Supplementary Materials: Visual Inference for a Social Network Model

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A Model Details

The continuous-time Markov chain (CTMC) family of models we use were first introduced in Snijders (1996). We describe their basic structure here, and full detail can be found in Snijders (1996); Snijders et al. (2010).

Rate Function: The rate function dictates when network changes are made and which actor can make them. An actor, i, is chosen make a change in its ties one of the other nodes j. In general, the rate function can include structural and node covariate parameters into account so that each actor has a different rate of change. However, we choose a simple rate function that is constant over all nodes in a given time period, because we focus on interpreting the parameters of the objective function which directly impact the overall network structure. We denote the rate from t_m to t_{m+1} as α_m for $m = 1, \ldots, M-1$, where M is the number of time points at which the network was observed. Using this notation, the waiting time to the next chance for actor i to make a change is exponentially distributed with expected value α_m^{-1} . Since the rate is the same for all actors, the waiting time for any actor to get the opportunity to change its set of ties is also exponentially distributed with expected value $(n\alpha_m)^{-1}$.

Objective Function: After actor i is selected to make a change, it randomly picks one of its current ties, x_{ij} , to change. Actor i aims to maximize the objective function f_i given the current state of the network, x and the node-level covariates, \mathbf{Z} . This function is defined as:

$$f_i(x, \boldsymbol{\beta}, \mathbf{Z}) = \sum_{k=1}^K \beta_k s_{ik}(x, \mathbf{Z}), \tag{1}$$

where $\boldsymbol{\beta} = (\beta_1, \dots, \beta_K)$ are additional model parameters, each associated with some statistics, $s_{i1}(x, \mathbf{Z}), \dots, s_{iK}(x, \mathbf{Z})$, calculated for actor i at the current network state x. At least two parameters must be included in the objective function: density and reciprocity (Ripley et al., 2017). We denote the density, or out-degree, parameter by β_1 and the associated

statistic as $s_{i1}(x) = \sum_j x_{ij}$ and we denote the reciprocity parameter by β_2 and the associated statistic as $s_{i2}(x) = \sum_j x_{ij}x_{ji}$. We will refer to the very simple model with only these two parameters in the objective function as model M1. We define additional parameters and models of interest in Section 2 Version 1.2-3 of RSiena (Ripley et al., 2013), the software we use to fit CTMC models to data, provides over 80 possible effects that can be included in the objective function.

The objective function $f_i(x, \boldsymbol{\beta}, \mathbf{Z})$ dictates the transition probability, p_{ij} of the network changing from its current state x to the state $x(i \rightsquigarrow j)$, which is identical to x except for x_{ij} : $x_{ij}(i \rightsquigarrow j) = 1 - x_{ij}$. The transition probability is

$$p_{ij} = \frac{\exp\{f_i(x(i \leadsto j), \boldsymbol{\beta}, \mathbf{Z})\}}{\sum_h \exp\{f_i(x(i \leadsto h), \boldsymbol{\beta}, \mathbf{Z})\}},$$
(2)

dictating which edge node i changes. Thus, the actor is more likely to make changes that increase the value of their objective function, and no change is most likely when any change decreases the value of the objective function.

A.1 Model Effects

The similarity measure is computed as:

$$sim_{ij}^{b} = \frac{\max_{hk} |b_h - b_k| - |b_i - b_j|}{\max_{hk} |b_h - b_k|}$$
(3)

where $\max_{hk} |b_h - b_k|$ is the range of number of bills authored by senators, and b_i , b_j are the number of bills authored by senators i, j repectively in the senate period.

The fitted values from repeated converged simulations are

A.2 Goodness-of-Fit Testing

The software RSiena contains methods for performing goodness-of-fit tests for the CTMC models. The sienaGOF() function performs goodness-of-fit testing as follows:

1. Auxiliary statistics, such as the cumulative outdegree distribution on the nodes, are computed on the observed data (\mathbf{u}_d) and on N observations simulated from the model $(\mathbf{u}_1 \dots \mathbf{u}_N)$.

