The Effect of Children on Women's Labor Supply: A Bayesian Replication Analysis

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Contents

Background

In 1998, Joshua Angrist and William Evans published an article called *Children and Their Parents' Labor Supply: Evidence from Exogenous Variation in Family Size* about the effect an additional child on labor supply. In general, outside the context of an experiment, it's hard to determine the true effect of children on adults' labor supply since fertility is endogenous. The authors note that many economists believe fertility and labor supply are "jointly determined." Varying research studies assess the effect of children on wages and vice versa. This study, conducted using a frequentist framework, using the "sibling-sex composition" as an instrumental variable (IV). The authors argue that an indicator variable for whether the first two children have the same sex is as if randomly assigned. The study finds that children lead to a reduction in labor supply for women–an outcome that remains significant even among the IV estimates. It also leads to lower wages on average and fewer weeks worked. The study identified small and null effects for men and college educated women with high wage husbands.

The causal effect of children on women's labor supply is important for many reasons: a reduction in women's labor supply could have positive effects on children's development, if women devote more time to caring for their children, or, if one values women's contributions to the labor market, small and null impacts may indicate that children do not pose an obstacle to women's career trajectories. Large negative impacts may

provide some explanation for the persistent gender wage gap. In 2020, women earned 84% of what men did (Pew Research Center, 2021). Given evidence in recent years of delayed family formation, particularly in large cities and urban areas, the impact of children on women's labor supply may be a motivating factor (Bui & Miller, 2018). The effect is both interesting in terms of causal research and the application of IV, but it's also meaningful for reasons Angrist and Evans don't even mention in their article.

In their paper, Angrist and Evans use data from the 1980 and 1990 Census Public Use Micro Samples (PUMS). They use a variety of restrictions to generate a sample of women ages 21-35 whose oldest child was less than 18 years of age and who have at least two children. While Angrist and Evans run their analysis on a second sample of married women, for this project I focus on the larger sample of all women–regardless of marital status. Additionally, I focus on women's earnings, not the binary outcome of whether they are in the labor force or the number of weeks worked. I previously replicated the findings in this paper using the frequentist two stage least squares (TSLS) approach to IV. Using the detailed sample restrictions that Angrist and Evans outline in their paper, I was able to replicate Tables 3, 6, and 7. The OLS and TSLS estimates that I replicated are below.

	All mothers			Married mothers			Married fathers		
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Estimation method	OLS	2SLS	2SLS	OLS	2SLS	2SLS	OLS	2SLS	2SLS
Instrument for *More than 2 children*	-	*Same sex*	*Two boys, Two girls*	-	*Same sex*	*Two boys, Two girls*	-	*Same sex*	*Two boys, Two girls*
Dependent variable									
Worked for pay	-0.173 (0.002)	-0.129 (0.026)	-0.122 (0.025)	-0.162 (0.002)	-0.124 (0.028)	-0.118 (0.028)	-0.008 (0.001)	0.006 (0.009)	0.003 (0.009)
Weeks worked	-8.768 (0.071)	-6.205 (1.133)	-5.886 (1.126)	-7.827 (0.089)	-5.833 (1.224)	-5.664 (1.216)	-0.850 (0.046)	0.604 (0.610)	0.452 (0.606)
Hours/week	-6.538 (0.062)	-4.777 (0.972)	-4.508 (0.966)	-5.854 (0.076)	-5.024 (1.033)	-4.837 (1.026)	0.217 (0.054)	0.803 (0.711)	0.727 (0.707)
Labor income	-3639.61 (33.55)	-2169.72 (536.41)	-2097.92 (533.66)	-3048.90 (39.71)	-1736.58 (555.74)	-1749.73 (552.43)	-1792.17 (102.26)	-355.51 (1356.42)	-414.19 (1348.97)
Ln(Family income)	-0.131 (0.005)	-0.046 (0.070)	-0.055 (0.069)	-0.132 (0.005)	-0.055 (0.060)	-0.058 (0.060)	-	-	-
Ln(Non-wife income)	-	-	-	-0.055 (0.006)	0.043 (0.072)	0.031 (0.071)	-	-	-

Figure 1: table 7

I only replicated this analysis with data from the 1980 Census, which is dated. Additionally, given time and processing constraints, I randomly sampled 3,000 records from the total dataset, which is around 400,000 records. A more precise estimate of the causal estimate would use more data. I hope that in replicating this analysis using Bayesian inference I will either strengthen (or contradict) the claims made by Angrist and Evans and provide a working example for updating this analysis with more recent data and larger datasets.

For the Bayesian analysis, I use the following methods: * a simple linear model with a normal PDF as the likelihood and `incwage` as the outcome * a simple linear model with a normal PDF as the likelihood and `log(incwage)` as the outcome * a two-stage model with a Probit in the first stage for the decision function of having an additional child and a normal likelihood in the second stage for the impact of children on `log(incwage)` * This approach is based off of the likelihood function in 2.3 of the sampleSelection vignette

```r
## load data
df <- read_dta("../00_data/sample1.dta")
df <- df %>%
  # create indicator for some college
  mutate(coll = if_else(str_sub(educus, 1, 1) == "8", 1, 0))

df_samp <- df %>%
  sample_n(3000)

df_samp <- df_samp %>%
  mutate(across(c("age", "age_fbirth"), ~ . - mean(., na.rm = T))) %>%
  mutate(l_incwage = if_else(incwage <= 0, log(1), log(incwage)),
         l_wkswork1 = if_else(wkswork1 <= 0, log(1), log(wkswork1)))

df_samp %>%
  group_by(samesex) %>%
  summarize(n = n())
```

```
## # A tibble: 2 x 2
##   samesex     n
##     <dbl> <int>
## 1       0  1434
## 2       1  1566
```

```r
# distribution of states
df_samp %>%
  group_by(stateus) %>%
  summarize(n = n()) %>%
  arrange(desc(n))
```

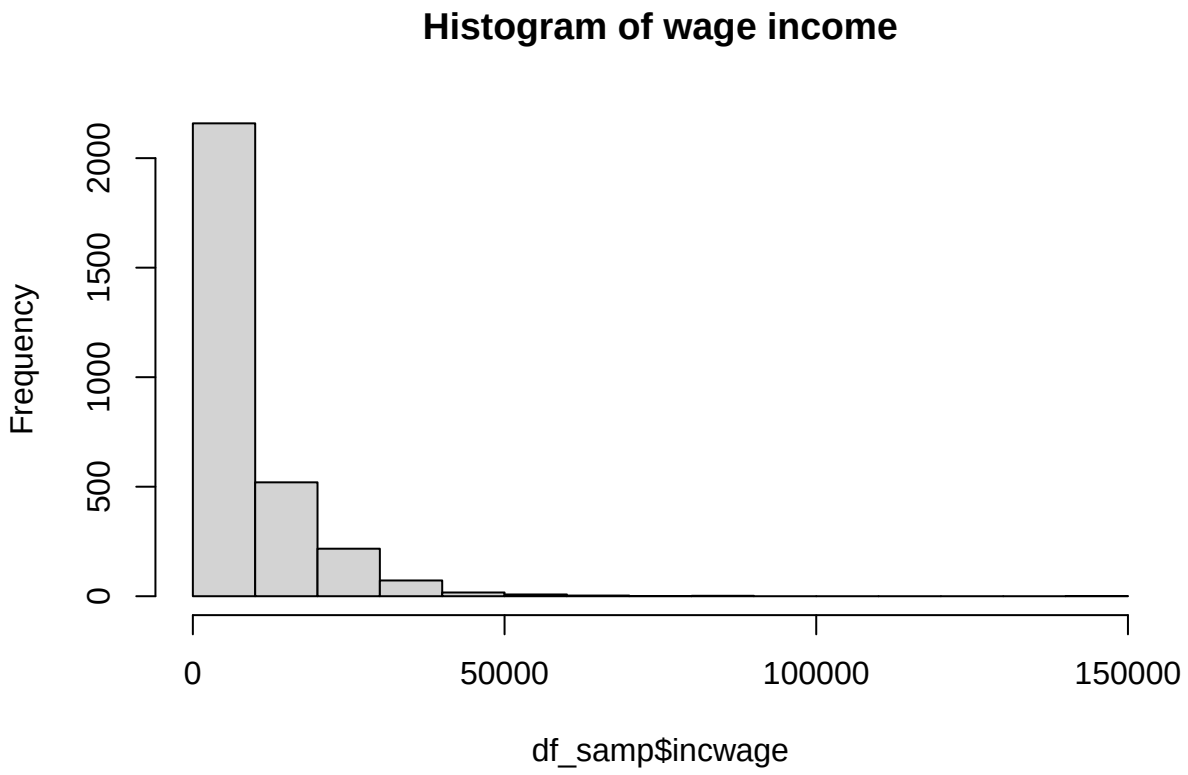
```
## # A tibble: 51 x 2
##              stateus     n
##            <dbl+lbl> <int>
##  1  6 [California]     257
##  2 48 [Texas]          214
##  3 36 [New York]       210
##  4 26 [Michigan]       165
##  5 17 [Illinois]       162
##  6 42 [Pennsylvania]   148
##  7 39 [Ohio]           137
##  8 18 [Indiana]        103
##  9 12 [Florida]         99
## 10 29 [Missouri]        80
## # ... with 41 more rows
```

```r
## distribution of education
df_samp %>%
  group_by(coll) %>%
  summarize(n = n())
```

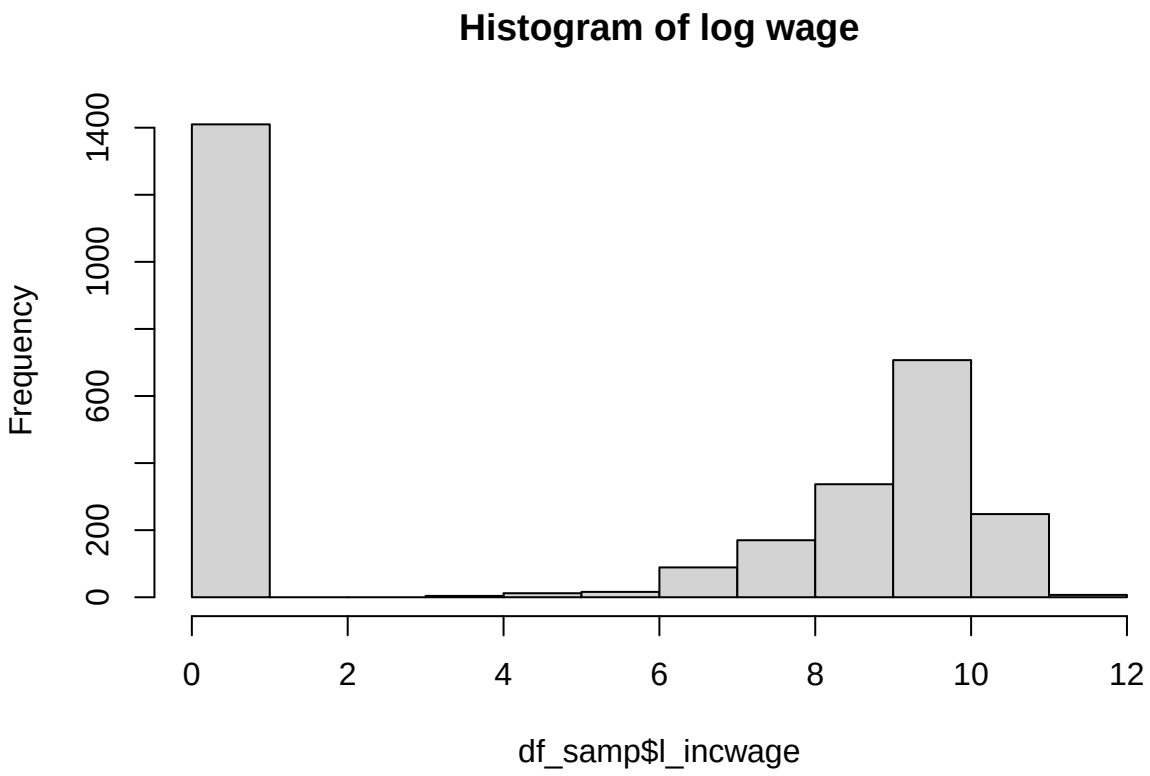
```
## # A tibble: 2 x 2
##    coll     n
```

```
##   <dbl> <int>
## 1     0  2202
## 2     1   798
```

```
hist(df_samp$incwage, main = "Histogram of wage income")
```




```
hist(df_samp$l_incwage, main = "Histogram of log wage")
```



Bayesian Analysis

Running with `rstanarm` for initial testing

```
# Running with rstanarm
post <-
  stan_glm(
    incwage ~ cnum_mt2 + age + age_fbirth +
      f_boy + s_boy + r_black + hisp + r_oth,
    data = df_samp,
    family = gaussian(),
    prior = cauchy(),
    prior_intercept = cauchy(),
    seed = 12345
  )
post
```

```
## stan_glm
##  family:       gaussian [identity]
##  formula:      incwage ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black +
##     hisp + r_oth
##  observations: 3000
##  predictors:   9
```

```
## ------
##             Median  MAD_SD
## (Intercept)  7667.8   258.5
## cnum_mt2    -3148.3   410.9
## age           537.0    57.1
## age_fbirth   -403.8    72.2
## f_boy          -0.1     3.7
## s_boy           0.0     3.4
## r_black      3113.0   609.1
## hisp            0.1     3.5
## r_oth           0.0     3.6
##
## Auxiliary parameter(s):
##       Median  MAD_SD
## sigma 10058.6   129.5
##
## ------
## * For help interpreting the printed output see ?print.stanreg
## * For info on the priors used see ?prior_summary.stanreg
```

```
post_log <-
  stan_glm(
    l_incwage ~ cnum_mt2 + age + age_fbirth +
      f_boy + s_boy + r_black + hisp + r_oth,
    data = df_samp,
    family = gaussian(),
    prior = cauchy(),
    prior_intercept = cauchy(),
    seed = 12345
  )
post_log
```

```
## stan_glm
##  family:       gaussian [identity]
##  formula:      l_incwage ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black +
##     hisp + r_oth
##  observations: 3000
##  predictors:   9
## ------
##             Median MAD_SD
## (Intercept)  5.3    0.2
## cnum_mt2    -1.6    0.2
## age          0.2    0.0
## age_fbirth  -0.3    0.0
## f_boy        0.0    0.2
## s_boy       -0.1    0.2
## r_black      1.3    0.3
## hisp         0.0    0.3
## r_oth        0.0    0.5
##
## Auxiliary parameter(s):
##       Median MAD_SD
## sigma 4.4    0.1
##
```

