

Supplemental Materials for
Bayesian Parametric Estimation of Stop-Signal Reaction Time
Distributions

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This supplement contains the detailed results of the posterior predictive model checks and the sensitivity analyses foreshadowed in the main text. In the first section, we present the posterior predictive model checks for the individual BPA analyses of the Bissett and Logan (2011) dataset. We present model checks using the observed signal–respond distribution and the observed response rate for each participant in the first as well as the second session of the experiment. In the second section, we present the results of a series of sensitivity analyses for the individual and the hierarchical BPA. First, we investigate the sensitivity of the shape of the estimated go RT and SSRT distributions to misspecification of the parametric form of the go RTs and the SSRTs. Second, we explore the sensitivity of the estimated go and stop parameters to misspecification of the group–level distribution of the individual μ_{go} , σ_{go} , τ_{go} , μ_{stop} , σ_{stop} , and τ_{stop} parameters.

Posterior Predictive Model Checks

This section presents the results of the posterior predictive model checks of the individual BPA analyses of the Bissett and Logan (2011) experiment. Posterior predictive model checks are frequently used procedures in Bayesian inference to assess the absolute goodness of fit of a proposed model (e.g., Gelman & Hill, 2007; Gelman, Meng, & Stern, 1996). In posterior predictive checks, we assess the adequacy of the model by generating new data (i.e., predictions) using the posterior distributions of the parameters obtained from fitting the model. If the model adequately describes the data, the predictions based on the model parameters should closely approximate the observed data.

We formalized the model checks by computing posterior predictive p–values (e.g., Gelman & Hill, 2007; Gelman et al., 1996). We first defined a test statistic T , and computed its value for the observed data: $T(data)$. For each of the $i = 1, \dots, N$ draws from the posterior distribution of the parameters, we sampled new stop–signal data, $data^* = (data_1^*, data_2^*, \dots, data_N^*)$, using the ex–Gaussian assumption. Lastly, we calculated the test statistic T for each $data_i^*$: $T(data_i^*)$. The posterior predictive p–value is given by the fraction of times that $T(data^*)$ is greater than $T(data)$. The posterior predictive p–value compares thus the observed value of the test statistic to its sampling distribution under the assumptions of the BPA. Extreme p–values close to 0 or 1 (e.g., lower than 0.05 or higher than 0.95) indicate that the BPA does not describe the observed data adequately. For each participant we conducted two posterior predictive analyses using different test statistics.

Signal–Respond Distribution

In the first posterior predictive analysis, we compared the observed signal–respond distribution to the signal–respond RTs predicted by the posterior distribution of the model parameters. The model check was performed only for the SSD with the highest number of observed signal–respond RTs in order to obtain stable observed and predicted signal–respond RT distributions. For each participant, we randomly selected $N = 1000$ parameter vectors from the joint posterior of μ_{go} , σ_{go} , τ_{go} , μ_{stop} , σ_{stop} , and τ_{stop} . Then, we generated 1000 stop–signal datasets using the 1000 parameter vectors, the chosen SSD and the corresponding number of stop–signal trials. We used the median of the signal–respond RTs of the observed and the predicted distributions as test statistic. For each participant,

Table 1: Posterior predictive p-values for the median of the signal-respond RT distribution and the response rate for the Bissett and Logan (2011) experiment computed from the parameter estimates from the individual BPA.

Participant	Session	P-value Median	Minimum p-value RR	Maximum p-value RR
1	1	0.64	0.11	0.91
	2	0.13	0.25	0.73
2	1	0.67	0.02	0.78
	2	0.34	0.32	0.77
3	1	0.44	0.10	0.79
	2	0.24	0.11	0.67
4	1	0.59	0.17	0.95
	2	0.08	0.11	0.85
5	1	0.96	0.02	0.78
	2	0.60	0.43	0.54
6	1	0.91	0.27	0.94
	2	0.88	0.16	0.81
7	1	0.77	0.13	0.70
	2	0.09	0.10	0.98
8	1	0.98	0.03	0.95
	2	0.95	0.14	0.90
9	1	0.57	0.05	0.90
	2	0.52	0.05	0.62
10	1	0.41	0.28	0.86
	2	0.66	0.11	0.77
12	1	0.40	0.18	0.94
	2	0.04	0.04	0.26
13	1	0.69	0.08	0.92
	2	0.85	0.22	0.51
15	1	0.68	0.29	0.76
	2	0.80	0.06	0.92
16	1	1.00	0.30	0.96
	2	0.99	0.14	1.00
18	1	0.11	0.25	0.61
	2	0.49	0.14	0.80
19	1	0.87	0.10	0.71
	2	0.60	0.03	0.62
20	1	0.00	0.33	0.96
	2	0.93	0.23	0.71
21	1	0.12	0.09	0.72
	2	0.30	0.10	0.72
22	1	0.15	0.06	0.77
	2	0.41	0.26	0.43
23	1	0.00	0.07	0.97
	2	0.84	0.16	0.87

Note. P-value Median = posterior predictive p-value for the median of the signal-respond RT distribution on the SSD with the highest number of observed signal-respond trials; Minimum p-value RR = the lowest posterior predictive p-value for the response rate computed for the SSDs that contained at least 10% of the trials; Maximum p-value RR = the highest posterior predictive p-value for the response rate computed for the SSDs that contained at least 10% of the trials.

the 1000 predicted signal–respond RT distributions were compared to the observed signal–respond RT distribution, using posterior predictive p–values and visual inspection of the distributions.

Figure 1 and Figure 2 shows the observed go RT and signal–respond RT distributions, and 100 randomly chosen predicted signal–respond RT distributions in the first and the second session of the Bissett and Logan (2011) experiment, respectively. For the majority of the participants, the predicted signal–respond RT distributions (i.e., gray lines) adequately followed the shape of the observed signal–respond RT distribution. Also, the predicted signal–respond RTs were generally faster than the observed go RTs (i.e., dashed line), a common finding that follows from the architecture of the horse–race model (Logan & Cowan, 1984). Lastly, the average of the medians of the predicted signal–respond distributions closely matched the observed median. This result is also evident from the posterior predictive p–values listed in the second column of Table 1. The posterior predictive p–values for the majority of the participants are well within the 0.05–0.95 range, indicating that the BPA adequately accounted for the median of the observed signal–respond RTs.

Response Rate

In the second posterior predictive analysis, we compared the observed response rates to the response rates predicted by the posterior distribution of the model parameters. The model check was performed for the SSDs that featured at least 10 % of the total number of stop–signal trials. For each participant, we generated 1000 stop–signal datasets using the 1000 parameter vectors selected for the first posterior predictive analysis, the chosen SSDs and the corresponding number of stop–signal trials. We computed posterior predictive p–values for each participant on each SSDs separately, where we used the observed and predicted response rates as test statistic.