Model	\hat{lpha}_1	\hat{lpha}_2	\hat{lpha}_3	\hat{eta}_1	\hat{eta}_2	\hat{eta}_3	\hat{eta}_4	\hat{eta}_5	\hat{eta}_6
M1	2.441	2.46	2.204	-4.903	4.893	_	_	_	-
M3	2.44	2.46	2.204	-4.902	4.893	-3.45	_	_	_
M4	2.438	2.461	2.211	-4.918	4.898	_	3.34	_	_
M5	2.442	2.459	2.206	-4.917	4.89	_	_	10.091	_
M6	2.443	2.461	2.205	-4.911	4.881	_	_	_	1.329
M7	2.441	2.459	2.21	-4.923	4.892	_	2.374	6.966	0.205

Table 1: The mean estimates from repeated fits of our models of interest. When simulating from these models, these are the estimates that we will use unless otherwise stated.

2. The mean $\overline{\mathbf{u}}$ and covariance matrix \mathbf{S} are computed from the N simulations, and the Mahalanobis distance, $d_M(\mathbf{u}_d)$ from the observed statistics to the distribution of the simulated statistics is computed:

$$d_M(\mathbf{u}_d) = \sqrt{(\mathbf{u}_d - \overline{\mathbf{u}})' \mathbf{S}^{-1} (\mathbf{u}_d - \overline{\mathbf{u}})}$$
(4)

- 3. The Mahalanobis distance for each of the N simulations is calculated and $d_M(\mathbf{u}_d)$ is compared to this distribution of distances.
- 4. An empirical p-value is found by computing the proportion of simulated distances found in step 4 that are as large or larger than $d_M(\mathbf{u}_d)$.

B Data

Details of how this data can be downloaded are provided by François Briatte at github. com/briatte/congress. In the US Senate, senators often show support for a piece of legislation by co-sponsoring a bill authored by one of their colleagues. In a co-sponsorship network, ties are directed from senator i to senator j when senator i signs on as a co-sponsor to the bill that senator j authored. There are many hundreds of ties between senators when they are connected in this way, so we simplify the network by computing a single value

Goodness-of-Fit: Outdegree distribution period 1

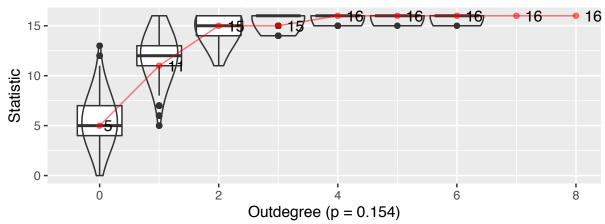


Figure 1: An example of what a goodness-of-fit plot from RSiena looks like. The overlaid boxplots and violin plots show the distribution of each of the outdegree count values on the simulated networks, and the red points and lines are the observed data values.

for each senator-senator collaboration called the weighted propensity to co-sponsor (WPC). This value is defined in Gross et al. (2008) as

$$WPC_{ij} = \sum_{b=1}^{B_j} \frac{Y_{ij(b)}}{c_{j(b)}} \left(\sum_{b=1}^{B_j} \frac{1}{c_{j(b)}} \right)^{-1}$$
 (5)

where B_j is the number of bills in a congressional session authored by senator j, $c_{j(b)}$ is the number of co-sponsors on senator j's b^{th} bill, where $b \in \{1, \ldots, B_j\}$, and $Y_{ij(b)}$ is an indicator variable that senator i co-sponsored senator j's b^{th} bill. This measure ranges in value from 0 to 1, where $WPC_{ij} = 1$ if senator i is a co-sponsor on every one of senator j's bills and $WPC_{ij} = 0$ if senator i is never a co-sponsor any of senator j's bills. To simplify the problem, we construct a network with binary edges as follows:

$$x_{ij} = \begin{cases} 1 & WPC_{ij} > 0.25 \\ 0 & WPC_{ij} \le 0.25 \end{cases}$$
 (6)

so that only strong ties between senators are in the network.