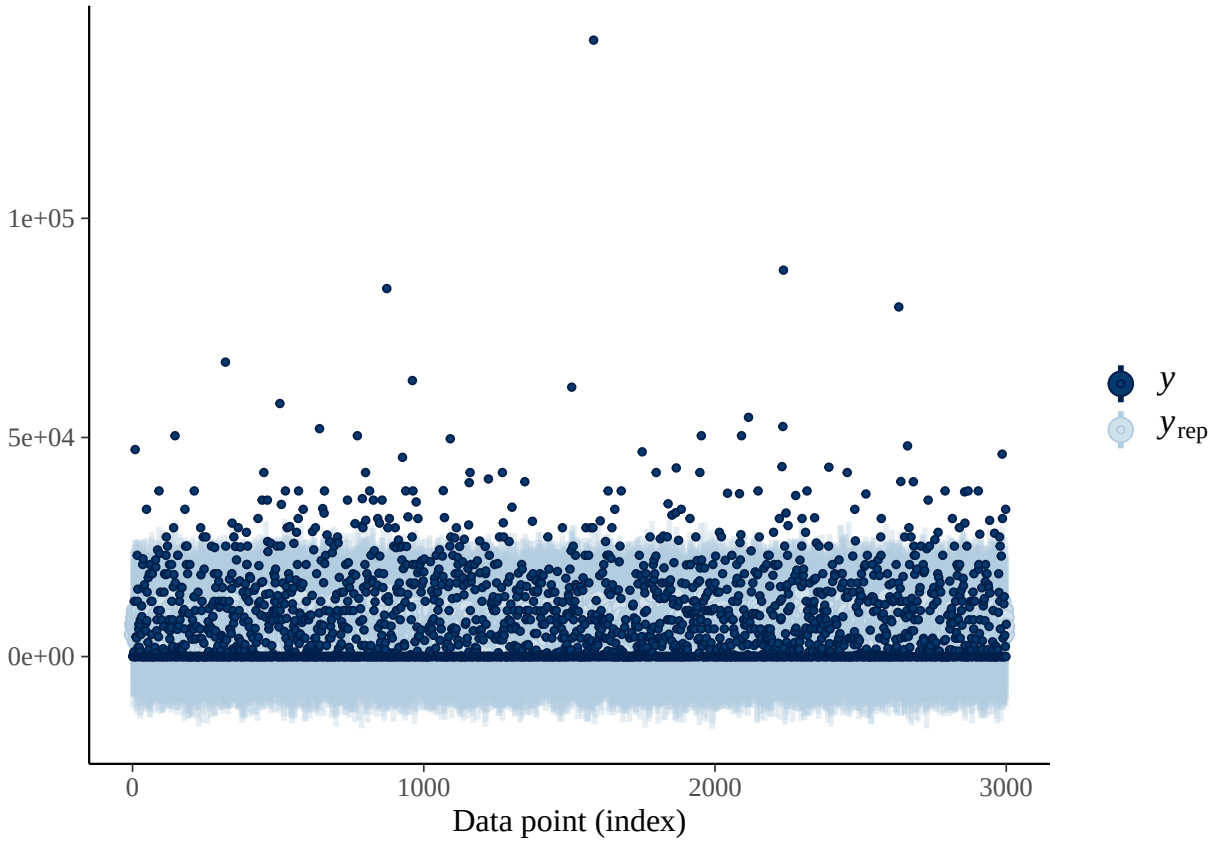
```
## ------
## * For help interpreting the printed output see ?print.stanreg
## * For info on the priors used see ?prior_summary.stanreg
```

Using the output generated by rstanarm we can run some posterior preditive checks.

```
pp_check(post, plotfun = "loo_intervals")
```

```
## Running PSIS to compute weights...
```

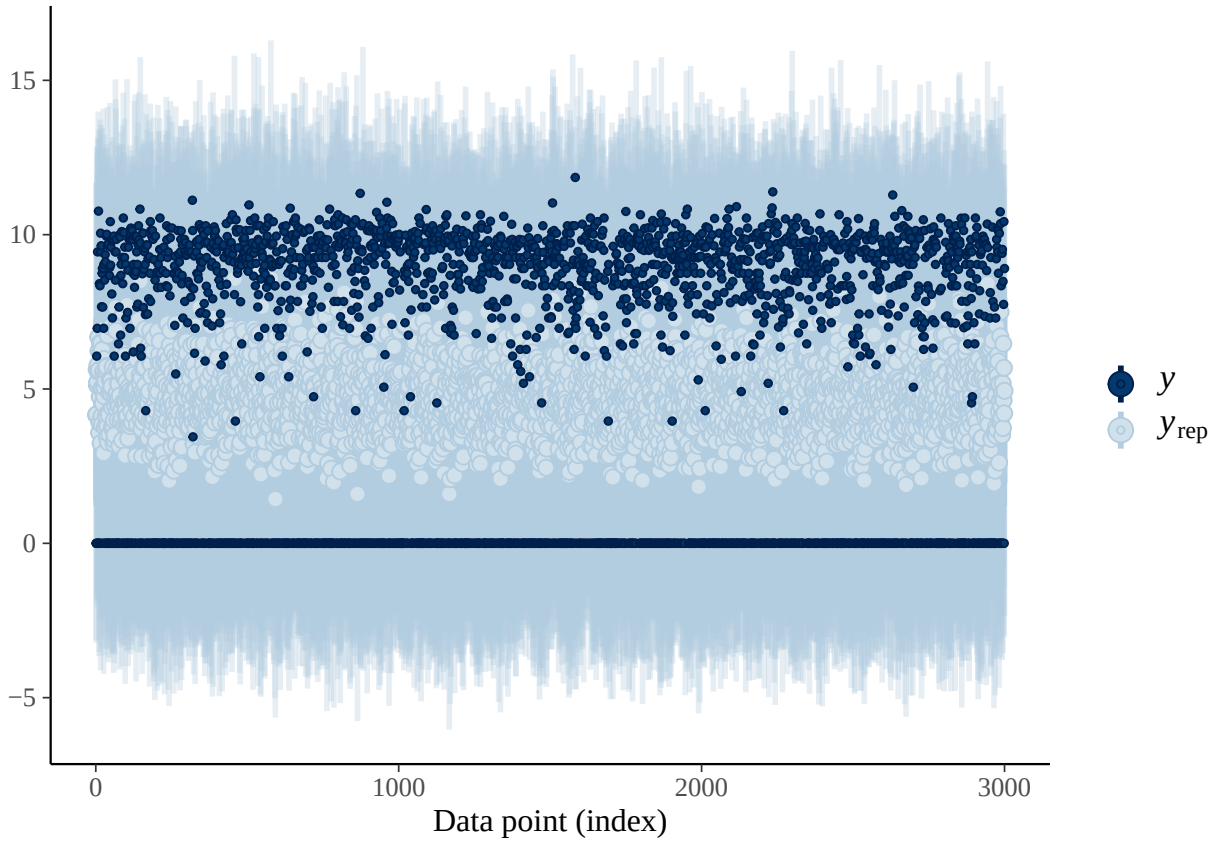
```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
```



The plot above shows the 100% intervals for the LOO predictive distribution. There are some extreme observed values of y, which the model does not predict, and the model predicts negative values of y, which are not substantively possible since the outcome is income.

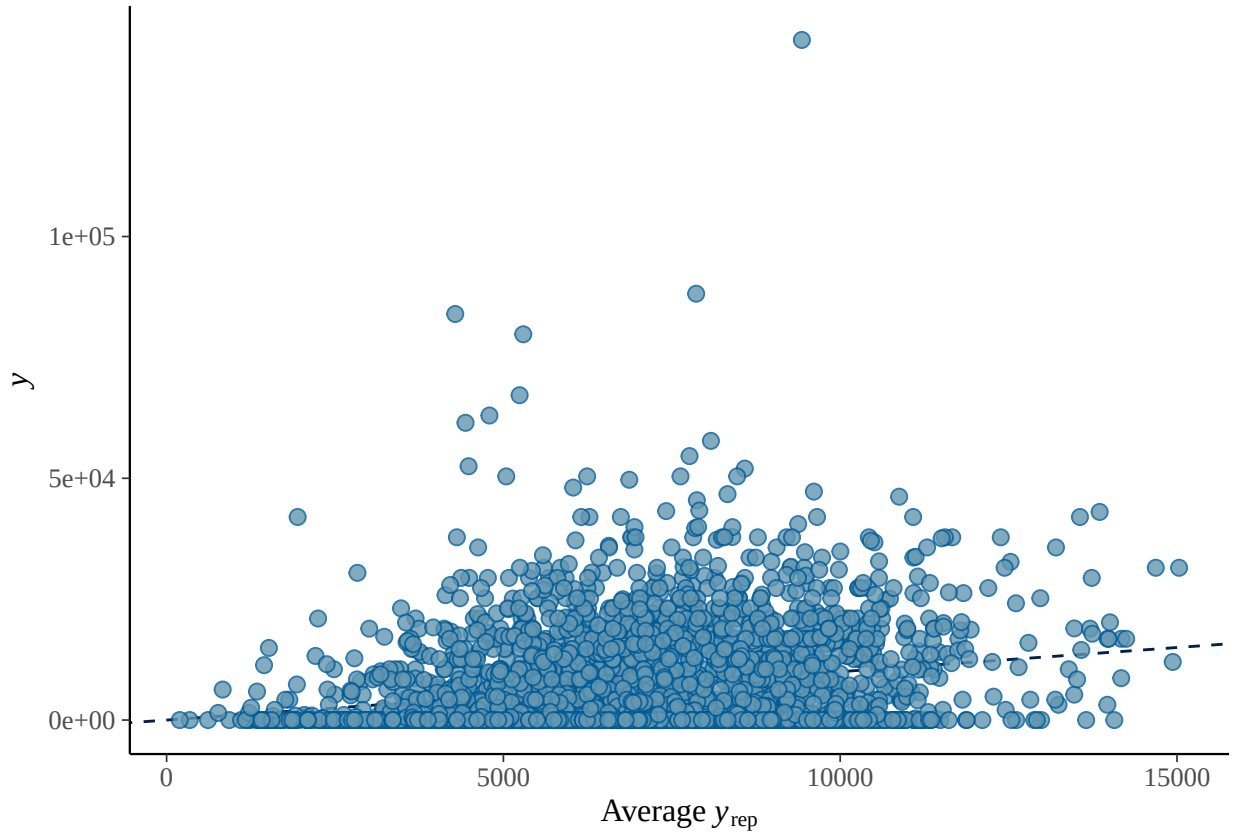
```
pp_check(post_log, plotfun = "loo_intervals")
```

```
## Running PSIS to compute weights...
```



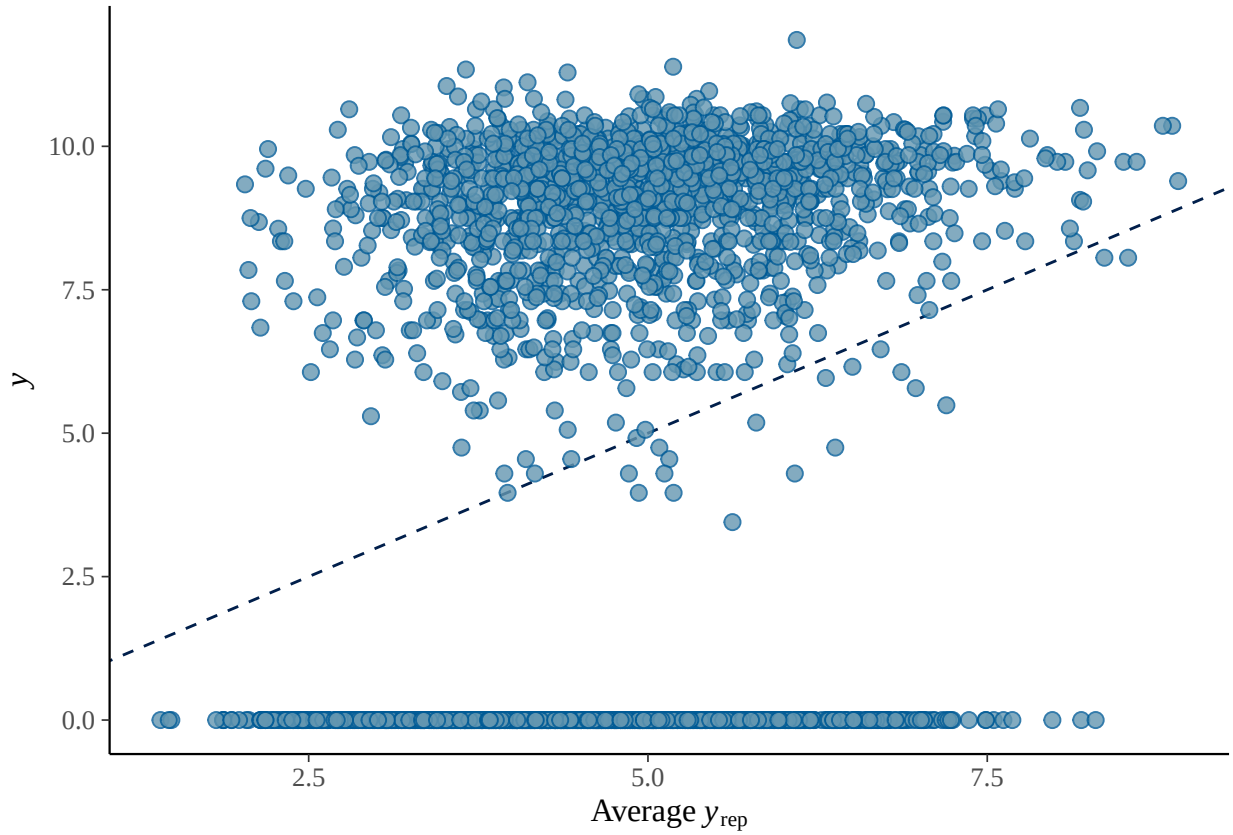
The plot is similar to the previous one, but shows the LOO predictive distribution for the log-transformed outcome. The LOO distribution predicts values of y that tend to be more extreme than the actual observed values of y. It also shows that there are many observed values at either 0 or 10 in log units, or $0 compared to approximately $20,000.

```
pp_check(post, plotfun = "scatter_avg")
```



This plot uses the untransformed outcome. The average predicted values of y tend to predict higher values y than are observed, which the flat linear trend demonstrates.

```
pp_check(post_log, plotfun = "scatter_avg")
```



This plot uses the log-transformed outcome. The average predicted values of y don't predict the extreme values of y as well. For example, the average predicted value may be 7 when the observed value is 0. However, overall the linear trend does suggest that the average predicted values of y *do* predict the observed values of y well; the incorrect predictions may cancel each other out.

Linear model with untransformed outcome

- This is based on the`linear.stan` file as shown in class, although I produce `log_lik` and `yrep` output as well.

```
# display stan code
writeLines(readLines("linear.stan"))
```

```
## #include quantile_functions.stan
## data {
##   int<lower = 0> N; // number of observations
##   int<lower = 0> K; // number of predictors
##   matrix[N, K] X;   // matrix of predictors
##   vector[N] y;      // outcomes
##   int<lower = 0, upper = 1> prior_only;   // ignore data?
##   vector[K + 1] m;                        // prior medians
##   vector<lower = 0>[K + 1] scale;             // prior scale values
##   real<lower = 0> r;
## }
## parameters {
```

```
##   vector[K] beta;
##   real alpha;
##   real<lower = 0> sigma;
## }
##
## model { // log likelihood, equivalent to target += normal_lpdf(y | alpha + X * beta, sigma)
##   if (!prior_only) target += normal_id_glm_lpdf(y | X, alpha, beta, sigma);
##   target += normal_lpdf(alpha  | m[1],   scale[1]);
##   target += normal_lpdf(beta | m[2:K + 1], scale[2:K + 1]);
##   target += exponential_lpdf(sigma | r);
## }
##
## generated quantities {
##   vector[N] log_lik;
##   vector[N] yrep;
##   {
##     vector[N] mu = alpha + X * beta;
##     for (n in 1:N) {
##       log_lik[n] = normal_lpdf(y[n] | mu[n], sigma);
##       yrep[n] = normal_rng(mu[n], sigma);
##     }
##   }
## }
```

```
# use normal priors
m <- c(8000, -2000, 0, -300, -40, -40, 2000, 2000, 2000)
s<- c(500, 3000, 600, 400, 140, 140, 3000, 3000, 3000)
```

```
# define covariates
cov <- c("cnum_mt2", "age", "age_fbirth", "f_boy", "s_boy", "r_black", "hisp", "r_oth")

# generate stan data
stan_data <- list(N = nrow(df_samp), K = 8, y = df_samp$incwage,
                                        X = df_samp[, cov],
                                        prior_only = TRUE, m = m,
                                        scale = s,
                                        r = 1)
```