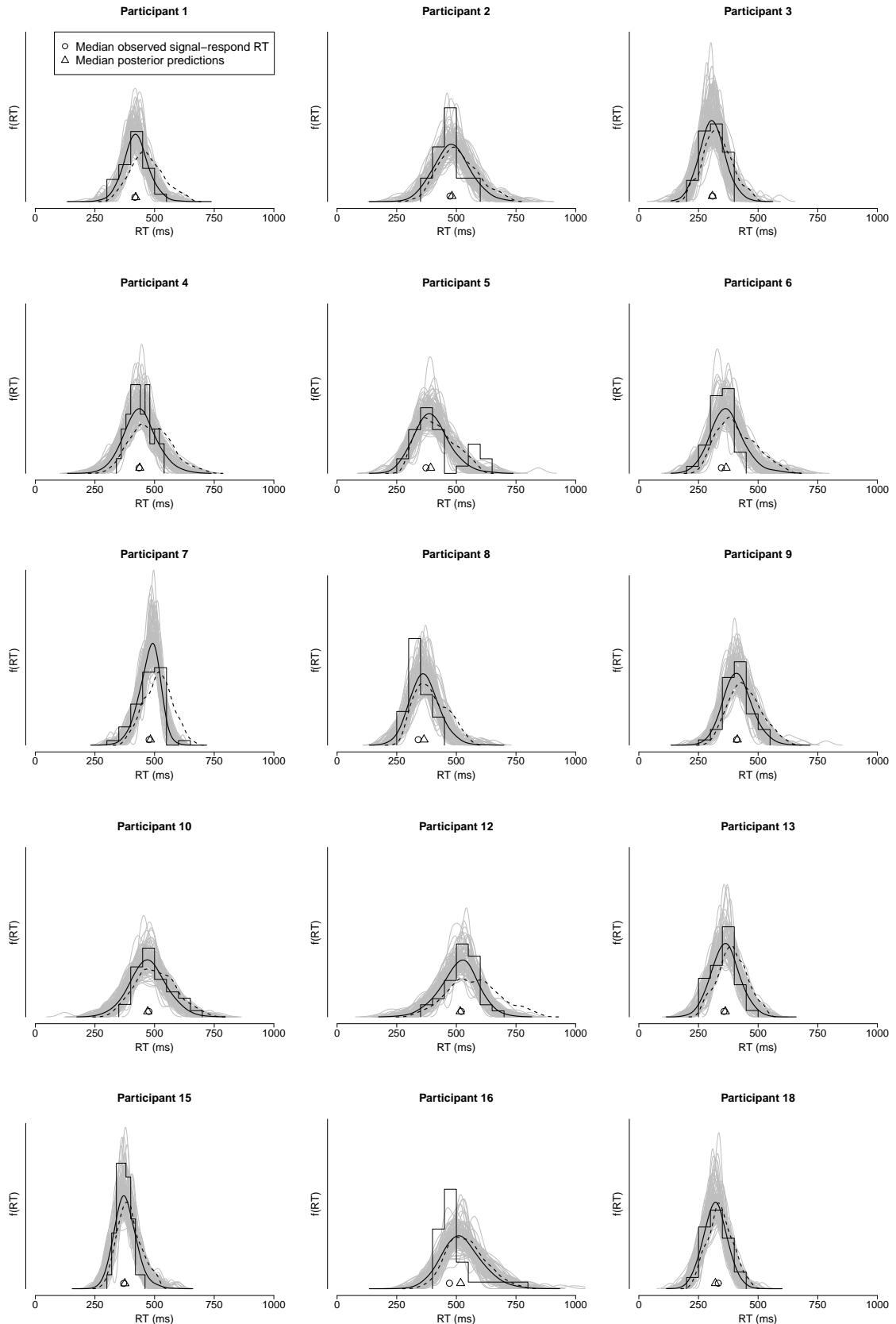
The third and the fourth column of Table 1 show the minimum and the maximum of the posterior predictive p–values for the response rates across the various SSDs. For most participants, the minimum and maximum of the p–values all lie between 0.05 and 0.95, corroborating our previous conclusion of satisfactory model fit using the median of the signal–respond RTs. To summarize, the results of the posterior predictive model checks indicated that for most participants the BPA provided plausible parameter estimates that adequately describe the observed data.

Robustness Analyses

This section presents the results of a series of robustness analyses that examined the sensitivity of the estimated go RT and SSRT distributions to misspecification of the individual and the group–level distributions assumed by the BPA.

Individual BPA

In this section, we investigate the sensitivity of the shape of the estimated go RT and SSRT distributions to misspecification of the parametric form of the go RT and SSRT distributions. We generated synthetic datasets where the go RTs and the SSRTs were drawn from shifted log–normal distributions with plausible parameter sets. The synthetic datasets



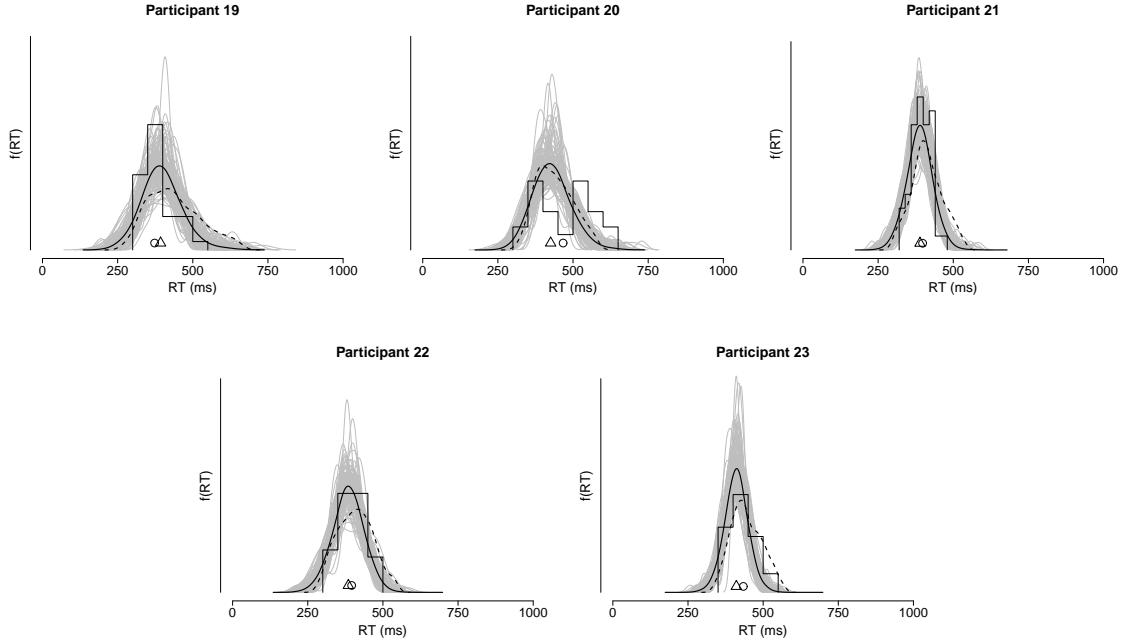
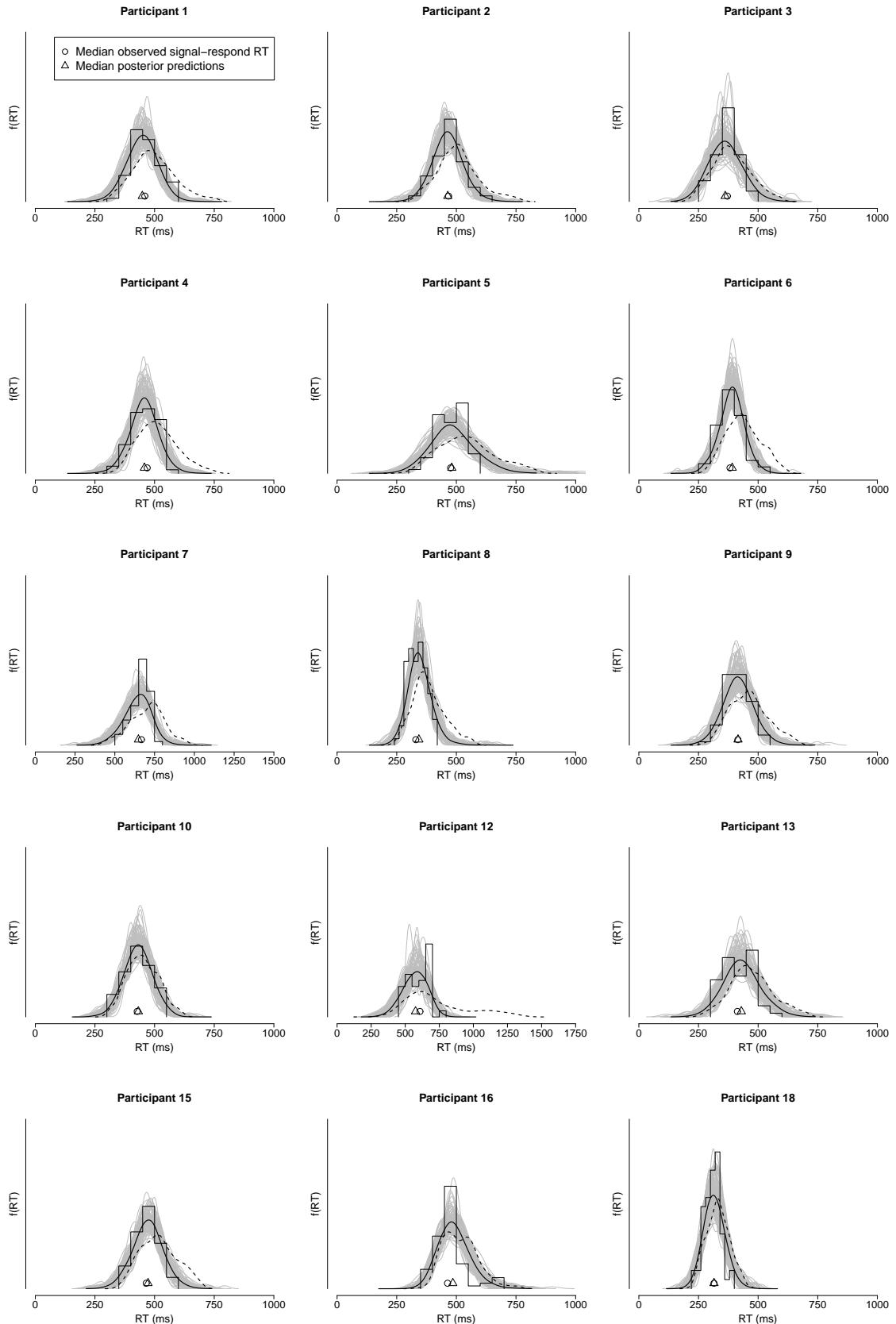


Figure 1. : Predicted and observed signal-respond RT distributions for the first session of the Bissett and Logan (2011) experiment. See text for a detailed description of the posterior predictive analyses. The histogram shows the observed signal-respond RT distribution. The gray lines show 100 randomly chosen predicted signal-respond RT distributions. The solid black line gives a predicted signal-respond RT distributions based on the mean of the posterior predictions. The circle indicates the median of the observed signal-respond RTs. The triangle indicates the median of the predicted signal-respond RTs. The median of the predicted signal-respond RTs is computed as the mean of the medians of the predicted signal-respond RT distributions. The dashed line shows the observed go RT distribution.

were then fit with the individual BPA that erroneously assumed that the go RTs and the SSRTs follow an ex-Gaussian distribution.

