

FACES

phil newsome (12.5.2024)

here() starts at /Users/philnewsome/Downloads/usc/coursework/Bayesian_Stats/final project

This is cmdstanr version 0.8.1.9000

- CmdStanR documentation and vignettes: mc-stan.org/cmdstanr
- CmdStan path: /Users/philnewsome/.cmdstan/cmdstan-2.35.0
- CmdStan version: 2.35.0

A newer version of CmdStan is available. See ?install_cmdstan() to install it.
To disable this check set option or environment variable cmdstanr_no_ver_check=TRUE.

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

Warning: package 'brms' was built under R version 4.3.3

Loading required package: Rcpp

Loading 'brms' package (version 2.22.0). Useful instructions can be found by typing `help('brms')`. A more detailed introduction to the package is available through `vignette('brms_overview')`.

Attaching package: 'brms'

The following object is masked from 'package:stats':

`ar`

Warning: package 'modelsummary' was built under R version 4.3.3

`modelsummary` 2.0.0 now uses `tinytable` as its default table-drawing backend. Learn more at: <https://vincentarelbundock.github.io/tinytable/>

Revert to `kableExtra` for one session:

```
options(modelsummary_factory_default = 'kableExtra')
options(modelsummary_factory_latex = 'kableExtra')
options(modelsummary_factory_html = 'kableExtra')
```

Silence this message forever:

```
config_modelsummary(startup_message = FALSE)
```

Warning: package 'posterior' was built under R version 4.3.3

This is posterior version 1.6.0

Attaching package: 'posterior'

The following objects are masked from 'package:stats':

`mad`, `sd`, `var`

The following objects are masked from 'package:base':

`%in%`, `match`

Warning: package 'bayesplot' was built under R version 4.3.2

This is bayesplot version 1.11.1

- Online documentation and vignettes at mc-stan.org/bayesplot

- bayesplot theme set to bayesplot::theme_default()

- * Does `_not_` affect other ggplot2 plots

- * See `?bayesplot_theme_set` for details on theme setting

Attaching package: 'bayesplot'

The following object is masked from 'package:posterior':

`rhat`

The following object is masked from 'package:brms':

`rhat`

Warning: package 'ggplot2' was built under R version 4.3.2

Warning: package 'patchwork' was built under R version 4.3.3

Research Questions

- (1) Does machiavellianism predict fear recognition accuracy at the prenatal timepoint? (linear regression model)
- (2) Does machiavellianism and fear accuracy predict change in amygdala response to fear faces across the transition to fatherhood? (multiple regression model)

	N	Mean	SD	Min	Max	Histogram
hit_rate_pre	34	0.62	0.27	0.18	1.07	
hit_rate_post	22	0.72	0.29	0.21	1.33	
raw_accuracy	22	0.78	0.18	0.40	1.00	
me_pre	30	43.17	7.62	32.00	65.00	
lamyg_mean_prenat	34	0.07	0.15	-0.24	0.34	
ramyg_mean_prenat	34	0.08	0.14	-0.38	0.32	
lamyg_mean_postpart	22	0.16	0.16	-0.10	0.46	
ramyg_mean_postpart	22	0.14	0.15	-0.09	0.43	
lamyg_change	22	0.06	0.24	-0.23	0.60	
ramyg_change	22	0.04	0.20	-0.24	0.40	

Variables

- 'hit_rate_pre' : prenatal unbiased hit-rate (raw accuracy and differential accuracy combined)
- 'raw_accuracy': fear recognition accuracy
- 'lamyg_mean_change' : change in left amygdala activation to fear>rest contrast
- 'ramyg_mean_change' : change in right amygdala activation to fear>rest contrast
- 'me_pre': prenatal machiavellianism