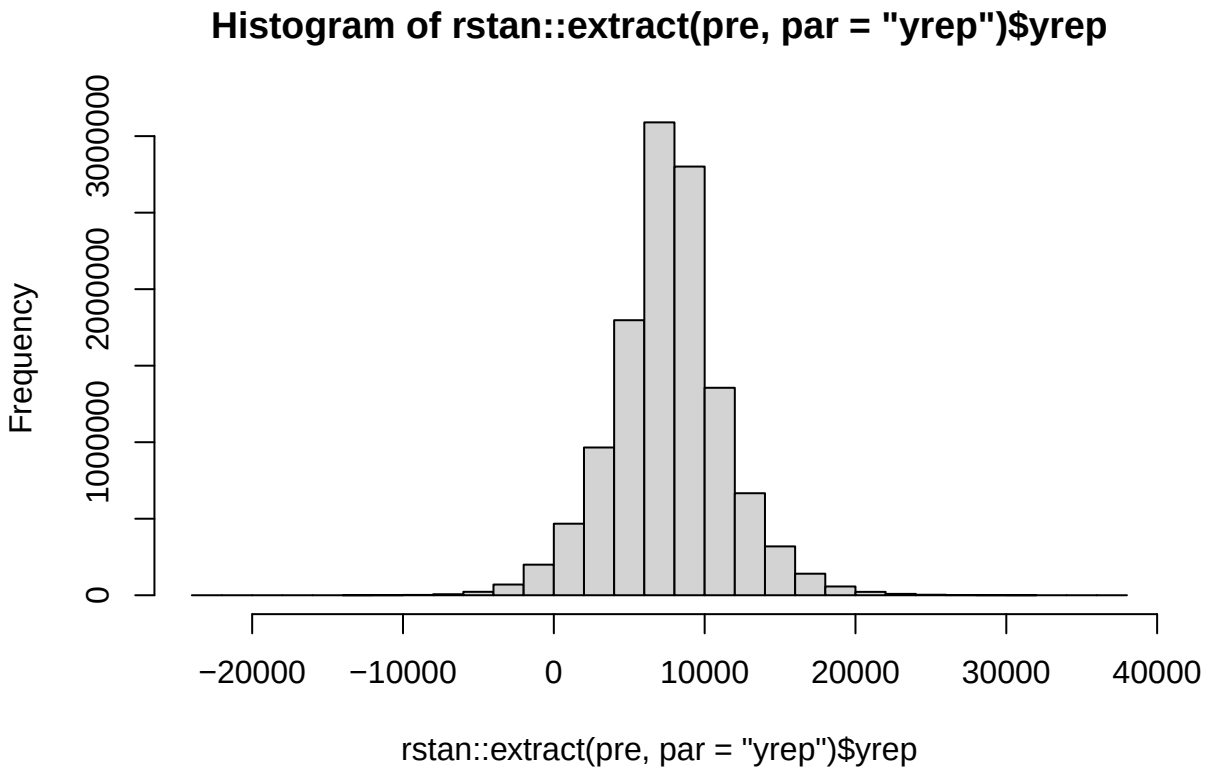
```
# call stan for prior predictive distribution checks
pre <- stan("linear.stan", data = stan_data, seed = 12345)
# print output
print(pre, pars = c("alpha", "beta", "sigma"))
```

```
## Inference for Stan model: linear.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##             mean se_mean      sd     2.5%      25%      50%     75%   97.5%
## alpha    7996.38    5.81  488.37  7030.90  7664.50  8003.21 8330.94 8925.42
## beta[1] -2017.94   32.63 2977.93 -7862.70 -4000.97 -2049.15  -18.79 3763.79
## beta[2]     7.21    6.36  577.61 -1133.33  -380.62    12.72  393.62 1121.94
## beta[3]  -305.60    4.62  391.34 -1083.30  -565.93  -306.14  -38.00  443.63
## beta[4]   -40.20    1.76  143.18  -307.95  -138.38   -40.02   57.07  239.75
```

```
## beta[5]   -40.35    1.58  141.06  -315.41  -135.64   -40.99   53.78  233.61
## beta[6]  1984.00   33.23 2991.23 -4025.77   -43.42  1991.59 4011.57 7806.12
## beta[7]  2023.87   34.37 2983.72 -3784.26     9.21  2016.28 4012.96 7767.03
## beta[8]  2062.00   32.01 2941.47 -3614.49    44.11  2041.59 4080.40 7729.61
## sigma       1.01    0.01    1.05     0.02     0.27     0.67    1.40    3.86
##         n_eff Rhat
## alpha    7066    1
## beta[1]  8328    1
## beta[2]  8244    1
## beta[3]  7187    1
## beta[4]  6626    1
## beta[5]  7943    1
## beta[6]  8104    1
## beta[7]  7534    1
## beta[8]  8447    1
## sigma    5857    1
##
## Samples were drawn using NUTS(diag_e) at Mon May 16 18:20:35 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

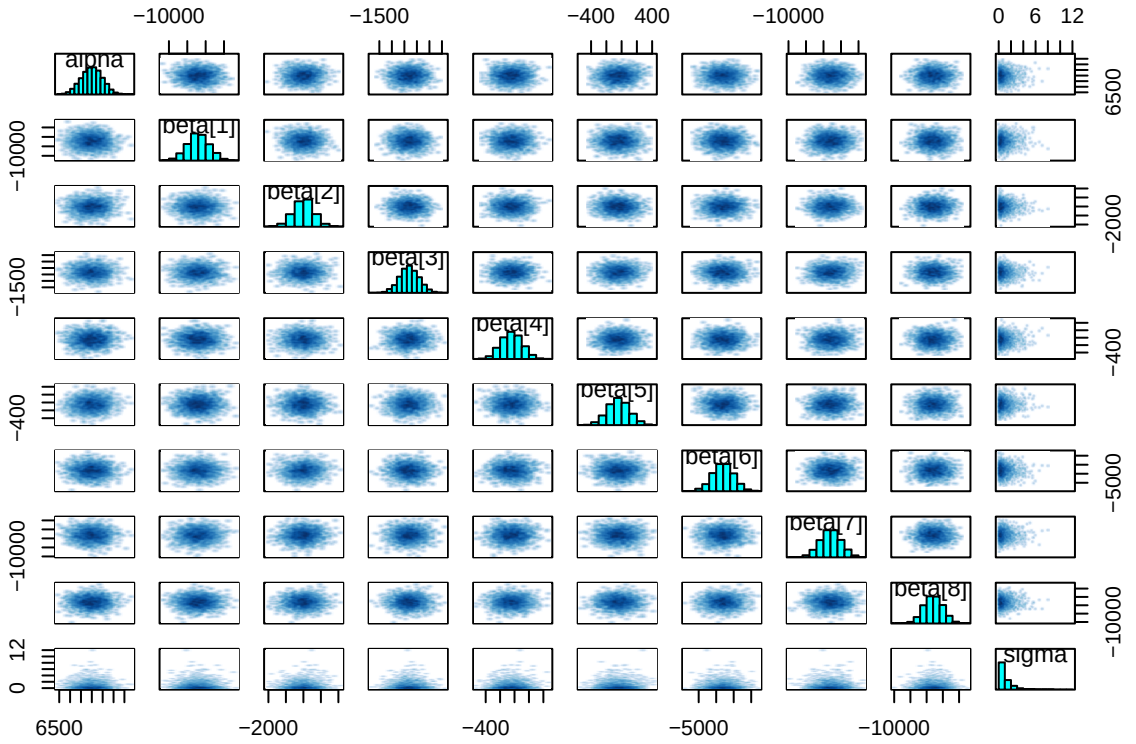
There were no issues running the model with `prior_only = TRUE`. The values of the parameters, as the pairs plot shows below, are all approximately normal.

```
hist(rstan::extract(pre, par = "yrep")$yrep)
```



The predicted values of y are slightly skewed to the right and are centered around $7,000. The prior predictive distribution also generates negative values of y, which are not realistic.

```
pairs(pre, pars = c("alpha", "beta", "sigma"))
```



The pairs plot does not indicate any major issues with the parameters as indicated by the prior distributions.

```
loo(pre)
```

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.

##
## Computed from 4000 by 3000 log-likelihood matrix
##
##               Estimate           SE
## elpd_loo -7.653539e+17 5.026072e+16
## p_loo     7.653539e+17 5.026072e+16
## looic     1.530708e+18 1.005214e+17
## ------
## Monte Carlo SE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##                          Count Pct.    Min. n_eff
## (-Inf, 0.5]   (good)        0    0.0%  <NA>
##  (0.5, 0.7]   (ok)          0    0.0%  <NA>
```

```
##    (0.7, 1]   (bad)         0    0.0%  <NA>
##    (1, Inf)   (very bad) 3000  100.0%  0
## See help('pareto-k-diagnostic') for details.
```

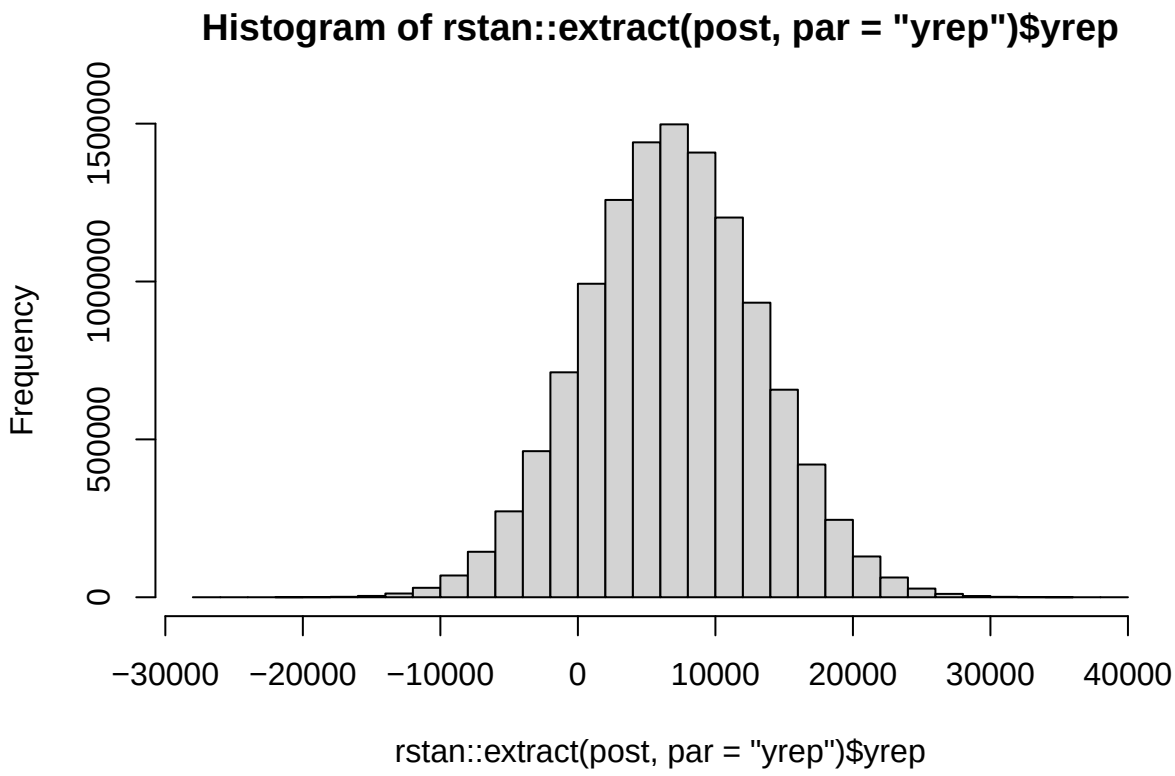
All 3,000 observations have Pareto K estimates > 0.7, which is an indication of outliers in the data and possibly model specification. The fact that `p_loo >> p` further indicates that the model is badly misspecified. Given the Pareto K estimates, the `elpd_loo` is inaccurate and should not be analyzed.

```
stan_data$prior_only <- FALSE
post <- stan("linear.stan", data = stan_data, seed = 12345)
# print output
print(post, pars = c("alpha", "beta", "sigma"))
```

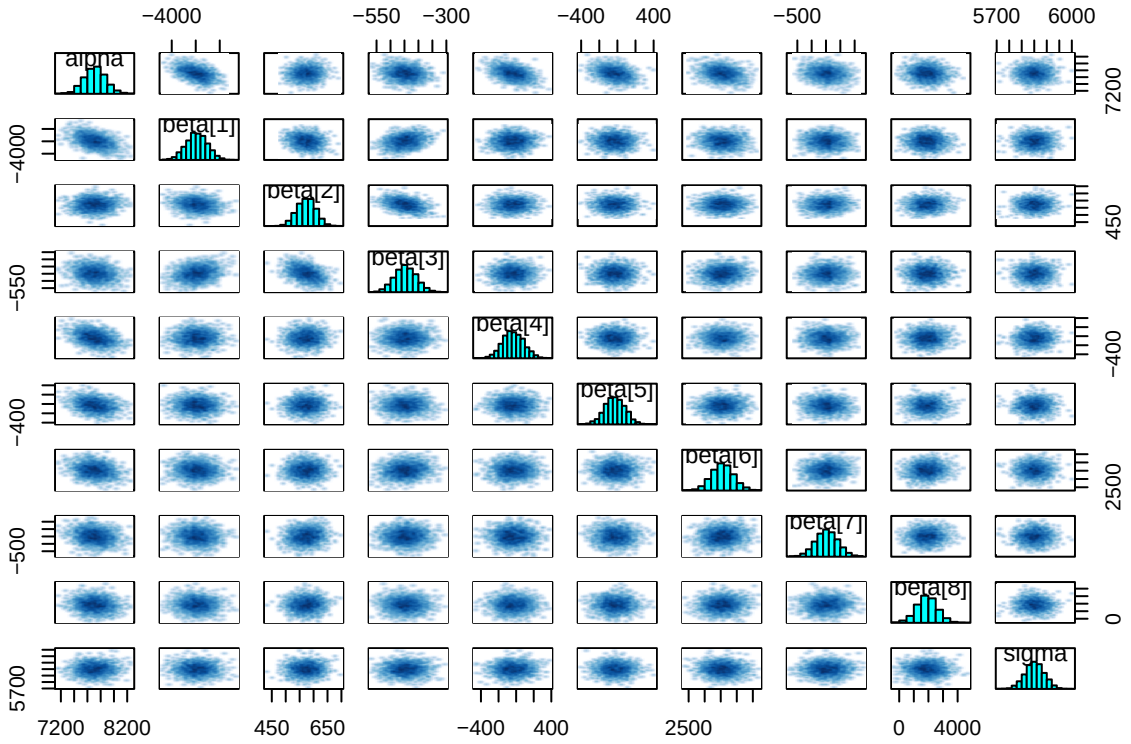
```
## Inference for Stan model: linear.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##             mean se_mean     sd     2.5%      25%      50%      75%    97.5%
## alpha    7714.59    2.83 161.96  7408.76  7606.55  7714.60  7823.96  8030.16
## beta[1] -3479.04    3.42 220.90 -3915.05 -3629.53 -3478.32 -3327.64 -3054.51
## beta[2]   573.89    0.50  33.35   508.30   551.16   575.05   596.50   636.26
## beta[3]  -446.38    0.65  39.39  -522.25  -472.32  -446.29  -419.61  -369.30
## beta[4]   -33.94    1.77 120.61  -267.13  -115.77   -36.34    49.57   202.58
## beta[5]   -27.33    1.67 113.09  -255.07  -104.30   -28.27    49.70   193.38
## beta[6]  3555.77    4.88 339.75  2893.42  3326.30  3554.06  3782.12  4251.18
## beta[7]   524.76    5.54 388.10  -248.31   264.36   522.88   787.92  1293.15
## beta[8]  1902.38   10.32 708.34   475.61  1437.43  1892.31  2373.83  3294.42
## sigma    5851.55    0.47  38.25  5776.61  5826.41  5851.82  5877.08  5924.98
##         n_eff Rhat
## alpha    3265    1
## beta[1]  4184    1
## beta[2]  4515    1
## beta[3]  3704    1
## beta[4]  4643    1
## beta[5]  4610    1
## beta[6]  4850    1
## beta[7]  4913    1
## beta[8]  4713    1
## sigma    6672    1
##
## Samples were drawn using NUTS(diag_e) at Mon May 16 18:24:57 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

Similar to the OLS results in Angrist and Evans' paper, the stan output shows that children negatively affect earnings. The 95% credible interval shows a decrease in earnings between \$3,915 and \$3,054.