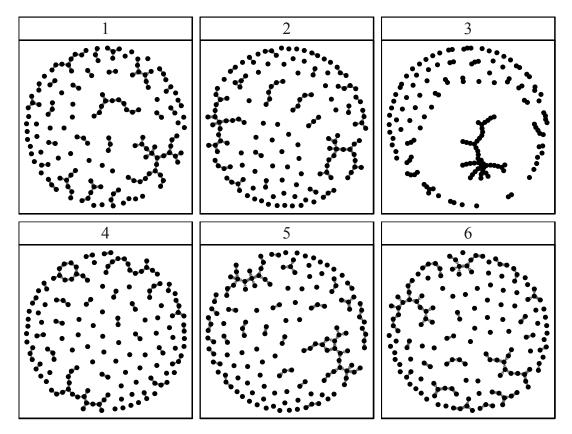


Figure 2: Lineup 3132, which led to rejection of the null hypothesis that $\beta_3 = 0$. The network simulated from model M3 is found in panel $\sqrt{16} - 1$, and the remaining panels show networks simulated from model M1.

C Lineups

D Results

D.1 Lineup Summaries

Table 2: Here is a caption. Put stuff here later

Lineup	Difficulty	Type	Param.	Rep 1	Rep 2	Rep 3	Global p-val.
	Easy	1	eta_1	$38/40^{\ddagger}$	$26/32^{\ddagger}$	$20/36^{\dagger}$	$< 10^{-4}$ ‡

Med.	1	eta_1	$22/31^{\ddagger}$	$15/31^\dagger$	$29/41^{\ddagger}$	$< 10^{-4\ddagger}$
Hard	1	eta_1	8/26	7/30	$22/38^{\dagger}$	0.02**
Easy	-1	eta_1	$20/23^{\ddagger}$	$25/26^{\ddagger}$	$19/20^{\ddagger}$	$< 10^{-4\ddagger}$
Med.	-1	eta_1	$25/36^{\ddagger}$	13/28**	$24/26^{\ddagger}$	$< 10^{-4\ddagger}$
Hard	-1	eta_1	$15/31^\dagger$	6/23	9/37	0.066*
Easy	1	eta_2	$15/23^{\ddagger}$	$34/36^{\ddagger}$	$33/37^{\ddagger}$	$< 10^{-4\ddagger}$
Med.	1	eta_2	$32/42^{\ddagger}$	$24/26^{\ddagger}$	$30/40^{\ddagger}$	$< 10^{-4\ddagger}$
Hard	1	eta_2	$23/32^{\ddagger}$	$19/21^{\ddagger}$	7/29	$< 10^{-4\ddagger}$
Easy	-1	eta_2	$24/38^{\ddagger}$	$18/28^{\ddagger}$	$19/27^{\ddagger}$	$< 10^{-4\ddagger}$
Med.	-1	eta_2	5/26	3/22	6/31	0.465

378
)77*
205
)34**
301
$10^{-4\ddagger}$
015**
038**
$10^{-4\ddagger}$
001 [†]
002 [†]

Hard	1	eta_4	10/23**	3/37	10/29*	0.205
Easy	-1	eta_4	11/41	10/25*	7/33	0.139
Med.	-1	eta_4	2/27	12/29**	14/37*	0.11
Hard	-1	eta_4	6/37	5/38	4/21	0.541
GoF	GoF	eta_4	$13/16^{\ddagger}$	7/20	$29/34^{\ddagger}$	$< 10^{-4\ddagger}$
Easy	1	eta_5	$17/26^{\dagger}$	8/21*	$27/38^{\ddagger}$	$< 10^{-4\ddagger}$
Med.	1	eta_5	2/21	11/37	$21/27^{\ddagger}$	0.019**
Hard	1	eta_5	8/30	13/30**	7/27	0.08*
Easy	-1	eta_5	$35/38^{\ddagger}$	$23/35^{\ddagger}$	$24/26^{\ddagger}$	$< 10^{-4\ddagger}$
Med.	-1	eta_5	$18/36^{\dagger}$	14/31**	17/40**	0.005^\dagger