Methods.

The go RTs were generated from a shifted log-normal distribution with the mean and standard deviation of the underlying normal distribution set at 6 and 0.2 respectively, and a shift added to the resulting RTs of 50 ms. The SRRTs were generated from a shifted log-normal distribution with a mean of 5, a standard deviation of 0.3, and a shift parameter of 50. Therefore, the mean and the standard deviation of the true go RT distribution was 462 and 83 ms, respectively. The mean and the standard deviation of the SSRT distribution was 205 and 48 ms, respectively. The SSDs were set to 150, 200, 250, 300, and 350 ms. The above parameter values and SSDs resulted in $P(\text{respond} \mid \text{stop-signal}, \text{SSD} = 150) = 0.12$, $P(\text{respond} \mid \text{stop-signal}, \text{SSD} = 200) = 0.28$, $P(\text{respond} \mid \text{stop-signal}, \text{SSD} = 250) = 0.50$, $P(\text{respond} \mid \text{stop-signal}, \text{SSD} = 300) = 0.69$, and $P(\text{respond} \mid \text{stop-signal}, \text{SSD} = 350) = 0.84$.



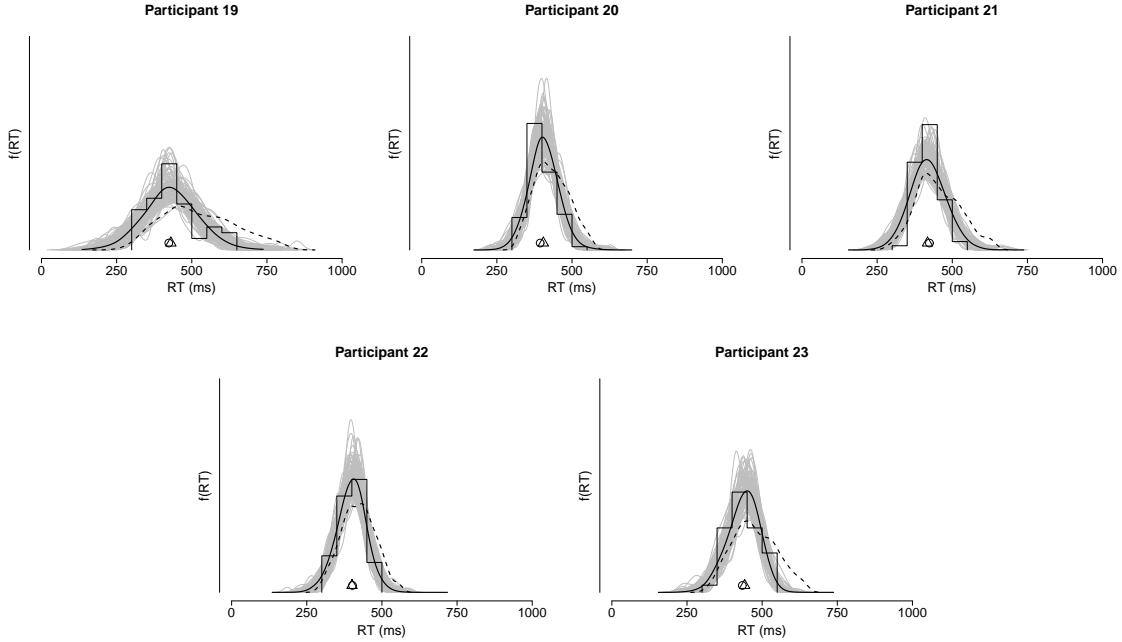


Figure 2. : Predicted and observed signal-respond RT distributions for the second session of the Bissett and Logan (2011) experiment. See text and Figure 1 for details.

We conducted four sets of simulations that varied the number of go and stop-signal trials, with 100 datasets for each set. For the first set, each dataset contained 4,500 go trials and 5×300 stop-signal trials. For the second set, each dataset contained 2,250 go trials and 5×150 stop-signal trials. For the third set, each dataset contained 750 go trials and 5×50 stop-signal trials. For the fourth set, each dataset contained 375 go trials and 5×25 stop-signal trials. The estimated ex-Gaussian μ_{stop} , σ_{stop} , and τ_{stop} parameters were constrained to be equal across the five SSDs.

We fit the datasets with the ex-Gaussian based individual BPA using WinBUGS. We ran three MCMC chains and used overdispersed starting values to confirm that the chains have converged to the stationary distribution ($\hat{R} \approx 1$). The first 500 samples of each MCMC chain were discarded. The reported SSRT distribution estimates are based on $3 \times 4,000$ recorded samples.

Results.

Figure 3 and Figure 4 show the estimated go RT and SSRT distributions, respectively, based on the posterior medians from the ex-Gaussian based BPA for the 100 replications. Figure 5 and Figure 6 show the mean and the standard deviation of the go RT and SSRT distributions, respectively, computed using the posterior medians from the ex-Gaussian based BPA across the 100 replications. As shown in the figures, the ex-Gaussian based BPA recovered the shape, the mean, and the standard deviation of the true shifted log-normal go RT and SSRT distributions with little bias even with relatively few go and stop-signal trials. Naturally, as the number of trials increased, the bias and uncertainty of

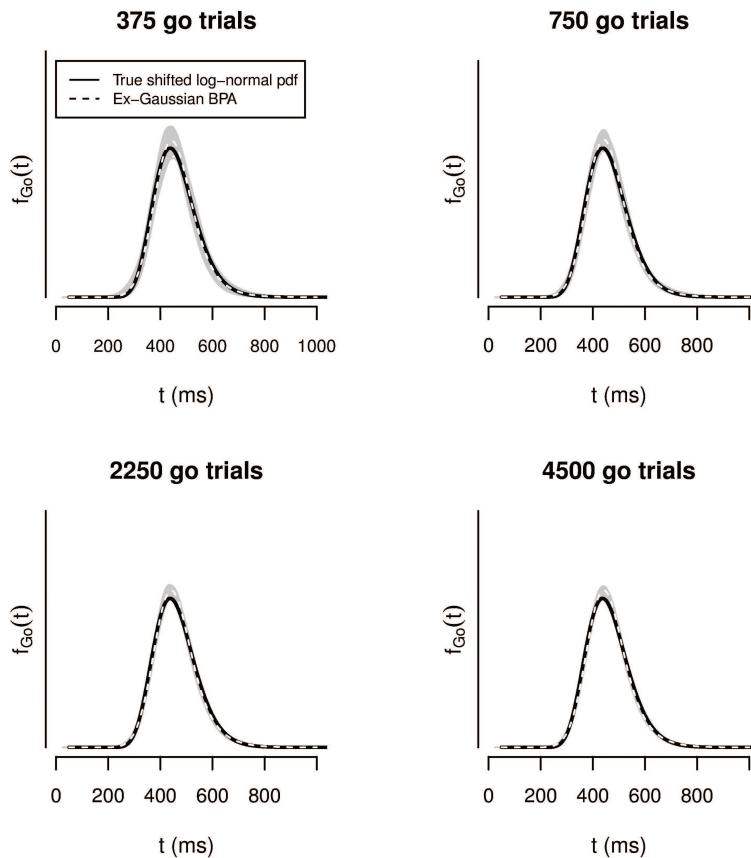


Figure 3. : Go RT distributions estimated using the individual BPA with misspecified go RT and SSRT distributions. The solid black lines show the true shifted log–normal go RT distribution. The dashed white line shows a go RT distribution based on the mean of the posterior medians of the go parameters from the ex–Gaussian based BPA across the 100 replications. The gray lines show the go RT distributions based on the posterior medians of the go parameters for the 100 replications.

the estimates decreased. Note that the SRRT distributions and their mean and standard deviation are slightly more biased and are estimated with larger uncertainty than the go RT distributions. This result is to be expected because the go distributions are estimated based on the go RTs as well as the signal–respond RTs. The go distributions are therefore better constrained by the data than the SSRT distributions.

