean parameter estimation, $\bar{\beta}$.
7. Compare mean parameter estimations learned form the Monte Carlo experiments with the baseline slope parameters to evaluate relative bias. Because the true underlying parameters associated with the networking variable is unknown, the above noted Monte Carlo experiments evaluate parameter bias based on how the observed coefficients (i.e. slopes estimated from Model 1-6) deviate from the quantities learned from repeated random samples through the simulation. In theory, the two values should converge over a large number of repeated samples and the difference should be minimal in a single sample with large n. In other words, the bias evaluated here has a relative nature. We compute relative bias of parameter estimates as a promotion using $\frac{|\bar{\beta}-\beta|}{\beta}$, where $\bar{\beta}$ is the average parameter estimate summarized based on 1000 valid Monte Carlo simulations and β denotes the baseline values (parameter estimated based on actual data). A relative bias greater than 5% is considered as substantial. Because we fixed the stochastic component μ in all models, the mean estimated slope parameter in each model is a function of sample size (n) and measurement uncertainty embedded in each simulated networking variable. In this way, we can compare how the relative bias change cross models using different networking measures but with the same simulated sample size.

References

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Curtis, S. McKay. 2010. "BUGS Code for Item Response Theory." *Journal of Statistical Software* 36(1):Code Snippet 1.

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Treier, Shawn and Simon Jackman. 2008. "Democracy as a Latent Variable." *American journal of Political Science* 52(1):201–17.