Hard	-1	eta_5	4/36	4/33	2/28	0.715
GoF	GoF	eta_5	9/21**	$21/24^{\ddagger}$	$14/16^{\ddagger}$	$< 10^{-4\ddagger}$
Easy	1	eta_6	$18/32^{\dagger}$	$19/25^{\ddagger}$	$31/35^{\ddagger}$	$< 10^{-4\ddagger}$
Med.	1	eta_6	$28/36^{\ddagger}$	$23/30^{\ddagger}$	$23/34^{\ddagger}$	$< 10^{-4\ddagger}$
Hard	1	eta_6	$29/35^{\ddagger}$	10/36	12/30**	0.002^\dagger
Easy	-1	eta_6	$19/30^{\ddagger}$	$27/35^{\ddagger}$	$18/26^{\ddagger}$	$< 10^{-4\ddagger}$
Med.	-1	eta_6	4/25	3/37	8/27	0.499
Hard	-1	eta_6	7/33	1/35	9/24*	0.435
GoF	GoF	M7	$17/20^{\ddagger}$	$14/28^{\dagger}$	$28/37^{\ddagger}$	$< 10^{-4\ddagger}$

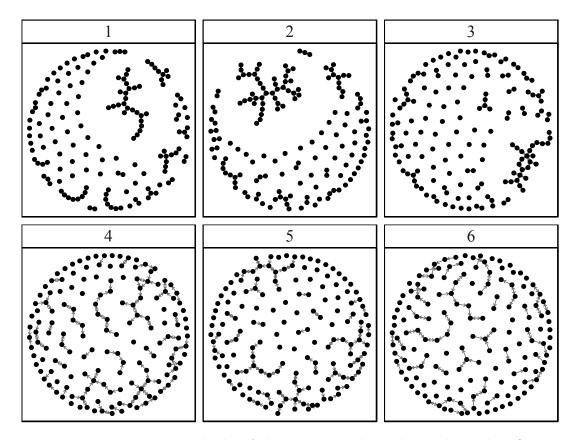


Figure 3: Lineup 3133, which resulted in failure to reject the null hypothesis that $\beta_3 = 0$. The network simulated from model M3 is found in panel $\sqrt{25} - 4$, and the remaining panels show networks simulated from model M1. 16 of 27 viewers picked plot two as most different.

D.2 Significance Testing

D.3 GoF

D.4 Visual Power

We expand portions of Figure 4 in Figures 9-11. These figures show the same prediction regions as in Figure 4, plus some additional predictions outside of the data range shown in light gray. Again, the points represent the results from the experiment. In all three of these figures, the lack of symmetry is apparent. In the reverse lineup scenario shown in Figure 11, the probability of prediction is consistently far less than the probability of prediction in the regular lineup scenario. This demonstrates that the visual signal of one plot from M4 among five plots from M1 is much stronger than that of one plot from M1

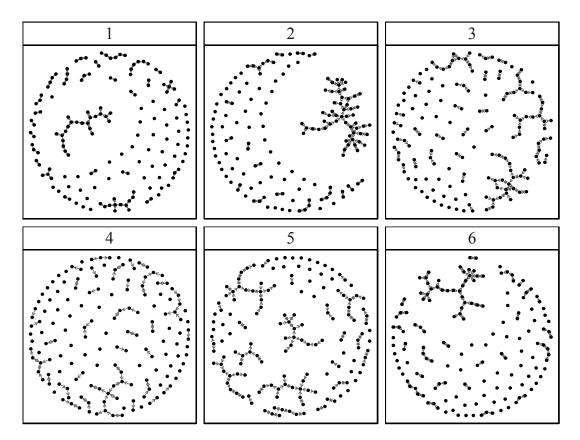


Figure 4: The goodness-of-fit lineup which resulted in failure to reject the null hypothesis. The null model for this lineup is M4. Only 7 of 20 viewers of this lineup selected the data plot as the most different from the others. The most commonly chosen panel was number four, which has a relatively simple structure compared to the other panels.

among five plots from M4. We posit that the latter is a more difficult task because it involves noticing a *lack of structure* as opposed to the presence of *more* structure. We can see a similar effect in Figure 10. At a value of $\beta_5 = 20$, the model predicts a probability of about 0.60 that a new viewer of a new lineup will identify the alternative data plot. At a value of $\beta_5 = -20$, however, the model predicts this same probability to be about 0.40. This again demonstrates that the presence of structure is detected more frequently and at smaller values than the absence of structure.