More Variables

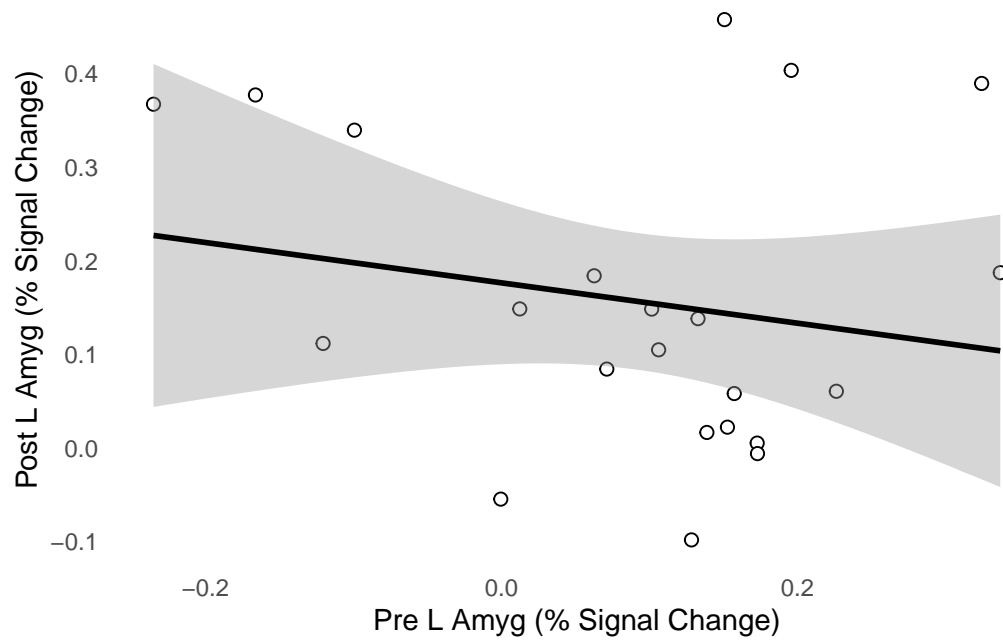
- 'lamyg_mean_change' : change in left amygdala activation to fear>rest contrast
- 'ramyg_mean_change' : change in right amygdala activation to fear>rest contrast

Table @tbl-summarize shows summary statistics

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 12 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

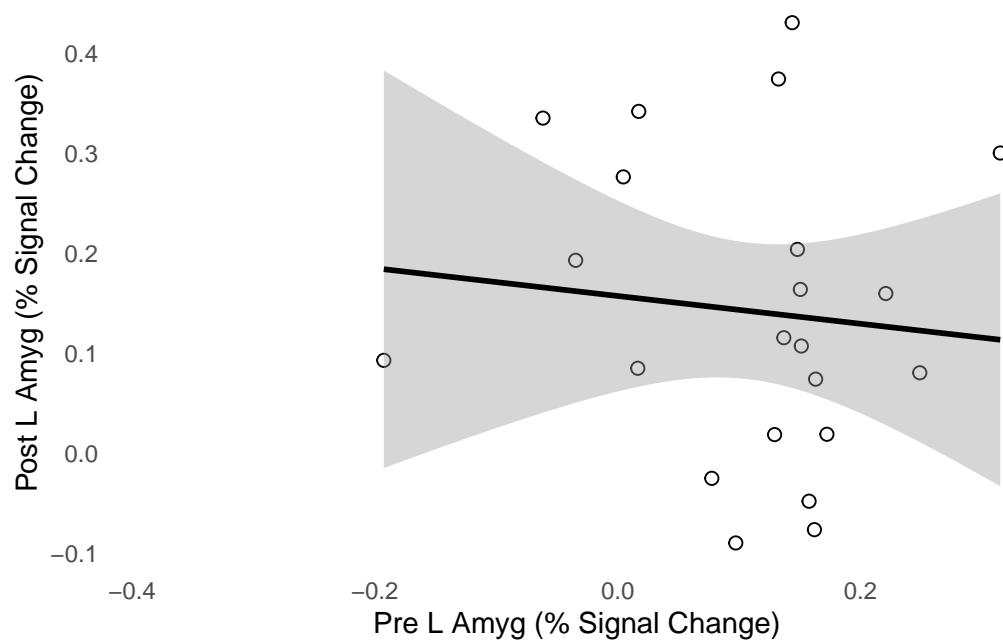
```
Warning: Removed 12 rows containing missing values or values outside the scale range
(`geom_point()`).
```



``geom_smooth()` using formula = 'y ~ x'`

Warning: Removed 12 rows containing non-finite outside the scale range (``stat_smooth()``).

Removed 12 rows containing missing values or values outside the scale range (``geom_point()``).



Model 1

Let $RAW = \text{raw_accuracy}$, $ME = \text{me_pre}$

$$\begin{aligned} RAW_i &\sim N(\mu_i, \sigma) \\ \mu_i &= \beta_0 + \beta_1 ME_i \end{aligned}$$

priors:

$$\begin{aligned} \beta_0 &\sim N(0, 2) \\ \beta_1 &\sim N(0, 10) \\ \sigma &\sim \text{Student-t}(4, 0, 1) \end{aligned}$$