In summary, the sensitivity analyses indicated that the individual BPA is robust to misspecification of the parametric form of the go RT and SSRT distributions. Even when the go RTs and the SSRTs were drawn from shifted log–normal distributions, the ex–Gaussian based BPA excellently approximated the shape of their distribution. This result is not surprising because the ex–Gaussian is very flexible and can accommodate a wide range of distributional forms. Unless the go RTs and the SSRTs are left skewed or bimodal – an unlikely scenario for RT distributions – the ex-Gaussian is likely to provide an adequate

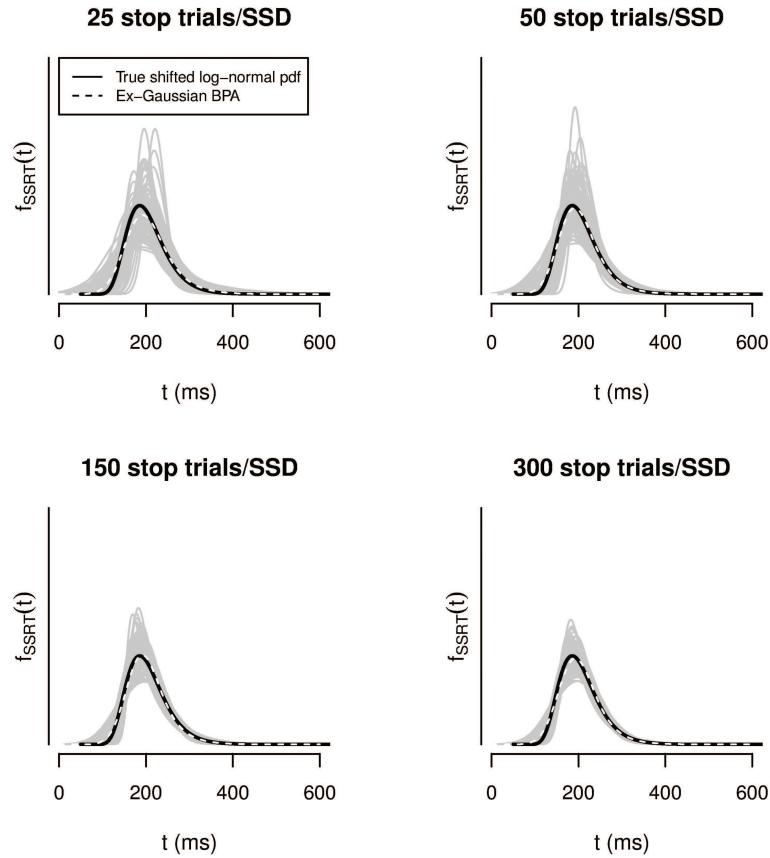


Figure 4. : SSRT distributions estimated using the individual BPA with misspecified go RT and SSRT distributions. The solid black lines show the true shifted log–normal SSRT distribution. The dashed white line shows a SSRT distribution based on the mean of the posterior medians of the stop parameters from the ex–Gaussian based BPA across the 100 replications. The gray lines show the SRRT distributions based on the posterior medians of the stop parameters for the 100 replications.

description of their distribution.

Hierarchical BPA

In this section, we explore the sensitivity of the estimated go and stop parameters to misspecification of the group–level distribution of the individual μ_{go} , σ_{go} , τ_{go} , μ_{stop} , σ_{stop} , and τ_{stop} parameters. We generated synthetic datasets where the individual go and stop parameters were drawn from uniform or bimodal group–level distributions with plausible parameter sets. The individual parameter values were used to generate stop–signal data using the ex–Gaussian distribution. The synthetic datasets were then fit with the hierarchical BPA that erroneously assumed that the individual μ_{go} , σ_{go} , τ_{go} , μ_{stop} , σ_{stop} , and τ_{stop} parameters came from truncated normal distributions.

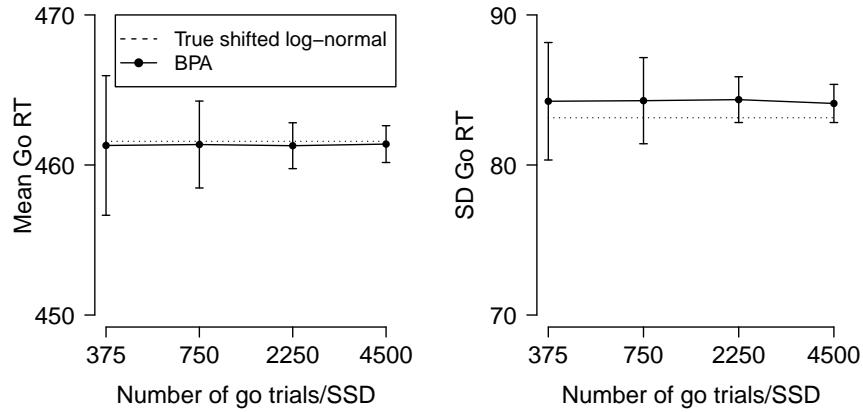


Figure 5. : Mean and standard deviation of the go RT distribution estimated using the individual BPA with misspecified go RT and SSRT distributions. The dashed lines give the true mean and standard deviation of the shifted log–normal go RT distribution. The black bullets show the mean and standard deviation of the go RT distribution computed using the mean of the posterior medians of the go parameters from the ex–Gaussian based BPA across the 100 replications. The vertical lines indicate the size of the standard error across the 100 replications.

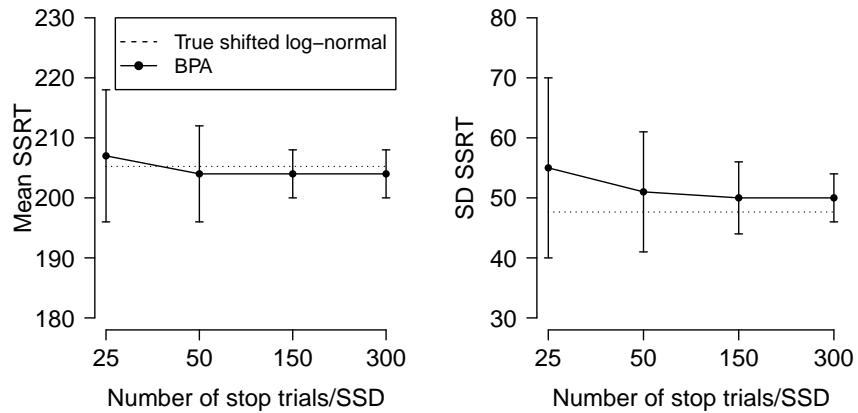


Figure 6. : Mean and standard deviation of the SSRT distribution estimated using the individual BPA with misspecified go RT and SSRT distributions. The dashed lines give the true mean and standard deviation of the shifted log–normal SSRT distribution. The black bullets show the mean and standard deviation of the SSRT distribution computed using the mean of the posterior medians of the stop parameters from the ex–Gaussian based BPA across the 100 replications. The vertical lines indicate the size of the standard error across the 100 replications.

Methods.

We ran two sets of simulations, each containing four synthetic datasets. Each dataset contained the stop–signal data of $j = 1, \dots, J$ participants. Across the four datasets, we varied the number of participants and the number of go and stop–signal trials. The first dataset contained the stop–signal data of 25 synthetic participants each responding to 300 go trials and 100 stop–signal trials. The second dataset contained the stop–signal data of 25 synthetic participants each responding to 1,200 go trials and 400 stop–signal trials. The third dataset contained the stop–signal data of 100 synthetic participants each responding to 300 go trials and 100 stop–signal trials. The fourth dataset contained the stop–signal data of 50 synthetic participants each responding to 600 go trials and 200 stop–signal trials.

In the first set of simulations, the individual go and stop parameter values were drawn from uniform group–level distributions. In the second set of simulations, the individual go and stop parameter values were drawn from bimodal group–level distributions that were created by the mixture of two truncated normal distributions. The generating parameter values of the group–level uniform and the normal distributions are shown in Table 2. In each set of simulations, the individual parameters were then used to generate stop–signal data for each participant using the ex–Gaussian distribution. For computational efficiency, we used a single SSD per participant that produced a $P(\text{respond} \mid \text{stop–signal})$ equal to 0.50.

In each set of simulations, we fit the four datasets with the misspecified hierarchical BPA using WinBUGS. We ran three MCMC chains and used overdispersed starting values. The first 3,000 samples of each MCMC chain were discarded. The reported parameter estimates are based on $3 \times 7,750$ recorded samples.

Results.