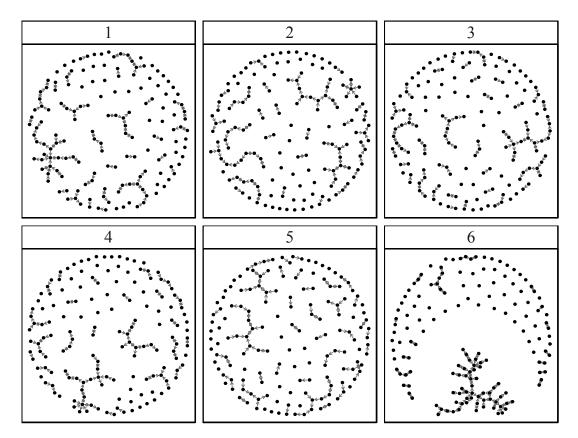


Figure 5: The linear resulting in the smallest p-value rejecting the null hypothesis. Surprisingly, this another repetition for M5 as the null model. The data are in panel 6.

Lineup ID	parameter	# ID	Total Views	p-value
3131	β_3	4	29	0.60654
3132	β_3	26	31	0.00001
3133	β_3	2	27	0.80053
3141	eta_4	10	23	0.03420
3142	eta_4	3	37	0.77965
3143	eta_4	10	29	0.09619

Table 3: Experiment results for the two parameters for which we performed significance tests. # ID indicates the number of participants who identified the alternative data plot. There were three lineups for each parameter, so there are three results for each plot.

References

Gross, J. H., Kirkland, J. H., and Shalizi, C. R. (2008), "Cosponsorship in the U.S. Senate: A Multilevel Two-Mode Approach to Detecting Subtle Social Predictors of Legislative

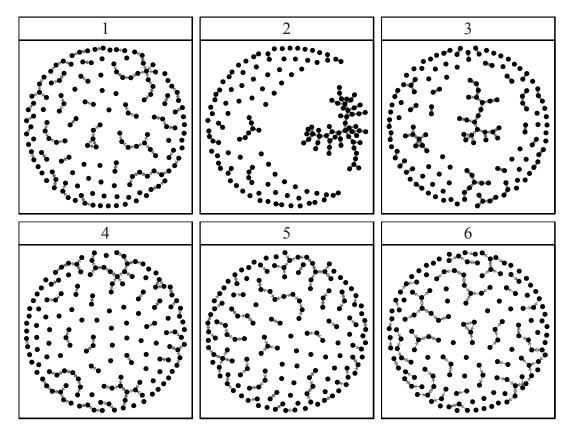


Figure 6: One repitition of a goodness-of-fit linear testing model M7. The senate data are shown in panel two, and it is evident that none of the other five panels, which show data simulated from model M7, come close to creating the large connected component that is central to the structure of the senate data.

Support," Unpublished Manuscript.

Ripley, R., Boitmanis, K., and Snijders, T. A. (2013), RSiena: Siena - Simulation Investigation for Empirical Network Analysis, r packa ge version 1.1-232.

Ripley, R. M., Snijders, T. A., Boda, Z., Vörös, A., and Preciado, P. (2017), "Manual for RSiena," Tech. rep., https://www.stats.ox.ac.uk/~snijders/siena/RSiena_Manual.pdf.

Snijders, T. A., van de Bunt, G. G., and Steglich, C. E. (2010), "Introduction to stochastic actor-based models for network dynamics," *Social Networks*, 32, 44 – 60, dynamics of Social Networks.