Model 2

Let $RAW = \text{raw_accuracy}$, $ME = \text{me_pre}$, $\Delta LAMY = \text{lamyg_change}$

$$\begin{aligned} \Delta LAMY &\sim N(\mu_i, \sigma) \\ \mu_i &= \beta_0 + \beta_1 ME_i + \beta_2 RAW_i \end{aligned}$$

priors:

$$\begin{aligned} \beta_0 &\sim N(0, 2) \\ \beta_1 &\sim N(0, 1) \\ \beta_2 &\sim N(0, 10) \\ \sigma &\sim \text{Student-t}(4, 0, 1) \end{aligned}$$

Model 3

Let $RAW = \text{raw_accuracy}$, $ME = \text{me_pre}$, $\Delta RAMY = \text{ramyg_change}$

$$\begin{aligned} \Delta RAMY &\sim N(\mu_i, \sigma) \\ \mu_i &= \beta_0 + \beta_1 ME_i + \beta_2 RAW_i \end{aligned}$$

priors:

$$\begin{aligned} \beta_0 &\sim N(0, 2) \\ \beta_1 &\sim N(0, 1) \\ \beta_2 &\sim N(0, 10) \\ \sigma &\sim \text{Student-t}(4, 0, 1) \end{aligned}$$

Model 1 Analysis

Results

The chains mixed well.