```
hist(rstan::extract(post, par = "yrep")$yrep)
```




```
pairs(post, pars = c("alpha", "beta", "sigma"))
```



There are some correlations (e.g., a negative linear trend between `alpha` and `beta[1]`), but there are no major divergences and the marginal distributions are all approximately normal.

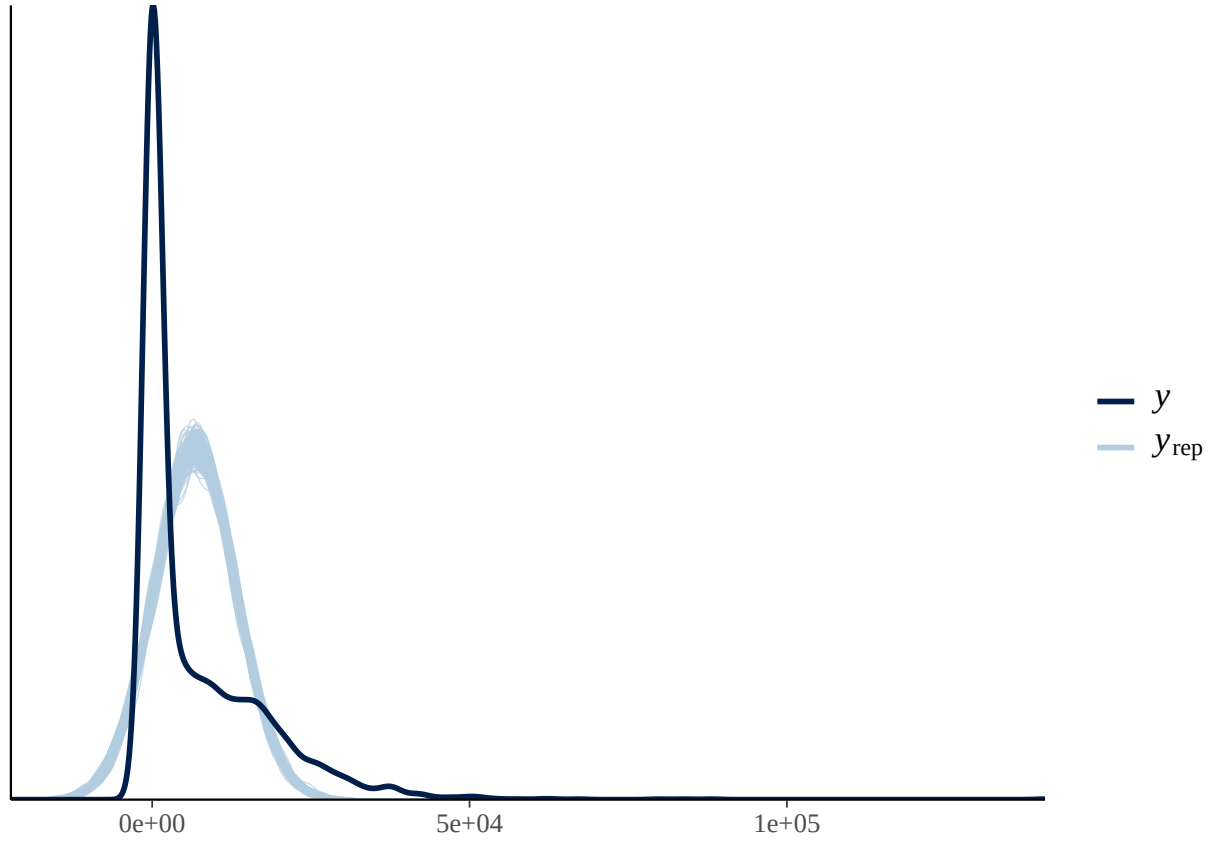
```
loo(post)
```

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.

##
## Computed from 4000 by 3000 log-likelihood matrix
##
##          Estimate    SE
## elpd_loo -33227.9 345.4
## p_loo        44.9  13.2
## looic     66455.8 690.8
## ------
## Monte Carlo SE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##                          Count Pct.    Min. n_eff
## (-Inf, 0.5]   (good)     2996  99.9%   1279
##  (0.5, 0.7]   (ok)          2   0.1%   562
##    (0.7, 1]   (bad)         1   0.0%   38
##    (1, Inf)   (very bad)    1   0.0%   7
## See help('pareto-k-diagnostic') for details.
```

Most Pareto K values are now less than 0.5, which indicates that `elpd_loo` is estimated with high accuracy for most observations. However, the `p_loo` is still higher than the number of parameters (though not

significantly so), which may indicate weak predictive capability of the model. This makes sense, since the observed and predicted values of y do not overlap.

```
pp_check(as.numeric(stan_data$y),
  rstan::extract(post, par = "yrep")$yrep[sample(1:length(stan_data$y), size = 150), ],
  ppc_dens_overlay
)
```



This plot visually shows the difference between the predicted values of y and the observed values of y. The observed values of y tend to be lower than the predicted values and there are more outliers in the observed data. The predicted values of y comprise a smoother normal distribution.

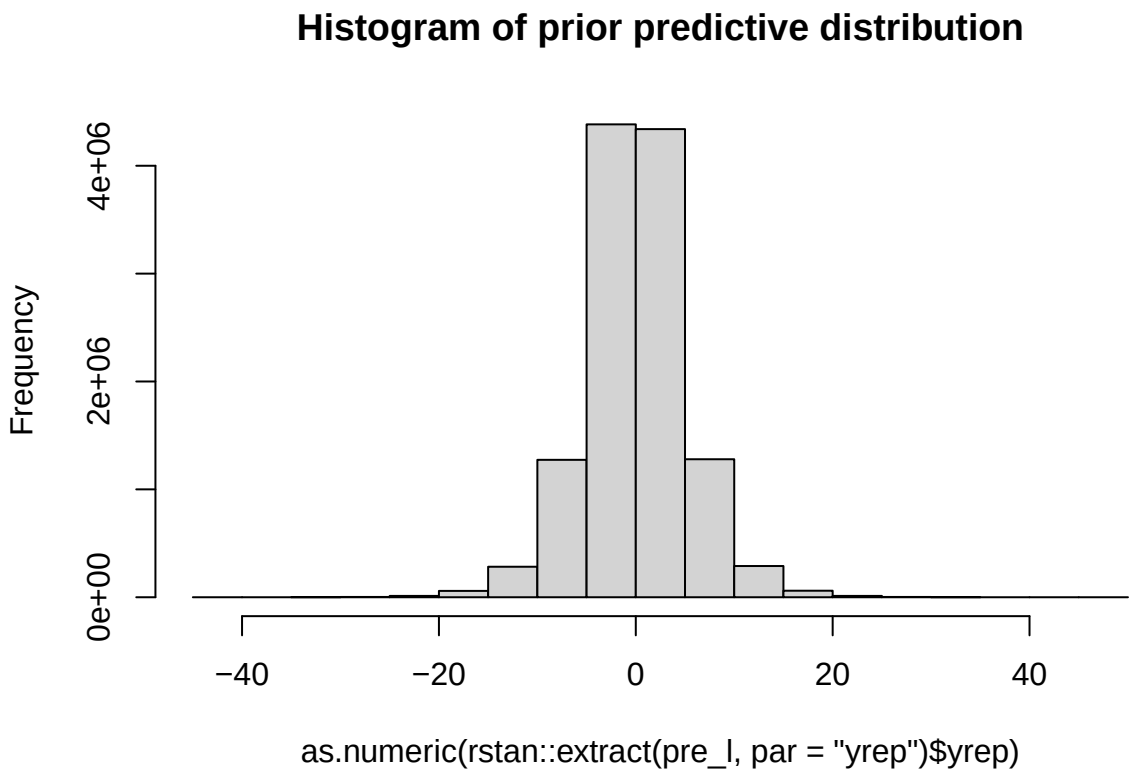
Linear model with log-transformed outcome

```
# set generic priors
m <- rep(0, 9)
s<- rep(1, 9)

stan_data$y <-  df_samp$l_incwage
stan_data$m <- m
stan_data$scale <- s
stan_data$prior_only = TRUE

pre_l <- stan("linear.stan", data = stan_data, seed = 12345)
```

```r
# print output
print(pre_l, pars = c("alpha", "beta", "sigma"))
```

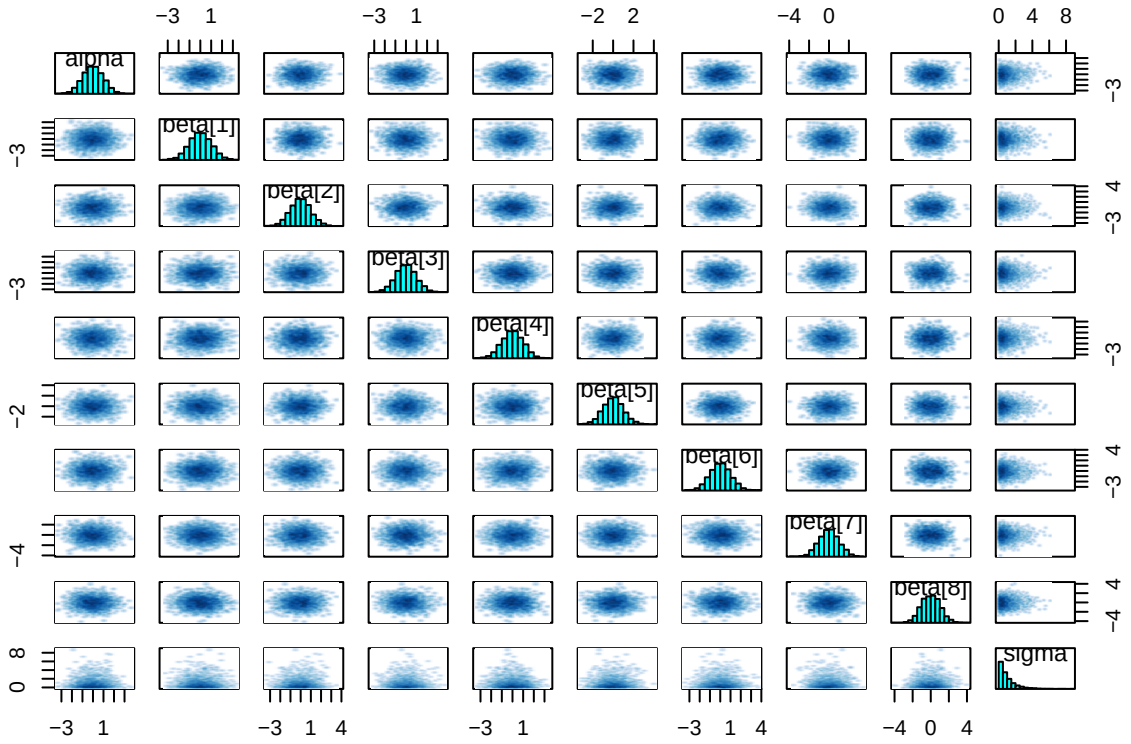
```
## Inference for Stan model: linear.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##          mean se_mean   sd  2.5%   25%   50%  75% 97.5% n_eff Rhat
## alpha    0.00    0.01 0.97 -1.89 -0.67  0.00 0.68  1.86  6371    1
## beta[1]  0.00    0.01 1.01 -1.97 -0.70  0.00 0.69  1.98  8306    1
## beta[2] -0.01    0.01 0.99 -1.95 -0.67 -0.01 0.64  1.98  7545    1
## beta[3]  0.00    0.01 0.97 -1.88 -0.65 -0.01 0.64  1.89  6362    1
## beta[4]  0.00    0.01 1.01 -1.99 -0.66  0.01 0.70  1.90  7275    1
## beta[5]  0.00    0.01 1.00 -1.95 -0.67  0.01 0.67  2.04  6800    1
## beta[6]  0.02    0.01 1.01 -1.96 -0.67  0.02 0.69  1.99  7851    1
## beta[7]  0.00    0.01 1.00 -1.92 -0.68  0.00 0.67  1.96  7598    1
## beta[8]  0.00    0.01 1.03 -1.98 -0.73  0.00 0.72  2.03  9306    1
## sigma    0.99    0.01 0.99  0.03  0.29  0.68 1.37  3.69  5330    1
##
## Samples were drawn using NUTS(diag_e) at Mon May 16 18:28:14 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

```r
hist(as.numeric(rstan::extract(pre_l, par = "yrep")$yrep),
     main = "Histogram of prior predictive distribution")
```



Since the outcome is now in log units, the prior predictive distribution is much narrower. It is still approximately normal.

```
pairs(pre_l, pars = c("alpha", "beta", "sigma"))
```



The prior marginal distributions for all parameters are approximately normal except for sigma, which is exponential.

```
loo_pre <- loo(pre_1)
```

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
```

```
loo_pre
```

```
##
## Computed from 4000 by 3000 log-likelihood matrix
##
##               Estimate             SE
## elpd_loo -5.499785e+12 105568780434.6
## p_loo     5.499785e+12 105568780378.4
## looic     1.099957e+13 211137560869.2
## ------
## Monte Carlo SE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##                            Count Pct.    Min. n_eff
## (-Inf, 0.5]   (good)         0    0.0%  <NA>
##  (0.5, 0.7]   (ok)           0    0.0%  <NA>
##    (0.7, 1]   (bad)          0    0.0%  <NA>
##    (1, Inf)   (very bad) 3000  100.0%  0
## See help('pareto-k-diagnostic') for details.
```