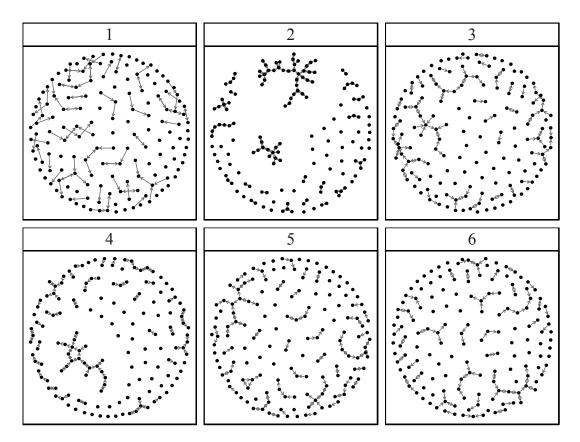


Figure 7: In our experiment, 52.8% of viewers of this plot selected the plot from the alternative model, M4. The "reverse" of this lineup is given in Figure 8, where 41.4% of viewers selected the plot from the alternative model, M1. Here, the alternative plot is $\sqrt{25} - 3$.

Snijders, T. A. B. (1996), "Stochastic actor-oriented models for network change," *Journal of Mathematical Sociology*, 21, 149–172.

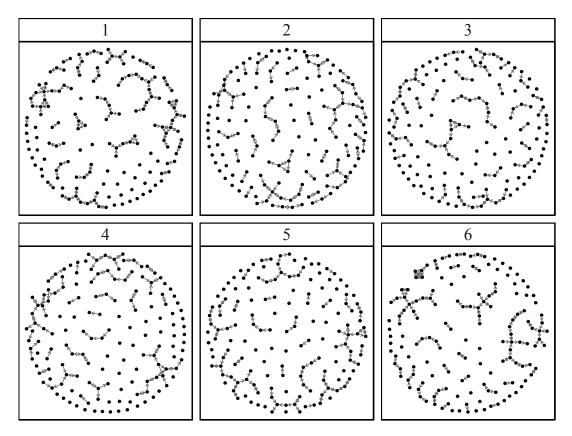


Figure 8: In our experiment, 41.4% people viewing this lineap selected the plot from the alternative model, M1. Here, the alternative plot is $\sqrt{25} - 1$. The other five plots were simulated from model M4.

Model	Replicate	Data Picks	Total Viewers	p-value
M3	1	29	36	< 0.0001
	2	13	18	0.0004
	3	16	20	< 0.0001
M4	1	13	16	< 0.0001
	2	7	20	0.1150
	3	29	34	< 0.0001
M5	1	9	21	0.0414
	2	21	24	< 0.0001
	3	14	16	< 0.0001
M7	1	17	20	< 0.0001
	2	14	28	0.0093
	3	28	37	< 0.0001

Table 4: An overview of the results from the 12 goodness-of-fit lineup tests.

Parameter	Estimate	Std Error	<i>p</i> -value	Odds Multiplier
$\overline{\eta_{1+}}$	37.3	6.57	$< 10^{-4\ddagger}$	$> 10^4$
η_{1-}	-9.93	3.47	0.0040^{\dagger}	$< 10^{-4}$
γ_{1+}	75.36	13.53	$< 10^{-4\ddagger}$	$> 10^4$
γ_{1-}	-14.5	4.8	0.0030^{\dagger}	$< 10^{-4}$
η_{2+}	-6.83	4.47	0.1260	0.001
η_{2-}	-17	2.24	$< 10^{-4\ddagger}$	$< 10^{-4}$
γ_{2+}	13.77	7.45	0.0640^{*}	$> 10^4$
γ_{2-}	-229.16	31.31	$< 10^{-4\ddagger}$	$< 10^{-4}$
η_{3+}	-2.8	0.95	0.0030^\dagger	0.061
η_{3-}	-2.64	0.81	0.0010^{\dagger}	0.071
γ_{3+}	4.47	1.39	0.0010^{\dagger}	87.36
γ_{3-}	-1.11	0.61	0.0690*	0.33
η_{4+}	-2.08	0.95	0.0290**	0.125
η_{4-}	-2.69	1.32	0.0420**	0.068
γ_{4+}	4.25	2.15	0.0480**	70.11
γ_{4-}	2.4	2.19	0.2720	11.02
η_{5+}	-5.84	2.99	0.0510^{*}	0.003
η_{5-}	-4.69	0.86	$< 10^{-4\ddagger}$	0.009
γ_{5+}	3.26	1.76	0.0630^{*}	26.05
γ_{5-}	-2.18	0.39	$< 10^{-4\ddagger}$	0.113
η_{6+}	-1.16	1.23	0.3430	0.313
η_{6-}	-5.93	1.28	$< 10^{-4\ddagger}$	0.003
γ_{6+}	5.76	3.52	0.1020	317.35
γ_{6-}	15.09	3.6	$< 10^{-4\ddagger}$	$> 10^4$
σ_δ^2	0.564			
σ_{ϵ}^2	0.342			