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: raw_accuracy ~ me_pre
Data: faces (Number of observations: 21)
Draws: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
       total post-warmup draws = 8000
```

Regression Coefficients:

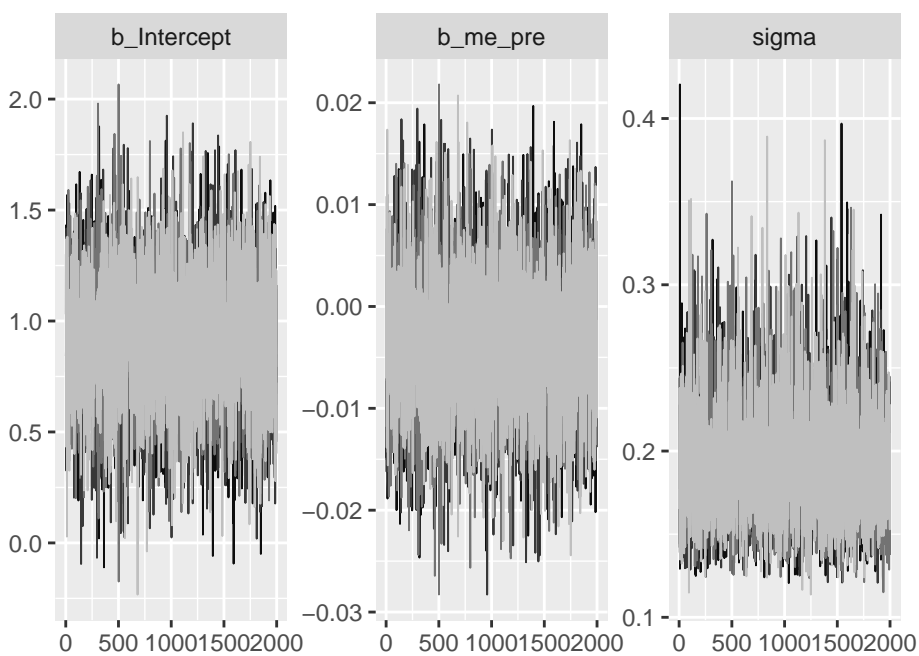
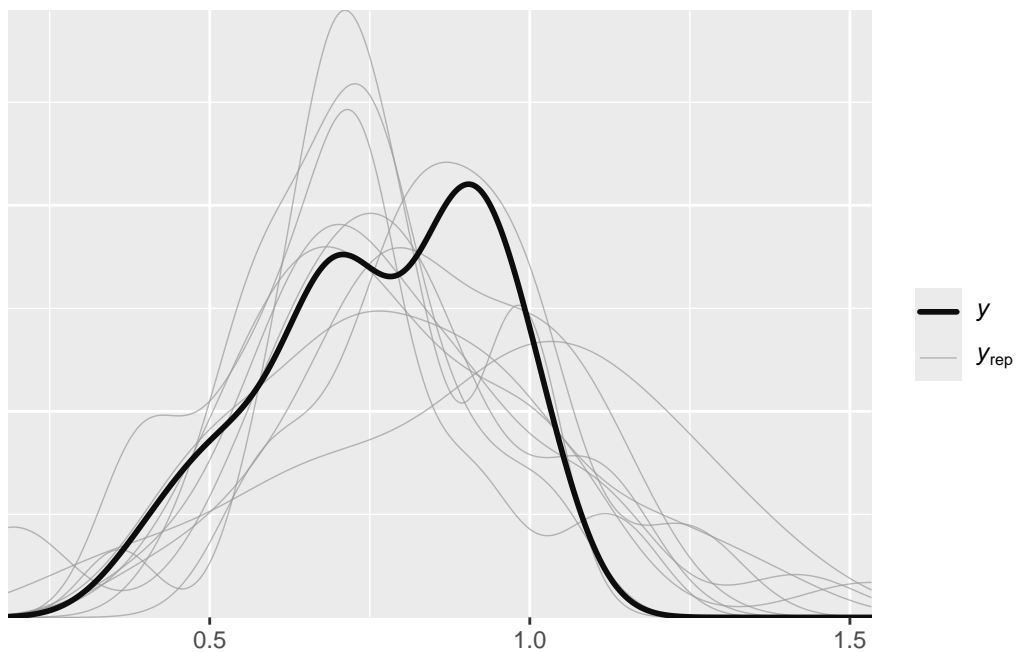
	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	0.92	0.29	0.35	1.48	1.00	7283	5347
me_pre	-0.00	0.01	-0.02	0.01	1.00	7324	4975

Further Distributional Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	0.19	0.03	0.14	0.27	1.00	5561	4812

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS and Tail_ESS are effective sample size measures, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

Using 10 posterior draws for ppc type 'dens_overlay' by default.



@tbl-summ-fit shows the posterior distributions

Table 1: Posterior summary of the model parameters.

variable	mean	median	sd	mad	q5	q95	rhat	ess_bulk	ess_tail
b_Intercept	0.92	0.92	0.29	0.27	0.45	1.39	1	7282.56	5347.31
b_me_pre	0.00	0.00	0.01	0.01	-0.01	0.01	1	7324.46	4975.09
sigma	0.19	0.19	0.03	0.03	0.15	0.26	1	5561.20	4811.62

Using all posterior draws for ppc type 'intervals' by default.

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

i This can happen when ggplot fails to infer the correct grouping structure in the data.

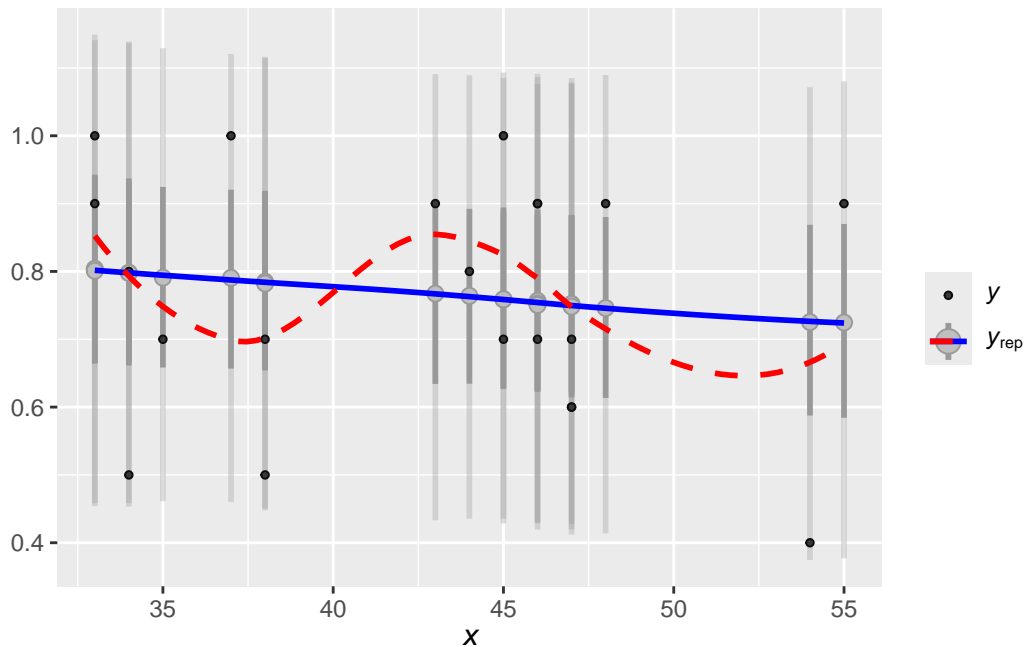
i Did you forget to specify a `group` aesthetic or to convert a numerical variable into a factor?

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

i This can happen when ggplot fails to infer the correct grouping structure in the data.

i Did you forget to specify a `group` aesthetic or to convert a numerical variable into a factor?



Model 2 Analysis

Results

The chains mixed well.

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: lamyg_change ~ raw_accuracy + me_pre
Data: faces (Number of observations: 21)
Draws: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
       total post-warmup draws = 8000
```