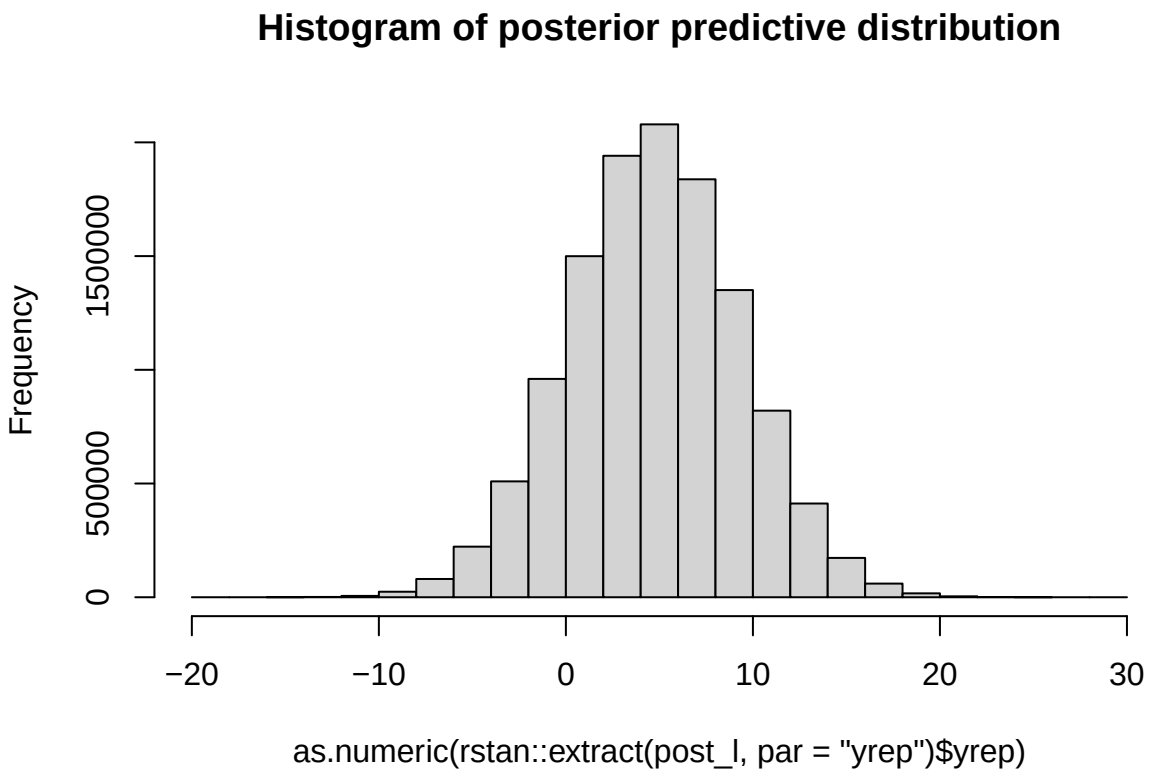
All 3,000 observations have Pareto K estimates > 0.7, which is an indication of outliers in the data and model specification.

```
stan_data$prior_only = FALSE
post_l <- stan("linear.stan", data = stan_data,
                                        seed = 12345)
# print output
print(post_l, pars = c("alpha", "beta", "sigma"))
```

```
## Inference for Stan model: linear.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##          mean se_mean   sd  2.5%   25%   50%   75% 97.5% n_eff Rhat
## alpha    5.14    0.00 0.16  4.83  5.03  5.14  5.25  5.45  3068    1
## beta[1] -1.50    0.00 0.17 -1.84 -1.62 -1.50 -1.38 -1.15  4196    1
## beta[2]  0.24    0.00 0.02  0.19  0.22  0.24  0.26  0.29  4394    1
## beta[3] -0.29    0.00 0.03 -0.35 -0.31 -0.29 -0.27 -0.23  4199    1
## beta[4]  0.09    0.00 0.16 -0.23 -0.02  0.09  0.20  0.41  3833    1
## beta[5] -0.04    0.00 0.16 -0.35 -0.14 -0.03  0.07  0.27  4104    1
## beta[6]  1.25    0.00 0.25  0.78  1.08  1.25  1.41  1.74  4042    1
## beta[7]  0.02    0.00 0.28 -0.52 -0.18  0.01  0.22  0.57  4571    1
## beta[8]  0.00    0.01 0.49 -0.95 -0.33  0.01  0.32  0.95  4287    1
## sigma    4.42    0.00 0.06  4.31  4.38  4.42  4.46  4.53  4483    1
##
## Samples were drawn using NUTS(diag_e) at Mon May 16 08:48:10 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

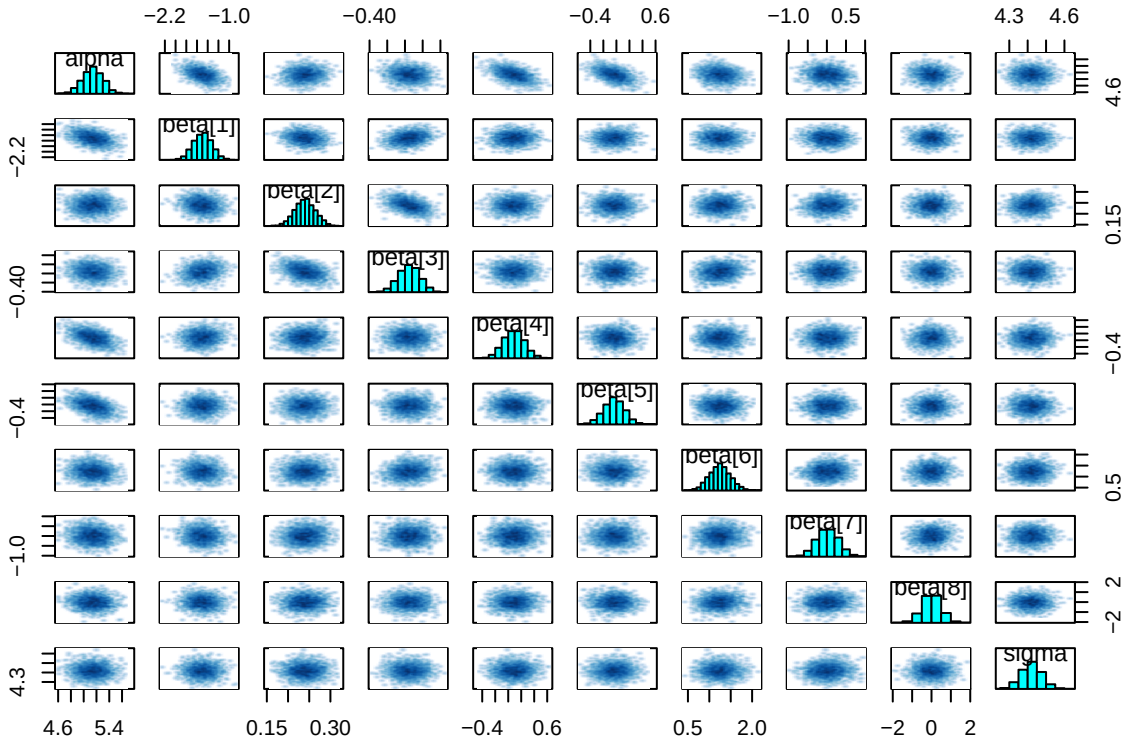
The stan output suggests that children have a negative effect on earnings, decreasing earnings by about 1.5 log units. If earnings were equal to log(10) (i.e., approximately \$22,000). This would be a decrease of around \$17,000, or about 77%.

```
hist(as.numeric(rstan::extract(post_l, par = "yrep")$yrep),
     main = "Histogram of posterior predictive distribution")
```



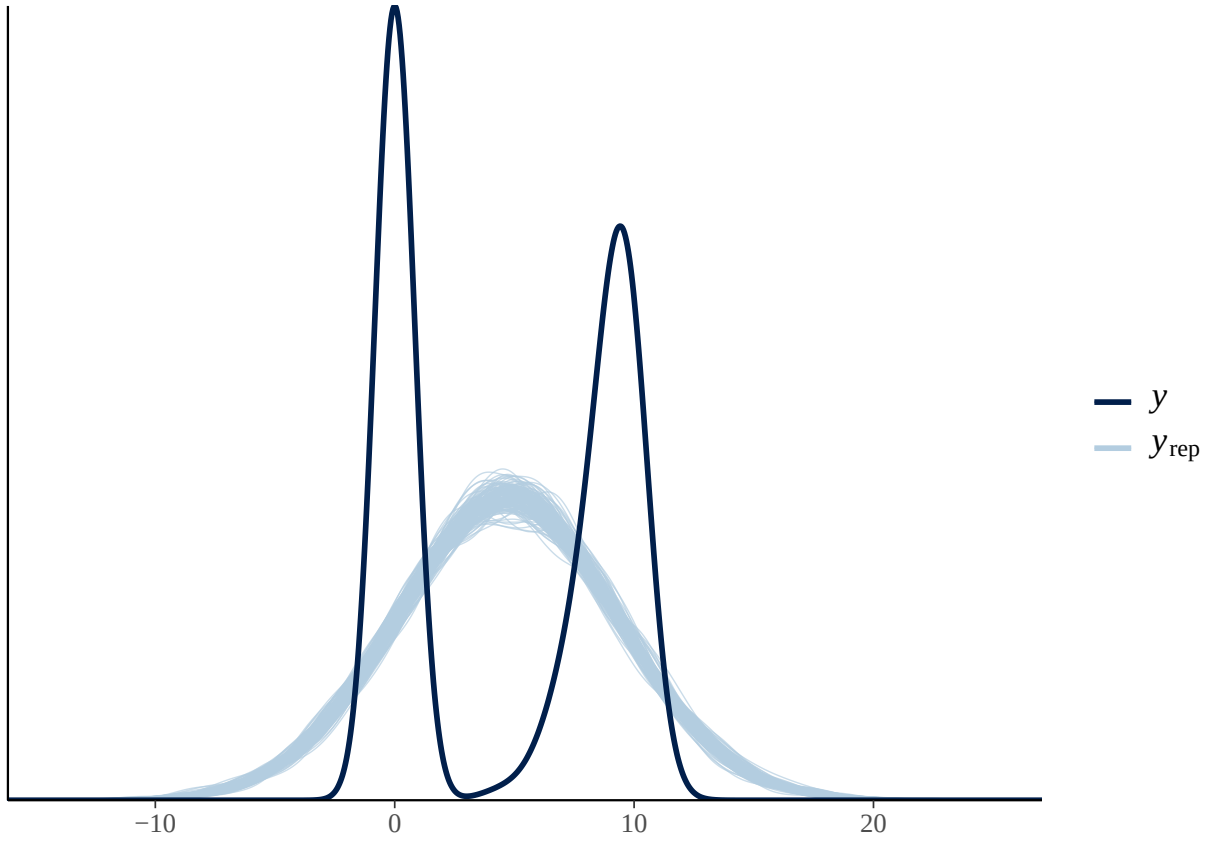
The negative values of the posterior predictive distribution are no longer impossible given the outcome is log-transformed. The distribution is approximately normal, although slightly skewed to the left.

```
pairs(post_l, pars = c("alpha", "beta", "sigma"))
```



The pairs plot shows some bivariate dependencies between `alpha` and `beta[1]` and `beta[4]` as well as between `beta[2]` and `beta[3]`. There are no divergent transitions and the marginal distributions of the parameters are approximately normal, with some skewness to the left or the right.

```
pp_check(as.numeric(stan_data$y),
  rstan::extract(post_l, par = "yrep")$yrep[sample(1:length(stan_data$y),
                                                   size = 150), ],
  ppc_dens_overlay
)
```



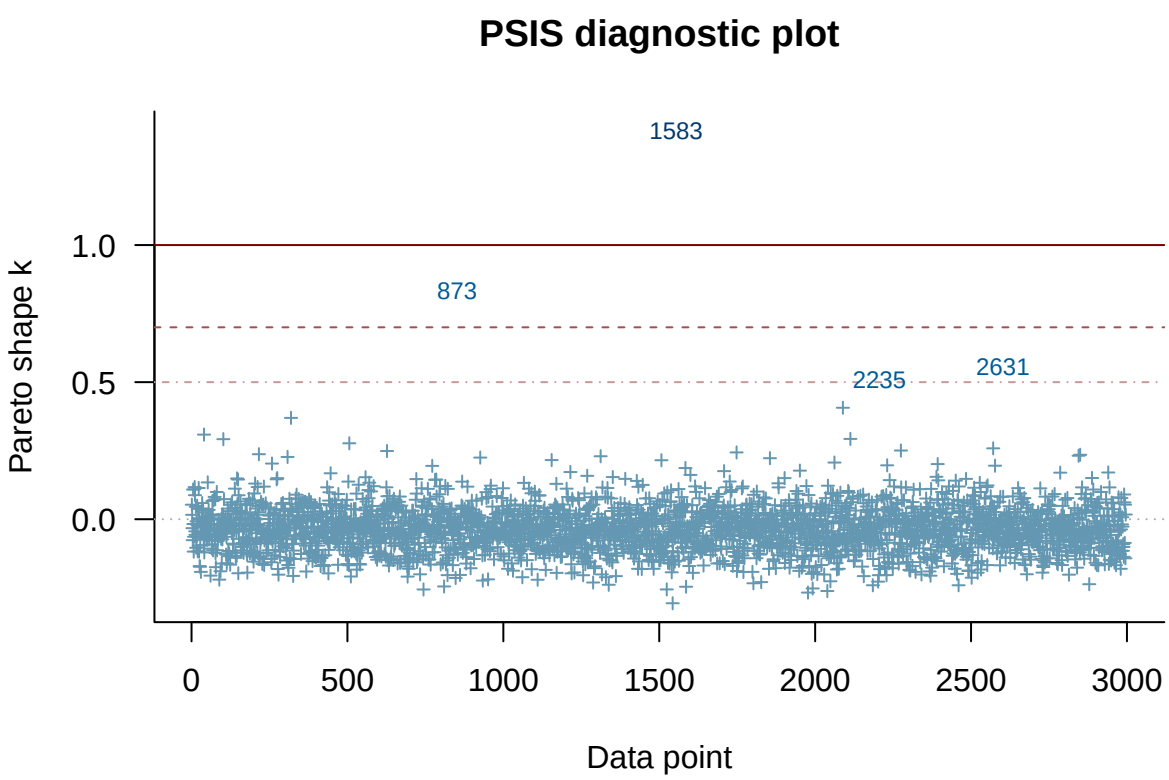
The observed values of y have two peaks: one closer to 0 and the other farther away. This demonstrates that there are likely two groups: those who do not work at all and those who are working already. Consequently, the posterior predictive distribution, which is still approximately normal, does not approximate the observed values of y as well. It tends to predict values of y that are in the middle of both peaks for the observed values of y.

```
loo_post <- loo(post_1)
loo_post
```

```
##
## Computed from 4000 by 3000 log-likelihood matrix
##
##          Estimate   SE
## elpd_loo  -8721.1 15.1
## p_loo         8.5  0.2
## looic     17442.3 30.1
## ------
## Monte Carlo SE of elpd_loo is 0.0.
##
## All Pareto k estimates are good (k < 0.5).
## See help('pareto-k-diagnostic') for details.
```

```
plot(loo(post), label_points = TRUE)
```

```
## Warning: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
```




```
loo_compare(loo_pre, loo_post)
```

```
##        elpd_diff     se_diff
## model2  0.000000e+00  0.000000e+00
## model1 -5.499785e+12  1.055688e+11
```

All Pareto k estimates are < 0.5, which means that importance sampling is able to estimate the `elpd_loo` with accuracy. Additionally, the `p_loo` is lower than for the priors.

The comparison of the prior and posterior models indicates that the posterior distribution is a better fit for the data in terms of the prediction.

Graphical models

- Graphical models provide a visual for understanding the difficulties with identifying causal effects, particularly with endogenous predictors like fertility.
- The DAG below illustrates the IV approach as outlined in Angrist and Evans' paper.

```
library(dagitty)
```

```
## Warning: package 'dagitty' was built under R version 4.1.3
```

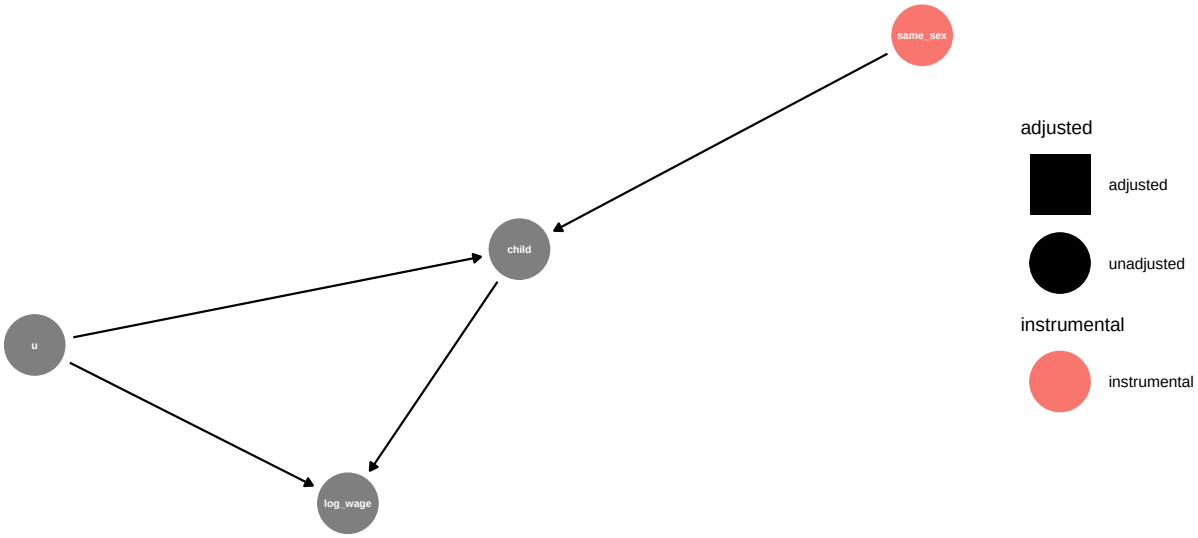
```
library(ggdag)
```