The estimated posterior medians of the individual go and stop parameters for the uniform generating group–level distributions are shown in Figure 7, Figure 8, Figure 9, and Figure 10. With respect to the go parameters, the μ_{go} , σ_{go} parameters are estimated very well with the misspecified hierarchical BPA regardless of the number of participants and the number of trials. Low values of τ_{go} are slightly overestimated. The bias, however, decreases as the number of participants and especially as the number of trials increase. With respect to the stop parameters, the results are less straightforward. Many individual parameters have failed to reach convergence. The figures therefore depict only those stop parameter estimates that have properly converged. The μ_{stop} parameters are estimated relatively well with the misspecified hierarchical BPA regardless of the number of participants and the number of trials. The results for σ_{stop} and τ_{stop} are unfortunately less encouraging. For the smallest dataset (i.e., Figure 7), none of the σ_{stop} parameters have converged. For the other datasets, low values of σ_{stop} are overestimated and high values of σ_{stop} are underestimated regardless of the size of the dataset. Similarly, low values of τ_{stop} are overestimated and high values of τ_{stop} are underestimated. Nevertheless, the correspondence between the true and the estimated τ_{stop} seems to increase as the size of the dataset increases.

The estimated posterior medians of the individual go and stop parameters for the bimodal generating group–level distributions are shown in Figure 11, Figure 12, Figure 13, and Figure 14. With respect to the go parameters, the true μ_{go} , σ_{go} , and τ_{go} parameters are estimated very well with the misspecified hierarchical BPA regardless of the number of par-

Table 2: Generating parameters of the group-level uniform and bimodal prior distributions for the robustness analyses for the hierarchical BPA

Parameter	Uniform Lower	Uniform Upper	Normal Mean I	Normal SD I	Normal Mean II	Normal SD II
μ_{go}	200	600	300	40	550	60
σ_{go}	1	180	40	30	120	10
τ_{go}	1	120	40	5	100	20
μ_{stop}	80	300	170	25	240	15
σ_{stop}	1	60	30	10	70	15
τ_{stop}	1	70	40	15	90	20

Note. Uniform Lower and Uniform Upper are the lower and the upper bounds of the uniform group-level distributions used to generate the individual parameters. Normal mean I and Normal SD I are the mean and standard deviation of the truncated normal group-level distributions used to generate the first sample of the individual parameters. Normal mean II and Normal SD II are the mean and standard deviation of the truncated normal group-level distributions used to generate the second sample of the individual parameters.

ticipants and the number of trials. Again, the results are less straightforward with respect to the stop parameters. Many individual parameters have failed to reach convergence. The figures therefore depict only those stop parameter estimates that have properly converged. High values of μ_{stop} seem to be slightly underestimated in datasets with a small number of trials (i.e., Figure 11 and Figure 13). In contrast, in datasets with a relatively large number of trials, the μ_{stop} parameters are estimated relatively well with the misspecified hierarchical BPA. Further, high values of σ_{stop} are severely underestimated. Nevertheless, the correspondence between the true and the estimated σ_{stop} seems to increase as the number of participants and especially as the number of trials increase. Lastly, high values of τ_{stop} are overestimated. The bias, however, decreases as the number of participants and especially as the number of trials increase.

In sum, the sensitivity analyses indicated that the hierarchical BPA is relatively robust to misspecification of the group-level distribution of the individual go parameters. Even when the true go parameters were drawn from uniform or bimodal group-level distributions, the hierarchical BPA with truncated normal group-level distributions provided accurate individual go parameter estimates. Unfortunately, the hierarchical BPA is less robust to misspecification of the group-level distribution of the individual stop parameters. When the true stop parameters were drawn from uniform or bimodal group-level distributions, the hierarchical BPA with truncated normal group-level distributions resulted in biased parameter estimates, particularly for the σ_{stop} and τ_{stop} parameters. Fortunately, the bias typically decreased as the number of participants and especially as the number of trials increased. The finding that the go parameters are more robust to misspecification of the group-level distributions is not surprising. The go parameters are estimated based on the go RTs as well as the signal-respond RTs. Also, the analyses – similar to a typical stop-signal study – featured three times as many go trials as stop-signal trials. As a result, the go parameters are more strongly constrained by the data and are less strongly influenced by their group-level distribution than the stop parameters.

The sensitivity analyses also indicated that misspecification of the group-level prior distributions often results in convergence problems. We therefore recommend researchers to carefully monitor the convergence of the individual parameter estimates. If there are reasons to suspect that the hierarchical assumptions are violated, we advise users to inspect the distribution of the individual go and stop parameters obtained either from the individual BPA or from the hierarchical BPA with very weak priors for the group-level parameters. If these preliminary analyses indicate that the distribution of the individual parameters substantially deviates from normality, one may use the unconstrained individual go and stop parameters. Alternatively, if substantive knowledge of the form of the group-level distributions is available, the hierarchical BPA may be adapted to accommodate the desired (mixture) distribution.

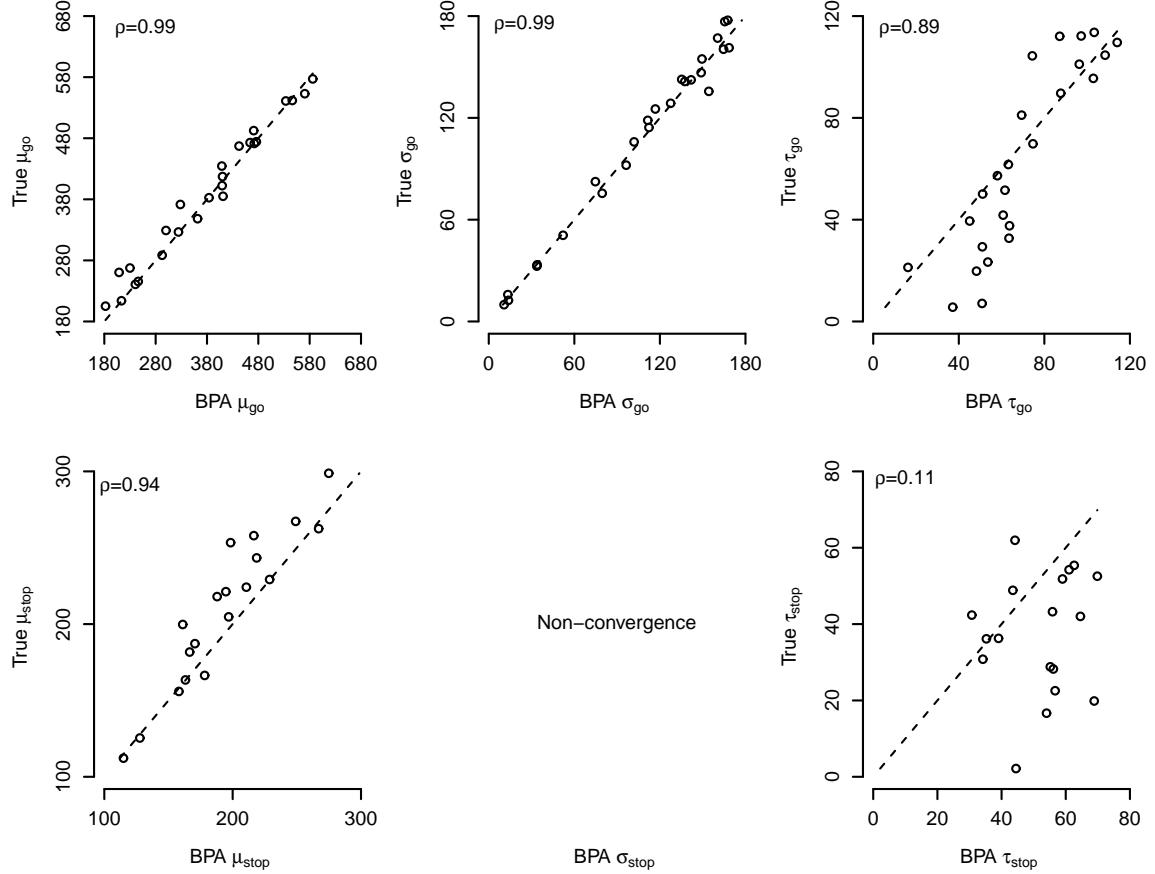


Figure 7. : Posterior medians from the hierarchical BPA with misspecified group-level distributions for the go and the stop parameters. The dataset was generated using uniform group-level distributions for the individual go and stop parameters. The dataset features 25 synthetic participants, each responding to 300 go trials and 100 stop-signal trials on a single central SSD. The dataset was fit with the hierarchical ex-Gaussian based BPA with misspecified truncated normal group-level distributions for the individual go and stop parameters. The value in the top left corner in each panel gives the correlation between the true and the estimated parameters. Note that none of the individual σ_{stop} parameters have reached convergence.