Regression Coefficients:

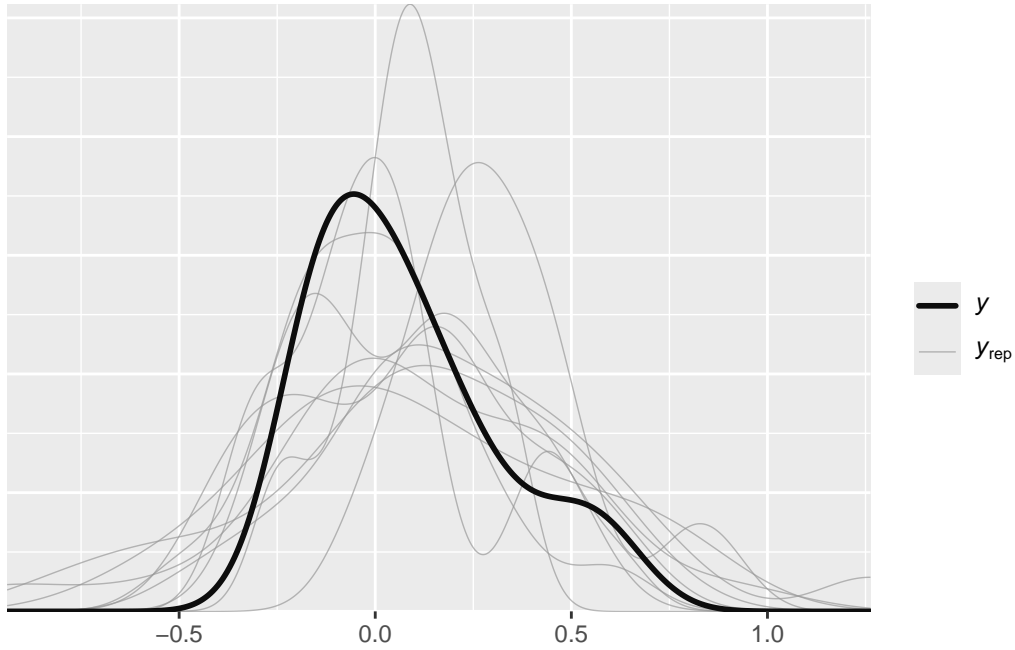
	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	0.09	0.47	-0.85	1.00	1.00	8081	5531
raw_accuracy	-0.29	0.31	-0.90	0.35	1.00	8078	5219
me_pre	0.00	0.01	-0.01	0.02	1.00	8071	5151

Further Distributional Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	0.25	0.05	0.18	0.36	1.00	6118	5270

Draws were sampled using `sampling(NUTS)`. For each parameter, `Bulk_ESS` and `Tail_ESS` are effective sample size measures, and `Rhat` is the potential scale reduction factor on split chains (at convergence, `Rhat = 1`).

Using 10 posterior draws for ppc type 'dens_overlay' by default.