```
## Warning: package 'ggdag' was built under R version 4.1.3
```

```
##
## Attaching package: 'ggdag'
```

```
## The following object is masked from 'package:stats':
##
##     filter
```

```
# visualizing the instrumental variables problem
dagify(log_wage ~ child + u, child ~ same_sex + u, exposure = "child",
       outcome = "log_wage", latent = "u") %>%
  ggdag_instrumental(text_size = 2) + theme_void()
```



IV

- The likelihood function is based on 2.3 in the sampleSelection vignette

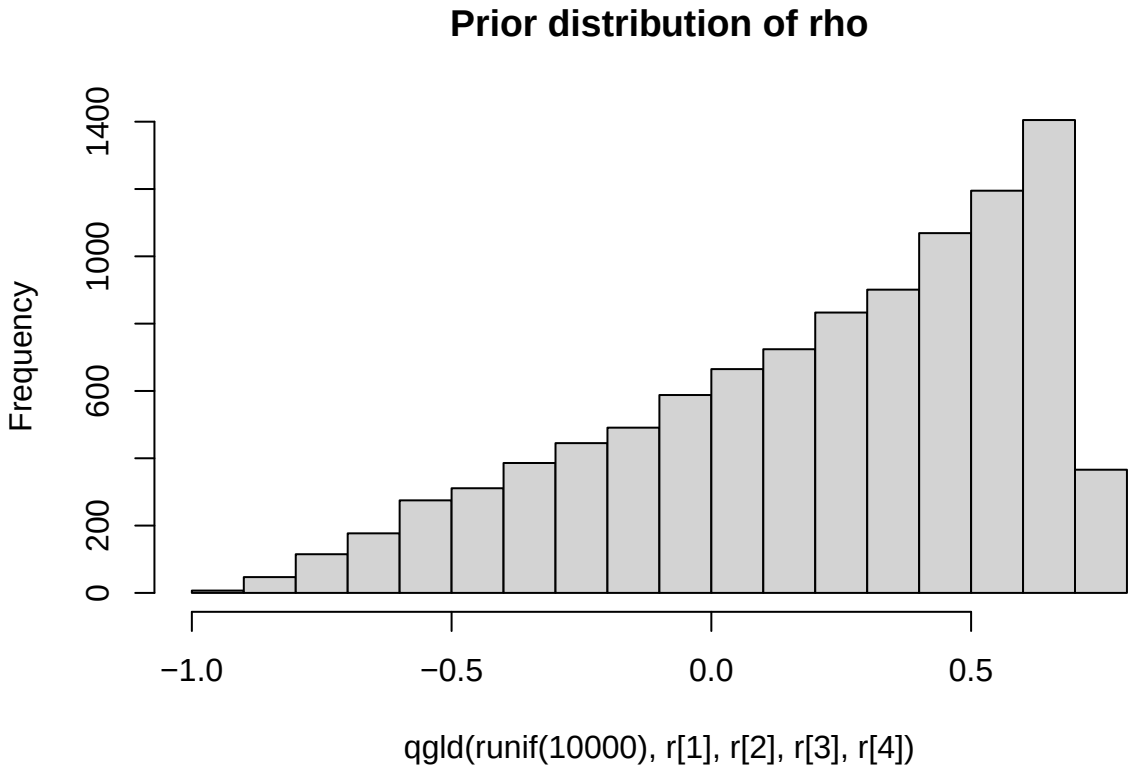
```
source(file.path("GLD_helpers.R"))
# set prior for rho with gld solver bounded
# allow rho to take on values between -1 and 1
a_s <- GLD_solver_bounded(bounds = -0.9:1, median = 0.3, IQR = 0.6)
```

```
## Warning in GLD_solver_bounded(bounds = -0.9:1, median = 0.3, IQR = 0.6): no asymmetry and steepness
## effective bounds are -0.939028894871395 and 0.722768561999757
```

```
r <- c(0.3, 0.6, a_s[1], a_s[2])
r
```

```
##                           asymmetry   steepness
##  0.30000000  0.60000000 -0.87521436  0.03133668
```

```
hist(qgld(runif(10000), r[1], r[2], r[3], r[4]),
     main = "Prior distribution of rho")
```




```
# display stan code
writeLines(readLines("iv_bin.stan"))
```

```
## #include quantile_functions.stan
## data {
##   int<lower = 0> N;
##   int<lower = 0> N_child;
##   int<lower = 0> N_nochild;
##   int<lower = 0> K; // number of predictors
##   matrix[N_child, K + 1] X_child_s;
##   matrix[N_nochild, K + 1] X_nochild_s;
##   matrix[N_child,  K] X_child;
##   matrix[N_nochild, K] X_nochild;
##   vector[N_child]  y_child;
##   vector[N_nochild] y_nochild;
##   int<lower = 0, upper = 1> prior_only;
##   vector[5] m;
##   vector<lower = 0>[5] scale;
##   vector[4] r;
```

```
## }
##
## parameters {
##   real<lower = 0> sigma;
##   real<lower = 0, upper = 1> p; // CDF for rho
##   real alpha0;
##   vector[K + 1] alpha1; // includes additional column for samesex pred
##   real beta0;
##   vector[K] beta1;
##   real beta2;
## }
##
## transformed parameters {
##   real<lower = -1, upper = 1> rho = gld_qf(p, r[1], r[2], r[3], r[4]);
##   vector[N_child]  mu_child  = beta0 + X_child*beta1 + beta2;
##   vector[N_nochild] mu_nochild = beta0 + X_nochild*beta1;
##   vector[N_child] eta_child = alpha0 + X_child_s * alpha1 +
##       rho / sigma * (y_child - mu_child);
##   vector[N_nochild] eta_nochild = alpha0 + X_nochild_s * alpha1 +
##       rho / sigma * (y_nochild - mu_nochild);
##
##   real conditional_sd = sqrt(1 - square(rho));
## }
##
## model {
##   if (!prior_only) {
##     target += normal_lpdf(y_child  | mu_child, sigma);
##     target += normal_lpdf(y_nochild | mu_nochild, sigma);
##
##     target += normal_lcdf(0 | -eta_child, conditional_sd);
##     target += normal_lcdf(0 | eta_nochild, conditional_sd);
##   }
##   target += normal_lpdf(alpha0  | m[1], scale[1]);
##   target += normal_lpdf(alpha1  | m[2], scale[2]);
##   target += normal_lpdf(beta0   | m[3], scale[3]);
##   target += normal_lpdf(beta1   | m[4], scale[4]);
##   target += normal_lpdf(beta2   | m[5], scale[5]);
##   target += gamma_lpdf(sigma | 2, 2);
## } // implicit: p ~ uniform(0, 1)
##
## generated quantities {
##   vector[N] log_lik;
##   int moves_rep[N];
##   vector[N] yrep;
##   real mu;
##   {
##     for (n in 1:N_child) {
##       log_lik[n] = normal_lpdf(y_child[n] | mu_child[n], sigma) +
##                    normal_lcdf(0 | -eta_child[n], conditional_sd);
##       mu = mu_child[n];
##
##       /* intermediate outcome: if they have an additional child */
##       moves_rep[n] = normal_rng(eta_child[n], conditional_sd) > 0;
##       if (moves_rep[n] == 0) mu -= beta2; // subtract beta if not
```

```
##       yrep[n] = normal_rng(mu, sigma); // sample outcome from new normal distribution
##     }
##
##     for (n in 1:N_nochild) {
##       log_lik[N_child + n] = normal_lpdf(y_nochild[n] | mu_nochild[n], sigma) +
##                         normal_lcdf(0 | eta_nochild[n], conditional_sd);
##       mu = mu_nochild[n];
##
##       /* intermediate outcome: if they have an additional child */
##       moves_rep[N_child + n] = normal_rng(eta_nochild[n], conditional_sd) > 0;
##       if (moves_rep[N_child + n] == 1) mu += beta2; // add beta if yes
##       yrep[N_child + n] = normal_rng(mu, sigma); // sample outcome from new normal distribution
##     }
##   }
## }
```

```
# subset the data
df_child <- df_samp %>%
  filter(cnum_mt2 == 1)

df_nochild <- df_samp %>%
  filter(cnum_mt2 == 0)

# reset covariates
cov <- c("age", "age_fbirth", "f_boy", "s_boy", "r_black", "hisp", "r_oth")

# set stan data
stan_data_iv <- list(N = nrow(df_samp),
                     N_child = nrow(df_child),
                     N_nochild = nrow(df_nochild),
                     K = 7,
                     X_child_s = df_child[, c("samesex", cov)],
                     X_nochild_s = df_nochild[, c("samesex", cov)],
                     X_child = df_child[, c(cov)],
                     X_nochild = df_nochild[, c(cov)],
                     y_child = df_child$l_incwage,
                     y_nochild = df_nochild$l_incwage,
                     prior_only = TRUE,
                     m = rep(-0.1, 5),
                     scale = rep(0.3, 5), r = r)
```

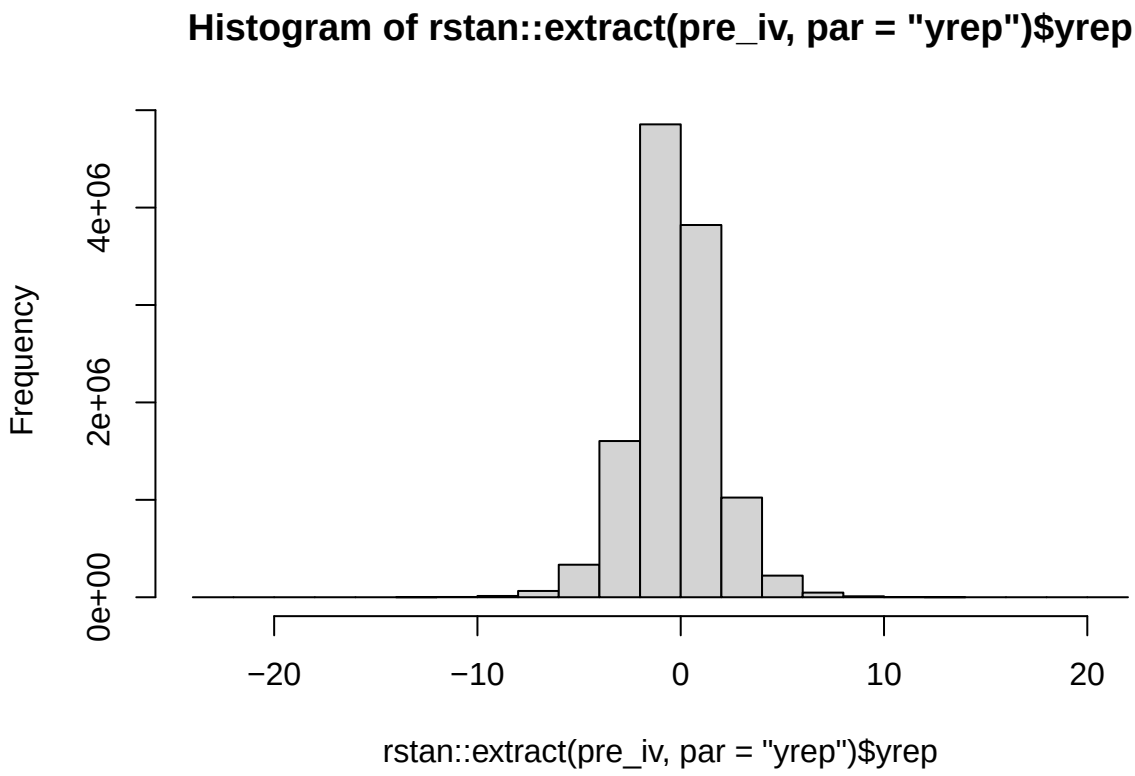
```
# call program without data for prior predictive checks
pre_iv <- stan("iv_bin.stan", data = stan_data_iv, seed = 1234)
print(pre_iv, pars =
        c("alpha0", "alpha1", "beta0", "beta1", "beta2", "sigma", "rho"))
```

```
## Inference for Stan model: iv_bin.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##            mean se_mean   sd  2.5%   25%   50%  75% 97.5% n_eff Rhat
## alpha0    -0.10    0.00 0.31 -0.72 -0.30 -0.10 0.10  0.50  8300    1
## alpha1[1] -0.10    0.00 0.30 -0.66 -0.30 -0.10 0.10  0.47  8472    1
```

```
## alpha1[2] -0.10    0.00 0.29 -0.66 -0.28 -0.10 0.09  0.48  9568    1
## alpha1[3] -0.10    0.00 0.30 -0.69 -0.30 -0.10 0.11  0.51  8857    1
## alpha1[4] -0.10    0.00 0.30 -0.70 -0.30 -0.10 0.09  0.48 10157    1
## alpha1[5] -0.10    0.00 0.31 -0.69 -0.30 -0.09 0.11  0.49  7979    1
## alpha1[6] -0.10    0.00 0.30 -0.71 -0.31 -0.10 0.11  0.48  8589    1
## alpha1[7] -0.10    0.00 0.29 -0.67 -0.29 -0.10 0.10  0.46  9680    1
## alpha1[8] -0.10    0.00 0.30 -0.70 -0.30 -0.11 0.10  0.49  7614    1
## beta0     -0.10    0.00 0.30 -0.68 -0.32 -0.11 0.11  0.48  9655    1
## beta1[1]  -0.10    0.00 0.30 -0.71 -0.30 -0.10 0.10  0.49  8619    1
## beta1[2]  -0.10    0.00 0.30 -0.69 -0.30 -0.10 0.09  0.49  8998    1
## beta1[3]  -0.10    0.00 0.30 -0.69 -0.31 -0.10 0.09  0.50  9737    1
## beta1[4]  -0.10    0.00 0.30 -0.69 -0.30 -0.11 0.10  0.50  8970    1
## beta1[5]  -0.10    0.00 0.30 -0.68 -0.29 -0.10 0.10  0.50  7880    1
## beta1[6]  -0.09    0.00 0.29 -0.66 -0.29 -0.09 0.10  0.48  8064    1
## beta1[7]  -0.10    0.00 0.29 -0.66 -0.30 -0.10 0.10  0.47  8828    1
## beta2     -0.10    0.00 0.30 -0.69 -0.31 -0.10 0.11  0.48  8796    1
## sigma      1.01    0.01 0.71  0.13  0.48  0.85 1.35  2.79  7311    1
## rho        0.21    0.01 0.39 -0.67 -0.06  0.29 0.54  0.71  6054    1
##
## Samples were drawn using NUTS(diag_e) at Mon May 16 18:38:29 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

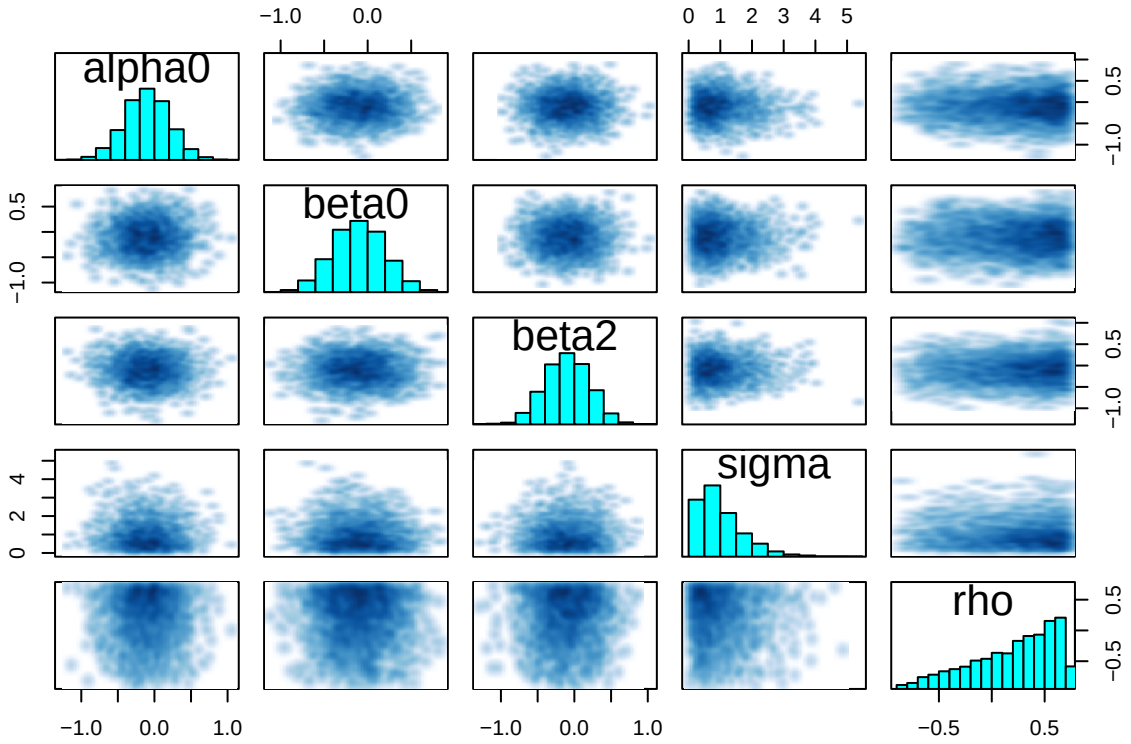
The draw from the prior distributions for the parameters make sense, given the priors.

```
hist(rstan::extract(pre_iv, par = "yrep")$yrep)
```