Table 5: Summary of the results from fitting the model given in Equation 4. Significance levels: * - < 0.10; ** - < 0.05; † - < 0.01; ‡ - < 0.001

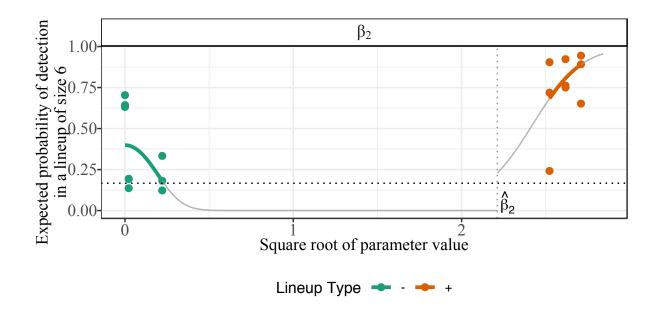


Figure 9: The top middle panel of Figure 4 expanded to show greater detail. The square root of the parameter value is shown on the x-axis. For this parameter, as its value approaches zero, the probability of identifying the alternate data model decreases, then increases, which is noticeably different from the pattern exhibited by the others. Again, a horizontal line is drawn at 1/6, the chance of selecting the data plot at random.

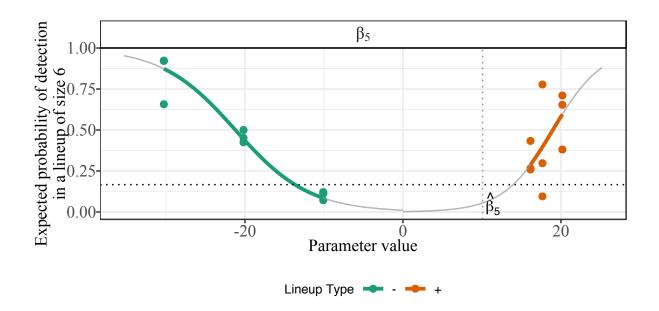


Figure 10: The bottom middle panel of Figure 4 expanded to show greater detail. The parameter value is shown on the x-axis. This parameter most closely follows our hypothesis shown in Figure 2. However, the result is not symmetric. According to the model, people will detect the effect at lower values and with greater frequency as the value increases when it is positive instead of negative.

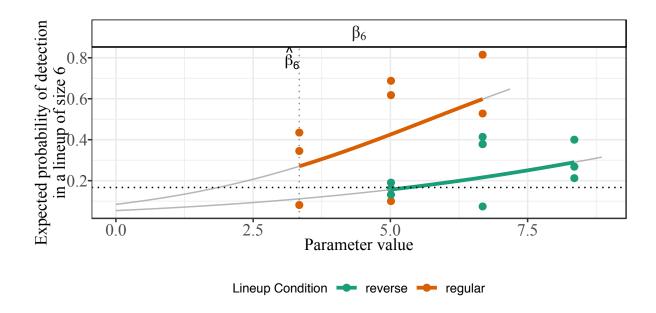


Figure 11: The bottom right panel of Figure 4 expanded to show greater detail. The parameter value is shown on the x-axis. The "reverse" lineup has a much flatter slope than the "regular" lineup, which means the participants had a harder time detecting a more simple M1 structure among many more complex M4 structures. Reversing the lineup scenario was not symmetric as we hypothesized.