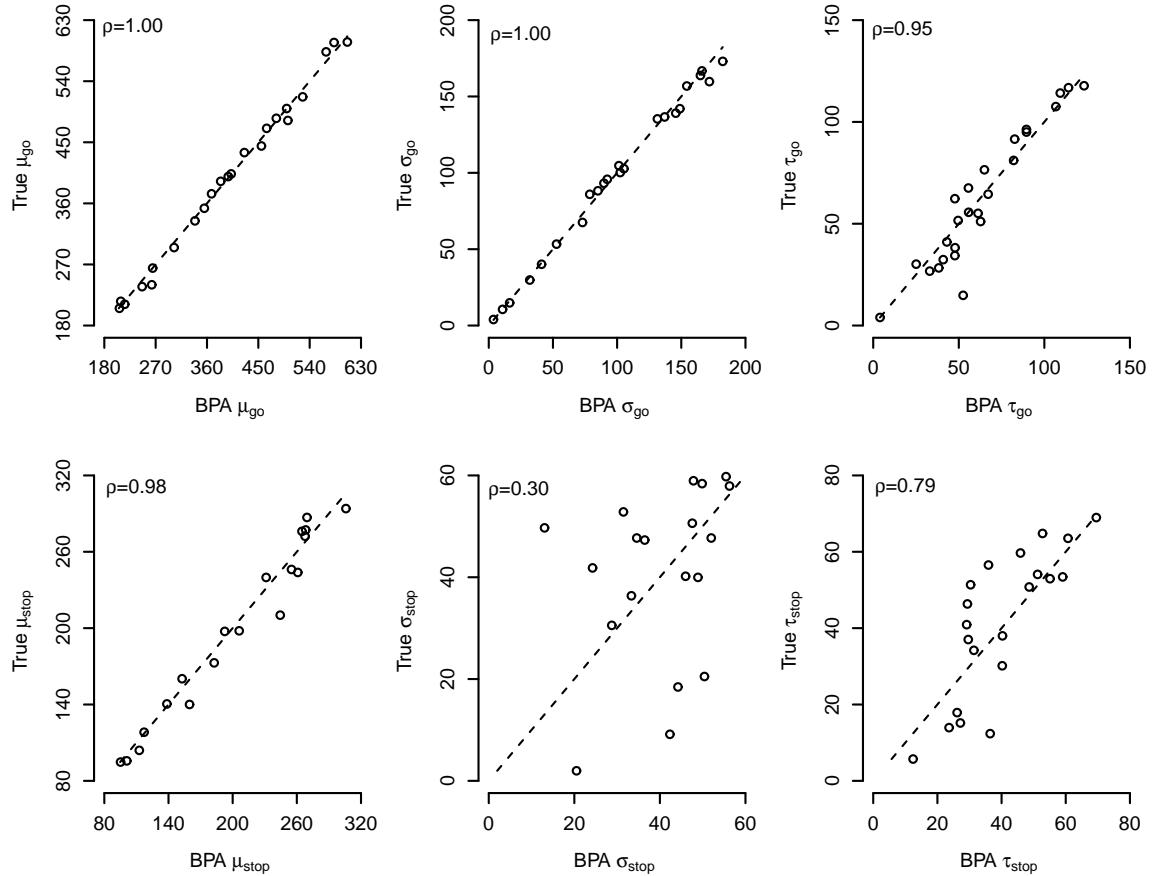


Figure 8. : Posterior medians from the hierarchical BPA with misspecified group-level distributions for the go and the stop parameters. The dataset was generated using uniform group-level distributions for the individual go and stop parameters. The dataset features 25 synthetic participants, each responding to 1200 go trials and 400 stop-signal trials on a single central SSD. The dataset was fit with the hierarchical ex-Gaussian based BPA with misspecified truncated normal group-level distributions for the individual go and stop parameters. The value in the top left corner in each panel gives the correlation between the true and the estimated parameters.

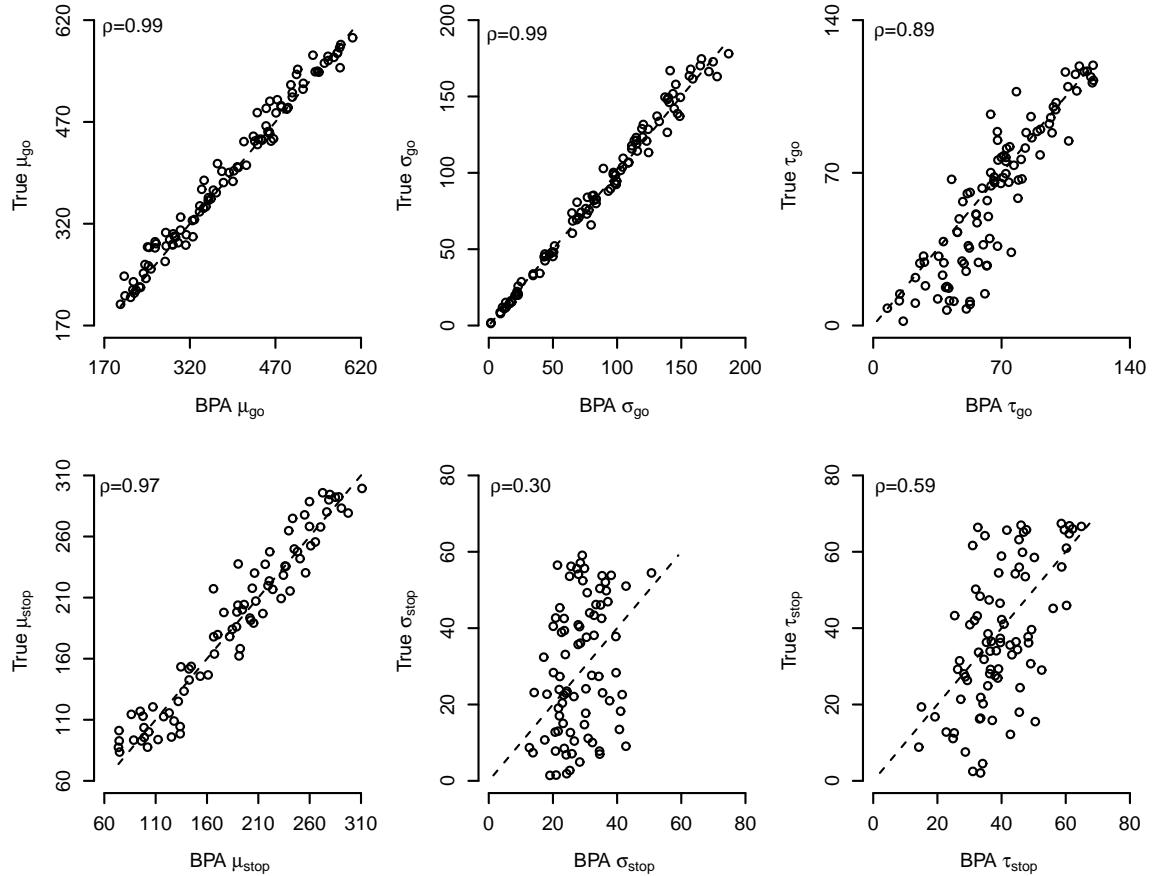


Figure 9. : Posterior medians from the hierarchical BPA with misspecified group-level distributions for the go and the stop parameters. The dataset was generated using uniform group-level distributions for the individual go and stop parameters. The dataset features 100 synthetic participants, each responding to 300 go trials and 100 stop-signal trials on a single central SSD. The dataset was fit with the hierarchical ex-Gaussian based BPA with misspecified truncated normal group-level distributions for the individual go and stop parameters. The value in the top left corner in each panel gives the correlation between the true and the estimated parameters.