The predicted values of y seem reasonable. In log units they range from -10 to 10, which is approximately 0 to $22,000.

```
pairs(pre_iv, pars = c("alpha0", "beta0", "beta2", "sigma", "rho"))
```



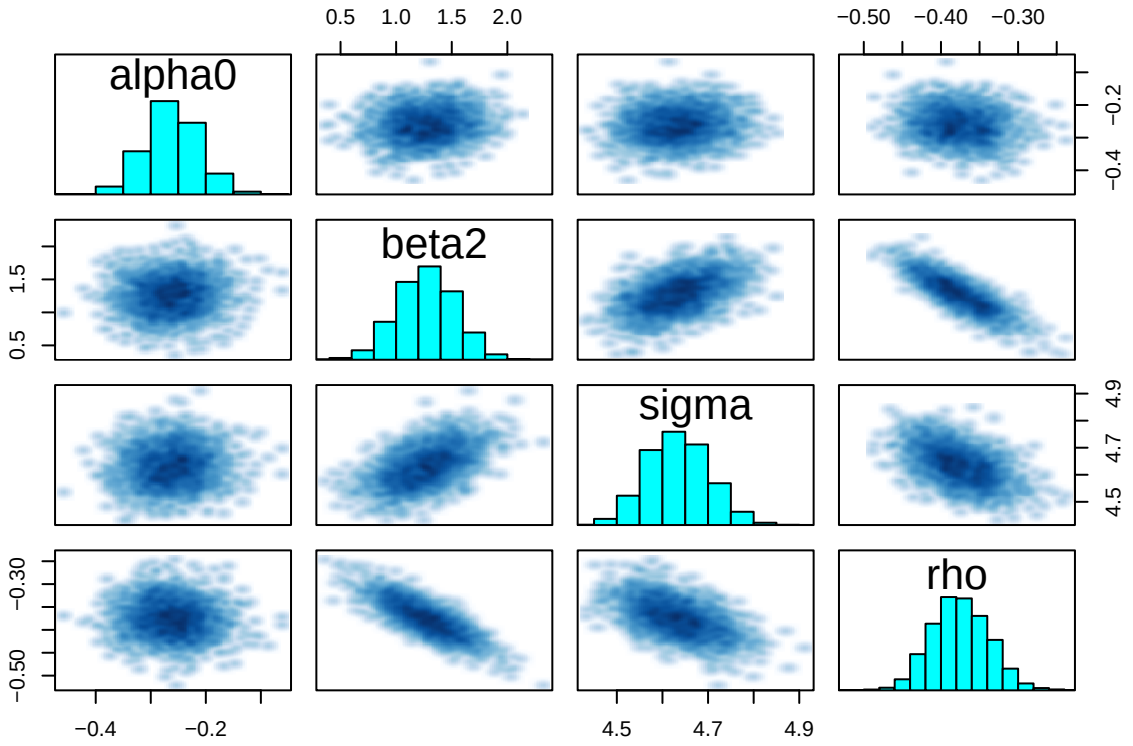
The bivariate plots are primarily blobs and show no bivariate dependence relationships. Except for sigma and rho, the marginal distributions are approximately normal.

```
stan_data_iv$prior_only <- FALSE

post_iv <- stan("iv_bin.stan", data = stan_data_iv, seed = 1234)
print(post_iv, pars = c("alpha0", "alpha1",
                        "beta0", "beta1", "beta2", "sigma", "rho"))
```

```
## Inference for Stan model: iv_bin.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##            mean se_mean   sd  2.5%   25%   50%   75% 97.5% n_eff Rhat
## alpha0    -0.26       0 0.05 -0.36 -0.29 -0.26 -0.23 -0.17  4243    1
## alpha1[1]  0.12       0 0.04  0.04  0.09  0.12  0.15  0.21  6630    1
## alpha1[2]  0.08       0 0.01  0.07  0.08  0.08  0.09  0.09  5977    1
## alpha1[3] -0.13       0 0.01 -0.15 -0.14 -0.13 -0.13 -0.11  5629    1
## alpha1[4] -0.17       0 0.05 -0.26 -0.20 -0.17 -0.14 -0.08  7702    1
## alpha1[5] -0.07       0 0.05 -0.17 -0.11 -0.07 -0.04  0.02  6079    1
## alpha1[6]  0.23       0 0.07  0.09  0.18  0.23  0.28  0.37  7567    1
## alpha1[7]  0.30       0 0.08  0.13  0.24  0.30  0.35  0.46  6755    1
## alpha1[8]  0.37       0 0.14  0.09  0.28  0.36  0.46  0.65  7746    1
## beta0      3.43       0 0.16  3.13  3.32  3.43  3.54  3.76  3432    1
## beta1[1]   0.16       0 0.03  0.11  0.14  0.16  0.18  0.21  4796    1
## beta1[2]  -0.17       0 0.03 -0.23 -0.19 -0.17 -0.14 -0.10  4889    1
```

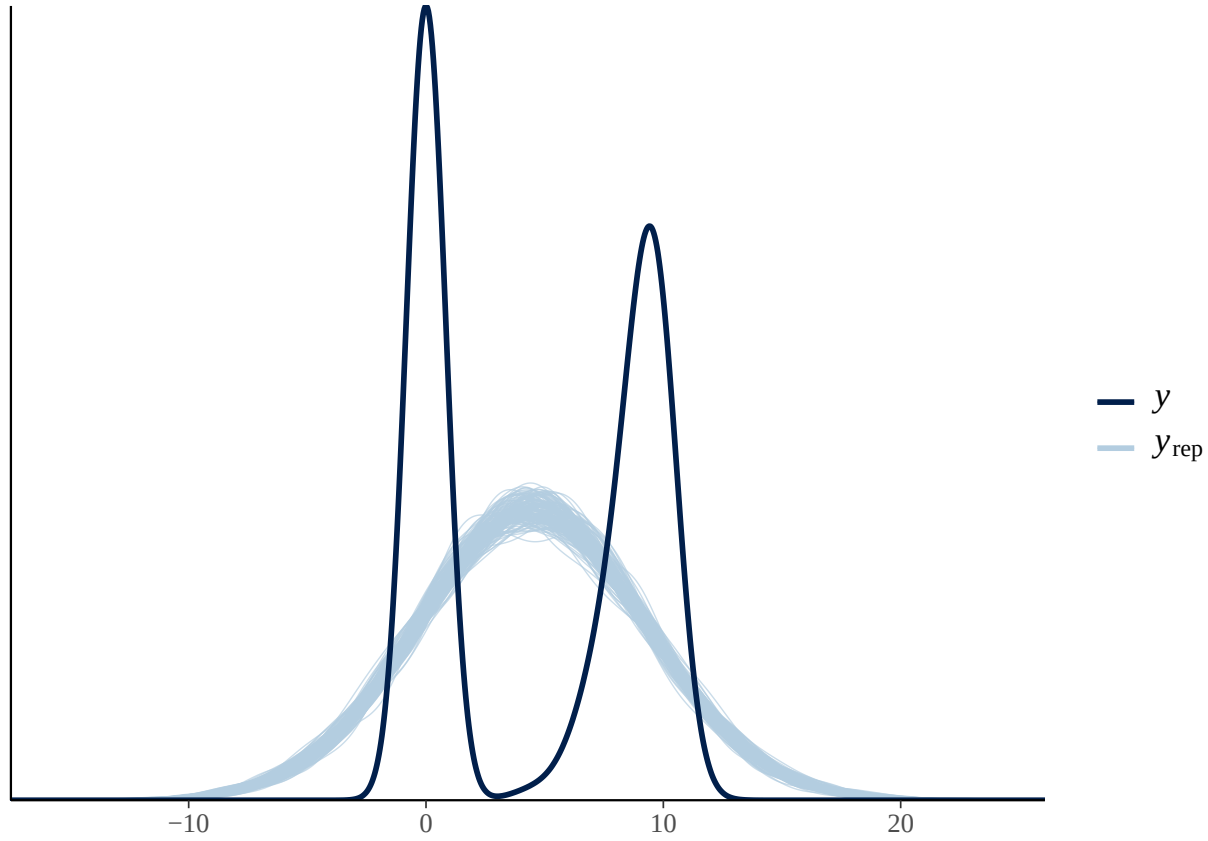
```
## beta1[3]    0.52       0 0.14  0.23  0.42  0.51  0.61  0.79  7008    1
## beta1[4]    0.37       0 0.14  0.10  0.27  0.37  0.46  0.63  5310    1
## beta1[5]    0.75       0 0.20  0.37  0.62  0.75  0.89  1.15  6017    1
## beta1[6]   -0.07       0 0.21 -0.49 -0.22 -0.07  0.07  0.34  7809    1
## beta1[7]   -0.11       0 0.27 -0.63 -0.28 -0.11  0.07  0.43  7620    1
## beta2       1.27       0 0.26  0.76  1.09  1.27  1.45  1.77  2903    1
## sigma       4.63       0 0.07  4.51  4.59  4.63  4.68  4.77  3933    1
## rho        -0.38       0 0.04 -0.44 -0.40 -0.38 -0.35 -0.30  3034    1
##
## Samples were drawn using NUTS(diag_e) at Mon May 16 20:29:44 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

```
pairs(post_iv, pars = c("alpha0", "beta2", "sigma", "rho"))
```



There is a linear trend between `beta2` and `rho`. However, it has not impacted the sampling as there are no divergent transitions or other warnings. There are no funnel shapes or other irregularities that would be cause for concern.

```
pp_check(c(as.numeric(stan_data_iv$y_child),
           as.numeric(stan_data_iv$y_nochild)),
  rstan::extract(post_iv, par = "yrep")$yrep[sample(1:nrow(df_samp),
                                                    size = 150), ],
  ppc_dens_overlay
)
```




```
loo_post_iv <- loo(post_iv)
loo_post_iv
```

```
##
## Computed from 4000 by 3000 log-likelihood matrix
##
##          Estimate   SE
## elpd_loo -10597.5 23.1
## p_loo        15.0  0.2
## looic     21195.0 46.2
## ------
## Monte Carlo SE of elpd_loo is 0.0.
##
## All Pareto k estimates are good (k < 0.5).
## See help('pareto-k-diagnostic') for details.
```

Re-run with weeks worked outcome

```
# set stan data
stan_data_iv <- list(N = nrow(df_samp),
                     N_child = nrow(df_child),
                     N_nochild = nrow(df_nochild),
                     K = 7,
```

```
                  X_child_s = df_child[, c("samesex", cov)],
                  X_nochild_s = df_nochild[, c("samesex", cov)],
                  X_child = df_child[, c(cov)],
                  X_nochild = df_nochild[, c(cov)],
                  y_child = df_child$wkswork1,
                  y_nochild = df_nochild$wkswork1,
                  prior_only = FALSE,
                  m = rep(-0.1, 5),
                  scale = rep(1, 5), r = r)

post_iv_wk <- stan("iv_bin.stan", data = stan_data_iv, seed = 1234)
print(post_iv_wk, pars = c("alpha0", "alpha1",
                           "beta0", "beta1", "beta2", "sigma", "rho"))
```

```
## Inference for Stan model: iv_bin.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##            mean se_mean   sd  2.5%   25%   50%   75% 97.5% n_eff Rhat
## alpha0    -0.26    0.00 0.05 -0.36 -0.29 -0.26 -0.22 -0.17  4658    1
## alpha1[1]  0.13    0.00 0.05  0.04  0.10  0.13  0.16  0.22  6389    1
## alpha1[2]  0.08    0.00 0.01  0.07  0.08  0.08  0.09  0.10  5697    1
## alpha1[3] -0.13    0.00 0.01 -0.15 -0.14 -0.13 -0.13 -0.11  6230    1
## alpha1[4] -0.18    0.00 0.05 -0.27 -0.21 -0.18 -0.15 -0.09  6125    1
## alpha1[5] -0.08    0.00 0.05 -0.18 -0.11 -0.08 -0.05  0.01  5624    1
## alpha1[6]  0.27    0.00 0.07  0.13  0.22  0.27  0.32  0.42  7011    1
## alpha1[7]  0.32    0.00 0.08  0.16  0.27  0.32  0.38  0.49  7067    1
## alpha1[8]  0.51    0.00 0.16  0.20  0.40  0.50  0.61  0.81  8320    1
## beta0     12.93    0.01 0.61 11.74 12.51 12.94 13.36 14.11  4648    1
## beta1[1]   1.02    0.00 0.13  0.77  0.93  1.02  1.11  1.27  5987    1
## beta1[2]  -0.77    0.00 0.15 -1.06 -0.87 -0.77 -0.67 -0.48  5608    1
## beta1[3]   3.17    0.01 0.63  1.91  2.75  3.18  3.59  4.43  6561    1
## beta1[4]   2.51    0.01 0.61  1.33  2.11  2.52  2.91  3.71  6310    1
## beta1[5]   3.17    0.01 0.81  1.58  2.63  3.18  3.70  4.80  6091    1
## beta1[6]  -0.08    0.01 0.81 -1.72 -0.61 -0.07  0.46  1.49  7362    1
## beta1[7]   0.05    0.01 0.95 -1.82 -0.59  0.05  0.69  1.90  7081    1
## beta2      5.29    0.01 0.92  3.48  4.68  5.29  5.90  7.09  3891    1
## sigma     22.45    0.00 0.32 21.85 22.24 22.45 22.66 23.09  5369    1
## rho       -0.36    0.00 0.03 -0.42 -0.38 -0.36 -0.34 -0.29  3880    1
##
## Samples were drawn using NUTS(diag_e) at Mon May 16 20:42:18 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

Re-run two-stage model for college subgroup

```
# subset the data
df_samp2 <- df %>%
  filter(coll == 1) %>%
  sample_n(3000) %>%
```

```
  mutate(across(c("age", "age_fbirth"), ~ . - mean(., na.rm = T))) %>%
  mutate(l_incwage = if_else(incwage <= 0, log(1), log(incwage)),
         l_wkswork1 = if_else(wkswork1 <= 0, log(1), log(wkswork1)))

df_child <- df_samp2 %>%
  filter(cnum_mt2 == 1)

df_nochild <- df_samp2 %>%
  filter(cnum_mt2 == 0)

# set stan data
stan_data_iv <- list(N = nrow(df_samp2),
                     N_child = nrow(df_child),
                     N_nochild = nrow(df_nochild),
                     K = 7,
                     X_child_s = df_child[, c("samesex", cov)],
                     X_nochild_s = df_nochild[, c("samesex", cov)],
                     X_child = df_child[, c(cov)],
                     X_nochild = df_nochild[, c(cov)],
                     y_child = df_child$l_incwage,
                     y_nochild = df_nochild$l_incwage,
                     prior_only = FALSE,
                     m = rep(-0.1, 5),
                     scale = rep(0.3, 5), r = r)

post_iv_coll <- stan("iv_bin.stan", data = stan_data_iv, seed = 1234)
print(post_iv_coll, pars = c("alpha0", "alpha1",
                             "beta0", "beta1", "beta2", "sigma", "rho"))
```

```
## Inference for Stan model: iv_bin.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##            mean se_mean   sd  2.5%   25%   50%   75% 97.5% n_eff Rhat
## alpha0    -0.47       0 0.05 -0.57 -0.50 -0.47 -0.44 -0.38  4329    1
## alpha1[1]  0.10       0 0.05  0.01  0.07  0.10  0.13  0.19  6511    1
## alpha1[2]  0.08       0 0.01  0.06  0.07  0.08  0.08  0.10  5957    1
## alpha1[3] -0.11       0 0.01 -0.12 -0.11 -0.11 -0.10 -0.09  6800    1
## alpha1[4] -0.05       0 0.05 -0.15 -0.09 -0.05 -0.02  0.04  6218    1
## alpha1[5]  0.01       0 0.05 -0.08 -0.02  0.01  0.05  0.10  7010    1
## alpha1[6]  0.03       0 0.08 -0.13 -0.03  0.03  0.08  0.18  6707    1
## alpha1[7]  0.09       0 0.11 -0.12  0.01  0.09  0.16  0.30  9768    1
## alpha1[8] -0.04       0 0.12 -0.29 -0.13 -0.04  0.04  0.20  8046    1
## beta0      4.17       0 0.15  3.89  4.06  4.17  4.26  4.46  3497    1
## beta1[1]   0.16       0 0.03  0.10  0.14  0.16  0.18  0.22  5149    1
## beta1[2]  -0.26       0 0.03 -0.31 -0.28 -0.26 -0.24 -0.20  5079    1
## beta1[3]   0.28       0 0.14  0.00  0.19  0.28  0.38  0.57  6574    1
## beta1[4]   0.44       0 0.14  0.17  0.35  0.45  0.54  0.72  5671    1
## beta1[5]   1.24       0 0.21  0.82  1.10  1.24  1.38  1.65  8341    1
## beta1[6]   0.14       0 0.25 -0.34 -0.02  0.14  0.30  0.62  8385    1
## beta1[7]   0.22       0 0.25 -0.28  0.06  0.22  0.39  0.72  8046    1
## beta2      1.04       0 0.26  0.52  0.87  1.05  1.22  1.55  3156    1
## sigma      4.57       0 0.07  4.44  4.52  4.57  4.62  4.71  4150    1
```

```
## rho       -0.39       0 0.04 -0.46 -0.42 -0.39 -0.37 -0.31  3186    1
##
## Samples were drawn using NUTS(diag_e) at Mon May 16 20:47:55 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

Frequentist example (for reference)