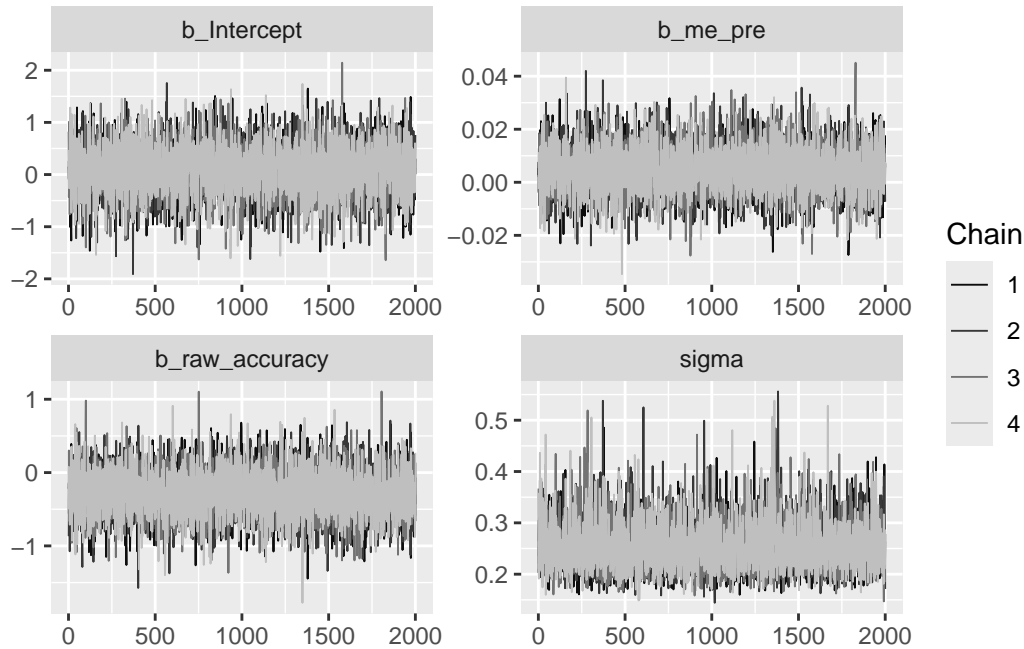


Table 2: Posterior summary of the model parameters.

variable	mean	median	sd	mad	q5	q95	rhat	ess_bulk	ess_tail
b_Intercept	0.09	0.09	0.47	0.46	-0.67	0.85	1	8080.76	5530.93
b_me_pre	0.00	0.00	0.01	0.01	-0.01	0.02	1	8071.11	5151.43
b_raw_accuracy	-0.29	-0.29	0.31	0.31	-0.79	0.23	1	8078.40	5218.91
sigma	0.25	0.25	0.05	0.04	0.19	0.34	1	6118.33	5269.50

Using all posterior draws for ppc type 'intervals' by default.

Using all posterior draws for ppc type 'intervals' by default.

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

i This can happen when ggplot fails to infer the correct grouping structure in the data.

i Did you forget to specify a `group` aesthetic or to convert a numerical variable into a factor?

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
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Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

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Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

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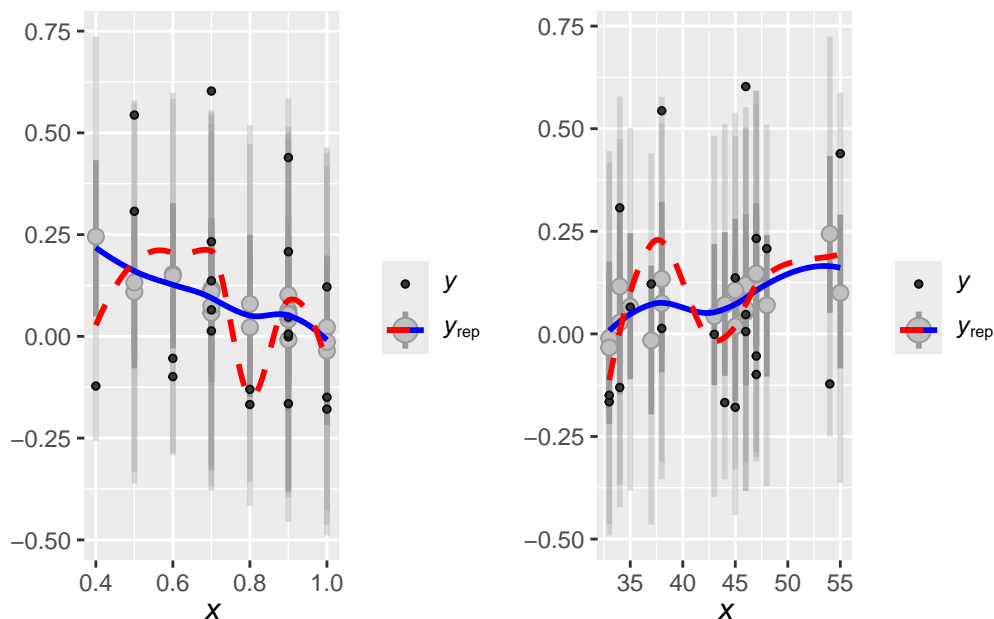
i Did you forget to specify a `group` aesthetic or to convert a numerical variable into a factor?

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Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

i This can happen when ggplot fails to infer the correct grouping structure in the data.

i Did you forget to specify a `group` aesthetic or to convert a numerical variable into a factor?



Model 3 Analysis

Results

The chains mixed well.