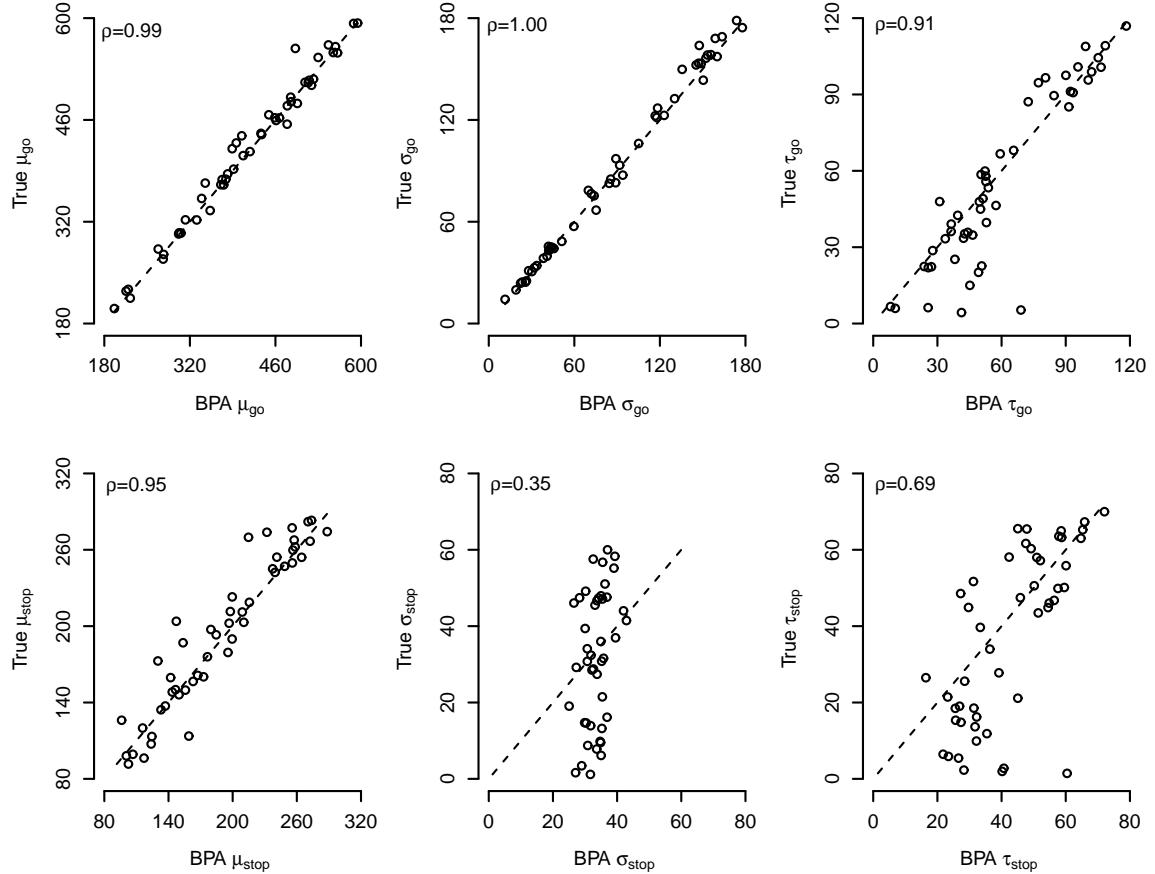


Figure 10. : Posterior medians from the hierarchical BPA with misspecified group-level distributions for the go and the stop parameters. The dataset was generated using uniform group-level distributions for the individual go and stop parameters. The dataset features 50 synthetic participants, each responding to 600 go trials and 200 stop-signal trials on a single central SSD. The dataset was fit with the hierarchical ex-Gaussian based BPA with misspecified truncated normal group-level distributions for the individual go and stop parameters. The value in the top left corner in each panel gives the correlation between the true and the estimated parameters.

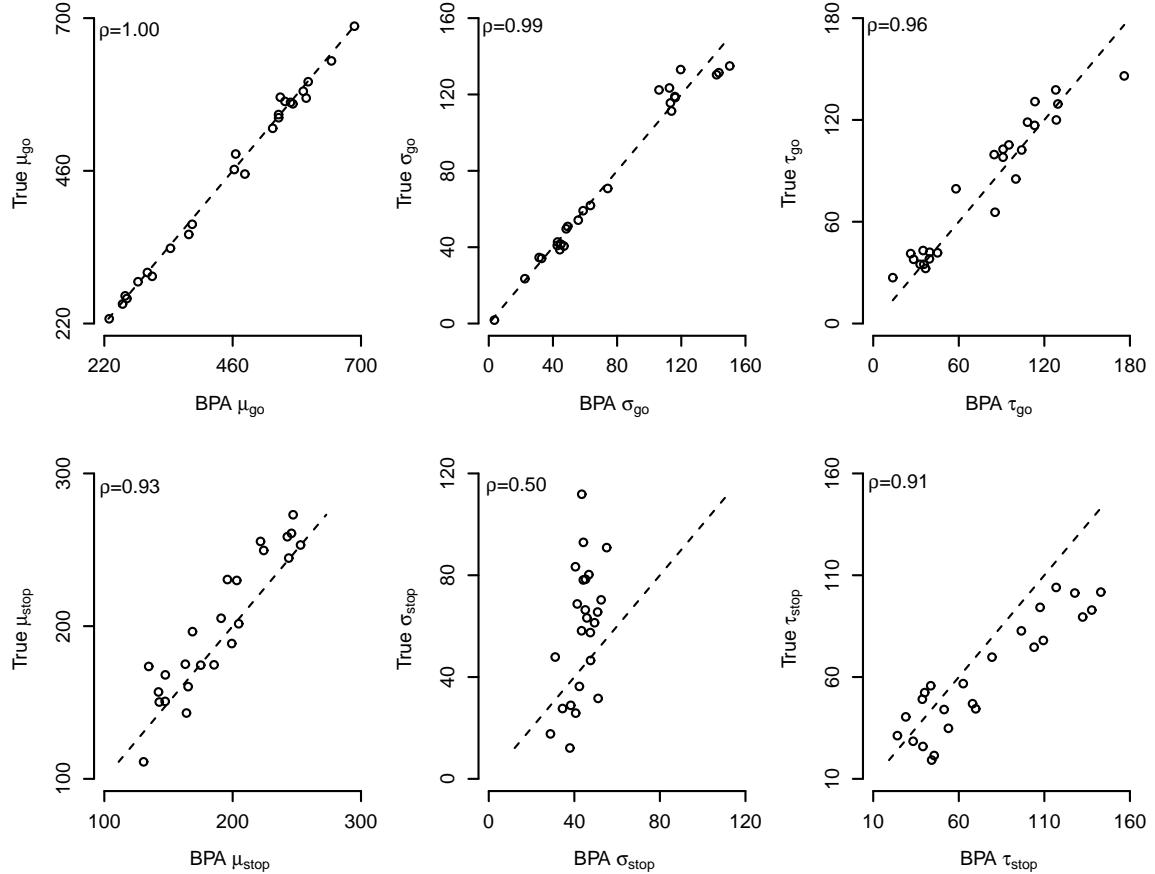


Figure 11. : Posterior medians from the hierarchical BPA with misspecified group-level distributions for the go and the stop parameters. The dataset was generated using bimodal group-level distributions for the individual go and stop parameters. The dataset features 25 synthetic participants, each responding to 300 go trials and 100 stop-signal trials on a single central SSD. The dataset was fit with the hierarchical ex-Gaussian based BPA with misspecified truncated normal group-level distributions for the individual go and stop parameters. The value in the top left corner in each panel gives the correlation between the true and the estimated parameters.

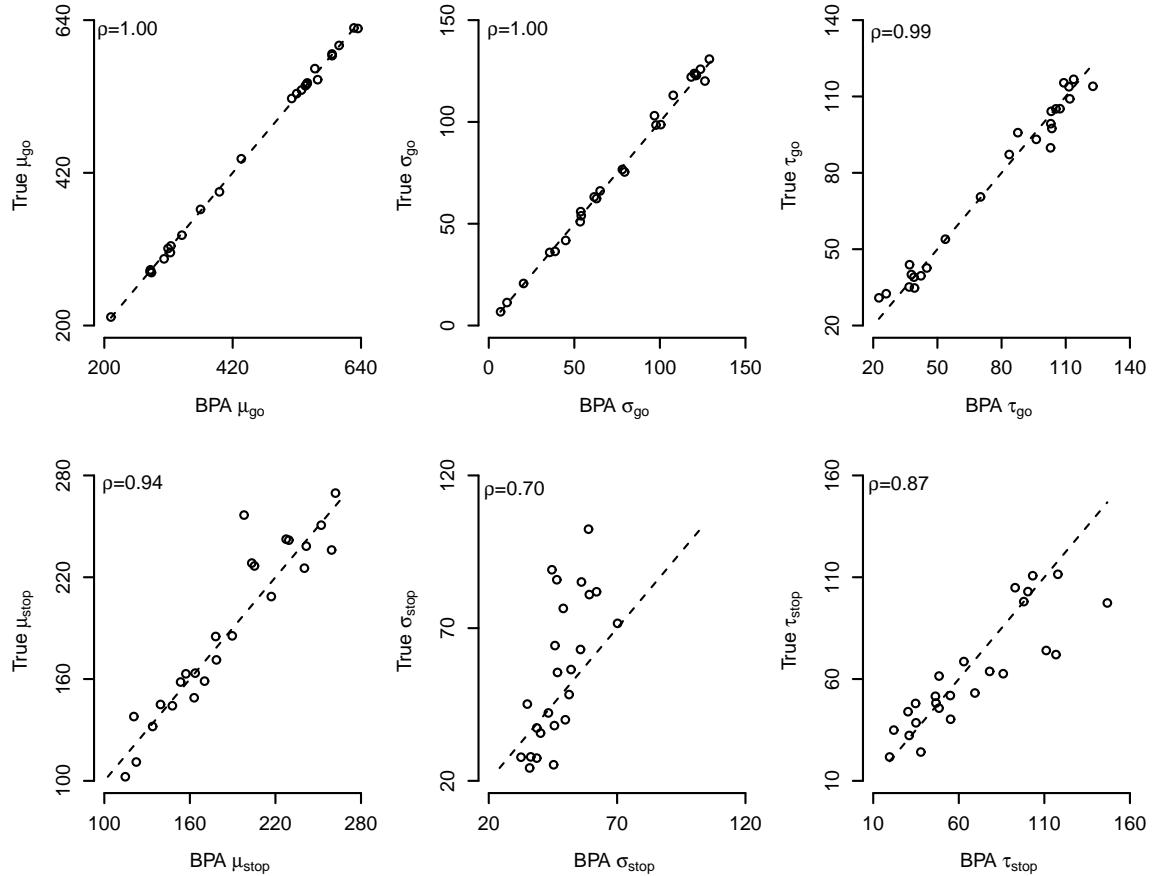


Figure 12. : Posterior medians from the hierarchical BPA with misspecified group-level distributions for the go and the stop parameters. The dataset was generated using bimodal group-level distributions for the individual go and stop parameters. The dataset features 25 synthetic participants, each responding to 1200 go trials and 400 stop-signal trials on a single central SSD. The dataset was fit with the hierarchical ex-Gaussian based BPA with misspecified truncated normal group-level distributions for the individual go and stop parameters. The value in the top left corner in each panel gives the correlation between the true and the estimated parameters.