```
# output using the sample
# outcome is log wage
twostage_fit <- treatReg(
selection = cnum_mt2 ~ samesex + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
outcome = l_incwage ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
data = df_samp
)
summary(twostage_fit)
```

```
## --------------------------------------------
## Tobit treatment model (switching regression model)
## Maximum Likelihood estimation
## Newton-Raphson maximisation, 3 iterations
## Return code 8: successive function values within relative tolerance limit (reltol)
## Log-Likelihood: -10567.72
## 3000 observations: 1808 non-participants (selection 0) and 1192 participants (selection 1)
##
## 20 free parameters (df = 2980)
## Probit selection equation:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.339548   0.050289  -6.752 1.75e-11 ***
## samesex      0.146264   0.049109   2.978 0.002921 **
## age          0.081076   0.007319  11.077  < 2e-16 ***
## age_fbirth  -0.132303   0.009109 -14.524  < 2e-16 ***
## f_boy       -0.136818   0.048226  -2.837 0.004585 **
## s_boy       -0.041062   0.048317  -0.850 0.395474
## r_black      0.232856   0.074290   3.134 0.001739 **
## hisp         0.358673   0.087225   4.112 4.03e-05 ***
## r_oth        0.533439   0.161498   3.303 0.000968 ***
## Outcome equation:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.84718    0.80165   6.047 1.66e-09 ***
## cnum_mt2    -0.52134    1.95110  -0.267 0.789330
## age          0.21123    0.06201   3.406 0.000667 ***
## age_fbirth  -0.24230    0.09490  -2.553 0.010721 *
## f_boy        0.06666    0.18468   0.361 0.718169
## s_boy       -0.08369    0.16570  -0.505 0.613539
## r_black      1.19006    0.30784   3.866 0.000113 ***
## hisp        -0.13850    0.38704  -0.358 0.720477
## r_oth       -0.21774    0.67182  -0.324 0.745885
##    Error terms:
##       Estimate Std. Error t value Pr(>|t|)
## sigma   4.4436     0.1182  37.603   <2e-16 ***
```

```
## rho    -0.1500     0.2640  -0.568     0.57
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## --------------------------------------------
```

```
# outcome is incwage
twostage_fit <- treatReg(
selection = cnum_mt2 ~ samesex + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
outcome = incwage ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
data = df_samp
)
summary(twostage_fit)
```

```
## --------------------------------------------
## Tobit treatment model (switching regression model)
## Maximum Likelihood estimation
## Newton-Raphson maximisation, 14 iterations
## Return code 8: successive function values within relative tolerance limit (reltol)
## Log-Likelihood: -33697.15
## 3000 observations: 1808 non-participants (selection 0) and 1192 participants (selection 1)
##
## 20 free parameters (df = 2980)
## Probit selection equation:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.297627   0.046299  -6.428  1.5e-10 ***
## samesex      0.115191   0.036460   3.159 0.001597 **
## age          0.071116   0.007091  10.028  < 2e-16 ***
## age_fbirth  -0.123429   0.008708 -14.175  < 2e-16 ***
## f_boy       -0.151919   0.046287  -3.282 0.001042 **
## s_boy       -0.054922   0.046272  -1.187 0.235349
## r_black      0.173898   0.073363   2.370 0.017834 *
## hisp         0.321245   0.085154   3.773 0.000165 ***
## r_oth        0.436578   0.160011   2.728 0.006401 **
## Outcome equation:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1357.36     494.52   2.745  0.00609 **
## cnum_mt2    12102.63     670.16  18.059  < 2e-16 ***
## age           121.20      71.09   1.705  0.08831 .
## age_fbirth    272.96      87.12   3.133  0.00175 **
## f_boy         705.57     453.91   1.554  0.12019
## s_boy         283.06     452.86   0.625  0.53198
## r_black      2221.94     714.83   3.108  0.00190 **
## hisp        -1454.92     832.00  -1.749  0.08045 .
## r_oth       -1014.44    1561.98  -0.649  0.51610
##    Error terms:
##         Estimate Std. Error t value Pr(>|t|)
## sigma  1.238e+04  2.421e+02   51.12   <2e-16 ***
## rho   -7.848e-01  1.758e-02  -44.65   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## --------------------------------------------
```

```r
# outcome is incwage
twostage_fit <- treatReg(
selection = cnum_mt2 ~ samesex + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
outcome = incwage ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
data = df_samp
)
summary(twostage_fit)
```

```
## --------------------------------------------
## Tobit treatment model (switching regression model)
## Maximum Likelihood estimation
## Newton-Raphson maximisation, 14 iterations
## Return code 8: successive function values within relative tolerance limit (reltol)
## Log-Likelihood: -33697.15
## 3000 observations: 1808 non-participants (selection 0) and 1192 participants (selection 1)
##
## 20 free parameters (df = 2980)
## Probit selection equation:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.297627   0.046299  -6.428  1.5e-10 ***
## samesex      0.115191   0.036460   3.159 0.001597 **
## age          0.071116   0.007091  10.028  < 2e-16 ***
## age_fbirth  -0.123429   0.008708 -14.175  < 2e-16 ***
## f_boy       -0.151919   0.046287  -3.282 0.001042 **
## s_boy       -0.054922   0.046272  -1.187 0.235349
## r_black      0.173898   0.073363   2.370 0.017834 *
## hisp         0.321245   0.085154   3.773 0.000165 ***
## r_oth        0.436578   0.160011   2.728 0.006401 **
## Outcome equation:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1357.36     494.52   2.745  0.00609 **
## cnum_mt2    12102.63     670.16  18.059  < 2e-16 ***
## age           121.20      71.09   1.705  0.08831 .
## age_fbirth    272.96      87.12   3.133  0.00175 **
## f_boy         705.57     453.91   1.554  0.12019
## s_boy         283.06     452.86   0.625  0.53198
## r_black      2221.94     714.83   3.108  0.00190 **
## hisp        -1454.92     832.00  -1.749  0.08045 .
## r_oth       -1014.44    1561.98  -0.649  0.51610
##    Error terms:
##         Estimate Std. Error t value Pr(>|t|)
## sigma  1.238e+04  2.421e+02   51.12   <2e-16 ***
## rho   -7.848e-01  1.758e-02  -44.65   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## --------------------------------------------
```

```r
## outcome is weeks worked
twostage_fit <- treatReg(
  selection = cnum_mt2 ~ samesex + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
  outcome = wkswork1 ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
  data = df_samp
)
```

```
summary(twostage_fit)
```

```
## --------------------------------------------
## Tobit treatment model (switching regression model)
## Maximum Likelihood estimation
## Newton-Raphson maximisation, 5 iterations
## Return code 8: successive function values within relative tolerance limit (reltol)
## Log-Likelihood: -15321.01
## 3000 observations: 1808 non-participants (selection 0) and 1192 participants (selection 1)
##
## 20 free parameters (df = 2980)
## Probit selection equation:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.341321   0.050105  -6.812 1.16e-11 ***
## samesex      0.152167   0.047691   3.191  0.00143 **
## age          0.080980   0.007329  11.049  < 2e-16 ***
## age_fbirth  -0.131915   0.009128 -14.451  < 2e-16 ***
## f_boy       -0.131687   0.048258  -2.729  0.00639 **
## s_boy       -0.046461   0.048283  -0.962  0.33600
## r_black      0.233100   0.074208   3.141  0.00170 **
## hisp         0.355926   0.087030   4.090 4.43e-05 ***
## r_oth        0.526677   0.160625   3.279  0.00105 **
## Outcome equation:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  25.60241    5.08082   5.039 4.96e-07 ***
## cnum_mt2    -14.69935   12.45436  -1.180  0.23799
## age           1.60771    0.38286   4.199 2.76e-05 ***
## age_fbirth   -1.65273    0.59381  -2.783  0.00542 **
## f_boy         0.06335    0.97283   0.065  0.94808
## s_boy        -0.48786    0.82204  -0.593  0.55291
## r_black       7.48252    1.66266   4.500 7.04e-06 ***
## hisp          0.34884    2.15017   0.162  0.87113
## r_oth         2.99973    3.62649   0.827  0.40821
##    Error terms:
##       Estimate Std. Error t value Pr(>|t|)
## sigma  21.7586     0.8857  24.568   <2e-16 ***
## rho     0.1910     0.3418   0.559    0.576
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## --------------------------------------------
```

```
# output using full data
# outcome is log wage
twostage_fit <- treatReg(
selection = cnum_mt2 ~ samesex + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
outcome = l_incwage ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
data = df_samp
)
summary(twostage_fit)
```

```
## --------------------------------------------
## Tobit treatment model (switching regression model)
```

```
## Maximum Likelihood estimation
## Newton-Raphson maximisation, 3 iterations
## Return code 8: successive function values within relative tolerance limit (reltol)
## Log-Likelihood: -10567.72
## 3000 observations: 1808 non-participants (selection 0) and 1192 participants (selection 1)
##
## 20 free parameters (df = 2980)
## Probit selection equation:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.339548   0.050289  -6.752 1.75e-11 ***
## samesex      0.146264   0.049109   2.978 0.002921 **
## age          0.081076   0.007319  11.077  < 2e-16 ***
## age_fbirth  -0.132303   0.009109 -14.524  < 2e-16 ***
## f_boy       -0.136818   0.048226  -2.837 0.004585 **
## s_boy       -0.041062   0.048317  -0.850 0.395474
## r_black      0.232856   0.074290   3.134 0.001739 **
## hisp         0.358673   0.087225   4.112 4.03e-05 ***
## r_oth        0.533439   0.161498   3.303 0.000968 ***
## Outcome equation:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.84718    0.80165   6.047 1.66e-09 ***
## cnum_mt2    -0.52134    1.95110  -0.267 0.789330
## age          0.21123    0.06201   3.406 0.000667 ***
## age_fbirth  -0.24230    0.09490  -2.553 0.010721 *
## f_boy        0.06666    0.18468   0.361 0.718169
## s_boy       -0.08369    0.16570  -0.505 0.613539
## r_black      1.19006    0.30784   3.866 0.000113 ***
## hisp        -0.13850    0.38704  -0.358 0.720477
## r_oth       -0.21774    0.67182  -0.324 0.745885
##    Error terms:
##       Estimate Std. Error t value Pr(>|t|)
## sigma   4.4436     0.1182  37.603   <2e-16 ***
## rho    -0.1500     0.2640  -0.568     0.57
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## --------------------------------------------
```

```
# outcome is incwage
twostage_fit <- treatReg(
selection = cnum_mt2 ~ samesex + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
outcome = incwage ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
data = df
)
summary(twostage_fit)
```

```
## --------------------------------------------
## Tobit treatment model (switching regression model)
## Maximum Likelihood estimation
## Newton-Raphson maximisation, 2 iterations
## Return code 8: successive function values within relative tolerance limit (reltol)
## Log-Likelihood: -4430972
## 393424 observations: 235996 non-participants (selection 0) and 157428 participants (selection 1)
##
## 20 free parameters (df = 393404)
```

```
## Probit selection equation:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.46665        Inf       0        1
## samesex      0.16728        Inf       0        1
## age          0.08736        Inf       0        1
## age_fbirth  -0.12399        Inf       0        1
## f_boy       -0.02370        Inf       0        1
## s_boy       -0.02166        Inf       0        1
## r_black      0.22249        Inf       0        1
## hisp         0.39007        Inf       0        1
## r_oth        0.20072        Inf       0        1
## Outcome equation:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1877.92        Inf       0        1
## cnum_mt2    -4732.90        Inf       0        1
## age           656.17        Inf       0        1
## age_fbirth   -467.49        Inf       0        1
## f_boy         -59.73        Inf       0        1
## s_boy         -56.46        Inf       0        1
## r_black      4035.09        Inf       0        1
## hisp          668.99        Inf       0        1
## r_oth        2545.61        Inf       0        1
##    Error terms:
##        Estimate Std. Error t value Pr(>|t|)
## sigma 1.011e+04        Inf       0        1
## rho   6.626e-02        Inf       0        1
## --------------------------------------------
```

```
## outcome is weeks worked
twostage_fit <- treatReg(
  selection = cnum_mt2 ~ samesex + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
  outcome = wkswork1 ~ cnum_mt2 + age + age_fbirth + f_boy + s_boy + r_black + hisp + r_oth,
  data = df
)
summary(twostage_fit)
```

```
## --------------------------------------------
## Tobit treatment model (switching regression model)
## Maximum Likelihood estimation
## Newton-Raphson maximisation, 5 iterations
## Return code 8: successive function values within relative tolerance limit (reltol)
## Log-Likelihood: -2007688
## 393424 observations: 235996 non-participants (selection 0) and 157428 participants (selection 1)
##
## 20 free parameters (df = 393404)
## Probit selection equation:
##               Estimate Std. Error  t value Pr(>|t|)
## (Intercept) -0.4576671  0.0201526  -22.710  < 2e-16 ***
## samesex      0.1545277  0.0043312   35.678  < 2e-16 ***
## age          0.0874500  0.0006507  134.392  < 2e-16 ***
## age_fbirth  -0.1243074  0.0007832 -158.727  < 2e-16 ***
## f_boy       -0.0233507  0.0041711   -5.598 2.17e-08 ***
## s_boy       -0.0215013  0.0041710   -5.155 2.54e-07 ***
## r_black      0.2233266  0.0064154   34.811  < 2e-16 ***
```

```
## hisp         0.3885330  0.0076323   50.906  < 2e-16 ***
## r_oth        0.2003231  0.0134156   14.932  < 2e-16 ***
## Outcome equation:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  11.15897    0.43660  25.559  < 2e-16 ***
## cnum_mt2    -20.96142    0.82311 -25.466  < 2e-16 ***
## age           1.87335    0.02838  66.009  < 2e-16 ***
## age_fbirth   -1.90350    0.03865 -49.247  < 2e-16 ***
## f_boy        -0.22988    0.07073  -3.250 0.001153 **
## s_boy        -0.27325    0.07068  -3.866 0.000111 ***
## r_black       7.19897    0.12977  55.476  < 2e-16 ***
## hisp          1.27515    0.17567   7.259 3.91e-13 ***
## r_oth         3.59341    0.23463  15.315  < 2e-16 ***
##    Error terms:
##       Estimate Std. Error t value Pr(>|t|)
## sigma 22.09152    0.10216  216.24   <2e-16 ***
## rho    0.33802    0.02117   15.97   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ---------------------------------------------
```

Conclusion