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: ramyg_change ~ raw_accuracy + me_pre
Data: faces (Number of observations: 21)
Draws: 4 chains, each with iter = 4000; warmup = 2000; thin = 1;
       total post-warmup draws = 8000
```

Regression Coefficients:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	0.02	0.41	-0.79	0.82	1.00	7710	5330
raw_accuracy	-0.07	0.27	-0.59	0.48	1.00	8552	5746
me_pre	0.00	0.01	-0.01	0.02	1.00	7666	5570

Further Distributional Parameters:

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	0.22	0.04	0.15	0.31	1.00	6603	5846

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS and Tail_ESS are effective sample size measures, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

Using 10 posterior draws for ppc type 'dens_overlay' by default.

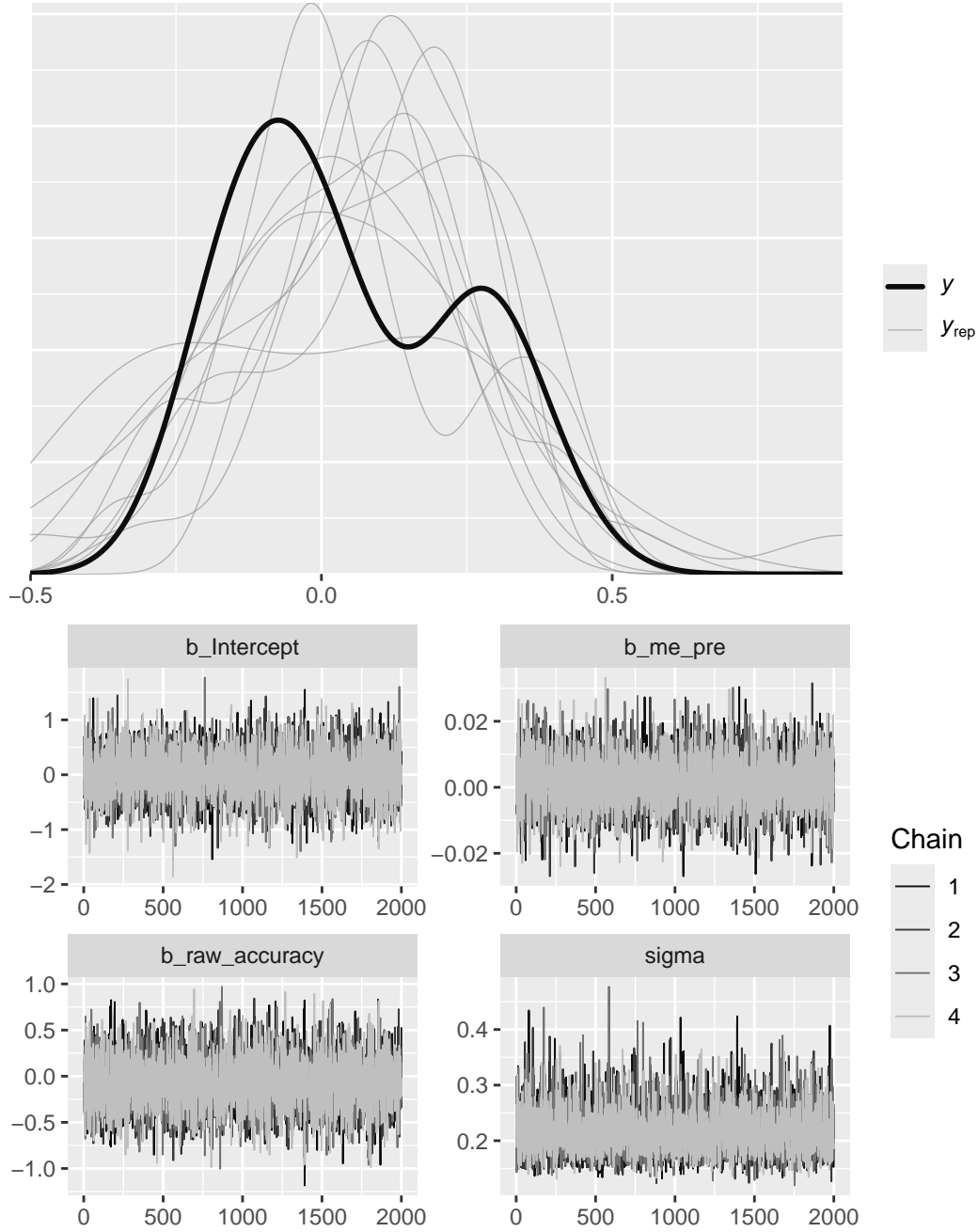


Table 3: Posterior summary of the model parameters.

variable	mean	median	sd	mad	q5	q95	rhat	ess_bulk	ess_tail
$b_{\text{Intercept}}$	0.02	0.03	0.41	0.38	-0.64	0.69	1	7709.71	5330.03
$b_{\text{me_pre}}$	0.00	0.00	0.01	0.01	-0.01	0.01	1	7665.95	5569.52

variable	mean	median	sd	mad	q5	q95	rhat	ess_bulk	ess_tail
b_raw_accuracy	-0.07	-0.07	0.27	0.26	-0.51	0.37	1	8551.90	5746.41
sigma	0.22	0.21	0.04	0.04	0.16	0.29	1	6602.67	5845.85

Using all posterior draws for ppc type 'intervals' by default.

Using all posterior draws for ppc type 'intervals' by default.

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

i This can happen when ggplot fails to infer the correct grouping structure in the data.

i Did you forget to specify a `group` aesthetic or to convert a numerical variable into a factor?

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`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
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Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

i This can happen when ggplot fails to infer the correct grouping structure in the data.

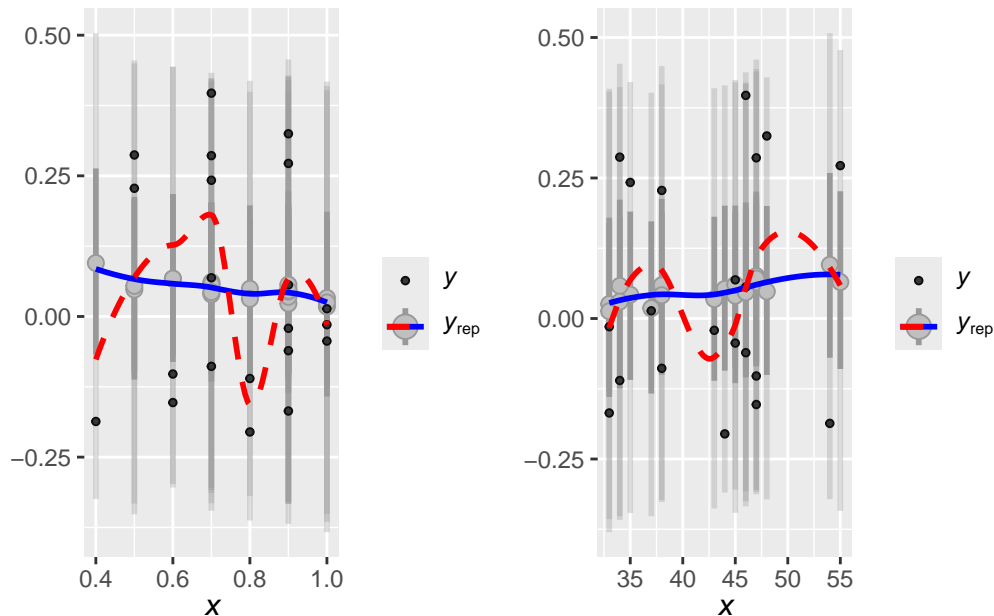
i Did you forget to specify a `group` aesthetic or to convert a numerical variable into a factor?

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```


Warning: The following aesthetics were dropped during statistical transformation: ymin and ymax.

i This can happen when ggplot fails to infer the correct grouping structure in the data.

i Did you forget to specify a `group` aesthetic or to convert a numerical variable into a factor?



save plots