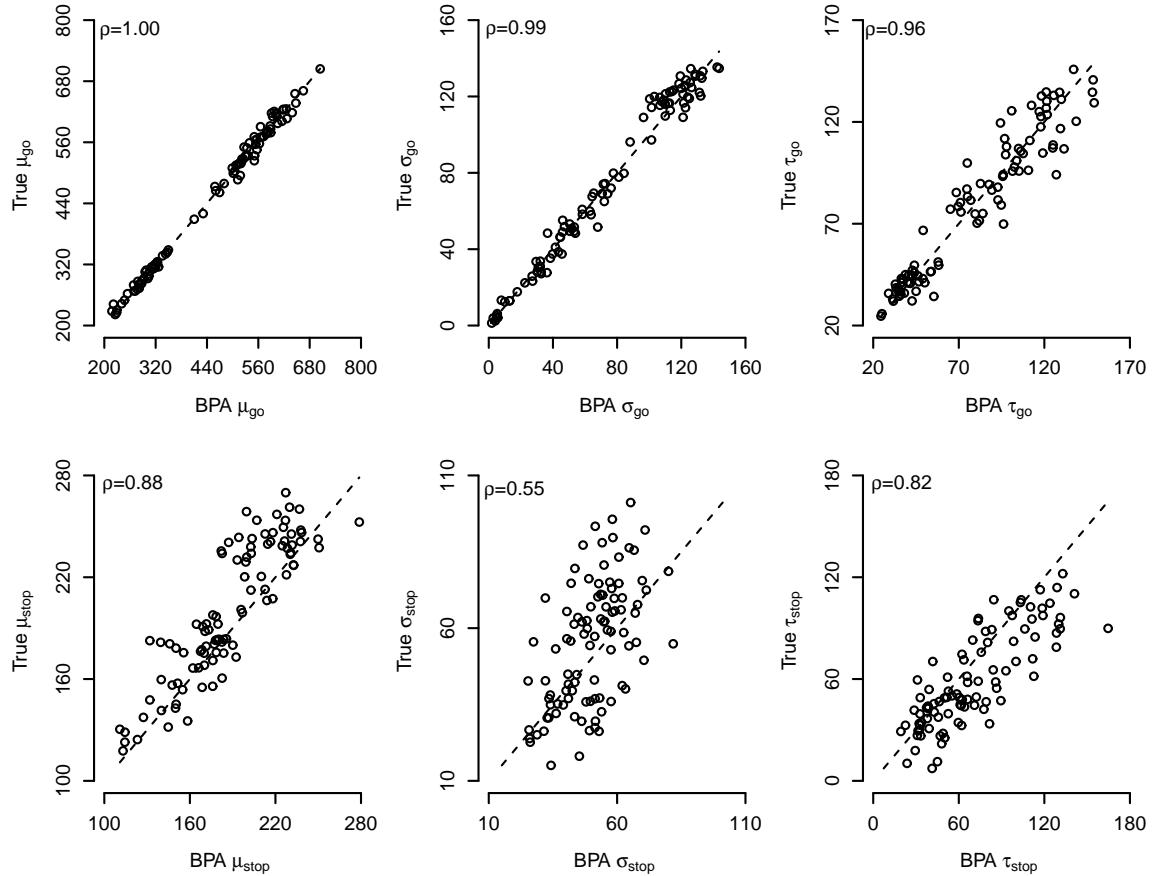


Figure 13. : Posterior medians from the hierarchical BPA with misspecified group-level distributions for the go and the stop parameters. The dataset was generated using bimodal group-level distributions for the individual go and stop parameters. The dataset features 100 synthetic participants, each responding to 300 go trials and 100 stop-signal trials on a single central SSD. The dataset was fit with the hierarchical ex-Gaussian based BPA with misspecified truncated normal group-level distributions for the individual go and stop parameters. The value in the top left corner in each panel gives the correlation between the true and the estimated parameters.

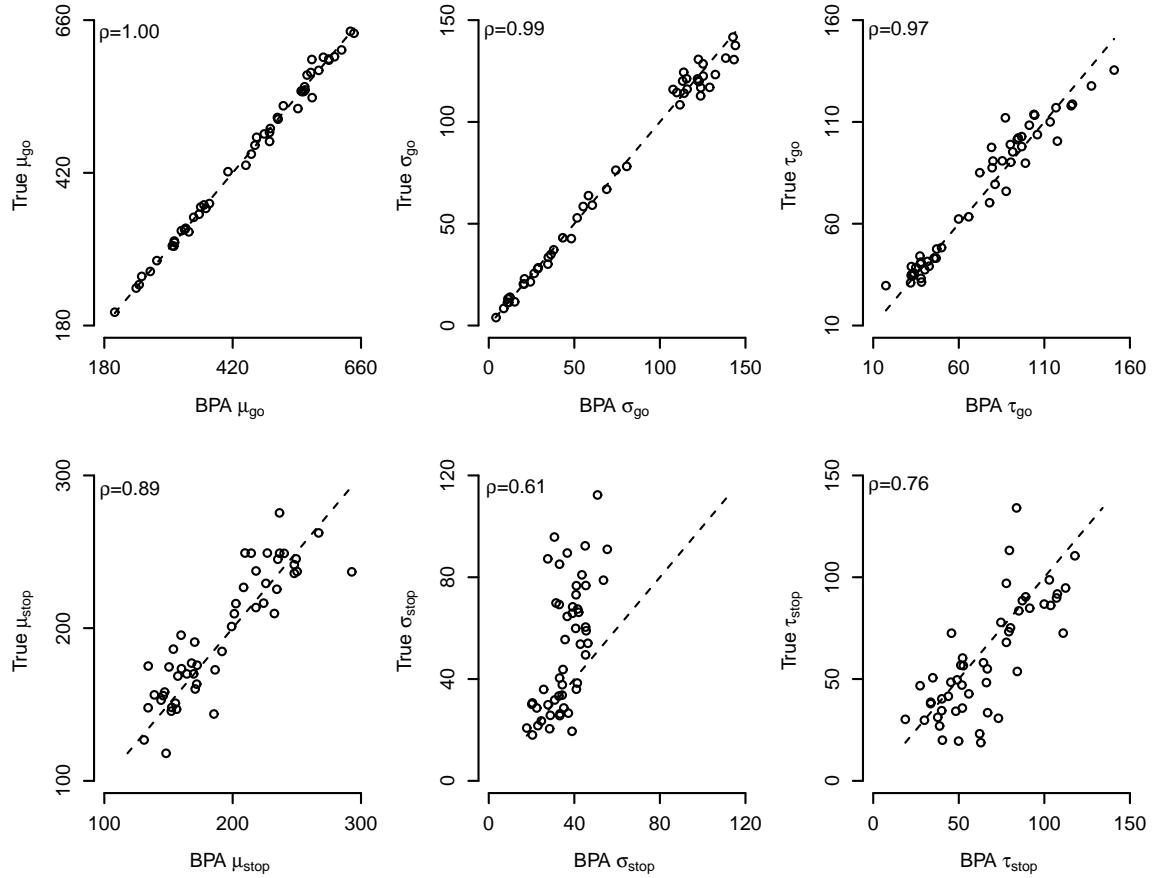


Figure 14. : Posterior medians from the hierarchical BPA with misspecified group-level distributions for the go and the stop parameters. The dataset was generated using bimodal group-level distributions for the individual go and stop parameters. The dataset features 50 synthetic participants, each responding to 600 go trials and 200 stop-signal trials on a single central SSD. The dataset was fit with the hierarchical ex-Gaussian based BPA with misspecified truncated normal group-level distributions for the individual go and stop parameters. The value in the top left corner in each panel gives the correlation between the true and the estimated parameters.

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