```
save_plot <- function(plot, filename, width = 10, height = 6) { ggsave(filename = filename,
  plot = plot, width = width, height = height, dpi = 300) }
```

Save plots from different models

Model 1 plots

```
ggsave("m1_pp_check.png", pp_check(m1), width = 10, height = 6, dpi = 300)
ggsave("m1_marginal_plot.png", pp_check(m1, type = "intervals", x = "me_pre") +
  geom_smooth(se = FALSE, col = "blue") + geom_smooth(aes(y = y_obs), se = FALSE,
  col = "red", linetype = "dashed"), width = 10, height = 6, dpi = 300)
```

```
png("m1_trace_plot.png", width = 10, height = 6, units = "in", res = 300) mcmc_trace(draws_df_m1,
pars = c("b_Intercept", "b_me_pre", "sigma")) dev.off()
```

Model 2 plots

```
ggsave("m2_pp_check.png", pp_check(m2), width = 10, height = 6, dpi = 300)
ggsave("m2_combined_plot.png", m2_combined, width = 16, height = 6, dpi = 300)
png("m2_trace_plot.png", width = 10, height = 6, units = "in", res = 300) mcmc_trace(draws_df_m2,
pars = c("b_Intercept", "b_me_pre", "b_lamyg_mean_prenat", "sigma")) dev.off()
```

Model 3 plots

```
ggsave("m3_pp_check.png", pp_check(m3), width = 10, height = 6, dpi = 300)
ggsave("m3_combined_plot.png", m3_combined, width = 16, height = 6, dpi = 300)
png("m3_trace_plot.png", width = 10, height = 6, units = "in", res = 300) mcmc_trace(draws_df_m3,
pars = c("b_Intercept", "b_me_pre", "b_ramyg_mean_prenat", "sigma")) dev.off()
```